SciLifeLab Infrastructure Report to the International Evaluation Committee

2024

SciLifeLab

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Welcome to the International Evaluation of the SciLifeLab Infrastructure 2024

Dear International Evaluation Committee (IEC) Members,

We are happy to welcome you to the 2024 International Evaluation of the SciLifeLab Infrastructure. Your acceptance to serve on this distinguished committee is greatly appreciated, and we eagerly anticipate your insights and recommendations.

The Science for Life Laboratory, or SciLifeLab, was established approximately 15 years ago through a collaborative effort between KTH Royal Institute of Technology, Karolinska Institutet, Stockholm University, and Uppsala University. SciLifeLab has evolved significantly ever since. In 2013, it was designated as Sweden's premier national research infrastructure for molecular biosciences, and was recently expanded to include sites in Gothenburg, Linköping, Lund, and Umeå, hence reflecting a true national organization.

Beyond its infrastructural role, SciLifeLab fosters a vibrant research community, supports early-career group leaders (SciLifeLab fellows), and offers training opportunities for postdoctoral researchers and doctoral students. In 2022, we proudly became the hub for the Data-Driven Life Science (DDLS) initiative, a 3.1 billion SEK program funded by the Knut and Alice Wallenberg Foundation, aimed at enhancing data- and AI-driven life science competence, recruitment, and training over a 12-year period across 11 partner organizations. Hence, SciLifeLab today is lot more than a national infrastructure, but the national infrastructure still remains the foundation for SciLifeLab.

Your role as evaluators is critical in shaping the future direction of SciLifeLab infrastructure, particularly in determining how the government funding should be allocated to maximize benefits to the academic community in Sweden in the coming years. This evaluation is pivotal for maintaining our infrastructure at the forefront of rapidly evolving technologies and research domains.

The upcoming IEC meeting in Uppsala from April 15–18, 2024, provides an opportunity for in-depth discussions and evaluation of each platform and unit.

This international evaluation, part of a series conducted every four years, plays a crucial role in guiding the strategic development of SciLifeLab. Following previous evaluations in 2016 and 2020, we have adopted a platform-centric organization, allowing for more dynamic evolution within our operational units also in between evaluations.



Thank you once again for your commitment to this important evaluation process. Your contributions are vital to ensuring that SciLifeLab continues to excel as a leader in molecular biosciences infrastructure and research.

Warm regards,

Olli Kallioniemi, SciLifeLab Director

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I. SciLifeLab Infrastructure Terms and Conditions for Funding

Abbreviations

CBCS	Chemical Biology Consortium Sweden (Unit)
CBGE	Chemical Biology and Genome Engineering (Platform)
CG	Clinical Genomics (Platform)
DC	SciLifeLab Data Centre
DDD	Drug Discovery and Development (Platform)
ESS	European Spallation Source
FAIR	Findable, Accessible, Interoperable, and Reusable
FTE	Full time equivalent
GMS	Genomic Medicine Sweden
GU	University of Gothenburg
HU	Head of Unit
IAB	SciLifeLab International Advisory board
IEC	International Evaluation Committee
IMT	Integrated Microscopy Technologies (Unit)
ISB	Integrated Structural Biology (Platform)
KAW	Knut and Alice Wallenberg Foundation
KI	Karolinska Institutet
KPI	Key Performance Indicator
KTH	KTH Royal Institute of Technology
LiU	Linköping University
LU	Lund University
MAX IV	Swedish National synchrotron
MG	SciLifeLab Management Group
NBIS	National Bioinformatics Infrastructure Sweden
NGI	National Genomics Infrastructure
NRM	Naturhistoriska riksmuséet (Swedish Museum of Natural History)
NSC	National SciLifeLab Committee
ÖRU	Örebro University
PB	Planetary Biology Capability
PCO	Platform Coordination Officer
PD	Platform Director
PI	Principal Investigator
PLP	Pandemic Laboratory Preparedness Capability
PM	Precision Medicine Capability
PMG	Platform Management Group
PSD	Platform Scientific Director
Sahlgrenska	Sahlgrenska University Hospital, Gothenburg
SEK	Swedish Krona (currency: 100 SEK = 8,95 EUR / 9,71 USD)
SLU	Swedish University of Agricultural Sciences
SME	Small and medium-sized enterprises
SNIC	Swedish National Infrastructure for Computing
SU	Stockholm University
TDP	SciLifeLab Technology Development Project
TH	SciLifeLab Training Hub
UmU	Umeå University
UU	Uppsala University
VINNOVA	Sweden's Innovation Agency
VR	Vetenskapsrådet (Swedish National Research Council)
DDLS program	SciLifeLab and Wallenberg National Program for Data-Driven Life Science
SMC	Swedish Metabolomics Centre (Unit)
CMSI	Chalmers Mass Spectrometry Infrastructure (Unit)
ISS	In Situ Sequencing (Unit)
SP	Spatial Proteomic (Unit) or Structural Proteomics (Unit)
SMS	Spatial Mass Spectrometry (Unit)
ST	Spatial Transcriptomics (Unit)
CSF	CRISPR Functional Genomics (Unit)

International Evaluation Committee



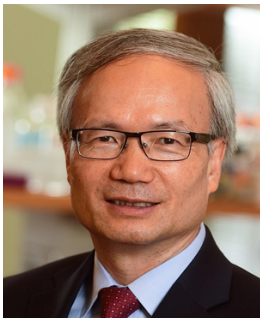
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More information about the IEC members can be found on the SciLifeLab website.

About this report

The present report is divided into three parts:

- Part I: Instructions to International Evaluation Committee (IEC)
- Part II: General overview of SciLifeLab and the research infrastructure, including descriptions and plans of the three SciLifeLab capabilities Precision Medicine, Planetary Biology, Pandemic Laboratory Preparedness, and the support functions Training Hub and Data Centre.
- Part III: Platform reports with metrics, descriptions of technologies and development plans for 2025–2028



Part I. Instructions to the International Evaluation Committee (IEC)

Introduction

The mission of the national SciLifeLab infrastructure is to provide a broad spectrum of cutting-edge technologies, instrumentation, and expertise to life science researchers within academia, healthcare, and industry across Sweden. The infrastructure operations are distributed across 11 Swedish universities and is organized into ten platforms (*Figure* 1). The platforms in turn comprise units offering specialized technologies, instrumentation, and dedicated expert resources. A general presentation of the SciLifeLab infrastructure is given in the *About SciLifeLab* section in this part of the report.

An important component in ensuring that SciLifeLab provides an up-to-date infrastructure with cutting-edge technologies are the international evaluations performed every fourth year. The evaluations are arranged prior to the upcoming governmental research bill, which dictates the budget and mission for the SciLifeLab infrastructure for the next four-year period. The current international evaluation is the third of its kind (the first one was carried out in 2016).

Guided by recommendations from the international evaluation, and input from universities and the National SciLifeLab Committee (NSC) representing the user community, SciLifeLab will decide on implementation of new operations or technology areas, and in parallel, if necessary, phase-down funding of units or technologies that are regarded as not as current, or if they otherwise no longer fulfil the criteria to serve as national SciLifeLab infrastructure unit. Decision on organization and funding of the infrastructure for the years 2025–2028 will be taken by the SciLifeLab Board in November 2024.

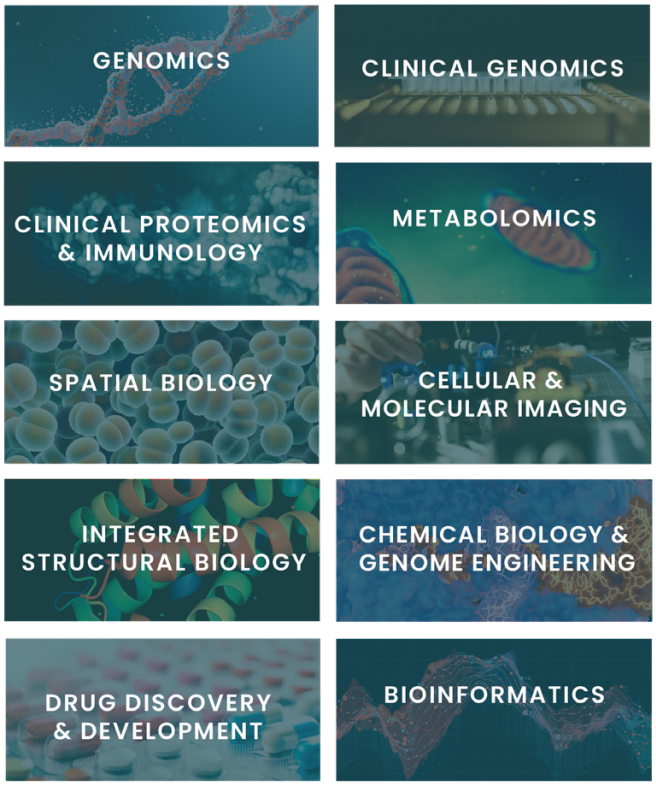


Figure 1. The SciLifeLab infrastructure platforms

Platform Plans and Technology Survey 2023

The infrastructure platforms are main responsible for keeping the technologies within their respective area constantly up-to-date. However, with the upcoming new funding period 2025–2028, for which SciLifeLab has asked for strengthened financial support from the government, there might be possibilities to perform larger strategic changes and invest in new operations and technologies urgently needed by the Swedish research community.

The platform reports, presented in Part II of this report, are based on the strategic planning carried out by the platforms and on the results from the national *Technology Survey* performed by SciLifeLab in June–September 2023.

The Technology Survey was arranged to engage and get input from the whole Swedish life science community on operations/technologies/services that today are missing and considered suitable as national SciLifeLab infrastructure services in the future. A similar survey was performed prior to the last international evaluation in 2020. In the survey, we asked for proposals on:

1. New cutting-edge technologies, instruments, services, and technological capabilities
2. Existing infrastructure operations, currently not part of SciLifeLab, (e.g. local core facilities), to be included in the international evaluation in 2024 for potential incorporation into the national SciLifeLab infrastructure from 2025.

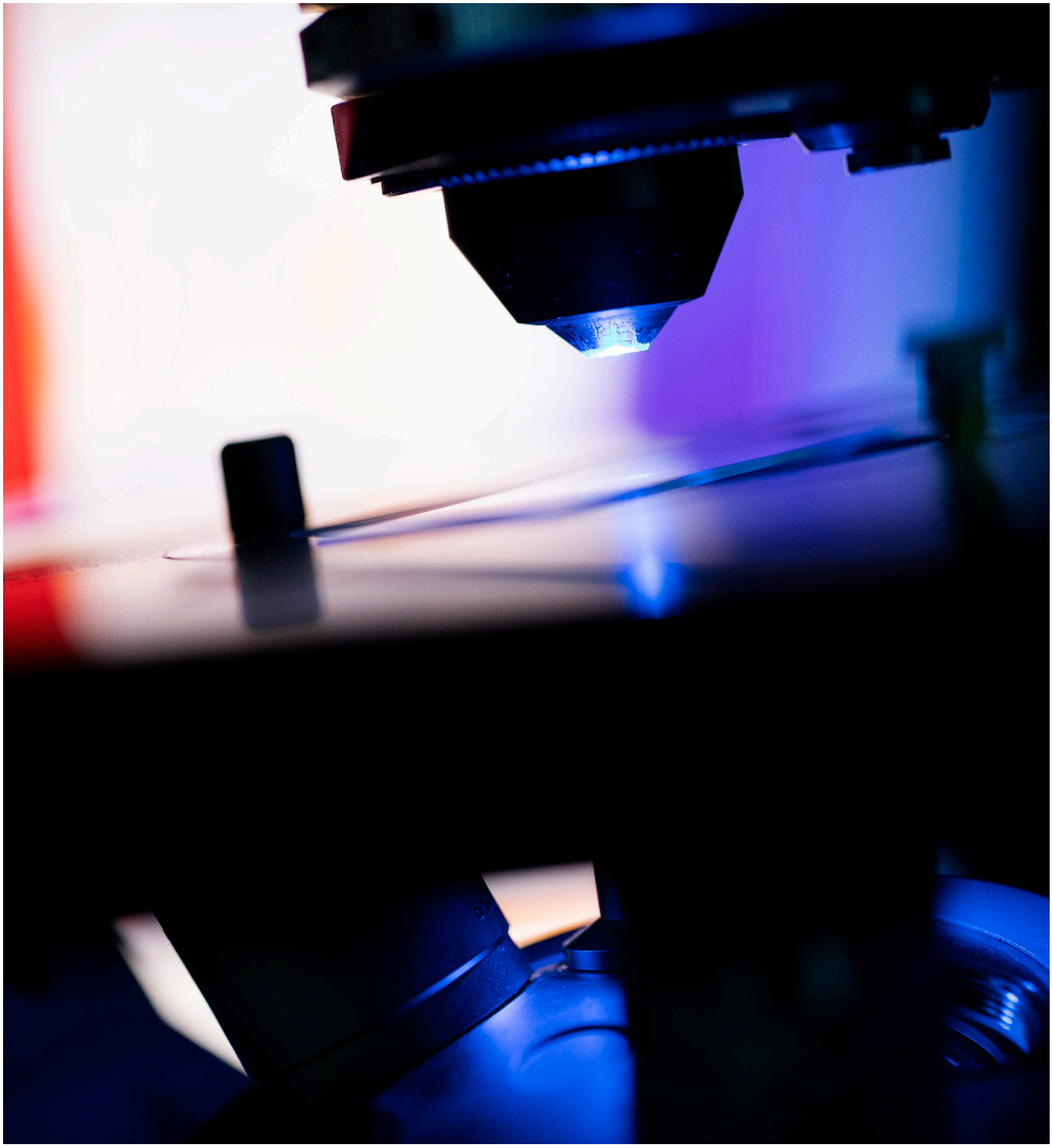
The survey resulted in 47 submitted suggestions on new technologies and 36 suggestions on infrastructure operations. The suggestions were reviewed internally by the SciLifeLab Management Group, the SciLifeLab Site Directors, the Platforms, and the leadership for the SciLifeLab Capabilities “Precision Medicine”, “Planetary Biology”, and “Pandemic Laboratory Preparedness”.

In the assessment, it was emphasized that new operations/technologies should be

a. nationally unique and internationally competitive in the field of biomolecular life sciences,
b. have a potential to reach a large national user base, and
c. provide complementary and synergistic opportunities within and across SciLifeLab platforms.

As a result of the review process, 10 of the proposed operations/technologies/services from the survey were selected for inclusion in the platform plans for the international evaluation. The proposed operations/technologies are described in Part III of this report under the respective SciLifeLab platform for which they have been incorporated in the 2025–2028 plans.

Since the 10 Technology Survey proposals are additions to the plans already developed by the platforms and involve operations currently not part of SciLifeLab, we would like IEC to evaluate these separately.



International Evaluation 2024

The international evaluation of the SciLifeLab infrastructure 2024 consists in short of

i. individual pre-evaluation done by each IEC member
ii. the IEC meeting in Uppsala
iii. the IEC report, a joint evaluation report from IEC with consensus grades and assessments. In addition, we would like input and recommendations in the IEC report on the centrally coordinated SciLifeLab functions Precision Medicine, Planetary Biology and Pandemic Laboratory Preparedness, Training Hub and Data Centre.

The timeline for the IEC is as follows:

March 5	*Infrastructure Report* and *Evaluation Portal* made available to IEC
April 5	*Deadline* for submission of individual *pre-evaluation* by IEC members via our Evaluation Portal
April 9	*Pre-evaluation result* made available to the IEC
April 15	Informal introduction meeting and dinner with SciLifeLab management in Uppsala
April 16–18	*IEC Meetings* with the infrastructure platforms in Uppsala
May 10	*Deadline* for submission of the *IEC Report* to SciLifeLab

Individual Pre-evaluation (deadline April 5)

As the first step in the evaluation, each IEC member is asked to perform an individual pre-evaluation of the SciLifeLab infrastructure in our web-based Evaluation Portal (Anubis) by April 5.

All material for the pre-evaluation is given in this report. The infrastructure steering document *SciLifeLab Terms and Conditions for Funding* is also available as background information (*Appendix I*, downloadable through the Evaluation Portal).

To facilitate the joint IEC assessment of the infrastructure, the individual pre-evaluations will be compiled into a summary report that will be distributed to the IEC reviewers prior to the IEC meeting in Uppsala. Please, note that this document will not be distributed to any other stakeholders and is intended to serve as an internal calibration tool for the IEC only.

Entities to Evaluate

For practical reasons, we have for this evaluation introduced the term *Entity*, which is defined as a part of the infrastructure that is the subject to a separate assessment. There are in total 23 *Entities* to evaluate. Based on similarity in technologies and/or user base, we have divided the current platform operations into 13 *Entities*. In addition, the operations/technologies suggested via the Technology Survey are presented as 10 separate *Entities*.

Thus, an *Entity* could either be:

1. A SciLifeLab platform with highly integrated units and/or units with similar technologies and/or user base (n = 7)
2. Part of a SciLifeLab platform with highly integrated units and/or units with similar technologies and/or user base (n = 6)
3. An operation, technology, or service offering suggested via the Technology Survey, to potentially be incorporated into the SciLifeLab infrastructure (n = 10) marked in blue in the table below.

Table 1 gives an overview of the evaluation *Entities*, in the order presented in the Platform plans section (Part III of this report) and in the Evaluation Portal. *Entities* corresponding to proposals on new operations/ technologies suggested via the Technology Survey, currently not part of the SciLifeLab infrastructure, are shown in blue.

Table 1. Overview of the evaluation *Entities*, E1–E21. *Entities* corresponding to proposals on new operations/technologies suggested via the Technology Survey, currently not part of the SciLifeLab infrastructure, are marked in blue

Platform	Evaluation Entity [1]	Evaluation Entity Nr	SciLifeLab Units (white) / Additional Evaluation Entity (blue) [2]
Genomics	Genomics	E1	Ancient DNA National Genomics Infrastructure
Clinical Genomics	Clinical Genomics	E2	Clinical Genomics Gothenburg Clinical Genomics Linköping Clinical Genomics Lund Clinical Genomics Stockholm Clinical Genomics Umeå Clinical Genomics Uppsala Clinical Genomics Örebro
		E3	SiMSen-Seq
Clinical Proteomics and Immunology	Affinity-based Proteomics	E4	Afiinity Proteomics Stockholm Affinity Proteomics Uppsala Autoimmunity and Serology Profiling
	MS-based Proteomics	E5	Global Proteomics and Proteogenomics Glycoproteomics and MS Proteomics
		E6	Clinical Mass Spectrometry Facility
Metabolomics	Metabolomics	E7	Chalmers Mass Spectrometry Infrastructure Swedish Metabolomics Center
	Exposomics	E8	Exposomics
Spatial Biology	Spatial Biology	E9	In Situ Sequencing Spatial Proteomics Spatial Mass Spectrometry
Cellular and Molecular Imaging	Cryo-EM	E10	Cryo-EM
	Integrated Microscopy Technologies	E11	Integrated Microscopy Technologies Gothenburg Integrated Microscopy Technologies Stockholm Integrated Microscopy Technologies Umeå
		E12	Lund University Bioimaging Centre – LSFM Network Node
		E13	NanoSIMS
Integrated Structural Biology	Integrated Structural Biology	E14	Structural Proteomics Swedish NMR Centre
		E15	Macromolecular Crystallography Support and FragMAX
		E16	ProLinC
Chemical Biology and Genome Engineering	Chemical Biology and Genome Engineering	E17	Chemical Biology Consortium Sweden Chemical Proteomics CRISPR Functional Genomics
		E18	Morphological Profiling and Automated Patch Clamp Profiling
		E19	Cell and Gene Therapy Core
Drug Discovery and Development	Drug Discovery and Development	E20	Integrated Units
Bioinformatics	Bioinformatics	E21	AIDA Data Hub Support for Computational Resources BioImage Informatics Support, Infrastructure and Training
		E22	LU-Fold
		E23	PReSTO

[1] Evaluation Entities based on current SciLifeLab operations
[2] Evaluation Entities based on suggestions from the Technology Survey, currently not part of the SciLifeLab infrastructure

Genomics (Entity 1)

The genomics platform (*Entity* 1) consists of one of the largest SciLifeLab units, National Genomics Infrastructure (NGI), with significant funding from the Swedish Research Council (VR), and the small, niched Ancient DNA unit, that works in close collaboration with NGI. When assessing the Genomics operations, we would like the evaluators to pay attention to the additional statistics for NGI showing user distribution and user publications categorized based on the separate technologies that the unit offers. These statistics will enable the evaluators to give more specific feedback with regards to individual technologies provided by the platform.

Clinical Genomics (Entities 2 and 3)

The Clinical Genomics (CG) platform (*Entity* 2) offers genomic services and expertise to the translational and clinical research community, as well as to clinical trials. The platform also develops and adapts new technologies to advance diagnostics within healthcare. With nodes at all seven Swedish medical faculties with associated university hospitals, the CG platform has full national outreach in bridging academia and healthcare. Besides the scientific impact on translational and clinical research in Sweden, we also ask the evaluators to consider the platform's societal impact by enabling improved diagnostics, treatment and follow up of patients diagnosed with serious illnesses. We also ask the evaluators to separately assess the plans to integrate the *SiMSen-Seq* technology (*Entity* 3), developed by the Translation Genomics Platform at University of Gothenburg, as a part of Clinical Genomics platform from 2025.

Clinical Proteomics and Immunology (Entities 4–6)

We have for the evaluation divided the Clinical Proteomics and Immunology platform into two entities, Affinity-Based Proteomics (*Entity* 4) and Mass Spectrometry (MS)-Based Proteomics (*Entity* 5). It should however be stressed that the platform has an overall joint mission to collaboratively assist users within proteomics technologies. Affinity Based Proteomics contains two units: Affinity Proteomics with nodes in Stockholm and Uppsala, and the Stockholm-based Autoimmunity and Serology Profiling unit. MS-based Proteomics constitutes of the Global Proteomics and Proteogenomics unit in Stockholm and the Glycoproteomics and MS Proteomics unit in Gothenburg. The MS-Based Proteomics plans include a proposal to extend operations towards clinical MS research and implementation. The proposal, Clinical Mass Spectrometry Facility (*Entity* 6) involves the current SciLifeLab units in Gothenburg and Stockholm, but also a facility in Lund that is not part of SciLifeLab, and we would therefore like the evaluators to assess this suggestion separately.

Metabolomics (Entities 7 and 8)

The metabolomics platform consists of two units offering metabolomics support to users, Swedish Metabolomics Centre (SMC) in Umeå and Chalmers Mass Spectrometry Infrastructure (CMSI) in Gothenburg, respectively, (*Entity* 7) and the Exposomics unit (*Entity* 8) in Stockholm providing services within MS-based exposomics technologies. The platform was established in 2021 after the last international evaluation, and the Exposomics unit was included with the status as a pilot unit since it was not operational as a service facility at that point. This is also the reason why we want the evaluators to assess the Exposomics unit separately with regards to development, performance and potential to become a national service provider long-term.

Spatial Biology (Entity 9)

Spatial Biology (*Entity* 9) was established as a new platform in 2021 after the last international evaluation. Notably, several of the technologies offered by the platform are developed by SciLifeLab researchers in close collaboration with the infrastructure. Even though the units within the platform were operative before 2021, the mission to offer integrated spatial biology technologies to users is new since 2021. The units of the platform are In Situ Sequencing (ISS) and Spatial Proteomics (SP), both located in Stockholm, and Spatial Mass Spectrometry (SMS) based in Uppsala. The reviewers should also note that Spatial Transcriptomics (ST), formally part of the National Genomics Infrastructure (NGI)/Genomics Platform, works in close collaboration with the Spatial Biology platform and is described in the plans. The publication output and user statistics for Spatial Transcriptomics can be found as part of the NGI technology-based infometrics (Spatial Omics).

Cellular and Molecular Imaging (Entities 10–13)

The Cellular and Molecular Imaging platform consists of the Cryo-EM unit with nodes in Stockholm and Umeå (*Entity* 10) and the three Integrated Microscopy Technologies (IMT) nodes in Gothenburg (CCI-CAT), Stockholm (ALM) and Umeå (UCEM-FIB-SEM) (*Entity* 11). Cryo-EM offers high-end microscopes in Stockholm and Umeå and operates through the CryoScreeNet with screening services in Gothenburg, Lund, and Uppsala. The Cryo-EM unit is also closely integrated with the Integrated Structural Biology (ISB) platform and is represented in the Platform Management Group of ISB. The three IMT nodes have each their specialized and nationally unique technologies, but have slightly different overall scope and mission, with the IMT Gothenburg and IMT Umeå nodes also serving as local core facilities at the respective universities. Two operations suggested in the Technology Survey that are currently not part of SciLifeLab are to be separately evaluated as potential additions to the platform: Lund University Bioimaging Centre (LBIC) in coordinating a national network in Light Sheet Fluorescence Microscopy (LSFM) (*Entity* 12), and NanoSIMS (*Entity* 13) as new technology and unit in Gothenburg.

Integrated Structural Biology (Entities 14–16)

The Integrated Structural Biology (ISB) platform (*Entity* 14) was formed in 2021 after the last international evaluation with the supplementary mission to coordinate the structural biology infrastructure landscape in Sweden towards the user community. The platform consists of the Swedish NMR Centre (SNC) with nodes in Gothenburg and Umeå and the Structural Proteomics (SP) units based in Lund, and the platform works closely with the Cryo-EM unit at the Cellular and Molecular Imaging platform (with representation in the ISB platform management), the national protein production network (PPS) (VR-funded infrastructure), the national synchrotron MAX IV, and the European Spallation Source ESS in Lund. As a result of the national Technology Survey, two additional operations are included as proposals in the platform plans for 2025–2028: Macromolecular Crystallography Support/FragMAX (*Entity* 15) to support users with protein crystallography and crystallography-based fragment screening and ProLinC (Entity 16) to support users with biophysical characterization. We would like IEC to evaluate these Entities separately.

Chemical Biology and Genome Engineering (Entities 17–19)

The Chemical Biology and Genome Engineering platform (*Entity* 17) specializes in chemical biology, chemical proteomics, and CRISPR technologies, integrating these disciplines through collaborative endeavors. The platform consists of three units, Chemical Biology Consortium Sweden (CBCS), Chemical Proteomics, and CRISPR Functional Genomics (CSF) that offer unit-specific support to users as well as integrated services across the units. As proposals via the national Technology Survey, we would also like the reviewers to separately assess the addition of Morphological Profiling and Automated Patch Clamp Profiling (*Entity* 18) as expanded technology offerings at CBCS, and Cell and Gene Therapy Core (*Entity* 19) as a potential new unit at the platform.

Drug Discovery and Development (Entity 20)

The Drug Discovery and Development (DDD) platform at SciLifeLab was established within SciLifeLab through a strategic Swedish governmental initiative in 2013 and has a dedicated funding stream from the government. The platform has a defined mission to support innovation by transforming academic research into validated early-stage drug development programs that are globally competitive for further investments. When reviewing the DDD platform is it important to keep these conditions in mind. We ask the evaluators for feedback on the design and performance of the current DDD model and advice for the future on how DDD should evolve, build long-term sustainability, and balance technologies and modalities to optimize the benefit to Swedish academic drug discovery.

Bioinformatics (Entities 21–23)

The Bioinformatics platform (*Entry* 21), branded through their VR-funding as the National Bioinformatics Infrastructure Sweden (NBIS), provides the Swedish Life Science community with expertise in bioinformatics and data science. Currently consisting of four units, AIDA Data Hub, BioImage Informatics, Support for Computational Resources, and Support Infrastructure and Training, the platform suggests further integration of the operations with a joint budget from 2025. The SciLifeLab funding of the platform is primarily intended for support of users of the SciLifeLab experimental platforms, however, it is important to note the Bioinformatics platform also receives considerable funding from other sources with separate terms and conditions. In addition to the current operations, we would like the evaluators to assess the proposals added via the national Technology Survey to extend the Bioinformatics platform with LU-Fold (*Entry* 22), supporting users with AlphaFold2 protein structure predictions, and PReSTO (*Entry* 23), a computational platform for structural biology.

Evaluation Criteria and Grading of *Entities*

We ask the evaluators to:

1) grade each *Entity* on a scale from 1 (low) to 9 (high) in terms of

a) relevance and impact of *current technologies, services and expertise* provided from a national and international perspective

b) *performance* 2021–2023 with regards to user base, user publication output, and platform/unit-specific mission and KPIs

c) strategic significance and impact of *development plans* 2025–2028 with regards to meeting future expected needs from the life science user community

Entities containing proposals on operations/technologies suggested via the Technology Survey should be graded correspondingly with regards to their current scope and mission as well as their potential value as part of the SciLifeLab national infrastructure from 2025.

2) provide written motivation of the grades. The feedback should consider all aspects of the operations and plans and include comments on individual units and technologies within the *Entity*.

Since the evaluator's expertise may vary across the technologies under review, we ask the IEC members in the pre-evaluation to indicate for each *Entity* their familiarity with the technology area and to abstain from evaluating a specific *Entity* if the field is beyond their expertise. Any conflicts of interests must also be declared.

The key criteria for evaluation of the SciLifeLab infrastructure technologies and operations are defined in the SciLifeLab steering document Terms and Conditions for Funding (Appendix I). According to these, SciLifeLab platforms and units should ideally:

- *Facilitate* world-leading research in molecular life sciences
- *Enable* research that otherwise would not be possible in Sweden
- Provide high-quality services to *academic researchers, industry, healthcare, and other organizations in Sweden*
- Serve *multiple research groups* in high-quality research projects *across the nation*
- Function in a *high-quality research environment* supporting continuous development of the technologies and services
- Operate according to *Good Infrastructure Practise* by ensuring high-quality and reproducible data production, using appropriate systems for recording and tracking data, and managing data by the principles of open access, FAIR and GDPR requirements
- Provide *internationally competitive services*
- Have a long-term plan for *instrumentation renewal, technology development*, data management and sharing, scientific domains and user communities being served, as well as for a sustainable and versatile funding base
- Provide complementary and *synergistic opportunities* within and across SciLifeLab Platforms
- Participate in *national coordination* of similar facilities at other universities in Sweden (when applicable)
- Promote *translational implementation* of research findings into healthcare, industry, and society (when applicable)

The grading and motivations below (with grades 9, 5 and 1, as examples) illustrate how to grade the Entities:

Grade 9: Nationally unique and internationally cutting-edge technologies, expertise, and services. Excellent fit within the SciLifeLab infrastructure. Broad, nation-wide, user base. Excellent plans including new high-impact technologies with potential to facilitate ground-breaking basic and/or translational research otherwise not possible in Sweden. Very high predicted importance for and impact on Swedish life science 2025–2028.

Grade 5: Nationally unique and internationally competitive technologies, expertise, and services. Good fit within the SciLifeLab infrastructure. User base somewhat biased towards local users, and/or some technologies might be available as services elsewhere including commercial providers. Plans are satisfactory, but some key technologies in the field are missing and/or some technologies provided are deemed out-dated or less relevant as national service. Medium predicted importance for and impact on Swedish life science 2025–2028.

Grade 1: The technologies/services provided that are neither nationally unique nor internationally competitive. Poor synergy and fit with other SciLifeLab platforms and units. User base is limited, and/or the unit is suited to assist mainly local users. Very low predicted importance for and impact on Swedish life science 2025–2028.

When grading, it is important to consider the size, total funding, years of operations, and type of technologies and services provided by the involved units in relation to user base, deliverables, and overall impact.

IEC Meeting in Uppsala, April 15–18

At the IEC Meeting in Uppsala, each of the platforms will briefly present their operations and development plans to IEC (ca 20 min), followed by a Q/A session (ca 40 min). There will also be allocated time for the IEC to discuss the grading and feedback to platforms and units, and for preparing the joint IEC Report. A preliminary program for the IEC Meeting is given below.

Preliminary program for IEC visit, April 15-18, 2024

Monday, April 15

18:00 **Welcome and Introduction to SciLifeLab**

20:00 **Dinner**

Tuesday, April 16

09:00 **Introduction, House-Keeping Rules**

09:15 **Genomics**

10:15 Coffee + IEC Discussions

10:45 **Clinical Genomics**

11:45 Lunch + IEC Working time

13:00 **Clinical Proteomics and Immunology**

14:00 IEC Discussions

14:30 **Metabolomics**

15:30 Coffee + IEC Discussions

16:00 **Spatial Biology**

17:00 IEC Discussions

19:30 **Dinner**

Wednesday, April 17

09:00 **Cellular and Molecular Imaging**

10:00 IEC Discussions + Coffee

10:30 **Integrated Structural Biology**

11:30 Lunch + IEC Working time

13:00 **Chemical Biology and Genome Engineering**

14:00 IEC Discussions

14:30 **Drug Discovery and Development**

15:30 Coffee + IEC Discussions

16:00 **Bioinformatics**

17:00 IEC Discussions

19:30 **Dinner**

Thursday, April 18

09:00 **Precision Medicine**

09:20 **Planetary Biology**

09:40 **Pandemic Laboratory Preparedness**

10:00 IEC Discussions + Coffee

10:30 **Training Hub**

10:50 **Data Centre**

11:20 Lunch + IEC joint evaluation

14:00 IEC Feedback

IEC Report to SciLifeLab (Deadline May 10)

We would like the IEC to compile and submit a final joint evaluation IEC Report to SciLifeLab by May 10, 2024, containing consensus grades of each of the *Entities* with appurtenant motivations and recommendations. In addition to the assessment of the infrastructure, we also ask the evaluators in the IEC Report to provide joint feedback and recommendations on the SciLifeLab Capabilities (Precision Medicine (PM), Planetary Biology (PB), and Pandemic Laboratory Preparedness (PLP), and the support functions Training Hub (TH), and Data Centre (DC). These are described in the *About SciLifeLab* section and will be presented and discussed at the IEC Meeting in Uppsala as well. More detailed instructions on the format of the IEC report will be provided in due time.

The Process after the International Evaluation

Based on the IEC report, the SciLifeLab Management Group and Site Directors will internally review the infrastructure during the spring and summer of 2024. The process will also involve input from the main Swedish universities, the National SciLifeLab Committee (NSC), the SciLifeLab Capabilities as well as discussions with the Platforms. A proposal on organization and funding of the infrastructure for 2025–2028 will be presented to the SciLifeLab Board in September 2024, and the decision on infrastructure funding and organization will be taken by the Board in November 2024.

Part II. About SciLifeLab



The SciLifeLab Strategic Objectives

To align the SciLifeLab stakeholders and agree upon a joint strategy, SciLifeLab has created a Roadmap to describe what the organization wants to achieve and why. The Roadmap focuses on what SciLifeLab can accomplish by maximizing the capacity of the Swedish life science ecosystem towards increased quality and international competitiveness of research through continued efforts on technology-driven infrastructure, as well as focus on data-driven life science. The Roadmap is currently under revision, where recent input from e.g. the SciLifeLab IAB will be considered. Below are given the five strategic objectives proposed for the updated Roadmap which taken together gives an overview of the current SciLifeLab activities and forward strategies of the organization.

1. Provide excellent and impactful life science infrastructure

SciLifeLab is committed to providing access to cutting-edge technologies, highly skilled staff scientists with technology expertise and multiple infrastructure services for its broad national user community. This will empower research endeavors across universities, health care, industries, and other life science disciplines in Sweden that would not otherwise be possible. SciLifeLab will keep the national infrastructure up to date through rigorous evaluations, technology development and agile adoption of new technologies. SciLifeLab supports and operates infrastructure at all major universities and has dedicated sites at Campus Solna (KTH, KI, SU) in Uppsala (UU, SLU), in Lund, Gothenburg (GU and CHT), Umeå (UmU and SLU) and in Linköping (LiU).

2. Facilitate the transformation of life science data into knowledge

Data-driven life science (DDLS): Open Data, AI, and knowledge. Life science is in a major transition that enables the data-driven research paradigm to be developed. SciLifeLab coordinates a national 12-year DDLS research program funded by the Knut and Alice Wallenberg Foundation. DDLS seeks to change how life science is practiced in the future, energized by data- and AI-driven opportunities. This includes recruitment, training, research school and collaborative programs as well as promoting open, real-time data sharing and rapid data cycles. As DDLS is hosted by SciLifeLab it derives benefit from the links to the data-producing infrastructure.

3. Strengthen capabilities, research communities and global partnerships

Currently, there are about 300 research group leaders with an association to SciLifeLab, across all sites, with a dedicated Campus Solna shared by KTH, KI and SU in Stockholm. SciLifeLab will continue to develop infrastructure in the best research environments, and conversely, strong research infrastructures promote cutting-edge research. SciLifeLab will develop technology- and data-driven capabilities in broad research areas that currently include: i) Precision Medicine, ii) Pandemic Laboratory Preparedness and iii) Planetary Biology. We bring together the technology and data infrastructure as well as researchers and all key stakeholders to promote these capabilities. SciLifeLab stands ready to repurpose

its infrastructure to help the society in acute crises, as demonstrated during the COVID-19 pandemic. We will also foster bottom-up research communities to be formed in specific research areas, supported by SciLifeLab infrastructure and the DDLS program. SciLifeLab is keen on forming international collaborations to enrich research and acquire diverse expertise and will continue to build on the strong partnership with EMBL as a model.

4. Attract scientific excellence and provide advanced training

SciLifeLab will continue to host a truly successful program focusing on recruiting and hosting young tenure-track SciLifeLab fellows at KTH, KI, SU and UU. Now the national DDLS program is underway to recruit and host computational biology group leaders at 11 partner organizations. We will provide joint networking and training programs to the various national fellow communities. The SciLifeLab training hub supports technology- and data-driven training with the help of cloud and AI technology. We arrange national PhD and postdoc training as part of the DDLS program and are increasingly considering life-long learning in technology and data-driven topics.

5. Support innovation and bridge-building for the benefit of society

As a national infrastructure, SciLifeLab is connected with 100s of academic, health care, government, international and industrial organizations as users, but also as contributors and collaborators. Some of the SciLifeLab platforms focus on translational and clinical research towards health care and industry applications. These include clinical genomics and the clinical proteomics and immunology platforms that promote diagnostic development across the country. The Drug Discovery and Development (DDD) platform has been a success story by screening hundreds of drug discovery leads and bringing them forward as dozens of licensed or venture-backed early-stage drug leads. These efforts are now complemented with the Proof-of-Concept grant program funded by the Knut and Alice Wallenberg foundation, which seeks to develop deep life science-based innovations to the marketplace. Building on all of these efforts, SciLifeLab is a powerhouse for strategic research initiatives, contributing to the health of people and the planet, to innovation and enterprises, and hence society at large.

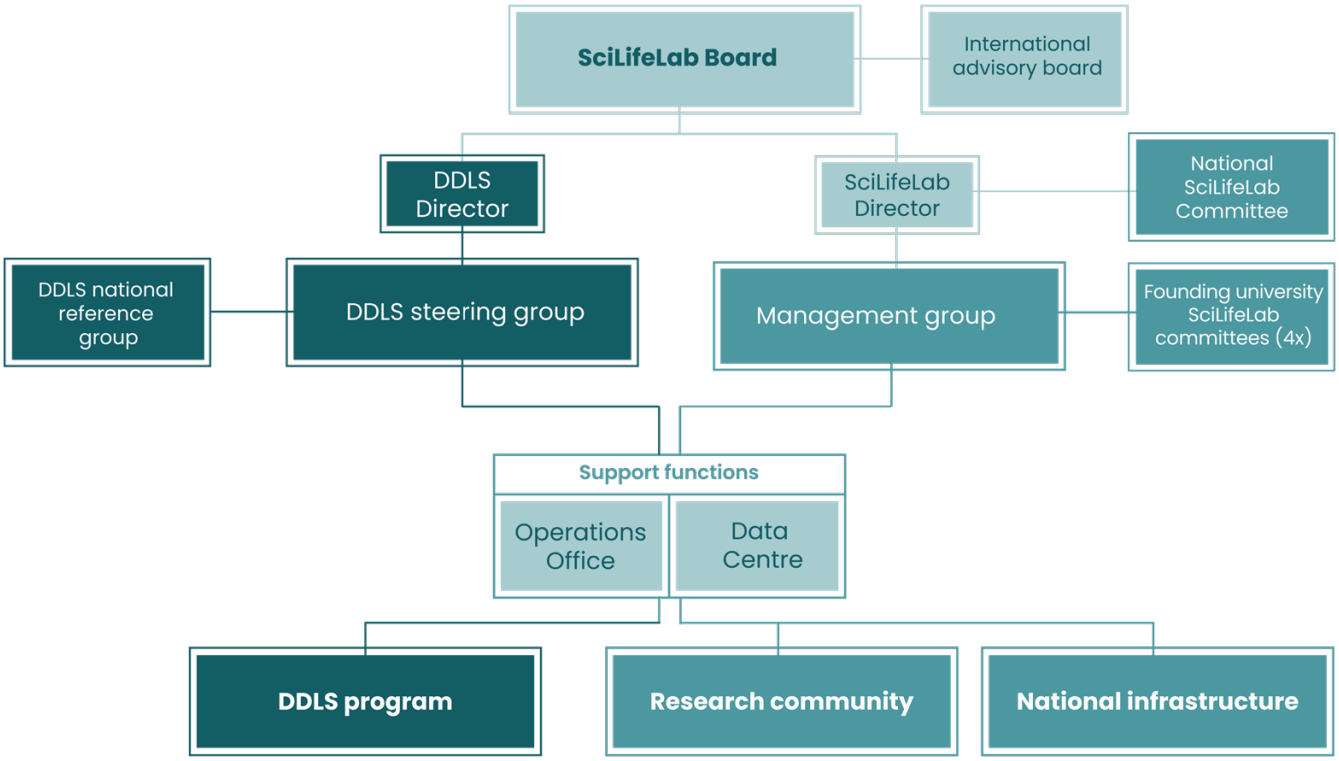


Figure 2. SciLifeLab organization. Efforts like Capabilities and Training Hub are transversal and involve all three pillars of SciLifeLab: Infrastructure, Research Community and DDLS.

SciLifeLab Organization and Funding

As a national infrastructure and collaborative organization across many universities, supported by several independently organized governmental and private funding sources, SciLifeLab as an organization has evolved from the original Stockholm-Uppsala centric research collaboration initiated in 2010 towards a complete nationally distributed organization where most functions operate under the National SciLifeLab Board, see *Figure* 2.

The legal, administrative, and financial host organization of SciLifeLab is KTH Royal Institute of Technology (KTH), though KTH shares this responsibility with the other founding universities Stockholm University (SU), Uppsala University (UU) and Karolinska Institutet (KI) through a formal agreement. The name and brand of SciLifeLab has over the years evolved into an umbrella, or a network, of various SciLifeLab associated activities besides the national infrastructure such as the strategic research area funding (SFO) supporting early-career group leaders (SciLifeLab fellows) at each of the original four founding universities and the SciLifeLab and Wallenberg National Program for Data-Driven Life Science (DDLS) with activities across 11 partners in Sweden.

Most of the infrastructure, the surrounding research environment and the SFO-financed fellows are located at the SciLifeLab sites in Stockholm (Campus Solna) and Uppsala (Navet). These two sites are also the base for the SciLifeLab management and operational support. However, the SciLifeLab operations are increasingly distributed, and as part of strengthening the coordination of the national mission, in 2021–2022 SciLifeLab sites were launched also in Gothenburg, Linköping, Lund and Umeå, see *Figure* 3.



Figure 3. SciLifeLab sites.

Organizational Bodies

Board. The SciLifeLab Board is the highest deciding body with the overall responsibility for national coordination and infrastructure funding. The Board is composed of the Chair and eight additional members of whom four are representing the founding universities KTH Royal Institute of Technology (KTH), Karolinska Institutet (KI), Stockholm University (SU) and Uppsala University (UU), three other Swedish universities, and one industry representative.

Management Group (MG). The MG consists of the SciLifeLab Director, Co-Director, Infrastructure Director (ID), and four Scientific Directors (SD), representing each of the founding host universities, as well as the Campus Solna Director.

SciLifeLab Site Directors. Each of the new sites in Gothenburg, Linköping, Lund and Umeå has an appointed Site Director. The Site Directors are increasingly consulted in national issues and will together with MG be involved in the follow-up work of the evaluation of the infrastructure 2024.

National SciLifeLab Committee (NSC). The NSC consists of representatives of experts from across Sweden with the task to oversee the national role of the SciLifeLab infrastructure from the user community perspective.

DDLS Steering Group (SG). The DDLS Director leads the steering group, which is the executive DDLS leadership that prepares decisions for the SciLifeLab Board. The DDLS SG also has close links with the 11 partner organizations through a national reference group with members close to the leadership at these organizations.

Operations Office (OO). The Operations Office supports the SciLifeLab Board, Directors, MG, the infrastructure, and the research community in coordinating, administering and the execution of proposed actions. OO also supports the DDLS Steering Group and the DDLS program.

Data Centre (DC). Data Centre (DC) coordinates and supports activities throughout the SciLifeLab infrastructure life cycle of data; from project planning, data production, data analysis, data sharing, to publishing and reuse of data. DC works closely with MG, OO, the infrastructure, universities, and the broad research community on data management and training. DC also has a major role in DDLS and its functions.

Training Hub (TH). SciLifeLab Training Hub was established in 2023 to consolidate and coordinate the training efforts across the SciLifeLab ecosystem, giving the life science community easy access to the SciLifeLab infrastructure knowledge, skills, and expertise.

SciLifeLab Capabilities. The SciLifeLab Capabilities, *Precision Medicine* (PM), *Planetary Biology* (PB), and *Pandemic Laboratory Preparedness* (PLP), are strategic initiatives constituting thematic focus areas aimed at addressing complex and demanding societal challenges. Each Capability has a Lead and co-Leads that are appointed by the Board.

International Advisory Board (IAB). The IAB is an independent, consultative body consisting of internationally leading experts from a broad range of fields of life sciences relevant for the SciLifeLab activities (for the current composition of the IAB, see below). The mandate of the IAB is to advise the SciLifeLab Board on strategic questions regarding the future of SciLifeLab from an international perspective.

SciLifeLab Board

- Ylva Engstrand, Chair, Stockholm University and member of the Royal Swedish Academy of Sciences
- Christoph Varenhorst, AstraZeneca, Industry representative
- Mikael Lindström Vice-rector KTH Royal Institute of Technology
- Mats Larhed Vice-rector Uppsala University
- Henrik Cederquist Deputy Vice President for Science, Stockholm University
- Martin Bergö Vice President, Karolinska Institutet
- Katrine Riklund Pro-Vice chancellor, Umeå University
- Carina Mallard Vice Chancellor, University of Gothenburg
- Lena Eliasson, Vice Dean, Faculty of Medicine, Lund University
- Gunilla Westergren-Thorsson, National SciLifeLab Committee Chair, Lund University, Co-opted member
- Andreas Muranyi Scheutz, Region Uppsala (adjunct, GMS representative)

SciLifeLab Management Group (MG) and Site Directors

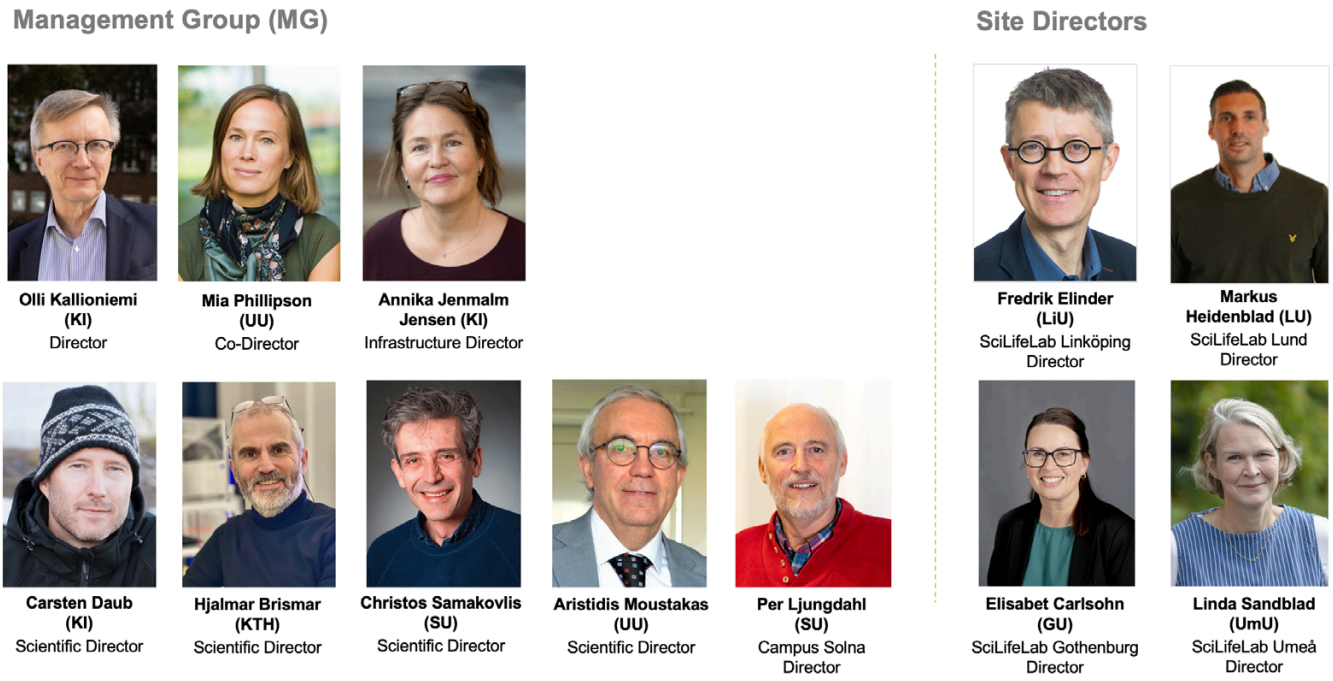


Figure 4. SciLifeLab Management Group and Site Directors

International Advisory Board 2024

- Sören Brunak, Chair, Novo Nordisk Foundation, Center for Protein Research, University of Copenhagen, Denmark
- Ruedi Aebersold, ETH Zürich, Switzerland
- Jo Bury, VIB, Belgium
- Sirpa Jalkanen, University of Turku, Finland
- Janet Jansson, Pacific Northwest National Laboratory, USA
- Iain Mattaj, Human Technopole Foundation, Italy
- Svante Pääbo, Max Planck Institute for Evolutionary Anthropology, Germany
- Kjetil Tasken, University of Oslo, Oslo University Hospital, Norway
- Sarah Teichmann, EMBL-EBI & Wellcome Sanger Institute, UK

National SciLifeLab Committee (NSC)

- Gunilla Westergren-Thorsson, Chair, Lund University
- Eva Hellström Lindberg, Karolinska Institutet
- Cristina Al-Khalili Szigyarto, KTH Royal Institute of Technology
- Sara Hallin, Swedish University of Agricultural Sciences, SLU
- Tanja Slotte, Stockholm University
- Tobias Sjöblom, Uppsala University
- Anders Fridberger, Linköping University
- Gustav Smith, University of Gothenburg
- Richard Lundmark, Umeå University

Funding

Up until 2019, the core SciLifeLab funding consisted of three separate funding sources from the government: national infrastructure funding (National), Drug Discovery and Development funding (DDD), and strategic research area funding (SFO) to the four founding universities. The SciLifeLab Board is the deciding body for the National and DDD funding, while the SFO funding is distributed directly to each of the four universities and is controlled by the SciLifeLab committees at these universities.

In 2020, new non-governmental funding sources were also introduced thanks to generous donations from Knut and Alice Wallenberg Foundation (KAW). The first funding was given in response to the global COVID-19 pandemic. This program was extended in late 2020 to continue for two more years and is now incorporated into the Pandemic Laboratory Preparedness capability. Through a major 3.1 BSEK donation from KAW, a national program on data-driven life science (DDLS) was then launched in 2021. The program is coordinated by SciLifeLab and has 11 partners.

In 2021 the four-year SciLifeLab budget from the government was increased for the budget period 2021–2024. The base funding to the infrastructure was in total increased by 150 MSEK for 2021–2024 (30 + 30 + 40 + 50 MSEK) and, in addition to that, SciLifeLab obtained funding from the government for Pandemic Laboratory Preparedness (PLP), 130 MSEK over 4 years (2021–2024). Thus, the total national infrastructure funding, including the DDD, was 309 MSEK for 2021, and has gradually increased to 344 MSEK in 2024. Taking all sources of funding together, there is a doubling of the SciLifeLab baseline funding by 2024, as compared to the level in 2020 (see *Table 2* and *Figure 5*).

Table 2. Funding to SciLifeLab 2020–2024.

	2020	2021	2022	2023	2024
Governmental funding (MSEK)					
Base funding NAT incl DDD	274.7	279.5	282.4	286.7	298.1
New NAT		30.0	30.0	40.0	50.0
PLP		40.0	30.3	30.7	31.8
SFO	161.8	164.5	166.3	168.5	174.4
Sum	*436.5*	*514.0*	*509.0*	*525.9*	*554.3*
Non-governmental funding (MSEK)					
COVID-19 program	35.0	87.5	52.5		
DDLS		7.5	40.4	177.9	320.4
Sum	*35.0*	*95.0*	*92.9*	*177.9*	*320.4*
Total	***471.5***	***609.0***	***601.9***	***703.8***	***874.8***

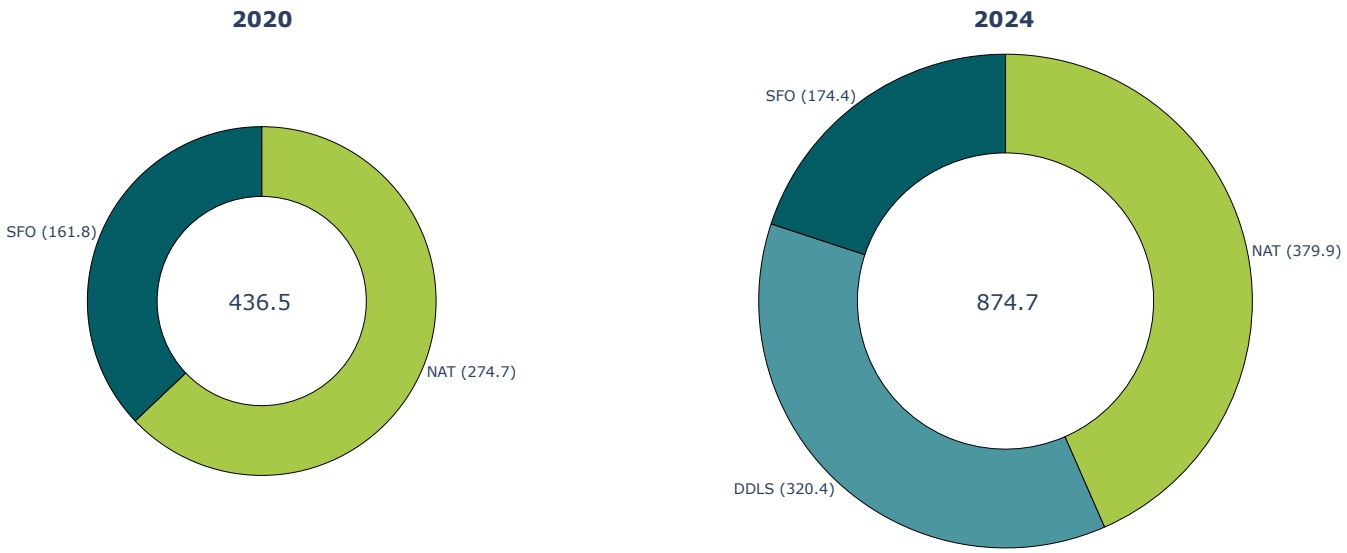


Figure 5. SciLifeLab funding. From 2020 to 2024, total funding to SciLifeLab have increased 100% from 436.5 to 874 MSEK (about 39 to 78 MEUR)

The SciLifeLab Infrastructure

The SciLifeLab research infrastructure, established in 2013, constitutes the backbone of SciLifeLab and is funded through a separate regulatory letter directly from the government. Together with the synchrotron radiation facility MAX IV and the European Spallation Source (ESS), both located in Lund, SciLifeLab is one of the three major national research infrastructures in Sweden, and the only one entirely dedicated to life science. The primary mission of the SciLifeLab infrastructure is to facilitate impactful research discoveries in Sweden by providing cutting-edge, unique, and complementary technologies, resources, and expertise to the life science research community. The infrastructure collaboratively assists users in projects ranging from basic to translational research and is well equipped to support large-scale research initiatives and societal grand challenges.

The SciLifeLab infrastructure has a national mission, and the technologies and services are offered to Swedish researchers on equal terms, regardless of academic affiliation. If demand exceeds capacity, a formal prioritization process with an external steering/advisory board is recommended. The infrastructure should also be accessible to researchers in sectors outside academia, including industry and healthcare, under a full-cost fee structure.

Organization – Platforms and Units

The SciLifeLab infrastructure is a large operation with over 600 staff scientists, spanning a broad range of technologies and service areas, and is organized into ten platforms. Each platform comprises units offering specialized services, technologies, instrumentation, and dedicated expert resources (*Figure* 6). The platforms are primarily designed by clustering units that share a common user base or offers similar technologies to maximize the cross-unit synergies. While built around platforms, SciLifeLab strongly emphasizes the importance of cross-platform interactions and collaboration to guide and serve users in an optimal fashion. As an example, the Swedish NMR Centre unit is organizationally part of the Integrated Structural Biology but is also involved in operations coordinated by the Metabolomics platform (by NMR-based metabolomics) and Chemical Biology and Genome Engineering platform (by NMR-based fragment screening). The SciLifeLab infrastructure operations are distributed over 11 universities across Sweden as illustrated in *Figure* 7.

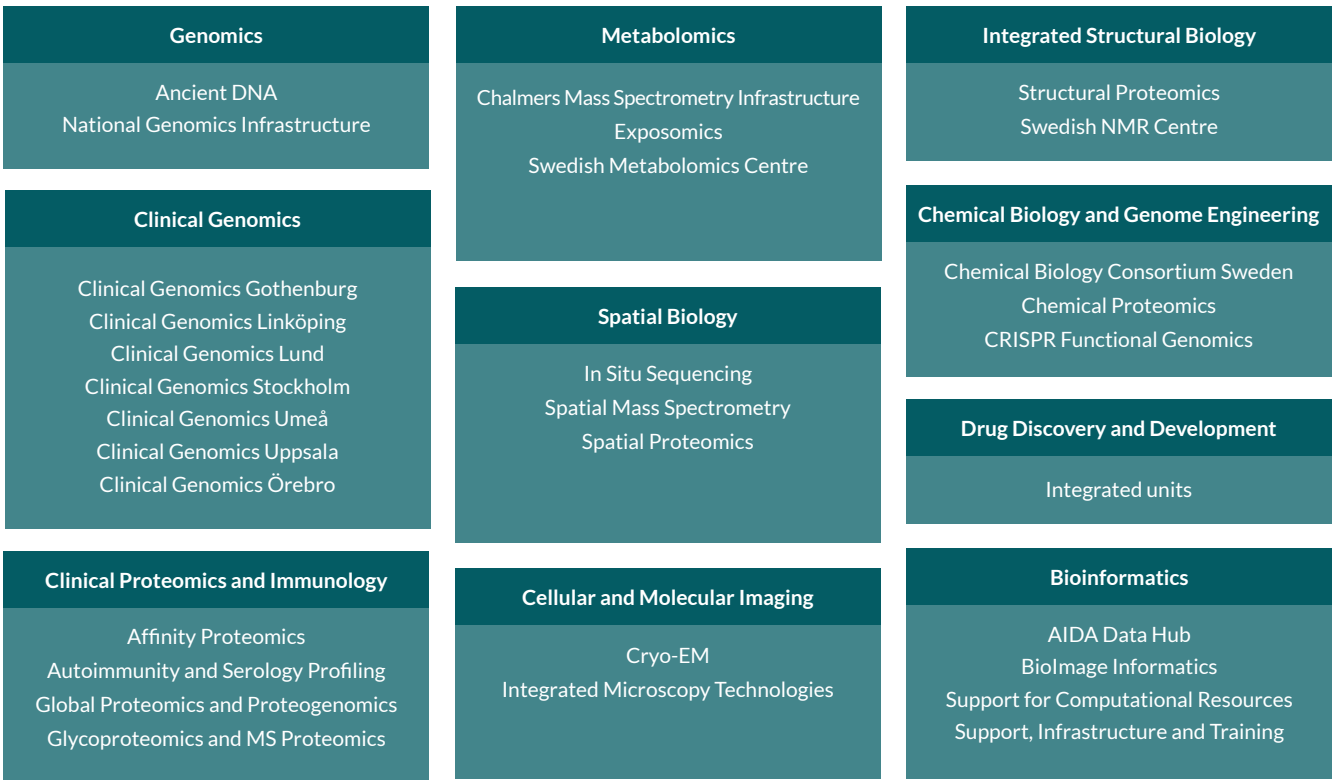


Figure 6. The ten Platforms and appurtenant Units of the SciLifeLab Infrastructure

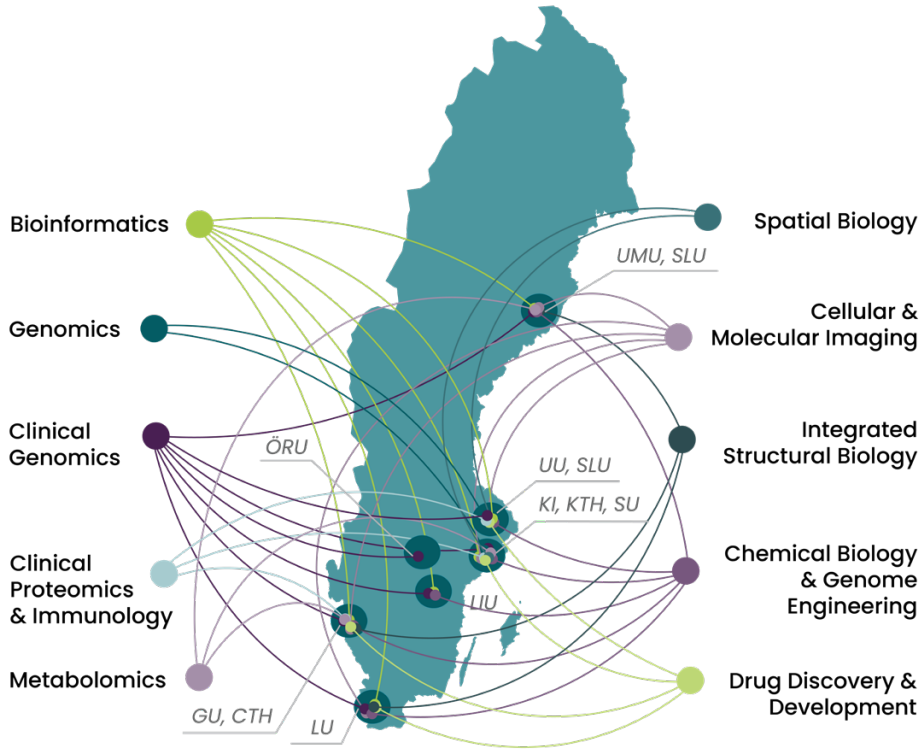


Figure 7. Distribution of platform operations across 11 Swedish universities

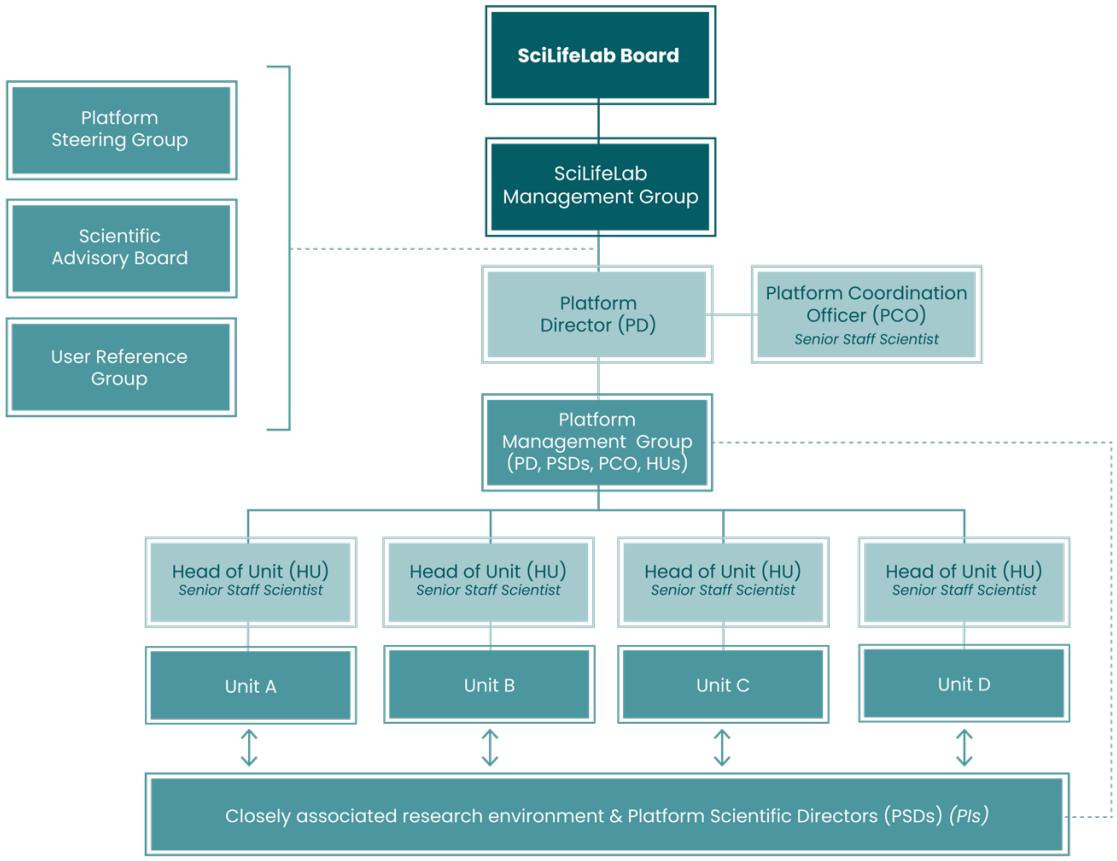


Figure 8. SciLifeLab platform organization chart

Platform Governance and Steering

Since 2021, SciLifeLab has implemented a platform-centric model for the infrastructure governance and operations. Compared to the previous organization, the platforms are given more mandate to make decisions on the platform level, and all platforms are annually provided dedicated funding from SciLifeLab that can be used for strategic development of the platform operations.

Each platform is managed by a Platform Management Group (PMG) led by a Platform Director (PD) that reports to the Infrastructure Director and the Management Group. Besides the PD (and Co-PD when applicable), the members of the PMGs constitute for most of the platforms of the Heads of Units (HU), the Platform Coordination Officer (PCO), and the Platform Scientific Directors (PSD). A generic platform organization chart is shown in *Figure 8*. The roles and responsibilities of PD, HU, PCO and PSD are described in more detail in the *SciLifeLab Terms and Conditions for Funding document* (Appendix I).

Funding

The allocation of the infrastructure funding from the government is decided annually by the SciLifeLab board, and the distribution including central administration and support functions for 2024 is shown in *Figure 9*. The direct support to the infrastructure operations is 245 MSEK (about 22 MEUR) and the distribution across the platforms is shown in *Figure 10*.

An expectation for a successful and sustainable SciLifeLab infrastructure unit is that, besides the SciLifeLab funding, it also attracts financial support from its host university(ies) and other funding sources. Equally important for sustainable operations are the user fees. SciLifeLab requires that all units charge user fees

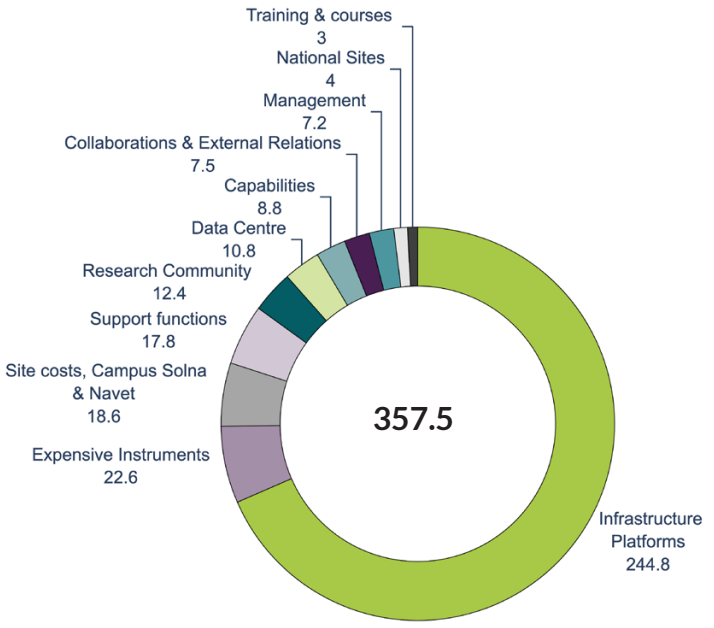


Figure 9. Allocation of SciLifeLab infrastructure funding 2024 (MSEK).

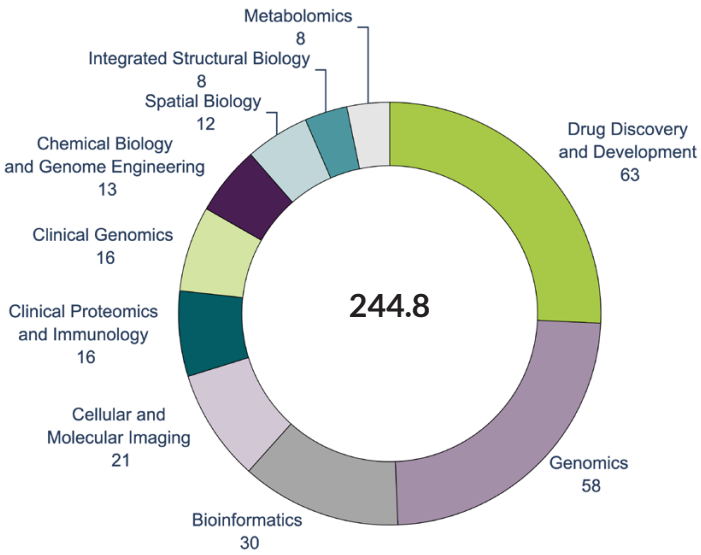


Figure 10. Distribution of SciLifeLab funding to platforms 2024 (MSEK).

according to pre-defined and documented cost models, including a full cost model for industry and healthcare users. In general, user fees cover the costs for reagents and consumables, but may also cover part of salaries, rents, and instrument related costs. Since the nature of services varies substantially between platforms and units, there is no standardized SciLifeLab user fee model. The individual user fee model for each unit is presented in more detail in the platform descriptions and plans (Part III in this report).

In 2023, the total user fees amounted 365 MSEK (about 33 MEUR) and most of the infrastructure platforms and units also attracted additional funding from e.g., the Swedish Research Council (VR), KAW, healthcare, their host universities, and other sources. The total funding from SciLifeLab and all other sources for the infrastructure in 2023 was 980.5 MSEK (about 87 MEUR), see *Figure 11*. Altogether, the funding enabled an infrastructure work force of about 630 staff scientists and technicians (corresponding to ca 490 FTEs) for 2023 of which 67% had a PhD.

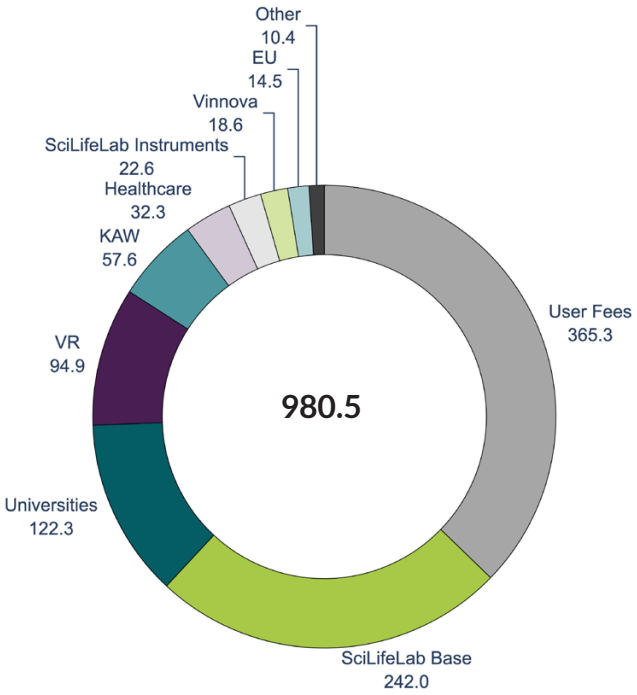


Figure 11. Total funding of the infrastructure 2023 including user fees (MSEK). VR: Swedish Research Council, KAW: Knut and Alice Wallenberg Foundation.

Users and Publications

The number of infrastructure users and their distribution across universities and non-academic sectors as well as the volume and impact of infrastructure user publications are key metrics that SciLifeLab monitors annually for each unit and for the whole infrastructure. The analyses presented in this section are global statistics for the entire infrastructure based on data reported from the units for 2023 and previously. Output and metrics for the individual infrastructure units are given in the platform descriptions and plans (Part III in this report).

User base

In 2023, there were close to 1,800 individual users of the SciLifeLab infrastructure (spread over 4,300 projects), and almost 1,600 of these were from academia. The distribution of the academic users based on the affiliation of the PI is shown in *Figure 12*. Notably, 58% of them were from universities or institutions outside of the SciLifeLab founding universities in Stockholm and Uppsala (KI, KTH, SU and UU), including 11% from international universities. In comparison, in 2017 the share of academic users outside the founding universities was only 40%. We believe that the current distribution of users demonstrates that the infrastructure has reached its potential as a true national asset for scientists and that it is internationally competitive. In addition to the individual users included in *Figure 12*, the bioinformatics unit Support for Computational Resources in Uppsala reported about 825 active user accounts spread across 2065 project owners across Sweden that utilized the data storage and computing capacities that the unit provides.

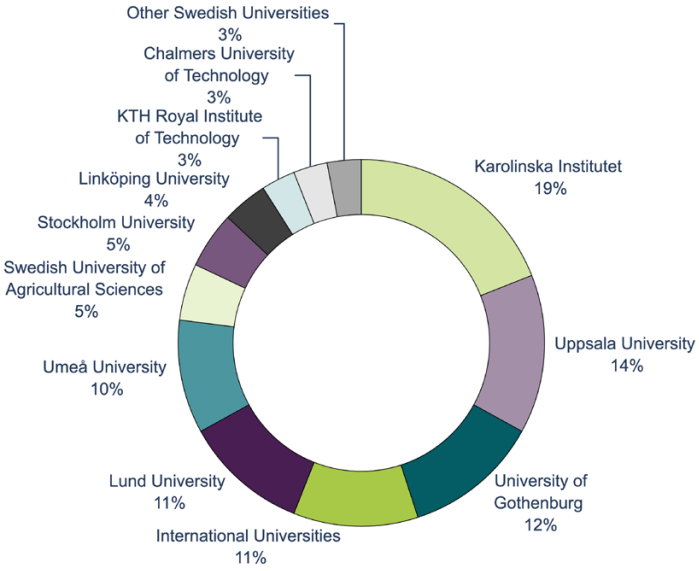


Figure 12. Distribution of unique academic infrastructure users 2023 (n = 1576) based on affiliation of the individual PIs.

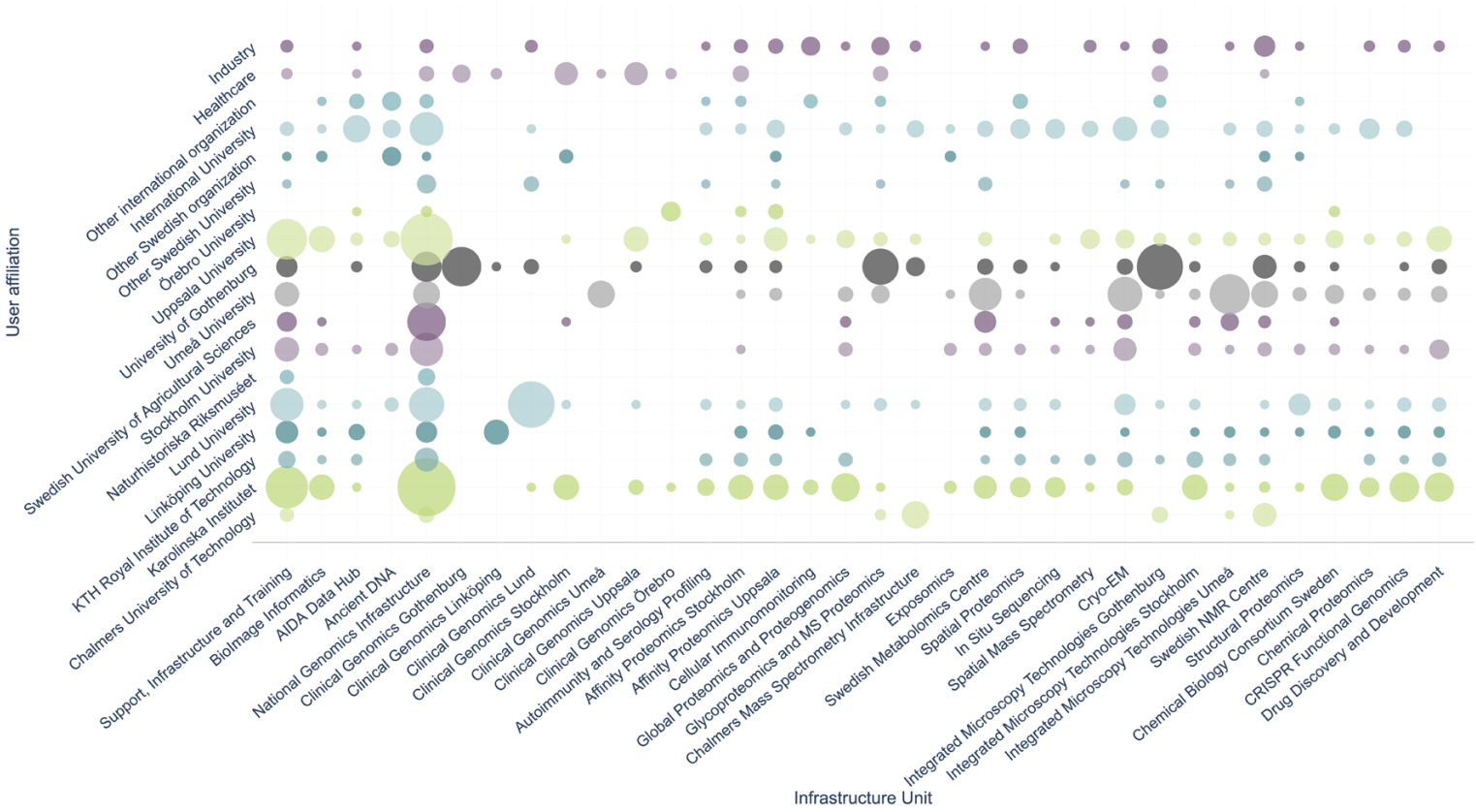


Figure 13. Distribution of the overall unique users 2023 from universities, healthcare, and industry (n = 1789) across all SciLifeLab infrastructure units. The size of the circles corresponds to the number of users.

The SciLifeLab infrastructure is also open towards non-academic researchers, and our recommendation is that up to 15% of the infrastructure services should be devoted to users from healthcare, industry, and other sectors. However, for the units on the Clinical Genomics platform that typically serve many healthcare users on a full-cost model, the fraction of non-academic users can be higher. Calculations based on estimated resource allocation for 2023 reported by the units, normalized by the total infrastructure FTE resources, show that 16% were allocated to projects from healthcare users (66 unique users), 3% on industry projects (73 unique users) and 1% on projects from other governmental organizations (24 unique users). Distribution of affiliations for all unique users across infrastructure units for 2023, illustrated in *Figure* 13, further demonstrates the utility on a national level and across sectors.

Publications

The infrastructure units continuously report the publications resulting from user-initiated projects and from the units internal technology development. In the SciLifeLab Publication Database[1], publications are labeled either as service (user-initiated projects where the infrastructure unit is acknowledged in the publication), collaborative (user-initiated collaborative project with unit staff as co-author of the publication) or technology development (unit-initiated technology development projects with unit staff as corresponding author of the publication). The total number of scientific papers from the SciLifeLab infrastructure remained relatively constant during 2018–2020, with around 600 publications annually, but increased significantly for 2021–2023, *Figure* 14. The increase can partly be explained by the inclusion of new units into the SciLifeLab infrastructure in 2021.

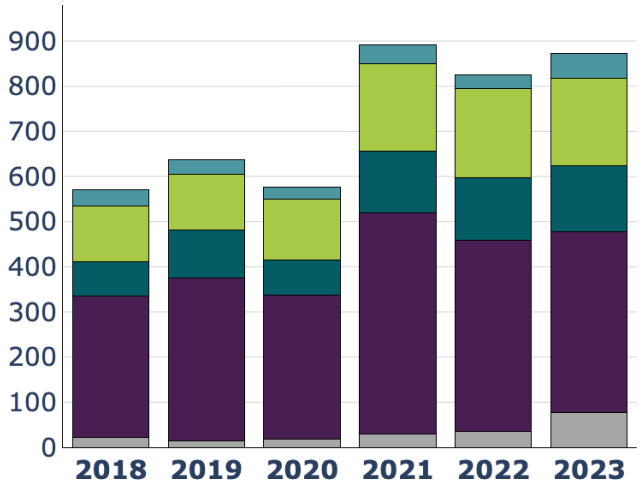


Figure 14. Infrastructure user publications 2018–2023 with Journal Impact Factor (JIF) distribution: JIF > 25 (blue), JIF 9–25 (light green), JIF 6–9 (dark green), JIF < 6 (purple), JIF unknown (gray).

[1] publications.scilifelab.se

An important mission of the SciLifeLab infrastructure is to promote and increase multidisciplinary research using several platforms, units, and technologies for addressing scientific questions. SciLifeLab monitors cross-unit usage based on the scientific publications by infrastructure users. Here, we have analyzed the 1688 infrastructure publications for 2022–2023, and of these 146 (9%) involved contributions from more than one infrastructure unit (excluding the Bioinformatics unit Support for Computational Resources), *Figure* 15.

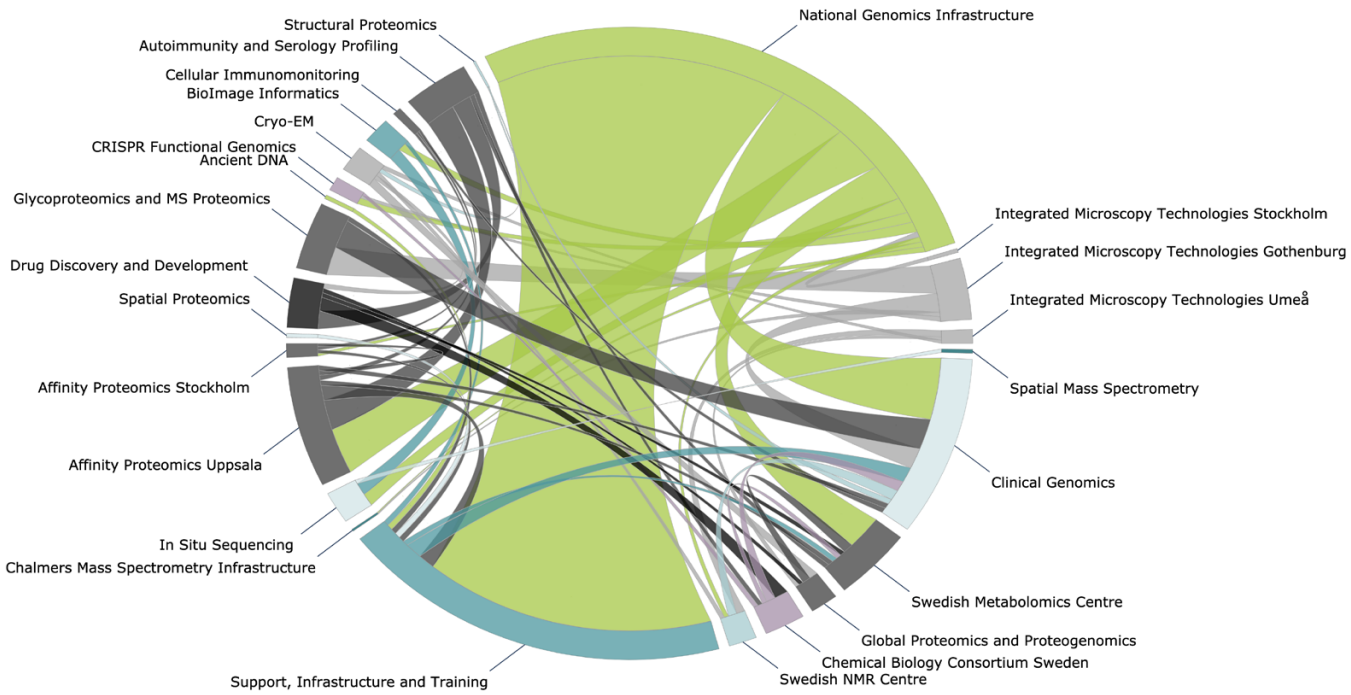


Figure 15. Circos plot illustrating cross-unit use based on infrastructure user publications 2022–2023 with two or more units involved (n = 146). The length of the circle segments corresponds to the number of cross-unit publications for each unit, and the ribbons connect the units that contributed to the publication with service, data, or analysis. The arcs of the plot are colored according to the SciLifeLab Platform. Publications based on use by a single unit only and those involving the Bioinformatics unit ScoRe (with only one additional unit) are not shown.

Technology Development and Renewal of Instrumentation

Continuous updating of technologies and services is essential for maintaining the SciLifeLab infrastructure at the cutting-edge. This is challenging due to the wide variety of technology areas, the complexity of nation-wide operations involving multiple universities, and the frequency of which upgrades of expensive instrumentation are required. To facilitate a continuous renewal, SciLifeLab has established four pillars for enabling infrastructure technology development and equipment upgrades:

1. Infrastructure units are allowed and encouraged to use up to 20% of their SciLifeLab funding for internal technology development, i.e., identifying and implementing new relevant technologies and protocols to complement existing capabilities.
2. SciLifeLab has arranged two calls for Technology Development Projects (in 2018 and 2021) for development and implementation of novel technologies as infrastructure services. Grants can be used to develop technologies in collaboration with external PIs and research groups, and we plan to launch this type of call on a regular basis.
3. Since 2018 SciLifeLab also arranges annual calls for funding of expensive instruments (in the range of 2 MSEK and above) for the infrastructure units. We reserve 15–20 MSEK annually from the national budget for this purpose to contribute to instrument depreciation costs.
4. Technology development by the research community closely associated with the infrastructure is an essential part of the SciLifeLab ecosystem. Projects in these research groups are often conducted in collaboration with infrastructure units, frequently resulting in new technologies that can be tested and implemented as service, as well as providing a scientific edge to the services offered.

SciLifeLab and Wallenberg National Program for Data-Driven Life Science (DDLS)

In 2020 the Knut and Alice Wallenberg Foundation (KAW) announced a 12-year funding initiative of 3.1 BSEK to support data-driven life science in Sweden. SciLifeLab as a national organization within the technology- and data-driven life sciences was entrusted with the coordination of the initiative, a collaboration with 10 Swedish universities and the Swedish Museum of Natural History.

The purpose of the program is to train and recruit the next generation of life scientists, to create a strong computational and data science base, and to strengthen the competencies in today's research society, thereby enabling every scientist to better analyze data patterns and integrate their data with the global data flows in life sciences. Furthermore, the program aims to strengthen national collaborations between universities, bridge the research communities of life sciences and data sciences, and create partnerships with industry, healthcare, and other national and international actors. The program focuses on four strategic areas for data-driven research, all of which are essential for improving the lives of people as well as animals and nature, detecting and treating diseases, protecting biodiversity, and creating sustainability.

The DDLS program is recruiting a total of 39 high-profile young group leaders (tenure-track DDLS fellows) in the four research areas to the participating partner organizations to expand excellence in data-driven life science research. Each fellow is offered a generous starting package with funding covering five years of their salary, and up two PhD student and two postdoc positions, as well as some running costs.

More information about the DDLS program can be found on scilifelab.se/data-driven. *DDLS is not part of the current evaluation by IEC.*

SciLifeLab Research Community

The SciLifeLab research community is promoted and maintained through several programs and initiatives with the common objectives to encourage excellence, team science, technology development, and collaborations across borders and sectors. Below are listed a few examples of these efforts *(SciLifeLab Research Community is not part of the IEC evaluation).*

SciLifeLab Fellows Program. The SciLifeLab Fellows program is a career program aiming at strengthening Swedish research in molecular biosciences, on a long-term perspective leading to societal impact for Sweden. The host universities KI, KTH, SU and UU provide an advantageous economic starting package and together with SciLifeLab a strong interdisciplinary research environment in close proximity to a cutting-edge research infrastructure. The recruitment of excellent researchers in international competition provides an influx of new and fresh knowledge and ideas to drive the development of the SciLifeLab research environment. Currently, there are 22 active fellows in the program and 21 alumni fellows.

SciLifeLab Group Leaders. The SciLifeLab Group Leader (SGL) concept aims at creating empowered communities by defining members of the community that are key to SciLifeLab and its development, particularly the infrastructure, locally as well as nationally. Further objectives are to promote collaborations within and across universities, sites, and disciplines (e.g. through tailored calls), strengthen laboratory and computational technology development by promoting and further connecting the SGLs, and increase SciLifeLab presence, visibility, and impact nationally through SGLs acting as "ambassadors" for SciLifeLab. Currently, there are > 300 approved SciLifeLab Group Leaders.

Program for Academic Leaders in Life Science (PALS). PALS is a collaboration between SciLifeLab, the DDLS program and the four Wallenberg Molecular Medicine Centers at Umeå, Linköping, Lund and Gothenburg. With PALS, the scope of the collaboration is expanded from molecular medicine to also include the diverse areas of life science that the SciLifeLab and DDLS communities represent, including 10 universities and the Museum of Natural History, and more than 150 fellows. The PALS program brings opportunities for experimental and computational scientists to meet and establish multi-disciplinary collaborations.

SciLifeLab Capabilities, Training Hub, and Data Centre

During 2021 and 2022 SciLifeLab launched three strategic initiatives, referred to as *Capabilities*, constituting thematic focus areas aimed at tying together the SciLifeLab infrastructure, research community and DDLS program to create increased opportunities in addressing complex and demanding societal challenges. The three SciLifeLab capabilities are *Precision Medicine* (*PM*), *Planetary Biology* (*PB*), and *Pandemic Laboratory Preparedness* (*PLP*), and these are presented in more detail below.

SciLifeLab *Training Hub* (*TH*) was launched in 2023 as a strategic initiative and central support function responsible for training support, resources, and tools available to the SciLifeLab ecosystem. Once fully operational, it will serve the infrastructure platforms with training support and resources, in addition to supporting the SciLifeLab research environment and its strategic initiatives.

Data Centre (*DC*) is a strategic SciLifeLab initiative and central support function responsible for services, resources, and support for IT and data-related issues. DC serves the infrastructure platforms but also supports operations and management, research programs, strategic initiatives, and represents SciLifeLab in national and international collaborations on issues regarding data and IT. As data-driven research has become pivotal to the SciLifeLab future, including the launch of the DDLS research program, DC is an established core function of SciLifeLab. The DC infrastructure support is managed through close interaction with the platforms, providing IT solutions and software services, advice on data flow design, and assistance in preparing operational plans or grant proposals. New services developed or procured by DC often originate in platform requirements, followed by collaboration projects piloting and evaluating prospective services.

Representatives for the Capabilities, Training Hub and Data Centre will present their activities and plans at the IEC meeting in Uppsala on April 18. As part of the IEC report to SciLifeLab, we would like IEC´s input and future recommendations on the PM, PB, PLP, TH and DC efforts.



Precision Medicine Capability

Background and organisation

Sweden has high ambitions to be a global leader in precision medicine, and SciLifeLab plays a pivotal role in advancing genomics-based precision medicine into healthcare through the Clinical Genomics platform. To strengthen Swedish research in precision medicine using SciLifeLab´s full range of technology and data capabilities, the Precision Medicine (PM) Capability was established in June 2021.

The PM Capability team consists of three scientific leads Päivi Östling (chair), Åsa Johansson and Janne Lehtiö and a scientific coordinator Eva Berglund. To connect the PM capability effort with key stakeholders in the Swedish precision medicine landscape, we have established an advisory expert group, with representatives from the SciLifeLab infrastructure and Data Center, Biobank Sweden, Genomic Medicine Sweden (GMS), as well as clinical precision medicine expertise from the healthcare sector. The PM Capability team works in close collaboration with the Data-Driven Life Science (DDLS) Precision Medicine and Diagnostics (PMD) expert group, with Janne Lehtiö being the lead also for the DDLS-PMD research area, and the associated Data Science Node team.

Funding

The PM Capability has a budget from SciLifeLab of 5.15 MSEK for 2024 which is used for salaries for the scientific leads (20%) and coordinator (50%). The remaining SciLifeLab funding is directed towards Clinical Technology Development Projects (see below), community building activities and outreach. We have also successfully obtained external funding of 55.3 MSEK for 2023-2027. The externally funded projects include one project that we lead: *National infrastructure to support clinical trials in precision medicine with cutting edge technologies*, funded by the Swedish Research Council (14.7 MSEK 2023-2027), where we will launch a call for Letter-of-Interest for Multimodal Precision Medicine Projects (see below).

The external funding, as outlined in the “Collaborative projects” section, has also enabled the establishment of a cross-platform multidisciplinary operational team at SciLifeLab dedicated to precision medicine. This team supports new developments within the technology infrastructure and co-develops infrastructure for sensitive data with key stakeholders.



Figure 1. Strategic objectives in SciLifeLab's Roadmap for Precision Medicine.

Operations and key achievements 2021–2024

An important first task has been to formulate a *strategy for SciLifeLab's role in precision medicine.* SciLifeLab's Roadmap for Precision Medicine, which was approved by the SciLifeLab board in May 2023, describes the vision and mission for SciLifeLab within precision medicine and outlines four strategic objectives (*Figure 1*).

Vision: Sweden is a world-leading nation in precision medicine

Mission: To be a key player in acceleration of research and implementation of precision medicine through technology- and data-driven approaches

The PM Capability has engaged in a range of *internal community-building* activities with the SciLifeLab infrastructure, research community and the DDLS program. For example, we have organized workshops at the SciLifeLab infrastructure meeting Facility Forum and group leader retreat and have actively engaged in several platform-specific meetings. We have also arranged two annual symposia in collaboration with DDLS-PMD, and co-organized the yearly complex diseases conference with GMS. In 2023, we organized a precision medicine session that featured presentations and a panel discussion with local experts during the four SciLifeLab Days in Gothenburg, Lund, Linköping and Umeå.

External outreach includes organization and participation of several national and international scientific conferences. To increase societal awareness about the significance of cutting-edge research infrastructure for precision medicine, we have arranged panel discussions in the political forum the "Almedalen Week", and engaged with for example Sweden's Ministry of Health and Social Affairs in questions related to precision medicine.

Overall plans for 2025–2028

The PM Capability team will interact with the SciLifeLab technology and data infrastructure through community-building events, training activities and proof-of-concept projects. Towards this, we have recently launched two types of calls for collaborative projects between our infrastructure and clinical researchers. These projects will contribute to strengthening the precision medicine research community, including researchers, infrastructure staff, healthcare professionals and industry. The initiative will also enhance our capacity to generate high-quality data for clinical studies in accordance with FAIR (Findable, Accessible, Interoperable and Reusable) principles. Furthermore, in collaboration with the technology experts from our platforms, we plan to write and publish a white paper that highlights how SciLifeLab, as a research infrastructure, can accelerate advancements in precision medicine. Through these activities, we will enhance awareness of the existing potential in precision medicine and outline the necessary steps towards achieving greater societal impact.

Clinical Technology Development Projects

In collaboration with the Pandemic Laboratory Preparedness (PLP) Capability, we have launched a call for Clinical Technology Development Projects where SciLifeLab technologies can solve unmet clinical and diagnostics needs. The aims of the call are to support the SciLifeLab infrastructure in adapting methods or assays towards well-defined clinical applications and strengthen their connection to clinical researchers and healthcare. The call will launch 5-6 projects with a budget of 3-500 000 SEK for one year and applicants must include both a technology infrastructure representative and a clinical researcher.

Letter-of-Interest for Multimodal Precision Medicine Projects

We have also launched a call for Letters-of-Interest to co-develop multimodal data generation on clinically relevant samples. Multi-modal data will be generated from patient cohorts to evaluate sample flow to SciLifeLab, as well as sample flow and sharing between technology platforms, to demonstrate the feasibility of operating practices in generating data for clinical studies. Similarly, these proof-of-concept projects will provide an opportunity to assess the potential of aligning bioinformatic pipelines and introduce the use of common meta-data models to create interoperable data across platforms. This will increase our internal competence in generating interoperable data from clinical samples of limited quantity in timeframes needed for clinical studies.

Inventory of needs for training within precision medicine

Jointly with the Training Hub, we are conducting a survey directed towards infrastructure staff, the research community, healthcare professionals and industry to assess needs of training within precision medicine as well as available courses. The results of the survey will help us prioritize what type of training material or courses should be made accessible for the community through the Training Hub. We hope to engage technology experts from the infrastructure and other experts in precision medicine in developing open digital courses within the areas highlighted in the survey.

White paper on precision medicine technologies with the SciLifeLab infrastructure

We plan to arrange a workshop in May 2024, bringing together technology experts from the SciLifeLab infrastructure and representatives from large-scale precision medicine initiatives in Sweden. The focus of the workshop will be on the cutting-edge technologies available at SciLifeLab and their current and potential future use for precision medicine. After the workshop, we will jointly write a white paper with the tentative title "*Leveraging a national research infrastructure to accelerate precision medicine research and implementation*".

Community-building, collaboration and outreach

Planned activities include i) continued organization of the seminar series *Clinical Talks* and the annual DDLS symposium in Precision Medicine and Diagnostics; ii) co-organization of two workshops at the SciLifeLab infrastructure event *Facility Forum* in June; and iii) organization of a panel discussion at the political forum *Almedalen in June*. Furthermore, we will actively continue aligning our activities to other key stakeholders in the field on a local, national and international level.

Collaborative projects

We are partner in several externally funded large collaborative initiatives, including:

- *Testing and Experimentation Facility for Health AI and Robotics* (TEF-Health), funded by the European Digital program (36 MSEK, 2023-2027).
- Two projects with Genomic Medicine Sweden (GMS) aiming to connect the National Genomics Portal (NGP) containing clinical sequencing data with the DDLS-PMD data portal to increase data access within Sweden and implement data analysis tools developed at SciLifeLab at the NGP.
  – *Systemdemonstrator för nationellt tillgängliggörande av omikdata för vård, forskning och innovation* from Vinnova (3,6 MSEK, 2024-2027).
  – *Skalbar nationell datadelning av omikdata för vård, forskning och innovation* from SWELife and Vinnova (1 MSEK, 2023- 2025).
- *Digifor1HealthSE: För effektivt och hållbart nyttjande av hälsodata genom integrering av DIGITAL-projekten och GMS i Sverige* (2024-2027).

Developing service packages for industry

The DIGITAL program-funded TEF-Health project is a large-scale EU-wide effort to offer a combination of physical and virtual testing services through a one-stop-shop to support to AI- and robotics development. The services are targeted towards small and medium-sized enterprises (SMEs) and include *physical testing facilities* (hospital and laboratory platforms, compute infrastructures) and *virtual testing facilities* (data access, expertise in AI as well as legal, ethical compliance and certification). This project is relevant for precision medicine development at SciLifeLab as it binds together technology- and data-driven aspects and will push us towards forming more unified service access by aligning user journeys, cost models and access points to testing facilities, to sensitive research data to software tools and enable us to participate in virtual research environment development together with the DSN.



Planetary Biology Capability

The rationale behind the SciLifeLab Planetary Biology (PB) Capability is the need for coordinated transdisciplinary efforts to comprehensively understand biodiversity on Earth – from single molecules and cells to individual species, communities, ecosystems, and their role and impacts on the planet: Life in the environmental context (*Figure 1*). The concept enables us to understand and tackle pressing societal challenges related to climate change, the biodiversity crisis, and biome degradation. PB aims to promote collaboration and efficient use of molecular life science approaches and infrastructure for a better understanding of the biology and biodiversity of ecosystems and our planet.

Mission and vision

Mission: To enable extensive and efficient use of SciLifeLab's full technology portfolio and resources to support and accelerate research in the PB research domain and promote translation to natural resource management and planetary stewardship. To connect and empower a multidisciplinary research community to tackle big questions and pressing challenges in ecology, evolution, and biogeochemistry.

Vision: Sweden will have a leading role in data-driven biodiversity and environmental research.

Organization and governance

The Capability is led by Olga Vinnere Pettersson (SciLifeLab) and Stefan Bertilsson (SLU), with support from three co-leads: Jacob Höglund (UU), Nathaniel Street (UmU) and Anders Andersson (KTH). The Capability Scientific Coordinator is Anabella Aguilera (SLU).

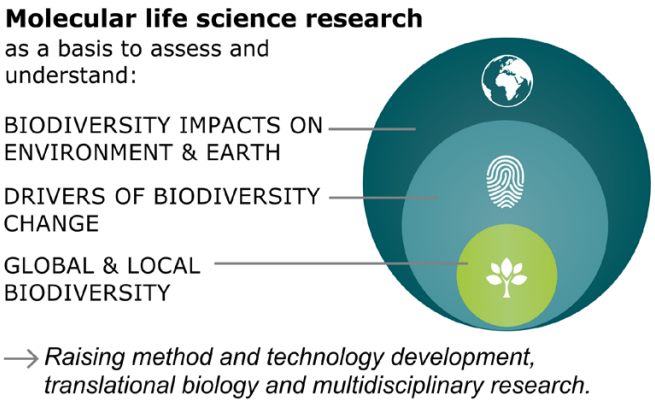


Figure 1. Planetary Biology Concept. Research in molecular life sciences allows us to describe and understand the drivers and meaning of diversity: what changes are happening, what are the underlying mechanisms, and what is the impact of those changes on ecosystems and planetary health.

Personnel and expertise

The leadership represents different organizations and different research foci across the technology and biology spectrum: OVP – Genomics and technology development for non-model organisms, SciLifeLab infrastructure representative, SB – microbial ecology, aquatic sciences and biogeochemistry, Jacob Höglund – conservation biology and population genetics, NS – plant biology and plant-microbe interactions, AA – environmental genomics and biodiversity informatics, AAg – ecophysiology and ecotoxicology.

Funding

PB is currently funded exclusively by SciLifeLab. The need for additional support has been articulated in SciLifeLab feedback to the coming research bill. We have ambitions to attract funds for a competence center, either from national funding agencies (e.g. VR, Formas) or private foundations supporting research and innovation. The capability will support focused collaborative grant applications from PB researchers, aiming to expand the capability "bottom-up". PB aspires to partner with international life science centers (e.g. EMBL) and be a national hub for Swedish participation in international efforts. Finally, PB will engage in dialogue with relevant government agencies and industrial partners to bring resources to the PB community and the Capability.

Operations and key achievements/KPIs 2021–2024

A kick-off meeting was held in Spring 2023 with national representation from >50 participants. This was followed by active participation in all SciLifeLab Days at Lund, Gothenburg, Umeå, and Linköping sites where local PB ambassadors were appointed. We organized a panel debate at the Democracy week at Almedalen to initiate contacts with governmental agencies and industry stakeholders. In 2023, we prepared a PB roadmap and engaged in collaborative dialogue, not only with the PB research community, but also with the DDLS area "Evolution and Biodiversity" and their DDLS fellows. To map the infrastructure and support needs of our research community, we conducted our own technology survey and communicated its results to SciLifeLab leadership. To expand our reach, this year PB is co-organizing and contributing to a number of scientific events, e.g. Nordic ecology society OIKOS meeting in Lund and the Long-Read Sequencing meeting in Uppsala. We are organizing the first PB conference "Molecules to Ecosystems" in Gothenburg (September 2024). PB partnered with the EMBL-led TREC (TRaversing European Coastline) expedition to support the sampling efforts in Sweden with field assistants and logistics. PB is extensively engaged in the European Reference Genome Atlas (ERGA) with OVP as a vice-chair and JH as a Swedish representative at ERGA Council.

Overall plans 2025–2028

Contribution to the development of the SciLifeLab infrastructure

PB has surveyed its community for feedback on user experience with SciLifeLab infrastructure regarding non-model organisms, environmental science and multidisciplinary biology. We have approached the technology platforms, in particular Genomics and Bioinformatics, to identify untapped potential for catering to the needs of PB researchers. In this way, we support: (*a*) SciLifeLab infrastructure with coordinated user feedback, and (*b*) PB research community by acting as brokers and lobbyists. We want to advocate for the development of methods, technologies and data analysis tools that will help SciLifeLab to accommodate not only the needs of biomedical researchers, but also the PB community.

In the longer term, given resources, we see the Capability providing direct support to researchers, stakeholders and infrastructure providers in adhering to the Nagoya protocol (and other legal frameworks relevant for handling of genetic and biological resources) – a sorely needed function.

PB aims to provide a "sample pre-processing" service to biodiversity researchers, enabling efficient extraction and cleanup of biomolecules or biomaterials for downstream high-throughput handling across the SciLifeLab technology platforms. Such a service does not fit in the existing platform structure, but PB could build this, thereby improving quality and cost-efficiency for the researcher while taking workload off the platforms. Currently, these often struggle with user-provided samples in challenging matrices. This service could be a flagship operation for the capability and cement our role as a conduit for excellent biology research beyond biomedicine.

Expected involvement by the platforms to your operation

Our survey has demonstrated that there are: (*a*) major needs for centralized development of methods and tools for work with non-model organisms and challenging environmental samples, (*b*) a willingness of the community to collaborate with the infrastructure to develop such methods, (*c*) strong motivation from the infrastructure side to develop and adopt new methods of analysis that are required. PB seeks to identify opportunities to fund the platforms to engage in technology development activities that go beyond day-to-day operations. This would include the DDLS program, the Bioinformatics platform and the SciLifeLab Data Center (DC). Finally, we fully endorse several existing platform initiatives, such as the "Open lab" at the Genomics platform.

Synergies and collaboration with other Capabilities/ Training Hub/Data Centre

PB involves research and applications related to One Health, e.g. spread of antibiotic resistance, zoonotic diseases and ecotoxicology. This enables extensive synergies with PLP in the environmental context of infectious agent monitoring. Such synergies in the broader area of infection biology could potentially involve PM as well. PB, PLP and PM leaderships have already taken first steps to explore this further.

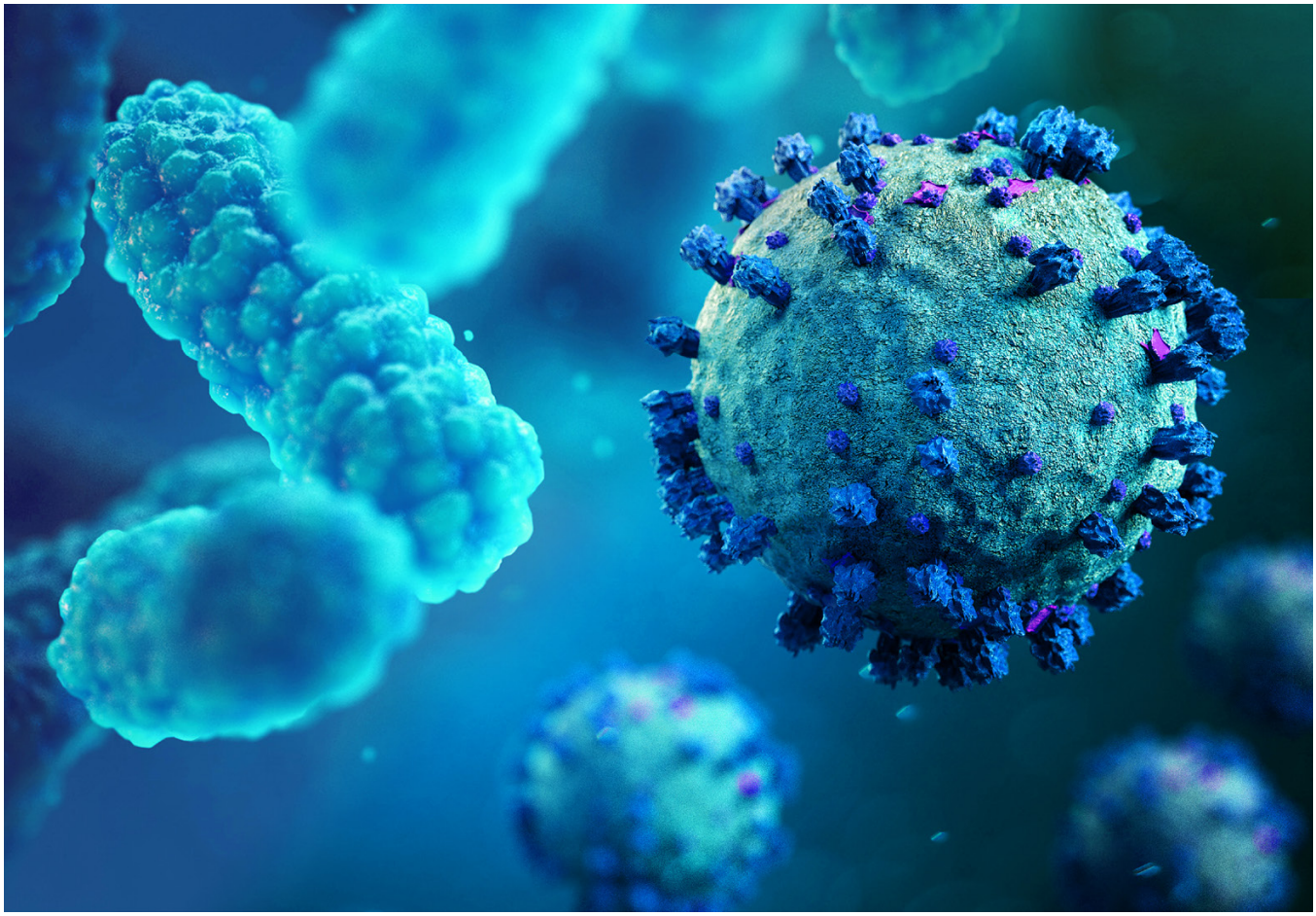
PB sees potential in partnering with the Training Hub (TH). We have established a collaboration within the scope of the PB-supported Biodiversity Genomics Europe (BGE) consortium and are preparing the first SciLifeLab online lab course in advanced genomics of non-model organisms, where the TH plays an important role. We want to continue this collaboration in organizing a summer research school, and other PB-related training. We have engaged DC in establishing a common open web-platform for sharing methods, SOPs and protocols for non-model organisms. We plan to collaborate with DC to establish, promote and disseminate proper metadata standards and FAIR principles in our community. PB will (in dialogue with DC and DDLS) map the community needs in data processing tools, databases, as well as legal and administrative support to conduct global-scale PB research.

Collaboration with external national and international organizations, healthcare, and industry

International level. The most prominent current collaborating partner is EMBL - the pioneer of the PB concept. Apart from supporting the Swedish leg of the TREC expedition, we are exploring possibilities for joint grant applications to foster the relationship between our two organizations, benefitting both SciLifeLab and the national PB community. In particular, we are planning upcoming multinational data collection actions to evaluate European ecosystem health and biodiversity using data driven approaches.

PB is involved in several global biodiversity genomics initiatives: the Earth BioGenome Project, ERGA and BGE. This provides a platform to lobby for biodiversity conservation and bioeconomy development at the European level. PB has collaborations with the Sanger Institute (UK) and the Sanger-lead Darwin Tree of Life program. Our Capability is also actively contributing to ecosystem-scale research infrastructure (e.g. eLTER, EMBRC) and ecosystem-centered research networks (e.g. Global Lake Ecological Observatory Network). Industrial collaborations are yet to be developed.

National level. PB has established contacts with several national governmental agencies within its scope (e.g. Swedish Agency for Marine and Water Management, Environmental Protection Agency), non-profit organizations (e.g. WWF, Naturskyddsföreningen), industry (e.g. Stora Enso, environmental consulting agencies such as Calluna and technology development companies such as Readily Diagnostics) as well as parliament members at the national and European level. Attempts to establish a direct link with the Ministry of Climate and Industry are progressing (although slowly). We are actively initiating contacts with representatives from those industries that are now being obliged to operate under the EU sustainability goals and habitat protection directives. Such enterprises would directly benefit from SciLifeLab infrastructure and molecular monitoring systems which are being developed in our research community.



Pandemic Laboratory Preparedness Capability

Mission and vision

During the COVID-19 pandemic, SciLifeLab repositioned the infrastructure and coordinated research, technologies and data handling to support society, health care and governmental agencies by delivering data important for strategic decision making in how to handle i) the spread of the infection and ii) the national vaccination program. This provides a model on how a national life science infrastructure can contribute to critical challenges or acute crises in the society and go from a "peace-time to a crisis-time" operation. The Pandemic Laboratory Preparedness (PLP) Capability at SciLifeLab was established in 2021 as a result of SciLifeLab integrational work during the pandemic. It is a 4-year program for national pandemic laboratory preparedness, financed by a special grant of 130 MSEK from the Swedish government. The main aim of the program is to provide SciLifeLab, in consultation with the Public Health Agency of Sweden (FoHM), abilities to build laboratory capacities for pandemics to support health care, clinical laboratories as well as public and commercial sectors but not to replicate or create competing clinical testing capacity. The aim is achieved by strengthening technical facilities for molecular analyses, increasing the capacity to analyze large amounts of data and by supporting research and method development required for increased understanding of infections that can cause pandemics. Relevant research fields include diagnosis, analysis of infection biology, disease pathogenesis, immunity and drug and vaccine resistance of viruses, bacteria and other disease-causing agents.

Organization and governance

The steering committee of the PLP capability (see *Figure 1*) is composed of experts within infection biology research, project management and organization and has ample experience in heading national and international research

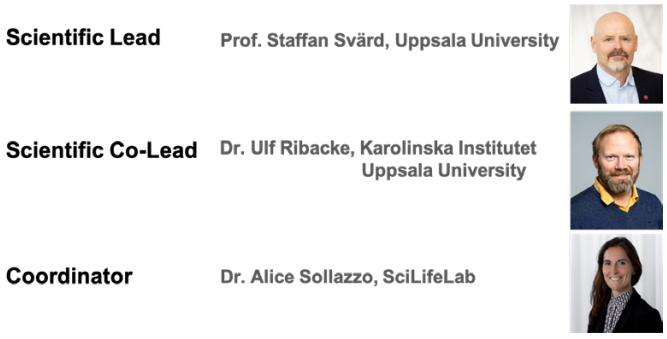


Figure 1. Staffan Svärd, UU, is scientific lead for the PLP program, Ulf Ribacke, KI and UU is co-lead since 2023 and Alice Sollazzo is program coordinator.

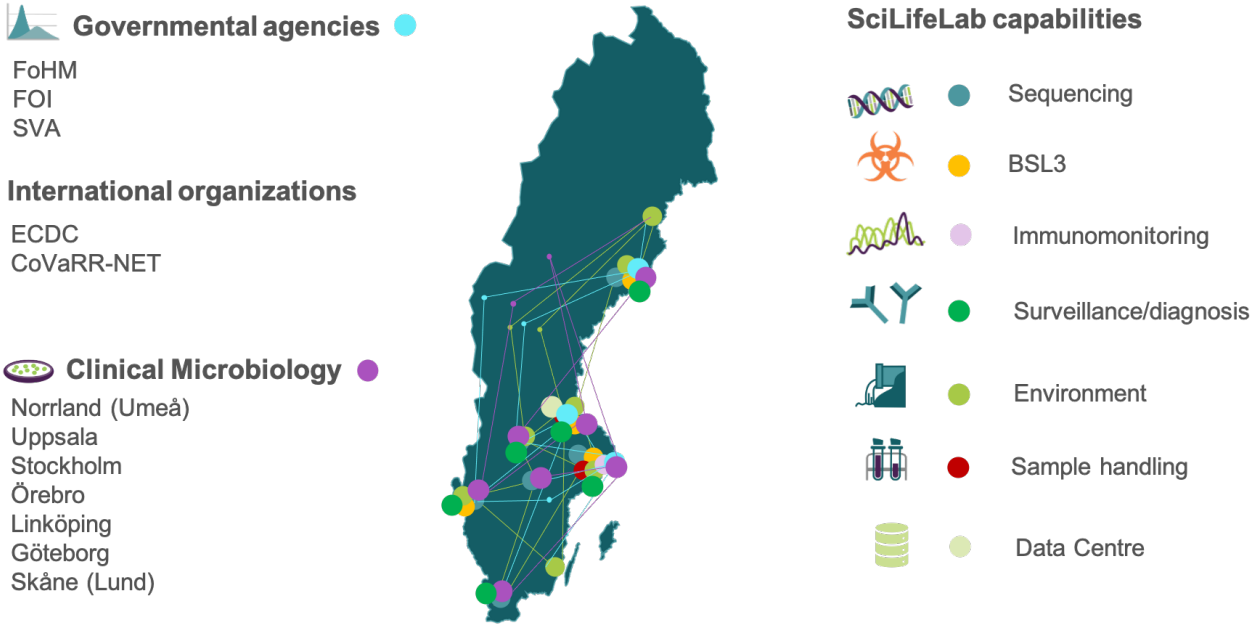


Figure 2. The PLP network with focus areas.

collaborations and networks. The development and work of the PLP program is performed in consultation with key Swedish governmental agencies such as SVA and FOI and decisions are taken in dialog with the Public Health Agency of Sweden, the SciLifeLab Management Group and approved by the SciLifeLab Board.

Personnel and expertise

Since the start in 2021, the PLP network has expanded via open, competitive grant calls and consists today of 23 separate units spread throughout the country and different research environments, all focusing on different areas within pandemic laboratory preparedness. The network now consists of about 200 collaborators. The main focus areas are DNA/RNA sequencing and metagenomics, BSL3 operations, immunomonitoring, diagnosis and surveillance, environmental analyses, sample and data handling (*Figure* 2). The PLP units are well integrated into SciLifeLab infrastructure (*Figure* 3). Thus, the PLP network has become a unique platform that joins the broad level of expertise needed to handle ongoing and future pandemic threats.

Funding

The PLP receive governmental funding given to SciLifeLab to build laboratory capacity to be better prepared for future pandemics (40 MSEK in 2021 and 30 MSEK per year 2022-2024, in total 130 MSEK). The absolute majority of this funding has been distributed through open and competitive grant applications. The future funding of the PLP program is not guaranteed and we have made new justifications for continued funding in the government research proposition. Continued funding will be key to our active work to retain and further develop the established PLP capabilities also in the post-pandemic phase.



Figure 3. The PLP network is integrated into the SciLifeLab platforms. The size of PLP symbol reflects involvement of the platform in PLP.

Operations and key achievements/KPIs 2021–2024

The network have played a very important role during the COVID-19 pandemic. Most of the sequencing of SARS CoV2 virus variants in Sweden has been performed within the network, as well as large scale serology studies, viral inhibition assays and estimates of vaccine efficiencies, detection and sequencing of SARS CoV2 virus variants in waste water analyses and sharing of research data via the COVID-19 /Swedish Pathogens portal. Collaborations have been established with the seven major clinical microbiology labs at the university hospitals (mainly via the Clinical Genomics platform), governmental agencies (FoHM, SVA and FOI), and international organizations (ECDC, CoVaRR-NET (Canada). In August 2023, the first PLP network meeting was held with participants from all units and collaborators and it showed that it is a strong and established national network. The PLP meeting initiated the writing of a road map for the PLP network 2025 to 2028.

Overall plans 2025–2028

Being able to retain and further develop the PLP network and the capabilities and technologies developed within is of great importance for the national ability to handle future pandemic threats. Already in the current state, had the network been at place at the onset of the COVID-19 pandemic, Sweden would have stood a better chance to respond rapidly and with high accuracy early in the pandemic. In addition, the work performed by the PLP capabilities in the post-pandemic phase will be of great value to several branches of general research, including infection biology, immunology, or antibiotic resistance. Epidemiology and biology of infection is also one of the four research areas of the DDLS program (DDLS EBI), in which PLP will play an important role. PLP will also contribute to the application of new methods to study infections and the microbiome, such as metagenome sequencing for research and diagnostics.

SciLifeLab and the PLP capability has shown a unique ability to strengthen basic and clinical research and technology development at universities, hospitals, authorities and companies during and between pandemics through the strong life-science infrastructure and research network established.

The PLP network is now focusing on five main areas.

1. Support and coordination of team-science efforts in the PLP network
2. Support of technique and technology development important for the study of pandemic pathogens and their pathobiology
3. National and international cooperation and collaboration with other research infrastructures and networks
4. Support of data management, sharing and open publication during and between pandemics via the Swedish Pathogens portal.
5. Integration of pandemic laboratory preparedness capabilities within SciLifeLab platforms, the Planetary Biology and Precision Medicine capabilities and the DDLS program in research area Epidemiology and Infection Biology

During 2024 the PLP program will continue to improve resources to be used in pandemics but with the added gain that these can also be used in other SciLifeLab activities, such as infrastructure support of infection research and precision medicine. Therefore, one aim is to make important PLP resources part of the SciLifeLab infrastructure portfolio from 2025 and to retain collaborations with the clinical microbiology laboratories to maintain and develop the capabilities needed for future pandemics.

Training Hub

SciLifeLab Training

Training is recognized as an important part of each platform's service portfolio. During 2023, SciLifeLab Infrastructure contributed to the delivery of >140 training events, reaching almost 3000 participants spread across the life science community. SciLifeLab Trainers are the staff-scientists and affiliated researchers across the SciLifeLab ecosystem that design, develop and deliver short-form training to the community and across the SciLifeLab platforms where over 400 FTEs (staff-scientists) are employed.

Training Hub

In 2023 Training Hub was launched as a new core entity within SciLifeLab with the vision to become the national go-to-place for life science technology- and data-driven lifelong learning. We will do this by consolidating the wealth of knowledge, skills and expertise from the breadth of the SciLifeLab ecosystem and to disseminate via the newly launched SciLifeLab Training Portal. Training Hub will support making the training (materials) openly and nationally accessible in addition to FAIR (Findable, Accessible, Interoperable, Reusable). Training Hub recognizes training materials as research material, which should follow the CoARA practices.

Operations

Training Hub is in the early phase of establishment and will during the next phase establish the organization and models of the support to be provided. The aim is with our training tools, resources and expertise to establish the Training Hub as a recognized central support function to the SciLifeLab ecosystem. The end result will assure that quality training activities are designed, developed and delivered from SciLifeLab to the life science community. Once fully operational, Training Hub will provide the SciLifeLab entities and groups with technical infrastructure and support in training to ensure quality across the Training Life Cycle (Plan-Design-Develop-Deliver-Evaluate) (*Figure 1*). Training Hub team aims to offer personalized training support in the form of training and pedagogy expert help and guidance on tailored learning paths.

Governance, organization/team and funding

Training Hub aims to concretize its governance structure in SciLifeLab during 2024/2025 with the SciLifeLab Management and Board. Training Hub operations are led by the Head of Training (Jessica Lindvall) and together with the Training Manager (Nina Norgren) oversees the daily operations of the team of Systems Developers and Scientific Training Officers. The tech-team consists of the

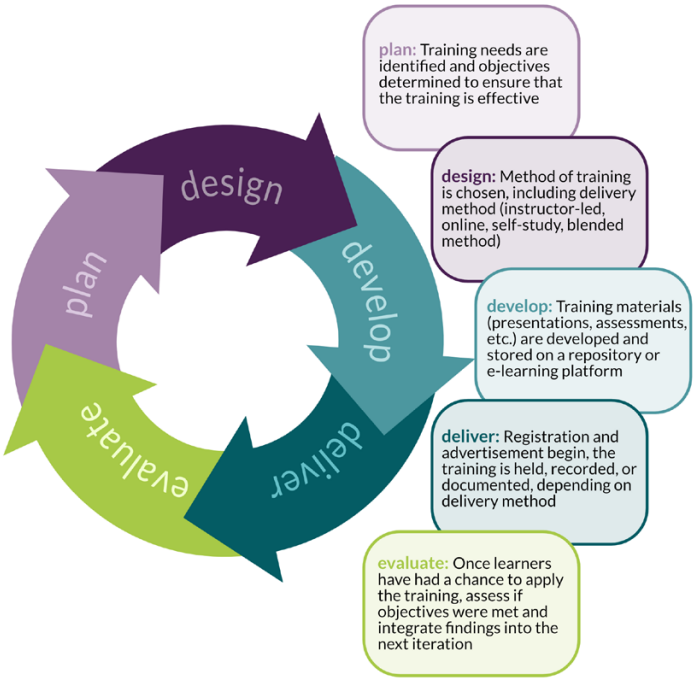


Figure 1. Outline of the Training lifecycle and its phases (plan-design-develop-deliver-evaluate).

Systems Developers and a Scientific Training Officer with the UX perspective. The Scientific Training Officers consist of 3 individuals with training and/or pedagogy expertise.

In 2023, SciLifeLab Training Hub received a 4-year grant (~11 MSEK, 2023-2026) from the Swedish Research Council with the aim to increase accessibility to SciLifeLab Infrastructure using training and lifelong learning. Together with the national funding from SciLifeLab (~2.8 MSEK 2024) and KAW/SciLifeLab DDLS funding (~2.8 MSEK 2024/2025) Training Hub have been able to recruit 3 Scientific Training Officers and 2 Systems Developer (incoming spring 2024). In addition, Data Centre has allocated 1 Systems Developer (recruited fall 2023) to work 100% with the Training Hub. This has enabled us to build the necessary infrastructure in parallel to launching the pedagogy and training support for the SciLifeLab entities to use. By the end of 2024 we envision the Training Hub team to consist of 6 FTEs divided on the Systems development team and the Scientific Training Officers team in addition to roles of the Training Manager and the Head of Training.

As *Table 1* shows, the Training Hub does not yet have a "sustainable" funding mechanism within SciLifeLab i.e the national funding granted only on a year-to-year basis, and within DDLS for a 2-year phase. In order to plan and work towards a sustainable training support and service model for the SciLifeLab ecosystem to enjoy, we therefore hope SciLifeLab recognizes the need for a more long-term budget planning.

Table 1. Funding scheme for Training Hub 2023–2026.

Year	SciLifeLab National	DDLS	National Research Council
2024	2,863,000	2,864,000	3,241,000
2025	-	2,864,000	2,013,000
2026	-	-	2,269,000

Interactions and synergies

across SciLifeLab

Design, development and delivery of training are activities that every SciLifeLab entity engages in. Training Hub will support both technically and with expertise to ensure quality across the Training lifecycle. Thus, Training Hub activities are transversal across the ecosystem (as shown in *Figure* 2) and will ensure knowledge transfer both internally and externally to stakeholders. Training Hub is to collaborate and interact with every platform and unit, Data Centre, Operation Office, SciLifeLab Sites, Capabilities as well as being involved in the DDLS program. For the DDLS Program, Training Hub aims to offer both the technical training support as well as training expertise for DDLS fellows and their teams. In addition, Training Hub aims to co-create, together with the DDLS fellows and Infrastructure experts, a DDLS training catalogue to support the fostering of the Sweden-based life science research community in data-driven life science. In addition, Training Hub is involved in the development and delivery of the DDLS Research School.

with national and international training entities

Training Hub has established connections and has ongoing collaborations both on a national and international level (*Figure* 2). We also foresee an increase in the requests for training collaborations and connections, both nationally and internationally, which will enable SciLifeLab to further connect outward. Of particular highlight is the Training Hub's affiliation with ELIXIR, where the Head of Training via NBIS/ELIXIR-SE (the SciLifeLab Bioinformatics Platform) is one of the Executive Committee members for the ELIXIR Training Platform. In addition, Training Hub collaborates with EMBL, EMBL-EBI, VIB and Human Technopole. Nationally, Training Hub is connected to ENCCS (the EuroCC National Competence Center Sweden) that provides high-performance computing training and support for industry, academia and public administration. In addition, collaboration and connections with SND (Swedish National Data service) is ongoing.

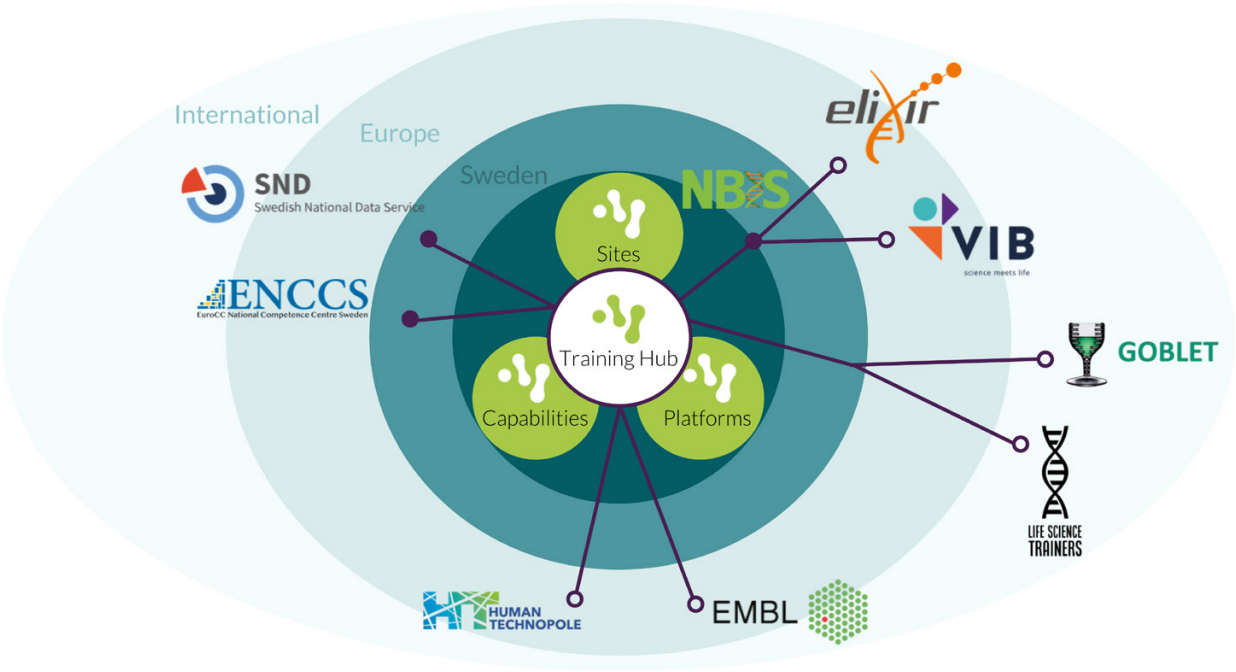


Figure 2. Training Hub connections and collaborations on the level of 1) internal SciLifeLab, 2) national, 3) European, and 4) international levels.

Key achievements 2023 – 2024

- During Q2 to Q3 in 2023 Training Hub onboarded 3 Scientific Training Officers and 1 Systems developer
- February 2024, we launched phase I of the Training Portal, a technical platform which directs training tools, opportunities, and resources for capturing and delivering knowledge at SciLifeLab.
- In 2023 and 2024 we will deliver Train-the-Trainer courses, an introductory course on Organisational Learning, How to make your training material FAIR course, and a course on Open Science. The aim is to upskill the community in training-related skills and to build a community of trainers who can ensure SciLifeLab training to be sustainable, quality-assured, Open, and FAIR.
- Continue to add training resources to the Training Portal as to support the community with training structure and guidelines.
- In 2024 launch a smörgåsbord of regular events and forums where the community receive collaborative support and discussion with the training experts at the Training Hub i.e the Scientific Training Officers. Examples of events and forums are:
  – Regular Training coffee sessions, forums where trainers can meet and discuss training
  – Consultations i.e. opportunity for the community to book short 1-to-1 meetings with dedicated questions related to training.
- In 2024 continue and finalize the support projects started with:
  – Planetary Biology (NGI), which will result in the delivery of a wet-lab course in June 2024. Training Hub supports across the full Training Life Cycle, from planning to evaluation of the course
  – Clinical Genomics are planning a series of Master Classes i.e 14 recorded sessions with the aim to transfer the knowledge of the platform to the community and future staff-scientists of the platform
  – Precision Medicine, as part of their work plan, are doing a gap-analysis and need assessment analysis across their stakeholder groups of which Training Hub is supporting. The gap-analysis will be followed by an inventory analysis of what training opportunities and training material is already available.
- 2023 publications from collaborative training projects
  – An international consensus on effective, inclusive, and career-spanning short-format training in the life sciences and beyond, Williams JJ, Tractenberg RE, Batut B, Becker EA, Brown AM, et al. (2023), PLOS ONE 18(11): e0293879. https://doi.org/10.1371/journal.pone.0293879
  – Phyton in a week - Conceptual tests for learning and course development, Christopher Blöcker, Thomas Mejtoft, Nina Norgren (2023), The 19th CDIO International Conference (Trondheim)

Overall plans 2025 – 2028

The overall challenge will be to adapt and integrate AI use into the Training services and to upskill the learners and trainers in AI readiness. This needs to be integrated both across the technical infrastructure as well as within the pedagogical training support offered. In order to ensure the delivery of quality training SciLifeLab need to establish support structures covering both technical infrastructure and pedagogical support that will cover the needs across the Training lifecycle. Apart from the portal, we will also set up and offer: Learning Management Systems for course delivery, administration systems for easy course administration, course templates and frameworks for making it easy to set up course structures according to OPEN and FAIR principles, etc.

In the next phase, Training Hub will continue its establishment with the technical infrastructure in parallel with the pedagogy and training support offerings to the SciLifeLab ecosystem. We will during 2024 launch regular Training Coffee sessions where trainers and instructors can meet to discuss challenges and peer-support each other in different training activities and for Training Hub to present the provided support. We will also set-up consultation opportunities for SciLifeLab affiliated staff to book for short questions regarding training, courses etc.

We are aware that Training Hub support processes are needed to be set-up on a broader scale. However, with the current resources, Training Hub is not able to meet the support demand from every SciLifeLab entity in a 1-to-1 relationship. Therefore, the need to set-up agnostic and general support structures that reaches the broader mass in one go is crucial. Also, the more support we can build into the technical platform the better.

Data Centre

SciLifeLab Data Centre (DC) is a part of the central SciLifeLab organization, providing digital infrastructure services for the life science field and leading strategic technical developments for data driven life science at SciLifeLab. In addition to its role in strategy and coordination for SciLifeLab on data and IT issues, including the DDLS program, the unit develops and operates a range of services for users in management, operations, infrastructure and the general research community. Principles of FAIR and Open Science are at the heart of DC, and the unit aims to empower research- and infrastructure communities with tools and services, for example enabling production-level hosting of community generated content, including data, computational services, AI models, knowledge support and training.

Data Centre operated digital infrastructure services have users at all infrastructure platforms, in operations and management, and we estimate that services reach over 100,000 international users annually for both DC-developed and -hosted data services and resources.

Most SciLifeLab DC services can be accessed through the national data platform at data.scilifelab.se.

Vision and mission

The vision of SciLifeLab Data Centre is to position Sweden at the global forefront of data-driven life sciences research. The DC mission is to facilitate world class research and enhancing research quality by offering a suite of impactful services. DC contributes to open science and removes barriers to reuse of research outputs, and participates at the highest international level in technology development and shaping best practices and standards for data-driven life sciences research.

Organization and governance

The SciLifeLab Data Centre is fully governed by the SciLifeLab board, and has no separate steering group. It is not an infrastructure platform, but a fulfils both a supporting role and a strategic, leading role to ensure SciLifeLab stays at the cutting edge of digitalising life science infrastructure. The Head of Data Centre is responsible for DC and is appointed by the SciLifeLab board, reporting to the SciLifeLab Director. The Head of DC is also adjunct to the SciLifeLab Management Group and the DDLS steering group.

The SciLifeLab Data Centre gets is assignments and oversight from the SciLifeLab board. The purpose already from the start was to serve both the infrastructure units and the research community, with a focus on maximizing the scientific impact of SciLifeLab output through FAIR and Open Science, but also to fulfil a strategic role strengthening SciLifeLab itself. DC has also been tasked to represent SciLifeLab towards national and international stakeholders in issues regarding data and IT, and to lead and organize the Data support and Databases operational area of DDLS, approximately 20% of the total DDLS budget.

To ensure oversight, DC management regularly meets the SciLifeLab/DDLS directors and management/steering groups to report progress and updates on services and planning.

The Data Centre is not assigned to provide, for example,

1. General IT support;
2. Bioinformatics analysis support;
3. Bespoke platform/technology specific development;
4. Own-operated hardware or bespoke compute- and storage services for infrastructure.

Personnel and expertise

To fulfil its assignments, DC has organized itself in five operational areas: Administration and Coordination, Data Science Services, Research Data Management Services, IT Systems and Infrastructure, and Open Science. Each operational area is led by a manager, and all DC staff reports to one of the managers. The operations of DC is led by its management group consisting of the Head and Vice Head of DC, the managers of the operational areas, the DC CTO, and the process owner for development.

Today, the SciLifeLab Data Centre employs 38 staff (22 M, 16 F, 36.4 FTE) in its two offices at UU and KTH. 29 out of the 38 staff have roles as system developers, data engineers, or data stewards, and 19 have a PhD. Nine staff members are employed as project leaders, project coordinators, IT specialists and in administration.

DDLS Data Science Nodes employ 12 staff: system developers, data engineers, and data stewards/coordinators. Staff are employed at the DDLS Data Science Node host universities and are embedded at the local organisations, but fully integrated in the work of the DC operational areas to develop services for the SciLifeLab national data platform. Their work is led from DC under the oversight of the DDLS Steering Group. In addition to this, four staff members are fully embedded at the national compute- and storage e-infrastuctures UPPMAX (at UU) and NSC (at LiU) to facilitate access and increase capacity for life science users in general, and in particular the DDLS program.

Although it is commonly considered difficult to recruit skilled technical staff to IT- and data areas in academia because of direct competition with industry, DC has successfully attracted highly competent staff, including in very competitive areas such as Kubernetes specialists, AI/MLops engineers and information security. 16 nationalities are represented in the group, with diverse backgrounds from different academic fields and industry.

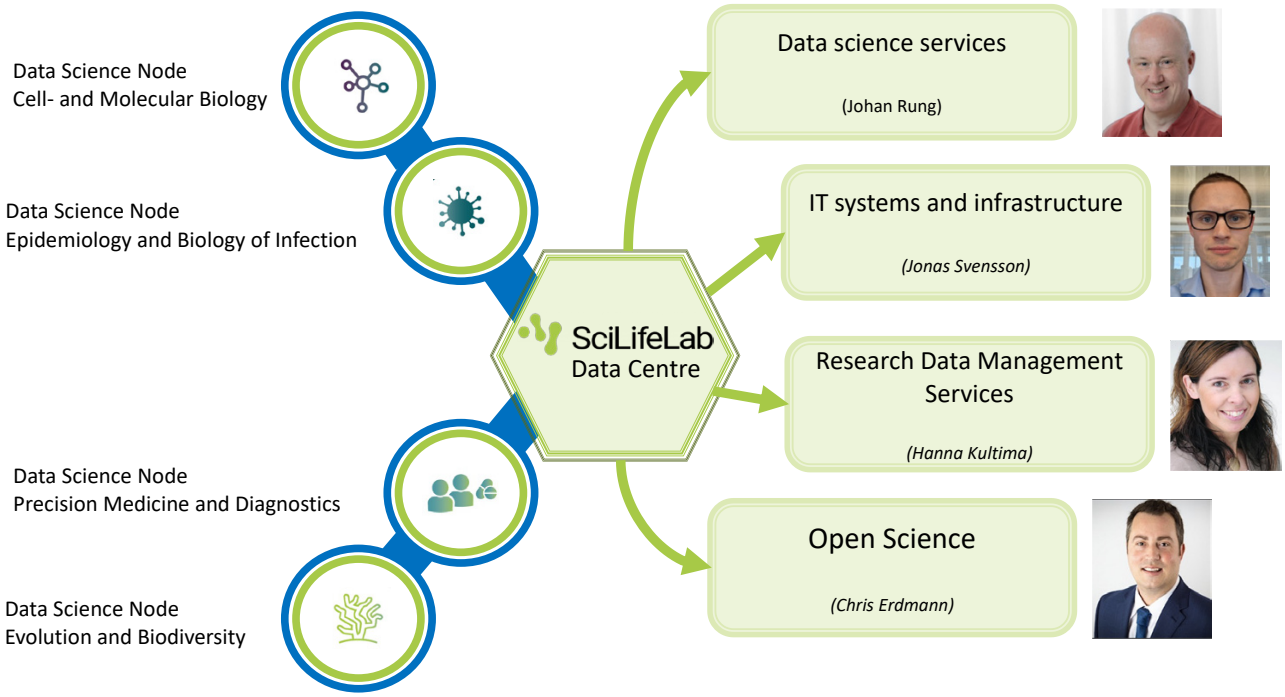


Figure 1. SciLifeLab Data Centre is organized in operational areas that develop and operate services, with personnel in the Data Centre and the associated DDLS Data Science Nodes.

DC often recruits directly from abroad or from industry, demonstrating that investments such as the DDLS program not only strengthens Sweden's ability to recruit to new teaching positions, but also to technical positions in digital infrastructure.

DC is led by a management group with strong academic background in life science, physics and data science, and long experience with research infrastructure. The group takes an active role with SciLifeLab management to shape SciLifeLab's strategy in the data domain. The Head of Data Centre has a Research Infrastructure Fellowship from the Swedish Foundation for Strategic Research.

Funding and external relations

SciLifeLab Data Centre, including the associated Data Science Nodes, is funded through several sources with approximately 70 MSEK annually, of which 9 MSEK is national funding covering the basic operations and support of core services for SciLifeLab operations and infrastructure. The generous additional funding through the DDLS program enables DC to develop and operate services for the data-driven life science research community. Additional funding to DC includes the pandemic preparedness program, Horizon Europe funding, and a highly competitive grant from the Swedish Foundation for Strategic Research for research infrastructure fellows received by the Head of DC.

Services in production with a major running cost component (for example the Data Delivery System) will operate on a user fee model starting later in 2024.

DC participates in external international projects such as the BY-COVID Horizon project for Pandemic Preparedness of pathogens data. DC is not part of the Swedish ELIXIR node, as NBIS constitutes the node itself, but the unit collaborates closely with NBIS and bilaterally with partners in the ELIXIR network. DC also has strong international collaborations with, for example, EMBL-EBI, CSC (Finland), McGill University (Canada), Global Alliance for Genomics and Health, VIB (Belgium), Michael J Fox Foundation, San Diego Supercomputer Center, Research Software Alliance, and CERN. The unit also engages in communities such as nf-core, where one DC developer participates in the nf-core central team. DC also drives engagement in key strategic initiatives such as CoARA for research assessment, and ADORE.software for FAIR and sustainable research software.

SciLifeLab Data Centre is listed by the European Open Science Cloud (EOSC) Steering Board in its catalogue of best practices (zenodo.org/records/7574165).

Services

SciLifeLab Data Centre has a solid service catalogue, available to researchers, infrastructure units and operations and management. Although all services are widely available and have users in all groups, we categorize them below to discuss in the context of each stakeholder group.

Services for management and operations

SciLifeLab increasingly prioritises data-driven science, and that also reflects in the activities that are carried out by Operations Office and the management team of directors. Therefore, the Data Centre participates in essentially every aspect of management and operations at SciLifeLab. This work is not only through providing support services, but to actively participate in a leading role in strategic and operational planning, as well as in event planning, external relations etc. For example, the Data Centre has a key role in communication with the government offices regarding SciLifeLab's coordination for European projects and AI strategy.

For the Operations Office and management, DC provides systems developed in-house for data collection from the infrastructure, for reporting and surveying, a publications database, and a system called Anubis to handle proposal submissions and the accompanying review process. Virtually all reporting for all parts of SciLifeLab, as well as all calls and proposals, are operated using DC systems and support, as well as data processing, analysis, visualisations and writing for reports. For example, Anubis has to date handled over 40 calls for SciLifeLab, involving more than 750 proposals and 3,000 reviews. The publication databases contains over 15,000 publications.

DC also participates in the infrastructure planning and coordination activities, and maintains a data policy and terms and conditions for infrastructure related to FAIR and Open Science. DC has driven the process of SciLifeLab signing up to the Coalition for Advancing Research Assessment (CoARA), and leads the work on research assessment development through its Open Science unit.

Data Centre does not provide general IT-support, as this is provided by the host universities. At Campus Solna, there is IT-support from KTH for campus-specific services through agreements between Solna Site Support and KTH. DC collaborates closely with KTH IT around the IT environment, as a user itself, but also regarding consolidation and coordination of services provided by KTH. Some of these have traditionally been organized as Solna-specific while in reality having a national scope, such as the scilifelab.se domain, the Google workspace, and the operation of infrastructure owned compute- and storage servers. Since 2023, the Data Centre employs an IT manager that bridges the national data operation at SciLifeLab and the IT division at KTH. Since early 2024, Data Centre also has a full organizational unit at KTH IT, and the ability to employ and take costs both at Uppsala University and KTH IT, greatly facilitating the national coordination of services. See *Table 1*.

Table 1. SciLifeLab Data Centre services for operations and management.

Service	Description
Publication database	System developed in-house to store publication data, providing a search and browse interface and an Application Programming Interface to find publications produced by researchers affiliated with SciLifeLab (including Fellows) or based on infrastructure services. The system is also a reporting tool for the platforms. publications.scilifelab.se
Reporting portal	System developed in-house to support the various reporting processes at SciLifeLab where infrastructure units, fellows or projects in SciLifeLab programs are required to report back, including annual reporting, IEC and IAB reporting.
Anubis	System for call-proposal submissions and handling of the review process, used in essentially all SciLifeLab activities involving calls and proposals and reviewing.
ProjectPlace	Project management system primarily used by Operations and Management.
www.scilifelab.se	Main SciLifeLab web site, where DC provides a web developer and participates in project management and planning for the SciLifeLab web.
Bibliometry, reporting analytics, reporting data management	DC is strongly engaged in SciLifeLab reporting, not only by the development and operation of the publications databases but also in the analysis of reporting data directly for the reports, provisioning of publications data and bibliometric analysis, and visualisations and collaborations with university libraries.
IT systems coordination	DC coordinates with KTH regarding IT services needed for its operations, but also engages in planning future directions and the consolidation of services that are required for SciLifeLab to operate on the national level, for example regarding Identity- and Access Management.
Infrastructure management and coordination	Infrastructure management and coordination at SciLifeLab requires the participation of DC regarding for example policies for Open Science, events, national coordination, collaborations with key international partners such as EMBL and VIB, etc.
Training Hub portal technical infrastructure	DC collaborates closely with SciLifeLab Training Hub, and supports TH with system development and hosting of the TH portal.
Photo bank	Nextcloud based photo- and picture library used by SciLifeLab communications team.

Services for infrastructure units

SciLifeLab Data Centre supports infrastructure units through close interaction with the service platforms, providing IT solutions and software services, advice on data flow design, and assistance in preparing operational plans or grant proposals. New services developed or procured by DC often originate in platform requirements, followed by collaboration projects piloting and evaluating prospective services. There is a particularly close collaboration between DC and the Bioinformatics platform, NBIS, regarding data management and FAIR. For example, DC and NBIS develop brokering submissions of data produced by SciLifeLab platforms to the appropriate repositories at EMBL-EBI through interactions with the platform, researchers in the project, and EMBL-EBI curators, and they together operate a Data Management helpdesk.

A central service to platforms is a system developed in-house for data delivery, already deployed in production at the Genomics platform with over 1,000 projects delivered and > 500 TB data transferred to users across Sweden. It is built on a cloud-based storage system and on-the-fly encryption enabling the transfer and storage of sensitive data.

The philosophy of DC is to make data sharing an integral part of the research process, linking data-producing platforms and research projects rather than being used passively for data publishing at the end of the research project. DC aims to build and operate well structured and supported production level services based on strong IT, and puts considerable effort on legal work and information security.

Data Centre services are used by all platform units, and provides fundamental systems often used daily at the infrastructure operations without knowing the role of DC in providing them.

DC order portals have to date handled over 15,000 service projects in eight instances. The unit also provides collaborative tools and team science software to facilitate work across the national organisation of SciLifeLab. For example, this includes commonly used software platforms such as Confluence, Jira, Nextcloud and Slack. This has proven to be very important for community building. Our Slack workspace brings approximately 2,000 users at infrastucture and research communities together, where DC both operates and supports the main SciLifeLab workspace and provides own workspaces for platforms, e.g., Genomics Platform and NBIS.

DC and SciLifeLab infrastructure units often share frustration over the limited ability of DC to provide technology specific solutions or bespoke development for specific units. This is because the growth of DC comes entirely from DDLS which can not be used to directly support specific infrastructure units. The current infrastructure funding to DC is at the same level since 2020 and consists of 6 FTE (including DC management and administration) serving all ten platforms as well as the SciLifeLab management and operations. However, DDLS funding is used for services that broadly stimulates the impact of SciLifeLab infrastructure in their interaction with researchers, such as the development of meta-data management, data delivery services and service hosting.

A gap is the facilitation of compute- and storage capacity for infrastructure. Researchers can utilize NAISS, the national e-infrastructure supporting active research, but infrastructure units are left to plan and implement their own services, as DC has neither ther capacity nor the assignment to provide C&S services to infrastructure. The capacity and staff at infrastructure units themselves to deal with this is varying and many units struggle. The ability to provide access to C&S capacity, from a consolidated platform, that can be provided for a fee is a high priority for DC but would require investments from SciLifeLab.

SciLifeLab platforms serve users at, primarily, Swedish universities, and the data produced in service projects is under the full governance of each organisation. Therefore, it is not feasible for SciLifeLab to build large repositories holding and serving the produced data, but rather to provide services that in other ways support projects and create added value for Swedish research on an opt-in basis. See *Table 2*.

Table 2. SciLifeLab Data Centre services for infrastructure units.

Service	Description
Data Delivery System	Cloud-based system facilitating data delivery and storage for units. It can also provide some other services, including feedback forms. DDS is developed in close collaboration with the infrastructure units and is in production at the Genomics platform, with 17 additional units piloting the system as of early 2024. delivery.scilifelab.se
Order Portal	A web-based management system that, amongst other things, enables infrastructure units to communicate with their users. It is currently used at multiple units and allows for the configuration of platform-specific instances.
NextCloud	File management system à la Dropbox, with DC-managed storage provided via SUNET, enabling file sharing and editing for platforms and operations. DC provides several solutions for infrastructure based on Nextcloud, including custom data management infrastructure to for example AIDA Data Hub, as well as SUNET based solutions to the Drug Discovery and Development platform.
Slack	Cloud-based communication system for rapid work communication.
Jira	Project management system.
Confluence	A system provided by Atlassian for wiki-style collaborative workspaces.
Storage	KTH operates a storage service that can be utilized by platforms, and currently has around 3 PB of storage of which 1.7 is currently allocated. DC is currently working with KTH to utilize this platform on the national level for infrastructure.
Google workspace	Document editing and sharing, and email access using Google.
TypeForm	Survey tool for user feedback or other service related surveys.
Protocols.io	System for open sharing of protocols used by the infrastructure units.
Infrastructure consultations and coordination	Supports infrastructure with expertise on data management, IT workflows, Open Science and FAIR, data science systems, AI and software engineering. Provided both at request, and through web based guidelines and documentation.
Helpdesk	Support helpdesk. In 2023 handled approximately 2,000 tickets.

Services for researchers

Since the start, one of the key assignments to the Data Centre is to provide the research community with impactful services. DC actively engages with individual projects from their adaptation of DC services, to support good data practices and Open Science. DC also engages directly with external research projects to strengthen strategic development central to SciLifeLab, such as AI, health data, scientific software engineering, collaborations with biobanks and sample collections, and image data applications.

It is important to DC to work in a scaleable way towards researchers. Therefore, our model is primarily to provide services and digital infrastructure with broad reach and impact, rather than focusing on direct support to individuals groups or units. In particular, we provide the national data platform where research- or service outputs generated by the user community itself can reach the widest possible audience in a sustainable production environment through service- and model hosting, and general data repositories.

Because of the DDLS program, DC can put considerable effort to develop production level services for research, listed below. The SciLifeLab Data Repository is a Figshare based general data repository with a data steward support team. The repository holds around 500 datasets that have been downloaded over 130,000 times. SciLifeLab Serve is a unique system that has received much attention internationally, being an open source platform for hosting and serving compute applications, computational notebooks, and AI models. It currently hosts over 70 different community developed services, operating on a small but adequate compute cluster with both GPU and CPU resources. The service greatly facilitates the hosting process and could scale several orders of magnitude given stronger back-end C&S.

The Swedish Pathogens Portal has been exceptionally successful and has been highlighted both by Swedish government and the European Commission as a model for future repositories that not only provide actual data resources but also hosts compute services, information, standards and data management support towards a

specific community. The portal was started as the Swedish COVID-19 Data Portal, and was launched rapidly as the first national data portal at the start of the pandemic in 2020. Building on a national mandate, an associated research program at SciLifeLab, and an international collaboration with EMBL-EBI, the portal became the go-to place for the Swedish COVID-19 research community. Because it was developed on an open source license, the portal code was shared internationally and approximately 15 other national portals opened, based on the Swedish one. As we now has moved into a new phase for Pandemic Preparedness, the portal is repurposed for general infectious diseases and pathogen data, and is now the only full national portal in the EMBL-EBI-led Pathogens network. The portal engages the DDLS community through an editorial committee of early career scientists including DDLS fellows, providing scientific advice, content and editorial support.

At the start of the DDLS program, DC was assigned to lead the operational work for the DDLS program data services and resources, as the hub of a national network for life science data across the participating universities. That includes strengthening the compute- and storage capacity required to operate the data platform, often through coordination with other e-infrastructure centres across Sweden. The strategy is to complement e-infrastructure services provided by other national providers or the universities, and the focus areas are services hosting platforms with Kubernetes, and data sharing services equipped with considerable capacity for data storage. A close collaboration has been established with the National Supercomputer Centre (NSC) at Linköping University, hosting the KAW-funded resource Berzelius.

Compute- and storage infrastructure for research in Sweden has gone through a transition in the last two years, and the organization has moved from a university consortium with centre at Uppsala University (SNIC) to a consolidated assignment to Linköping University for the operation of national resources (NAISS). This has sometimes caused uncertainty in the community and the already fragmented landscape in Sweden for Compute- and Storage is now in transition. SciLifeLab aims to be a strong representative for the life science community, and DC led a requirements analysis for life science and infrastructure for sensitive data, delivered on assignment to the new NAISS organization in early 2023.

12 staff members at DC are placed at four DDLS Data Science Nodes. These nodes are organized by four DDLS partner universities in Sweden and will develop research area specific data services, linking the DC-developed national data platform with strong local environments for data services and -infrastructure. The nodes have gone through formation and organization during the first phase of DDLS and are becoming fully operational in 2024. See *Table 3*.

Table 3. SciLifeLab Data Centre services for researchers.

Service	Description
SciLifeLab Data Repository	General data repository powered by Figshare. A service to publish data and other information with a persistent Digital Object Identifier (DOI). figshare.scilifelab.se
Swedish Pathogens Portal	National Pathogens data portal, providing a web portal for data, services, information and guidelines regarding infectious disease research and pandemic preparedness. Partner in the Pathogens platform together with EMBL-EBI. pathogens.se
SciLifeLab Data Platform	A technical environment offering data-centric tools and databases, service- and data hosting, as well as an overarching web portal to support and accelerate data-driven life science research in Sweden. data.scilifelab.se
SciLifeLab Serve	A platform developed in-house to host and share compute applications (for example Shiny and Dash apps), computational notebooks (Jupyter), and trained machine learning models (PyTorch, Tensorflow). serve.scilifelab.se
Hosting services	DC hosts storage and services for infrastructure units and the research community. DC manages the compute and storage resources and a Kubernetes-based container management system.
Data Stewardship Wizard	A web-based tool for storing and maintaining structured data management plans (DMPs), facilitating their use by SciLifeLab researchers and infrastructure users. The system supports DMP formats as required by the SciLifeLab research programmes and the Swedish Research Council. SciLifeLab participates in the national coordination of DMPs led by the Swedish Research Council.
SciLifeLab FAIR storage	A data sharing service powered by combining large scale object storage, data management plans, the data repository and data stewardship support. Researchers can allocate relative large data for long term use, provided continued FAIR sharing of research outputs and maintenance of updated DMP.

The future of digital research infrastructure at SciLifeLab

After the investments in SciLifeLab as a strategic research environment for life science came in 2010, it was soon realized that the impact of the research investment would be greatly elevated through national infrastructure services with access to support and instrumentation, not possible to procure for individual research groups. The national infrastructure funding for SciLifeLab started in 2014, and has since then built a strong and successful operation of currently ten major infrastructure platforms. These are serving the research field, but also driving technology development and access to cutting edge technologies, and strengthening recruitment of technical expertise to Sweden.

In 2021, the DDLS program started with a major funding from Knut and Alice Wallenberg foundation. The program has already greatly impacted the future of life science research in Sweden through building the competence in the field, but it is not a program aimed at building infrastructure in itself. It is now becoming increasingly clear that to enable the strong impact and international recognition that SciLifeLab has built in as a national infrastructure for experiment-driven science with technologies and instrument services and support, a similar investment in digital research infrastructure is needed. The Data Centre is now the digital arm of SciLifeLab research infrastructure organization, and national infrastructure platform support is also provided to, in particular, the Bioinformatics platform (NBIS) to operate in the area.

In the near future, we can expect that units will want to increasingly provide digital infrastructure such as domain specific Large Language Models (LLMs), customized development environments with tools for MLops, testbeds with software engineering support, reference data resources with added-value curation, and many other services. These would need operations with technical staff, data scientists, compute and storage infrastructure, legal support, information security processes, administration and economy management. This is very analogous to today's instrument-driven infrastructure platforms. The Data Centre now provides services that pilot this type of infrastructure, for example the SciLifeLab Serve system that can host community-developed computational services and AI models.

SciLifeLab will actively work to establish digital research infrastructure as a domain, and new investments that will enable the full scaling up to match the demands from the DDLS program coming into full operation.

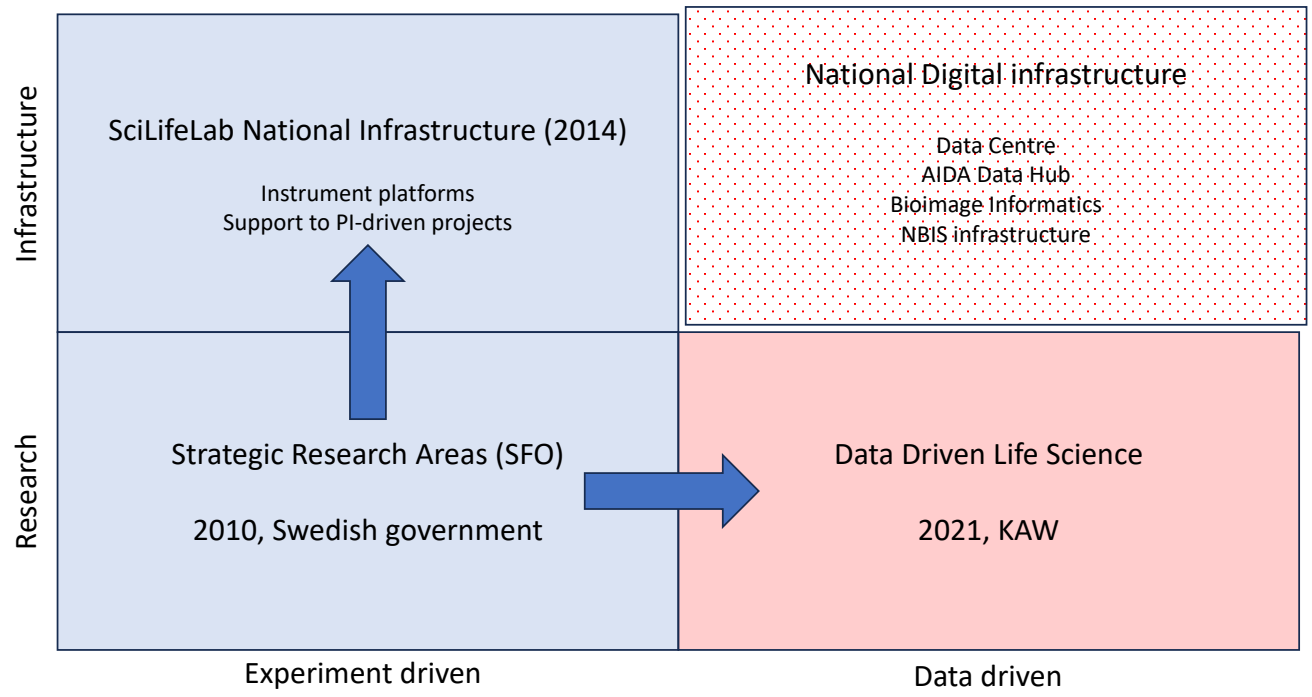


Figure 2. The recent transformation of life science research into data-driven science enabled by the DDLS research program has not yet been met with an investment in digital research infrastructure, apart from the DC services enabled by the DDLS and some specific investment by existing national infrastructure funding at SciLifeLab.





Part III. Platform Reports

Instructions to the Platforms

Below are the generic instructions given to the Platforms/Evaluation *Entities* on what items to primarily address in their reports.

- Platform organization and governance
- Overall platform development and key achievements 2021–2024
- Platform specific KPIs
- Overall platform plans 2025–2028
- Platform Strategic Budget 2025–2028
- Expertise, technologies, and services offered
- Competence/background of staff and plans for keeping/attracting competent staff scientists
- User base (current and expected 2025–2028)
- Procedure for prioritization of projects
- User fee model(s)
- Scientific environments and synergies with these (closely associated research groups as well as national/international networks). Provide a few examples of representative publications and indicate the association of the PI with the unit(s).
- Plans for development including new technologies/ service offerings 2025–2028
- Plans for data handling and analysis 2025–2028 including a plan on how to make data open and FAIR
- Current bottlenecks (if any) that prevent
  (i) the unit from meeting the user demand
  (ii) the data generated to be efficiently shared and transformed to knowledge, publications, and translations
- Describe how the above items will be addressed in the plans 2025–2028
- NBIS – current support and needs for 2025–2028.
- Data Centre – current support and needs for 2025–2028.
- Synergies and current/planned collaborations with and contributions to
  i) other SciLifeLab units and platforms
  ii) the SciLifeLab capabilities PM, PB and PLP
- Collaboration with industry, healthcare, and other organizations
- Current training offerings and plan for 2025–2028.
- Briefly motivate and explain budget requests 2025–2028

Infographics

In addition to the material submitted by the platforms according to the instructions above, Operation Office and Data Centre have prepared background information, statistics and metrics for the platforms and units that are presented in the report. The content is described below.

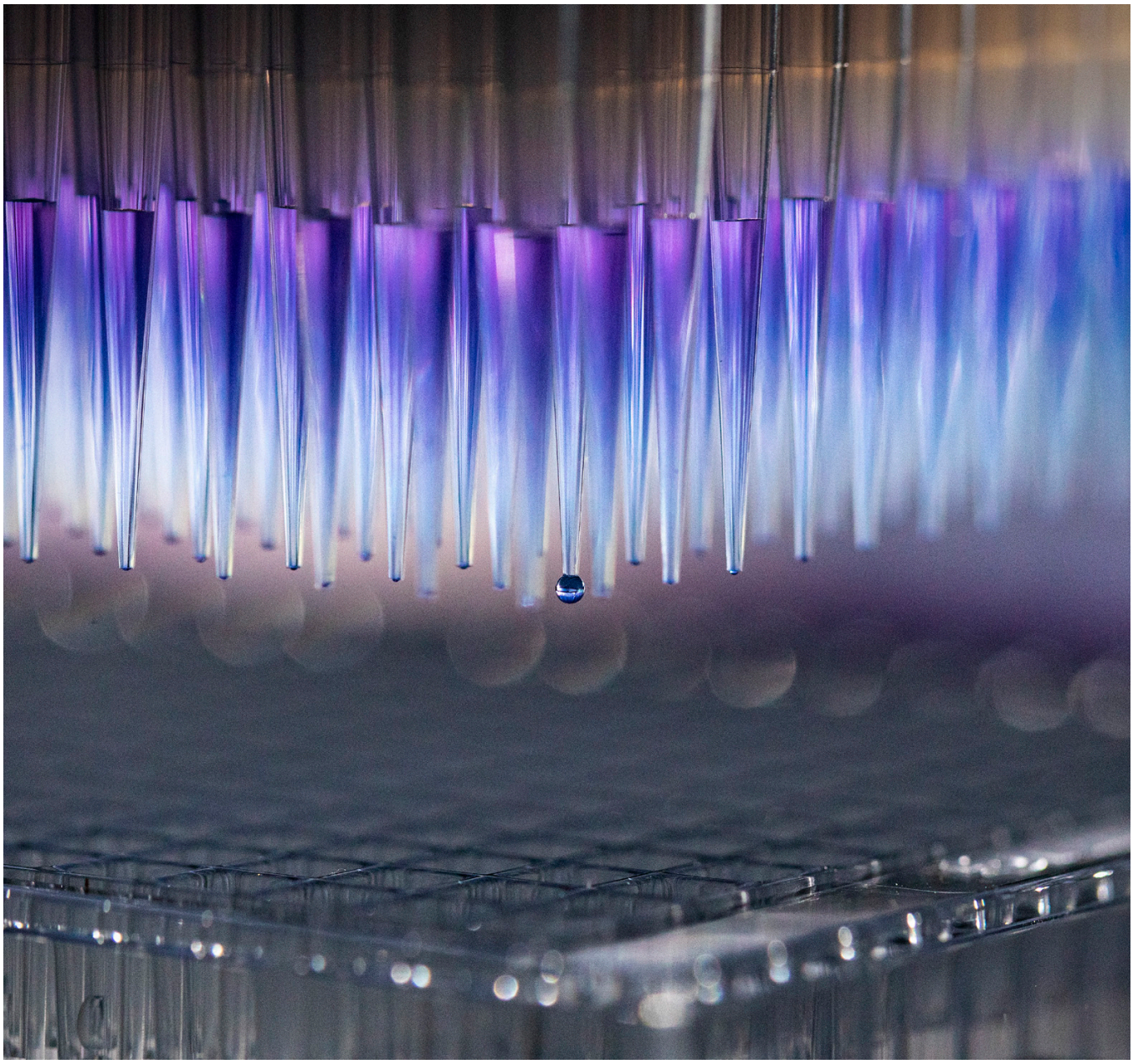
Platform Information (First Page for Each platform)

- Platform Director (PD), Platform Co-Director (Co-PD), and Platform Coordination Officer (PCO)
- Vision and mission statements
- Map of Sweden with location of units, including new suggested operations.
- Table with current SciLifeLab funding (2024) and requested annual SciLifeLab funding 2025–2028. The numbers are taken from the budgets provided from the platform and units, using the mean values for 2025–2028.
- Pie charts with the distribution of total current funding (2024) and distribution of total requested/ predicted annual funding 2025–2028 for the platform. The numbers are taken from the budgets provided from by the platform and units, using the mean values for 2025–2028.

Unit Infographics (Presented under the *Entity* for which the unit is represented)

- Head of Unit (HU) – The HU is responsible for the operations
- Host University(ies)
- Year when the unit became part of the SciLifeLab infrastructure
- SciLifeLab funding 2024
- Other funding 2024 (other infrastructure funding and instrument funding)
- User fees 2024 (predicted)
- Platform Scientific Director (PSD) – The PSD is a scientific advisor associated with the unit
- Links to the Unit web page and user publications in the SciLifeLab publication database
- Statistics on user publications 2021, 2022 and 2023 (by type of publication and journal impact factor, respectively)
- Number of Technology Development publications 2021–2023
- Total number of unique PIs and geographical user distribution 2021, 2022 and 2023.
- Unit-specific KPIs (up to three bullets provided by the unit).

Please note that we have not prepared user statistics for the new operations/technologies from the *Technology Survey* suggested to be included into the infrastructure but asked for this information to be reported separately in the description of these *Entities*.





Ancient DNA unit in Uppsala. Photo: Mikael Wallerstedt

Genomics Platform

Basic Information

Platform Director: Tuuli Lappalainen, KTH Royal Institute of Technology

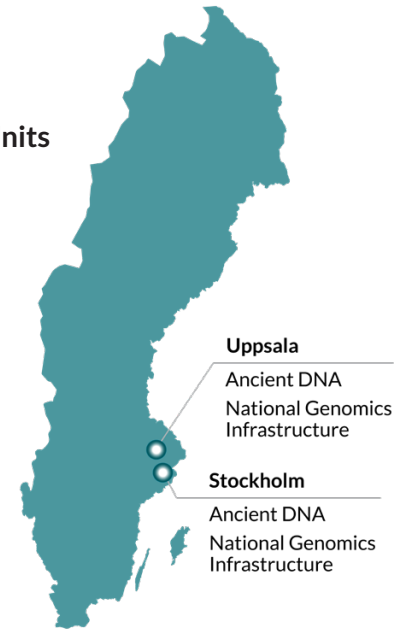
Platform Co-Director: Lars Feuk, Uppsala University

Platform Coordination Officer: Magnus Lundgren, Uppsala University

Platform vision: To provide world-leading expertise and technology in genomics to empower world-class research, industrial development, and applications that benefit society

Platform mission: To operate a world-leading genomics infrastructure that provides state-of-the-art technology and expertise, drives technology development, and supports its users in applying genomics across the spectrum of life sciences

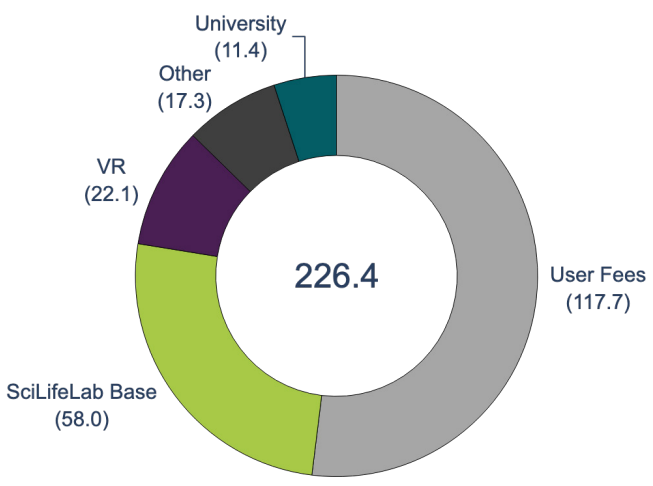
Location of Units



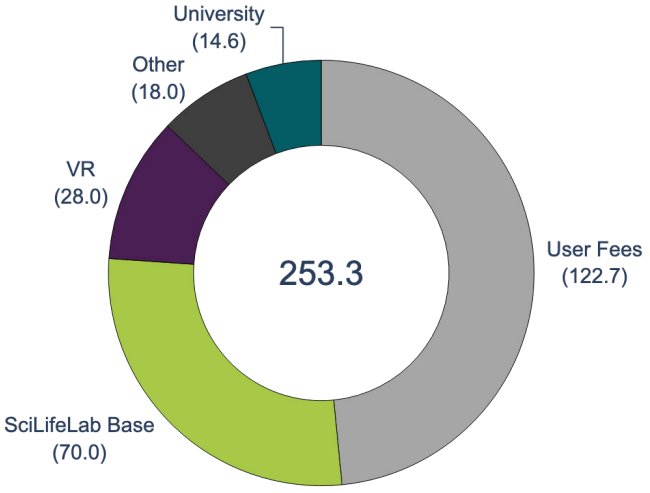
SciLifeLab Funding

Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Ancient DNA	3.1	4.6
National Genomics Infrastructure	53.3	63.0
Platform Strategic Funding	*1.6*	*2.4*
Total SciLifeLab Funding	**58.0**	**70.0**

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E1 Genomics

The Genomics Platform consists of two units: the National Genomics Infrastructure (NGI) and Ancient DNA, with closely related services in genomics expertise and technology. They enable internationally competitive research in a wide range of research fields across the entire spectrum of life sciences (*Figure* 1). In addition to providing access to cutting-edge services for genomics, a major part of the platform's operations is devoted to evaluating and introducing new methods, instruments and protocols in collaboration with users and companies, or through internal development. The platform provides comprehensive scientific support to its users and education and outreach in the form of seminars, workshops, and webinars for the Swedish research community, and participates in higher education courses. The infrastructure provides state-of-the art data processing, quality control, and delivery. The platform is a partner in many national and international collaborative projects and is a key part of the biomolecular research ecosystem in Sweden.

NGI is a large national infrastructure and one of the major sequencing centers in Europe with 87 FTE. It operates as one unit, integrating its two locations in Stockholm and Uppsala and the four consortium organizations, with KTH Royal Institute of Technology being the host institute. Ancient DNA provides internationally unique services with a staff of 4 FTE and locations in Stockholm and Uppsala. The Platform's main funding sources are SciLifeLab, the Swedish Research Council (VR), the host universities, and the Knut and Alice Wallenberg Foundation (KAW).

Platform organization and governance

The platform governance structure is shown in *Figure* 2. The platform steering group meets 6 times a year and makes major decisions and guides the platform strategy as defined in its Terms and Conditions document. In 2022 the platform's first dedicated scientific advisory board was appointed consisting of leading European experts in diverse areas on genomics, and they provide strategic advice via yearly meetings. The platform management group (PMG) is chaired by the platform director, Professor Tuuli Lappalainen (KTH), appointed in 2021, and a co-director Professor Lars Feuk (UU), appointed in 2022. The new platform leadership are active scientists with international visibility and significant competence in genomic technologies and applications as well as in infrastructure operations. The PMG meets every two weeks and has nearly daily communications via electronic channels. The PMG has overall operational responsibility and prepares platform strategy as well as grant applications and reports to funding agencies.

NGI is also a Swedish Research Council (VR) funded national infrastructure, with multiple subunits (*Figure* 2) and specific regulations regarding its governance. The Ancient DNA unit is part of the VR-funded Swedigarch and ArchLab national infrastructures. As NGI comprises a major part of the platform, the platform steering group, management group, director and co-director also serve in these roles for NGI as a VR infrastructure. Swedigarch and

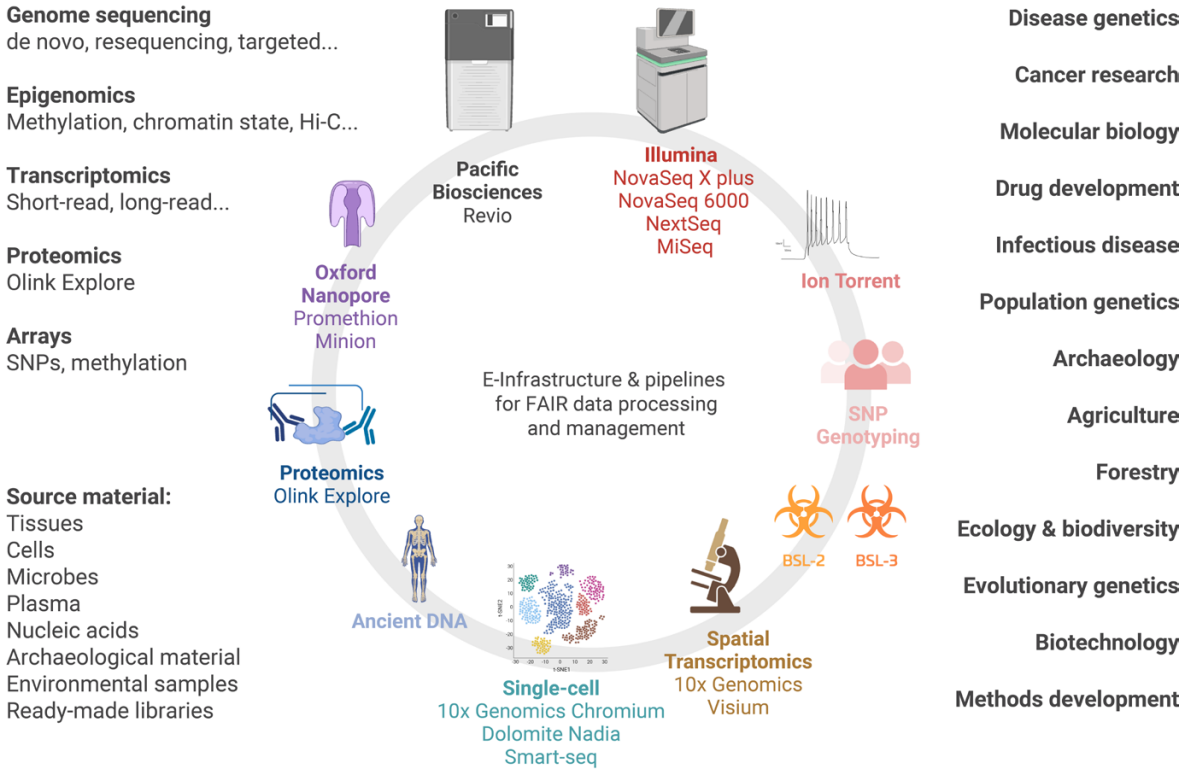


Figure 1. Technologies, services and applications of the Genomics platform in 2024.

ArchLab include operations outside of the platform, and they are governed by separate management and steering groups. Ancient DNA, as well as NGI's individual subunits, have internal decision-making structures for decisions that only concern each unit. The platform has a clearly defined structure of information flow and decision-making at each level (subunit, unit, management group, steering group, SciLifeLab management).

Platform development and achievements 2021–2024

During the last few years, the field and platform projects have shifted the balance from simply increasing sequencing throughput to more elaborate ways of turning various biological problems into sequencing readouts and applications, often with a higher informativeness and resolution per sample (*Figure 3*). These protocols and

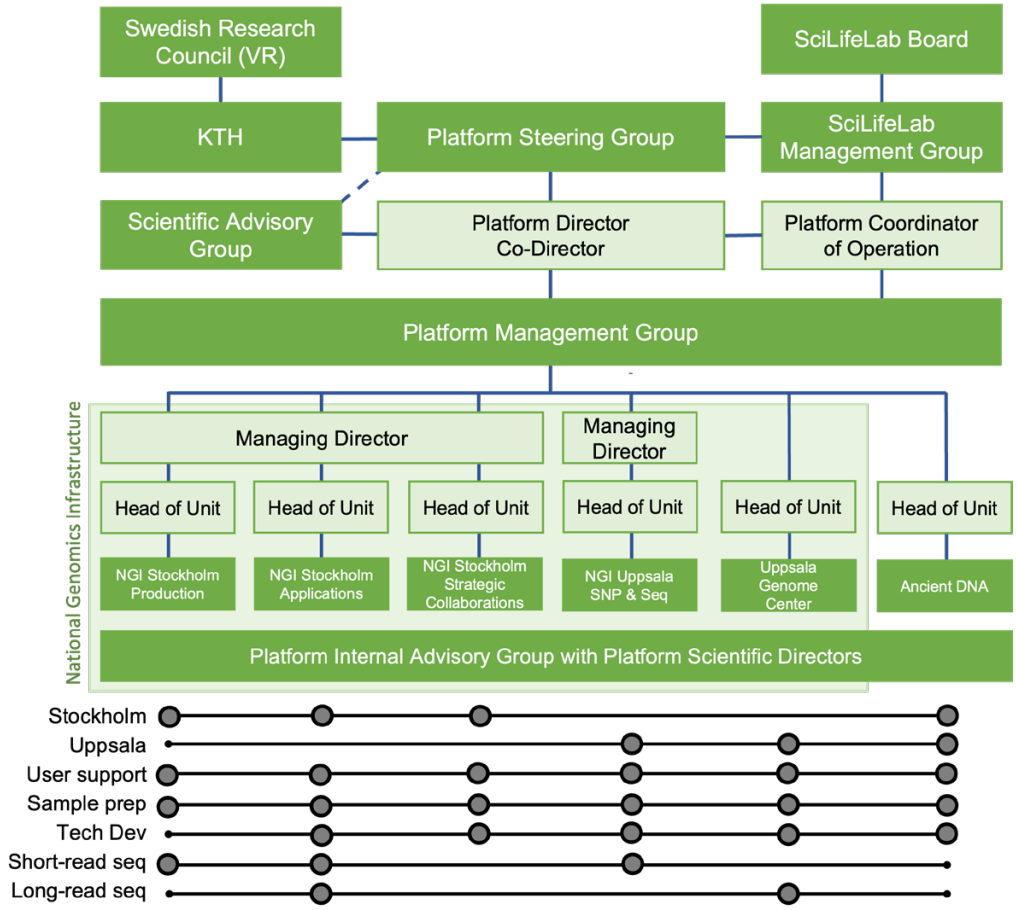


Figure 2. Genomics Platform organogram and unit focus areas.

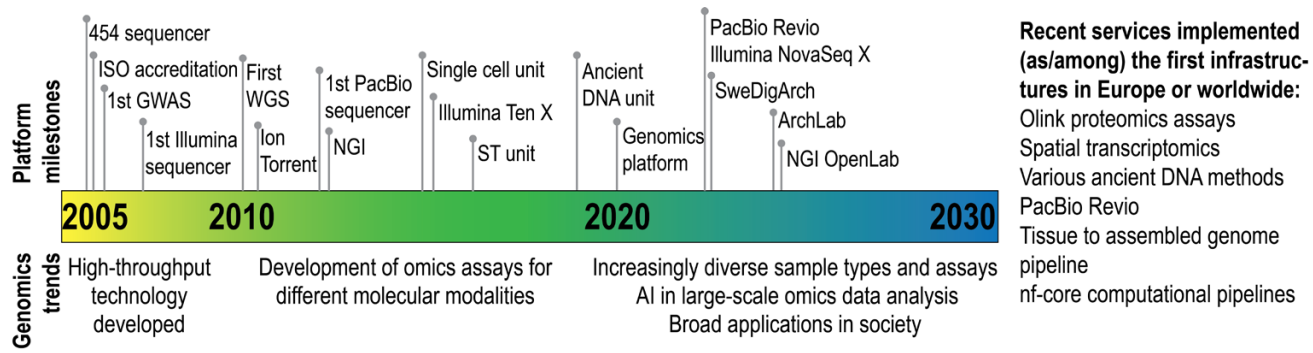


Figure 3. Development of the Genomics platform and major trends in genomics.

their development are highly labor-intensive rather than simply relying on higher data throughput. This transition is reflected in the number of samples, projects and sequenced bases.

Governance

The platform appointed a new director, professor Tuuli Lappalainen (KTH) in 2021, and a new co-director, professor Lars Feuk (Uppsala University) in 2022, bringing in a new generation of energetic and committed leadership. Furthermore, the platform has appointed its first Scientific Advisory Board consisting of leading genomics experts in Europe. Professor Stefan Bertilsson became chair of the steering group in 2022. Under the new leadership, the platform and its units have become more integrated under a shared vision, a clear decision-making structure, and active strategic development of partnerships, internal operations, and technology and service portfolio.

Development of the user base

The platform is widely used by researchers from all major universities and university colleges in Sweden, as well as by companies, and international researchers and others. In 2023 NGI performed 1084 user projects for 511 PIs, of which 235 were new users. These numbers correspond to a stable or slightly increasing long-term trend, including a steady proportion of new users. The PIs are from all major Swedish universities and several governmental research institutes, with NGI's consortium universities (KTH, KU, UU and SU) together representing 55% of all PIs. Ancient DNA initiated operation in 2019, and had 41 users in 2023, representing a 70% growth from 2022 with wide range of national and international academic researchers, museums, government organizations and companies. This reflects the increasing adoption of the methodology among biologists and archaeologists, not in the least after the Nobel Prize to Svante Pääbo in 2022 for his development and application of ancient DNA methodology.

Technologies in novel molecular modalities and sample types at NGI

The platform has co-developed and implemented multiple new technologies that expand the scope of genomics to new molecular modalities and finer resolutions (*Figure* 3). The Olink Explore technology uses a sequencing readout for a highly scalable protein quantification, and, working together with Olink Proteomics (a Swedish company), NGI was the first facility in the world to provide this rapidly expanding technology as a service in collaboration with the Proteomics Platform. In 2022-23 the formerly independent SciLifeLab Eukaryotic Single Cell and Microbial Single Cell units merged with NGI, resulting in dedicated single-cell genomics teams in the Stockholm and Uppsala sites. NGI thus provides a comprehensive single cell service that supports samples from most organisms using plate-based methods, 10x Genomics technology including emerging services in multi-omics and fixed cells, as well as other assays. NGI has been an early adopter of the world-leading 10x Genomics Visium technology and provides cutting-edge services for analysis of both fresh-frozen and FFPE tissues, and a new assay with Oxford Nanopore full-length transcriptome sequencing. NGI has strengthened its internal coordination of technology development by forming an active R&D group, and by recruiting a new head of strategic collaborations who works across the platform units.

Development of ancient DNA analysis

The ancient DNA unit has developed and implemented laboratory methods for analysis of DNA in soft tissue, sediments and other material, to complement analysis of bone material, which is the most common type of material analyzed by the unit. The unit is also performing an extensive comparison of single strand library preparation protocols for ancient DNA, which are important especially for highly degraded DNA, which will be followed by implementation of single strand library preparation as a service. The unit has developed and implemented data analysis services and pipelines relating to analysis of e.g., kinship, population genetics, metagenomics (incl. pathogens), and phenotypic traits. The Ancient DNA unit is also developing both laboratory and computational services relating to analysis of ancient and herbarium plant DNA, which is a rapidly expanding field.

Tissue to genome assembly pipeline

NGI developed a pipeline for high quality de novo genome assemblies, starting from extraction of high molecular weight DNA from diverse biospecimens followed by

sequencing by PacBio and/or ONT long read, Illumina Omni-C and RNA sequencing, and finishing with assembly and annotation of the genome. Solutions have been put in place so that different experimental protocols, run at different NGI sites, are coordinated and applied to each sample. The bioinformatics pipeline was developed in close collaboration with NBIS. Solutions for sharing data between the two national infrastructures have been developed that do not require active user involvement until an finished annotated assembly is delivered.

New generation of sequencing instruments

NGI is one of the first European genomics facilities acquiring the Illumina NovaSeq X Plus and PacBio Revio instruments, with both instrument types installed in the spring of 2023. These sequencing instruments represent the latest generation of technology in short- and long-read sequencing with dramatic improvements in throughput and cost. These instrument purchases were supported by the Swedish Research Council, SciLifeLab and the Knut and Alice Wallenberg Foundation. NGI is in the process of acquiring the Element Aviti instrument, which will be installed in 2024, further diversifying the sequencing instrumentation at the platform.

Bioinformatics

The large-scale data generation at NGI has required a parallel development of tools and pipelines for data handling and analysis. The platform actively supports the sequencing data analysis core- and user-community for example with Arteria, an open-source automation system for sequencing data processing developed for sequencing core facilities (arteria-project.github.io; Dahlberg et al., 2019 GigaScience) and the nf-core project, a community-based and highly successful effort initiated at NGI to collect curated data analysis pipelines (nf-co.re; Ewels et al., 2020 Nature Biotechnology). The nf-core project, founded in 2018 to collaborate and curate a set of best-practice bioinformatics pipelines, hosts > 50 pipelines for different types of analysis, with > 8000 users on Slack and 4000 twitter followers. The SAREK pipeline for germline or somatic variant detection from WGS data is one of the popular nf-core pipelines developed in part by NGI (sarek.scilifelab.se; (Garcia et al., 2020 F1000Research). Another example of software originally developed at NGI includes MultiQC, a tool for aggregating the results from bioinformatics analyses into a single report (multiqc.info; (Ewels et al., 2016 Bioinformatics).

New e-infrastructure and data delivery system

The four NGI host universities provided funding in 2021 to establish a modern HPC cluster (Miarka) for NGI, together with its storage system (Vulpes), hosted by UPPMAX. The new cluster also included a GPU node. In 2021 the SciLifeLab Data Centre and NGI co-developed a new Data Delivery System for user data.

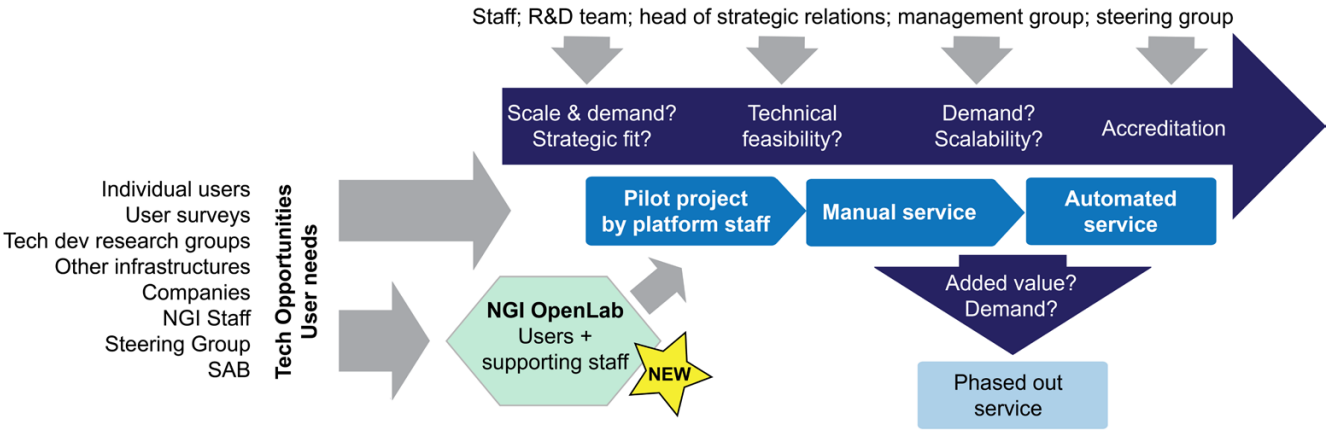


Figure 4. The flow of assays and technologies from novel opportunities to established services.

Infographics: Statistics and Metrics for Genomics Units

Ancient DNA

Read more: Webpage, Publications Database

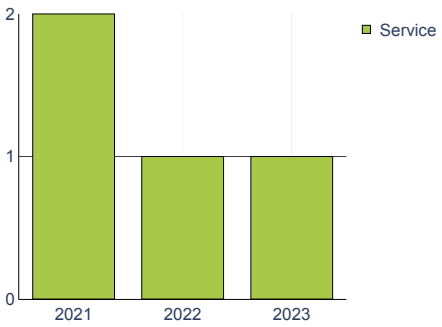
Basic Information

HU: Magnus Lundgren
Host University: UU, SU
SciLifeLab unit since: 2017
FTEs: 3.83
PSD: Mattias Jakobsson, Anders Götherström

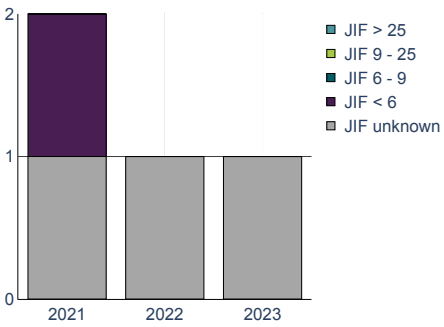
Funding 2023 (kSEK)

SciLifeLab: 3000
Other: 1433
User Fees: 771

Publications by category

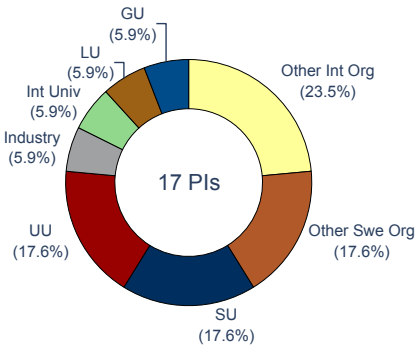


Publications by JIF

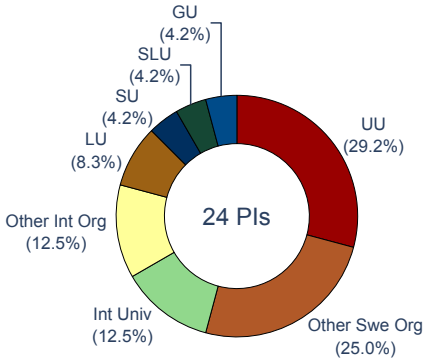


No. of Tech Dev Publications 2021 - 2023: 1

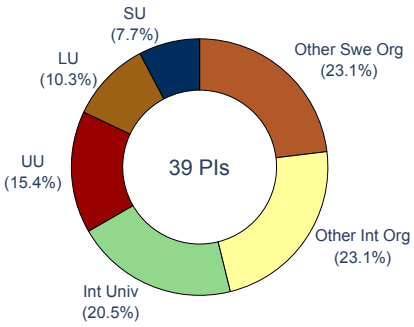
Users 2021



Users 2022



Users 2023



- *Offers for 174 user projects provided, with 90 projects completed or initiated (61 with users in Sweden)*
- *Analysis of 773 individuals completed or initiated as part of user projects*
- *Services provided to 52 unique users, representing 33 organizations in 15 countries*

National Genomics Infrastructurew (cont. on next page)

Read more: Webpage, Publications Database

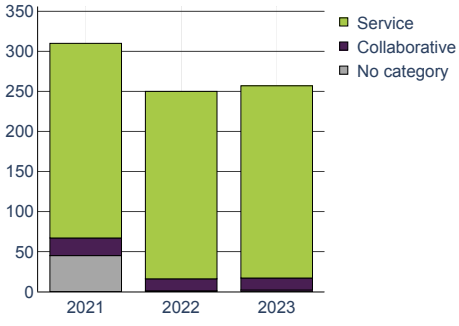
Basic Information

HU: Tuuli Lappalainen (Genomics PD), Lars Feuk (Genomics Co-PD), Ellen Sherwood (MD), Jessica Nordlund (MD), Susanne Hellstedt Kerje, Ulrika Liljedahl, Anja Mezger, Robert Månsson
Host University: KI, KTH, SU, UU
SciLifeLab unit since: 2013
FTEs: 86.95
PSD: Johan Ankarklev, Fabien Burki, Carsten Daub, Lars Feuk, Ulf Gyllensten, Joakim Lundeberg, Jessica Nordlund, Ellen Sherwood

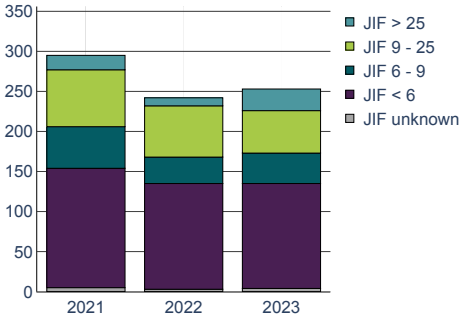
Funding 2023 (kSEK)

SciLifeLab: 51500
Other: 47697
User Fees: 115199

Publications by category

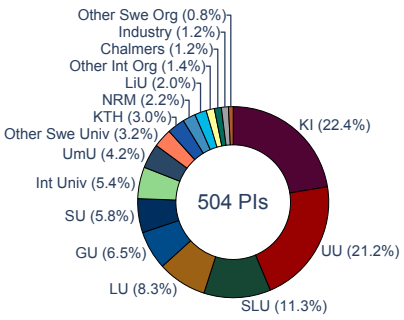


Publications by JIF

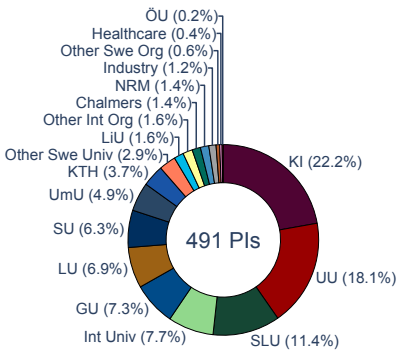


No. of Tech Dev Publications 2021 - 2023: 8

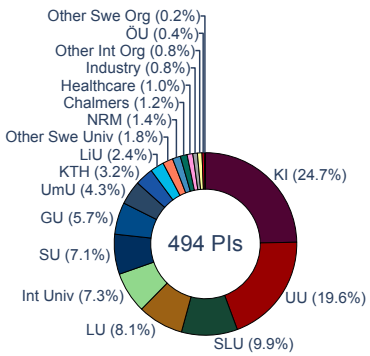
Users 2021



Users 2022

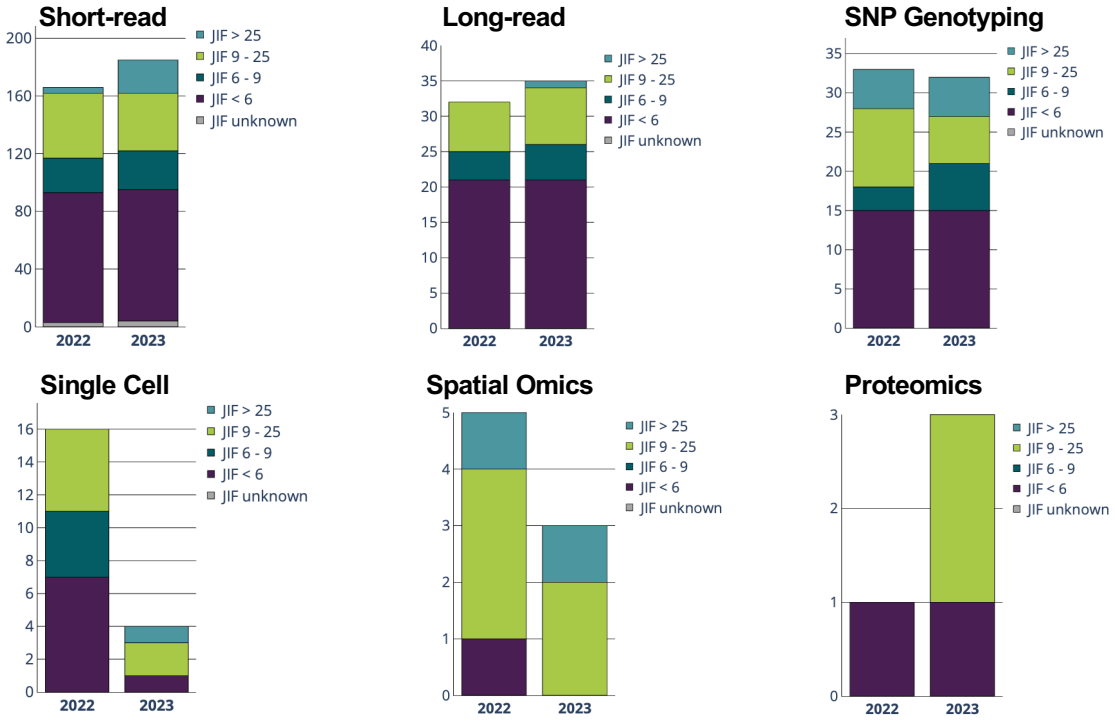


Users 2023

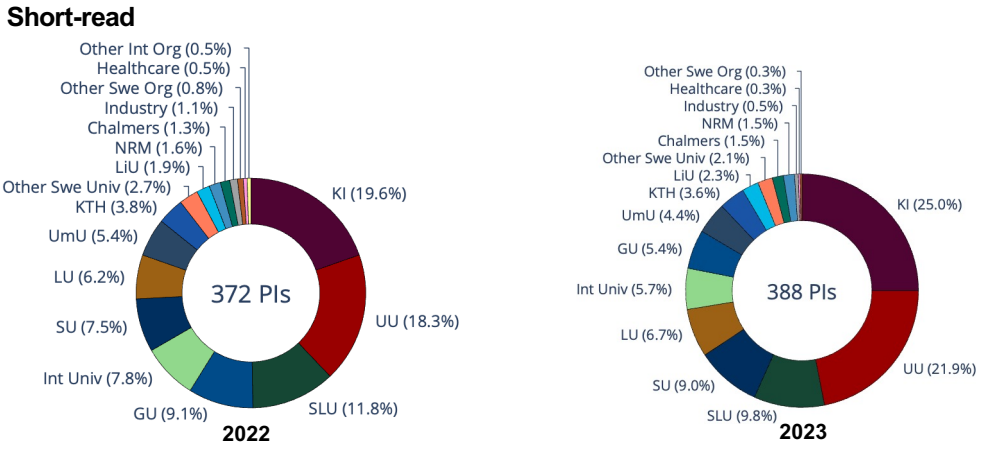


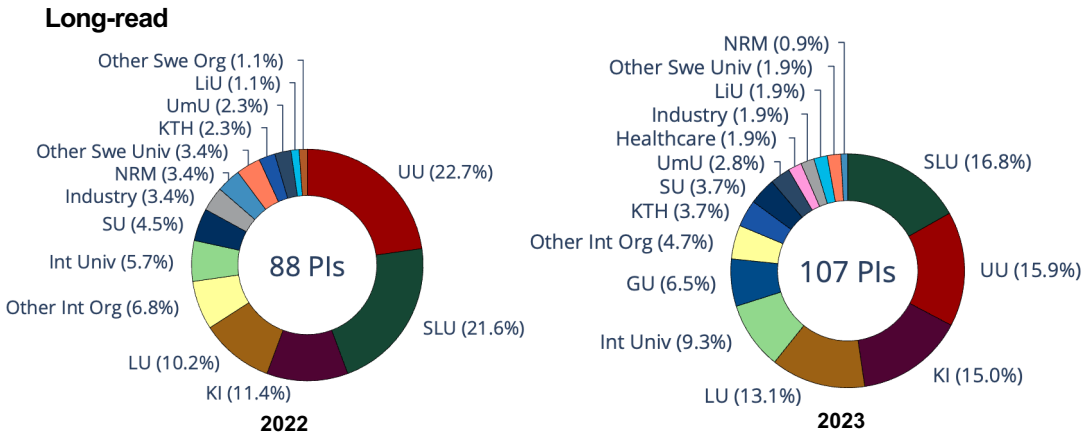
- *In 2023, NGI performed 1084 user projects for 511 PIs, of which 45% are not from NGIs consortium universities*
- *A steady number of hundreds of new users annually (235 new users in 2023)*
- *In 2023, NGI analyzed 60,388 samples in sequencing projects and 20,022 in genotyping projects*

Publications by Technology Category 2022–2023

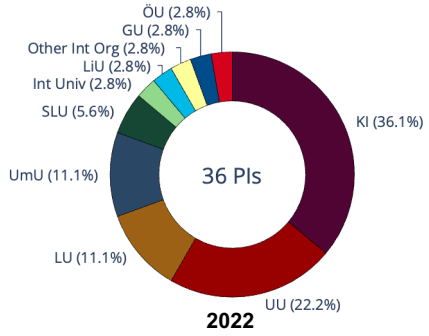


Users by Technology Category 2022–2023

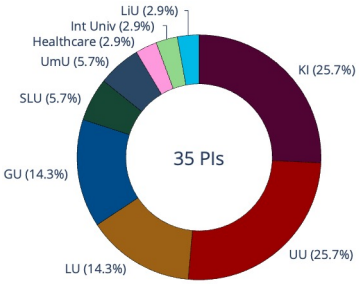




SNP Genotyping

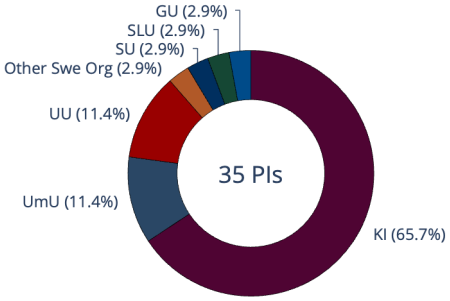


2022

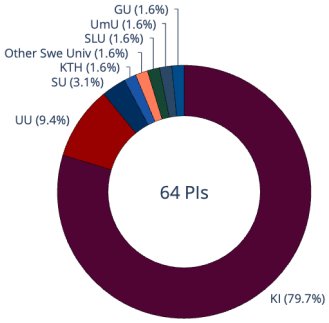


2023

Single Cell

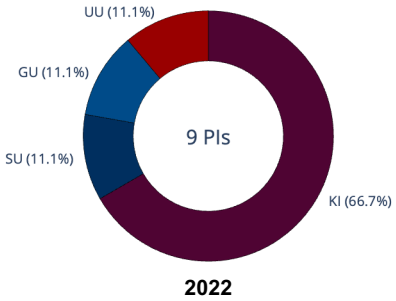


2022

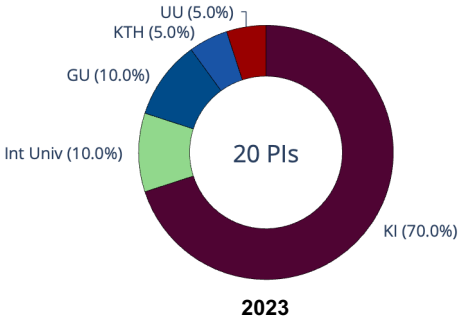


2023

Spatial Omics

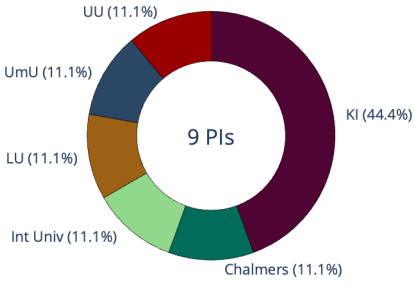


2022

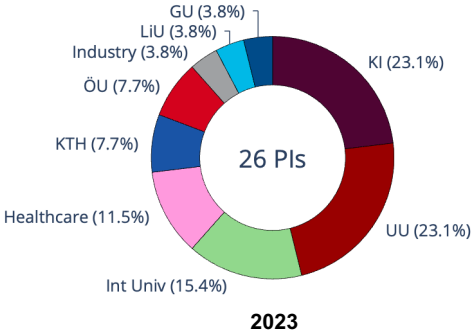


2023

Proteomics



2022



2023

Platform plans 2025-2028

The Genomics platform seeks to continue the high quality, quantity and scope of services in the 2025-2028 period. Working in a rapidly developing field, new and improved methods and analysis tools are continuously becoming available, and the Genomics platform is in an excellent position to offer the best assays to the Swedish and international research community. The platform seeks to strengthen its role not only as a service provider but as a hub of expertise and implement new collaborative ways to serve its users across diverse fields of biomolecular science.

New service model: NGI OpenLab

In the funding period 2025-2028, the platform seeks to establish a new way to support its users by establishing NGI OpenLab, an accessible genomics lab space with instrumentation and consultative staff support. This will allow users to prepare samples for genomics assays and test new methods independently or with guidance from NGI's experts. NGI OpenLab will bridge an increasing demand of researcher needs especially for highly specialized ad hoc protocols that are not feasible for NGI staff to test and set up as standard services (*Figure* 4). Metagenomics, microbiome analysis, biodiversity, functional genomics, single cell assays and technology development are examples of areas where users would greatly benefit from NGI OpenLab. The increasing number of assays using live tissue or cells as starting material is an area where we see the OpenLab as vital. Importantly, NGI OpenLab would also allow NGI to host courses for hands-on training in genomics, which is currently limited by restricted access and space in the ISO17025 accredited facilities needed for high-throughput data production. This training would educate and empower the research community to pursue cutting-edge genomics methods and applications.

We seek to pilot OpenLab in BMC Uppsala in 2024 and expand it to Solna in 2025-2028 when suitable premises become available. It is available to all users in Sweden, and we envision that some users may travel to Uppsala or Stockholm to use the OpenLab. In the future, the concept could be further expanded in the future to national SciLifeLab sites, potentially in collaboration with the Clinical Genomics Platform and SciLifeLab Capabilities, and even adopted by platforms outside the realm of genomic assays. We envision a powerful combination of local genomics expertise and facilities for sample preparation - sometimes with remote consultation with experts elsewhere in the country - and subsequent shipping to NGI for analysis that requires expensive large-scale instrumentation.

Expertise, technologies, and services

The Genomics platform enables internationally competitive research in a wide range of research fields, supported by the platform's service portfolio of different technologies (*Figure* 5) and the comprehensive support in project planning. In addition to the fields focused on specific biological applications, many Platform users work on genomics technology development. The platform assists projects on all scales using the most modern technology and comprehensive instrumentation (*Figure* 6).

As a large and decade-old infrastructure, NGI is not reliant on individual research groups in its strategic or scientific development. However, it collaborates closely with numerous academic research groups working on technology development and applications, especially within the vibrant SciLifeLab technology development community. The Ancient DNA unit is operationally independent and benefits from and contributes to the strong ancient DNA research environments at Uppsala University Human Evolution research program and the Stockholm University/Swedish Museum of Natural History Centre for palaeogenetics.

Key services and technologies and development plans for 2025-2028 are described below.

Project planning. Consultative support to the users is one of the most important platform services, and a unique feature not available from e.g. commercial providers. The platform's project coordinators meet with users to ensure an optimal project design to achieve the best possible results and advice on current best practices and methods for the users to optimize their use of time, biospecimens and funding. Since 2020, most project consultations are conducted remotely via Zoom. During the 2025-2028 period we will explore how to further enhance user support across the country, potentially with a more networked model together with the Clinical Genomics platform and SciLifeLab nodes.

New sequencing technologies. There are several notable recent advances in sequencing technology. For instance, a 2023 study proposed a method to detect proteins and their modifications by passing them through nanopores, similar to DNA sequencing (Martin-Baniandres,.et al. Nat. Nanotechnol. 2023). Emerging sequencing companies, Element Biosciences and Singular Genomics, are also developing instruments that can be used for other types of molecules besides DNA, often in a spatial context. The platform is currently testing these technologies and anticipates many opportunities to arise in 2025-28.

Human whole genome sequencing. NGI offers several options for human whole genome sequencing (WGS). High throughput human genome re-sequencing is typically performed using automated protocols and the Illumina NovaSeq sequencing instruments. WGS is also offered using long-read sequencing on both PacBio Revio and Oxford Nanopore PromethION, allowing for reference independent de novo assembly and improved structural variation analysis. Long-read WGS is a rapidly growing application due to the increases in quality and affordability, as demonstrated by workflow for PacBio Revio WGS of rare disease patient samples, developed by NGI in collaboration with Genomics Medicine Sweden (Eisfeldt et al. medrXiv 2023).

	Complex diseases	Rare disease & cancer risk	Molecular biology	Cancer biology	Infectious diseases	Ecology & biodiversity	Evolutionary genomics	Agriculture and forestry	Archaeo-logy	Dominant technology	Typical specimens
WGS short read	**	***		***	**	**	**	***	*	Illumina	DNA, seq libraries
WGS long read		**		**	*	*	***	**		PacBio, ONT	DNA, tissue
Targeted sequencing	*	***		**	***	*	*	*		All seq platforms	DNA
SNP genotyping	***							**		Illumina array	DNA
RNA-seq short read	***	**	***	***	**	**			*	Various prep + Illumina	RNA
RNA-seq long read			**	**		*	***			PacBio, ONT	RNA, tissue
Proteomics	***	**	*	***						Olink + Illumina	Plasma
Epigenomics	***	*	***	***						Various	Tissue, DNA, etc
scRNA-seq	*	*	***	***	*					10x, others + Illumina	(Fixed) cells
Microbial genomics			**		***	***	*		*	Various + Illumina	Tissue, soil etc. extracts
Spatial transcriptomics		*	**	***						10x Visium + Illumina	Tissue
Ancient DNA					*	*	**	*	***	Custom prep + Illumina	Bone, ancient tissue
User-made libraries	*	*	***	**	*	*	*	*	**	Illumina	Sequencing library
Typical species	Human	Human	Human, model	Human	Microbes, humans	All non-human	All non-human	Domestic species, trees	Human		

Figure 5. Summary of the Genomics Platform technologies and the importance of each of them across different fields and applications. Altogether, the platform provides all major genomics assays and technology platforms and serves the entire scope of biomolecular science

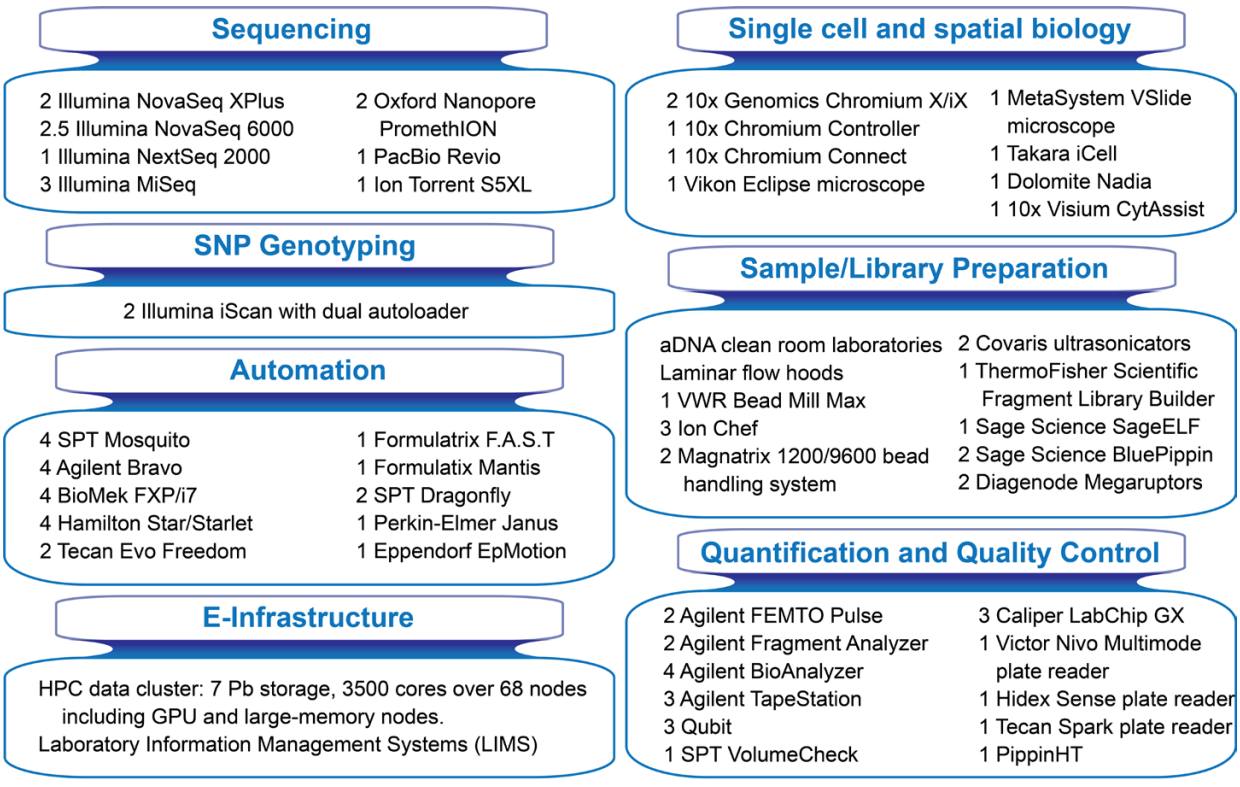


Figure 6. Genomics platform instrumentation (Q2 2024)

Non-human eukaryotic genome sequencing. Sequencing of non-human genomes for model organism research, evolutionary biology and comparative genomics is performed on all NGI sequencing platforms. NGI has generated a pipeline for high quality de novo genome assemblies, starting from extraction of high molecular weight DNA from diverse biospecimens followed by sequencing by PacBio HiFi or ONT long read, Illumina Omni-C and RNA sequencing, and finishing with assembly and annotation of the genome (the latter performed by NBIS). The increased capacity of the PacBio Revio and the platform's funding and involvement in the Biodiversity Genomics Europe consortium will drive further development in this field.

Microarrays and targeted sequencing. SNP genotyping is offered on all scales, from few to millions of SNPs, in projects ranging from 10s to tens of thousands of samples. DNA methylation analysis of a genome-wide panel of CpG sites accounts for 4,000 of the ~40,000 samples genotyped on average per year at NGI. All of the SNP genotyping and DNA methylation array processes are automated and supported by liquid handling robots and an in-house developed laboratory information system, Chiasma. There is continued demand and strategic interests in maintaining microarray services. NGI also offers a range of targeted sequencing applications including RAD-seq, exome sequencing and amplicon sequencing with both long- and short-read instruments. Despite decreasing sequencing costs, these remain valuable approaches, for example by enabling affordable population genetics in species that lack SNP arrays (e.g., Creel 2019 Sci Rep), and by enabling target enrichment combined with long-read sequencing for clinical diagnostics (Höijer et al., 2022 Nature Communications).

Functional Genomics. RNA sequencing is one of the most popular assays at NGI, and analysis of epigenetic marks provides further functional readouts. The main applications are strand-specific RNA sequencing, DNA methylation analysis using enzymatic conversion (Methyl-seq), microRNA sequencing, ATAC-seq and ChIP-seq. On PacBio Revio and Oxford Nanopore PromethION, full-length transcript sequencing using long reads is offered, as well as methylation pattern analysis of native DNA. New protocols for direct native RNA sequencing with Oxford Nanopore will enable improved isoform analysis and epitranscriptomic readout. We foresee ongoing interest and support for diverse functional genomics assays.

Microbial genomics and metagenomics. Genomics has become a powerful tool for analyzing microbial communities and their interactions with the environment and/or host organisms. Small microbial genomes are sequenced on Illumina, PacBio, and Oxford Nanopore sequencers, with ongoing technology development to decrease library preparation cost. There is also a steady demand in metagenomics, including e.g. total DNA sequencing or targeted sequencing of 16S ribosomal RNA genes as well as microbial single cell approaches. The platform is working on methods development to advance these analyses, which will also benefit from NGI Open where users can develop tailored solutions for specific organisms and sample types.

Single cell genomics. NGI is the national hub for single cell services within SciLifeLab, coordinating with other platforms and units across the organization. In 2022-23 the formerly independent Eukaryotic Single Cell and Microbial Single Cell units merged with NGI, forming a strong hub for single-cell analyses. NGI aims to continue offering a comprehensive single cell service that supports samples from most eukaryotic and prokaryotic organisms, using plate-based methods (Smart-Seq, whole genome amplification assays, single-cell WGBS), 10x Genomics technology, and emerging technologies enabling multi-omics readsouts and for fixed cells. NGI will continue to develop and evaluate methods for cutting-edge single cell analysis, recent examples include WGS of single cells (Hård et al., 2023, Nature Communications) and highly multiplexed barcoding of scRNA-seq libraries (Gezelius et al., 2024, NAR Genomics and Bioinformatics). Due to increased interest and decreasing cost of single cell WGS, in particular from the planetary biology community, NGI is currently evaluating different single-cell WGS solutions in collaboration with SciLifeLab researchers.

Spatial sequencing. Spatial transcriptomics technology services are operationally and financially part of NGI, with the Spatial Biology platform contributing to the strategic development of this technology. We foresee ongoing development of cutting-edge services in spatial sequencing and combination of multiple spatial technologies as a collaboration between the two platforms. We are currently evaluating expanding multi-omics readouts with a new 10X Genomics multiplexed protein-labeling kit (31 targets + custom antibodies), which fits with regular Visium workflow, and the Pixelgen technology (80 cell-surface proteins) in collaboration with the Proteomics Platform. We will explore new approaches to increase resolution and capture area, including with new sequencing instruments that provide spatial data. We will establish assays that combine the standard Visium workflow with bacterial and fungal RNA detection, enabling the study of host-pathogen interactions (e.g., Sounart et al. 2023 Genome Biology), and expand our services to plant tissues.

Affinity Proteomics. The Olink Proteomics Explore assay combines proximity extension assay with a sequencing readout for measuring protein abundance. In 2021 NGI spearheaded a service in collaboration with the SciLifeLab Affinity Proteomics Unit Uppsala from the Clinical Proteomics and Immunology platform, and thus became the first certified core lab in Europe to offer high-throughput multiplexed protein analysis by sequencing.

This has been very successful (e.g., Alvez et al. 2023 Nature Communications) and we anticipate increased demand for this growing technology area.

Ancient DNA. The ancient DNA unit provides services relating to laboratory and computational analysis of ancient DNA in different types of human and animal remains and sediments. The services include concrete advice on how ancient DNA analysis can support research in archaeology, biology, medicine and related areas. The unit advice on selection of samples for ancient DNA analysis and have extensive experience of optimal sampling of the irreplaceable material studied. The unit performs extraction of DNA and library preparation procedures appropriate for ancient DNA in a cleanroom environment. Data analysis services include validation of ancient DNA and analysis sex chromosomes, kinship, maternal/paternal ancestry, prevalence of pathogen DNA, and traits, as well as metagenomic and population genetic analyses. The unit can provide complete analysis packages to address specific research questions or requested desired parts of such projects. Future developments include comparing, developing and implementing procedures for single strand library preparation for the benefit of analysis of especially highly degraded DNA. The unit will also develop and implement new and improved services relating to analysis of sedimentary ancient DNA, and ancient and herbarium plant DNA, with regard to both laboratory procedures and data analysis. Procedures for metagenomic data analysis, e.g., for analysis of pathogens inhuman and animal remains, will be developed to reduce computational load and analysis time.

Computational tools for automated processing and analysis of sequencing data. Increasing data volumes in genomics necessitates automated data processing systems. As described above, the platform actively supports the sequencing data analysis core- and user-community and initiated and developed the nf-core project (nf-co.re; Ewels et al., 2020 Nature Biotechnology). With funding from the Chan Zuckerberg Initiative Essential Open-source Software and accompanying Diversity and Inclusion programs, NGI continues to be a partner in developing the community and backbone of nf-core. Overall, the nf-core community continues to build every kind of bioinformatics pipeline for new sequencing instruments and data types. NGI has recently introduced Sequera Platform into its operation; a web-based launch and monitoring tool for NextFlow, leading the way towards a hybrid HPC/cloud environment, which later can be shifted towards cloud-based analysis. As the NGI HPC cluster ages, there will be a gradual transition to cloud computing during the 2025-2028 period. This will require investment in development of tailored tools and pipelines that make local systems compatible with cloud-based resources, while maintaining data integrity and security.

Quality assurance

The platform has implemented several practices to fulfill its mission to deliver data of the highest quality in a timeframe that is suitable for the users. Many of NGI's sequencing and genotyping processes have been accredited by SWEDAC according to the ISO/IEC 17025 quality standard. SWEDAC audits each site annually. In addition to the laboratory and bioinformatics methods, accreditation encompasses instruments, premises, management, computer systems, data security, contacts with users and suppliers, continuous development, and staff education. These organizational practices also benefit assays that are not themselves accredited. Data is delivered to the users after in-house quality control and includes a detailed metadata report of sample processing steps. The Ancient DNA unit will recruit additional staff for laboratory work, bioinformatic analysis and project coordination to meet the increasing demand for services and allow improved turn-around times for projects. Further, with increasing project volume, the unit will implement improved procedures and systems for project management.

Research and Development

The platform has a strong track record of development of new genomics protocols, in addition to adoption and setup of new methods from commercial providers. NGI has an internal R&D team that follows the latest developments in the field, plans R&D projects, and pursues opportunities for collaborations and external funding. The Ancient DNA unit pursues technology development projects alongside user projects and in collaborative projects. As shown in *Figure* 4, the platform systematically collects input of user needs and novel technologies from multiple sources, with multiple evaluation steps for assays to move from pilot projects to established assays. NGI OpenLab will also provide data of emerging assays for the platform's portfolio development (see above). In addition to assay or domain-specific technology development discussed above, key areas of methods development that are relevant across diverse technologies include:

Decreasing the cost of library preparation, which has kept constant while sequencing costs have decreased. NGI is currently working on adapting the splinted-ligation library preparation method, SPLAT, developed at NGI (Raine et al., 2017 Nucleic Acids Research, Raine et al., 2022 Sci Rep) into a highly scalable, flexible library preparation workflow for pooled sequencing of large numbers of barcoded samples (upSPLAT-seq). Another way we minimize costs is by automatization (including in long-read sequencing) and miniaturization of library preparation reactions, enabled by new pipetting robots and staff with expertise in robot programming. Already implemented methods for cost-efficient sequencing of many samples include RAD-seq and a concept we call 'User QC' where we do no QC of samples

or libraries prior to library preparation or sequencing. This last method can be run using half reactions to further reduce the cost for the user.

Large-scale pooling to utilize high-throughput sequencing. Efficient use of the increasing sequencing throughput– such as 25 billion reads from the NovaSeq X 25B flow cell – across projects of all scales requires efficient pooling of samples and projects without compromising quality. Here, NGI is developing methods for a cost-efficient and rapid library pool quantity and quality detection with Oxford Nanopore MinIon prior to a massive, expensive sequencing run. This extra QC step will allow for pooling of user made library pools seeing how the indexes used will be certain and can be run as a stand-alone service, or as a compulsory step for ready-made library users needing less data than one unit (lane or flow cell) of sequencing.

Tools for laboratory and data management to track samples, annotate data and manage projects is an area where NGI has a long track-record. It is regarded by other core facilities as a leader in the field of laboratory management, evidenced by the numerous visits from other core facilities. NGI develops software for management systems and opens these systems to the public. For example, the NGI application programming interface package Genologics (pypi.org/project/genologics) allows automated interaction with the Illumina Basespace Clarity LIMS and has become widely used by other sequencing facilities worldwide. The Ancient DNA unit is reviewing options for LIMS and data management as operation is expanding.

Staff development

The competence and experience of the platform staff in laboratory analysis, bioinformatic processing, project planning and management of operation have been critical to the success of the Genomics platform. Maintaining an excellent, safe and inclusive workplace environment and opportunities for staff development continue to be of top priority for the platform. The platform closely follows and contributes to the ongoing development of career pathways for staff scientists and infrastructure personnel at Swedish universities. The platform has programs for staff exchange and rotation of tasks, and support participation in conferences and educational programs as well as in networking in fields relating to the platform's operation.

User base, projects and fees

The Genomics platform is open to all Swedish researchers on equal terms and accepts all projects that meet standards for ethical and relevant research. The platform also accepts international projects as service projects if capacity is available, or as part of international collaborations or infrastructures. Projects that require more than 5% of the capacity of the requested technology platform are subjected to Steering Group approval. Projects are entered into the queue on a first come-first serve basis after the quality control of samples, with a fast track for sequencing ready-made libraries.

The platform charges user fees to cover reagent costs as well as a subset of the operating costs. The user fees for Swedish academic users are subsidized relatively to the total cost, which is charged from industry and international users. In 2023-2024 the platform has been preparing a revision of its user fee model to increase equity towards users of different assays, to stabilize cost recovery against fluctuations e.g. in reagent costs, and to increase transparency that allows better support for strategically important services. This model will be implemented gradually during 2024-2025. The Ancient DNA unit will revise its user fee model to allow a larger percentage of the unit's funding to consist of user fees and meet the increasing range and volume of user projects.

While we do not anticipate major changes in our user base, we foresee and pursue growth particularly in the following user segments: a) Ancient DNA users - the trend has been increasing, the technology is more established, and the applications are getting wider recognition; b) Planetary biology community - already a major user group, with the planned investments in technology and applications creating novel opportunities; c) Industry users - with increasing awareness of genomics services particularly among small and medium-sized companies.

Training and outreach

The platform provides multiple forms of training and outreach activities and has historically had an important role in increasing the competence in genomics in Sweden. This includes helping researchers that are new to genomics to enter the field and pursue successful projects, as well as education of expert users in state-of-the-art methods of the rapidly evolving field.

Project planning meetings. When a user contacts the platform via the web portal or email, the project representatives are offered a consultation meeting with project coordinators. This can take place in advance of scientists' grant applications or at the stage of project initiation. The goal is to ensure an optimal project design to achieve the best possible results and provide advice on current best practices and methods for the users to optimize their use of time, biospecimens and funding. This direct communication with researchers has an important educational function and disseminates information about the platform services to the Swedish research community. Project planning meetings are one of the most important activities of the platform.

Seminars and meetings. The platform regularly organizes a wide variety of webinars, seminars, and scientific meetings, often in collaboration with technology providers. Topics of recent events range from ancient DNA to plasma proteomics. The largest event arranged by the platform is

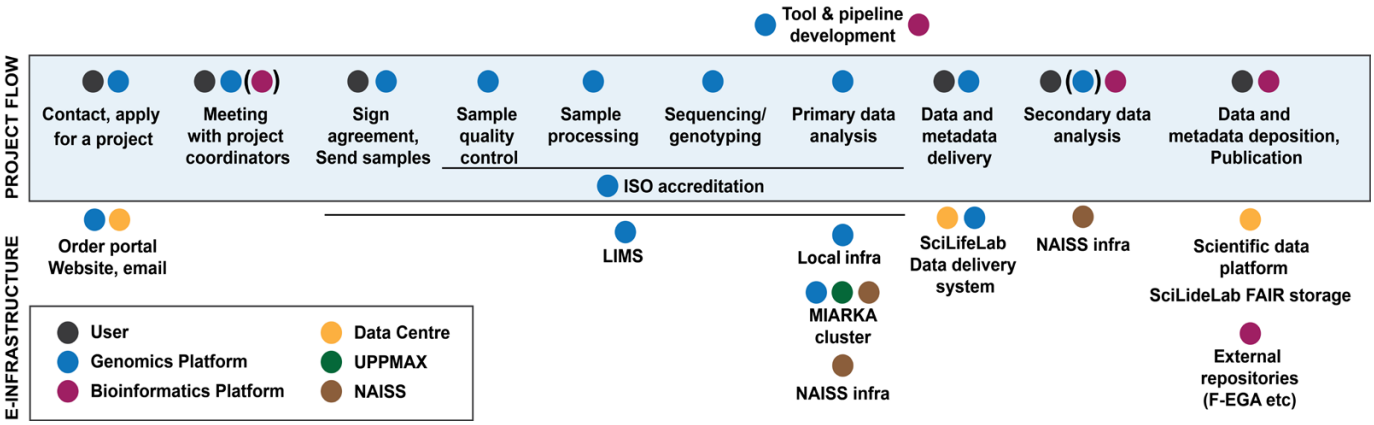


Figure 7. User projects at NGI (and partially at ancient DNA), with an emphasis on e-infrastructure for data handling.

the highly appreciated, internationally attended Long-Read Uppsala Meeting. It has been held five times since 2015, most recently in the University Main Building in Uppsala with > 300 participants in November 2022. The platform also takes part in SciLifeLab and university outreach events and hosts many site visits. Since 2020 the platform has worked towards making events available online or in hybrid format, in order to gain a broader audience across all of Sweden and reduce the environmental impact of travel. The platform's seminars often consist of high-quality scientific presentations by prominent guest speakers and users, followed by project consultations.

Online educational material. Educational material, including recorded seminars, lectures, and symposiums, is made available to researchers across Sweden through the NGI and SciLifeLab YouTube channels. Information to NGI's user community regarding educational activities is posted on the NGI website (ngisweden.scilifelab.se), sent through newsletters, and announced on Twitter (@ngisweden) and LinkedIn. NGI also publishes on its website technical notes, such as evaluations of sample and library preparation protocols, experimental design guidelines, experimental protocols and test data sets. In 2024 and onwards these activities will be increasingly organized in collaboration or coordination with the SciLifeLab Training Hub.

University education. The platform participates in education at universities across Sweden, with staff giving lectures on topics related to all platform activities in courses ranging from undergraduate, to master, doctoral and postdoctoral level. The staff supervise MSc student thesis projects and occasionally co-supervise PhD students or post-docs working with technology development. The platform also frequently hosts lab tours where students learn about, for example, how laboratory automation is used for high throughput genomics. During the coming funding period, our vision with the NGI OpenLab is to be able to host graduate-level hands-on courses in library preparation and sequencing.

Data handling and sharing

The platform has a strong track record in maintaining e-infrastructure that is necessary for its operation, developing computational tools, and supporting its users in receiving data and metadata in useful formats (*Figure* 7).

The platform devotes substantial efforts to managing and handling genomic data that it produces, and sufficient resources for maintaining independent expertise in software and hardware is essential for its operations. The platform does processing of the raw data it produces for quality control reasons, and to provide the users with both primary raw data and secondary data files that can more easily be interpreted and analyzed. The users that need help in analyses that address biological questions are referred to the Bioinformatics Platform. The two platforms are long-term partners in developing and standardizing data analysis pipelines according to gold standards of the field. This includes software solutions for managing, tracking and automating data processes, as well as in-house expertise for systems development and administration. NGI has a strong track-record in developing world-leading tools in this area (see above). The Ancient DNA unit is part of the Swedish National Infrastructure for digital archaeology (Swedigarch), which is developing systems for analyzing, managing and sharing archeological data, including ancient DNA data.

A large proportion of the data produced is of sensitive nature (genetic information from a living person with an existing identification key), and NGI has leading expertise in appropriate handling of such data. All its systems and routines have been configured to comply with GDPR. This includes personal non sensitive information as well, such as management of user accounts in the order portal.

The pre-processing of raw sequencing and genotype data is performed using in-house resources, while the primary analysis, including quality control and report assembly of short-read sequencing data takes place at NAISS/UPPMAX. A backup copy of the raw data is sent for medium-term storage (16 months) on tape at NAISS/PDC Center for High Performance Computing. In 2025-2028 the platform will be increasingly adopting cloud services instead of local

e-infrastructure. Here, the platform is preparing to use services built by NAISS, as well as commercial options. NGI has recently introduced a new data delivery system co-developed with SciLifeLab Data Centre.

The data is owned by the user, with the platform providing support for open access and FAIR data handling. The project agreement with the PI includes a section about the open access policy requirements for research funded by the Swedish Research Council. The platform ensures that delivered data is in the correct format and that corresponding metadata are available for upload to public databases. The major goal for 2025-2028 is to streamline data FAIRification and metadata collection pipelines even further. The platform actively provides expert feedback to Data Centre's plans and solutions for FAIR data.

Collaborations within SciLifeLab

The Genomics Platform is an integral part of the ecosystem of infrastructures in SciLifeLab and collaborates with many of them. *The Bioinformatics Platform* (NBIS) has a close long-term relationship with the Genomics platform and NGI, summarized in *Figure 7*. The platforms collaborate in outreach and education, user support and project design, and development of novel tools and pipelines. The platforms have clearly defined responsibilities for user data analysis support. The bioinformatics platform is also the primary support provider for data deposition. NGI and NBIS are also joint applicants in the EU-initiative Genome of Europe within the Beyond 1M Genomes project. *SciLifeLab Data Centre* provides tools and services in data management and platform operations. In 2021-2022 NGI and Data Centre co-developed a new data delivery system for NGI and other SciLifeLab units, and the Genomics platform actively provides feedback on FAIR data sharing services that the DC develops. *The SciLifeLab Clinical Genomics Platform* focuses on developing genomics assays for clinical diagnosis and clinical trials, and it works closely with Genome Medicine Sweden and the healthcare system. Conversely, the Genomics platform serves the full scope of biomolecular science and does not provide clinical testing. The platforms maintain close contact on practical and strategic levels, e.g., they share sequencing instrumentation and collaborate on assay development and single cell genomics services. The platforms are currently planning the development of a national strategy for genomics infrastructures, with the goal to ensure excellent user service and efficient use of resources. *The SciLifeLab Proteomics Platform and the Genomics platform* have had a productive collaboration in pioneering the Olink Explore proteomics service, and are exploring further expanding these collaborations e.g., in single cells. *The SciLifeLab Spatial Biology Platform* focuses on analysis of cellular and tissue biology at spatial resolution using primarily imaging technologies. Spatial transcriptomics is operationally and financially part of NGI, with Spatial Biology contributing to its strategic development. *The SciLifeLab Crispr Functional Genomics unit* offers functional genomic screens using the CRISPR/CAS9 system and uses NGI for their sequencing read-out. *The SciLifeLab Training hub* provides opportunities to enhance Genomics platform training efforts for example by improving access to online training materials and helping with practicalities related to organizing courses or recording video materials.

The Planetary Biology, Pandemic Laboratory Preparedness and Precision Medicine Capabilities and the corresponding research communities all use genomics approaches and our platform services, and the representatives from our platform participate in events by each community. We are engaged in particularly active conversations with the Planetary Biology capability leadership about the needs of the community and how to meet them, as discussed above. Of the platform's projects one third target species other than human or model organisms. The platform has performed sequencing and methods development for COVID-19 wastewater sequencing and has good connections to the infectious disease community. With a large part of the platform projects linking to the biomedical community, it is well positioned to contribute to the Precision Medicine Capability, in close coordination with the Clinical Genomics platform.

External collaborations

The platform has important national collaborations. *National Academic Infrastructure for Supercomputing in Sweden* (NAISS) is an important partner for compute and storage needs, including cloud computing (see above and *Figure 7*). *Genomic Medicine Sweden* is an important driver in translating genomic innovation into clinical practice. While its closest SciLifeLab infrastructure partner is the Clinical Genomics Platform, the Genomics platform also supports projects funded via GMS e.g. by evaluating the benefits of cutting edge technologies in clinical diagnostics of specific patient groups. *Biobank Sweden* is developing national routines for biobanking and sample access and is an important source of samples processed by NGI. The Ancient DNA unit is part of VR-funded national infrastructures, the *Swedish national infrastructure for digital archaeology (Swedigarch)* supporting improved and combined analysis of archaeological data, and the *Swedish national infrastructure for archaeological research laboratories* (*ArchLab*) to provide a wide range of archaeological research methods to the research community. *Heritage Science Sweden*, a network including the Ancient DNA unit, promotes the use of scientific analysis of cultural heritage material.

The platform units take part in multiple international projects, networks, and consortia. NGI is a partner and work-package co-lead in the *Biodiversity Genomics Europe* project funded by EU Horizon during 2022-2026 ti to generate and annotate genome assemblies for up to 500 diverse species, build barcode reference libraries

for key indicator species for biomonitoring, and develop and coordinate protocols. NGI has been a key partner in the *European Advanced Infrastructure for Innovative Genomics* (EASI-*Genomics*) project funded 2019-2023 by the EU Horizon 2020 –INFRAIA-2018 program, and now an application is being prepared for a 2-year project to plan for an application to build a European strategic research infrastructure (ESFRI). NGI is a work package leader in this application. The *European Infrastructure for Translational Medicine* (EATRIS) is a research infrastructure that provides access to expertise and technologies for translational medicine. EATRIS consists of over 80 academic centers across Europe, where Uppsala University hosts the Swedish node. NGI has been a long-standing active member in EATRIS, for example through the Horizon 2020 flagship project, EATRIS-plus (funded 2020-2024), which delivered a multi-omic toolbox for future Personalized Medicine (motbx.eatris.eu). *Integrating platforms for the European Research infrastructure on Heritage Science* (*Iperion HS*) is an EU-funded infrastructure where the Ancient DNA unit participates as a provider of trans-national access to analysis of ancient DNA for approved projects.

Budget request

The budgets forms show an integrated budget for each cost category. Allocation of subsets of the funds for specific purposes is described below. The budgets are calculated with a 2% annual inflation increase.

Platform Strategic Budget

Costs

- We request support for staff that work on cross-platform tasks. This is important for a large platform with a high degree of activity in governance and operations that spans the units and nodes.
  – Support for Platform Coordinating Officer, so that total SciLifeLab support covers 20% of salary
  – 15% salary support for Platform co-director
  – 25% support for a platform administrator
  – 50% support for Head of Strategic Relations
- Platform Technology Development Project call was first piloted in 2023 and it was a success; these were small-scale project proposals from our staff, reviewed by our steering group
- The annual SciLifeLab Genomics retreat

Revenues

We ask for 2 MSEK support from SciLifeLab - a modest increase from previous levels. We work actively together as a platform and appreciate the support towards this.

National Genomics Infrastructure

NGI's budget is a realistic extrapolation of the budgets and actual expenses of past years. We foresee providing services and support at a similar level as before, with additional investment into NGI OpenLab and into support for services for the Planetary Biology community.

Costs

- NGI's most valuable asset is our expert staff. This includes
  – 9.3 FTE for governance and administration, including directors, managers and heads
  – 16.6 FTE for user support and project coordination
  – 9.9 FTE of team leaders for laboratory and computational staff
  – 45.3 FTE of laboratory staff, *including 2 additional staff for OpenLab R&D support*
  – 14 FTE of bioinformaticians working directly with data
  – 19 FTE of e-infrastructure staff including systems developers, administrators and bioinformaticians
- The majority of NGI's operational costs comes from reagents and instrument maintenance.
- NGI's e-infrastructure costs consist of hardware as well as services from NAISS and Data Centre. During the 2025-28 period we foresee shifting towards cloud-based infrastructure, i.e. paying for e-infrastructure more as a service rather than as hardware depreciation.
- Instrument depreciation costs come from major equipment, including sequencers, pipetting robots and other automation, sample preparation and quality control instruments, and others. In 2024 depreciation costs were lower than long-term trends, which are the basis of the 2025-2028 budget. E-infrastructure is not included here.
- The premise, LKP and overhead costs are according to the current rates at KTH, UU, KI and SU

Revenues

- SciLifeLab funding. We request funding from SciLifeLab according to the following model
  – 2024 funding level as a starting point; we believe we have performed well and fulfilled our mission towards our users and the SciLifeLab community. Thus, we request funding for NGI's core services to continue at a corresponding level to before, with an inflation increase of 3.4% for 2024->2025. Note that due to the heavy inflation of the past years and the unfavorable exchange rate, the current level of funding is lagging behind the actual increases in costs.

– In the 2024 funding we include the funding for formerly independent units for Eukaryotic and Microbial Single Cell Genomics. These services will continue, now as an integrated into NGI, in 2025-2028 (with MSCG operations reorganized to support microbial and metagenomics broadly). We request that their funding would continue as before, but now as an integral part of NGI's budget.
– Funding for a new service model of NGI OpenLab: +6 MSEK / year for a) 2 FTE, b) 0.75 MSEK for 100 m2 of lab space at Solna and BMC, c) 1.75 MSEK for basic consumables, service contracts, etc., d) 1 MSEK/year for depreciation of a startup instrument package with total value of 4 MSEK.

- We project a modest increase in the university co-funding; however this is still a provisional number
- NGI receives substantial funding from The Swedish Research Council. For the funding period 2025-2028 NGI received outstanding reviews and was one of the few infrastructures to be awarded an inflation increase, thus providing support for operations at the present level.
- We project maintaining a similar level of external funding
- User fees for Swedish academic users cover the reagents and a subset of NGI's operational costs. International and non-academic users pay user fees that cover full cost.

Ancient DNA

The Ancient DNA unit's key asset is its expert staff, followed by the clean-room laboratories. The budget represents an estimation of the needs with increasing demand for the units current and planned services.

Costs

- The budget includes the following costs for staff
  – 2.3 FTE (2.8 from 2025 and onwards) for research engineers performing laboratory work
  – 1 FTE for bioinformatician performing data analysis
  – 1 FTE for a 50/50 bioinformatician/project coordinator from 2025 onwards
  – 0.8 FTE for head of unit for administration and project coordination
  – Operations costs including reagents, equipment maintenance, DNA sequencing (by NGI), travel etc.
- Premises costs for offices and laboratories at Uppsala University and Stockholm University
- Depreciation costs for acquired equipment
- Inflation increase 2% annually

Revenues

- SciLifeLab funding, based on the 2024 level with 2 % annual increase to compensate for inflation, and funding for a 50/50 bioinformatician/project coordinator from 2025 onwards to manage the increasing project and data volume
- Funding from the Swedish Research Council for the units participation in the Swedigarch and Archlab national research infrastructures
- Funding by university SFO to support operation and development
- User fees

Table 1. Genomics – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Personnel	664	1 300	1 326	1 353	1 380
Platform Coordinating Officer	92	95	97	99	101
Platform Co-Director	212	215	219	224	228
Platform Administrator	-	250	255	260	265
Head of Strategic Relations	360	740	755	770	785
Platform technology development project call	166	300	306	312	318
Platform retreat	370	400	408	416	424
Platform Director	150	150	150	150	150
Platform Coordination Officer	200	200	200	200	200
Sum costs (kSEK):	**1 550**	**2 350**	**2 390**	**2 431**	**2 471**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*1 200*	*2 350*	*2 390*	*2 431*	*2 127*
Sum revenues (kSEK):	**1 200**	**2 350**	**2 390**	**2 431**	**2 471**

Table 2. National Genomics Infrastructure (NGI) Budget

Costs	2024	2025	2026	2027	2028
Personnel 87 FTEs (2024) -> 89 FTEs (2025–2028)	90 767	95 802	97 778	99 753	101 728
Operations (total)	108 345	111 919	114 226	115 776	118 120
Reagents and other small purchases	86 528	90 016	91 872	93 728	95 584
Lab service contracts, all licenses	12 407	12 203	12 563	12 867	13 174
E-infrastructure	7 536	7 915	7 970	7 323	7 468
Staff support (travel, training and conferences)	1 874	1 785	1 822	1 858	1 895
Premises	9 156	9 353	9 546	9 738	9 931
Instrument depreciations	13 642	17 112	17 465	17 817	18 170
Other	1 656	582	594	606	618
Sum costs (kSEK):	**223 566**	**234 768**	**239 609**	**243 690**	**248 567**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*53 303*	*61 110*	*62 370*	*63 630*	*64 890*
University co-funding	10 287	12 310	13 950	13 950	13 950
Swedish Research Council	20 810	24 655	26 655	27 655	27 655
External grants (various)	17 282	17 460	17 820	18 180	18 540
User fees	116 450	119 302	118 940	120 633	123 715
Sum revenues (kSEK):	**218 132**	**234 837**	**239 735**	**244 048**	**248 750**

Table 3. Ancient DNA budget

Costs	2024	2025	2026	2027	2028
Personnel 4.3 FTEs (2024) -> 5.8 FTEs (2025–2028)	4 873	6 601	6 733	6 868	7 005
Operations	675	850	867	884	902
Premises	1 049	1 223	1 235	1 249	1 263
Instrument depreciations	73	73	73	73	44
Sum costs (kSEK):	**6 670**	**8 747**	**8 908**	**9 074**	**9 214**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 105*	*4 417*	*4 505*	*4 596*	*4 687*
University co-funding	-	-	-	-	-
Swedish Research Council	1 319	1 344	1 371	1 380	1 380
SFO Uppsala University	500	500	500	500	500
SFO Stockholm University	600	600	500	500	500
User fees	1 200	1 900	2 050	2 150	2 200
Sum revenues (kSEK):	**6 724**	**8 761**	**8 926**	**9 126**	**9 267**





Clinical Genomics Unit in Linköping. Photo: Mikael Wallerstedt

Clinical Genomics Platform

Basic Information

Platform Director: Thoas Fioretos, Lund University

Platform Co-Director: Lucia Cavelier, Karolinska Institutet

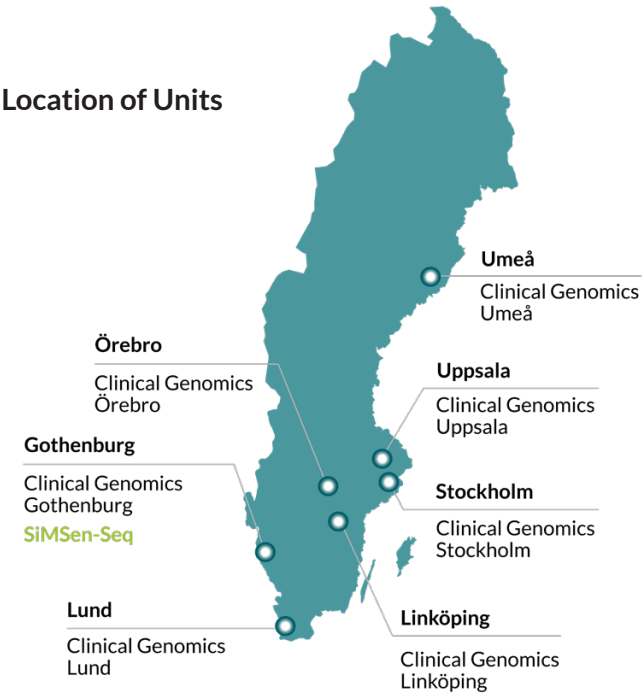
Platform Coordination Officer: Eva Berglund, Uppsala University

Platform vision: Positioning Sweden as a global leader in translating genomic discoveries into clinical practice and societal impact.

Platform mission:

1. To provide world-class support for translational research and clinical studies.
2. To adapt and optimize new genomic technologies for tomorrow's healthcare.
3. To contribute to a direct patient and societal impact by promoting precision medicine.

Location of Units

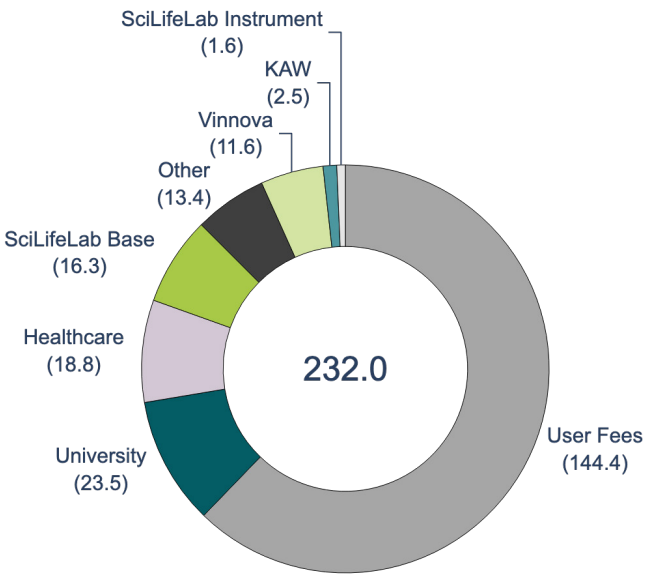


SciLifeLab Funding

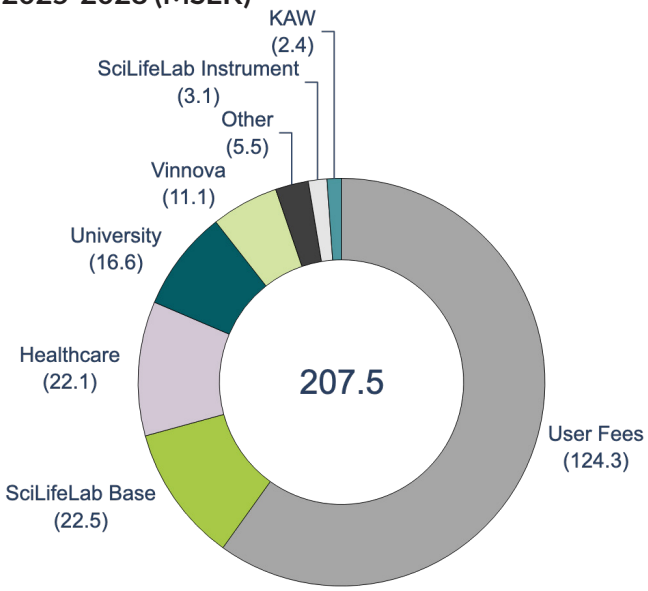
Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Clinical Genomics Gothenburg	2.2	2.5
Clinical Genomics Linköping	0.8	1.0
Clinical Genomics Lund	2.2	2.5
Clinical Genomics Stockholm	5.2	4.5
Clinical Genomics Umeå	0.8	1.0
Clinical Genomics Uppsala	2.6	2.8
Clinical Genomics Örebro	0.8	1.0
SiMSen-Seq for Ultrasensitive Detection of Nucleic Acids*	0.0	0.5
Platform Strategic Funding	*1.8*	*6.7*
Total SciLifeLab Funding	**16.3**	**22.5**

*Proposed to be included in the platform

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E2 Clinical Genomics

Platform organization and governance

The Clinical Genomics (CG) platform was established in 2014 to meet the increasing demands by the translational research community to leverage genomic technologies towards improved diagnostics and treatment. Today, the platform has full national outreach with nodes at all seven Swedish medical faculties, working in close collaboration with the respective university hospital (*Figure 1*). Given that Swedish healthcare is organized into autonomous regions, the national coverage is critical for ensuring equal access to services provided by the platform and accelerating the implementation of new diagnostics in healthcare throughout the country.

The Platform is coordinated nationally by the Platform Director (PD), together with a co-PD, the Platform Coordination Officer (PCO) and a vice-PCO (*Figure 1*), and this group meets twice a month. In addition, each month this team meets with the Platform Scientific Directors and Heads of Units from each node, as well as the Research Data Manager, to exchange information, strategize and organize across nodes: this is the Platform Management Group.

The international Scientific Advisory Board (SAB) provides expertise, insights, and recommendations to ensure that the platform operates according to the latest advances and best practices in the field. Meetings with the SAB are held twice per year and a platform retreat for all platform staff is held once a year.

Platform organization and governance

The CG platform provides expertise and cutting-edge genomic services tailored for the translational and clinical research community and for clinical trials. Our current key technologies include short- and long-read sequencing, transcriptome and methylome analysis, single-cell and spatial analysis, and ultrasensitive variant detection. These core technologies are complemented with diagnostic and medical expertise, mainly within rare diseases, solid tumors, hematology and infectious diseases. With this unique combination of technological and medical expertise, we can provide a comprehensive end-to-end service including understanding of clinical needs and guidance on experimental design, technical assay development, software development, quality assurance, and clinical interpretation.

Our assays and analyses are developed with clinical implementation in mind, which entails rigorous benchmarking, quality assurance activities and, in some cases also ISO accreditations. Often, our services are established in a manner that supports clinical studies with prospective patient recruitment and real-time analyses and are also preparing for the changes required by the European In Vitro Diagnostic Regulation (IVDR).

In addition to our research services, our platform spearheads the development, validation, and implementation of genomic-based methods for individualized patient care and precision medicine at a national scale, in collaboration with the national precision medicine program Genomic Medicine Sweden (GMS), which was initiated by our platform in 2018 (see section "Collaboration with industry, healthcare, and other organizations"). Within our platform, development of new diagnostic tests often starts with collaborative research projects to optimize laboratory and bioinformatic workflows, and is followed by a careful

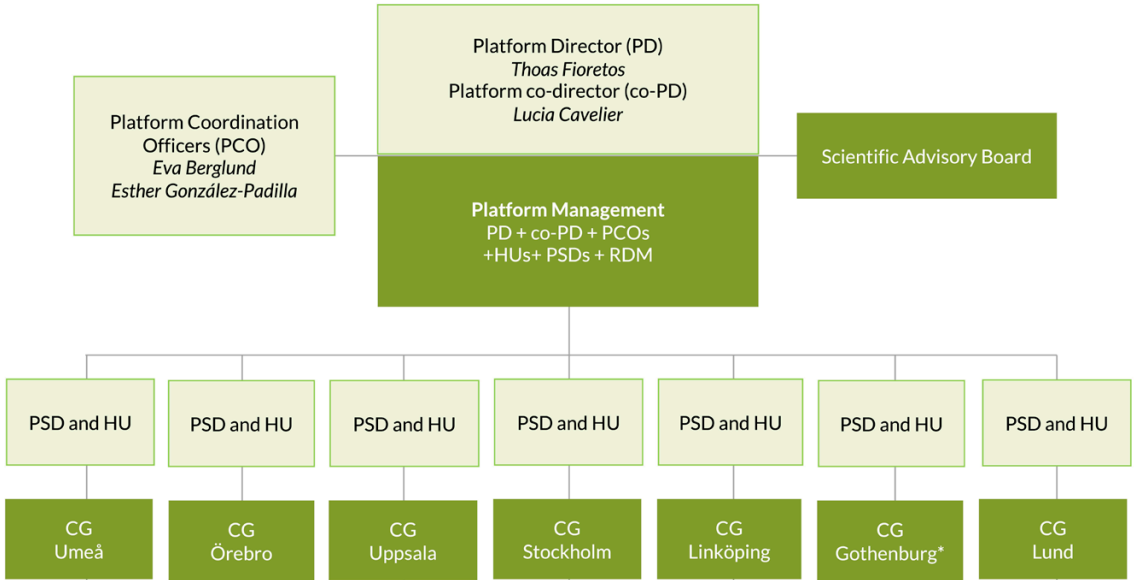


Figure 1. Organization of the CG platform with seven nodes. The Scientific Advisory Board includes Beatrice Melin, Dag Undlien, Eva Hellström Lindberg, Finn Cilius Nielsen and Katja Kivinen. *The SimSen-Seq technology will be incorporated into CG Gothenburg.
PSD, Platform Scientific Director; HU, Head of Unit; RDM, Research Data Manager.

validation process, whereby the analytical performance is evaluated with respect to specificity, sensitivity and reproducibility. In addition, aspects such as turnaround-time and cost are assessed. Our platform has access to large cohorts of samples for clinical validation and once a new diagnostic test has been implemented, healthcare normally takes over the clinical diagnostic service (*Figure 2*).

Personnel and plans for recruiting and retaining excellent staff scientists

The platform has a total personnel count of 165 (117 FTEs), of which 58% are female and 50% hold a PhD. The team includes molecular biologists, bioinformaticians, software developers and other IT professionals, clinical laboratory geneticists and medical doctors. We thus combine technical expertise in assay development, including bioinformatics and software engineering, with clinical expertise in assay needs and performance.

Several efforts are ongoing to promote competence and career development for platform staff. We offer site visits and exchange of personnel between nodes to promote knowledge transfer, networking, and collaboration. Staff members are encouraged to grow professionally by for example task shifting (paid training to acquire new skills followed by taking over responsibility for the task) and increased mobility between academia and healthcare. Furthermore, we are active drivers in a national network aiming to establish career paths for research infrastructure personnel.

Users, projects and scientific environments

User base

The presence of CG nodes at all seven medical faculties in Sweden ensures national accessibility for researchers and healthcare and enables close, personal support. As a result, there is a high and increasing demand for the expertise and services provided by our platform. Since 2020, the number of users has increased by 55% (from 182 to 282) and the number of projects per year has increased by 78% (from 385 to 686). In addition to researchers and healthcare, we serve industry and governmental agencies, including the Public Health Agency of Sweden and the National Forensics Authority. We expect a further extended user base in the coming years as a result of new technologies and services being introduced, a larger demand for genomic characterization as part of clinical trials, and the increased focus on precision diagnostics and precision medicine within research, healthcare and society.

User fee models

Academic users benefit from a subsidized cost. Cost models are based on a cost per sample, on reagent costs, and/or on hourly fees for experimental work and bioinformatics. Collaborative projects can be further subsidized or covered by joint grants. For industry and healthcare users, we apply a full-cost model. Work is ongoing on implementation of the new government ordinance relating to how research infrastructures can charge for their services.

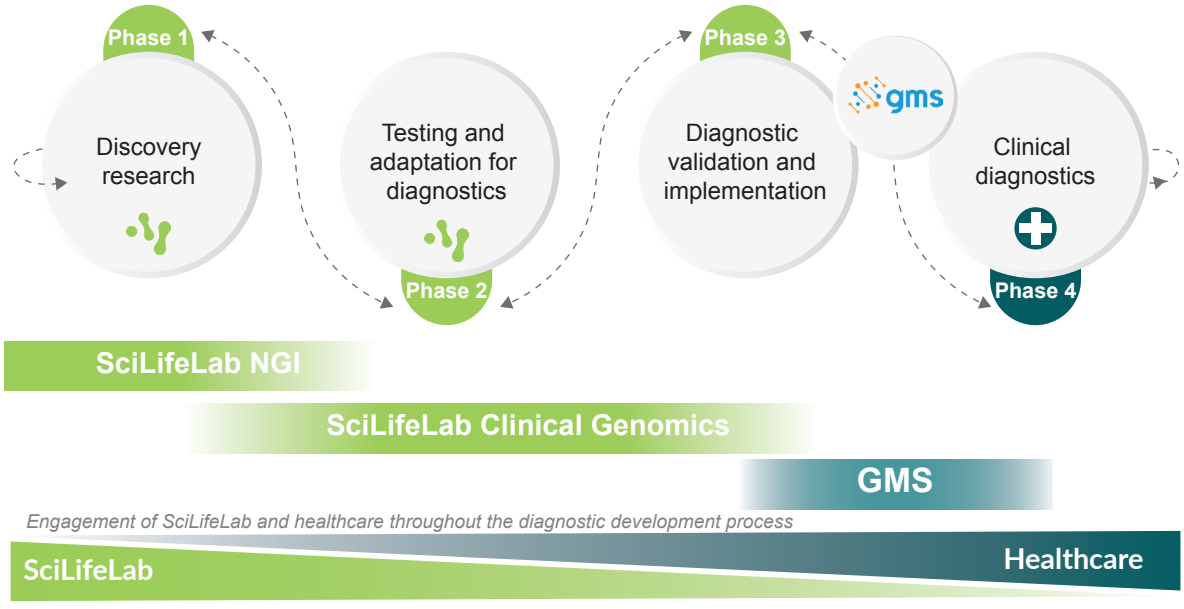


Figure 2. Schematic outline of the diagnostic development process. The CG platform operates in phase 2 and 3 and provides expertise, technology development, and services to translational and clinical researchers, as well as clinical trials. The CG Platform also works in close collaboration with National Genomics Infrastructure (NGI) in multiple diagnostics development projects and with GMS, the national initiative for precision medicine, to facilitate the implementation of genomics-based precision diagnostics and precision medicine in Sweden.

Project prioritization

The platform provides service for clinical and translational research, either on a first-come first-served basis or prioritized based on clinical need. Collaborative development projects are prioritized based on the expected importance of the development work for future research service projects or healthcare applications. Project requests are typically directed to a specific node and assessed by the local management group. If the node initially contacted is not best suited to provide the requested service, projects are referred to another node within the platform or to NGI.

Scientific environments

Each CG node has well established collaborations with academic and clinical researchers, with nodes having established a network of affiliated scientific experts. Our platform scientific directors are active in translational and clinical research, and most of them have dual affiliations to academia and healthcare ensuring that development efforts align with clinical needs. We also work closely with clinical researchers active within our key alliance partner GMS. Our scientific environments also include Data Driven Life Science (DDLS) fellows and researchers within the Wallenberg Centre for Molecular Medicine (WCMM) network. These collaborations critically promote technology development, leading to new services for research as well as new diagnostic tests in healthcare. For examples of publications, see "Platform development and key achievements 2021–2024".

International networks

The CG platform actively participates in several international networks, including the Nordic Alliance for Clinical Genomics, the Global Alliance for Genomics and Health, the European '1+ Million Genomes' Initiative, several European reference networks for rare diseases and the European Liquid Biopsy Society. Through participation in these networks, we liaise with Nordic and European peers to facilitate cross-border learning, harmonization of processes, quality assurance of analyses, and data sharing in order to support discovery and diagnostics.

Infographics: Statistics and Metrics for Clinical Genomics Units

Clinical Genomics

Read more: Webpage, Publications Database

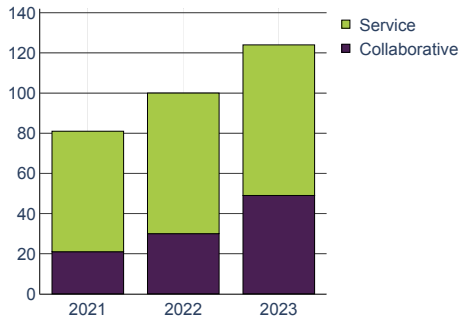
Basic Information

PD: Thoas Fioretos
Co-PD: Lucia Cavelier
Host University: GU, LiU, LU, KI, KTH, UmU, UU, ÖRU
SciLifeLab platform since: 2014
FTEs: 117

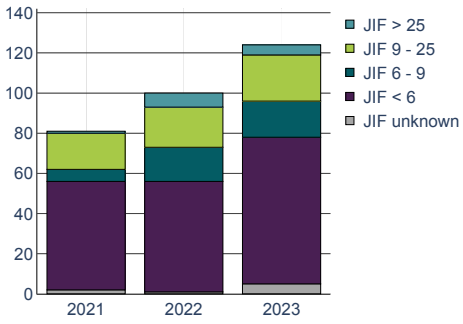
Funding 2023 (kSEK)

SciLifeLab: 14100
Other: 59455
User Fees: 146546

Publications by category

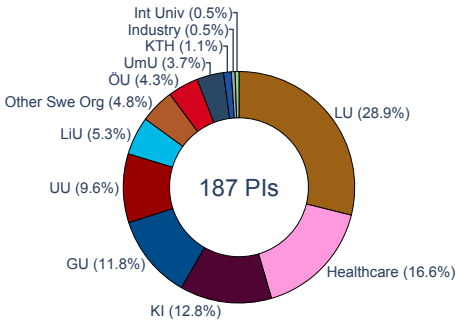


Publications by JIF

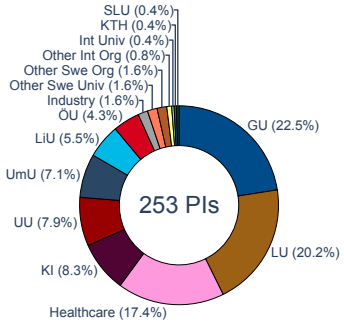


No. of Tech Dev Publications 2021 - 2023: 12

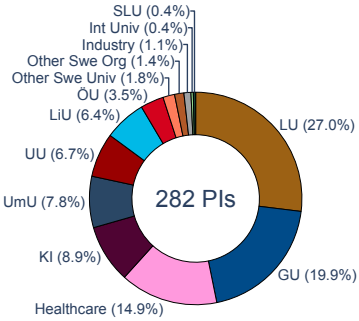
Users 2021



Users 2022



Users 2023



- *Key contributors to >300 scientific publications 2021-2023.*
- *Supported >10 clinical studies and co-developed tests performed on >190,000 patient samples in healthcare 2021-2023.*
- *Played an instrumental role in implementation of precision diagnostics and medicine in Sweden.*

Platform development and key achievements 2021–2023

The CG platform played a transformative role in providing genomics-based services for translational and clinical research, clinical trials, and in the development and implementation of new genomics-based diagnostics within healthcare at the national level. Our achievements were also recently highlighted by our Scientific Advisory Board: "Clinical Genomics is no doubt an internationally leading technology platform making a true impact for genomics-based translational and clinical research as well as for the entire Swedish precision medicine landscape". Our key achievements during 2021-2024 are summarized in *Figure* 3 and include:

New services and instruments

- Implementation of a range of *new end-to-end services tailored to meet translational and clinical research needs*, including cancer gene panels and whole-genome sequencing assays, long-read sequencing, ultra-sensitive detection, epigenetic profiling, single cell and spatial analyses, metagenomics, new bioinformatics pipelines, and data visualization tools. These are spearheaded by our technology focus areas (see "Plans for development including new technologies/service offerings 2025–2028").
- Secured funding for the acquisition of new high throughput sequencers (Illumina NovaSeq X, Pacific Biosciences Revio) at several nodes to continue driving cost reductions and enabling new applications.

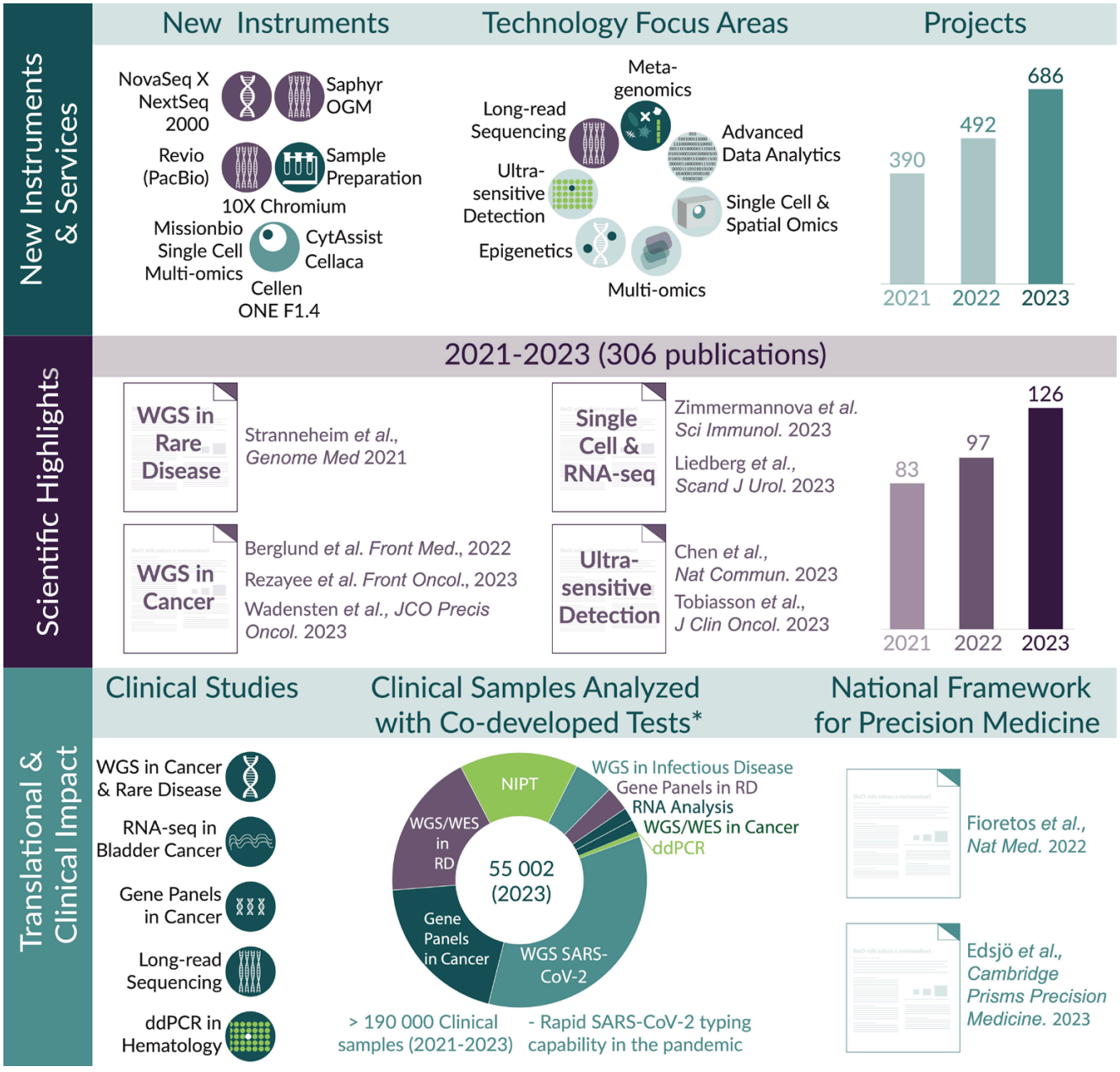


Figure 3. Schematic summary of key achievements 2021-2023, including New Instruments & Services, Scientific Highlights, and Translational & Clinical Impact. *Indicates the number of clinical samples analyzed in healthcare with tests that were co-developed by the CG Platform.
Abbreviations: WGS, whole-genome sequencing; WTS, whole-transcriptome sequencing; ddPCR, droplet digital PCR; WES, whole-exome-sequencing; NIPT, non-invasive prenatal testing.

Scientific highlights

Services offered by the platform resulted in 306 *scientific publications* 2021-2023. Among these, 28 articles were published in scientific journals with an impact factor >9. Examples include:

- Implementation of WGS for rare inherited disease in healthcare that resulted in ~40% of patients receiving a clear diagnosis and to the discovery of more than 30 new disease-causing genes (Stranneheim et al, *Genome Med* 2021: PMID: 33726816).
- Development and validation of a new method for ultra-sensitive detection of disease-driving mutations in hematologic malignancies (Chen et al., *Nat Commun* 2022; PMID: 35821208).
- Methods development and support with multimodal single cell sequencing demonstrating that tumor immunogenicity can be restored with dendritic cell reprogramming (Zimmermannova et al., *Sci Immunol* 2023; PMID: 37418548).
- Critical technology development demonstrating that patient-specific measurable residual disease predicts outcome in myelodysplastic syndrome after hematopoietic stem-cell transplantation (Tobiasson et al., *J Clin Oncol* 2024; PMID: 38232336).

Translational and Clinical Impact

The platform played a crucial role in supporting several pioneering clinical studies, utilizing a variety of assays including gene panels, whole-genome sequencing (WGS), gene expression analysis, and digital PCR. Additionally, we were instrumental in translating new genomic technologies into healthcare, showcasing our significant societal impact by facilitating improved diagnostics, treatment, and follow-up of patients diagnosed with serious illnesses. Notable examples include:

- We launched a national clinical study, in partnership with GMS, investigating the clinical utility of WGS and whole-transcriptome sequencing (WTS) in acute leukemia (Berglund et al., *Front Med*, 2022; PMID: 35402448).
- With GMS we are conducting a clinical study investigating the diagnostic yield of WGS and WTS as standard for all children diagnosed with cancer in Sweden, including establishment of multi-disciplinary molecular tumor boards. Initial results from this study revealed a refined diagnosis in 50% of cases and identification of actionable targets in 26% of the patients (Wadensten et al., *JCO Precis Oncol* 2023; PMID: 37384868).
- Support with WTS was provided for a large-scale multicenter study aiming at translating gene expression-based molecular stratification of bladder cancer into clinical practice (Liedberg et al., *Scand J Urol* 2023; PMID: 36540001).
- More than 190,000 *patient samples* were analyzed during 2021-2023 in healthcare with clinical tests co-developed by our platform.
- We played a critical role in the development of comprehensive gene panels for improved diagnostics of *hematologic malignancies and solid tumors at the national level*, resulting in more than 5000 clinical samples being analyzed with these panels in 2023.
- We rapidly developed and scaled up new methods for the diagnosis and monitoring of SARS-CoV-2 variants, sequencing >100,000 SARS-CoV-2 isolates during 2021-2023.
- By providing expertise, technology development and services to our key alliance partner GMS, we jointly established a *framework for implementing precision medicine at the national level* (Fioretos et al., Nat Med 2022; PMID: 36123428; Edsjö et al., *Cambridge Prisms Precision Medicine* 2023).

Plans for development including new technologies/service offerings 2025–2028

During the ongoing funding period, we have witnessed an increased focus on precision diagnostics and medicine in Sweden and internationally, along with an increased demand for our services. To meet the user needs, we continuously engage in technology development, as collaborative projects with researchers, GMS and clinical laboratories, or as internal projects. For example, major technology development is performed as part of clinical studies in collaboration with GMS. We also strive to maintain an up-to-date instrumentation, to continue driving quality improvements (e.g., long-read sequencing) and cost reduction (e.g., short-read sequencing on NovaSeq X).

To ensure tracking of the newest developments in key areas, we have defined seven translational *Technology Focus Areas*, each coordinated by one node. New technologies are implemented as services as they mature in each technology focus area. Depending on demand, services are subsequently disseminated to other nodes, ensuring a streamlined and efficient use of resources and expertise. The coordinating node is responsible for organizing meetings, workshops and webinars with internal and external stakeholders, as well as coordinating grant applications and internal technology development publications within the area. Our plans for 2025-2028 for each area include:

Long-read sequencing

Recent advancements in long-read sequencing technologies enhance the identification of SNVs, structural variants, repeat expansions, and methylation profiles, potentially providing a comprehensive diagnostic tool. Implemented clinical tests include SARS-CoV-2 and BCR:ABL1 fusion gene sequencing. We foresee a dramatic

increase in long-read sequencing in clinical research and diagnostics over the next few years. Major development projects, being undertaken in collaboration with the National Genomics Infrastructure (NGI), include: i) Increasing the diagnostic yield in rare disease above the 40% reached by short-read WGS, by detecting challenging variants and facilitating phasing ii) Replacing laborious methods, such as chromosome analysis, currently used in cancer diagnostics; iii) Facilitating assembly of complete microbial genomes with reduced turnaround time compared to current culture-dependent methods, used for species identification, antibiotic resistance prediction and epidemiological surveillance; iv) Detecting all classes of structural variants, also in genomic regions that are difficult to investigate by sequencing, using optical mapping.

Multi-omics

Multiple data layers improve diagnostic yield in several disease areas. For example, transcriptome sequencing facilitates interpretation of genomic variants in regulatory and intronic regions as well as identification of abnormal expression and splicing patterns, allelic imbalances and gene fusion events in cancer. Having established bioinformatic workflows for detection of these types of events, in the next few years we shall further refine these and integrate other modalities with DNA data into a joint variant prioritization model along with methylation data for analysis of gene inactivation. During the next funding period, we plan, with the Clinical Proteomics and Immunology platform, to explore offering a joint service in proteogenomics.

Epigenetics

Recent years have witnessed the development of methylation-based classifiers for several cancer types and the CG platform is instrumental in assessing the clinical utility of this tool for correct identification and treatment of central nervous system tumors. We are now in the process of implementing this for improved diagnostics in healthcare. New clinician-friendly methylation analysis pipelines providing end-to-end data handling with minimal coding will be expanded and refined. We are also contributing to the development and implementation of a new classifier for brain tumors used to support an international clinical trial with diagnostic methylation profiling. We shall collaborate with NGI to develop methylation analysis workflows for long-read and adaptive sequencing, particularly with a view to perioperative high speed real-time classification. Future plans also include creating profiles for cardiopulmonary and infectious diseases.

Ultrasensitive detection

Ultra-sensitive assays for identification of low frequency mutations play a crucial role in cancer diagnosis, prognosis and monitoring treatment response. No single method meets all criteria for number of markers screened, sensitivity, time-efficiency, and cost-efficiency. We therefore use a combination of methods, including digital PCR, deep sequencing with unique molecular identifiers, and superRCA, and we plan to incorporate the SimSen-Seq technology for highly sensitive multi-marker detection as a national service by our platform (see section on Translational Genomics Platform). We have developed and implemented diagnostic tests for several cancers using liquid biopsies (i.e., detection of variants in circulating tumor DNA), a rapidly expanding area. A major development project is a clinical study in myelodysplastic neoplasms utilizing digital PCR and super RCA post stem-cell transplantation for early relapse prediction and optimized treatment.

Single-cell and spatial omics

In recent years, single-cell and spatial omics applications have demonstrated great potential to advance translational research and future healthcare diagnostics, prognostics, and disease monitoring, e.g. in cancer and autoimmune diseases. Due to an increasing demand for these technologies in the translational and clinical research space, the platform has established single-cell transcriptomics, epigenetics, and multimodal applications as services using two complementary technologies (10x Genomics and MissionBio). For spatial analyses, we currently provide services using two instruments (NanoString GeoMx and 10x Genomics CytAssist). Looking ahead, we shall further develop single cell and spatial omics technologies to meet clinical needs, enhance cost-effectiveness, throughput, and efficiency, particularly for analyzing low-input samples, collaborating with other platforms (mainly NGI and Spatial Biology) for broader modalities (e.g., proteomics) and spatial omics at single-cell or sub-cellular levels (in situ sequencing).

Metagenomics

Comprehensive analysis of microbial and host genetic material holds great potential for diagnosis and treatment of infectious disease. As part of the G3P project (see PLP section below), we have established clinically validated, rapid metagenomic sequencing assays for detection of known and unknown pathogens as well as antimicrobial resistance, along with providing publicly available bioinformatic pipelines. We serve as the technical backbone for several national projects, partnering with, for example, GMS, the Public Health Agency of Sweden and the Swedish Defence Research Agency. Future development plans include evaluation and benchmarking of different approaches for human background depletion or microbial enrichment before sequencing (in collaboration with NGI) and development of antimicrobial resistance prediction using long-read sequencing.

Advanced data analytics

Clinical bioinformatics and AI play a crucial role in translating large-scale datasets into actionable insights for personalized medicine, disease diagnosis, prognosis, and treatment planning. One area to explore is the optimization of current algorithms, following open source standards and FAIR guidelines. We shall also work towards the integration of diverse data types, such as electronic health records, imaging data, and omics data, to create comprehensive patient profiles for more holistic insights. Another area includes the implementation of AI-driven decision support systems and conducting regular evaluation and validation of these AI models to ensure their outcome is reliable and relevant. The main purpose is to promote collective efforts towards increased scalability in diagnostics, improving outcomes and healthcare delivery.

Plans for data management and secondary use 2025–2028

To meet the increasing demands in data management and FAIR sharing, the CG platform recently appointed a dedicated Research Data Manager to develop a roadmap with short- and long-term goals. With this, we will ensure a unified framework across the different nodes targeting data storage, annotation standards and FAIR compliance for secondary use. Furthermore, we will collaborate with key infrastructures such as Federated-EGA Sweden, DDLS Data Science Nodes, SciLifeLab's Data Centre, GMS National Genomic Platform (NGP) and the European Genomic Data Infrastructure (GDI) project. Our key objectives are to: 1) create a user support package assisting with data management plans, ethical approval applications, and informed consents, 2) align metadata specifications with leading national (e.g., NGP) and international initiatives (e.g., GA4GH), 3) establish streamlined procedures for data annotation and delivery to national and international repositories, and 4) establish dynamic learning systems, aiming at enhancing data interpretation and fostering the generation of the new insights.

Data Centre – current support and needs for 2025–2028

The Data Centre currently deploys MethylR, a tool developed by the CG platform for the analysis and visualization of methylation data. Going forward, we will benefit from enhanced access to high-performance computing and cloud-based data delivery for other applications through the Data Centre, as the volume of data generated increases and new analytical programs with applications to precision diagnostics and precision medicine are developed. In addition, gaining access through a simple protocol to existing frameworks and tools for data management plans and data publishing will accelerate our compliance towards the FAIR principles.

NBIS – current support and needs for 2025–2028

Synergies with the Bioinformatics platform (NBIS) include joint personnel (0.5 FTE), knowledge transfer through thematic meetings, as well as strategic sessions. The CG platform also contributes to NBIS courses and the Swedish Bioinformatics Advisory Program. Additionally, NBIS and DDLS representatives have engaged in several bioinformatics events organized by the CG platform. In 2023, the CG platform engaged in the annual NBIS retreat to delineate actionable points to strengthen our intra-platform collaboration. A main goal for 2025–2028 is to develop reproducible bioinformatic tools together. Beyond this, support from NBIS could expand to several key areas: i) collaborative development of bioinformatic pipelines, ii) early guidance to our users on bioinformatics downstream analysis of the data generated by the CG platform, and iii) facilitating access to NBIS domain experts in bioinformatics, advanced analytics, databases, tools and data management to the CG platform personnel.

Current training offerings and plan for 2025–2028

In collaboration with the Training Hub, we are currently developing a digital master class in Clinical Genomics, to be launched in 2024. Lectures will be held by all CG nodes according to area of expertise, and topics will include current and future clinical applications of genomics in different disease areas, molecular technologies, bioinformatics and clinical variant interpretation. The course is aimed for professional development of CG platform personnel as well as the larger SciLifeLab and healthcare communities.

We are also involved in other training activities, including organizing the EMBL course for liquid biopsies, contribution to NBIS courses, regular university courses, and organization of workshops connected to bioinformatic tools or our technology focus areas. For example, we are responsible for the course "Molecular Techniques and Data Analysis in Precision Medicine" given within the first Swedish Master's degree program in Precision Medicine at Uppsala University. Another example is the well-attended first epigenetics workshop covering tumor classifiers, methylation panels and long-read sequencing and including a number of outside speakers, as well as clinicians, clinical geneticists, bioinformaticians, staff from precision medicine, DDLS fellows and researchers, held in February 2024.

The CG platform also plays a key role as trainers and teachers for healthcare professionals and clinical researchers in the field of genomic medicine/precision medicine. For example, we participate in educational activities hosted collaboratively with GMS, for example lunch seminars and various e-courses.

Challenges and bottlenecks to meet user demands

Infrastructure maintenance and development

A challenge during 2025–2028 will be to maintain our infrastructure at the cutting-edge level due to the rapid technological development in the field as well as to ensure that we meet the increasing and more challenging demands from projects in the translational research and clinical trial settings. For example, long-read sequencing is rapidly maturing and several clinical applications are expected to shift from short- to long-read sequencing during the upcoming funding cycle. We also foresee a major demand for sequencing at even lower cost to enable clinical applications of somatic whole-genome sequencing, spatial and single-cell sequencing, all requiring large amounts of data. We also expect a strong increase in demand for various counting-based applications as they enter translational and clinical use; this includes proteomics-based assays such as Olink plasma protein quantification and Pixelgen single-cell spatial proteomics for cell surface protein quantification and localization. Finally, we foresee a strong increase in the number of samples to be processed as studies shift from single-time point diagnostic analyses to applications with repeated analyses per patient, including applications such as early detection as well as post-diagnostic monitoring during remission for early detection of relapse. These applications require large sample processing capacity, rapid turnaround and processing in real-time, coupled with low cost to allow for frequent screening of each subject/patient.

Recruiting and retaining personnel

A bottleneck that we are facing is staff turnaround. Bioinformaticians, software developers and IT experts in particular have become vital for conducting science using high-throughput technologies but are often lured away by higher salaries and more established career paths in industry. As of today, universities and university hospitals both face challenges in recruiting and retaining these key competencies. Our efforts for addressing this challenge are described under "Personnel and plans for recruiting and retaining excellent staff scientists".

Synergies and collaborations within SciLifeLab

National Genomics Infrastructure (NGI)

We collaborate extensively with NGI, with synergies including shared instrumentation, joint technology development, knowledge exchange and shared personnel. Current collaborative projects comprise development of both wet-lab protocols and bioinformatic pipelines within short-read, long-read and single-cell sequencing. Several additional joint projects are planned, for example within spatial sequencing. Furthermore, the CG platform and NGI provide joint services for users, for example in different phases of a project, e.g. where initial analyses are performed at NGI and subsequent prospective sample collection and real-time analyses at the CG platform.

Precision Medicine (PM) capability

Precision medicine is a core activity of the CG platform which we address by: i) providing end-to-end service for clinical research, ii) supporting clinical trials with validated assays, iii) developing and implementing diagnostic assays in collaboration with healthcare, and iv) constituting the technical backbone of GMS. Within the next funding period, we will continue to drive our efforts in implementing a sustainable and nationally harmonized infrastructure to promote precision diagnostics and precision medicine at the national level (Fioretos et al, *Nat Med* 2022). We contribute with expertise to the PM capability team and strategic expert group. We are also a critical partner of the project "*National infrastructure to support clinical trials in precision medicine with cutting edge technologies*" funded by The Swedish Research Council, which aims to leverage SciLifeLab's technological platforms and capabilities to attract and promote clinical trials in Sweden.

Pandemic Laboratory Preparedness (PLP) capability

The CG platform was instrumental in providing services and developing resources during the Covid-19 pandemic. During early 2021 several healthcare regions reached out to their local CG node with a need to rapidly establish SARS-CoV-2 typing capability. Within 5-6 weeks we established this capability to sequence, analyze and upload data to national and international data repositories. This effort has been instrumental and allowed the public health officials to monitor in real-time the diversity of infectious strains and the dynamics of molecular evolution during the outbreak. In total, we sequenced over 100,000 isolates for healthcare and public health authorities during 2021-2023. Coordinated by our platform, the PLP project Genomics-based Pandemic Preparedness Portfolio (G3P) established a resilient capability in relation to viral outbreaks. This is a collaboration between key SciLifeLab infrastructures, GMS, and the centralized, high-capacity National Pandemic Center. The consortium provides a national capability consisting of high analytical capacity, rapid delivery of results and a portfolio of complementary technologies including centralized and federated data generation and combined analysis capability to mitigate risks associated with a single critical infrastructure.

Planetary Biology (PB) capability

While planetary biology is not a main focus of the CG platform, several bioinformatic pipelines originally developed by the platform to support clinical research have found wider applicability in biodiversity research. This includes pipelines for processing, analyzing and visualizing RNA-seq, small RNAs and methylation array data, which can be used for different types of species and environmental samples.

Collaboration with industry, healthcare, and other organizations

The CG platform maintains a large network in the national and international research communities, organizations and industries, where our close connections to healthcare and GMS makes us a particularly valuable partner for technology development, testing and translation.

Healthcare

The integration of the CG platform with all seven Swedish university hospitals provides a strong link between SciLifeLab and healthcare. We have close relations with Regional Cancer Centers, Genomic Medicine Centers, Precision Medicine Centers and Centers for Rare Diseases, ensuring that novel diagnostic methods developed by the platform are introduced into national care programs and support clinical trials.

Genomic Medicine Sweden (GMS)

Our platform initiated the national precision medicine program GMS in 2018 upon recognizing that the Swedish healthcare system was lagging behind in offering harmonized services for genomics-based precision medicine. Our platform continues to provide expertise and services in genomic technologies to GMS, while GMS is focused on the harmonized national implementation of precision medicine into healthcare, on ethical and legal aspects, health economy, patient engagement, and on establishing a national genomics platform for the storage and sharing of data primarily generated within healthcare.

Biobanks

The CG platform has close connections to the national biobanking infrastructure Biobank Sweden. Biobank Sweden coordinates centers at the university hospitals and provides access to high quality samples for research as well as rare samples needed for validation purposes.

Innovation and Industry

We are actively involved in the rapidly growing genomics-based precision diagnostics community, collaborating with industry leaders like Bristol-Myers Squibb, Illumina, Oxford Nanopore Technologies, Rarity Bioscience, and Incyte. Together, we test new products, innovate diagnostic methods, and contribute to clinical studies, making Sweden more attractive for clinical trials. This not only benefits patient access to cutting-edge diagnostics but also reduces costs for novel healthcare treatments.

E3 SiMSen-Seq

Current operations – funding, expertise, technologies, and services offered

The Translational Genomics Platform (TGP), founded in 2017 at University of Gothenburg (UGOT) and Sahlgrenska University hospital, is a research infrastructure focused on *ultrasensitive sequencing applications* using liquid biopsies, allowing highly sensitive and accurate detection of individual disease-associated molecules. TGP is supported by the Wallenberg Center for Molecular Medicine with ~2.5 MSEK/year. Additional financing as part of consortium has been obtained through different funding organizations, including Sweden's Innovation Agency (~30 MSEK, 2019-2023), Swelife -Medtech4Health (3 MSEK, 2021-2023) and FORMAS (3.7 MSEK, 2022-2024). The TGP expertise covers all aspects of ultrasensitive DNA/RNA analysis, including liquid biopsy handling, pre-analytics, nucleic-acids analysis, and data analysis, with a primary focus on digital sequencing technologies. The core technology, named *SiMSen-Seq*, was invented by Prof. Anders Ståhlberg at UGOT in collaboration with Tony Godfrey, Boston University (Ståhlberg et al., *Nat Protocol* 2017: PMID: 28253235). The technology offers digital resolution with close to error-free sequencing with minimal quantification biases. In addition, the approach is flexible and easy to adapt to a wide range of applications, such as detection of circulating tumor-DNA in essentially any tumor entity, immune repertoire profiling, and detection of environmental DNA. A key application is personalized SiMSen-Seq panels for circulating tumor-DNA detection in cancer patients that enable precision medicine. Here, patients are sequenced at diagnosis using whole genome sequencing, whole exome sequencing or comprehensive gene panels. Then, patient-specific mutations are selected and monitored over time.

Currently, services are only provided to selected research collaborators. By integrating expertise and services into the SciLifeLab Clinical Genomics platform, it will become possible to offer services for researchers nationwide, as well as to facilitate introduction of the technology into healthcare.

Scientific environment

The TGP has close collaboration with several national and international academic partners (e.g. Karolinska Institute, Lund university, Chalmers University of Technology, Boston University, Oslo University, and University of Graz), Research Institutes of Sweden (RISE), governmental agencies (National Forensics Center) and industrial partners (including SMEs). In addition, the TGP actively participates in several networks including the Liquid Biopsy working group within Genomic Medicine Sweden (GMS) and the European Liquid Biopsy Society. Pending approval, *the aim is now to integrate the SiMSen-Seq technology, currently part of TGP, into the SciLifeLab Clinical Genomics (CG) node at University of Gothenburg*, one of seven nodes within the national CG platform. CG Gothenburg has a close collaboration with the Center for Medical Genomics, Clinical Genetics and Genomics at Sahlgrenska University Hospital, enabling transfer of services into healthcare. Sequencing equipment and resources for data analysis are shared between the Sahlgrenska Academy at UGOT and the Sahlgrenska University Hospital via CG Gothenburg. Technology development is also carried out at Sahlgrenska Center for Cancer Research, UGOT, which is in close proximity to CG Gothenburg.

User base

The TGP is currently involved as a partner in >30 projects, mostly translational and clinically oriented. The project portfolio consists of research projects, within areas such as cancer, transplantation medicine, immunology, forensics and cardiovascular diseases, with main focus on cancer management and applications related to diagnostics, prognostication, monitoring of treatment efficiency and early detection of treatment resistance and relapse. Partners include academia, research institutes, health care and industry. Supported TGP projects have resulted in >60 research articles, 4 patent applications, and 2 start-up companies.

By the incorporation of the *SiMSen-Seq technology* into CG Gothenburg, several ongoing projects will benefit significantly as the analyses can be offered as a service with increased throughput, allowing larger sample cohorts to be examined. The expected user base in 2025 is ~15 PIs. Initially, services will be offered at CG Gothenburg and then disseminated to other nodes within the CG platform to cover an expected 50% yearly increase of users. We foresee that a full integration of this technology into the SciLifeLab portfolio will provide novel opportunities for the Swedish research community and by providing end-to-end service solutions, non-experts will be able to utilize this technology in exciting new applications and research areas.

Complementarity and synergistic opportunities within and across SciLifeLab platforms

Today, the TGP is already collaborating with several platforms within SciLifeLab. For example, we interact closely with CG Gothenburg by utilizing their equipment and computational resources. Another interaction is with the National Genomics Infrastructure (NGI), where we perform whole genome and whole exome sequencing. Most of our projects utilize liquid biopsies, where we often assess more analytes than nucleic acids, including proteins and metabolites which could be monotonized by analysis provided within the Clinical Proteomics and Immunology platform and the Metabolomics platform. Furthermore, we support GMS with identification of mutations at cancer diagnosis that are monitored in liquid biopsies.

Plans for incorporation of the operations into CG Gothenburg

The services provided by the TGP consist of clinical sample analysis and novel technology development. We now aim to offer ultrasensitive sequencing, especially SiMSen-Seq, to end users as a service at CG Gothenburg (2025), and to disseminate the technology and services to the other CG nodes depending on the demand nationally (2026). The initial services will include pre-analytics, analytics and bioinformatics where users may use one or several of these services. The first applications will include handling of liquid biopsies and analysis of circulating tumor-DNA in cancer management, as well as immune repertoire profiling, using the established clinical workflow of the SiMSen-Seq technology. New technologies and applications will continuously be incorporated as research services provided by CG platform during 2025–2028.

Budget request

Our platform has made a profound impact in promoting Swedish translational and clinical research and in developing and implementing new diagnostic assays within healthcare. The current SciLifeLab funding to our platform is 16.3 MSEK, which constitutes ~7% of the total platform budget (including user fees). In the budget for 2025-2028, we request a *yearly funding of on average* 23.5 MSEK, i.e. an increase by 6.2 MSEK (38%). Considering that we have had a significant positive impact on clinical research, public health and patient care, rapid progress in technology and the need for continued innovation and implementation going forward, we believe that the suggested increase of the SciLifeLab funding is timely and well justified.

We request that 6.65 MSEK of the total funding (28%) is allocated as a *Platform Strategic Budget*. As it requires a major investment in time to lead a platform with 117 FTEs and seven nodes at different universities and an extensive range of key partnerships to maintain, we are in need of increased resources for coordination (1 FTE) and compensation for our Platform Directors (0.5 FTE). To reach our goals within data management and data sharing, we also need to maintain our research data manager (0.5 FTE). Importantly, to remain responsive to the dynamic nature of the field, we request that 3.5 MSEK per year is allocated for projects within our translational technology focus areas, the nature of which will be decided on a yearly basis by the PMG. The Platform Strategic Budget also includes funding for our annual platform retreat and a few additional strategic and thematic meetings.

As detailed in the *Node-specific budgets*, we request that 15.3 MSEK per year (65%) is allocated directly to the nodes to support personnel and operations. Given that we foresee an increasing demand for ultrasensitive detection (e.g., of circulating tumor DNA), we specifically request that 1 MSEK per year during 2025-2026 is allocated to incorporate the SiMSen-Seq technology as a service within our platform, spearheaded by the CG Gothenburg node (see "SiMSen-Seq for ultrasensitive mutation detection").

Should the requested total budget not be allocated, we welcome a discussion on prioritization between the different budget items.

Table 1. Clinical Genomics – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Platform coordination officers 0.8 FTEs (2024) -> 1 FTE (2025–2028)	850	1 200	1 200	1 200	1 200
Research data manager 0.5 FTEs (2024) -> 0.5 FTE (2025–2028)	582	600	600	600	600
Platform directors 0.15 FTEs (2024) -> 0.5 FTE (2025–2028)	225	750	750	750	750
Strategic projects within Technology Focus Areas		3 500	3 500	3 500	3 500
Meetings (annual platform retreat, PMG meetings, focus meetings, outreach)	93	600	600	600	600
Sum costs (kSEK):	**1 750**	**6 650**	**6 650**	**6 650**	**6 650**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*1 750*	*6 650*	*6 650*	*6 650*	*6 650*
Sum revenues (kSEK):	**1 750**	**6 650**	**6 650**	**6 650**	**6 650**

Table 2. Clinical Genomics Gothenburg Budget

Costs	2024	2025	2026	2027	2028
Personnel 22 FTEs (2024) ->30 FTE (2024-2028)	25 500	26 100	26 800	27 400	28 100
Operations	2 500	2 700	2 900	3 100	3 300
Premises	1 400	1 400	1 400	1 400	1 400
Instrument depreciations	3 000	3 300	3 600	3 900	4 200
Translational Genomics Platform (SiMSen-Seq, implementation, knowledge transfer, suppport and dissemination)	-	1 000	1 000	-	-
Sum costs (kSEK):	**32 400**	**34 500**	**35 700**	**35 800**	**37 000**

Revenues [1]	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*2 174*	*2 500*	*2 500*	*2 500*	*2 500*
SciLifeLab funding (Translational Genomics Platform: SiMSen-Seq)	-	1 000	1 000	-	-
University Co-financing	9 600	9 600	9 600	9 600	9 600
University Hospital Co-Financing	4 300	4 730	5 203	5 723	6 296
SciLifeLab Pandemic Preparedness	380	-	-	-	-
GMS Vinnova, SweLife and other national initiatives	7 800	7 800	7 800	7 000	7 000
User fees	7 300	8 030	8 833	9 716	10 688
Sum revenues (kSEK):	**31 554**	**33 660**	**34 936**	**34 540**	**36 084**

[1] All funding is approved for 2024, 2025-2028 are prognosis

Table 3. Clinical Genomics Linköping Budget

Costs	2024	2025	2026	2027	2028
Personnel 3 FTEs (2024) -> 3.5 FTEs (2025–2028)	2 420	2 840	2 930	3 027	3 127
Operations	260	400	500	500	500
Premises	148	186	186	186	186
Instrument depreciations	-	740	740	740	740
Sum costs (kSEK):	**2 828**	**4 166**	**4 356**	**4 453**	**4 553**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*828*	*1 000*	*1 000*	*1 000*	*1 000*
University co-funding	828	1 000	1 000	1 000	1 000
GMS or other national initiatives within precision medicine	476	500	500	500	500
Pandemic Preparedness (transferred to 2024)	381				
Other (local research grants)		600	600	500	500
User fees	650	800	1 000	1 200	1 400
Sum revenues (kSEK):	**3 163**	**3 900**	**4 100**	**4 200**	**4 400**

Table 4. Clinical Genomics Lund Budget

Costs	2024	2025	2026	2027	2028
Personnel 12 FTEs (2024) -> 12 FTEs (2025–2028)	12 323	11 478	11 799	12 152	12 515
Operations	19 472	22 240	23 770	25 780	27 991
Premises	2 300	2 300	2 300	2 300	2 300
Instrument depreciations	5 632	4 533	3 067	2 643	1 985
Other	4 619	130	130	130	130
Sum costs (kSEK):	**44 346**	**40 680**	**41 066**	**43 005**	**44 921**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*2 174*	*2 500*	*2 500*	*2 500*	*2 500*
LU-Medfak	2 680	2 480			
LU-MedFak instrument (equipment, frontline large-scale sequencer)	4 600				
LU-Stemtherapy [1]	1 000	1 000	1 000		
SciLifeLab instrument	360	360	360		
SciLifeLab-Pandemic	381				
KAW- instrument	1 250	1 250	1 250	1 250	1 250
Vinnova GMS [1]	1 760	1 700	1 700	1 700	1 700
Financer FoU (RS) [2]	7 250	2 500	2 500	2 500	2 500
User fees	20 795	22 874	25 162	27 678	30 446
Sum revenues (kSEK):	**42 249**	**34 664**	**34 472**	**35 628**	**38 396**

[1] Uncertain funding
[2] Uncertain funding from 2026

Table 5. Clinical Genomics Stockholm Budget

Costs	2024	2025	2026	2027	2028
Personnel 40 FTEs (2024) -> 25 FTEs (2025–2028) [1]	35 000	30 000	25 000	25 000	25 000
Operations [2]	50 000	30 000	30 000	30 000	30 000
Premises	4 500	4 500	4 635	4 774	4 917
Instrument depreciations [3]	8 000	6 200	5 200	4 200	2 400
OH	10 000	7 000	7 000	7 000	7 000
Sum costs (kSEK):	**107 500**	**77 700**	**71 835**	**70 974**	**69 317**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*5 175*	*4 500*	*4 500*	*4 500*	*4 500*
University co-funding (KI) [4]	1 800	1 800	1 800	1 800	1 800
GMS and other national precision medicine initatives [4]	1 500	200	500	500	-
Funding agency: SciLifeLab PLP-1 G3P	450	-	-	-	-
KAW (novaseq X instrument depreciation)	1 250	1 250	1 250	1 250	750
University co-funding (KI) (PacBio Revio depreciation)	1 000	1 000	1 000	1 000	1 000
User fees	95 000	66 000	60 000	60 000	60 000
Sum revenues (kSEK):	**106 175**	**74 750**	**69 050**	**69 050**	**68 050**

[1] Reduced staffing due to some personnel will need to move to hospital side as analyses are transferred there
[2] Reduced expenses due to lower sequencing costs and selected analyses being transferred to healthcare
[3] Includes only current instrumentation, but there will be additional instruments purchased at some point
[4] Not decided for 2025-2028 (decision expected in Q3-Q4'2024)

Table 6. Clinical Genomics Umeå Budget

Costs	2024	2025	2026	2027	2028
Personnel 4.5 FTEs (2024) -> 6 FTEs (2025–2028)	4 181	5 181	5 581	5 692	5 806
Operations	250	500	1 000	1 000	1 000
Premises					
Instrument depreciations	600	600	600	600	600
Sum costs (kSEK):	**5 031**	**6 281**	**7 181**	**7 292**	**7 406**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*828*	*1 000*	*1 000*	*1 000*	*1 000*
University co-funding	1 000	1 000	1 000	1 000	1 000
Pandemic Prepardness (transferred to 2024)	380				
GMS	730				
ALF	1 000	1 000	1 000	1 000	1 000
Kempe Foundations	600	600	600	600	600
Other		1 000	1 000	1 000	1 000
User fees	650	1 650	2 550	2 800	2 800
Sum revenues (kSEK):	**5 188**	**6 250**	**7 150**	**7 400**	**7 400**

Table 7. Clinical Genomics Uppsala Budget

Costs	2024	2025	2026	2027	2028
Personnel 20.5 FTEs (2024) -> 23 FTEs (2025–2028)	24 431	25 400	26 500	26 800	27 400
Operations	4 731	5 000	5 500	5 900	6 400
Premises	280	350	400	450	500
Instrument depreciations	481	279	186	-	-
Sum costs (kSEK):	**29 923**	**31 029**	**32 586**	**33 150**	**34 300**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*2 588*	*2 800*	*2 800*	*2 800*	*2 800*
University co-funding (SFO) [1]	750	750	750	750	750
SciLifeLab instrument grants for depreciation	279	279	186	-	-
SciLifeLab Pandemic preparedness	381	-	-	-	-
ALF infrastructure [1]	3 500	3 500	3 500	3 500	3 500
ALF instrument grants for depreciations at UU	202	-	-	-	-
Vinnova, SweLife, other funding for national initiatives (GMS etc) [1]	2 007	2 000	2 000	2 000	2 000
User fees	13 500	14 000	15 500	16 000	17 000
Salary funding at Uppsala University Hospital/Region Uppsala	6 691	7 700	7 900	8 100	8 200
Sum revenues (kSEK):	**29 898**	**31 029**	**32 636**	**33 150**	**34 250**

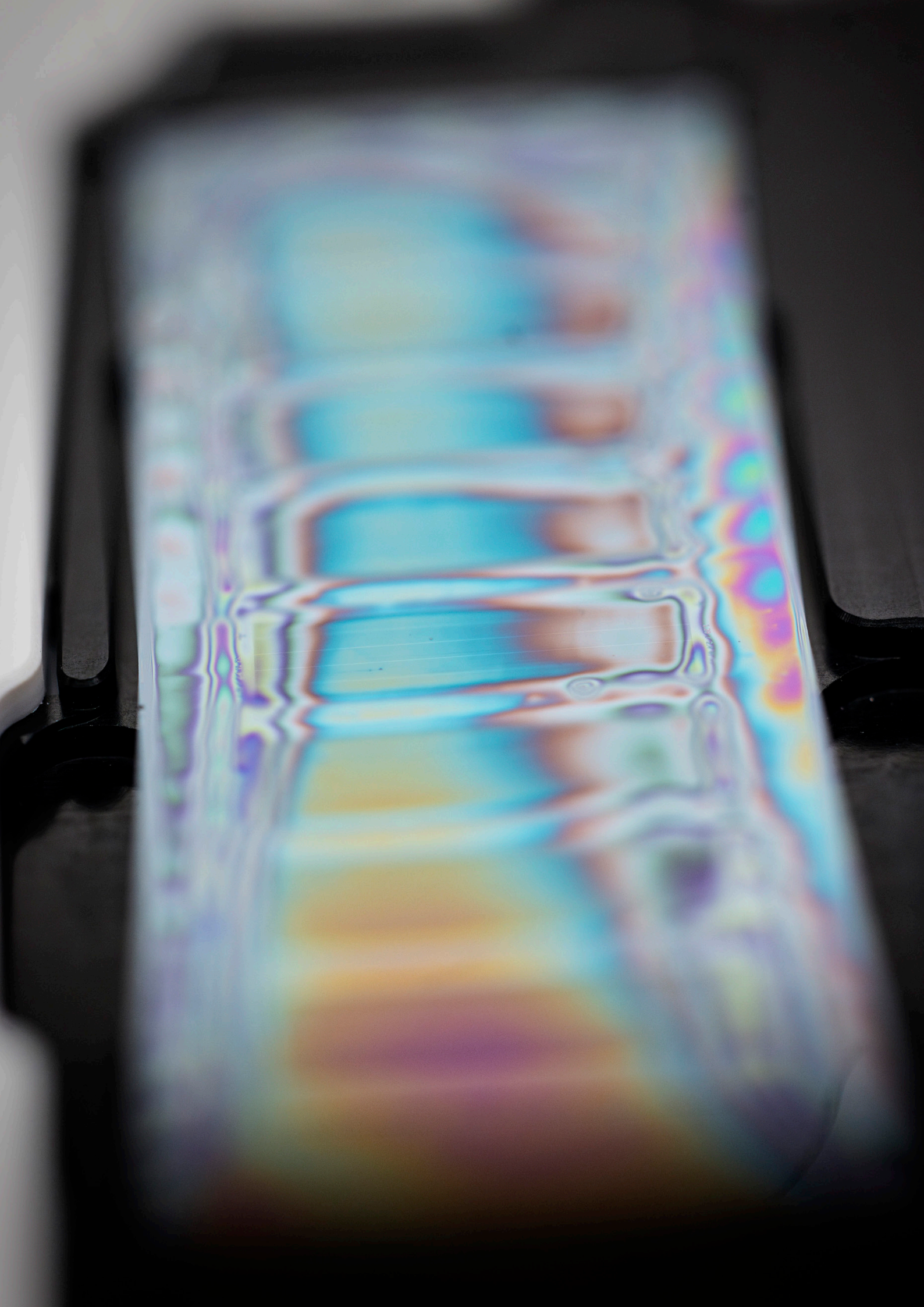
[1] Approved for 2024, 2025-2028 prognosis

Table 8. Clinical Genomics Örebro Budget

Costs	2024	2025	2026	2027	2028
Personnel 4 FTEs (2024) -> 6 FTEs (2025–2028)	4 281	4 709	5 180	5 698	6 267
Operations (services, licenses, reagents, data storage and backup)	6 357	6 992	7 692	8 461	9 307
Premises	73	75	77	240	264
Instrument depreciations	1 134	1 564	1 564	4 364	4 364
Sum costs (kSEK):	**11 844**	**13 340**	**14 512**	**18 762**	**20 202**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*828*	*1 000*	*1 000*	*1 000*	*1 000*
University co-funding	237	261	287	315	347
Hospital co-funding	3 107	3 418	3 759	4 375	5 077
Grants for instruments [1]	932	1 362	1 362	4 162	4 162
SciLifeLab Pandemic preparedness	474	-	-	-	-
User fees	6 500	7 000	7 500	8 000	8 500
Sum revenues (kSEK):	**12 078**	**13 040**	**13 908**	**17 853**	**19 086**

[1] 2025-2028 prognosis





Global Proteomics and Proteogenomics unit. Photo: Mikael Wallerstedt

Clinical Proteomics and Immunology Platform

Basic information

Platform Director: Masood Kamali-Moghaddam, Uppsala University

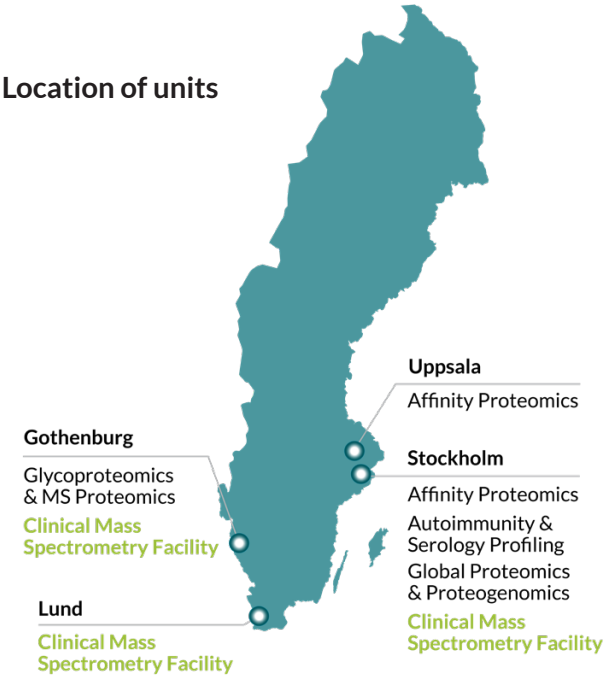
Platform Co-Director: Claudia Fredolini, KTH Royal Institute of Technology

Platform Coordination Officer: Claudia Fredolini, KTH Royal Institute of Technology

Platform vision: Impacting scientific discoveries and life science community by leading-edge proteomics services

Platform mission: Advancing scientific discovery, personalized medicine and global health through cutting-edge proteomics

Location of units

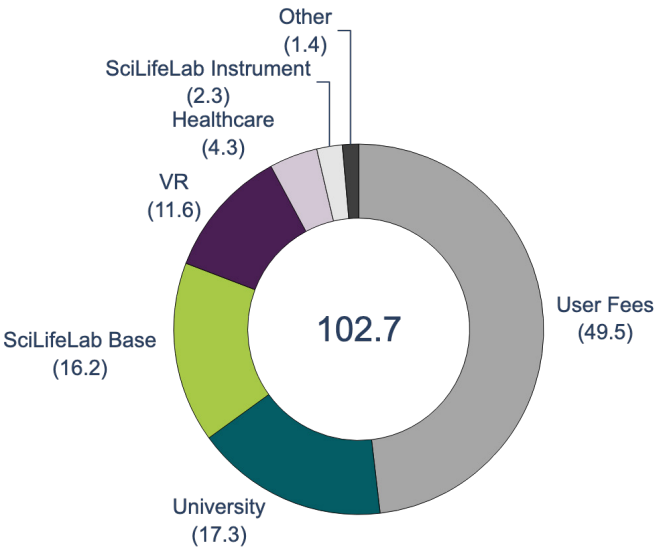


SciLifeLab Funding

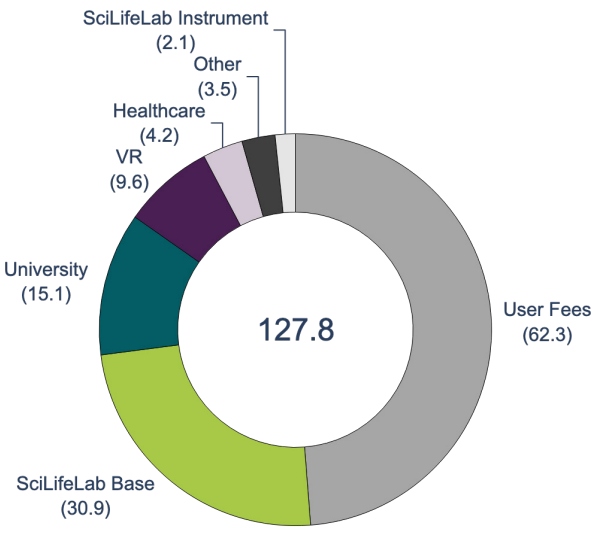
Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Afiinity Proteomics Stockholm	3.1	4.6
Affinity Proteomics Uppsala	3.1	4.6
Autoimmunity and Serology Profiling	3.0	4.8
Global Proteomics and Proteogenomics	3.6	4.9
Glycoproteomics and MS Proteomics	2.6	4.5
Clinical Mass Spectrometry Facility*	0.0	6.0
Platform Strategic Funding	*0.8*	*1.5*
Total SciLifeLab Funding	**16.2**	**30.9**

*Proposed to be included in the platform

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



Clinical Proteomics and Immunology Platform

Platform organization and governance

The Clinical Proteomics and Immunology (CPI) was formed in 2021 after the re-organization of the former Proteomics and Metabolomics platform. Today, CPI provides research support in proteomics by offering state-of-the-art mass spectrometry (MS), affinity proteomics and single cell analyzing tools.

The CPI platform is composed of five units located at five Swedish Universities: Autoimmunity and Serology Profiling (ASP, KTH); Affinity Proteomics with one node in Stockholm (APS, KTH) and one node in Uppsala (APU, UU); Glycoproteomics and MS-proteomics (GMP, GU), Global Proteomics and Proteogenomics (GPP, KI) and the Clinical-MS (CMS, LU, KI, GU), which has been suggested to include from 2025.

Each unit is managed by a Head of Unit (HU), with responsibility for personnel, budget and operative activities. HUs are also responsible for the scientific and the strategic development of the units together with the Platform Scientific Directors (PSD). PSDs are in most cases the principal investigators of research groups to which the units are associated. Units and research groups work synergistically by developing and implementing new technologies and assays.

The Platform Director (PD) and Co-Director (Co-PD) are responsible for the activities in the Platform Management Group (PMG), which includes all the PSDs and HUs. The PDs and PMG overlook the platform budget and deliverables. The Co-PD also acts as Platform Coordination Officer (PCO). The PCO coordinates operations and communication in the platform, organizes the PMG and HU meetings, and represents the platform in outreach events and PCO forums (*Figure 1*).

The PD and Co-PD/PCO meet every week and HUs meets biweekly to discuss platform operations. The PMG meets four times per year to evaluate platform achievement and discuss strategies and direction for future development. The PMG is supported by an international advisory board, which is currently composed of representatives and experts from Academia and Industry – Prof. Claudia Langenberg, is an expert in computational medicine and program leader at Charité - Universitätsmedizin Berlin; Prof. Darragh Duffy is the group leader of the Translational Immunology lab at the Institut Pasteur, Paris, his research interest lies in the mechanisms behind inter-individual differences in immune responses. PhD. Maria Lagerström-Fermer is the Head of Clinical Innovation and Business Planning at AstraZeneca. The members of the advisory board provide their complementary perspective and suggestions for platform scientific development.

Overall platform development and key achievements 2021–2024

Proteomics technologies are developing rapidly and today have reached a prominent role in the different disciplines of biological research. CPIs technologies provide tools and services to study detailed protein level regulation such as protein turn over, post-translational modification, protein interactions all the way to in-depth quantitative proteome analysis of cell and tissues. Sub-proteomes such as clinically relevant plasma and other body fluids proteomes provide organism level biological information, often in informative time series, whereas other methods can be harnessed to study sub-cellular proteomes and organelles. Recent technology developments both in affinity and MS-based proteomics have propelled high throughput capabilities allowing large sample series to be analyzed as well as improved sensitivity towards single cell proteomics.

In the Swedish research landscape of the last ten years, proteomics has assumed a prominent role, demonstrated by the Swedish Proteomics Society (SPS) established in 2001 and, by the Human Protein Atlas (HPA) started in 2003. Our platform and associated research corona is also key contributor on important infrastructures such as the National Swedish Infrastructure for Biological Mass Spectrometry (BioMS), Svenska masspektrometrisällskapet (SMSS), and the development of a large numbers of cutting-edge technologies for proteomics analysis, such as Proximity Extension Assay (PEA) commercialized by the Swedish spin-off company Olink (recently acquired by Themo Fisher).

The CPI platform development in the past four years focused on the creation of a comprehensive proteomics infrastructure integrating state-of-the-art mass spectrometry (MS) and affinity proteomics to support research excellence with high-performance instruments and unique multidisciplinary competences.

Starting in 2021, with an already highly competitive range of analytical instruments and methods for proteins profiling, quantification and characterization, we have continued to update our portfolio introducing a number of new technologies such as the Bruker single-cell proteomics TIMS-TOF and TIMS-TOFs with the Evosep LC system to reach the automation and throughput required in the analysis of clinical samples. Furthermore, an Orbitrap Eclipse Tribrid MS and Exploris 480 was acquired to enhance structural and quantitative analysis of glycoproteins, glycolipids and proteoglycans as well as phosphoproteins; and most recently Asymmetric Track Lossless (Astral) analyzer MS under purchase,

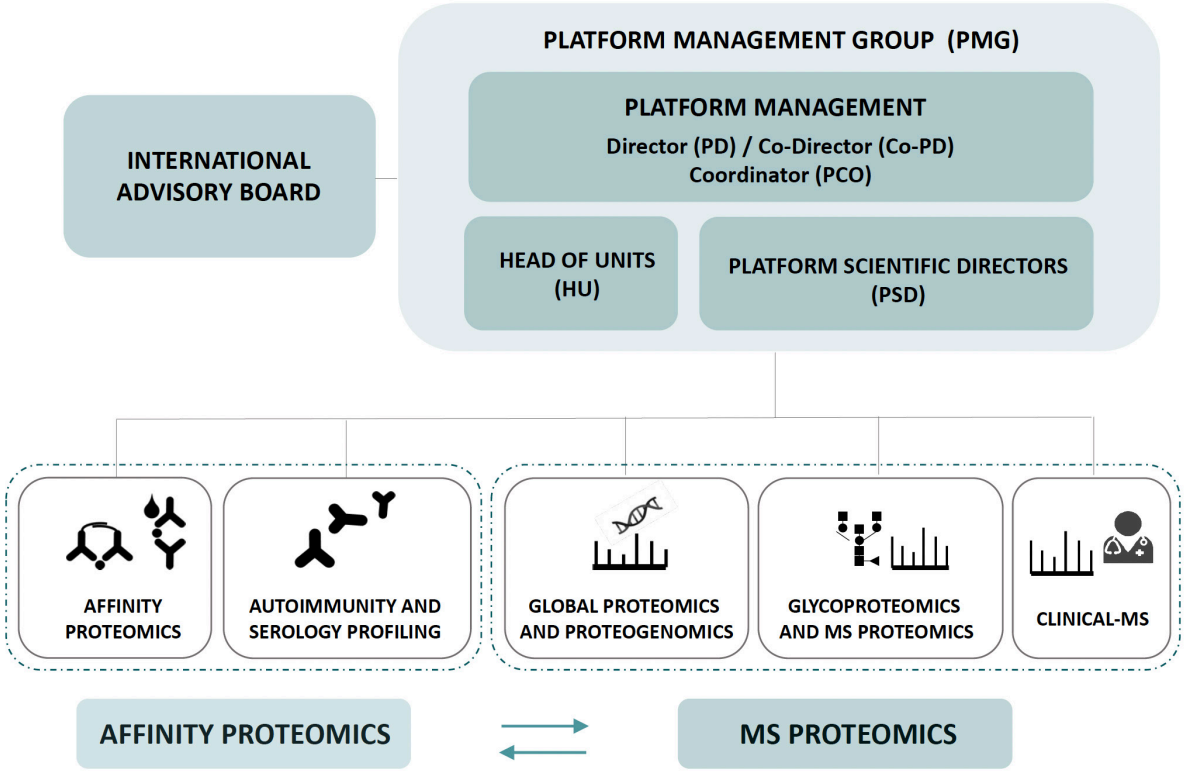


Figure 1. Platform organogram.

partly financed by SciLifeLab instrument call. In 2021, the SciLifeLab Explore Lab was established as a collaboration between the CPI and the Genomics platform to offer Olink Explore assays, as these require next generation sequencing readout for the simultaneous measurement of several thousand proteins. In 2023, we updated Explore to the latest version Explore-HT with up to 5,400 target proteins. In addition, CPI improved the depth of profiling of humoral immune and auto-immune response by a new planar array that includes 1,500 full-length proteins.

Knowing the international omics research landscape, we truly believe in the unique research opportunities inherent in the complementarity of MS and affinity proteomics. Therefore, in 2022, with the support by SciLifeLab funding, the GPP and the AP Uppsala and Stockholm units initiated a collaborative project to better understand the analytical features and proteome coverage capacity of MS and affinity-based proteomic technologies. The goal is to develop a unique plasma biomarker discovery pipeline based on in-depth MS plasma proteomics and Olink Explore that is seamlessly coupled with targeted quantitative affinity assay and MS-based PRM assays for biomarkers validation.

To highlight one of the many contributions, the platform has provided a tremendous and impactful research support during the COVID-19 pandemics, which led to CPI's prominent role in the Pandemic Laboratory Preparedness (PLP) and Precision Medicine (PM) capabilities.

During the first wave of the COVID-19 pandemic, a high performance multiplexed SARS-CoV-2 serology assays were developed by a multidisciplinary team. The assays were later offered by the ASP unit supporting research in various aspects of the immune-response to Sars-Cov-2. More than 200,000 plasma and serum samples were analyzed in less than two years. The AP units have also contributed substantially to the large serological effort by exploring different sample types and technologies. The Uppsala node analyzed a similar number of samples as ASP but with a focus on variants post wild-type, neutralizing antibodies and mucosal samples whereas AP-Stockholm introduced microsampling based sample collection and automated analysis to facilitate population studies and biomarkers monitoring. Biomarkers quantification in microsampling devices and alternative body fluids (eg. interstitial fluid, saliva, breath), remained an important direction of development for AP-Stockholm due to the high impact of low-invasive sampling in clinical proteomics and precision medicine.

Another equally important achievement was the creation of a pandemic sample center to facilitate handling of clinical specimens between university hospitals and SciLifeLab units.

Overall platform plans 2025–2028

In the period of 2021-2023, our platform has seen a remarkable development in unbiased MS-proteomics and targeted affinity-proteomics. Moreover, the reorganization of the platform at the management level has facilitated collaborations among units enhancing the overall impact of our proteomics contribution to the national and international scientific community, as described above.

The variety and versatility of our portfolio of proteomics technologies are now encouraging us to broaden our scope moving from "Clinical Proteomics" into "Proteomics". Opening up to all domains of biological protein-related research, we have initiated a closer collaboration with the Planetary Biology capability.

At the same time, we will strengthen our clinical proteomics capacity to provide an even more incisive support to the PM and PLP capabilities. Therefore, we plan to introduce (i) a Clinical MS-unit, dedicated to national trial support, diagnostic decision support, patient molecular phenotype and a harmonized service portfolio initially covering three university hospitals in Sweden and (ii) an affinity proteomics hub that will support an "immunoassay"-based pipeline for bio fluids biomarker discovery and validation. Clinical researchers will have access to powerful cutting-edge affinity-proteomics screening technologies, and to emerging advanced quantitative immunoassays for laboratory medicine as well as to microsampling and POC devices.

Our technology portfolio, which is managed by very competent staff, will be updated with the latest instruments and technologies in the field of proteomics such as new development in MS instrumentation, alternative affinity-based methods for proteome-wide analysis (eg. the Aptamer based SOMAscan assay >10,000 targets); and platforms for high throughput monoclonal antibody (mAb) characterizations (eg. the surface plasmon resonance (SPR)-based technology Carterra LSA). Our overall ambition as a platform is to provide harmonized procedures for project handling, proteomics workflows, data processing pipelines and data delivery. High priority will be to guarantee high quality standards in data generation and to provide the most reliable protein and biomarker analysis options as services to healthcare and industry. To achieve this, certification for ISO 17025 and GLP certification from SWEDAC are being discussed (also to align to the Genomics and Clinical Genomics platforms).

We aim, furthermore, at the developing of digital tools for our users to store, visualize, and deliver proteomics data. This will aid us in serving clinical decision-making support systems and establish internal data management systems similar to those already existing for genomics data sharing such as The Molecular Tumor Board Portal (mtbp.org).

For platform-centric budget, see page 114.

E4 Affinity-Based Proteomics

Affinity-based assays are arguably the clinically most useful, robust and high throughput tools for protein analysis of human samples. Most of today's diagnostic methods are though still single-plex version of these immunoassays (e.g. ELISAs, COBAS Roche, Immulite Siemens, etc). Recent breakthroughs in affinity-based assays have, however, enabled the simultaneous measurement of thousands of proteins within a wide range of concentrations as exemplified by the PEA and SOMAScan where thousands of proteins are detected in parallel. Technologies such as xMAP Microbead-Based Multiplex arrays (xMAP, Luminex), Quanterix' Single Molecule Arrays (SiMoA), MesoScale electrochemiluminescence (MSD) and Ella automated microfluidic assays (ProteinSimple) have furthermore shown to be especially powerful in the automation, versatility and quantification of low abundant clinical biomarkers. These recent technologies are outperforming existing clinical immunoassays and MS-based assays.

The AP and ASP units provide Swedish researchers with access to a unique affinity-based toolbox for protein-centric precision medicine research through the integration of in-deep individual phenotyping by mean of high multiplex (> 5,400 proteins) protein profiling, with accurate protein quantification to support the initial steps of biomarkers validation and translation into clinical applications.

The CPI platform currently includes two Affinity-based units, Affinity Proteomics - AP, with two nodes hosted by KTH in Stockholm and by in Uppsala University, respectively (scilifelab.se/units/affinity-proteomics) and the Autoimmunity and Serology Profiling - ASP, hosted by KTH (scilifelab.se/units/autoimmunity-profiling).

The two units, already equipped with nearly all of the aforementioned affinity technologies, represent reference laboratories for Swedish and international researchers interested in performing affinity proteomics analysis. All the units have shown the capability to support large population studies in collaboration with public entities (Swedish Public Health Agency, FoHM), large Swedish consortia; population-based biobanks and pharma companies. Every year, APS, APU and ASP together support more than 100 researchers and generate data for almost 100 scientific publications (publications.scilifelab.se). The users of our units belong mostly to Swedish academia (>70%), and the rest is a mix of industry, healthcare and international users. For 2023, the units supported 193 projects and ran in total 92600 samples.

KPI's

- Projects (2023): 193
- Number of samples (2023): 92600

Infographics: Statistics and Metrics for Affinity Proteomics Units

Affinity Proteomics Stockholm

Read more: Webpage, Publications Database

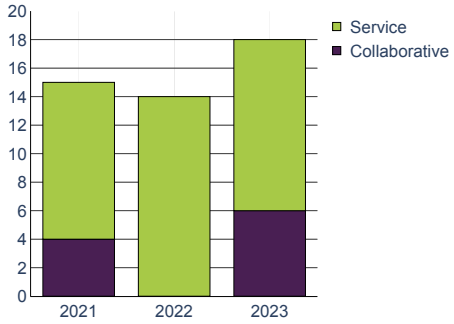
Basic Information

HU: Claudia Fredolini
Host University: KTH
SciLifeLab unit since: 2013
FTEs: 4
PSD: Jochen Schwenk

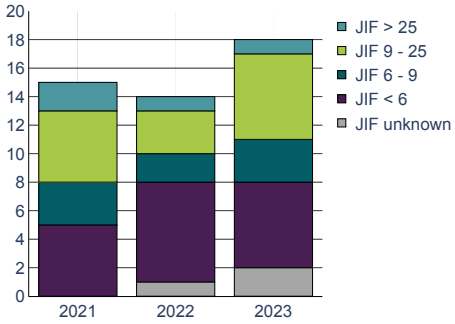
Funding 2023 (kSEK)

SciLifeLab: 3000
Other: 280
User Fees: 9000

Publications by category

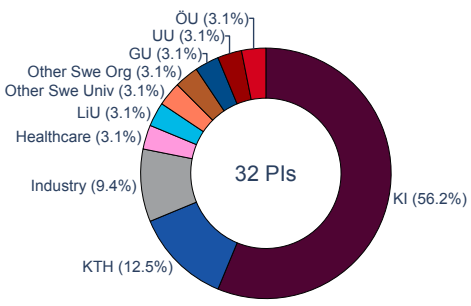


Publications by JIF

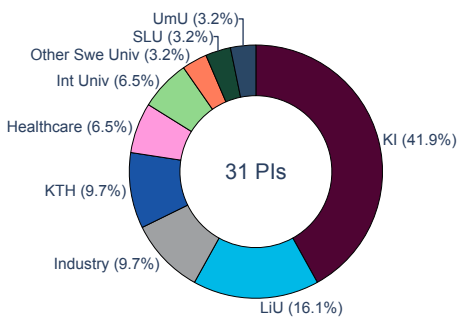


No. of Tech Dev Publications 2021 - 2023: 3

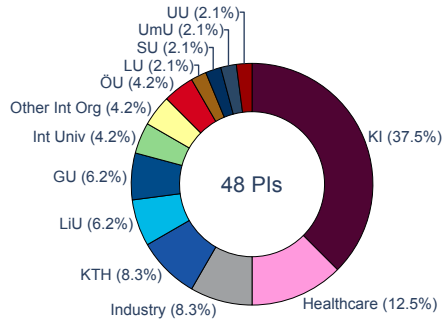
Users 2021



Users 2022



Users 2023



Affinity Proteomics Uppsala

Read more: Webpage, Publications Database

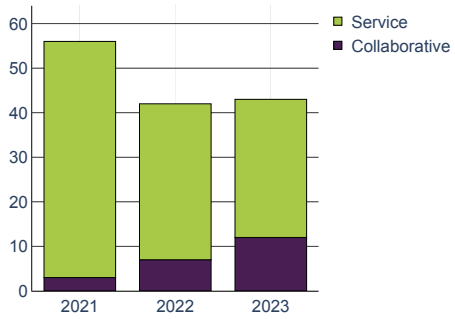
Basic Information

HU: Mikael Åberg
Host University: UU
SciLifeLab unit since: 2021
FTEs: 6
PSD: Masood Kamali-Moghaddam

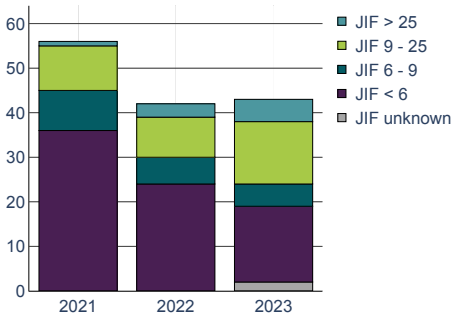
Funding 2023 (kSEK)

SciLifeLab: 3000
Other: 1780
User Fees: 31156

Publications by category

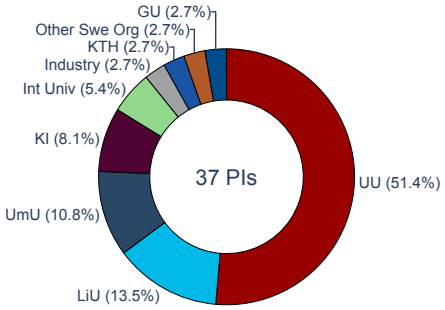


Publications by JIF

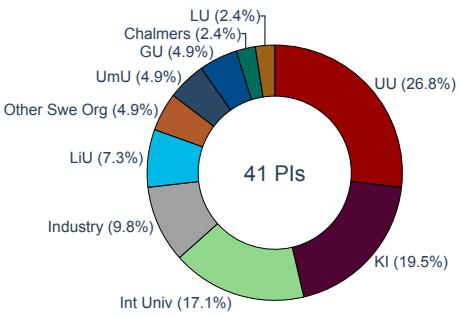


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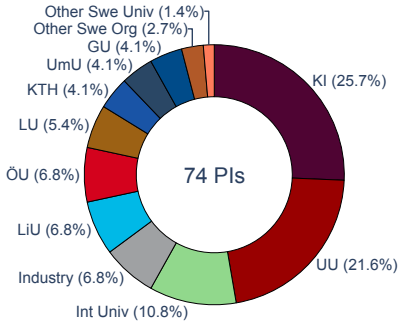
Users 2021



Users 2022



Users 2023



Autoimmunity and Serology Profiling

Read more: Webpage, Publications Database

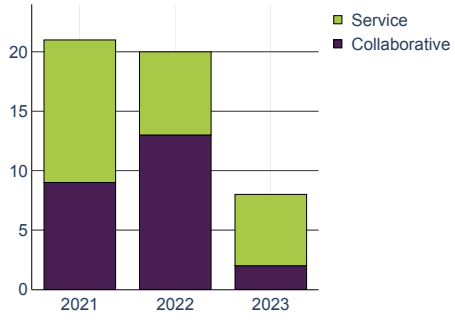
Basic Information

HU: Ronald Sjöberg
Host University: KTH
SciLifeLab unit since: 2013
FTEs: 4.3
PSD: Peter Nilsson

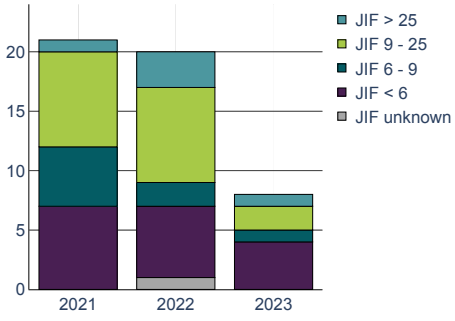
Funding 2023 (kSEK)

SciLifeLab: 2900
Other: 700
User Fees: 1000

Publications by category

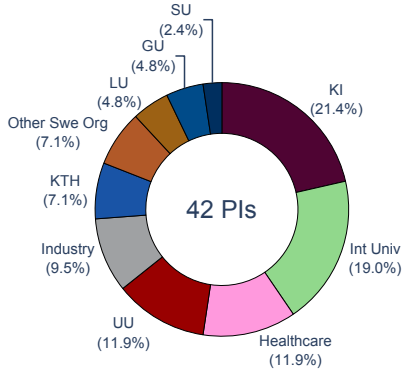


Publications by JIF

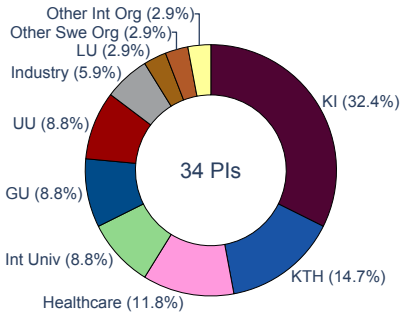


No. of Tech Dev Publications 2021 - 2023: 4

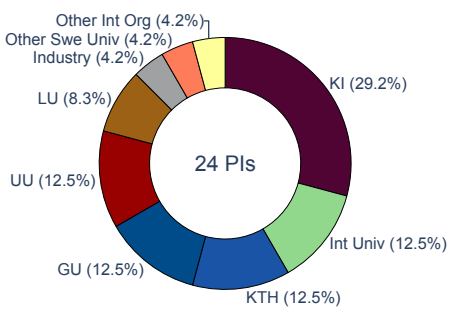
Users 2021



Users 2022



Users 2023



Expertise, technologies, and services offered

Affinity Proteomics (AP Stockholm and Uppsala)

Affinity-Proteomics (AP) is particularly suitable for the analysis of endogenous and exogenous proteins, extracellular vesicles and pathogens (eg. viral particles) in body fluids, cell supernatants and other liquid specimens. It is a powerful tool both on its own and as a vital part in multiomics studies combined with e.g. genomics and/or metabolomics. Low-plex ultra-sensitive quantitative assays can be used to validate novel panels of biomarkers, to monitor known proteins associated with disease progression and response to treatment as well as therapeutics drugs analogs. Proximity Ligation Assays (PLA) with dual and triple antibody recognition represent an advanced alternative to immunohistochemistry. Selected services provided by the AP are described in brief below.

- Proteome-wide profiling of body fluids, cells supernatants, cell/tissue lysates, extracellular vesicles (EVs) and viral particles.
- Highly sensitive absolute quantification of panels of biomarkers in body fluids, cell/tissue lysates, EVs, pathogen proteins and viral particles.
- Development of novel single and multi-plex immunoassays.
- Analysis of proteins-protein interactions and post-translational modifications in fixed cells, tissue sections and extracellular vesicles
- Analytical and research support for the development of diagnostic devices aiming at low invasive monitoring of protein biomarkers (eg. Dried Blood Spots (DBS), breath and interstitial fluid collectors, Point of Care (POC)).

Autoimmunity and Serology Profiling (ASP)

Profiling the antibody response to foreign or native antigens enable the exploration of the connection between infection, immune response, and autoimmunity. This connection, and the influence of autoantibodies, on disease pathologies have become of increasing interest for clinical research. The knowledge of autoantigens can be utilized for understanding disease onset and progression, as well as used for diagnostics and patient stratification. However, thorough screening of novel autoantigens requires access to high-throughput methodologies and large antigen libraries. The Autoimmunity and Serology Profiling (ASP) unit provides infrastructure and technologies for analysis of autoantibody repertoire in body fluids, as well as antibody validation using protein and peptide arrays.

Selected services provided by the ASP are described in brief below.

- Access to more than 42,000 human protein fragments generated by the Human Protein Atlas.
- Screening on the Secretome array, comprising of 1500 full-length secreted proteins.
- Serology (SARS-CoV-2) and autoantibody profiling in plasma, serum or CSF through screening on microarrays
- Epitope mapping and off-target analysis of affinity reagents as well as identified autoantibodies
- Custom designed protein array production using an Arrayjet Super Marathon with a JetMosphere Max™ and commercial protein and peptide arrays

Competence/background of staff and plans for keeping/attracting competent staff scientists

The affinity proteomics units have a long standing expertise in the field of proteomics. The main technologies currently available (Olink and Luminex) were developed by associate researchers and offered for the first time by our units in Sweden.

AP and ASP employ overall 18 scientists with relevant backgrounds and half of the team holds a PhD or above.

Unfortunately, academic salaries cannot compete with the private sector, therefore retaining personnel, in particular with a PhD level, can be challenging. However, our units are grounded on the vibrant international environment of SciLifeLab that offers attractive opportunities for continuous professional and personal growth (seminars, scientific events, training). The interest in continuously updating competence and skills is encouraged and all scientists (PhD and non-PhD level) have the opportunity to be involved in research, participate in conferences and take courses. While PhD level scientists can progress into infrastructure, academic careers and/or become leaders in start-up spun-out from collaboration with the units, the career path is currently limited for non-PhDs. Facilities are hybrid environments between academia and industry, and therefore an attractive opportunity could be to offer PhD programs dedicated to faculty careers similar to industry PhDs. Moreover, KTH and the Uppsala University are discussing the introduction of career path strategies also involving non-PhD level personnel similar to those adopted at KI.

Scientific environments and synergies with research groups, national/international networks

AP-Uppsala is hosted by the Department of Medical Sciences at Uppsala University and is connected to the Molecular Tools research program at the IGP Department (PIs M. Kamali-Moghaddam, U. Landegren and others). AP-Stockholm and ASP are hosted by the Division of Affinity Proteomics, Department of Protein Science at KTH where they are closely connected to Nilsson Lab and Schwenk Lab sharing lab environment and instrumentation. AP-Stockholm and AP-Uppsala, works synergistically as a

unique unit sharing project, personnel and premises/equipment when needed. Both units collaborate with the research labs. to develop new methods and technologies that can be later implemented as a service (Álvez MB, Nat Commun. 2023, Siegbahn, PLOS One 2023, K Suhre, Nature Reviews Genetics 2021, F Ribet, Adv Healthc Mater. 2023).

A highly performing, high-throughput and multiplex SARS-CoV-2 serology assay was developed by a multidisciplinary team from KTH (including Nilsson Lab) and SciLifeLab. The assay, now offered by the ASP unit, has been used to analyze more than 200,000 plasma and serum since the beginning of the pandemic [covid19dataportal.org], and contributed to high impact studies focusing on different aspects of the immune-response to Sars-Cov-2 and vaccines (S Hober, Clin Transl Immunology 2021; S Havervall, J Intern Med 2022, S Havervall , N Engl J Med. 2022).

The AP-Stockholm has equipment and expertise to develop multiplex quantitative immunoassays for body fluids biomarkers quantification and validation (Uhlén M, Sci Signal. 2019, RS. Häussler, Proteomics. 2019, Fredolini C, Sci Rep. 2019). In 2022, through the collaboration with JM. Schwenk (KTH), N Roxhed (KTH), O Beck (KI) and the company Capitainer AB, the unit introduced a semi-automated workflow for protein analysis in qDBS. The new pipeline enables to support biomarkers monitoring studies in large populations (N. Roxhed, Nat Commun. 2021). Furthermore, through the head of unit, C Fredolini, AP-Stockholm collaborates and/or has initiated new contact with researchers at KTH, KI, UU, Region Stockholm, MedTechLAb, and SciLifeLab Fellow, to name a few, A Russom, F Chiodi, K Alving, S. Alemann and E Setzgin.

Over the years a number of biotech start-up were developed within the Molecular Tool program in collaboration with AP-Uppsala (recently Sample Facts, Readily Diagnostics). Former start-ups are now entertaining close collaboration with the unit (eg. Olink Proteomics, Navinci Diagnostics, Vesicode).

AP- Uppsala recently collaborated with U. Landegren for the development of an homogeneous PCR-based assay for sensitive and specific detection of antibodies in serum or dried blood spots (DBS) (H. Zhao, N Biotechnol. 2022), and recently received a Proof of Concept grant (SciLifeLab's and Knut and Alice Wallenberg Foundation's program) for high-throughput analysis of specific antibody reactivity through the collaboration of the head of unit M Åberg with U. Landegren. The Unit, during the Covid-19 pandemic, started a collaboration with the Public Health Agency of Sweden and the PHA sponsored studies COMMUNITY (PI Charlotte Thålin, KI) and SÄBO (PI Mattias Forsell, UmU). The data produced is shared with the agency, CDC and WHO and have resulted in several publications in high impact journals (S Havervall, N Engl J Med. 2022, K Blom Lancet Infect Dis. 2023, L Vikström, Lancet Reg Health Eur. 2023). Furthermore, the affinity-proteomics units are connected, to the Human Protein Atlas Projects (HPA) to the international HUPO plasma proteome project (HPPP) and Human Brain Proteome Project (HBPP). AP-Stockholm and ASP are also part of the European infrastructure for translational medicine (EATRIS) and currently partners in the EU cluster project canSERV.

Procedure for prioritization of projects and user fee model(s)

The affinity-based proteomics units have a first-come-first-serve policy with highest priority given to national academic users. However, in periods of high request and limited access, a strict queue and prioritization system is applied. The submission of a project proposal is usually followed by an introductory meeting with the user. The projects are then assessed according to technical feasibility, current availability of the required capacity and resources, scientific potential, supporting preliminary data, significance of unit specific technologies, and if the proposed project supports unit development in competency and techniques. Priority is often given to user that are continuing a research project that the unit has supported previously to ensure continuity. The units usually accept all requests for large cohort protein profiling projects (e.g. EU projects) assuming that scientific quality has been thoroughly reviewed by the funding organization, while projects requiring new technology and/or methods development are more strictly evaluated. Priority is given to methods with the potential to become of broad interest for the Swedish research community, or to contribute to the unit development and can be established later as new services. The units follow a user-fee model where Swedish academic users are charged for reagents, consumables and a fee for instrument maintenance, while international and industry users also cover personnel cost.

User base (current and expected 2025–2028)

AP and ASP provide research support to Swedish and international academia, healthcare and industry, where international and industry users represent a minor part. The projects cover support research in a broad range of disciplines including Immunology, Microbiology, Cardiology, Neuroscience, Oncology, Clinical Chemistry but also Molecular Biology and Biomedical Engineering.

We have analyzed a number of large Swedish and International cohort studies including EU funded project (e.g. Psych-Strata, Pancaid, Discern, IMI-DIRECT); U-CAN, KARMA SNAC-K Swedish cohort, the Karolinska COVID19 Study Group, Scapis, EpiHealth, GÅS, SIMPLER, Swedish Twin-registry, PREDICT, U-CAN and Global Neurodegeneration Proteomics Consortium (GNPC) and other international projects funded by industry, private foundations or agencies (e.g. IMI-projects, HPA foundation, Gates Ventures, WHO, Public Health Agency of Sweden, NIH).

The number of PIs and projects has overall increased over the period 2021-2023 (from 150 to 193; ~25%) and based on the increased interest in data driven life sciences and precision medicine, we foresee this increase to continue for the period of 2025-2028.

Plans for development including new technologies/service offerings 2025–2028

The AP and ASP units are planning to join forces to create a new Swedish infrastructure that will support discovery and validation of clinical protein biomarkers in body fluids using affinity-based proteomics (Clinical AP). Benefiting from the large collaborative network of which the units are part of, a multidisciplinary environment gathering together clinicians, clinical researchers, experts in clinical chemistry and laboratory medicine, biomedical engineers and industry will be created. The new infrastructure will offer resources and competence to support translational proteomics research and to evaluate the analytical performances of emerging affinity proteomics technologies for clinical chemistry labs. Clinical-AP aims to provide a more incisive support to the Precision Medicine(PM) and Pandemic Laboratory Preparedness (PLP) capabilities. The current technology portfolio will be expanded acquiring the latest platform and instruments in the field.

AP-Stockholm, will continue to work at the interface between engineers and clinicians to support development and assessment of analytical performances and utility of new microsampling and point of care (POC) devices (N. Roxhed, Nat Commun. 2021, Hauser, Anal Chem. 2023). Due to an increase in demand for customized quantitative multiplex immunoassays (low-medium plex), and more in general for support in biomarkers validation, pipelines for assay development will be further optimized (eventually in collaboration with commercial partners). The Quanterix SP-X Imaging and Analysis System was recently acquired to expand the existing SiMoA equipment. Finally, alternative platforms for extensive protein profiling such as the SOMAscan system offered by SomaLogic or the newly established Alamar Bioscience NULISA are under evaluation. The SOMAscan assay is based on Slow Off-rate Modified Aptamer (SOMAmers) and enables the simultaneous quantification of >10000 proteins. In the US and UK, SOMAscan has already proven its immense capability to aid diagnostic testing. SomaLogic has recently partnered with Illumina, this may lead to a future expansion of the proteome profiling capacity adding NGS readout. SOMAscan is not available in any laboratory in Sweden and we believe it to be exceptional complement to the Olink Explore technology, eventually as further collaboration with NGI.

The ASP unit plan to introduce the system Carterra. Carterra LSA is based on surface plasmon resonance (SPR) which is a reliable and tested technology with proven advantages over similar systems for high throughput monoclonal antibody (mAb) characterizations. The Carterra LSA platform is well positioned to become the new gold standard for drug discovery and antibody therapeutics research and will be possibly acquired in collaboration with the Drug Development and Discovery (DDD) platform. Another forward-looking goal of APS will be to replace the current microarray spotter, the Arrayjet Super Marathon, with the next generation spotter, the Arrayjet Mercury.

Due to the high user interest and increased demand, AP-Uppsala plans to continue its investments in being a world leading core lab for high-throughput multiplex proteomics (eg Olink technology) and to be an early adopter of new panels, methods and sample types. Similarly to AP-Stockholm, we assist to an increased demand for single-plex or low-plex assays stemming from the larger screening studies. We use the Meso-Scale platform for new assay development. One example of implementing new sample types is by adapting the Explore platform for extracellular vesicle (EV) analysis. The field of EVs has greatly developed during the last decade and compelling evidence demonstrate their roles in health and disease, and their potential, amongst others, as a novel family of biomarkers and as promising drug delivery agents. A collaboration between MolTools/UU and the Akademiska hospital/UU has initiated to implement of a portfolio of technologies for EV analysis ranging from proteomics to flow cytometry to Nanoparticle Tracking Analysis.

Other applications/technologies that will be explored are single-cell proteomics based on molecular pixelation (by Pixelgen) eventually in collaboration with NGI Uppsala (due to a sequencing read out)).

Finally, leveraging on a successful pilot project conducted together with the DanioReadout service facility at Uppsala University, AP-Uppsala will explore the opportunity for affinity-based profiling of proteins in Zebrafish models developing customized assays.

Plans for data handling and analysis 2025–2028 including a plan on how to make data open and FAIR

AP and ASP generate protein level data on human sample materials; hence the data are made available as governed by the consent and as GDPR regulations. The raw and processed data are stored in our secure servers 20 core server and backed up to KTH's parallel distributed computing center, and then shared with PIs using password-protected links. PIs are encouraged to share the data using public repositories, handling affinity-proteomics data such as the COVID19 data portal (covid19dataportal.org) or similar alternatives.

However, since affinity-proteomics is a newer field in respect to MS-proteomics, most of the data repositories currently available are tailored to share exclusively MS data, hence the units has recently started an interaction

with Pride (ebi.ac.uk/pride) and the company Olink to develop a pipeline enabling the upload of affinity-based proteomics data on Pride.

The units aim as well at the development of a clinical decision support system (CDSS) for data delivery similar to the Molecular Tumor Board Portal (mtbp.org/welcome.php). The overall aim of the proposed CDSS will be to make affinity-proteomics data available to medical doctors, to encourage their use by medical doctors eventually as a complement to genomics data.

Current bottlenecks (if any) that prevent:

(i) the units from meeting the user demand

Lack of funding for staff. In the past years, the units have experienced an increase in project requests and numbers of samples to be analyzed per project. This confirms the interest in affinity proteomics technologies and demonstrates the competences in the Swedish and international scientific community, but it pushes our current resources to their limits. Due to the lack of staff available to take on yet another project, we had to, from time to time, deprioritized (i) activities dedicated to the improvement of our workflows and protocols (automation, standardization); (ii) projects requests involving the development of new methods tailored to answer specific biological questions; and (iii) requests for developing customized multiplexed immunoassays (eg. for validation and verification of panels of biomarkers). Hence, we are now in great need to increase of the base SciLifeLab funding. In addition, we are actively planning to create an affinity-proteomics infrastructure to attract additional funding (an application was submitted during the fall to Swedish Research Council-SRC (Inventory of needs 2023-Research infrastructure).

Long lab reconstruction works (AP-Stockholm and ASP). During 2023, a considerable limitation in the operations was experienced by the units in Solna due to inaccessibility of the main lab, as a reconstruction required to become compliant to BSL-2 specification took place over a long period of the year. The Solna-based units are still experiencing limitations due to lack of available laboratory space at SciLifeLab campus Solna, which have prevented them from acquiring additional technologies requiring large lab space.

(ii) the data generated to be efficiently shared and transformed to knowledge, publications, and translations

For projects involving the application of routine SOPs, unit's scientists are often not involved in the process that follows the generation and QC of the data up to the publication, and the units are only consulted during manuscript writing for collaborative projects. Unfortunately, some users do not feel comfortable sharing data and knowledge pertaining to their projects, and this lack of openness can limit the quality of the scientific output. Additionally, translation of candidate biomarkers into application is often limited by lack of funding to engage in the steps following the discovery phase. Here we see a strong need for a tighter collaboration between academic/clinical researchers and industry, thus we proposed an affinity proteomics infrastructure capable of facilitating these types of interactions.

NBIS – current support and needs for 2025–2028

Similarly, to the MS-proteomics units, we see an important need for bioinformatics support for study design, data analysis and interpretation (*see also above*). To ensure the necessary support, NBIS has previously agreed to create a direct contact with dedicated experts in proteomics data analysis to whom we can address our users. However, according to NBIS, they receive a very limited number of proteomics projects, eventually reflecting the choice of our users to perform data analysis on their own. To ensure the quality of downstream data processing, analysis and publication, it would be desirable to follow a standard procedure for review and acceptance of proteomics projects that would include a bioinformatician together with the team of experts in affinity-proteomics and clinical chemistry. We acknowledge that NBIS may not have the capacity to engage in all revisions of a project, however, such a procedure would guarantee a brief consultation to each project, limiting acceptance only to those designed to lead to a high-quality scientific outcome and publication.

Data Centre – current support and needs for 2025–2028

So far, the AP and ASP units have not received any meaningful support from the Data Centre. The AP unit (both Stockholm and Uppsala node) has reached out to ask for assistance but the requests have so far been turned down due to lack of resources, and our requests were eventually considered too specific for the Data Centre. Despite the units interest in some of the resources available to the whole SciLifeLab such as The Orderportal and the Data Delivery System (DDS) (*still in preparation*), we would expect Data Center to be available to discuss needs specifically associated to our area of support, including generation of an affinity proteomics data repository, development and maintenance of shiny apps for randomization of samples, power calculation etc. In one of the many examples that has yet to receive the required attention and support, Data Center could build a unified data sharing interface that could be connected to the university's data management system.

Synergies and current/planned collaborations with SciLifeLab units and capabilities) other SciLifeLab units and platforms

The AP units work in strong connections with the platforms of Genomics (Explore Lab) and Bioinformatics, AP-Stockholm has collaborated with the Drug Discovery and Development (DDD) platform (Human Antibody Therapeutics unit) for the screening of human antibody fragments against intact Sars-Cov-2). AP and ASP are particularly suited to support studies focused on the investigation of immune-response to infectious diseases and circulating proteins biomarkers. As mentioned previously, during the pandemic we provided an outstanding contribution through serology profiling and by establishing a protocol to facilitate surveillance studies using microsampling (>400000 samples analyzed and >80 publications). The units are currently co-financed by the PLP SciLifeLab program through two grants ((RePLP1 – Multiplex and high-throughput multi-disease serology – P. Nilsson, and PLP2 – Strengthening population health surveillance and epidemics monitoring by microsampling– C Fredolini). AP and ASP have participated in discussion and planning of the precision medicine (PM) capability roadmap, providing their expertise and perspectives, and are willing to contribute more concretely to aspects such as body fluid biomarker based strategies for population screening, early diagnosis and monitoring of the response to individual treatments.

Collaboration with industry, healthcare, and other organizations

The affinity proteomics units host a critical mass of affinity proteomics technologies and have established strong collaborations with companies providing instrumentation and reagents such as Luminex and Olink (e.g. as beta tester), Biotechne, Navinci AB. AP collaborates with biotech companies and supports the development and dissemination of microsampling devices such as: qDBS (Capitainer AB), breath collectors (Munplast AB, Breath Explore), plasma DBS (SampleFacts AB).

The units collaborate with a number of clinicians at Region Stockholm, the Swedish Public Health Agency (FoHM), and are connected with national and international organizations such as the Human Protein Atlas (HPA), the Human Proteome Organization (HUPO), the European Infrastructure for Translational Medicine (EATRIS).

Current training offerings and plan for 2025–2028

Heads of units and senior staff at the affinity proteomics units are engaged in training in the form of teaching in PhD and master level courses as guest lecturers or hosting PhD students at the unit to learn our methods and workflow. Our plan for 2025-2025 is to increase the awareness and understanding of emerging affinity proteomics technologies and their potentials in translational research among clinicians, industry and healthcare. PhD level courses open to national and international students and professionals are planned. The courses will be hosted respectively by Uppsala University (*Advanced Molecular technology and instrumentation for proteome analysis*) and KTH (*Affinity Proteomics for bio fluid biomarkers and precision medicine*). The units will be supported in generating digital training material and video-recorded work-shops by SciLifeLab Training Hub.

Budget Affinity-Based Proteomics

See page 114.

E5 MS-Based Proteomics

Recent developments of mass spectrometry (MS) have enabled proteome analysis to contribute profoundly on the analysis of biological and environmental systems by comprehensive molecular phenotype data and detailed molecular data of its components. Fields such as systems biology and meta-proteomics have catalyzed major leaps in our understanding of the world. And an increased throughput of in-depth proteomics has open the field to the analysis of large clinical cohorts required at a precision medicine era. In the context of precision medicine, the proteome represents the molecular phenotype that connects genotypes and phenotypes with mechanistic details of biological systems, ultimately leading to the identification of new actionable biomarkers and drug targets. MS analysis is arguably the most versatile and powerful tool for global protein analysis of biological systems and for detailed analysis of molecular structures and protein networks. Access to the latest MS instrumentation, methods and expertise need to be made available for all competitive projects, regardless of local resources, to provide Swedish researchers the opportunity to integrate powerful molecular phenotype analysis in their research. MS-based proteomics fulfills all criteria of a national research infrastructure by following rapid development in the field with heavy infrastructure investment needs, high demand on domain specific expertise, and a wide range of MS-applications spread over the life science field. Biological MS provides an important data layer to allow for example to connect genotypes with molecular phenotypes, images to molecular structural data or subcellular protein location down to variant and protein modification level, or as a vital part of precision medicine.

The CPI platform currently includes two MS-based units, Global Proteomics and Proteogenomics- GPP, located at KI, (scilifelab.se/units/global-proteomics-and-proteogenomics) and Glycoproteomics and MS-proteomics-GMP, located at GU (scilifelab.se/units/glycoproteomics-and-ms-proteomics) serving wide range of projects across the country and domains of biological and biomedical research. The aim is also to strengthen our capacity to perform clinical MS by introducing a dedicated Clinical MS-proteomics unit (described separately below). The units have obtained and maintained a critical mass of funding and expertise to ensure a cutting-edge instrument park as well as highly skilled personnel that provides service in broad range of MS-based proteomics applications to encompass the needs of the Swedish life science community. Services include global quantitative proteomics (QMS) and proteome profiling, in-depth proteomics, interaction or network studies by affinity purification or proximity labeling prior to MS and post-translational modification (PTM) analysis. The service facilities have also acquired vast expertise and developed SOP on various types of samples and sub-proteome analysis, such as exosomes, paleo-proteomics, model and biodiversity analysis on animals, plants, bacteria as well as consultation on project design in biological mass spectrometry. In addition, the units provide world leading support on specialized applications in glycoproteomics, glycomics, proteogenomics and clinical MS-based proteomics.

Infographics: Statistics and Metrics for MS-Based Proteomics Units

Global Proteomics and Proteogenomics

Read more: Webpage, Publications Database

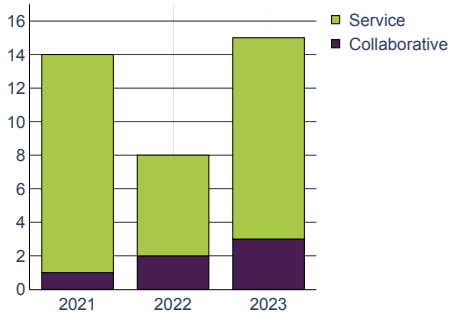
Basic Information

HU: Maria Pernemalm
Host University: KI
SciLifeLab unit since: 2017
FTEs: 7.8
PSD: Janne Lehtiö

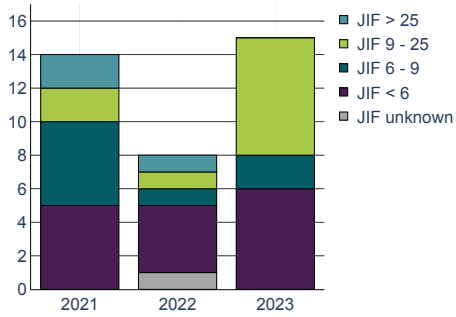
Funding 2023 (kSEK)

SciLifeLab: 3500
Other: 14942
User Fees: 3570

Publications by category

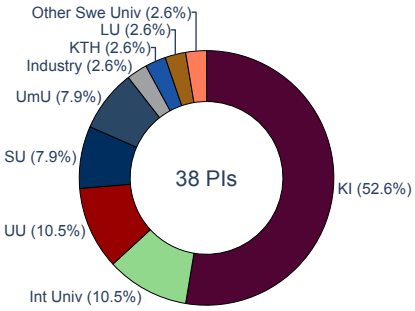


Publications by JIF

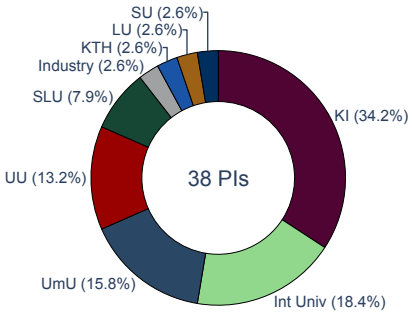


No. of Tech Dev Publications 2021 - 2023: 14

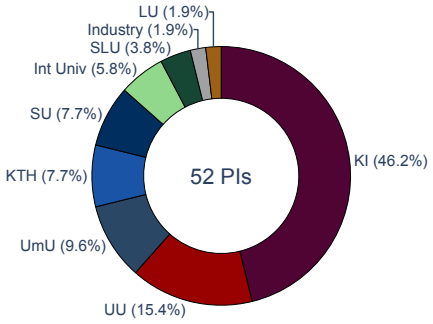
Users 2021



Users 2022



Users 2023



Glycoproteomics and MS Proteomics

Read more: Webpage, Publications Database

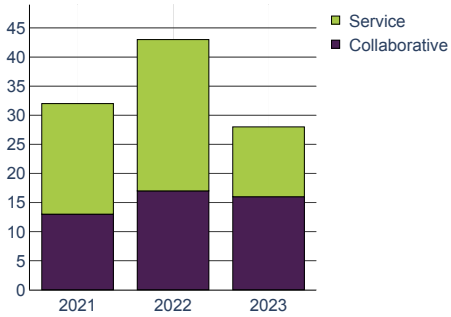
Basic Information

HU: Carina Sihlbom Wallem
Host University: GU
SciLifeLab unit since: 2021
FTEs: 12.1
PSD: Ekaterina Mirgorodskaya

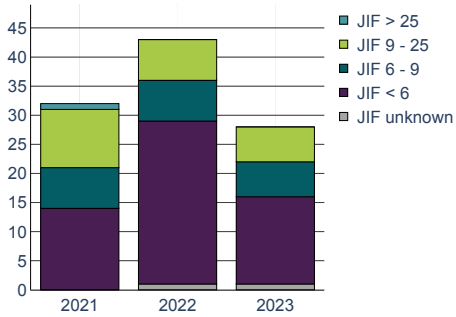
Funding 2023 (kSEK)

SciLifeLab: 2500
Other: 17790
User Fees: 5506

Publications by category

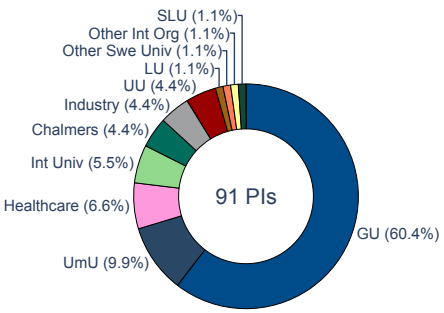


Publications by JIF

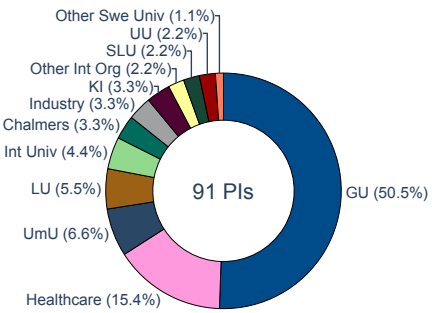


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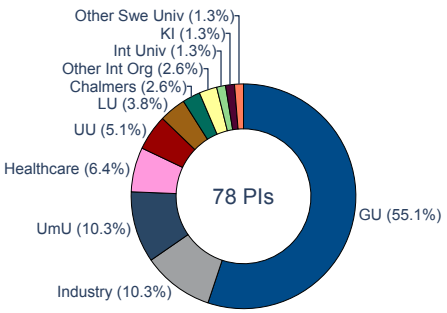
Users 2021



Users 2022



Users 2023



Expertise, technologies, and services offered

Global Proteomics and Proteogenomics – GPP

Proteogenomics combines proteomics information with sample specific genomic information and can be used to discover novel protein coding regions/genes and to provide protein level-evidence to confirm the protein coding potential of a gene; thereby improving genome annotation. In addition, proteogenomics can also be used to detect novel proteoforms/variants by patient specific protein sequence analysis based on DNA or RNA sequencing data for pQTL analysis, analyze impact of mutations and SNPs on post-translational modification or protein localization and create customized databases for analyzing novel and variant peptides based (on putative gene models, long non-coding RNAs etc.), meta proteomics, xeno-proteomics to study host-virus interactions and 6RF whole genome searches for *de-novo* use of peptide level data for genome annotation. Selected services provided by the GPP are described in brief below.

- Personalized proteomics -Individual sequence-based search database generation for variant analysis at the protein level coupled with in-depth quantitative proteome analysis.
- Disease state/Variant proteomics – Database supplemented with all known SNPs and disease-causing genetic alterations. (Can be used when sample specific sequence data is not available.)
- Unbiased proteogenomics in any species with a sequenced genome – Three/Six frame translation of genome generated database searches for protein coding genome annotation.
- XenoProteomics – Database suppl. with proteins/peptides from disease causing pathogens.
- Meta proteomics – Proteogenomics analysis based on metagenomics database generation.

Glycoproteomics and MS proteomics – GMP

The structural and functional signatures of proteins PTMs are essential for cellular signaling and cell-to-cell communication and interactions, furthermore PTMs increase the genome generated functional space and diversity of proteomes by many folds. Protein glycosylation holds a special position among PTMs due to the immense structural diversity, which makes glycoproteomics a challenging research field. The unravelling of glycan interactions in cell biology and the establishment of glycan biomarkers from clinical samples are expected to become increasingly important. Glycoproteomics is based on MS technologies used for global or directed analysis of proteins, glycans and glycoconjugates in various biological samples. It combines available methodologies to address the complexity of a glycoproteome. Proteins carrying glycosylation are identified and quantified. The glycan localization, sites occupancy and microheterogeneity are determined. To accomplish this a series of enrichment strategies, fragmentation techniques as well as bioinformatic tools are available in the research support. Selected services provided by the GMP are described in brief below.

- Structural characterization, global analysis and quantification of N- / O-linked glycopeptides.
- Screening and characterization of free oligo-saccharides and liberated glycans from glycolipids and glycoproteins for comparative glycomics.
- Analysis of glycosaminoglycans and proteoglycans
- Identification and relative quantification of phosphorylation and other modifications.
- Global quantitative proteomics – eg Tandem-mass tags (TMT), samples analyzed in parallel.

Competence/background of staff and plans for keeping/attracting competent staff scientists

The MS units and affiliated researchers have a solid expertise in the proteomics field. The GPP unit was the first dedicated proteogenomics facility in the world and has continuously developed both analytical methods and downstream bioinformatics pipelines to improve the analysis. The unit currently employs 17 people all PhD level. The staff covers a broad range of expertise including mass spectrometrists, scientific programmers, molecular biologists, biochemists and engineers, many of which spend part of their position in research developing methods that are later implemented as services in the facility. The GMP unit consists of 13 people, with a majority of Ph.D. education and very long experience in experimental study design, analytical quality assurance, method development, and automation. The broad research competence comes from a variety of international institutes: UCSF, ETH Zurich, Max Planck Berlin, Boston School of Medicine, University of Southern Denmark, Inst Molecular Biotechnology in Vienna, Helmholtz Centre in Germany, Macquarie University in Sydney, Tallin University as well as the pharmaceutical industry. Our facilities have also extensive collaboration internationally with Nordic proteomics community, EUPA and HUPO.

To promote the career opportunities for infrastructure personnel, Karolinska institute has already adapted a career path for infrastructure personnel and the staff working in the facility have transferred their positions into this career path, ki.se/en/about/qualifications-portfolio-for-research-infrastructure-specialist-and-senior-research. University of Gothenburg is in progress to develop a similar career path strategy, also involving non-PhD levels, meanwhile providing financing for personal development and visits to conferences and courses.

Scientific environments and synergies with research groups, national/international networks

The GPP unit is closely connected to the Cancer proteomics group at KI headed by Professor Janne Lehtiö. The research group and the unit provide an ecosystem for knowledge transfer and co-development where methods developed in the research group can be adapted as a service in the GPP unit (Arslan, Nature Protocols 2022, Umer, Bioinformatics 2022, Lehtio, Nature Cancer, 2021). The links to the research group also provide continuous development for the facility staff and the possibility to engage in development projects. Nationally the unit is connected to Genomic Medicine Sweden (GMS) (genomicmedicine.se through the chair Richard Rosenquist Brandell, (Herbst, Nature comm, 2022) and in Europe the unit is engaged in the Cancer Core Europe network providing MS-analysis as well as being part in developing the molecular tumor board portal (MTBP), a clinical decision tool facilitating the interpretation of omics data (CCE/MTBP/DART) (Tamborero, Nature Med, 2020, Tamborero, Nature Cancer, 2022). Globally the unit is connected to the plasma proteome project (HPPP) through head of unit Maria Pernemalm (Deutsch, JPR, 2021). The bioinformatics team has collaborations with Pride (ebi.ac.uk/pride), where pride has implemented packages developed in the group create proteogenomics databases based on ENSEMBL resources (Umer, Bioinformatics 2022). Unit has collaborated and initiated new contacts with SciLifeLab and DDLS fellows active on the mass spectrometry field, namely Simon Elsasser (fellows alumni), Avlant Nilsson and Fredrik Edfors (DDLS fellows on precision medicine) and Andrea Fossatti (DDLS fellow in infection biology and epidemiology).

GMP is closely associated with Daniel Bojar, Assistant Professor of Chemistry and Molecular Biology at the University of Gothenburg, and selected talent of a yearly Forbes Magazine within the category of Science & Healthcare. A recent study has uncovered the powerful properties of breast milk across different animals, providing info for better infant formula design. GMP profiled milk glycomes via LC-MS/MS, discovered >100 novel glycan sequences, curated the dataset that constitutes an exhaustive overview of milk glycan biodiversity. (Jin C, Mol. Cell Proteomics, 2023). Proteoglycans (PGs) are composed of glycosaminoglycan (GAG) chains attached to various core proteins and are important for embryogenesis and normal homeostasis. MS-glycoproteomic approaches have been developed in collaboration with Professor Göran Larson and his group at Clinical Chemistry, Sahlgrenska University hospital. This provides a framework for future studies on site-specific functional analysis of PGs in human pathophysiology. (Nilsson J, Glycoconj J, 2023), (Noborn, Mol. Cell Proteomics, 2023). GMP is co-developing methods for relative protein quantification in extravesicles (EVs) with Jan Lötvall, Professor/ Chief Physician at Department of Internal Medicine and Clinical Nutrition, and his group at Krefting research center, GU. EVs can serve as biomarkers for several different diseases. Worldwide, intensive research is under way to develop EVs also into new strategies to treat various diseases. Results demonstrating that EVs from mesenchymal stem cells can inhibit inflammation in mice and that EVs are loaded with material that enhances their anti-inflammatory effect. (Park KS, J Nanobiotechnology, 2023).

Procedure for prioritization of projects/ Userfee models

Both MS units has a first-come-first-serve policy with academic priority prior to industry and certain priority for urgent PhD studies and papers in review process (at the GMP unit). Each project request is first discussed in a start-up meeting together with the user. In the process, selected unit experts discuss the project aim and feasibility, sample type, amounts, research hypothesis and relevance for MS-analysis, possibility of optimization and implementation of new methods and ethical approval, when applicable. The facilities have a user fee model based on direct costs related to each service (including costs for reagents, actual instrument time, personnel cost). All academic users pay a subsidized fee of approximately 30% of the full cost price whereas non-academic users (e.g. commercial users) cover the full cost of the project.

User base (current and expected 2025–2028)

Currently the GPP and GMP provide research support for both national and international academia, healthcare and to a minor extent industry. Together our 120 PI´s are covering many disciplines, such as Microbiology, Biomedicine, Clinical Chemistry, Neuroscience, Physiology, Odontology, Biological and Environmental Sciences, Chemistry and Molecular Biology, Cancer Center and Surgery divisions. We have seen increase both in the size of the projects as well as the number of projects and foresee this increase to continue due to new powerful MS instruments and increase in high impact publications in the proteomics field serving as templates for new users creating a demand.

Plans for development including new technologies/service offerings 2025–2028

Last year a mass spectrometer with a completely new mass analyzer named Astral (Assymetric Trac Lossless Analyser) was introduced by Thermo (Guzman, Nature Biotech 2024). The new Orbitrap Astral instrument represents the largest paradigm shift in technological innovation in MS since introduction of the Orbitrap mass analyzer in 2005. Together with the Chemical Proteomics unit at KI/SciLifeLab the GPP unit applied for partial funding SciLifeLab and the Astral will now be acquired during 2024. This will provide a very important technological advantage compared to earlier generations of MS instrumentations offering high resolution, mass accuracy and sensitivity at

unprecedented speed and will overall improve the quality and throughput of the service provided.

In parallel, single-cell proteomics area has made major developments and both units are currently setting up an analytical portfolio for single cell/rare cell populations/low amount samples utilizing the Bruker Single Cell Proteomics (SCP) MS (purchased during 2023). Early applications within GPP include for example immunopeptidomics for cancer neoantigen discovery and GMP is purchasing a Cellenone system for fluorescent or non-tagged specific cell selection in protected no-loss sample preparation.

Overall, we see an increased interest in MS-based proteomics for large cohorts of hundreds or thousands of samples. These larger cohorts demand high through-put and higher level of automation, which we are currently setting up using automated robotics workflow (Beckman Coulter) that will allow both units to introduce a high-throughput fast track service data independent acquisition service (DIA) service.

Both units are also intensely following and evaluating the development of a vast number of AI-based tools that are being developed for various steps in the MS-data analysis workflow, including for example AI based tools to predict peptide sequence based on MS2 fragment intensities, and MS intensity based on peptide sequence or to utilize the peptide sequence to predict the behavior in the ion mobility separation (Lazerar JPR 2023, Picciani Proteomics and Systems Biology 2023, Mann Alpha suite github.com/MannLabs), and we envision that this will transform the MS data processing in the units in the coming years. We will also facilitate development of AI tools for glycomic/glycoproteomic data analysis by supporting and providing comprehensive MS-based analytical tools to deliver reviewed and curated data to the scientific community working on the development of machine-learning tools.

The GMP unit will expand their PTM portfolio to biomedically important PTM modifications, that are relatively under-studied and of user interest. Collagen modifications (hydroxyproline, Lys-oxidation, Lys-glycosylation and native cross-linking), protein glycations, citrullination, methylation, lipoylation etc. will be investigated. Our established methods for the analysis of glycopeptide structures with LC-MS/MS will enable us to successfully study new classes of glycosylation, including GPI anchors, keratan sulfate and heparan sulfate glycosylations. Earlier glyco-applications highlighted the need for further development in tools for functional glycoproteomic studies. Various available protein solubility assays will be evaluated to provide additional biophysical information to the detected and quantified glycoforms.

The units are currently providing state-of-the-art protein QMS across a variety of biological/clinical projects, however, the relevant protein alterations are likely not only to occur on the protein abundance level, but also to involve changes in proteins' biophysical properties. These changes can be detected by measuring global protein solubility alterations. Chemical proteomic tools, originally developed to study protein-drug interactions, are now available to provide additional information on protein functions and interactions on a proteome-wide scale, opening possibilities to offer MS-based functional proteomic studies to our users (in synergy with Chemical proteomics unit), (Kurzawa *Nat Chem* Biol 2023).

Plans for data handling and analysis 2025–2028 including a plan open and FAIR data

Raw data from MS instruments is processed and searched using specific tools to annotate MS-spectra. The MS-raw data generated by the units and results files are currently made publicly available through the PRIDE repository proteomeXchange operated by EMBL-EBI to ensure open access to research data according to the FAIR principles. To make the applied methods more adherent to the FAIR principles, the GPP unit is currently migrating our protocols to Protocols IO (protocols.io), which will allow version tracking and assignment of a DOI for each protocol. The units are currently also improving our metadata handling in our in-house workflow-based pipeline to facilitate re-use of data. Sample submission forms include rich meta-data from start of the project.

Current bottlenecks (if any) that prevent

(i) the units from meeting the user demand. Over the last year costs related to all aspects of the facility operations, spanning from reagents to instruments, have drastically increased and we are very concerned that the grants are not increasing in the same pace. In order to maintain the same level of operations it is essential that the grants are following the general economic developments in society and particular developments in MS field. More importantly, in order to retain and attract skilled staff, there should also be economical prerequisites to lift the staff salary when the merits of the staff reach the higher levels in the career programs. We also see a trend, associated with increased demand of MS-analysis, that the industry highly values the competence of our staff and offers salaries way beyond our budget, and the replacement hiring of staff is more difficult due to global shortage in the field. Finally, we see growing demand on specialized clinical proteomics on prospective analysis mode to support clinical trials which is not feasible to develop using current resources, hence the separate plan for a dedicated national unit.

(ii) the data generated to be efficiently shared to provide cutting edge services, it is imperative that the units can develop and function to catalyze users to be early adaptors of new software solutions, data workflows and novel analysis capabilities. MS-data requires a range of domain specific data analysis workflows and such tools are continuously developed over time, hand-in-hand with the development of new instruments, wet-lab applications and conceptual advances. There is currently a lack of funding for personnel embedded in the MS units with computational, IT and bioinformatics skills. In addition, we also see a lack of downstream bioinformatics support with proteomics expertise (see below).

NBIS – current support and needs for 2025–2028

We see a great need among our users for bioinformatics support in interpreting and analyzing the MS-data using state-of-the-art bioinformatics methods. According to NBIS, a very limited number of MS-based proteomics projects receives NBIS support each year. This is a concern, and from our perspective, involving NBIS at an early stage during the project would be desirable and facilitate transfer of the project to NBIS. A closer link to the data generating units would allow knowledge transfer between the units and assure that up-to-date MS specific bioinformatics knowledge is maintained. To improve the connectivity between the data generating units and NBIS, the GPP unit has been involved in a pilot project and co-hosted and provided training in MS-based proteomics and proteogenomics to one integrated bioinformatician (employed by NBIS 2020-2022). With the fast developments in the AI field there is also a need to continuously evaluate and incorporate novel AI based MS-raw data analysis tools, that requires dedicated bioinformatics work, which is currently not being covered in the NBIS service.

Data Centre – current support and needs for 2025–2028

At present the GPP or GMP unit is not receiving any support from Data Centre. The unit has reached out to ask for assistance, for example with joint storage and data-portal for SciLifeLab generated MS-data (Stockholm, Gothenburg and Lund SciLifeLab facilities) allowing re-analysis for meta-data studies; with hosting of Molecular Tumor Board portal for clinical reporting of data, or assistance in raw data upload to proteomeXchange, but that has as of yet not been materialized.

Synergies and current/planned collaborations with SciLifeLab units and capabilities

The MS units have strong connections with the platforms in Integrated structural biology, Genomics, Bioinformatics, Chemical Biology, Metabolomics and Genome Engineering. Significant synergies with both the chemical MS, structural MS and clinical MS modules are generated by cross infrastructure workflows, coordinated actions, joint vendor deals and services within the MS-based proteomics field.

GPP and GMP is working closely with the precision medicine (PM) capability, providing protocols and expertise for MS-based proteomics applications. The GPP unit is establishing an advanced sample-prep lab at the Pathology department at Karolinska University hospital, to support clinical trials with sample handling and prep for parallel DNA, RNA and protein analysis. The sample-prep has also been engaged in the pandemic laboratory preparedness (PLP), setting up routines for sample flow from the infectious disease clinic at the Karolinska university hospital to the BSL3 laboratory in KI Huddinge. The aim is now to connect this to rapid autopsy/biopsy programs within the PLP framework. The GPP unit has been engaged in Covid-19 projects, (data.scilifelab.se/highlights/covimapp) (Babacic *Nature comms* 2023, Palma Medina, Respir Res 2022). The GMP unit analyzed carbohydrate structures on the receptor-binding domain of the SARS-CoV-2 spike protein which is important for its activity and for the design of future vaccine candidates (Samuelsson, ACS Infect Dis 2022). In the planetary biology (PB) capability, global QMS can be used for meta-proteomics and to elucidate how plants adapt to changing environmental conditions and climate change. Detailed knowledge is essential in e.g. crop (growth-yield) improvement efforts, germination rate, nutritional or allergenic content, resistance to pests and diseases or for predicting the response to future environmental challenges of which are projects in progress. Global QMS also allows for a comprehensive understanding of bacterial response to different treatments. Antibiotic and multi-drug resistant bacteria is one of the main global health threats. High-quality specie and strain specific genomes including mutations resistant genes generated by NGS are essential as protein databases. QMS can be applied in areas such as medicine, agriculture, natural- and environmental science to explore protein expression in resistant or drug-tolerant bacterial with non-resistant phenotypes, study bacterial adaptation to different growing conditions and bacterial catabolism and study pathogen-host cell interactions or response to bacteria in the host.

Collaboration with industry, healthcare, and other organizations

The common base between units generates a critical mass of instruments and expert scientists, generating possibilities to join forces to become a stronger partner for vendors, other nationally important infrastructures, the health care region and for specific areas such as the Swedish precision medicine initiative and the Wallenberg funded data-driven life science initiative. We have ongoing collaboration with Bruker, SLL region and VGR region. Other significant collaborators are national infrastructures BioMS, Swedish Proteomic Society, Genome Medicine Sweden and Biobank Sweden. The units are networking with international organizations within the biomolecular research field, eg. the association for biomolecular research facilities (ABRF), its European Counterpart Core Technologies for Life Sciences (CTLS), European Molecular Biology Organization (EMBO), European Proteomics Association (EuPA), the Human Proteome Organization (HUPO) and the American Society for Mass Spectrometry (ASMS).

Current training offerings and plan for 2025–2028

Both MS units provide two-weeks courses each year for PhD students, post-docs and staff; "Mass spectrometry-based proteomics, when and how?", "Proteomics: practicals with QMS and glyco-phosho-proteomics and "Omics data analysis: from quantitative data to biological information". The individual staff members are also frequently engaged as lectures in external master programs and courses including KTH and Chalmers. GPP co-hosts a bi-weekly national seminar series on zoom on MS-based proteomics organized together with BioMS, the Swedish Proteomics Society (SPS) and the SciLifeLab Integrative Structural Biology (ISB) platform. The units are open for providing custom-made work-shops or introduction for new users and are planning to provide video recordings to be published on-line and to be provided by SciLifeLab Training Hub.

E6 Clinical Mass Spectrometry Facility

Current operations – funding, expertise, technologies, and services offered

Precision medicine forms a paradigm shift in research with profound impact on health economy and democratization of healthcare by introducing measurable biomarkers as clinical decision support. SciLifeLab has successfully developed the national genomics research platform into a clinical genomics platform that has been instrumental for Swedish clinical research and implementation of precision medicine. Academy, healthcare, regulatory bodies, and industry have widely recognized the need for multi-omics to enter diagnostics and push precision medicine development. Indeed, many single proteins are used as clinical markers since decades, however, systems level proteome analysis and disease associated protein variants, is a large unused information-rich level of clinical biomarkers. Improved chromatography and especially mass spectrometry (MS) with high throughput analysis, new sensitive ion mobility TOF instruments (on market since 2021) and Orbitrap Astral MS (2023), have opened completely new opportunities to develop MS-analysis for clinical research. MS-analysis offers proteome wide analysis or rapid development of assays for protein variants and post-translationally modified proteins, not possible to scale up on any other analytical platform.

In 2022, the Swedish Research Council (SRC) granted BioMS, the national infrastructure in biological mass spectrometry, an instrumental grant to establish a national consortium in clinical MS distributed across the three BioMS nodes in Lund, Stockholm and Gothenburg. The consortium is co-financed by three universities and the local health care regions. In responses to the instrument funding, BioMS has acquired six mirrored state-of-the-art mass spectrometers with connected rapid liquid-chromatography systems and liquid-handlers for automated sample preparation, at each node representing an investment of 40 million SEK. These mirrored instrument platforms enable a massive increase in sample throughput, catalyzing the analysis of large and clinically relevant cohorts and to undertake synchronized prospective analysis for clinical trials at a national level. However, recent budget constraints at SRC have resulted in insufficient funding for personnel preventing the platform to reach its full potential.

Here we propose the SciLifeLab Clinical MS facility, distributed in Lund, Gothenburg and Stockholm to lead the clinical MS research and implementation. The combined effort from the SRC, local universities, health care regions and SciLifeLab will unlock the full potential of previous instrument investments and generate a

world unique opportunity to develop an internationally competitive cutting edge clinical MS facility. Dedicated development on standardization, methods on prospective analysis and related knowledge to define clinically meaningful biomarker readouts are urgently needed. This unit will address these outstanding challenges, bring new unique functions and generate data for SciLifeLab's and the Data Driven Life Science (DDLS) programs in precision medicine. We expect rapid build-up, leveraging experience from SciLifeLab's clinical genomics and collaborate with other Swedish and international key players in the area, such as Genome Medicine and AIDA medical imaging facility. A nationally synchronized consortium in clinical MS will further unlock as example (i) population-based investigations of massive clinical biobank sample collections (ii) make Sweden eligible as a partner in EU-financed Joint Networks of Expertise (JANE2) to provide services and tools to European cancer institutions and networks. Further, a high performing clinical MS facility will create new opportunities for development of multi-modal diagnostics as part of clinical research and place Sweden in unique position internationally for example in relation to EUs cancer and (iii) provide Sweden with unparalleled opportunities to establish a testbed for national prospective clinical trials for systematic development of proteome medicine.

Scientific environment

BioMS is a distributed national infrastructure with nodes in Gothenburg, Stockholm and Lund. The recent expansion of BioMS services towards a national consortium in clinical MS brings together Sweden's leading experts in biological mass spectrometry with scientists and clinical researchers from three health care regions. Such efforts provide new possibilities to support internationally recognized clinical research with unique MS capacity and expertise across Sweden as exemplified below:

- We have teamed up with SciLifeLab research faculty to develop proteome medicine with successful early examples. In the cancer field, we have demonstrated the clinical value of proteogenomics in patient stratification in Chronic Lymphoblastic Leukemia revealing novel proteome subtype with poor-prognosis distinct from genomic prognosis factors p53mutation and B-cell receptor pathway mutations (Herbst et al. Nature Communications). Further, in proteome driven multi-omics project with joint forces from Stockholm and Lund, we demonstrated that proteogenomics provides valuable patient stratification in lung cancer. (Lehtiö J et al., Nature Cancer). Both examples demonstrate our capability to develop discovery proteomics methods into high throughput proteome assays for large cohort studies suitable for new facility services.
- We have demonstrated the ability to develop a MS-based proteomics method for subtyping of cardiac amyloidosis, a protein aggregation related condition leading to heart failure. Endomyocardial biopsies were retrospectively analyzed directly from fresh frozen material, without the prior enrichment of amyloid deposits with laser microdissection. This timesaving method is now used as clinical decision support for correct treatment. (Noborn F, Amyloid 2022).
- We have formed a translational researcher network connecting research from the clinic for infectious diseases, emergency department, intensive care unit, and clinical microbiology with scientists active in systems biology, multi-omics, bioinformatics, and artificial intelligence (AI). The constellation has recently constructed the largest digital biobank to date in sepsis, comprised of data sets from rapid proteomics, and developed new strategies in explainable AI to determine key biological pathways associated with the development of sepsis. Furthermore, we have used the digital biobank to develop a sepsis digital twin patient model for precision medicine strategies in sepsis.
- We have also teamed up SciLifeLab development of clinical decision support tool MTB-portal, a digital tool that is used for reporting cancer genomics data to molecular tumor boards and for patient allocation in clinical trials ongoing (Tamborero D., Nature Cancer 2022). We are currently co-developing proteome module to gain expertise and address the need for data exchange within clinical research setting. As DDLS precision medicine area develops, our intended clinical MS facility can provide data and expertise for joint development in the proteome medicine field.

User base (current and expected 2025–2028)

Currently, there are multiple large effort collecting and analysing samples where requests and pilots has been carried out to include proteomics data. Examples of such efforts include SCAN-B cancer genomics and transcriptomics study in region Skåne, where we have already co-developed proteomics analysis from same biopsy used for transcriptomics, Predix clinical trial on breast cancer in Stockholm, FOCU.SE national cancer clinical trial, where we have contributed with a proteome sampling into the trial protocol. This trial is part of the PRIME-ROSE EU projects with seven similar national trials. There are requests to perform a standardized multicenter study from the Sepsis Alert study connecting 10 hospitals across Sweden and to analyse all the samples from the SWECRIT study. In combined, these studies provide already a big need for clinical MS services using the multi-site mirrored analysis platform at SciLifeLabs clinical MS facility. In addition, we expect that the platform will catalyse efforts in academic and translational research activities.

Complementarity and synergistic opportunities within and across SciLifeLab platforms

SciLifeLab, with its clinical genomics, tissue imaging, single cell omics and related data driven efforts in precision medicine forms an ideal setting for a dedicated clinical MS facility. MS-analysis can directly leverage sample specific genomics and transcriptomics data by forming proteogenomics search databases to provide induvial proteome information also considering sequence variants. Moreover, our intended facility has unique opportunity to develop population scale antibody based HTP assay based on the accurate MS-data to develop precision health research domain and for example provide molecular phenotype level to connect genotype and histopathological imagine data on large cohorts.

Plans for incorporation of the operations into the platform/MS-Based Proteomics

BioMS and our related SciLifeLab MS-facilities has a long-standing collaborative track record. We propose that three BioMS nodes form a coherent unit where the work is coordinated under one head-of-unit. But to materialize this plan, we urgently need funding for dedicated personnel and expertise to harmonize and develop prospective clinical MS research service. Here we can leverage the BioMS instrument park and with this grant launch a world unique development of harmonized facility for clinical MS-based proteomics in the SciLifeLab context.

Budget

See below.

Budget request

Platform Strategic Budget

CPI requests 5,700 kSEK over four years [2025-2028], 1,100 kSEK in the first year and 1,400 kSEK in the following years. The requested budget will be used as follow:

1. A substantial part will be used for financing 2-3 open call projects in which external researchers will be collaborating with at least two units of the platform to support the platform's strategic, technological and harmonization visions. The external researchers will participate and are required to co-finance the project. The applications will be evaluated by the platform's IAB and other external expert reviewers where it is necessary (eg. leaders of SciLifeLab capabilities).
2. Co-financing up to 10 smaller grants supporting further training and development of our employees such as participating in courses, workshops, conferences and short-term visits to other units, other platforms or relevant laboratories. This will require co-financing from the unit or hosting university.
3. Financing social activities for the platform employees such as annual retreat, and co-financing platform conferences, courses and outreach.

Budget Affinity-Based Proteomics

Affinity Proteomics-Stockholm (APS)

APS requests 18,400 kSEK for 4 years (2025-2028). corresponding to an average increase of 1,500 kSEK per year compared to previous grant period (2021-2024). The costs correspond to:

- Personnel: Increase from 4 FTE to 5 FTE.
- Operation: Reagents, consumables, service contracts for the instruments
- Other costs: Computers, software, courses, conferences

APS has been increasing the delivery capacity by 50% in the past three years. In order to meet the increased project requests and accordingly to our plan for development, we see the need for additional funding that will cover the salary of one additional FTE, and part of the costs for operations and premises resulting from the acquisition of new instruments.

Affinity Proteomics-Uppsala (APU)

APU requests 18,400 kSEK for 4 years (2025-2028), corresponding to an increase of 1,500 kSEK per year compared to the previous grant period (2021-2024). The costs correspond to:

- Personnel: Increase from 6 to 7 FTE

- Operation: Consumables, service contracts for the instruments
- Other costs: Computers, software, courses, conferences

APU has increased the number of projects from 51 to 99 and the number of PIs from 38 to 74 over the period of 2021-2023 whereas the number of samples were centered around 65 000 per year. Two research engineers were hired and trained at the end of 2023 and are working mainly with big cohort studies. To meet the rising demand of custom assays and the introduction of new methods we seek increased funding to cover the salary of one FTE (PhD) and the related operational cost.

Autoimmunity and Serology Profiling (ASP)

APS requests 19,390 kSEK for 4 years (2025-2028), roughly corresponding to an average increase of 1,800 kSEK per year compared to previous grant period (2021-2024). The costs correspond to:

- Personnel: Increase from 3 FTE to 4 FTE
- Operation: Reagents, consumables, service contracts for new instruments
- Other costs: Computers, software, courses, conferences

ASP is facing a return to pre-pandemic level of the more labor-intensive autoantibody screening projects and is additionally aiming at expanding its offerings of large-scale arrays, which requires a considerable investment into the preparation of the thousands of antigens necessary for constructing the arrays. The unit is additionally aiming to add a new instrument for high-throughput screening of monoclonal antibodies, which is expected to attract additional projects. The unit therefore see a need of an investment in funding for an additional FTE, and for operations and premises costs, until the new technology platforms have been established and self-sufficient in generated user fees.

Budget MS-Based Proteomics

Glycoproteomics and MS Proteomics (GMP)

GMP requests 18,000 kSEK for four years (2025-2028). corresponding to an increase of 2,000 kSEK per year compared to previous grant period (2021-2024). The costs correspond to:

- Personnel: Increase from 1.7 FTE to 3.0 FTE, keeping the team members FTE 11.1.
- Operation: Costs including gas, reagents, consumables, service contracts for the MSs
- Other costs: External IT costs not covered in OH, spare parts MS and LC system

GMP was a candidate unit and is now delivering with highest capacity, the unit has 80 PI's and increasing interest, which requires additional funding. Two years of negative balance will be compensated the next two years.

Global Proteomics and Proteogenomics (GPP)

GPP requests 19,500 kSEK for four years (2025-2028) corresponding to an increase of 1500 kSEK per year compared to previous grant period (2021-2024). This is due to that we are scaling up (planetary biology and single cell proteomics) and also because of the inflation (both salaries and operation costs have increased). The cost corresponds to:

- Personnel: Increase from 8 FTE to 11 FTE (scale up to planetary biology, single cell proteomics, and we also need to follow the AI development)
- Operation: Costs include gas and chemicals, reagents, MS-columns, consumables, and service contracts for the MS. Due to increase number of instruments, we have more capacity that also can meet the increased number of customers and samples (larger cohorts), resulting in increased operational costs. The prices for reagents, lab consumables etc. have in general increased, and a few reagents often use in our facility have increased extremely.
- Other costs: Workshops, computers, storage, spare parts MS and LC system, personnel education, software licenses, meetings, dissemination, etc.

Clinical Mass Spectrometry Facility

The clinical MS facility requests 24,000 kSEK for four years, corresponding to 6,000 kSEK per year, (2,000 kSEK for each BioMS unit year) between 2025-2028. The costs correspond to:

- Personnel: 1.25 FTE per site + 0.25 FTE coordinator/ manager. In total there will be 4 FTE, including an annual salary increase of 3% per year.
- Operation: Costs for operation including consumables such as evotips and upcoming service contracts for the MS and robotics
- Premises: Staff need writing space, lab space, samples need freezing space, etc

The operations are co-financed by the instrument costs for mass spectrometers and liquid handler robots from SRC and from the local universities (University of Gothenburg, Lund University and Karolinska Institute). In addition, all necessary equipment and lab freezers are co-financed by the SciLifeLab facility, the regional facilities and BioMS operation.

Table 1. Clinical Proteomics and Immunology – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Open Call projects x2 or x3 [1]		800	1 200	1 200	1 200
Training for employees	50	100	100	100	100
Platform retreat conference, courses and outreach		200	200	200	200
Premises and indirect costs [2]		84	84	84	84
"Pilot project in precision medicine using CAR-T therapy as model system"	400				
Platform Director	150	150	150	150	150
Platform Coordination Officer	200	200	200	200	200
Other					
Sum costs (kSEK):	**800**	**1 534**	**1 934**	**1 934**	**1 934**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*800*	*1 534*	*1 934*	*1 934*	*1 934*
Sum revenues (kSEK):	**800**	**1 534**	**1 934**	**1 934**	**1 934**

[1] Included the indirect costs
[2] Premises and indirect costs are calculated for only training and platform activities based on IGP's current model

Table 2a. Affinity Proteomics Stockholm Budget

Costs	2024	2025	2026	2027	2028
Personnel 4 FTEs (2024) -> 5 FTEs (2025–2028)	*4 100*	*5 040*	*5 253*	*5 410*	*5 572*
Operations (includes reagents)	8 580	8 900	9 000	9 400	9 700
Premises	397	420	441	463	486
Instrument depreciations	807	590	590	590	534
Other	176	220	230	241	253
Instrument depreciations (eventually planned acquisition) [1]		2 000	2 000	2 000	2 000
Sum costs (kSEK):	**14 060**	**17 170**	**17 514**	**18 104**	**18 545**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 100*	*4 300*	*4 650*	*4 650*	*4 800*
University co-funding					
Expensive Instrument SciLifeLab	280	280	280	280	280
SciLifeLab funding-PLP2	1 200				
User fees	9 500	10 550	10 700	11 300	11 500
Expensive Instrument SciLifeLab /VR Infra/other External fundings [1]		2 000	2 000	2 000	2 000
Sum revenues (kSEK):	**14 080**	**17 130**	**17 630**	**18 230**	**18 580**

[1] The fundings are not available yet, but acquisition of a new instrument/s is planned

Table 2b. Affinity Proteomics Uppsala Budget

Costs	2024	2025	2026	2027	2028
Personnel 6 FTEs (2024) -> 7 FTEs (2025–2028)	5 600	6 798	7 002	7 212	7 428
Operations	555	583	612	642	675
Premises	680	714	750	787	827
Instrument depreciations	1 800	1 690	1 590	1 290	720
Reagents	26 000	28 600	31 500	35 500	39 000
Sum costs (kSEK):	**34 635**	**38 385**	**41 454**	**45 432**	**48 650**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	3 105	4 600	4 600	4 600	4 600
University co-funding [1]	1 500	1 500	1 500	1 500	1 500
Scilifelab instrument grant	280	280	280	280	
User fees	30 000	32 600	35 500	39 500	43 000
Sum revenues (kSEK):	**34 885**	**38 980**	**41 880**	**45 880**	**49 100**

[1] Uncertain for the next years. If not provided, user fees have to increase

Table 2c. Autoimmunity and Serology Profiling Budget

Costs	2024	2025	2026	2027	2028
Personnel 3 FTEs (2024) -> 4 FTEs (2025–2028)	3 250	4 450	4 600	4 770	4 930
Operations	770	1 100	1 140	1 180	1 220
Premises	380	480	500	520	540
Instrument depreciations	700				
Instrument depreciations (eventually planned acquisition) [1]		1 400	1 400	1 400	1 400
Sum costs (kSEK):	**5 100**	**7 430**	**7 640**	**7 870**	**8 090**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 000*	*4 600*	*4 760*	*4 930*	*5 100*
University co-funding					
Pandemic Laboratory Preparedness	200				
Scilifelab expensive instruments	520				
KTH SFO expensive instruments	180				
User fees	1 200	1 430	1 480	1 540	1 590
Expensive Instrument SciLifeLab /VR Infra/other External fundings [1]		1 400	1 400	1 400	1 400
Sum revenues (kSEK):	**5 100**	**7 430**	**7 640**	**7 870**	**8 090**

[1] The fundings are not available yet, but acquisition of a new instrument/s is planned

Table 3a. Glycoproteomics and MS Proteomics Budget

Costs	2024	2025	2026	2027	2028
Personnel 11.1 FTEs (2024) -> 11.1 FTEs (2025–2028) [1]	12 231	12 480	12 720	12 980	13 240
Operations	3 948	3 950	3 950	3 950	3 950
Premises	2 645	2 650	2 650	2 650	2 650
Instrument depreciations	4 370	4 370	4 370	2 700	2 700
Other	1 846	1 850	1 850	1 850	1 850
Sum costs (kSEK):	**25 040**	**25 300**	**25 540**	**24 130**	**24 390**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028) [2]	*2 500*	*4 500*	*4 500*	*4 500*	*4 500*
University co-funding	12 650	11 000	11 000	11 000	11 000
VR	5 140	3 520	3 520	3 520	3 520
User fees	4 750	5 100	5 600	6 100	6 600
Sum revenues (kSEK): [3]	**25 040**	**24 120**	**24 620**	**25 120**	**25 620**

[1] We will keep the number of team members.
[2] Not a candidate unit any longer, the unit have about 80 pI's, and increasing requests from new users. Funding should be comparable with overall budget.
[3] Two years with negative result will be compensated the last two years.

Table 3b. Global Proteomics & Proteogenomics Budget

Costs	2024	2025	2026	2027	2028
Personnel 8 FTEs (2024) ->11 FTEs (2025–2028)	8 096	10 299	10 556	11 895	12 252
Operations	4 477	4 780	5 090	5 435	5 975
Premises	1 500	1 550	1 600	1 650	1 700
Instrument depreciations	8 137	7 473	7 175	6 239	3 965
Other (travel, meetings, education etc)	300	315	330	350	400
Sum costs (kSEK):	**22 511**	**24 417**	**24 751**	**25 569**	**24 292**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 623*	*4 500*	*4 500*	*5 000*	*5 500*
KI University co-funding (KI-BioMS co-funding)	1 900	2 590	2 590	2 590	2 590
Vetenskapsrådet (BioMS Clinical instrument) (depreciation, 2023-2027	2 400	2 400	2 400	1 800	
Vetenskapsrådet (BioMS, instrument) (yearly depreciation)2020-2024	300	1 600	1 600	1 600	1 600
Vetenskapsrådet (BioMS) Driftanslag	3 800	2 860	2 860	2 860	2 860
SLL/FoU (rent , personnel, and running costs)	3 493	3 500	3 500	3 500	3 500
KI/FoU (Dyr Utrustning I)	1 100				
Karolinska University Hospital/FoU (Dyr utrustning II)	840	840	840	840	420
SciLifeLab Expensive Instrument I	65				
SciLifeLab Expensive Instrument II	670	670	670	670	670
SciLifeLab Dyr Utrustning III (Astral) 60:40 (GPPG:CP facility)	480	960	960	960	960
RED Grant (50:50; Lehtiö:Roman)	50	100	100	100	100
User fees	4 000	4 400	4 750	5 650	6 100
Sum revenues (kSEK):	**22 721**	**24 420**	**24 770**	**25 570**	**24 300**

Table 3c. Clinical Mass Spectrometry Facility Budget

Costs	2024	2025	2026	2027	2028
Personnel 4 FTEs (2025–2028)		4 480	4 630	4 750	4 881
Operations (service contracts, evotips, LIMS etc)		1 560	1 650	1 800	1 950
Premises (freezer space, office, lab)		600	620	650	670
Other					
Sum costs (kSEK):	**-**	**6 640**	**6 900**	**7 200**	**7 501**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)		*6 000*	*6 000*	*6 000*	*6 000*
User fees		650	900	1 200	1 500
Sum revenues (kSEK):	**-**	**6 650**	**6 900**	**7 200**	**7 500**



Swedish Metabolomics Centre Unit in Umeå. Photo: Mikael Wallerstedt

Metabolomics Platform

Basic Information

Platform Director: Johan Trygg, Umeå University

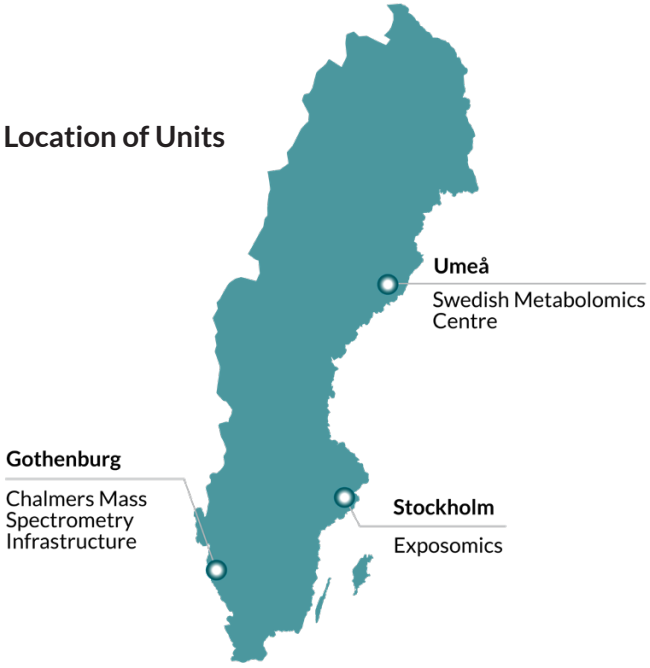
Platform Co-Director: Rikard Landberg, Chalmers

Platform Coordination Officer: Annika Johansson, Umeå University

Platform vision: Leverage world-class science by accurate assessment of small molecules from biological systems, exposures, and their interactions

Platform mission: National cutting-edge service for metabolomics, exposomics and small molecule analysis and data analytics support

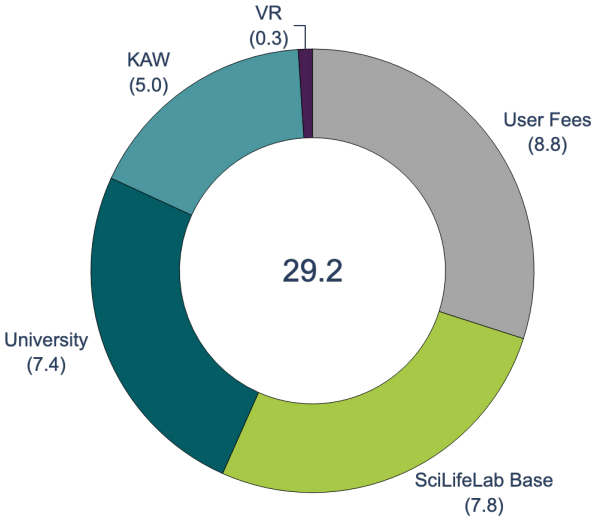
Location of Units



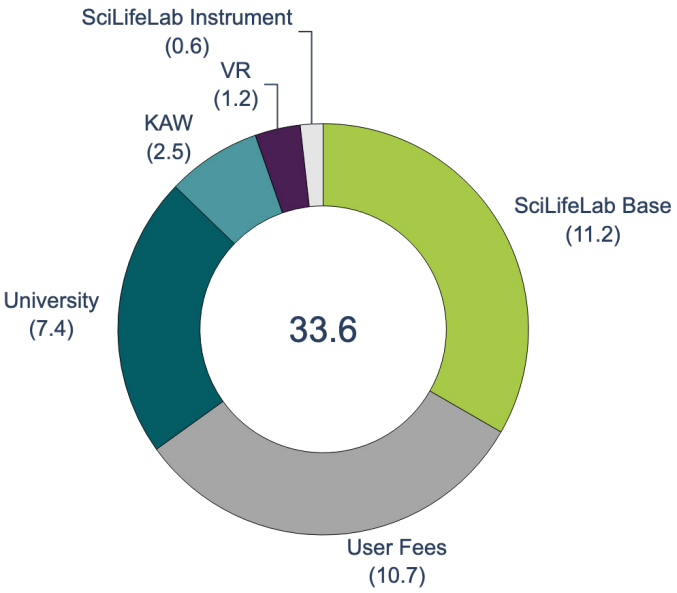
SciLifeLab Funding

Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Chalmers Mass Spectrometry Infrastructure	2.2	3.4
Swedish Metabolomics Center	2.5	3.0
Exposomics	2.6	3.3
Platform Strategic Funding	*0.6*	*1.6*
Total SciLifeLab Funding	**7.8**	**11.2**

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



Metabolomics Platform

Platform organization and governance

The Metabolomics Platform at SciLifeLab was formally established following an international evaluation in 2020. The Platform consists of three complementary units:

- *Swedish Metabolomics Centre (SMC)*, Umeå – Formed as a collaboration between Umeå University (UmU) and the Swedish University of Agricultural sciences (SLU). Since the establishment of SMC in 2013, the unit has been focusing on providing service for small to medium size studies (< 500 samples) for targeted- and untargeted metabolomics to balance project throughput, user accessibility and flexibility.
- *Chalmers Mass Spectrometry Infrastructure (CMSI)*, Gothenburg – Situated at Chalmers University of Technology (Chalmers). The main focus of CMSI is to provide service for large cohort studies with >500 samples, particularly projects within the domain of precision health. The complementarity of these two units (CMSI and SMC) allows comprehensive development and maintenance of niche services and analyses but at the same time allows projects and methods to be shared if needed. This allows the two units to flexibly adapt to the continuous flow of project and service requests.
- *Exposomics*, Stockholm – is hosted by Stockholm University (SU), in the Department of Environmental Science (ACES), and operates as the Exposomics Unit within the SciLifeLab Metabolomics Platform. With expertise in small molecule high resolution mass spectrometry in human and environmental samples, the SciLifeLab Exposomics unit is currently the first and only laboratory in Europe providing a national service dedicated to untargeted chemical exposomics.

In addition, the Swedish NMR Centre (SNC) from the SciLifeLab Integrated Structural Biology (ISB) platform, is associated with the Metabolomics platform to provide NMR-based metabolomics services and competence. For more in-depth information about NMR-based metabolomics, please see the material on the ISB Platform (p. 187).

After a new organization in February 2023, the Metabolomics Platform Management Group consists of the Director professor Johan Trygg (SMC), the Co-Director professor Rikard Landberg (Chalmers), the Head of Unit and Platform Coordination Officer Dr. Annika Johansson (SMC), the Platform Scientific Director professor Jonathan Martin (Exposomics), and the Head of Units Dr. Otto Savolainen (CMSI) and Dr. Stefano Papazian (Exposomics), along with the Platform Scientific Director professor

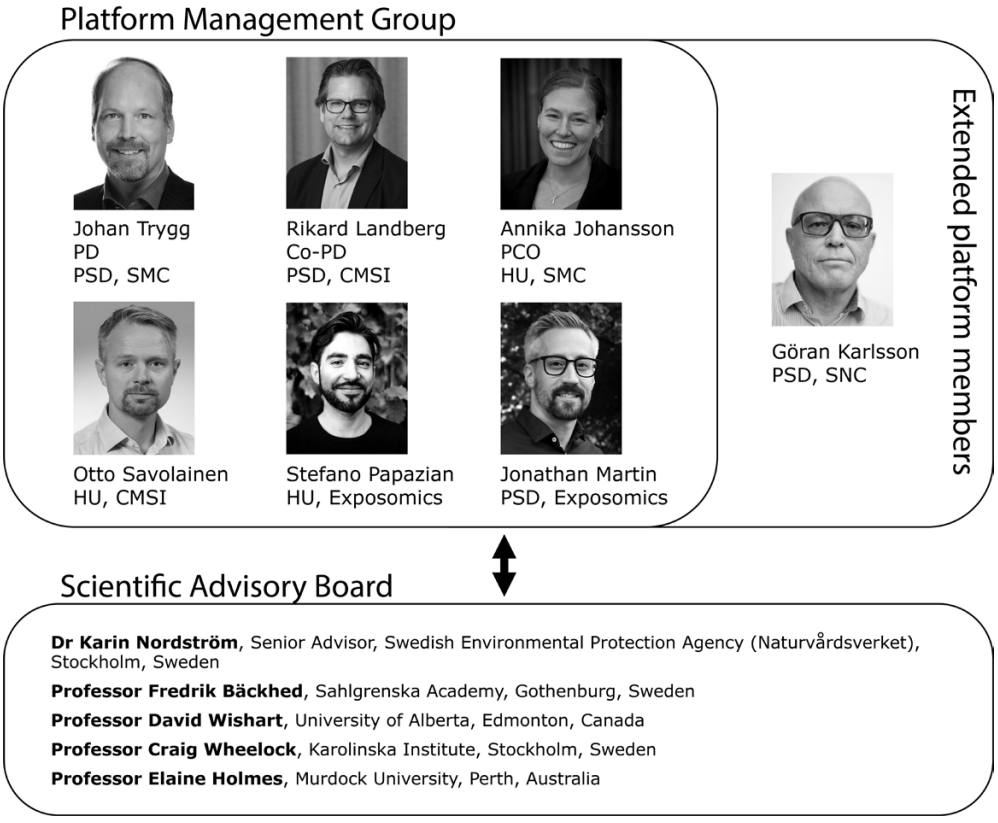


Figure 1. Platform organogram.

Göran Karlsson (SNC, Gothenburg). Further, the Platform's International Scientific and Stakeholder Advisory Group (see organogram) includes members from academia and governmental organizations, gathering broad multi-disciplinary expertise across metabolomics, chemometrics, computational metabolomics, precision medicine and precision health, contaminant biomonitoring, and planetary biology.

Platform development and key achievements 2021–2024

The new Metabolomics Platform organization was successfully established in SciLifeLab to meet the emerging demands for comprehensive analysis of the most downstream read-out of biological systems, metabolites, and also considering small-molecule exposures. Along with MS-based metabolomics and exposomics services, the recent inclusion of NMR-based metabolomics (SNC) renders the Platform unique at the international level and creates new research opportunities for integrating metabolomic and exposure profiling as a key technology in many research fields.

In 2022, the SciLifeLab strategic Platform budget was leveraged to increase the visibility of Exposomics unit and attract new users by launching the "Exposome-Metabolome Interaction" program. This was done as a public call to sponsor Swedish national projects aimed at understanding associations between environmental chemical exposures and the metabolome. Two projects were selected and given access to collaborative cross-unit services. Method development and analyses were completed in 2023, and data integration is underway. These projects should nicely illustrate the power of transdisciplinary multi-omic endeavors for understanding the role of environmental exposure in disease etiology.

The Platform units have also taken national leadership roles to support further infrastructure development and services for small molecule analysis. In 2023, two separate proposals were submitted by the Platform to the Swedish Research Council's (VR) national infrastructure needs inventory: 1) "*Exposome Sweden*" (PI Martin) headed by the Exposomics unit, which is a cross-cutting infrastructure for human and environmental health studies, coordinating among 6 Swedish universities and interfacing with the European research infrastructure for exposomics, EIRENE RI; and 2) "*The Swedish Metabolomics Platform*" submitted by SMC/CMSI, which integrates metabolomics research and services at 6 Swedish universities using the state-of-the-art MS and NMR technologies. By forming a comprehensive national platform, we will increase the visibility of metabolomics across the scientific community in Sweden and beyond, and gain benefit from joining forces in capacity building.

Training and outreach

As part of the Platform´s outreach activity, metabolomics and exposomics services are frequently advertised in meetings, lectures, seminars, and conferences to increase the awareness and visibility of this capacity provided nationally by SciLifeLab. This includes workshops dedicated to open science and FAIR tools with a focus on exposomics applications attended by high-profile research institutes (Yale, Columbia University, Mount Sinai, etc) as well as co-organizing meetings and knowledge sharing activities with NBIS with focus on mass spectrometry-based metabolomics and small molecule applications. In January 2024, SNC and SMC co-organized in Umeå the conference "*Metabolomics in Life Sciences*", focusing on mass spectrometry, NMR and computational metabolomics, attracting 120 participants and an impressive list of international speakers. During 2023, Chalmers has established a 3 year collaboration with Harvard and the metabolomics platform at Broad Institute at Harvard and MIT with the aim to conduct method comparison studies in metabolomics to allow large-scale replication studies using metabolomics samples from large Swedish and US cohort studies. Further, the Platform has been representing and directly involved in the Nordic Metabolomics Conference series, both Copenhagen 2022 and Trondheim 2023. In addition to these outreach efforts, the Platform has presented its growing needs for bioinformatic support and established stronger links to the NBIS platform. In 2024, we initiated a series of internal meetings titled "*Metabolomics and Exposomics Staff Seminars*" to facilitate knowledge exchange among staff from SMC, CMSI, Exposomics, SNC and Spatial-MS unit (Spatial biology Platform). These seminars aim to discuss new protocols, cutting-edge technologies, and foster interactions across units, and cross-Platform to enhance awareness and support for metabolomics within SciLifeLab.

Platform plans for 2025–2028

During 2023-2024, the Platform initiated a comprehensive evaluation of various blood microsampling techniques, aiming to assess their performance and reproducibility for large scale deployment. Particular emphasis is directed towards protocols tailored towards easily deployable microsampling, ideally suitable for self-sampling by subjects and to sustain integration with automated high-throughput analysis by NMR- and/or MS-based metabolomics, alongside parallel targeted and untargeted exposomics. If successful – these methods will be introduced as new service offerings in 2025-2026, thus enhancing our ability to support large-scale longitudinal metabolomics and exposomics investigations within national population cohorts.

Another focus will be to support SciLifeLab capability in precision medicine, facilitating support for clinical trials, high-throughput drug screening, and more effective patient stratification for existing medication, treatments, lifestyle interventions, or novel indications. In collaboration with clinical researchers, the Metabolomics Platform will introduce high-throughput metabolomics screening to complement existing drug screening methodologies, validating findings in patients and offering diagnostic tests to supplement existing drug testing platforms and available drugs in clinical settings.

In 2024, the Platform is formally establishing a Computational Metabolomics Group (CMG) that capitalizes on its expertise in chemometrics among existing staff, and ongoing collaboration with NBIS to ensure a geographically diverse representation from various nodes (>8 FTEs). The goal is to leverage and harness our existing data-driven domain experts in metabolomics, data analysis, and biochemical interpretation, to uniquely distinguish the Metabolomics Platform and foster cross-platform collaborations within SciLifeLab, all while adhering to FAIR and open science principles and GDPR-compliant protocols.

Throughout 2025-2026 the platform will continue building a comprehensive inventory of authentic reference standards relevant for the identification and quantification of both metabolites and xenobiotics. Mass spectral data will be systematically acquired for each compound and compiled into a common library to share with the metabolomics and environmental chemistry community through deposition in public depositories such as MassBankEU, MoNA, and others.

Data Centre and FAIR workflows

Integration of the Platform services into the SciLifeLab Order Portal and the new Data Delivery System is underway at the Exposomics unit, and will soon be extended to the metabolomics units. Further to support from the Data Centre, we have proposed the establishment of a cloud-based and GDPR-compliant data repository in order to store and exchange raw mass spectrometry data within SciLifeLab (but potentially integrated or linked to the EMBL MetaboLights ecosystem). A great additional resource would be a local ecosystem built around this repository to allow efficient data retrieval, integration, and visualization (e.g. via interactive dashboards), facilitating swift sharing of results with users. Moreover, creating such an open access repository for sharing laboratory protocols across Platforms (and users) would enhance the FAIRness of our workflows and increase the impact of SciLifeLab into addressing the overarching concern of reproducibility in science.

E7 Metabolomics

The Swedish Metabolomics Center (SMC) in Umeå (UmU and SLU), and the Chalmers Mass Spectrometry Infrastructure (CMSI) in Gothenburg (Chalmers), collectively offer complementary national metabolomics resources for standard- and high-throughput targeted and untargeted mass spectrometry (MS)-based measurements of metabolites, catering to researchers within the life sciences.

Technologies and services

Metabolomics analyses conducted at the units meet the demand of the research community by offering valuable insights into metabolic perturbations associated with genetics, environmental exposures (including diet, drugs, lifestyle, microbiota, etc.) as well as health and disease conditions. Our services facilitate functional discovery and prospective studies, where metabolomics particularly excels at determining the phenotypic response resulting from genetic manipulations or experimental treatments.

Our services provide users with excellent potential to accelerate advancements in molecular and planetary biology, precision medicine, healthcare, and other areas within life science research. We offer:

- Untargeted and targeted metabolite and lipid profiling on small to large sample cohorts
- Quantitative panels of metabolites ranging from food intake biomarkers and plant phytohormones
- Method development support, tailored to specific user needs
- Extended metabolite identification and substance confirmation
- Down-stream data processing and biological interpretation, in close collaboration with the users

In addition to the services above, both units maintain and support open access laboratories, offering researchers extensive training opportunities and the freedom to independently access a wide range of mass spectrometers, ranging from single quadrupole to high-end ion mobility and high-resolution MS instruments, empowering researchers with broad and versatile analytical capacity.

SMC became a SciLifeLab unit in 2017. From 2017-2021, CMSI operated as an integrated unit of the SMC. The rationale to transform CMSI to an independent unit in 2022 was the continued expansion and complementary profile of the unit. From a user perspective, the two units are complementary, with most small-medium projects performed by SMC, and large population cohort studies directed towards CMSI.

SMC (Umeå) has operated for >10 years as a national infrastructure with focus on prospective and functional discovery studies and developed a unique expertise to swiftly develop and adapt new methods to individual projects from a wide range of science domains, research questions, sample matrices and sample (plasma, cells, bacteria, plants, tissues etc.) and different sizes/volumes. Typical projects (between 20-500 samples) start with small or medium sized set of experiments that target specific questions in biology, biotechnology or medicine.

CMSI (Gothenburg) has operated since 2016 as an open academic infrastructure with the goal of providing cutting edge and efficient metabolomics services to the Swedish research community. CMSI has a primary focus on large sample sets from large interventions and population-based cohorts numbering in the thousands. In 2023, CMSI completed its largest metabolomics study involving more than 8000 individuals. Chalmers University is a member of a national cohort infrastructure, SIMPLER, and in this context, CMSI is responsible for generating both targeted and untargeted metabolomics data that will enrich a database of >14,000 individuals. The data generated will be open for use through project requests to SIMPLER.

Highly skilled staff scientists

While all Platform units have access to state-of-the-art, high-end instrumentation, the main strength of the Platform derives from its highly skilled and experienced staff. The two units, SMC and CMSI, have a total of 12.5 FTEs working to support platform users, supporting a variety of needs ranging from design of experiments from small targeted analyses to large metabolomics projects, data-processing, biochemical interpretation and reporting. Both units are actively engaged in method development initiatives aimed at advancing instrument and data analytical procedures to remain at the forefront of metabolomics analysis. Continuous competence development is facilitated by through opportunities for staff to contribute to a diverse range of projects, involving various techniques and method development for novel sample matrices and analyte classes.

SMC has eight people employed (7.5 FTEs) of which 6 have a PhD in metabolomics or mass spectrometry related topics. In May 2024, an experienced analytical chemist will join SMC to work at the interface between research and service, with a focus on internal method-development projects. CMSI has a total of 5.2 full-time staff equivalents (FTE) among which 2 PhD level staff scientists and 3 FTEs having MSc level education in a relevant field. Additionally, the unit has a long-term mission to recruit PhD level staff scientists experienced in metabolomics. This will help guarantee international competitiveness of the SciLifeLab metabolomics services in long term perspective, as also highlighted in the unit budget.

Infographics: Statistics and Metrics for Metabolomics Units

Chalmers Mass Spectrometry Infrastructure

Read more: Webpage, Publications Database

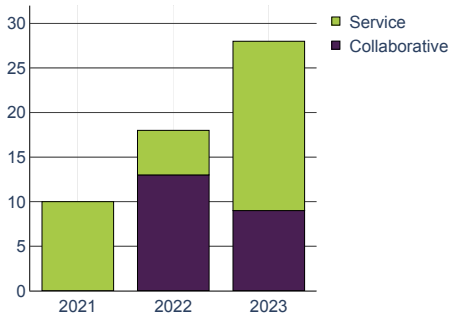
Basic Information

HU: Otto Savolainen
Host University: Chalmers
SciLifeLab unit since: 2021
FTEs: 6
PSD: Rikard Landberg

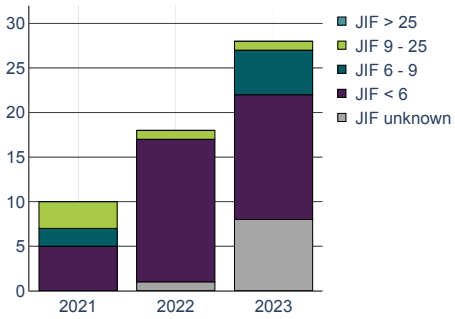
Funding 2023 (kSEK)

SciLifeLab: 2100
Other: 2067
User Fees: 4200

Publications by category

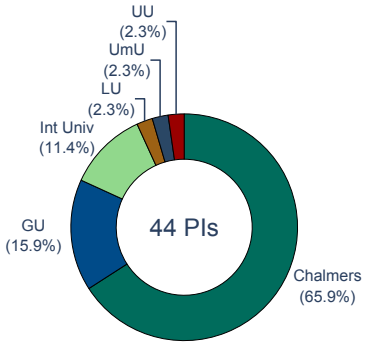


Publications by JIF

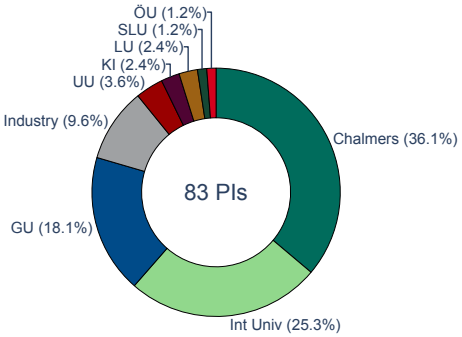


No. of Tech Dev Publications 2021 - 2023: 1

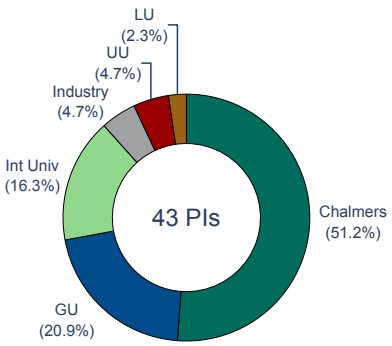
Users 2021



Users 2022



Users 2023



Swedish Metabolomics Centre

Read more: Webpage, Publications Database

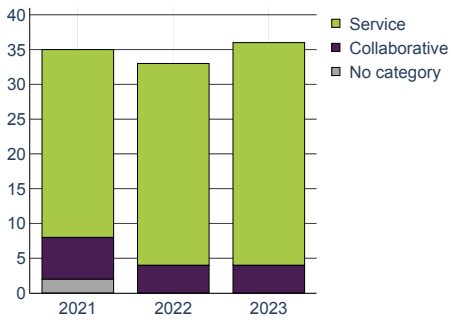
Basic Information

HU: Annika Johansson
Host University: SLU, UmU
SciLifeLab unit since: 2017
FTEs: 7.5
PSD: Johan Trygg

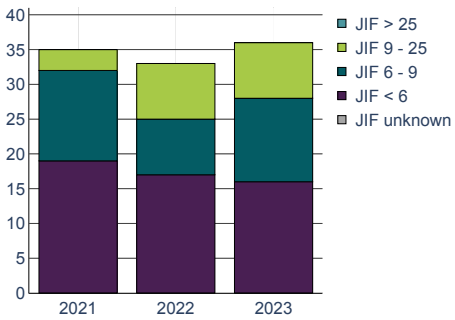
Funding 2023 (kSEK)

SciLifeLab: 2400
Other: 10000
User Fees: 3100

Publications by category

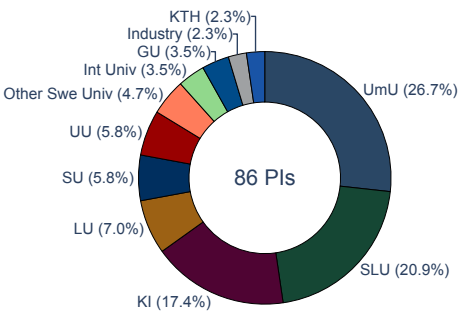


Publications by JIF

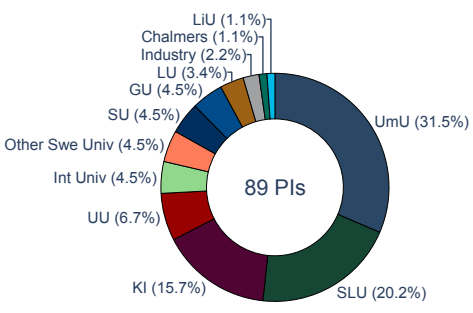


No. of Tech Dev Publications 2021 - 2023: 2

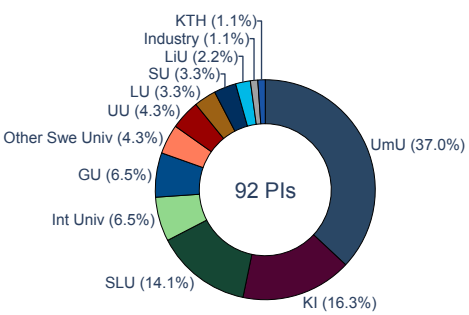
Users 2021



Users 2022



Users 2023



User base and user fee models

SMC is continuously providing support to projects coming from 90 PIs on a yearly basis, while CMSI annually serves 42-80 PIs in addition to provision of metabolomics data to the SIMPLER infrastructure that cater a large number of users of the data generated in different molecular epidemiological studies in medicine and health. Both units have a well distributed user base and cover all major research and university sites in Sweden (see unit statistics). Both units receive project requests through their corresponding websites, by email and by word of mouth, e.g. by researchers contacting the unit. Project requests are always followed by a preliminary start-up meeting with the responsible PI, to evaluate and discussed the project´s design, feasibility, and user expectations. Projects are normally prioritized on feasibility and expected timeline, not on their scientific merits. Upon acceptance, projects are placed in queue at the respective unit. User fees are calculated based on a full cost recovery model, including staff salaries, rent, service contracts, and consumables. Base funding for the units differs. SMC's is currently funded by KAW (Knut and Alice Wallenberg foundation) (ending in December 2026), SciLifeLab, and Universities co-funding, allowing extensive subsidies on instruments and personnel for Swedish researchers. International researchers are only partly subsidized, whereas full-cost recovery is applied for industrial partners. Similarly, CMSI has funding from Swedish Research council (VR; ending in 2024, with pending decision for prolongation), SciLifeLab and university co-funding, that subsidizes the costs for user fees for academic users. At both SMC and CMSI, all analytical steps from study design, sample preparation, data pre-processing and preliminary statistical evaluation are included in the service.

Excellent scientific environments

SMC is incorporated within the Umeå Plant Science Centre (UPSC), one of Europe's most highly ranked plant and forest biotechnology research environments. Over the years, unique databases for various plant species such as *Arabidopsis*, *Populus* and *Brassica* have been developed as well as highly specialized targeted methods for measuring plant hormones. This expertise is in excellent alignment with the Planetary biology capabilities within SciLifeLab. As an example, during 2023, Professor Stefan Jansson (responsible PI of the SMC at the department and a member of the SMC R&D team) integrated untargeted GC-MS metabolomics screening and targeted plant hormone analysis with transcriptomics. The study, published last year in *Nature Communications* (Lihavainen et al. 2023) revealed that the timing of deciduous leaf senescence in aspen trees depends not only on environmental changes but also on the ability of each genotype to sustain stress tolerance mechanisms mediated by the phytohormone salicylic acid.

Many key metabolites are found naturally at low abundance, are either unstable, or have low ionization efficiency, and thus they are often not detected in global untargeted metabolite profiling analysis. Instead, they require highly dedicated and optimized targeted methods especially if the sample quantity is limited, as in cell studies. As an example, SMC in collaboration with Professor Thomas Moritz at the Center for Basic Metabolic Research (University of Copenhagen), and a member of the SMC R&D team, developed and validated a method for quantification of key carboxylic acids (TCA cycle) at pM concentration ranges in 10,000 mouse myotube cells (Hodek et al 2023).

The research of Professor Johan Trygg and Henrik Antti at Umea University has, for last 20 years, contributed to develop and define our workflows at the Metabolomics Platform including chemometrics, data processing, and advanced data analysis portfolio. SMC has been involved in several EU-funded projects including MC BOLD Training Network, FP7 BioMargin, HUMAN and BatCure H2020 projects leading chemometrics and metabolomics method development. More specifically, SMC was key partner lab in elucidating biochemical pathways and linking clinical phenotypes to cancer, autoimmune- and age-related diseases.

CMSI is located at the Infrastructure Division in the Department of Life Sciences (LIFE) at Chalmers University of Technology. The co-location of CMSI together with the Chalmers NBIS node as well as the Chalmers DDLS data science node provides a rich environment offering the possibilities to bridge competencies across the national infrastructure borders. The host Department, LIFE, has a strong focus in utilizing MS-based analytics, including metabolomics, in various research questions. The close proximity to the Division of Food and Nutrition Science (FNS) and the Systems Biology Division at LIFE, has proven to be particularly beneficial and the CMSI platform has co-developed many wet-lab and data-analytical procedures over the years. These synergies have resulted in several publications (e.g. 1, 2, 3, 4, 5, 6) while other ongoing projects are yet to be published.

In addition to the Chalmers research environment, CMSI has a long-standing collaboration with infrastructure units at the Sahlgrenska Academy, most notably with the SNC, as well as the Proteomics Core Facility and the Wallenberg Laboratory which are integrative part of the Swedish National Infrastructure for Biological Mass Spectrometry (BioMS). Furthermore, CMSI (through Drs. Landberg, Savolainen, and Brunius) has strong and long-standing collaborations with Swedish and international research networks. Within the European Human Exposome Network (EHEN), collaboration is ongoing with leading European metabolomics platforms represented by Prof Kati Hanhineva (Uni Turku), Prof Seppo Auriola

(Uni Eastern Finland), and Dr. Pekka Keski-Rahkonen (International Agency for Research on Cancer) to establish commonalities in the measurable metabolome. A three-year collaboration with STINT-funding has been established between the Chalmers environment, and the Broad Institute at Harvard and MIT. The aim of this project is to harmonize and align metabolomics measurements across platforms to allow large scale replication studies in cohorts, encourage the exchange of staff, and enhance training of young investigators.

Future developments in 2025-2028

In addition to the future development plans mentioned at the Platform level, ongoing projects to develop and expand the services offered at the units will mainly focus on the development of large multiclass target panels, as well as fluxomics workflows.

Target panels

A major development focus will be given to implementing methods for broad scale coverage of the metabolome using targeted analysis panels, allowing the mapping and confident identification of hundreds to thousands of metabolites at once. These methods, which are available through collaborations with Prof Wishart of The Metabolomics Innovation Center (TMIC), will improve targeted metabolite coverage in research projects that strive for fast, low-cost access to easily interpretable metabolomics data. Moreover, this strategy will result in a more efficient use of resources by allowing untargeted metabolomics application to exploratory (discovery) studies. We anticipate offering a collection of assays for 1300-2000 targeted metabolites in standard matrices by 2025-2026. During 2021-2024, SMC developed HILIC-LC-MS methods applicable to both untargeted profiling and targeted analysis of several unstable key metabolites such as ATP/ADP, NAD/NADH, and other phosphate-containing compounds. These panels are being continuously expanded to build a broad, quantitative panel of polar metabolites.

Fluxomics and identification

Between 2024-2028, SMC will continue its ongoing efforts to advance mass spectrometry-based flux tracer and stable isotope incorporation studies, i.e. “fluxomics” aiding in the elucidation of metabolic pathways and relative kinetics of biochemical reactions. This ongoing development will be conducted in collaboration with researchers at UPSC and the research group led by Thomas Moritz at University of Copenhagen. Upon the establishment of a robust mass spectrometry protocol and a refined data handling strategy, the goal will be to introduce flux tracer analyses as either a fee-for-service option or a service for collaborative projects beginning in 2025.

As previously mentioned, metabolite identification poses a significant challenge in metabolomics. This is particularly relevant to the Planetary Biology domain, where the plant kingdom alone is estimated to contain >250,000 specialized secondary metabolites (natural products), and many prokaryotic microorganisms also harbor species-specific metabolites, many of which remain unidentified. To address this challenge, our Platform is collaborating with microbiology teams to investigate different bacterial strains based on their metabolite profiles. This initiative aims to establish an open access database of MS/MS spectra and retention times of both known and unknown metabolites characteristic to a specific bacterial strain or common among groups of prokaryotes. Furthermore, Laura Carroll, a newly recruited DDLS fellow at UmU, will join and contribute to the project applying machine learning approaches to mine the microbial genomes for novel biosynthetic gene clusters with the potential of biosynthesize novel secondary metabolites. The integration of metabolomics data with (meta)genome information will facilitate comprehensive exploration and understanding of microbial metabolic capacity, increasing our understanding of microbial biodiversity potentially leading to significant advancements in drug development.

Data handling and analysis 2025–2028

Metabolomics data, describing the behavior of thousands of molecules, are exceedingly complex. Extracting relevant information, prior to data analysis is performed, is a challenging task. We will develop and integrate AI/deep-learning-based approaches with existing workflows for a range of metabolomics data processing and modeling tasks. We achieved early success in developing a variant of a CNN-based U-net, coupled with multivariate analysis, to automate peak detection and integration from complex LC-MS metabolomics data. Moreover, the combination of genome scale metabolic models and dynamic flux modeling complement our existing systems biology and planned data integration approaches, in collaboration with other SciLifeLab platforms. The generation of high-quality biological data will encompass prospective clinical-based studies, where the design of experiments and related sample selection is critical. Implementing algorithms for continuous quality monitoring of untargeted MS-based analysis and assessing data quality will automate near real-time monitoring, ensuring stability over time and enabling interoperability and comparability. Computational development aimed at increasing data comparability, particularly by enhancing the opportunities for replication, data pooling, and meta-analysis, hold enormous potential to augment the value of metabolomics data for life science. Both units constantly receive high volume of projects and samples, resulting in substantial amounts of raw instrument data. However, staff resource is inadequate, both in terms of data-processing capacity

and the development of scalable workflows that aligns with user needs and support requirements. Metabolite identification emerges as a key bottleneck in converting data into knowledge. Thanks to a SciLifeLab technology development project, we initiated the development of a modular data-analytical pipeline adhering to FAIR principles and designed to enhance processing efficacy and efficiency. Integration and embedded resourcing support from SciLifeLab Data Center and NBIS platforms will enable us to make a significant impact on the DDLS program and Precision Medicine and Planetary Biology Capabilities.

Training and collaborations with industry

We identify both a need and opportunity to increase our training portfolio and collaboration with industry. In October 2024, SMC will arrange a workshop in collaboration with the metabolomics platform at FIMM, Institute for Molecular Medicine Finland and MIMS, Molecular Infection Medicine Sweden, Sweden. The target audience will be young researchers (PhD students and post-docs) without previous expertise in metabolomics. SMC also developed an extensive collaboration with Sartorius (sartorius.com), a global Life Science Research partner in life science and biopharmaceutical industry to increase AI/deep learning, multivariate data analysis and hybrid modeling expertise in support of metabolomics applications. One example includes genome-scale metabolic models combined with a comprehensive set of multi-omics and high-throughput data for biology modelling. Here, we are excited to continue collaboration with top pharmaceutical companies, technology providers, leading academics as well as regulatory agencies. Already planned, our developed methods, tools, and workflows will be made open source. Large international companies within the food industry such as Arla Foods, Lantmännen, Barilla and Oatly are applying metabolomics to a number different collaborative projects with Chalmers. This interaction is expected to increase over time.

E8 Exposomics

Exposomics

The concept of the "exposome" was introduced in 2005 to encourage more attention on complex environmental causes of disease. Exposomics complements existing omics profiling (e.g., genomics, metabolomics, transcriptomics and proteomics) by incorporating assessments of chemical and biological environmental exposures across an individual's lifespan, including internal and external influences. The chemical exposome can be comprehensively profiled by high-resolution mass spectrometry (HRMS). It consists of a vast and diverse range of small molecules, including synthetic industrial chemicals (e.g., PFAS), persistent global pollutants, pesticides, substances in consumer products, and natural chemicals present in our environment and diet. Diverging from traditional biomonitoring methods, which aim to understand population-wide exposure at single points in time, exposomics aims to characterize the complex mixtures of known and unknown exposures in individuals over their lifecourse.

The Exposomics Unit

The Exposomics unit is hosted by Stockholm University (SU), in the Department of Environmental Science (ACES), and operates as the Exposomics Unit within the SciLifeLab Metabolomics Platform. With expertise in small molecule high resolution mass spectrometry in human and environmental samples, the Exposomics unit is currently the first and only laboratory in Europe providing a national service dedicated to untargeted chemical exposomics.

Staff and expertise

As of 2024, the Exposomics unit is composed of two PhD level staff, i.e. the Head of Unit (since Nov. 2021) and recently a Lab Manager (recruited Jan. 2024). With shared expertise in analytical chemistry, GC/LC chromatography, Orbitrap mass spectrometry, metabolomics, exposomics, and data analysis, these 2 FTEs are, together, entirely responsible for delivery of services at the Exposomics unit. Additional support is provided as in-kind contribution by SU/ACES with a research engineer (0.25 FTE), and by the associated research group of Prof. Jonathan Martin (SU/ACES, and Exposomics Scientific Director).

Infographics: Statistics and Metrics for Exposomics Unit

Exposomics

Read more: Webpage, Publications Database

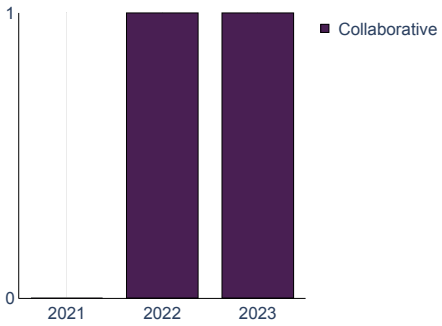
Basic Information

HU: Stefano Papazian
Host University: SU
SciLifeLab unit since: 2021
FTEs: 2.25
PSD: Jonathan Martin

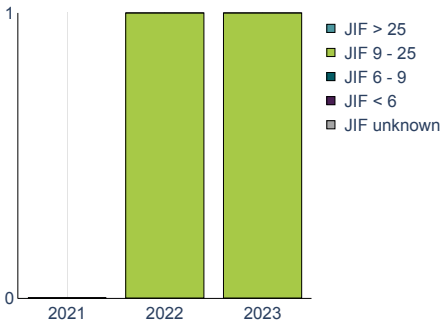
Funding 2023 (kSEK)

SciLifeLab: 2500
Other: 1100
User Fees: 1256

Publications by category

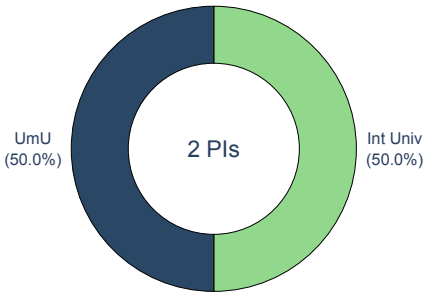


Publications by JIF

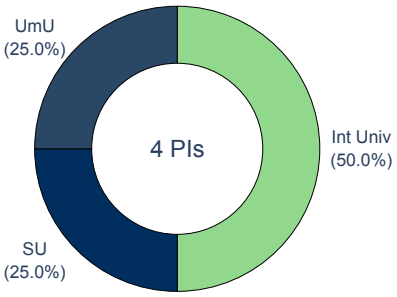


No. of Tech Dev Publications 2021 - 2023: 4

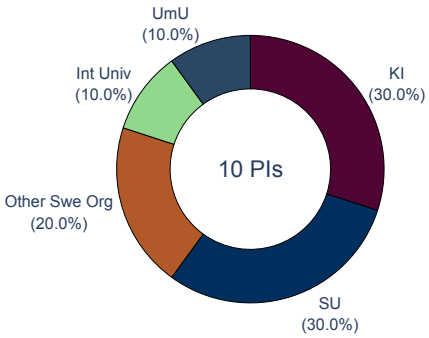
Users 2021



Users 2022



Users 2023



- *Translated chemical exposomics research methods into national services at SciLifeLab*
- *Demonstrated strong user base with growing national and international demand for exposomics*
- *"Exposome-Metabolome Interaction" flagship project performed as joint Platform cross-unit activity*

Unique technology

Exposomics shares conceptual similarities with the mass spectrometry-based metabolomics services offered at the metabolomics Platform, but has unique demands with respect to sample preparation, instrumental performance, method sensitivity, and downstream data processing. The workflows, now provided as a service by the unit, are globally unique and include state-of-the art methods developed at SciLifeLab in the Chemical Exposomics research group. Major technological achievements that are now being applied to user projects include specialty methods for enhanced chemical exposomics, for example by phospholipid removal cleanup of human plasma, and large volume injection with in-line solid phase extraction for environmental water samples. We also validated untargeted mass spectrometry workflows and advanced data processing applications of high-throughput spectral library and in silico structural annotation of small molecules (e.g., demonstrated for the discovery of environmental contaminants in air and water) using open science software (e.g., MS-DIAL) and public databases (e.g., MassBankEU, PubChemLite) to emphasize FAIR data management principles.

Services

The mission of the Exposomics unit is to provide our users with a broad range of chemical exposomics research tools to enable pioneering investigations into the complex effects of chemical pollution on human health and ecosystems. Exposomics methods are currently available to only a few select academic labs in the world, and none are offered commercially to date. At the Exposomics unit, we offer:

- specialized sample preparation conducted within an ultraclean BSL2 laboratory, ensuring meticulous control over background contamination;
- comprehensive trace molecular analysis by sensitive HRMS Orbitrap technology; liquid chromatography (LC; Q Exactive HF-X and Exploris 480) via electrospray and/or atmospheric pressure chemical ionization for wide-scope analysis of polar and semi-polar chemicals;
- combined multi-class targeted (180 analytes) and parallel untargeted LC-HRMS analysis with data-independent (DIA) and/or data-dependent (DDA) MS/MS acquisitions;

- gas chromatography (GC-HRMS; Q-Exactive) analyses to expand the chemical space coverage towards nonpolar analytes (e.g. polycyclic aromatic compounds, brominated flame retardants, legacy organochlorine pesticides, polychlorinated dioxins, and polychlorinated biphenyls).
- expertise in statistics and multivariate data analysis for evaluation of exposure markers.

User fee models

Ensuring nationwide accessibility remains a top priority for Exposomics unit. Users are considered on a first-come first-served basis, with academic users within Sweden receiving priority and subsidies. Following subsidies, exposomics services for national academic users typically range between 1800-2500 SEK/sample, depending on analytical requirements and project scale. This model currently sustains operational expenses while keeping the user fees affordable. Non-academic or international users are subject to higher per-sample costs, approximately 50% more than Swedish academic rates.

User base

Since start of operations in 2021, we have demonstrated a high demand for exposomics services with a strong user base that is rapidly growing. Through 2022-23 (and until Feb. 2024), we attracted a total of 16 projects (8 completed, 6 on-going, and 2 in preparation) primarily from users of national Swedish universities (SU, KI, UmU), but also international users, e.g. DTU (Denmark) and Siena University (Italy). Many of our users were especially satisfied with the quality of the data delivered and already initiated (or planned) follow-on projects for 2024-25.

Collaboration with industry, healthcare, and other organizations

Non-academic projects included those from Swedish environmental agencies (KEMI) and municipal water companies (SVOA) tasked with monitoring chemical safety and environmental health. Some national (and international) requests received in 2022-2024 from industry users were not prioritized due to the specific project´s narrow scope or our lack of internal resources. We anticipate an increase in requests from government agencies and primary healthcare institutions responsible for monitoring chemical pollutants in human blood or the environment (e.g., the Swedish Environmental Protection Agency), as well as from industries striving for environmental sustainability and circular economy practices, which are increasingly attentive to chemicals and associated impurities in commercial materials or new products.

Strategic "Exposome-Metabolome interaction" program

In 2022, strategic funding from SciLifeLab (Platform budget) was allocated to engage users of Exposomics, and to demonstrate cross-unit workflows at the platform. We invited national projects with a focus on exposome-metabolome interactions, and following an internal review, 2 out of 5 applications were selected. One fully supported project (recipient: C. Wheelock, KI) examines the link between traffic-related air pollution exposure and chronic obstructive pulmonary disease. Exposomics (LC-HRMS Orbitrap) and lipidomics (LC-Q-TOF) analyses were conducted on plasma and bronchoalveolar lavage fluid, and data integration is ongoing as a joint collaboration across institutions including KI, the University of British Columbia (CA) and Harvard Medical School (MA, USA), with a goal for publication in 2024. Another on-going project received support for method development on stools, plasma, and cerebrospinal fluid, with a focus on molecular exposures and amyotrophic lateral sclerosis (KI). Notably, a third project (also KI) despite not being selected, proceeded from external user fees for exposomics analyses on human biopsies to study the development of endometriosis (completed in 2023).

Synergy with research group and scientific environment

There are no globally harmonized methods for untargeted exposomics, thus the Exposomics unit collaborates with the Chemical Exposomics research group (SU, Martin) to facilitate the rapid translation of the newest technologies into the delivery of unique national services. The proximity to other research groups and units at Campus Solna (Stockholm), including infrastructure and DDLS fellows, as well as local bioinformatics expertise (NBIS), creates a rich multidisciplinary environment that makes SciLifeLab well positioned to integrate exposomics with e.g., genomics, proteomics, and metabolomics, enabling broader investigations into systems biology and precision health.

Technology development for new service offerings (2025–2028)

The Exposomics unit's technology development aims to expand its service offerings and advance exposomics contributions toward SciLifeLab research capabilities in Precision Medicine and Planetary Biology. Specifically, with regard to Precision Medicine, the Exposomics unit is undertaking development and validation of high-throughput methods for environmental contaminant exposure in human biofluids (J. Martin VR grant "HiChem"). These involve developing kits and protocols for collecting high-frequency low-volume samples (e.g., based on microsampler technology) to generate longitudinal data crucial for supporting large-scale epidemiological investigations on human disease, including environment-

wide association studies (EWAS). We also intend to produce and distribute passive air sampler kits for measuring personal airborne exposomes and global air pollution, based on novel PDMS-foam disk technology which already supports air quality research in European households with a focus on infants and young children (Horizon Europe project INQUIRE).

In the realm of Planetary Biology, the Exposomics unit is working on methods to assess chemical pollution impact on soil biodiversity by combining LC/GC-HRMS exposomics with monitoring of biodiversity composition via eDNA/metabarcoding (PALS grant in collaboration with DDLS fellow from Uppsala University; on-going). Moreover, the development of integrated workflows for DNA/RNA adductomics tailored to sentinel environmental species commonly used in Swedish and European marine monitoring programs is ongoing, in collaboration with users from SU. Future directions in technology development thorough 2025-2028 – contingent on SciLifeLab expensive instrument calls or external funding opportunities, may additionally result in new service offerings including:

- integration of LC-HRMS with ion mobility for higher confidence annotations in molecular discovery
- LC-HRMS structure-oriented screening xenobiotic transformation byproducts
- sensitive analysis of personal airborne exposome monitors by thermal desorption GC-Orbitrap.

Current bottlenecks and needs for operational scale-up

The Exposomics unit experienced rapid growth, expanding its services with strategic investments from SciLifeLab. These included acquiring modern mass spectrometry infrastructure and renovating lab spaces. However, to meet the increasing volume of user requests and project sizes, further investments in personnel and instrumentation are necessary. Time dedicated to post-instrument acquisition data processing and curation is currently the major bottleneck for small to medium-size projects (e.g. 50 to 500 samples; 1–4 months). Larger projects (e.g. >1000 samples) are currently unsustainable due to limited resources, necessitating additional investments in personnel and equipment to support technical development and operation scale-up (e.g. optimization of higher throughput sample preparation and chromatography). Thus, despite already receiving requests for large-scale projects (e.g. 12,000 human serum samples from the Swedish Twin Registry) current resources at the Exposomics unit (with only 2 FTEs) limit the unit's ability to support such endeavors.

NBIS, Data Centre, and FAIR data management

At the Exposomics unit, our philosophy is to use reproducible open science protocols and FAIR data management to meet the demands of the national research audience. We currently employ open science software for data processing, including advanced analysis techniques for high throughput spectral library searches and structural annotation of unknown molecules. To enhance collaboration with NBIS, the Exposomics unit have recently initiated the implementation of high-throughput data processing pipelines with modules tailored to exposomics data (e.g. including chemical identification, structural predictions, analogue search, and metadata annotation). This will help to sustain the high user demand for combined targeted and untargeted exposomics services, and further aid to undertake large projects which require extensive computational capacity.

Budget request

Platform Strategic Budget

Beginning in 2025, we propose an increased Platform budget allocation of 1 FTE dedicated to computational metabolomics, embedded within the Computational Metabolomics Group. This new FTE will split their efforts evenly (50-50) between method development and providing user project support in advanced data analytics. Furthermore, we anticipate funding available for an additional FTE in partnership with NBIS to develop metabolomics data analysis workflows.

We will continue to organize yearly retreats for the Metabolomics Platform personnel (SMC, CMSI, Exposomics), extending invitations to staff from SNC and Spatial Mass Spectrometry units to explore technological developments and foster collaborative across units and Platforms. To accelerate skill development of the Platform staff, we will launch a "*Staff Exchange Program*" enabling staff members to seek funding for internal exchanges within the Platform. Additionally, we will actively encourage international visits to further enrich expertise and collaboration. Part of the annual Platform-centric budget will be allocated towards method development within a designated common area, focusing on internal projects aimed at enhancing Platform methodologies and workflows. Starting in 2024 and extending through 2025-2028, the Platform-centric budget will continue to sponsor a seminar series targeted at the SciLifeLab community, aiming to showcase the potential of metabolomics in advancing precision health, physiology, molecular biology and environmental research. Every year, one or two international speakers will be invited to the Platform to visit our facilities, present their work, and engage in networking for collaborative opportunities.

Budget Metabolomics (SMC and CMSI)

To sustain SMC's ability to accommodate the high influx of users within a reasonable time frame, and to retain highly skilled personnel, we are requesting a 1000 kSEK increase in funding from 2027 onwards.

At present, SMC receives 2400k SEK in SciLifeLab support, in addition to the funding from KAW and co-funding from both SLU and UmU. As the KAW grant is set to end by 2026, and despite gradual adjustments to the current subsidies starting in summer 2024, we do not anticipate full offsetting the loss of the KAW grant solely through increased user fees. In addition, we will apply for grants from other sources to maintain the instrumental park and further develop our unit.

The current CMSI operational model has been built on an influx of projects with a very large sample number and the unit has been dimensioned accordingly. The increased visibility of SciLifeLab through the Gothenburg site is changing the operational landscape with 1) an increased request for project with a smaller sample number and an increased demand for data competence, and 2) Increased focus on mapping of the known metabolome than on unknown discoveries. This will result in as proportionally lower user fees (note the unproportionally high user fee amount in comparison to the operational budget and infrastructure dimension) in comparison to operational budget and in turn as increased demand on Metabolomics staff scientist competence. The budget reflects the change and includes an increase of 0.8 FTE PhD level Staff Scientist at the platform (new recruited staff) in comparison to 2023 (2 FTE PhD), 2024 (3 FTE PhD) level. In addition, we see an increased service cost as seen as increased operations costs of the relatively large instrument park in 2026–2028. Overall, the requested budget from SciLifeLab is one third of the overall facility budget.

Budget Exposomics

The current workload places large demand on the time of both staff (2 FTEs), which is required for lab maintenance, sample analysis, data processing and interpretation, as well as administration and communication with users. The growing volume of projects and users (ca. 1 MSEK/year in user fees) currently allows the Exposomics unit to cover operation costs (e.g. premises, consumables, small equipment depreciations). Additional funding for one more technical personnel (1 FTE) is essential to alleviate the bottleneck in sample preparation and data processing. This will enable the unit to meet yearly user demand, resulting in a sustainable rise in user fees (e.g., 2.5–3 MSEK/year) by 2026–2028. Consequently, this will facilitate further investments in equipment and technological development to scale-up operations in support of large-scale projects (e.g., >500–1000 samples) on a regular basis. Furthermore, the addition of 1 FTE would also afford more time to the Head of Unit and Lab Manager to organize exposomics courses and workshops at the SciLifeLab Training Hub, and to participate in international laboratory staff exchange programs (e.g., within the SciLifeLab-EMBL partnership framework).

Table 1. Metabolomics – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Platform Director	150	150	150	150	150
Platform Coordination Officer	200	200	200	200	200
Seminar series	20	20	20	20	20
Workshop SciLifeLab Metabolomics Personnel	70	80	80	80	80
Joint platform method development projects	160	160	160	160	160
Staff internal exchange / international visits		30	30	30	30
Computational Metabolmics group (1 FTE)		1 000	1 000	1 000	1 000
Sum costs (kSEK):	**600**	**1 640**	**1 640**	**1 640**	**1 640**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*600*	*1 640*	*1 640*	*1 640*	*1 640*
Sum revenues (kSEK):	**600**	**1 640**	**1 640**	**1 640**	**1 640**

Table 2. Chalmers Mass Spectrometry Infrastructure Budget

Costs	2024	2025	2026	2027	2028
Personnel 5.2 FTEs (2024) -> 6 FTEs (2025–2028)	4 968	6 018	6 139	6 261	6 387
Operations	2 050	2 100	2 800	2 820	2 840
Premises	527	687	701	715	724
Instrument depreciations	1 155	941	500	500	500
Sum costs (kSEK):	**8 700**	**9 746**	**10 140**	**10 296**	**10 451**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	2 174	3 200	3 300	3 400	3 500
University co-funding	1 767	1 800	1 820	1 850	1 870
VR Biological Mass Spectrom	300	600	600	600	600
User fees	4 500	4 100	4 200	4 300	4 400
Sum revenues (kSEK):	**8 741**	**9 700**	**9 920**	**10 150**	**10 370**

Table 3. Swedish Metabolomics Centre Budget

Costs	2024	2025	2026	2027	2028
Personnel 7.5 FTEs (2024) -> 7.5 FTEs (2025–2028)	7 500	8 100	8 200	7 500	7 500
Operations (Incl. service contracts)	4 500	4 500	4 500	4 500	4 500
Premises	1 050	1 050	1 050	1 050	1 050
Instrument depreciations	2 264	1 579	1 579		
Other (upgrade wet lab instruments)		300			
Sum costs (kSEK):	**15 314**	**15 529**	**15 329**	**13 050**	**13 050**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	2 484	2 500	2 500	3 500	3 500
University co-funding (UmU and SLU)	5 000	5 000	5 000	5 000	5 000
KAW	5 000	5 000	5 000		
User fees	3 000	3 200	3 500	4 600	4 600
Sum revenues (kSEK):	**15 484**	**15 700**	**16 000**	**13 100**	**13 100**

Table 4. Exposomics Budget

Costs	2024	2025	2026	2027	2028
Personnel 2.25 FTEs (2024) -> 3.25 FTEs (2025–2028)	2 900	3 400	3 900	4 050	4 150
Additional technical personell (TAs, PhD students)	200	100	100	100	100
Operations	350	400	650	850	1 000
Premises	400	420	440	460	480
Instrument depreciations & contracts (current)	1 500	1 500	1 500	1 500	600
Instrument depreciations & contracts (new)	-	100	1 200	1 400	1 400
Other (e.g. Travels)	30	30	40	40	40
Sum costs (kSEK):	**5 380**	**5 950**	**7 830**	**8 400**	**7 770**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	2 588	3 100	3 100	3 400	3 400
University co-funding (SFO/SU) Science Faculty, instrument depreciation	900	-	-	-	-
University co-funding (SU/ACES) - salaries, instrument depreciation	600	600	600	600	600
SciLifeLab Expensive Instrument Funding (2025-2027)	-	800	800	800	-
Exposome-Sweden VR Infrastructure Grant (2026-2028)	-	-	800	800	800
User fees	1 250	1 500	2 500	2 800	3 000
Sum revenues (kSEK):	**5 338**	**6 000**	**7 800**	**8 400**	**7 800**



In Situ Sequencing Unit. Photo: Mikael Wallerstedt

Spatial Biology Platform

Basic Information

Platform Director: Mats Nilsson, Stockholm University

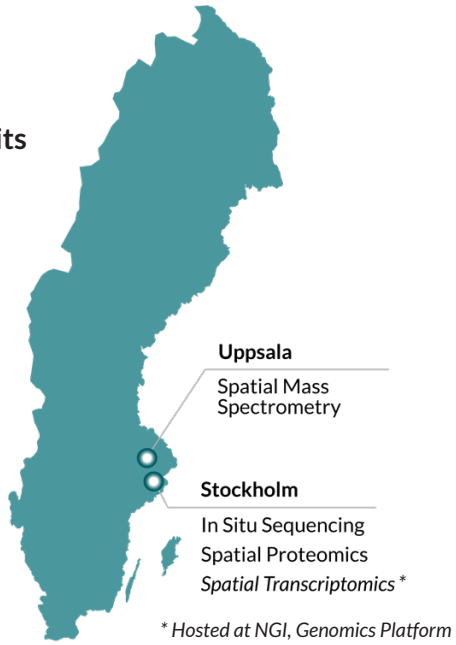
Platform Co-Director: Charlotte Stadler, KTH Royal Institute of Technology

Platform Coordination Officer: Charlotte Stadler, KTH Royal Institute of Technology

Platform vision: To develop and make spatial omics broadly accessible for deciphering biology across all major research fields

Platform mission: Provide service for advanced spatial analysis of biomolecules *in situ*

Location of Units

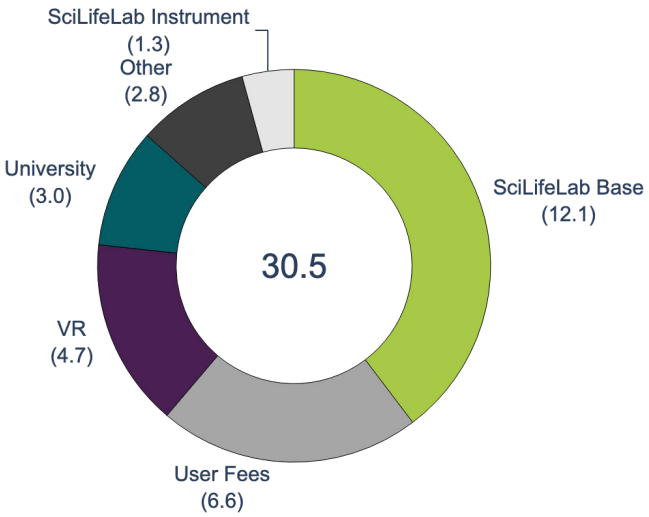


** Hosted at NGI, Genomics Platform*

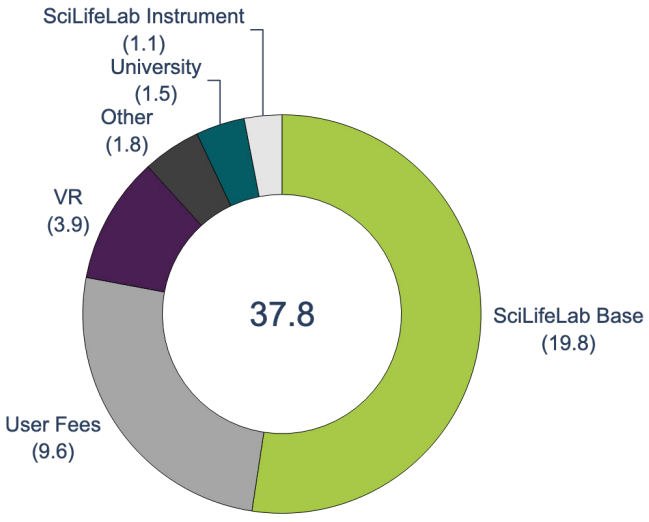
SciLifeLab Funding

Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
In Situ Sequencing	3.1	5.1
Spatial Mass Spectrometry	2.6	4.4
Spatial Proteomics	4.7	5.7
Platform Strategic Funding	*1.8*	*4.7*
Total SciLifeLab Funding	**12.1**	**19.8**

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E9 Spatial Biology

Platform organization and governance

The platform was formed after the evaluation in late 2020 with support from the International Advisory Board (IAB) and brings together cutting-edge technologies for spatial omics, including spatial transcriptomics and in situ sequencing that both have been developed by researchers at SciLifeLab and KTH/SU respectively. The expertise is divided across 4 *units* (ST - *Spatial Transcriptomics*, ISS - *in situ sequencing*, SP - *Spatial Proteomics and* SMS - *Spatial Mass Spectrometry*) with its own Head of Unit (HU) and covers all layers of omics in cells and tissue sections: genes, transcripts, proteins and small molecules (lipids, peptides, metabolites). The platform has been organized according to the SciLifeLab steering documents and is led by *platform director (PD) Mats Nilsson* and *co-PD Charlotte Stadler*. The platform currently has four closely associated research groups and scientific directors (PSD) and together with the HUs, PD and co-PD they form the Platform Management Group (PMG), equivalent to the platform steering group. Members of the PMG is also acting as steering group in the VR instrument grant received by the SB platform in 2021.

The Platform has also put together an extended platform management group (extended PMG) with representatives from the Bioinformatics platform, the Genomics Platform and Data Center to promote discussions and coordinate data analysis and single cell activities. An overview of the platform organization is shown below.

Overall platform development and key achievements 2021–2024

Platform specific KPIs 2023:

- 31 collaborative project publications and 18 platform technology publications since 2021 (ST not included)
- 19 of above publications in high impact journals (>9)
- Increased user base with 40 % since 2021 (70 PI in 2021, 98 PI in 2023)

Following the 2020 evaluation, the spatial biology platform was recognized as a capability with huge potential, given the emerging field of spatial omics and the existing expertise in this field at SciLifeLab. The platform steering and governance has come into place and has been described above. In 2021, the SB platform received 29,4 MSEK funding from VR Infrastructure to invest in instruments dedicated to the platform and to promote the infrastructure. Dedicated instrument funding of 6 MSEK has also been received from SciLifeLab from instrument calls in 2020 and 2023. These instruments, besides Vizgen's Merscope platform that was funded end of 2023, have now been installed and unique service using these instruments is now offered. *Since 2021, the number of unique users has increased from 70 to 98 in 2023*, showing the growing need and requests for the spatial omics service given by the platform. Due to efforts in outreach activities the overall fraction of *non-local users is now above 50 %*.

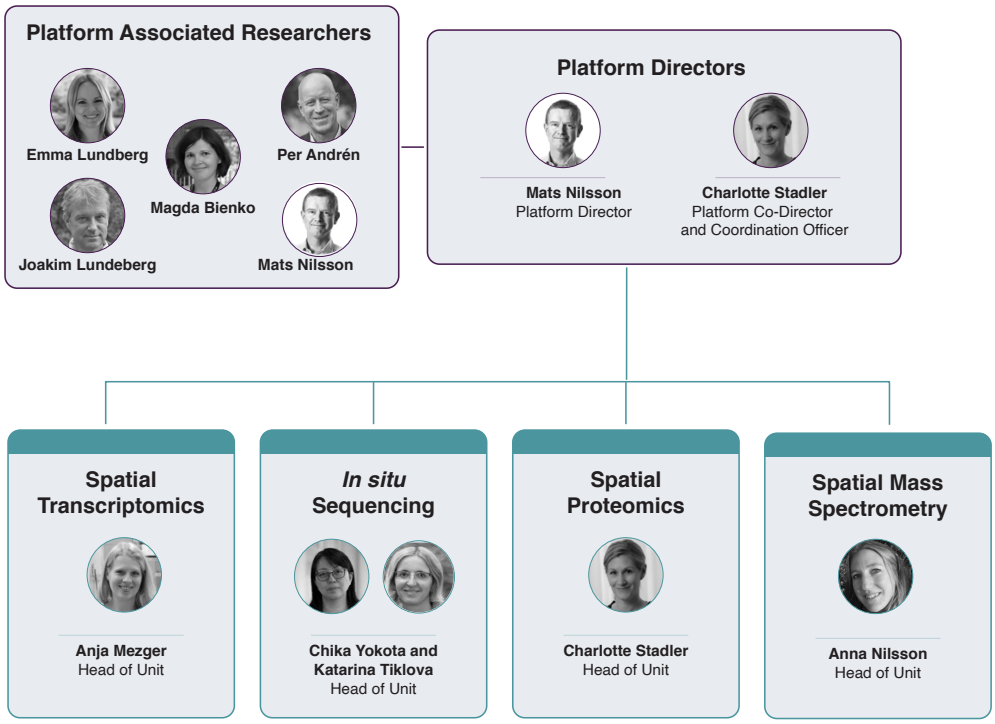


Figure 1. Platform organization as of today with appointed Head of units and associated research groups. From the start of the SB platform and until 2021, the platform also hosted the eukaryotic single cell genomics unit, now part of the Genomics platform as it is purely based on sequencing data without any spatial components.

The ISS and SP units have temporarily expanded their respective teams thanks to other funding sources (VR and EU funding) and increased funding from SciLifeLab since the mid-term evaluation in 2022. Together with the instrumentation this has increased the throughput in number of projects and possibilities for further internal development. Still, we are one of the smallest platforms at SciLifeLab with a total of 12 FTE employed in the units, excluding the ST unit that is operated as part of NGI and the Genomics platform. The platform has established close connections to many of the key industry players in the field, including 10x Genomics, Akoya Biosciences, Lunaphore, Bruker Daltonics and Waters, as well as contacts and collaborations with smaller companies to develop new tools and future service. From gained global reputation the platform will beta test new instrumentation from another global actor with start in spring 2024.

From the user side we see an increased number of projects in need of multiple spatial omics methods. In 2020 three of the platform PSDs received a VR-Research Environment Interdisciplinary grant (30 MSEK) for developing integrated spatial omics methods to study dementia. Since then, and in line with the Terms and Conditions from SciLifeLab, several projects across the platform units have been initiated to promote integrated omics method development. This includes combining *in situ* sequencing with multiplexed IF, *in situ* sequencing with spatial mass spectrometry and spatial transcriptomics respectively, and spatial transcriptomics with spatial mass spectrometry. The latter method integration method was recently published in *Nature Biotechnology* (PMID: 37667091). The platform has also received TDP funding (Technology and Development project) from SciLifeLab to combine multiplexed IF with the Phenocycler platform with DNA/RNA FISH. A few examples of integrated omics methods are shown below in *Figure* 2.

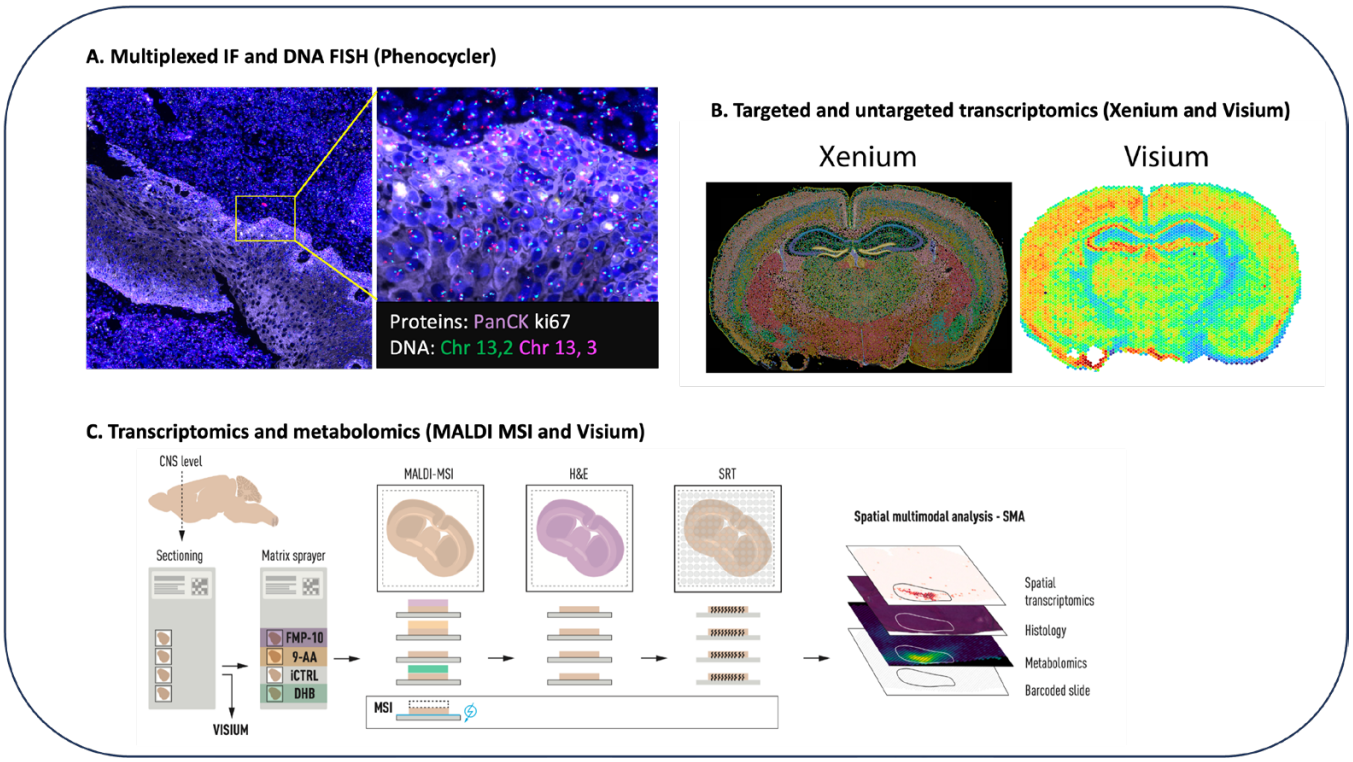


Figure 2. Three examples of ongoing technology development for integrated omics within the platform. (A) Integrated multiplexed IF and DNA FISH, (B) targeted and untargeted transcriptomics on the 10x platforms and (C) the already published method from integration of spatial metabolomics and transcriptomics using MALDI imaging and 10X Visium (Nature Biotechnology 2023, PMID: 37667091)

Infographics: Statistics and Metrics for Spatial Biology Units

In Situ Sequencing

Read more: Webpage, Publications Database

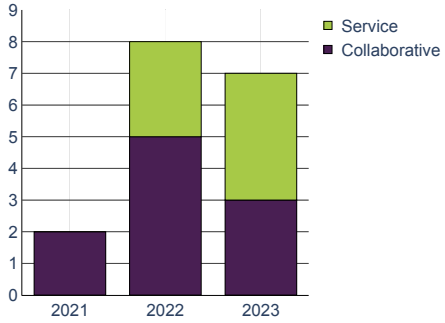
Basic Information

HU: Katarina Tiklova, Chika Yokota
Host University: SU
SciLifeLab unit since: 2019
FTEs: 2.4
PSD: Mats Nilsson

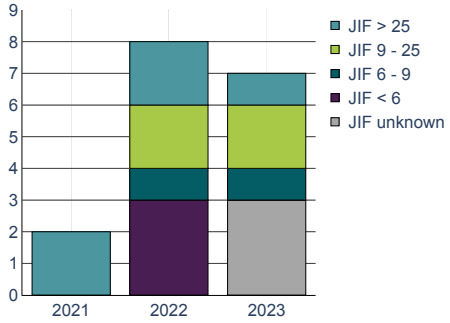
Funding 2023 (kSEK)

SciLifeLab: 3000
Other: 5068
User Fees: 1900

Publications by category

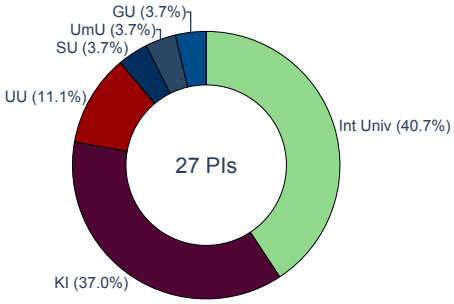


Publications by JIF

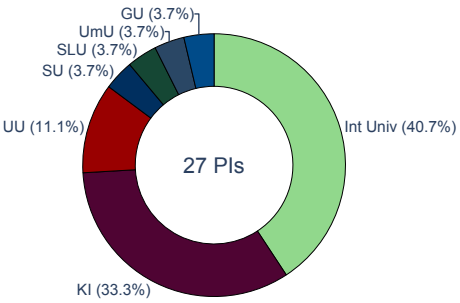


No. of Tech Dev Publications 2021 - 2023: 5

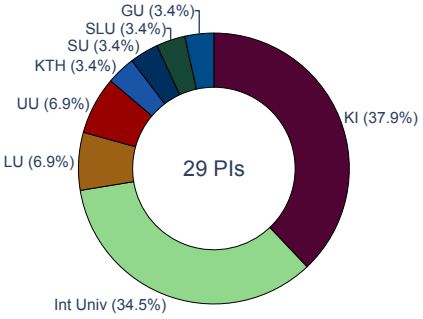
Users 2021



Users 2022



Users 2023



- *Provided service to 50 projects for 41 users across 8 national and 15 international universities and institutes 2021–2023.*
- *Organized the first spatial EMBO practical course: Spatial analysis of gene expression in tissues*
- *Installing and implementing service of the fully automated ISS system, two Xenium analyzers*

Spatial Mass Spectrometry

Read more: Webpage, Publications Database

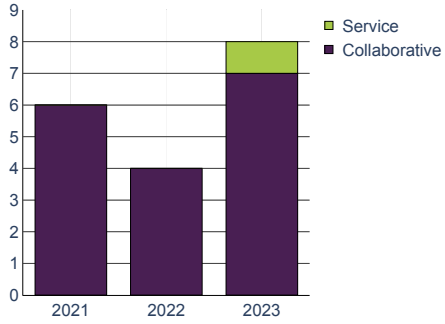
Basic Information

HU: Anna Nilsson
Host University: UU
SciLifeLab unit since: 2021
FTEs: 4.1
PSD: Per Andrén

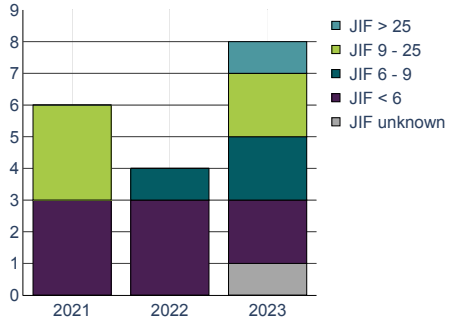
Funding 2023 (kSEK)

SciLifeLab: 2500
Other: 4000
User Fees: 155

Publications by category

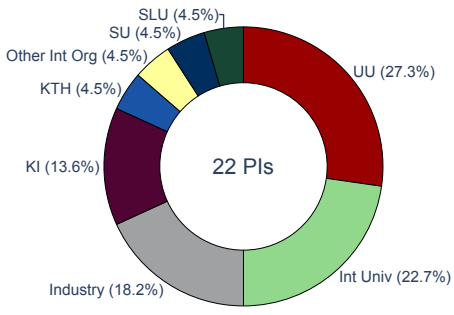


Publications by JIF

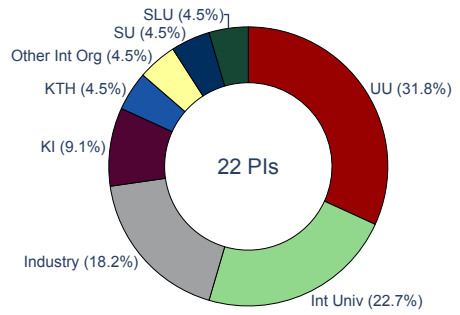


No. of Tech Dev Publications 2021 - 2023: 9

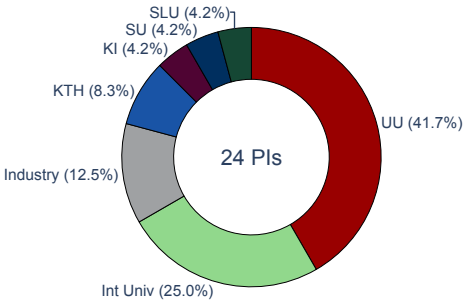
Users 2021



Users 2022



Users 2023



- *Provided service to more than 35 projects for 24 different users 2021–2023.*
- *Organized an international 3-day SMS workshop and symposium with >130 attendees (Regional MSI Spring Workshop)*
- *Developed a spatial multimodal analysis of transcriptomes and metabolomes in the same tissue section.*

Spatial Proteomics

Read more: Webpage, Publications Database

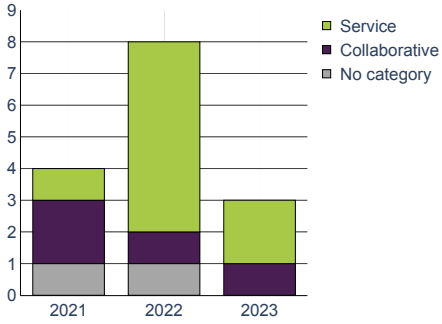
Basic Information

HU: Charlotte Stadler
Host University: KTH
SciLifeLab unit since: 2013
FTEs: 4.8
PSD: Emma Lundberg, Magda Bienko

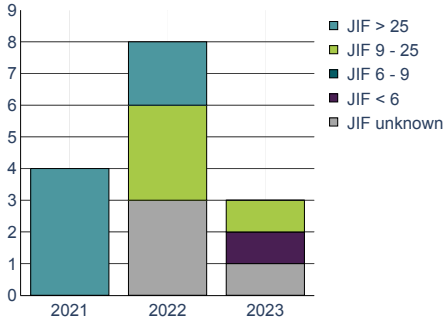
Funding 2023 (kSEK)

SciLifeLab: 4500
Other: 1550
User Fees: 1100

Publications by category

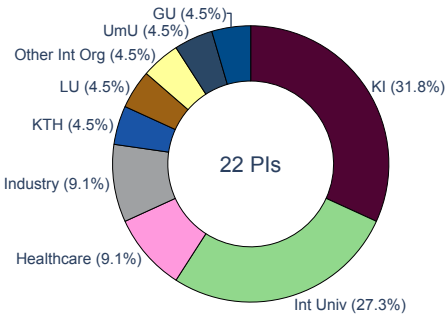


Publications by JIF

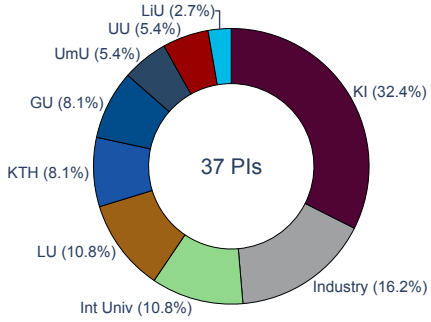


No. of Tech Dev Publications 2021 - 2023: 5

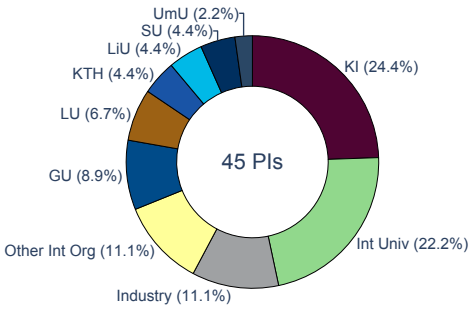
Users 2021



Users 2022



Users 2023



- *Increased user base with 100 % since 2021*
- *Established collaborations with 5 industry partners*
- *Selected beta test site for 3 new instruments 2021–2023*

Spatial Transcriptomics' KPI's

- *Access provided to 22 users across 12 different institutions, including industry and non-Swedish academia 2021–2023.*
- *318 samples were processed and analyzed 2021–2023, including a collaborative, large-scale project.*
- *3 new technologies in service: protein detection + Visium, CytAssist and ONT sequencing coupled with Visium*

Overall platform plans 2025–2028

Organization and operations

First of all, we suggest changing the name of the platform from Spatial Biology to Spatial Omics, to align with other SciLifeLab platforms and make the name more intuitive. After three years of operations and with a continuous increase in service requests, we see the importance of creating routines and operation systems that allows for additional scale up. This involves project management and data handling. We do not intend to grow the platform by changing the platform structure or increasing the number of units. We see a minor expansion of personnel within the different units and strive towards an equal number of FTE across the units. We believe at least 4 *FTE are needed in each platform unit* to enable further development and implementations of new services, and for engaging in other platform related activities such as the capabilities and the training hub. We anticipate closer interactions between unit personnel as more multi-omics projects are expected in the coming years.

As data generation capacity increases due of the recent instrument investments, we need to seamlessly integrate analysis with data generation. According to the SciLifeLab long term vision of more platform centric activities, *we aim to expand the platform centric resources with bioinformatics support (from 1 to 3 FTE) and with a project coordinator (1 FTE).* We will continue to collaborate with the Bioinformatics platform to leverage on this and propose to pay salary for experts employed within the Bioinformatics platform but operating within and between the spatial omics units and under their lead. This will benefit both platforms as the Spatial Biology have the in dept knowledge of what is currently needed to support our users, future needs and to support scale ups in the everyday work, while the BioInformatics platform will develop more expertise within the spatial omics field and multi omics integration.

Technology developments, increased service, and new research areas

We will continue our work with developing and implementing spatial multi omics services that span across several units. Two instrument platforms, 10x Visium and Lunaphore COMET, recently launched integrated transcriptomics and proteomics and this will be implemented as a service during 2024. We also work internally on the combination of Xenium and Phenocycler and COMET, to leverage on the large RNA panels from Xenium, and the image quality, resolution, and custom antibody panels of the spatial proteomics platforms. We are also working on integrating Xenium and Visium on the same slide, as well as MALDI imaging combined with Visium and Xenium. Through ongoing collaborations with Navinci Diagnostics, we are currently developing an integrated method for detecting protein interactions along with multiplexed imaging on the Phenocycler platform. This is further described under "new technologies and service offerings".

Connection to capabilities

We have so far been focused on generating data on model organisms, mostly human and mouse. As such, there are already many ongoing efforts within the *precision medicine capability*, initially within the spatial proteomics field, where highly multiplexed imaging contributes to in depth analysis of the tissue microenvironment and allows for cellular phenotyping, expression, and distribution of existing as well as potential new biomarkers that will aid in personalized treatment. As an example, the spatial proteomics unit is working together with clinicians at Karolinska Hospital for improving patient stratification for immunotherapies in bladder cancer. An antibody panel of existing diagnostic markers for primary diagnosis of lung cancer tumors has also been developed with support from a SciLifeLab TDP project grant. We anticipate our contribution to this capability to increase further, in line with the development of more spatial multiomics methods, with the advent of the automated Xenium platform and the CytAssist platform that enables Visium analysis on standard microscopy slides. In addition, the SMS unit has developed a protocol which needs minimal sample preparation and just one µl of cerebrospinal fluid (CSF). The developed protocol allows simultaneous analysis of numerous metabolites and neurotransmitters with high accuracy in a very time efficient matter (Analytical Chemistry, PMID 38059473). This approach identified significant metabolic differences between de novo Parkinson's disease and controls and offers swift detection of biomarkers in low sample volumes, promising for diagnostics of neurological disease.

We *plan to expand our service into diverse sample types* beyond model organisms, in line with the overall platform mission and vision to accelerate biology insights across diverse research areas. From discussions with the capability leads for *planetary biology* we intend to collaborate with the Genomics and Bioinformatics platform, to set up adjusted protocols and pipelines that allows for spatial profiling of other species and plants. Given our existing know how and instrumentation for spatial omics methods in our platform, the large operations and expertise within sequencing and generation of data pipelines within the

Genomics and Bioinformatics platforms, we believe SciLifeLab can make significant contributions to expand the use of spatial omics beyond the current focus areas. For spatially resolved transcriptomics, several projects on plants and other species with existing sequencing data and reference libraries has already been conducted on the Visium platform, for example on insects, sponges, amphibian and bird tissues. Further, we see huge potential for using the new Merscope platform for spatial profiling of non-model organisms, as it has a very flexible solution for custom panels of probes. We also see the feasibility for the *in-house* ISS chemistry for custom projects that also require sample processing optimizations. The spatial mass spectrometry methods offered are already compatible with plant samples and we have shown impact in this field through a number of publications on plant stress hormones and the characterization of cyclotides in violets (Scientific Reports, PMID:35115562, Front Plant Sciences, PMID: 30254654). This field is limited to reference compound databases that allows for identification of the compounds. For spatial proteomics, the opportunities for diverse species are limited to the availability of affinity reagents. However, we have initiated discussions for performing spatial proteomics in sections of *Zebra Finch*, using antibodies available for other bird species. To test and develop protocols for various species, we can make use of the well-defined antibody collection from the Human Protein Atlas program, all with known antigen sequences, to select suitable antibodies with high sequence homology.

For the *pandemic preparedness capability* the platform has previously collaborated with the Chemical Biology Genome Engineering (CBGE) platform and associated researchers to develop an assay combining cellular phenotypic screening using the HPA antibody resource, along with drug repurposing to identify new therapeutic targets for SARS CoV-2 (published on BioRxiv). This project, demonstrating the power between targeted phenotypic screening and drug repurposing was selected as a demonstrator project for the European Infrastructure of Translational Medicine (EATRIS) and as part of this, spatial proteomics data will be generated. Overall, we see that our ongoing work with integrated omics methods can be used to understand viral and other pathological conditions within infected cells, thereby supporting the pandemic preparedness capability.

Training and education

As a small platform of 12 FTE and with a high pressure on data generation and implementation of new methods and scale up activities, there is currently limited time to engage in training and education. However, we see it as important to share our knowledge and to educate the broader research community in this field and we hope to have the resources to do this more in the coming years when the platform grows. As a provider of expensive services that require unique instrumentation and technological expertise, practical courses on sample preparations and running the methods is not feasible for larger groups. Instead, we invite users with actual projects to join the activities when working on their samples when feasible. While we strengthen the connection to the Bioinformatics platform to further develop data analysis support, courses for analysis of the data we generate is a feasible approach. In addition, we can also contribute to data analysis course by providing training data sets containing single or multiple omics information. In this way we can also contribute to internal training of the staff within the Bioinformatics platform.

Overall, we hope for an expansion of the platform resources within the coming years, that will enable further contributions and engagements into various initiatives beyond data generation.

Technologies and services offered within the spatial biology platform

The four platform units offer a broad range of spatial omics methods to detect various types of molecules at different resolution and scale across different sample types. The overall principle is that the users deliver tissue blocks to be sectioned onto the respective glass slides, or tissue samples already sectioned on standard glass slides. Following this, single or multiple spatial omics data are generated by the platform experts. This includes full planning of experimental set-up, initial control and quality testing and possible optimizations needed. The data (sequence data, images and/or text files with extracted features) are then delivered to the user using various solutions depending on the unit and data type (implementation of the SciLifeLab data delivery system is ongoing). The service provided is a mix of commercial methods using cutting edge instrumentation, and unique in-house methods, protocols and custom assays. The overall service concept and representative images generated in the platform using the various technologies is shown in *Figure 3* and the technologies are summarized in *Table 1*.

Competence/background of staff and plans for keeping/attracting competent staff scientists

The team of leading scientists within and associated to the platform (*Prof Joakim Lundeberg and Prof Mats Nilsson*) has long experience from the field and have been developing some of the cutting edge spatial transcriptomics methods of today (Science PMID:27365449, Nature methods PMID:23852452, Nucleic Acids Res. PMID:32990747). The spatial proteomics expertise comes from previous work within the *Human Protein Atlas* (*HPA*) *project* (Science PMID: 28495876, Science PMID:25613900) and the research team of *Prof Emma Lundberg and Dr Charlotte Stadler*, previous member and PhD student of her team.

For the spatial mass spectrometry, *Prof Per Andrén* has contributed extensively to develop the methods and advancements of both MALDI and DESI (Nature Methods PMID 31548706, Nature Protocols PMID 34075230) and the staff has extensive competence within the field ranging from sample preparation, experience in using different types of SMS instruments, and data processing. Currently, all unit members have more than ten years of experience from working with the technologies and they also have experience within the field of analytical chemistry and method development. Together, this put the platform in an excellent position to continue developing the future integrated spatial omics services.

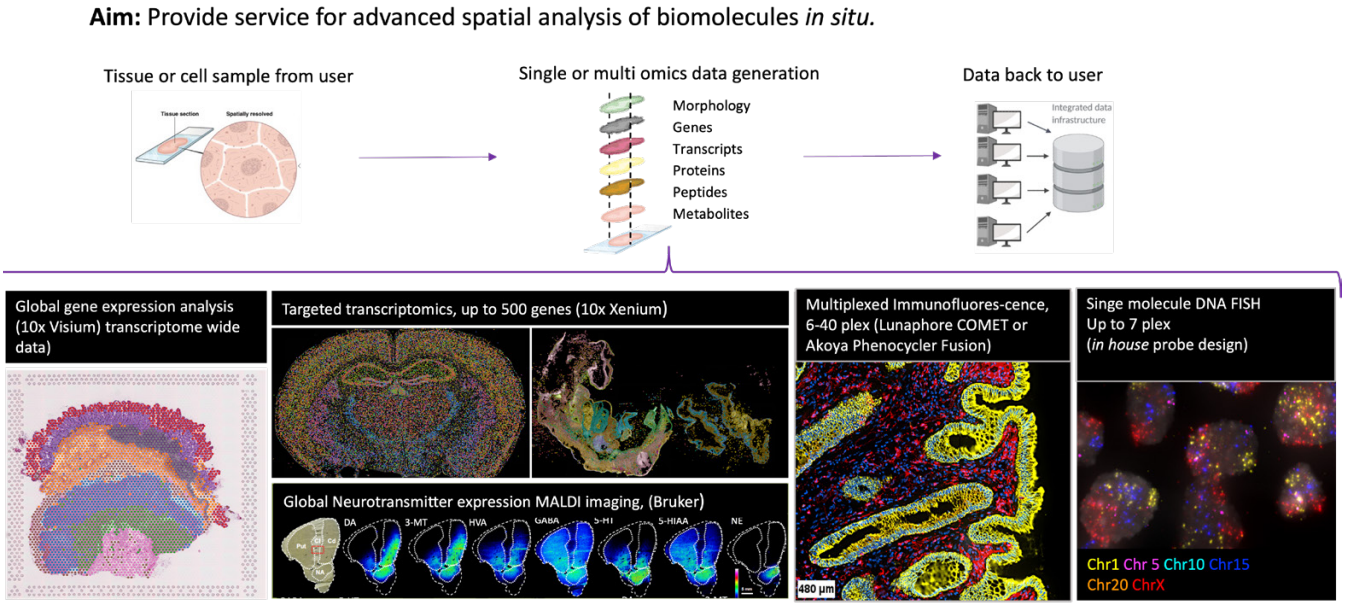


Figure 3. Overview of the platform service and examples of different spatial omics data generated within the platform using various instrumentation as well as in house expertise.

Table 1. Current services and methods offered at the Spatial Biology Platform units, along with overall features and feasibility. ST= Spatial Transcriptomics, ISS = in situ sequencing, SMS = Spatial Mass Spectrometry and SP = Spatial Proteomics.

Unit and technology	Omics type	Readout	Complexity	Sample requirements		Spatial resolution
				Fresh-frozen	FFPE	
ST - 10X Visium	RNA	NGS Sequencing Microscopy of tissue section	Transcriptome wide	✓	✓	Anatomical feature of 55 um
ISS - 10X Xenium	RNA	Microscopy	Predesigned panels up to 500 genes Custom panels	✓	✓	Sub-micron
ISS - In situ sequencing (in house)	RNA	Microscopy	Custom panels of up to 400 genes	✓	✓	Sub-micron
SP - sm RNA/DNA FISH	RNA/DNA	Microscopy	Custom in house probe design 1-6 targets	✓	✓	Sub-micron
SMS - MALDI Imaging	Small molecules < 20 kDa	Mass spectrometry	Mutliplexed, targeted or untargeted	✓	✗	Anatomical feature of 5 um
SMS - DESI Imaging	Small molecules < 20 kDa	Mass spectrometry	Mutliplexed, targeted or untargeted	✓	✗	Anatomical feature of 20 um
SP - Akoya Phenocycler	Proteins	Microscopy	Pre-conjugated antibodies > 40 proteins Custom conjugations	✓	✓	Sub-micron
SP - Akoya Phenocode/Opal	Proteins	Microscopy	Panels of 6 antibodies (TSA amplification)	✓	✓	Sub-micron
SP - Lunaphore COMET	Proteins	Microscopy	Custom antibody panels of 6-30 proteins	✓	✓	Sub-micron

We are fortunate to operate and offer service within this strong era of spatial omics, that has gained increased interest and attraction over the last years. However, we believe the most important factor for success of our platform is due to the strong collaborations across research groups and the units, and the competence within every member of the platform team. This strong constellation helps to keep every member knowledgeable of developments in the field. The personnel actively engage in and participate in both national and international conferences and workshops. This involvement is crucial for advancing scientific knowledge, fostering collaborations, staying abreast of advancements, and promoting the ongoing professional development of the research staff. As part of our platform strategic budget, we help to support these activities, by paying for participation in international conferences or courses relevant to the field. This is a dual win, as the team members gain new knowledge while also promoting the work of the platform on the international arena. In addition, personal development is an important factor for keeping the expert competence and we continuously invests in our staff to ensure that everyone is highly trained and can help users during their projects.

User base, project prioritization and user fee models

Since the platform was formed in 2021 the user base has steadily increased, going from supporting 70 unique users in 2021 to 98 in 2023. The implementation of several new instruments has significantly increased throughput, at the same time as the interest has further increased and we expect this scale up to continue over the coming years – possibly at even higher pace. Our user base is mainly academia with a smaller fraction of industry users and healthcare providers. The users are local, national as well as international. Since last evaluation we have worked hard to increase national spread of users. Webinars have been organized in Gothenburg, Linköping, Umeå and Örebro, as well as within the STorM network and other national workshops. The fraction of non-local users has increased from <40 % in 2020 to almost 60 % in 2023 indicating a strong national (and even international) interest (see user statistics), which is well in line with the SciLifeLab objective of supporting users at national scale.

As all our methods make use of ex vivo material, samples can easily be shipped from around the globe to our units in Stockholm and Uppsala, making the spatial biology service well suited for a research infrastructure serving a broader user base. With advancements in sample handling such as the CytAssist instrument used for Visium, we can accept sectioned tissue samples (fresh frozen and FFPE material) which users can easily ship from anywhere to the facilities in Stockholm. Our objective is to further broaden our user base by engaging other universities in Sweden, but also to increase the fraction of industry users to help support high operational costs. This will be accomplished through an expansion of outreach activities at these academic institutions and via the supplier companies.

After initial evaluation of feasibility, impact and required resources, projects are prioritized on a first come first serve model. However, exceptions are allowed for priority, such as rare sample material with specific timelines or revised experiments for publication. For most projects we offer a pilot study to access the feasibility to make a stop or go decision. In some cases, users are wait-listed (weeks-months depending on how extensive the project is). If the demand continues to increase, we have a plan to prioritize projects based more on scientific impact.

For the Swedish academic users, we charge for reagents and consumables, and a subset of operating costs. As the reagents are very expensive, only minor contributions to the operation costs, such as instrument running costs and service contracts are covered by user fees.

Scientific environments, synergies and collaborations

One of the overall strengths of the platform is the scientific environment with closely integrated units and pioneering research groups (see *Figure 1*). As described in other sections of the report, many technology development projects are ongoing across the units and together with the associated research groups. In total, *close to 20 technology development publication has come out from the platform.* There are close ongoing collaborations between the SMS, ST and ISS units and research groups on technical method developments for the integration of MALDI imaging with the Visium/Xenium and in situ sequencing technologies. There are initiated collaborations between the SP and ISS unit for development of a joint service on the Xenium and downstream proteomics instruments. The ST and SP units are closely interacting within several user projects applying Visium and downstream spatial proteomics at high resolution, although on consecutive sections, and a few user manuscripts are in preparation. There are planned collaborations between the SMS and the SP unit, for integration of a new MALDI-IHC protocol with multiplexed immunofluorescence.

The units are also connected with several additional research groups, either via the scientific directors or independently as part of collaborative user projects. The platform is well connected to several large-scale research projects and community programs including the *Human Protein Atlas*, *the Human Developmental Cell Atlas* initiative, ENABLE and EU projects PROMINENT, DISCERN, HUGODECA and DiscovAIR. Many of the units are also connected to National as well as European Infrastructure networks or research projects, including *EPIC-XS* and *EASI Genomics* (5-year consortia recently ended), *Euro Bioimaging*, *Int. MSI Soc.* and *CutCancer*, the latter funded by Horizon 2020 within the Mission Cancer focus area. Within SciLifeLab, collaborations with

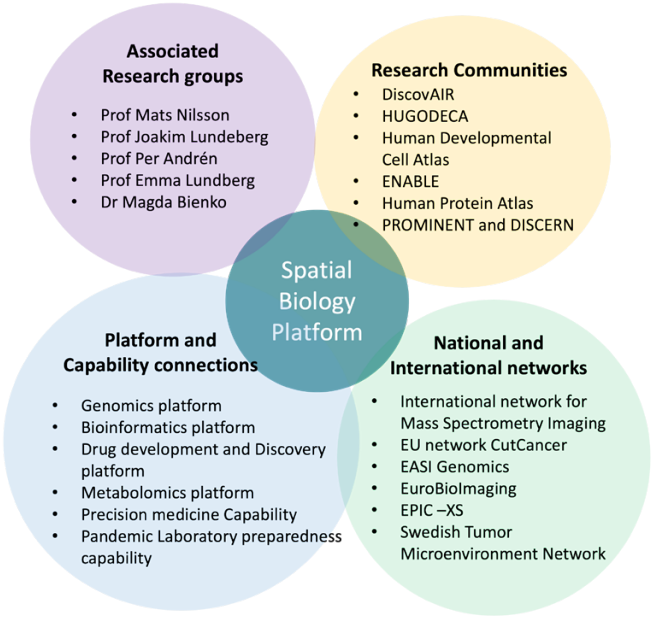


Figure 4. An overview of current and past platform external connections. Individual research group collaborations besides the directly platform associated research groups are not listed here.

the *Bioinformatics*, *Genomics*, *Metabolomics and DDD* platform exist, as well as activities towards the capability areas of SciLifeLab (described earlier). The SMS unit together with the metabolomics platform (Chalmers infrastructure for metabolomics, Gothenburg, Swedish NMR Centre, Gothenburg, Swedish metabolomics center, SLU and Umeå University, Exposomics, Stockholm) aim to promote synergies and pipelines that could benefit user projects. In addition, we have established collaboration with the DDD platform for certain projects involving the characterization of new candidate drug molecules. The overall interaction network is illustrated in *Figure 4*.

Collaboration with industry, healthcare, and other organizations

The platform has several ongoing collaborations regarding technology development with various industry partners in the field of spatial biology, many operating at the global market as key players. This includes the providers of the key instrumentation and technologies offered by the platform, including 10X *Genomics*, *Akoya Biosciencs*, *Lunaphore*, *Waters Corp.* and *Bruker Daltonics*. Together with the latter, the SMS *unit* is collaborating to develop a deep learning approach for single cell analysis based on morphological features of the images. This project is supported by a TDP grant to the unit from SciLifeLab. The *SMS and SP units* will also beta test new instrumentation from Waters and *Thermo Fisher Scientific* respectively. The SMS *unit* is also collaborating with *AmberGen Inc*, to develop and implement MALDI-IHC, allowing for simultaneous detection of larger protein markers using antibodies conjugated to mass-tags, on top of small molecules from the MALDI imaging to assign the expression of small molecules to specific cell types.

In addition, several collaborations with small or medium sized companies from start-ups to more established exist, with the aim to develop or implement new methods. An example is the collaboration between the SP *unit* and *Navinci Diagnostics*, where in situ proximity ligation assay (isPLA) is used in combination with the Phenocycler platform, to allows for direct protein interactions along with deep phenotypic profiling. The goal is to implement protein interactions as a new service within the platform service and precision medicine capability. Together with *Atlas Antibodies* the *SP unit* is beta testing a new method for achieving multiplexed IF on a conventional fluorescence microscope and using antibodies from the HPA project with the aim to make multiplexed IF more flexible for diverse protein markers, and present opportunities for labs without the expensive commercial instrumentation.

Besides technology driven companies, collaborations also exist with pharmaceutical companies, including Chiesi Farmaceutici S.p.A, where the SMS unit is conducting PK/PD studies in drug development projects. Another example is the collaboration with TreeFrog Therapeutics, for joint technology development for imaging of organoids. Several large pharma companies are (or have been) users of the platform services, for example Novo Nordisk, Roche and AstraZeneca. We expect and strive to increase industry connections further in the coming years.

An overview of current collaborations with industry is summarised in *Figure 5*.

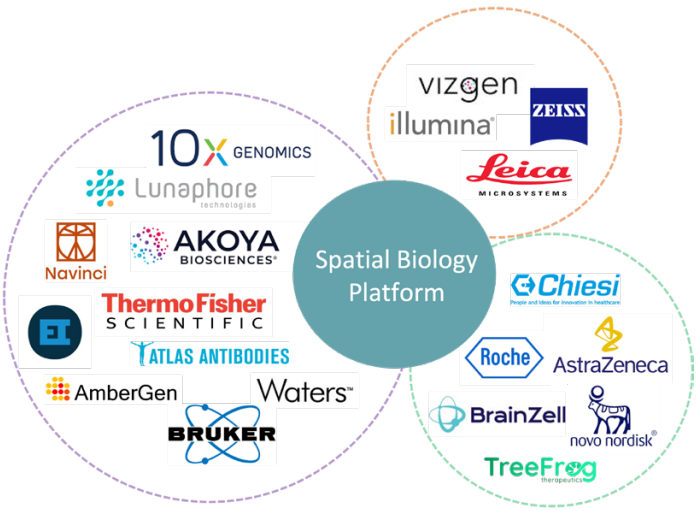


Figure 5. Platform industry connections. Industry collaborators are shown in purple circle, pure instrument suppliers in orange and industry platform users in green.

Plans for development including new technologies/service offerings 2025–2028

Several new service areas as well as methods for improved performance and throughput are planned to be implemented within the coming years. Some of the new services involve incorporation of the latest advancements made by commercial industry providers of instruments and technologies. These enhancements cover combined RNA and protein readouts for 10X Visium and Xenium, as well as improvement on the Phenocycler and COMET platform, and improved resolution on the Visium platform (Visium HD). Other new implementations and services are a result of *in house* developed integrated methods. These include service for *integrated metabolomics* and transcriptomics, DNA FISH with multiplexed immunofluorescence (mIF) and protein-protein interactions using *in situ* PLA along with multiplexed immunofluorescence, both on the Phencocycler platform. We will also complement the targeted transcriptomics area with the Merscope instrument and related service. Merscope is based on the FISH method with no amplification of the signal which is a method of choice for some projects and customers. With the human samples the challenge is the auto fluorescent signal which interferes with the currently used ISS method. Merscope is solving this problem with the tissue clearing method to remove the tissue but preserves the RNA. This will widen the service and possibilities which we provide. From internal development in sample preparations and protocols, the SMS unit will offer detection of new molecule classes and in FFPE material, as well as advancing the spatial resolution to surpass <1 µm through morphology-guided deep learning. This enables imaging of comprehensive molecular profiles at the individual cell level, capturing unique molecular fingerprints associated with each cell category. An overview of planned implementations and additional services is listed in *Table* 2.

As described in the overall platform plans, we will work with adaptation of technologies and methods to make them more applicable for non-model organisms and the planetary biology capability. Due to increased demand from users, including from the planetary biology community, the ST unit as part of NGI will invest resources to expand its services to be able to process plant tissues and to couple the normal Visium protocol with the detection of bacteria and fungi. The in-house ISS service allows for processing of non-mammalian tissues and cells, including bacterial and viral genes and upon concrete requests we plan for adaptation of the sample preparations to contributes to the planetary biology and well as the pandemic laboratory preparedness capabilities.

Table 2. Current services offered by the different units (ST= Spatial Transcriptomics, ISS = in situ sequencing, SMS = Spatial Mass Spectrometry and SP = Spatial Proteomics.

Unit and technology	Omics type	New service	Additional Comments
ST - 10X Visium	RNA (and proteins)	Multiomics - proteins added (> 30) Multispecies runs - microbes added	Improved spatial resolution (Visium HD 2 um)
ISS - 10X Xenium	RNA (and proteins)	Multiomics - proteins added Increased RNA complexity	Predesigned panels up to 5000 genes
ISS - In situ sequencing (in house)	RNA	Additional anlaysis support	Implementation of cell segmentation Increased sensitivity and sample feasibility
ISS - Vizgen MerScope	RNA (and proteins)	New Instrument platform	Expected service from Q1 2025
SMS - MALDI Imaging	Small molecules < 20 kDa	New molecule classes Increased lateral resolution by deep learning Multiplexed MALDI-IHC	Detection of glycans and tryptic peptides Single cell resolution Compabitle for FFPE sections
SMS - DESI Imaging	Small molecules < 20 kDa	Targeted metabolomics	Expected service Q1 2025
SP - Akoya Phenocycler	Proteins and (RNA/DNA)	Multiomics - RNA added (Akoya) DNA added (in house)	Launch of RNA assay Q4 2024 DNA FISH offering 2025
SP - Lunaphore COMET	Proteins and (RNA)	Multiomics - RNA added (1-12)	Launch of RNA assay Q1 2024 Expected service from Q3 2024
SP - in situ Proximity Ligation Assay	Proteins	New modality - protein interactions	Integrated isPLA and multiplexed IF on Phenocycler Expected service 2025

Plans for data handling and analysis 2025–2028

We endorse the FAIR data sharing principles (Findable, Accessible, Interoperable, and Reusable) and consider properly managed, accessible, and reusable data as a valuable and necessary resource for conducting research of high quality. For the spatial omics field, data generation is expensive and the substantial amount of information from these data sets should be used as broadly as possible. Hence, we encourage our users to follow these principles and do our best to provide them with necessary information to do so. Since we are a young platform setting up our entire organization and operations in the last 2 years, we are still developing in this area, and we see NGI and the data handling within the ST unit as a role model for how this could be organized. This will be increasingly important with the expected growth of the platform and number of projects in the coming years. While NGI possesses the necessary infrastructure and knowledge to process sensitive data and has worked closely with the SciLifeLab Data Centre to co-develop the data delivery system (DDS), the other units have since day one actively been pushing for a better data delivery system to our users. As our image-based data sets are large, this has been a challenge both for the platform and the users to handle. We have now successfully set up the use of the DDS system within the ISS unit and expect to connect the SP unit to this system during 2024. The generated data within the SMS unit are stored and analyzed using facility computer and raw data is stored on in-house NAS servers. Only the processed extracted data (excel-files) is delivered to the users. All data handling complies with GDPR. For the internal projects across units and research groups, we are planning to apply for SciLifeLab FAIR storage to enhance the data sharing with the FAIR principles.

As the platform resources are limited and entirely used to generate spatial omics data, support in data analysis from the units to our users is very limited. An exception is the ST unit, as operated within NGI which has extensive resources in data handling and analysis. NGI has since 2021 a two-year shared position with the Bioinformatics platform NBIS, which resulted in an nf-core pipeline for the analysis of 10x Visium data. Expertise on data analysis exist in the research groups connected to the platform, however the resources and same level of expertise is not available within the units. This is clearly reflected by the number of user publications from pure service projects compared to collaborative projects.

To develop and implement better data analysis support, we use most of the *strategic platform funding* (1.1 MSEK) to buy expertise from NBIS. Since the end of 2023, 1 FTE now works closely with the platform to support the units in their most urgent needs. This involves improvements of everyday activities within the units by implementing more automated data handling steps and scalable solutions to cope with more and larger projects, implementation of existing analysis pipelines from the research groups, as well as establishment of new analysis pipelines and tools developed within NBIS and specifically within the Bio Image Informatics Facility (BIIF). While the output data formats from the ST, ISS and SP units are open and allows for analysis using various analysis programs, the data from the SMS unit relies on vendor-specific data analysis software for image processing and are currently confined to on-site execution. Nonetheless, post-processing tasks such as statistics and correlation analyses can be conducted on exported data, offering flexibility in data analysis.

Despite recent initiation of bioinformatics support we already start to see valuable contributions to the platform. However, the resource of 1 FTE is far from enough and *we see the need for 3 FTE to support the platform* and for our users in the coming years. While it took some time to set up this arrangement with NBIS, we see this as a win-win model as NBIS has better opportunities to permanently employ experts that can then be paid for by our platform. We hope for an increase of our strategic platform funding from 2025 and intend to continue using the funding for this purpose as we see this as a major bottleneck to our operations and possibility to contribute to the broader research community.

Regarding data management the platform has so far had limited support from *Data Centre*. Since the platform started in 2021 and after pushing for a solution to an urgent problem, we concretely got help to setting up an FTP server that allowed some of the units to deliver their data to the users, avoiding portable hard drives for delivery of TB sized data. Our understanding is that DC develops many services, but there is lack of support to the platform to implement them into the operations. To be fair, the limited computational resources within the SB platform has also slowed down the implementation of new tools and routines. Recently, the platform got support to implement the use of the new Data Delivery System (DDS) and temporary storage is also supported by Data Centre. However, for sensitive data, this has been hampered by legal aspects as agreements has to be in place between DC and the Host University of the respective units, in our case different for every unit. We aim to connect all units to the DDS system during 2024.

Current training offerings and plan for 2025–2028

As part of the overall operations, the personnel within the units meet with current and future users to educate and consult about spatial omics applications. This number is much larger than the number of reported projects, and total *number of users the units have interacted with was 159 during 2023.* In addition, several educational outreach events have been held across Sweden and internationally. Many seminars have also been co-hosted with industry partners and our site has been a location for several European Tours organized by Akoya and Lunaphore. As members of the EU project consortium CutCancer, we provide ISS training, including wet lab work, imaging, and analysis to other members of the consortium. Similar activities were part of the EASI Genomics consortia and educational seminars were also held as part of EPIC-XS and within the National Microscopy Infrastructure (NMI). In 2025, we are planning to organize an ISS workshop for domestic participants. The SMS unit actively engages in comprehensive training programs for national and international master's and PhD students, covering essential aspects such as sample preparation, data acquisition, and advanced data analysis techniques. Many units also organize on-site training sessions and hands-on experiments with cutting-edge products for users with ongoing projects.

Budget request

For the coming years it will be crucial that reasonable resources exist in every unit, and we strive to balance the number of staff scientists between the units. *We believe at least 4 FTE per unit is needed* to allow for 1) testing and implementing new methods and protocols from the industry partners 2) contribute to platform internal development along with the associated research groups and 3) engage in platform related activities such as outreach, training and capability areas.

Therefore, the *ISS unit request additional funding to grow from 2.4 to 4 FTE* and funding to cover additional premises for the expansion of space that would be needed to also fit new instruments. For SP and SMS, the number of FTE will remain the same. *Note: ST is not covered by this budget as operating under NGI, part of the Genomics platform.*

As a platform with expensive instrumentation and reagents, all units *request funding to cover parts of the instrument service contract costs.* Many of the instruments have been under warranty until now but will require service contracts from 2024 and beyond, adding extra budget posts for the units that are currently not covered. We do not see these entire costs to be covered by user fees considering they are already charged for the expensive reagents that also has increased during the last 2 years (SP and ISS unit). We estimate to cover ≈ 25 % of the instrument service contract costs by user fees.

The *SMS unit* also request additional funding to cover costs when current co-funding from Uppsala University expires with no possibility for renewal.

As described in the report we see the need to *expand on data analysis resources*, to implement analysis pipelines, improve and automate current workflows and make them scalable with increased user projects and sample numbers, and to develop integrated omics analysis pipelines. We currently employ 1 FTE from NBIS using our *strategic platform funding* and now request increased *platform funding to cover 3 FTE* as a platform centric resource. In addition, we *request platform funding for a project coordinator* to set-up routines and workflows for multiomics projects that will increase during the coming years. Finally, we request *0.5 MSEK annually for reagents* to be used in further development of integrated omics service within the units. As the reagents are expensive (for ex one Xenium run detecting 300 genes is ≈ 80 kSEK and one Phenocycler run of 30 antibodies is 30 kSEK) we do not have any funding for such activities as user fees are already high to cover the reagents for the user project. Remaining budget posts for the strategic platform funding remains the same as current, including a platform retreat, some outreach activities/training/conference participation of the staff. 80 kSEK of the platform strategic budget is used to complement the PCO (Platform coordination officer) funding of 200 kSEK that is given to all platforms, to cover the salary costs of 20 % activity of the PCO.

Finally, the SB platform has applied to the Research Council as part of the inventory of research infrastructure. If successful, the platform will be invited to submit a full application for infrastructure funding. The decision on whether the platform will be invited to submit the actual application will be announced in June 2024. Funding of a successful application will start from 2026 and we intend to request funding for 5 FTE in this application.

Table 1. Spatial Biology – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Personnel 1 FTEs (2024) -> 3-4 FTEs (2025–2028)	1 000	3 000	3 000	4 000	4 000
Platform activities - retreat	150	150	150	150	150
Personnel participation conferences/outreach	70	100	100	100	100
Additional PCO salary to cover 20 % activity	80	80	80	80	80
Platform internal technology development - reagents	100	500	500	500	500
Platform Director	150	150	150	150	150
Platform Scientific Coordinator	200	200	200	200	200
Sum costs (kSEK):	**1 750**	**4 180**	**4 180**	**5 180**	**5 180**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*1 750*	*4 180*	*4 180*	*5 180*	*5 180*
Sum revenues (kSEK):	**1 750**	**4 180**	**4 180**	**5 180**	**5 180**

Table 2. In Situ Sequencing Budget

Costs	2024	2025	2026	2027	2028
Personnel (3 FTEs for 2024, and 4 FTEs from 2025)	3 140	4 355	4 486	4 620	4 759
Operations (reagents, R&D)	5 000	6 000	6 500	7 000	7 500
Premises	434	534	534	534	534
Instrument depreciations	2 280	2 280	2 280	2 280	800
Service contracts (3 instruments)	-	-	1 500	1 500	1 500
Other (co-funding for MERSCOPE)	1 000				
Sum costs (kSEK):	**11 854**	**13 169**	**15 300**	**15 934**	**15 093**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 105*	*4 700*	*4 700*	*5 400*	*5 400*
University co-funding	-	-	-	-	-
VR instrument grant (depreciations)	1 480	1 480	1 480	1 480	-
SciLifeLab fnstrument grant (depreciations)	700	700	700	700	700
Accumulayed funding previous year	2 500	1 200	1 200		
CutCancer (untill 2025)	300	300			
Additional funding X	-			500	500
User fees (reagents, 50% of service contracts)	5 000	6 000	7 300	7 900	8 500
Sum revenues (kSEK):	**13 085**	**14 380**	**15 380**	**15 980**	**15 100**

Table 3. Spatial Mass Spectrometry Budget

Costs	2024	2025	2026	2027	2028
Personnel 4.1 FTEs (2024) -> 4.1 FTEs (2025–2028)	4 053	4 175	4 259	4 344	4 431
Operations	766	1 250	1 250	1 250	1 250
Premises	680	748	763	778	794
Instrument depreciations	2 147	2 147	2 147	2 147	2 147
Sum costs (kSEK):	**7 646**	**8 320**	**8 419**	**8 519**	**8 622**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*2 588*	*3 600*	*4 500*	*4 750*	*4 600*
University co-funding					
VR-INFRA (2021-00189), instrument depreciation	1 000	1 000	1 000	1 000	1 000
UU - SciLifeLab	1 000	1 000	1 000	1 000	1 000
UU - Forskningsinfrastruktur (FISK)	2 000	2 000			
Accumulated for instrument depreciations (from FISK)			1 147	1 147	1 147
User fees	300	700	800	800	900
Sum revenues (kSEK):	**6 888**	**8 300**	**8 447**	**8 697**	**8 647**

Table 4. Spatial Proteomics Budget

Costs	2024	2025	2026	2027	2028
Personnel 4.8 FTEs (2024) -> 4.5 FTEs (2025–2028) (2.5 % increase/year)	4 939	5 000	5 125	5 253	5 385
Operations (reagents)	1 200	1 300	1 300	1 300	1 300
Premises	750	750	750	750	750
Instrument depreciations	1 600	1 600	1 600	1 600	
Service contract (Phencycler from 2024, COMET from 2025)	300	600	600	600	600
Sum costs (kSEK):	**8 789**	**9 250**	**9 375**	**9 503**	**8 035**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*4 658*	*5 500*	*5 625*	*5 750*	*5 900*
University co-funding	-				
VR (NMI)	600	750	750	750	750
VR instrument grant (depreciation)	1 000	1 000	1 000	1 000	
Scilife instrument funding (depreciation)	600	600	600	600	
VR and Scilife funding previous years (used after 2024)	650	-	-	-	-
User fees (reagents and 20 % instrument service contract contribution)	1 260	1 420	1 420	1 420	1 420
Sum revenues (kSEK):	**8 768**	**9 270**	**9 395**	**9 520**	**8 070**



Cryo-EM unit in Stockholm. Photo: Mikael Wallerstedt

Cellular and Molecular Imaging Platform

Basic Information

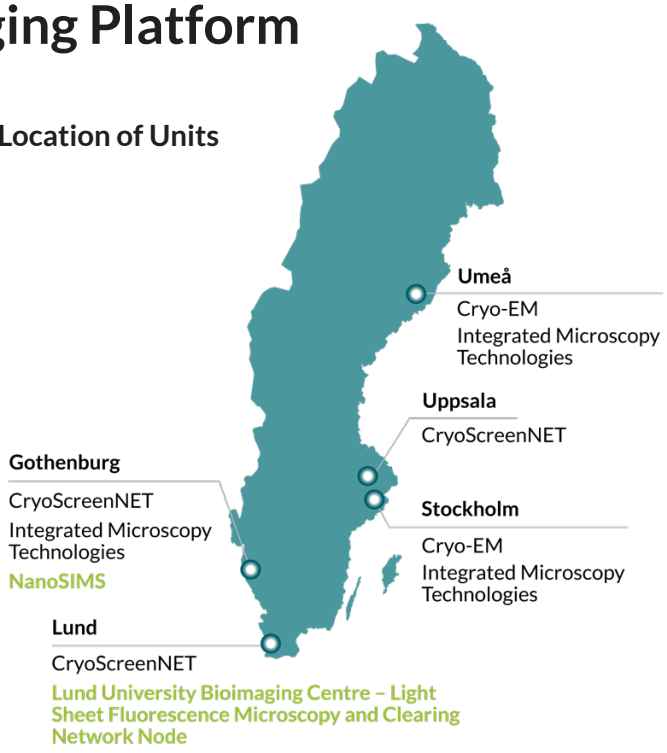
Platform Director: Marta Carroni, Stockholm University

Platform Coordination Officer: Rebecca Howard, KTH

Platform vision: Through its distinctively integrated platform for microscopy technologies and expertise, Cellular and Molecular Imaging (CMI) will support a strategic expanding range of state-of-the-art imaging methods, further develop multimodal approaches at the interface between supported applications, and disseminate these techniques to a growing range of cellular, structural, neuroscience and medical research fields

Platform mission: The CMI Platform enables research that requires imaging on various spatial scales, from the atomistic to organismal levels, leveraging and integrating advanced fluorescence and electron microscopy methods not generally accessible to individual research groups or local facilities

Location of Units

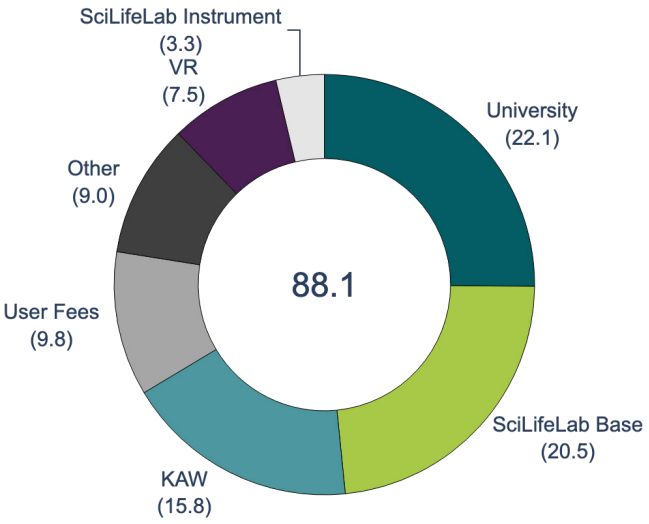


SciLifeLab Funding

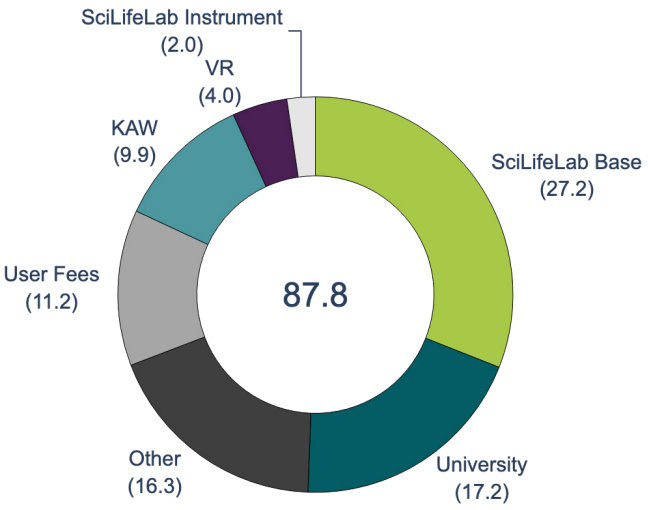
Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Cryo-EM	11.9	15.5
Integrated Microscopy Technologies Gothenburg	1.6	1.6
Integrated Microscopy Technologies Stockholm	3.6	4.3
Integrated Microscopy Technologies Umeå	1.6	1.6
Lund University Bioimaging Centre – Light Sheet Fluorescence Microscopy and Clearing Network Node*	0.0	0.8
NanoSIMS*	0.0	1.5
Platform Strategic Funding	*1.9*	*1.9*
Total SciLifeLab Funding	**20.5**	**27.2**

*Proposed to be included in the platform

Total funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



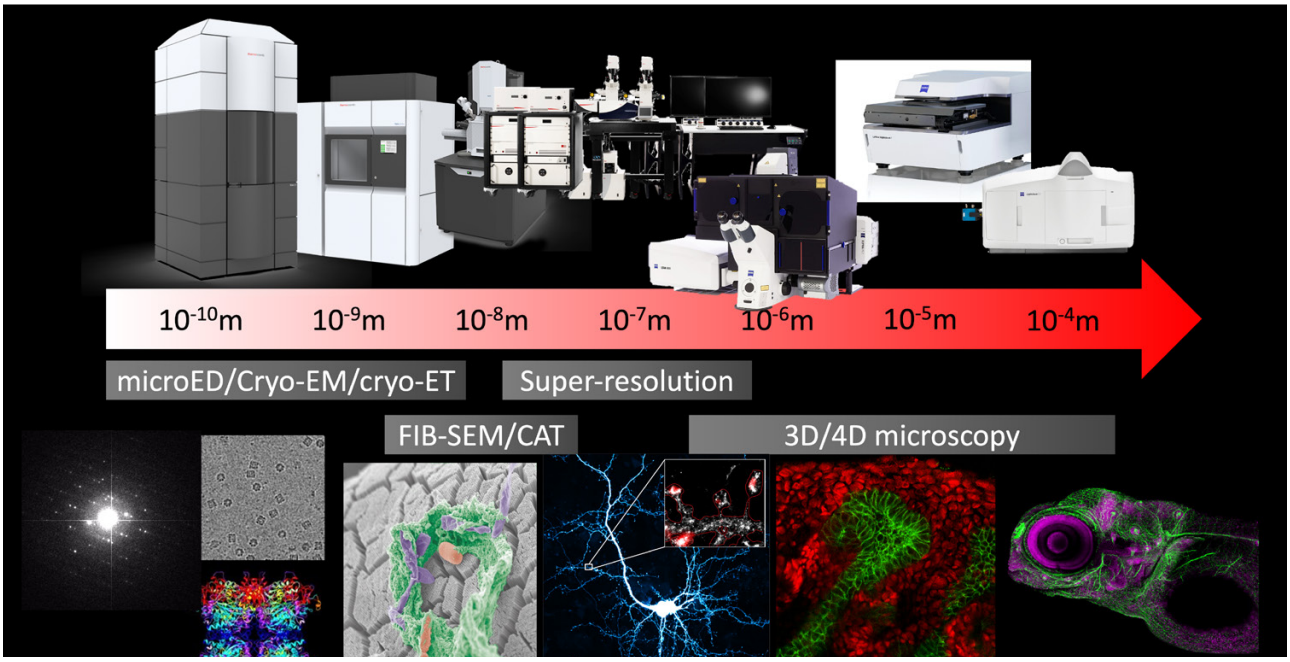


Figure 1. Overall purpose of the CMI platform

Cellular and Molecular Imaging platform

Platform organization and governance

According to the plan presented to the IEC under the previous evaluation for the 2021-2024 road map, the CMI platform has strengthened the focus on imaging technologies. The CMI platform consists currently of two Units: the Cryogenic Electron Microscopy (Cryo-EM) Unit and the Integrated Microscopy Technologies (IMT) Unit. More detailed descriptions of the Units are found below and in the Units sections. The platform is steered by the management group (PMG) which includes: the Platform Director, the Platform Coordination Officer, the Heads of Units of each node (HUs) and the Platform Scientific Directors (PSDs). The PMG meets remotely once a month, reports to the central SciLifeLab management group and communicates the information taken centrally to the Platform staff.

Twice a year, the eight members of the User Reference Group (URG) are invited to the PMG meetings in order to obtain feedback about the Platform operations, limitations and suggested improvements. The URG is composed of user community representatives, being themselves active users of one or several of our operations. Their insights have proven very useful in identifying problems, such as data handling issues and limitations and needs for expansion, such as requests for more capacity for high-resolution cryo-electron tomography (cryo-ET). The URG is asked to fill in a user survey, thus providing the Platform a written track of evaluations.

Once a year, and especially in preparation for important deadlines, the Platform meets also the two members of the International Reference Group (IRG), international experts in light and electron microscopy and in the operation of large infrastructures (Prof. Peijun Zhang, Diamond Light Source, and Prof. Timo Zimmermann, EMBL Imaging Centre). Having discussions with the IRG and recognizing similar challenges and goals in major infrastructure institutes in Europe is extremely important for the Platform and for SciLifeLab in general. The two Units of the CMI Platform have also regular meeting activities with other Platforms and Infrastructure entities. The IMT Unit is also part of the VR-funded National Microscopy Infrastructure (NMI) group and the Cryo-EM Unit is also associated to the SciLifeLab Integrated Structural Biology Platform, with monthly meetings and common retreats and courses organisation.

Overall platform development and key achievements 2021–2024

The *Cryo-EM Unit* has been in operation since 2016 as a unified entity with two main nodes, one in Umeå and one in Stockholm (at Campus Solna). The Cryo-EM Unit offers services in single particle analysis, cryo-ET and electron diffraction (microED). The main nodes also coordinate a cryo-EM screening network (CryoScreeNET), created in 2021, which is composed of three expert colleagues placed at the universities of Gothenburg, Uppsala and Lund, who are in charge of reaching out to the local communities, distant from Stockholm and Umeå, assisting with sample preparation and screening. The launch and implementation of the CryoScreeNET has been one of the key achievements under 2021-2024.

Additionally, the Unit has consolidated practices in microED screening and data acquisition – a capacity that started as a technology development project (TDP)

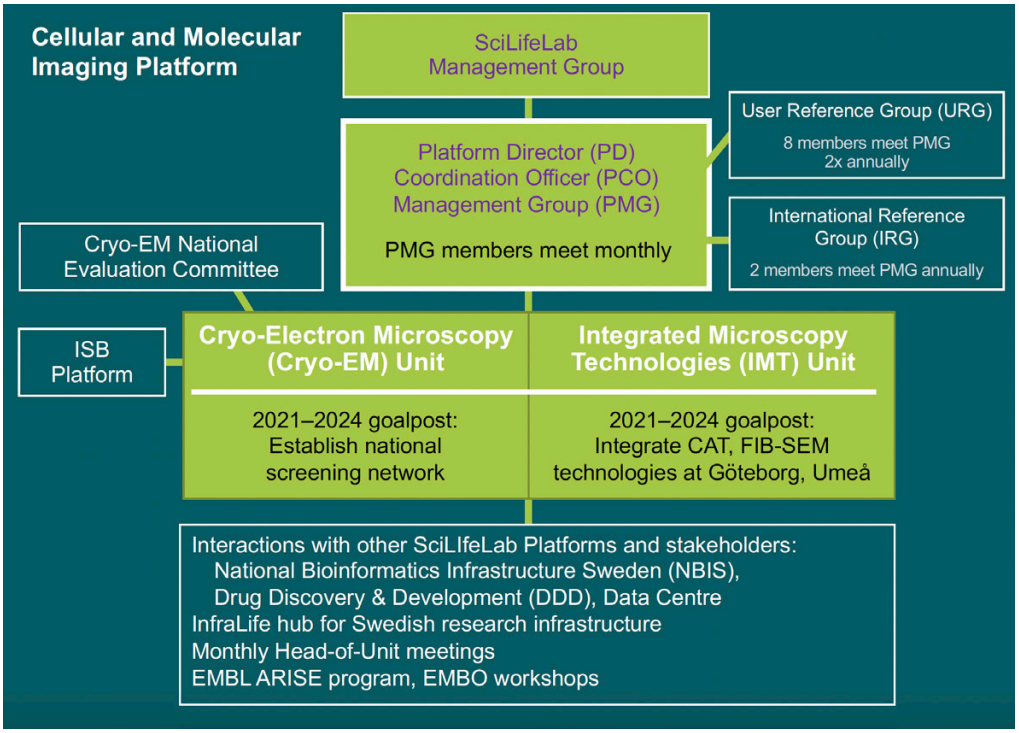


Figure 2. Platform organogram

between Stockholm University and SciLifeLab and has then expanded via site exchange between the Swedish sites and also to other Nordic and European sites.

During 2021-2024 the Unit has continued to strengthen the interactions with the other Nordic cryo-EM communities, in particular with the Danish centres in Copenhagen and Aarhus, as part of the cryoNET initiative, funded by the Wallenberg (Sweden) and NovoNordisk (Denmark) Foundations. In addition to the annual international cryoNET symposia, the cryoNET group has launched a workshop in "Advanced Cryo-EM Image Processing", with high-level speakers from all over the world, bringing the newest advances in data analysis to Nordic students and researchers, including industry users. The Unit has also strengthened contacts with industry by attracting users from biopharmaceutical companies and engaging in industry collaborations for methods development.

Another key achievement of the 2021-2023 period has been the incorporation of two new cryo-EM staff members, experts in single particle image processing, which are employed by National Bioinformatics Infrastructure Sweden (NBIS)within the DDLS program, but are physically located at the Cryo-EM Unit in Stockholm, working daily with the rest of the Unit staff. More details are found in the dedicated Cryo-EM Unit section below.

In terms of instrumentation, 2021-2023 has witnessed a significant step forward for the Unit with the acquisition of a Glacios microscope (Thermo Fischer Scientific) and major upgrades of the Titan Krios in Umeå, upgrades for microED at both nodes and acquisition of a new-generation blot-less system for sample preparation (Chameleon-TDPLabtech) in Stockholm. As part of the CMI Platform plan for 2025-2028, the Unit has started to work towards developing to maturity the service of cryo-ET (on thin specimens and cryo lamellae) for high-resolution cellular imaging and subtomogram averaging for in situ structural biology and cryo- and live correlative light and electron microscopy (cryo-CLEM). Instrumentation for CLEM (see more in the next section) has been recently acquired in Stockholm and was already present in Umeå, where a new Aquilos 2 FIB microscope has also been purchased. We aim to expand the cryo-FIB capabilities at both nodes to reach a broader community.

The *IMT Unit* was created in 2021 based on the existing Advanced Light Microscopy (ALM) facility at Campus Solna in Stockholm, operational since 2013. Since 2021, the IMT Unit includes ALM (IMT-Stockholm) plus two additional nodes: the Focused Ion Beam Scanning Electron Microscopy (FIB-SEM) node in Umeå (IMT-Umeå) and the Correlative Array Tomography (CAT) node in Gothenburg (IMT-Gothenburg). The IMT Unit offers services with a plethora of fluorescence microscopy techniques: SIM, FLIM, STED and single molecule localization microscopy (SMLM) for super resolution, single molecule measurement with fluorescence correlation spectroscopy (FCS and STED-FCS) for studying single molecule dynamics, expansion microscopy (ExM) and tissue clearing followed by lattice and light-sheet fluorescence microscopy for large biological volumes, FIB-SEM and CAT for cellular and tissue correlative microscopy. One of the key achievements of the IMT Unit in 2021-2023 has been the integration of the new technologies FIB-SEM and CAT. The Unit has run a pilot project on kidney multimodal imaging and particularly the design of a pipeline for sample preparation, transfer and adaptation to the multimodal

imaging approach. The FIB-SEM IMT-Umeå node has also engaged in collaborations with Luleå University for the usage of X-ray imaging as aid in identifying specific region of interest prior to FIB milling. The CAT IMT-Gothenburg node has attracted international collaborations (see details below) and, through the organisation of an international workshop, has raised the awareness about the potentials of CAT among the national Swedish community.

In line with the whole CMI Platform development plans towards correlative and multimodal imaging, the IMT Unit has recently acquired a MINFLUX microscope for molecules live tracking, which opens up the possibilities to perform a variety of studies for the study of molecular mechanism using fluorescence and cryo-EM in parallel.

The CMI Platform stands out, together with NBIS, as one of the top performing SciLifeLab platforms in terms of training and education, with more than 30 workshops and conferences organised in 2023 alone, with the participation of international speakers and covering most imaging techniques. Many staff members participate in international exchange internships, courses in leadership and management, and further training activities for the Platform personnel, collaborating with the NBIS Training Hub. In addition to courses, workshops and conferences, the Platform plays a strong role in the education of the research community via personalised and advanced technical consultation (e.g., cryo-EM drop-in service), continuous interaction with the users on data collection and analysis matters (e.g., cryo-EM Tuesdays user meetings). Such activities do not only involve the local Swedish community but also attract participation by international researchers.

The CMI Platform has also been very successful in securing substantial grants external to SciLifeLab, with 3 out of 7 Research Infrastructure grants from the Swedish Foundation for Strategic Research awarded to members of the Platform.

Overall platform plans 2025–2028

During 2025-2028, the CMI Platform plans to work on different fronts of development involving not only the Platform, but also other stakeholders at SciLifeLab. Specifically, the Platform will work towards:

1. Strengthening the interactions between the IMT and the Cryo-EM Units in order to push correlative and multimodal imaging both on the cellular and on the molecular scale. On the cellular and tissue scale, we will intensify the development of volumetric EM (FIB-SEM), CAT and CLEM to enable studies of complex cellular networks, organoids and tissues. On the molecular scale, we will work on the combination of cryo-EM, MINFLUX and CLEM to study molecular mechanisms using *in vitro* systems. For *in vivo* systems, and with the idea of adding a temporal component to imaging, we will push the development of super-resolution live imaging coupled to cryo-ET. These activities will involve expert research groups at different sites. We will organise Platform annual workshops focused on techniques as well as an annual retreat for all Platform staff.
2. Strengthening the interactions with NBIS for development of machine learning and AI tools in the analysis of images and other cellular and molecular data. This will imply collaborations, not only with NBIS, but also with the Integrated Structural Biology (ISB) Platform, the Data Centre and the DDLS Fellows.
3. Further development of operation practices useful for Precision and Personalised Medicine. At the moment, the Platform is involved in epitope mapping projects using cryo-EM and in pathological anatomy studies with STED imaging. We will try to involve further the medical and pharmaceutical communities for the usage of our advanced technologies in medical or diagnostic imaging.
4. Adding two new capabilities to the IMT Unit:
   – The nanoscale secondary ion mass spectrometry (NanoSIMS) facility in Gothenburg (NFG), providing access to the qualitative and quantitative analysis of biomolecules, elements, organic and inorganic compounds in the sample. The instrumentation is unique in the Nordics and it is hosted by AstraZeneca, thus offering strong interaction partnership with industry and emphasising the importance of the technique in the analysis of pharmaceuticals. The NFG personnel and the associated research groups are highly skilled and have developed unique methods for this distinctive technique. A detailed description of the current state and of planned the inclusion into the Platform are presented in the NanoSIMS section below.
   – A network for advanced light-sheet and clearing microscopy. Similar to CryoScreeNet, the network will serve to integrate knowledge and build a community in tissue clearing methods and light sheet imaging at the national level. IMT-Stockholm and the Lund Bioimaging Centre will organize the network, which will also include light sheet expertise in Gothenburg and Umeå. Light sheet imaging of entire cancer biopsies and combination with spatial transcriptomics and metabolomics can open interesting line of studies and method development at the Platform.

The Swedish research community, as well public health sectors and industry will benefit enormously from any of these CMI Platform advancements. Building up on the Platform training tradition, outreach and educational activities will be organised to involve as many as possible researchers, students and society in general. The constant advancements in technology and strengthening in networking and collaborations within the CMI Platform can make the platform a highly competitive partner at the European level.

E10 Cryo-EM

Expertise, technologies, and services offered

The Cryo-EM Unit offers extensive expertise and a full range of project services in single-particle cryo-EM screening and data collection, cryo-ET, cryo-lamella preparation using focused ion-beam SEM, microcrystal electron diffraction, negative stain EM and correlative light- and electron microscopy. In addition, more advanced sample preparation procedures for challenging projects are available, including next generation blot-free instrumentation for macromolecular samples and high-pressure freezing and waffle methods for cryo-lamella preparation from tissues and cells. Specifically, these services are made available to Unit users using the following instrumentation:

- Single-particle cryo-EM data acquisition on three 300 kV Titan Krios cryo-TEMs (two with Gatan/Ametek Bioquantum-K3, one with Selectris-Falcon 4i filter and direct electron detector) and two 200 kV systems (Glacios with Falcon 4i, Talos Arctica with Gatan K2).
- Cryo-electron tomography data acquisition on the above cryo-TEMs.
- Microcrystal electron diffraction (microED) data acquisition for small-molecule and macromolecular nanocrystal samples on the above cryo-TEMs.
- Focused Ion Beam (FIB) milling for cryo-lamellae of cells and microcrystals on an Aquilos DualBeam SEM and an Aquilos 2 Dual Beam SEM (will be available from Q3 2024).
- Sample preparation using next generation as well as standard methods (SPT Labtech Chameleon and TFS Vitrobots).
- Correlative light- and electron microscopy (cryo-CLEM) on Leica Thunder DM6 FS Leica DMi8 plus PRIMO grid micropatterning systems.

Alongside the experimental support outlined above, the Unit continuously provides project consultation, including all aspects from experimental design to advanced data analysis. This is performed via bi-weekly online drop-in service one-to-one consultation as well as bi-weekly user meetings. The Unit also organizes multiple national training courses annually, covering sample preparation, data acquisition and advanced data analysis. The Unit is involved in collaborative projects, courses and symposia organization with the other main cryo-EM nodes in the Nordics (Denmark and Finland) via the CryoNet community.

Since 2023 the CryoEM Unit, in collaboration with the NBIS platform and within the DDLS frame of activities, provides user support with advanced image processing. This support is accessible to the community via quarterly national project calls.

Recruitment and development of staff competence

The Unit staff come from a diverse background, ranging from electron microscopy to x-ray crystallography, computational biology, biochemistry and cell biology. All staff have undergone extensive training in multiple cryo-EM workflows, either before joining the Unit or during their time working there. The strong expertise of the Unit staff is highly valued among the user community and many of the Unit staff are engaged in research projects on a collaborative basis (within the 20% of their time set aside for competence development) as well as provide continuous consultation to both novice and experienced Unit users. Staff are also regularly invited as lecturers and teachers on international courses in cryo-EM.

Unit staff help organize advanced courses and symposia in cryo-EM where international experts are invited to teach and present. The Unit promotes exchange visits among Unit staff members with the CryoNet colleagues (Denmark) as well as with EMBL, within the EMBL-SciLifeLab exchange program.

As a way of being attractive for competent staff scientists, as well as keeping the current staff engaged, we plan to strengthen our collaborations with industry for instrument and service development (e.g. SPTLabTech and Wavebreak LLC). Moreover, in collaboration with the neighboring research community and with colleagues of the IMT Unit, we will work towards advanced integration of fluorescent and electron microscopy imaging.

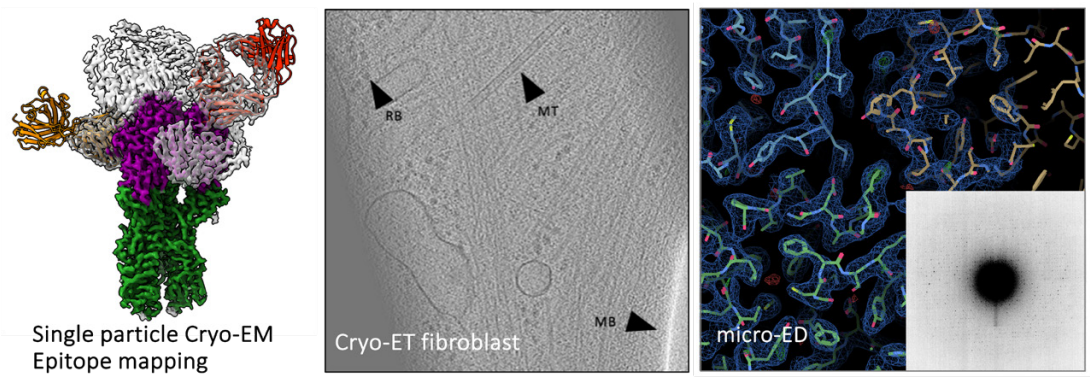


Figure 3. Examples of services/operations offered by the Cryo-EM Unit

Infographics: Statistics and Metrics for Cryo-EM Units

Cryo-EM

Read more: Webpage, Publications Database

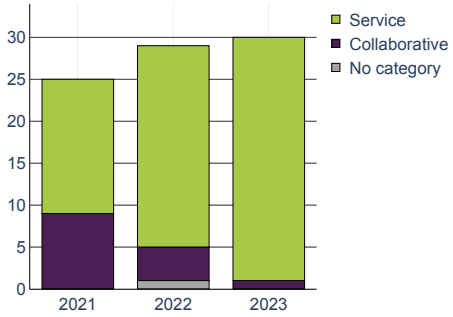
Basic Information

HU: Marta Carroni, Michael Hall
Host University: SU, UmU, GU, LU, UU
SciLifeLab unit since: 2016
FTEs: 9.25
PSD: Gunnar von Hejine, Linda Sandblad

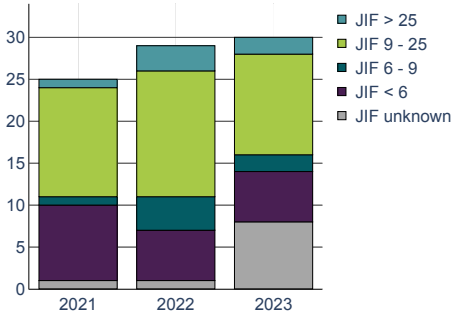
Funding 2023 (kSEK)

SciLifeLab: 11500
Other: 27947
User Fees: 4800

Publications by category

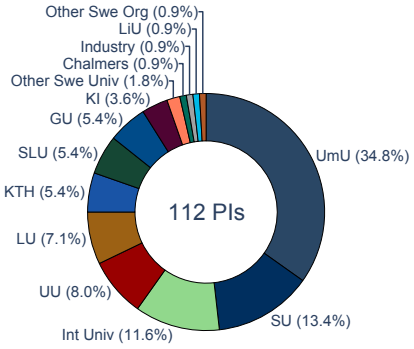


Publications by JIF

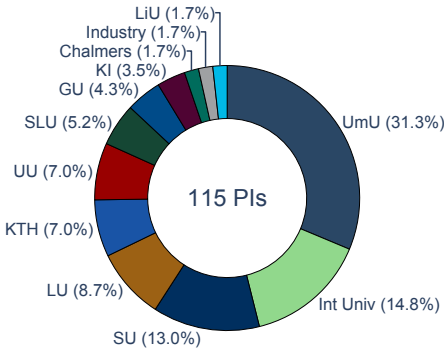


No. of Tech Dev Publications 2021 - 2023: 3

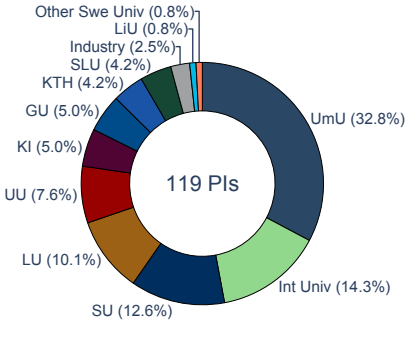
Users 2021



Users 2022



Users 2023



- *Education: 34 courses/workshops/conferences 2021–2023*

User base (current and expected 2025–2028)

During the first years of operation after its start in 2016 the Unit underwent a rapid user base expansion. This was due to strong interest in cryo-EM from the Swedish structural biology community, as well as outreach and training activities performed by the Unit. The user base has currently stabilized at 110-120 research groups from all major Swedish universities, as well as from minor Swedish universities, other Nordic and international universities and industry. The current core user base is formed by a large proportion of the current structural biology researchers in Sweden and these are expected to both continue and increasingly utilize the services provided by the Unit as one of their primary experimental methods during the 2025-2028 period.

In general, the Unit plans, in order to expand and diversify our user base, to engage more with the cellular, neuroscience and biomaterial communities. Thanks to the collaboration with the ISB and the bioinformatic (NBIS) platforms, we envision a growth in projects that involve cryo-EM in all its different flavours (single particle, cryo-ET and microED), in combination with NMR, mass spectrometry and structure prediction methods.

As a result of opening our services to other Nordic universities and industry as well as an increased focus on cellular tomography and *in situ* structural biology, we estimate that the user base may increase by 30-50 % until 2028.

Procedure for prioritization of projects

Instrument time is allocated through an annual block allocation group (BAG) application, where each applicant university is awarded a certain fraction of the available microscope time. A limited amount of time (5-10 %) is reserved for so-called rapid access (RA) projects, intended for new users who are not yet part of a BAG or users from smaller institutions or industry. After an initial evaluation of technical feasibility performed by the Unit staff, full evaluation of BAG applications and subsequent annual time allocation is performed by an external national evaluation committee. The allocation of time between participating research groups within a BAG is thereafter determined internally in each BAG. RA projects are continuously evaluated during the year by Unit staff. The same external national evaluation committee prioritizes the cryo-EM projects that apply for image processing support within the NBIS/WABI call (p. 245).

User fee models

The current fee model for academics is a flat fee (6000-8000 SEK / 24 h depending on instrument). The fee includes sample preparation, consumables, staff time and project consultation. After seven years without adjustment, this fee was increased by 80 % in 2023 in order to compensate for increased costs of consumables and instrument service contracts, and will very likely need to be further increased in the coming years. Industrial users pay the full cost of the instrument time and all consumables, service and staff support. A user-fee model is also being put in place for usage of the blot-less vitrification method Chameleon.

Scientific environments and synergies

The Cryo-EM Unit has since its inauguration worked closely with core cryo-EM research groups at Umeå University, Stockholm University and Campus Solna. This collaboration has been pivotal, both in driving technology and service development as well as for obtaining funding for new instrumentation.

At the Umeå node, the CMI Platform Scientific Director Dr. Linda Sandblad conducts her research in close collaboration with the Unit, both indirectly as a Unit user for her research on cytoskeleton structure, assembly and spatial organization and also directly via a SSF Research Infrastructure Fellow support grant for novel cryo-EM method development. Also closely associated with the Umeå node is Dr. Lars-Anders Carlsson, whose research group has pioneered the establishment of FIB-SEM workflows for cryo-ET in Sweden through his interest in the rearrangements of host-cell membranes by positive-sense RNA viruses. The successful operations and research output of the Unit have provided attractive conditions for the recruitment of new researchers, an example being Dr. Max Renner, an expert in cryo-ET, who also has rapidly become closely associated with the unit. Several long-term visiting researchers furthermore strengthen both method development and research integration. Prof. Irina Gutsche, holder of the 2023 Tage Erlander visiting professorship, extensively uses unit services for her development of new methods for investigation of the cellular structural proteome, using both single-particle and cryo-ET methods.

Alongside researchers tightly associated with the Unit, the Umeå node benefits from a strong local community in integrated structural biology, encompassing more than 20 research groups from many departments at the university as well as the Swedish Defense Research Agency. Besides cryo-EM they bring together research and extensive expertise in X-ray crystallography, NMR, molecular and quantum dynamics and time resolved wide angle X-ray scattering.

The Stockholm node of the Cryo-EM Unit has from the beginning been focused on generalized service to the Swedish research community. However, the physical location of the microscopes at Campus Solna, where research groups from the three major Stockholm Universities (Karolinska Institute-KI, Royal College of Technology-KTH and Stockholm University-SU) co-exist, has played an important role in shaping the research community around the Cryo-EM Unit. As an example, resulting from interactions with the immunology community at KI (Adnane Achour, Olle Kämpe), Uppsala (Nils Landegren) and Gothenburg University (Davide Angeletti), the CMI Platform Director Marta Carroni has recently obtained a SSF Research Infrastructure Fellow grant for the development of medically-relevant cryo-EM tools such as cryo-EM Polyclonal Epitope Mapping (cryo-EMPEM). Similarly, and in line with the strengthening of the whole CMI platform, Platform, having nodes of the Cryo-EM and IMT Units placed at the same premises in Campus Solna, together with SciLifeLab Fellow Ilaria Testa's research group, opens many possibilities for the development of advanced correlative light and electron-microscopy work. A collaboration with the group of Hanna Barriga and Molly Stevens at KI and Imperial College London (UK) has led to applications in the field of bio-nanoparticles. Collaborative work with bioinformaticians, Arne Elofsson at Campus Solna and Claudio Mirabello at Linköping University, has helped the Unit to integrate cryo-EM and AlphaFold predictions, especially important given the prospect of future cryo-ET data at medium-to-low resolution.

In addition to the Campus Solna environment, the Stockholm node of the Unit benefits from a strong local community of structural biologists, bioinformaticians and electron microscopists at the host Department of Biochemistry and Biophysics (DBB), and at the Department of Materials and Environmental Chemistry at Stockholm University (MMK). Research groups at DBB have been extremely successful in the past years in obtaining break-through results with support from the Cryo-EM Unit; among these, David Drew's membrane protein group will soon relocate to Campus Solna.

The collaboration with Xiaodong Zou's group at MMK has been very productive as it allowed the Unit to set up microED, and the same group is currently driving the development of advanced strategies for microED data collection (serialED) at the Unit. Unit staff has been very active in spreading the knowledge about microED, via visits to other cryo-EM nodes in the Nordics.

Uppsala and Lund universities have recently invested in their own Glacios microscopes, while Gothenburg has an older cryo-TEM for sample screening. These local facilities are integrated with the Cryo-EM Unit through the SciLifeLab CryoScreeNET initiative and receive funding for 0.5 FTE each. Staff at the Cryo-EM Unit and at the local screening facilities have regular weekly group and journal club meetings, and in-person visits take place throughout the year.

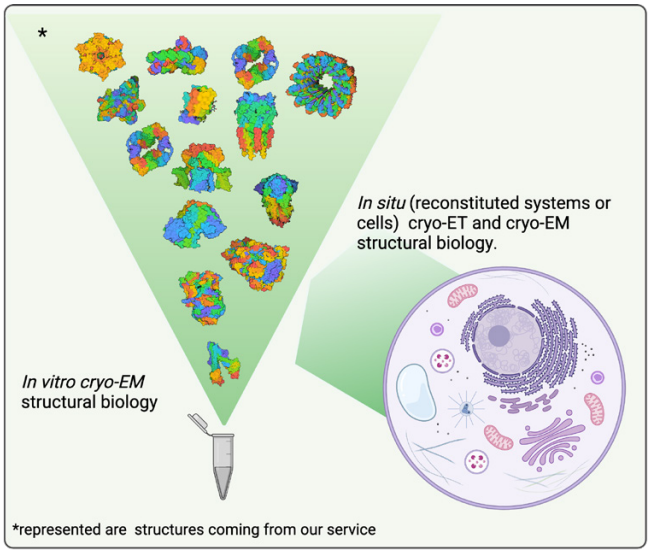


Figure 4. Future directions of the Cryo-EM Unit towards *in situ* structural biology

Plans for development including new technologies/service offerings 2025–2028

During 2021-2024, the Cryo-EM Unit has continued to provide extensive user training and service to the Swedish and Nordic scientific communities. Alongside this, the Unit has pursued three primary developmental objectives: (1) the establishment of CryoScreeNET, a national screening and cryo-EM expertise network, (2) improved throughput and data quality for existing high-demand services such as single-particle analysis for structural biology applications and (3) development of microED and cryo-CLEM capabilities within the Unit. All of these objectives have been achieved. CryoScreeNET is now well established, with staff members at Lund, Gothenburg and Uppsala Universities thoroughly integrated in the Unit, both personally as well as operationally. Major hardware upgrades to the Unit's previous two high-end instruments, as well as the acquisition of an additional screening microscope at the Umeå node and a second high-end microscope at the Solna node, have ensured that researchers are able to receive cutting edge quality data at high throughput. Finally, workflows for microED and cryo-CLEM have been well established at the Solna and Umeå nodes and are now being offered as services.

For the period 2025-2028 the Unit plans to pursue the following aims:

1. Increase capacity for *in situ* structural biology applications. Specifically, this requires an expansion of instrumentation for and expertise in FIB-SEM for cryo-lamella preparation. While this service has been available for many years at the Umeå node, capacity and national user interest has been limited and cryo-FIB capacity has not been present at all at the Stockholm/Campus Solna node. However, with in situ cryo-ET workflows now becoming increasingly well established and clearly representing a key method in the next evolutionary step of the field of structural biology – i.e. understanding macromolecular structure in its cellular context – it is a critical development for the Unit. In the short term, capacity will be increased by the expansion of current instrumentation with an Aquilos 2 FIB-SEM microscope at the Umeå node (Q2 2024). Long-term, it is a high priority for the Unit to establish cryo-FIB-SEM capabilities at both nodes, including instrument investment for higher throughput as well as knowledge transfer. The Unit staff at both nodes include experts in cryo-lamellae handling, high-resolution cryo-ET data collection and subtomogram averaging (see also *Integrated Structural Biology Platform Plans*, *Figure* 6, p. 191).
2. Expand services and expertise towards cell biology applications and well as perform method development on the associated technologies (cryo-ET, CLEM and FIB-SEM). Close collaboration with the IMT unit of the CMI platform will allow both to increasingly identify and facilitate projects for the analysis of cellular systems as well as integrate with methods such as super resolution light microscopy, CAT and FIB-SEM volume imaging. This development will be aided by the above described SSF Research Infrastructure Fellow support to Linda Sandblad.
3. Facilitate the usage and application of cryo-EM in medically relevant projects, including the development of robust pipelines for cryo-EM Longitudinal Epitope Mapping. This development will be aided by the above described SSF Research Infrastructure Fellow support grant to Marta Carroni.
4. Increase knowledge and technology transfer such that microED services become routine at both Unit nodes and also, where applicable, at the CryoScreeNET nodes. Spread the technical development of the newest practice in electron diffraction (e.g. serialED) from Zou's group at SU to all other cryo-EM centers in the Nordics.
5. Increase knowledge and technology transfer of the cryo-CLEM services, in combination with cryo FIB-SEM capabilities, so that good and efficient practices become operational at both Unit nodes and also, where applicable, at the CryoScreeNET nodes. In collaboration with the IMT Unit of the Platform as well as various research groups, work will be carried out to integrate super-resolution imaging and cryo-EM (both in live and frozen samples).
6. Increase the interaction with the bioinformatics research community and NBIS for the development of prediction tools that integrate cryo-EM and cryo-ET data. Work in this direction has been started within the collaborative SciLifeLab-funded technology development project BeyondFold. The large amount of data produced by the Unit are an important mine of information for bioinformaticians as well as for cryo-EM experts for the development of novel image-processing approaches.

For these lines of expansion towards atomic (diffraction and compounds), cellular imaging (cryo-ET, *in situ* structural biology and volume EM) and computational methods the cryo-EM Unit will organize outreach activities and courses, involving both the research community and students from across the country. Some of these courses will be organized in collaboration with the IMT Unit, as well as the ISB and the NBIS platforms, in an attempt to shape a new research community that uses integrated methods for structural biology and multimodal imaging.

Plans for data handling and analysis 2025–2028

The Unit produces a large amount of data (around 10Tb of data per day per high-end Krios microscope) which needs to be transferred to adequate storage space for processing. At the moment, data transfer is managed by the Unit's IT system administrators, whom also take care of local cluster facilities for data processing, when performed by the Unit staff. The local clusters, both in Umeå and in Stockholm are primarily meant for local research groups, that have funded their hardware and maintenance. Large national supercomputer clusters – e.g. BerzeLius, Tetralith – could in principle be used as processing hubs for the Swedish cryo-EM community, but various bottlenecks have so far prevented this from happening. Currently, the large majority of users perform data processing independently on local workstations. In the past years, the user community has repeatedly pointed to the lack of image processing and data handling as being a major bottleneck in the Units offered services.

Over the years, the Unit has developed: (i) an online system for direct booking and project tracking by the user (emhub.cryoem.se), (ii) a fortnightly drop-in service for personalized advice and (iii) an on-line open user meeting (20-40 attendants) to provide updates about the status of the instrumentation and to discuss all aspects of cryo-EM data acquisition and image processing. Recently, in an attempt to alleviate the need for image processing support demanded by the users, the Unit staff has welcomed two new members who help researchers who have limited knowledge of cryo-EM data analysis, or difficult image processing cases. This has been possible thanks to the strong collaboration with NBIS and the Wallenberg Foundation within the DDLS program. For more details, refer to the NBIS section of this report. Plans to enlarge the capacity of data analysis for cryo-EM and structural biology in general are under discussion with the NBIS and ISB platforms, also in line with the (6) plan described above. We consider that the current "embedding model" between NBIS and Cryo-EM, consisting in having bioinformatic staff with specific expertise working in daily contact with the data-generating platform, is particularly powerful.

In order to design possible solutions for more effective data handling and computational power accessibility, we think that a similar "embedding model" with the Data Center would be beneficial. At the moment, the Data Center is undergoing large expansion and discussions with the Unit about data transfer and data tracking, with per-dataset DOIs traceable all the way to the international repositories PDB and EMPIAR, have been taking place. However, for effective test and implementation, it is important that experts in data handling, system administration and specificities of cryo-EM data work closely together.

For the same reason, the Unit plans to work towards establishing a closer contact point with the supercomputer clusters in Sweden that could support the Swedish cryo-EM community. Currently, storage space and cryo-EM software optimization in terms of GPU usage are problems preventing the usage of the BerzeLiUs and Tetralith supercomputer clusters, other than for simple data analysis during short courses. A closer communication between the Cryo-EM Unit, NBIS, the Data Center, the steering committees at the supercomputer clusters and at DDLS will be necessary.

The creation of dataset-specific DOIs to be deposited together with PDB entries as well as the enforcements of raw and meta data deposition into EMPIAR will be important steps to push the Unit into more FAIR practices. Similarly, the whole user community will be invited to make usage of the SciLifeLab Data Centre Figshare servers, even for those that are not formally SciLifeLab associated, in order to make accessible data (e.g. scripts, figures, videos) that do not typically find a place in regular publications.

Current and planned collaborations and training

As presented above, in the current operations as well as for future plans (1-6) the cryo-EM Unit operates in proximity and collaborations with many other entities at SciLifeLab. Work with industry, collaboration with the DDD platform (part of the KTH BAG) as well as collaborative work with medical researchers, such as the cryo-EMPEM projects, position the cryo-EM Unit for a possible role within the Precision Medicine capability at SciLifeLab.

In terms of training, the Unit, together with the whole of the CMI platform, scores among the most active ones at SciLifeLab and aims at strengthening this training role also in collaboration with ISB and the InfraLife initiative.

E11 Integrated Microscopy Technologies

Expertise, technologies, and services offered

IMT offers a distributed network of three specialized nodes, each equipped with state-of-the-art technology and unique expertise in advanced light and electron microscopy.

- ALM (Advanced Light Microscopy, Stockholm) specializes in visualizing biological structures at the nanoscale, measuring single-molecule dynamics, and capturing high-resolution 3D images at ultrafast speeds.
- CCI-CAT (Correlative Array Tomography, Gothenburg) supports 3D correlative imaging using light and electron microscopy, combining structural (SEM and TEM) and molecular (LM) information. CCI-CAT also offer chemical analysis with MALDI-IMS and NanoSIMS technologies.
- UCEM-FIB-SEM (Focused Ion Beam Scanning Electron Microscopy, Umeå) provides isometric high-resolution 3D electron microscopy (down to 5 nm^3) and advanced sample preparation for correlative light and electron microscopy workflows.

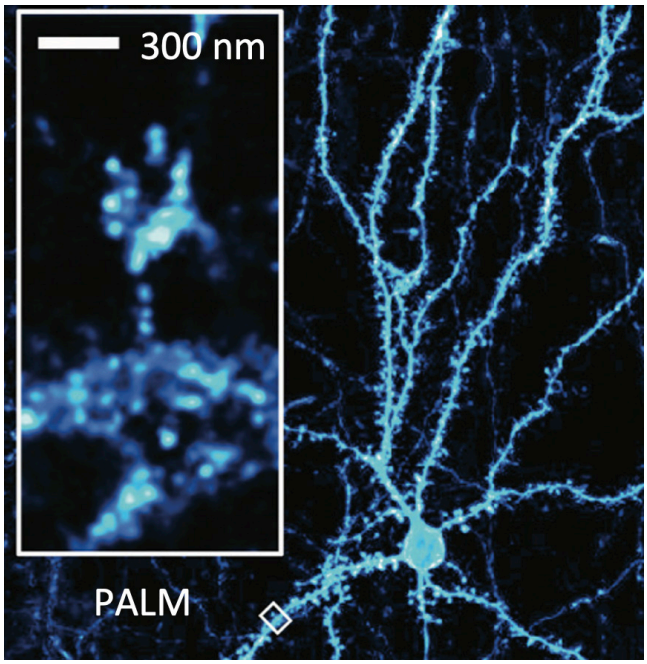


Figure 5. SMLM of neuronal proteins at the IMT-Stockholm node

Competence of staff scientists

IMT's team of highly skilled staff scientists ensures the quality and efficiency of the services. Each node boasts unique national expertise:

- ALM: Over 20 years of experience in super-resolution microscopy, 30+ years in fluorescence correlation spectroscopy, and 10+ years in light sheet/lattice light sheet microscopy. Continuous technology and competence development are an important part of the staff scientists job description.
- CCI-CAT: Unique expertise in the entire correlative multimodal imaging workflow, encompassing sample preparation, data acquisition from various techniques (SEM, TEM, LM, NanoSIMS, MALDI-IMS), and advanced image processing and analysis.
- UCEM-FIB-SEM: Unique expertise, with over 7 years of experience in combining 3D electron microscopy and lamella preparation. Continuous training, international collaborations, and workshops ensure that the staff competence is at the forefront. Additionally, the local team of highly skilled staff scientists in the Cryo-EM unit, foster a collaborative environment for continuous technology and competence development.

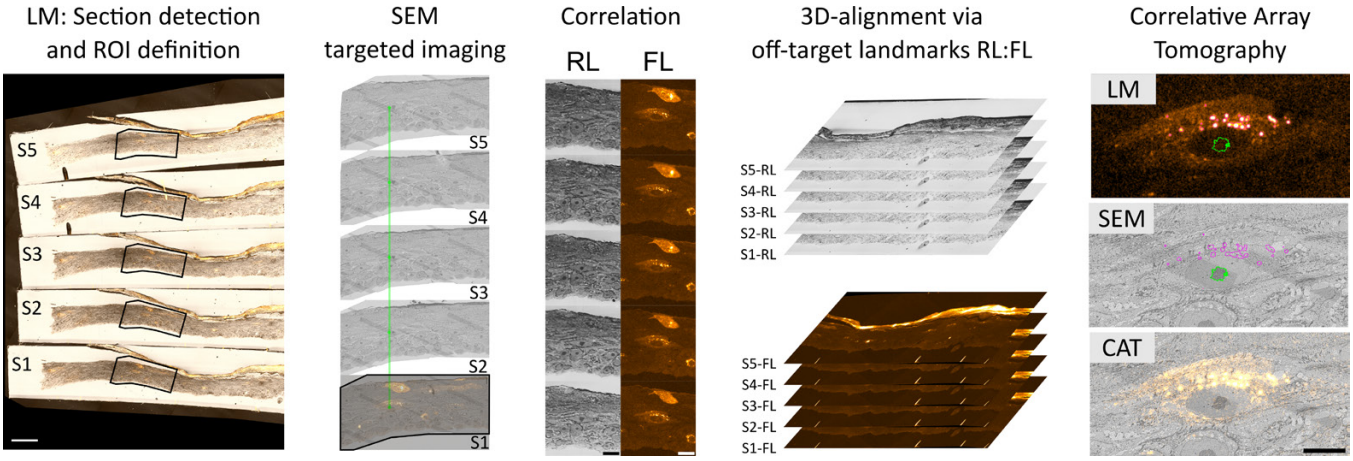


Figure 6. Representative project implementing CAT at the IMT-Gothenburg node. Left to right: light Microscopy (LM) images of sample sections were processed for stitching and shading correction. From these images, sections and regions of interest were defined. After post staining, these regions were imaged in the SEM. The process of z-alignment was carried out using off-target landmarks between reflected (RL: general morphology) and fluorescence (FL: cells of interest) channels, followed by alignment between SEM and RL off-target landmarks for CAT registration. Magenta segmentation shows areas of high fluorescence intensity, while green shows the nucleolus. Scale bars: LM: 100 µm; Correlation: 20 µm; CAT: 10 µm.

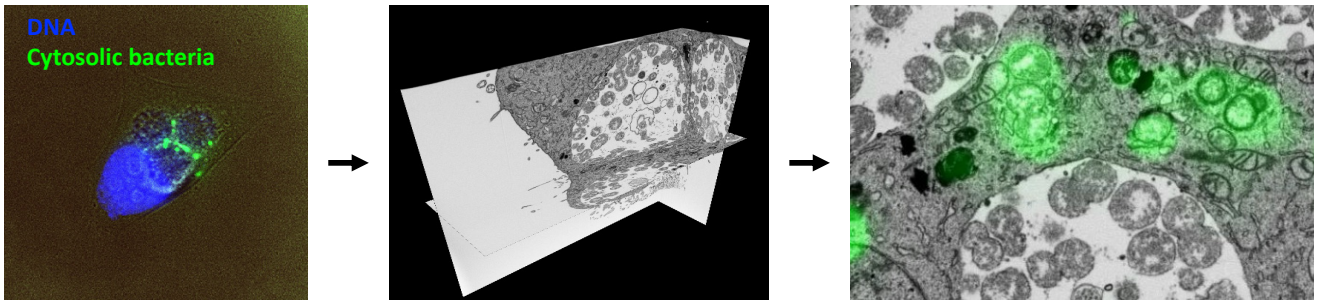


Figure 7. Implementation of CLEM on FIB-SEM volume imaging at the IMT-Umeå node. The fluorescent signal is aquired before sample preparation for FIB-SEM. A high-resolution volume is then acquired at the area of interest using FIB-SEM and the fluorescent signal can be correlated with the structure of interest.

Recruitment and development of staff competence

IMT recognizes the critical role of talented staff scientists in driving cutting-edge microscopy research. We have implemented a comprehensive strategy to retain and attract the best staff scientists at our specialized nodes.

Investing in Infrastructure and Stability:

- *State-of-the-art equipment*: Each node continuosly make investments in instrumentation, empowering the staff scientists to explore the frontiers of imaging technology.
- *Long-term funding commitments*: Financial stability contributes to sustained infrastructure development and is a most important factor to attract and retain the very best staff scientists.

Promoting Collaboration and Skill Development:

- *Collaborative research projects*: IMT promotes staff scientists to be involved and contribute with more than just imaging expertise in users research projects, fostering well-rounded expertise and valuable skill acquisition.
- *Collaborative multimodal imaging projects*: Encouraging such projects across the IMT nodes support innovation in this rapidly evolving field, leading to knowledge exchange and skill development among our staff scientists.
- *Training for future research infrastructure leaders*: IMT's participation in the H2020 project RItrainPlus (ritrainplus.eu) equips staff scientists with leadership skills, preparing them for potential future management roles within IMT or other research facilities.

By prioritizing infrastructure, collaboration, and skill development, IMT cultivates a stimulating environment where staff scientists can continuously refine their expertise and contribute significantly to advancements in microscopy and related research fields.

User base (current and expected 2025–2028)

ALM

- 2021-2024: Supported 128 PIs with 171 projects, training 203 users. This active community generated 44 scientific publications.
- 2025-2028: Projecting similar user base and publication output based on strong demand.

CCI-CAT

- 2021-2024: Supported 20 research groups (7 local GU, 3 national, 9 international, 1 industrial) in 28 correlative multimodal imaging projects, resulting in 4 publications (1 published, 3 in preparation).
- 2025-2028: Anticipate increased demand for CAT technology, driving user base expansion.

UCEM-FIB-SEM

- 2021-2024: Supported 14 researchers (8 local UmU, 4 national, 2 international) with volume electron microscopy, resulting in 3 publications, with more in progress. The FIB-SEM is frequently used for sample preparation for the cryo-EM, contributing significantly to instrument usage. (publications from this usage is reported under the cryo-EM facility)
- 2025-2028: Anticipate increased demand for FIB-SEM technology, leading to a larger user base.

Procedure for prioritization of projects

IMT offers user access via a project portal (nmi.scilifelab.se).

- *Experienced users*: Can often directly submit project proposals outlining research objectives and microscopy needs.
- *New users*: Can via the portal access consultations with node staff for technology selection and proposal guidance.

Proposals undergo review by Heads of Units and staff scientists, ensuring technical feasibility and scientific merit within available techniques. IMT encourage collaboration between users and staff scientists to develop tailored project plans for successful data acquisition. In case of limited capacity, project prioritization is made based on technical feasibility and scientific merit.

Infographics: Statistics and Metrics for Integrated Microscopy Technology Unit Nodes

Integrated Microscopy Technologies Gothenburg [1]

Read more: Webpage, Publications Database

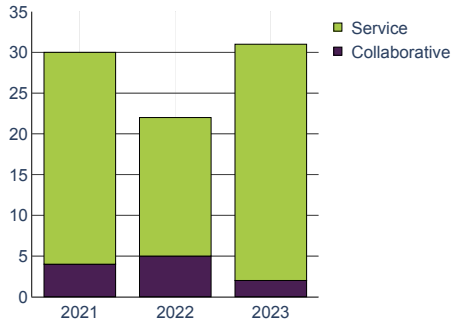
Basic Information

HU: Julia Fernandez-Rodriguez
Host University: GU
SciLifeLab unit since: 2021
FTEs: 7
PSD: Julia Fernandez-Rodriguez

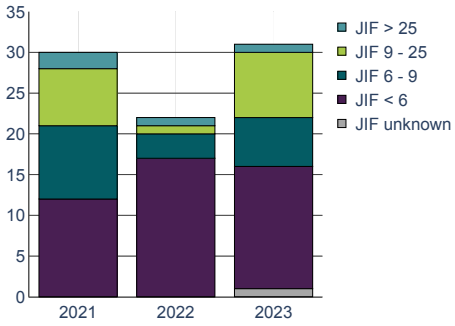
Funding 2023 (kSEK)

SciLifeLab: 1500
Other: 8170
User Fees: 2000

Publications by category

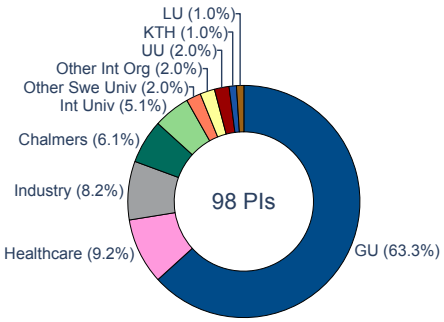


Publications by JIF

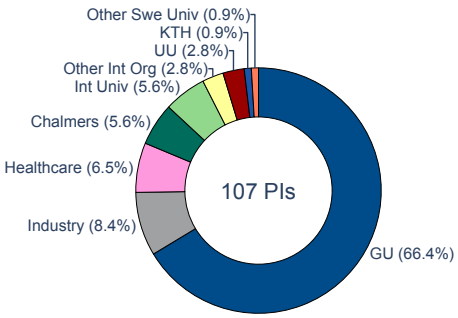


No. of Tech Dev Publications 2021 - 2023: 4
SciLifeLab Technology (CAT)-Specific Publications 2021–2023: 1

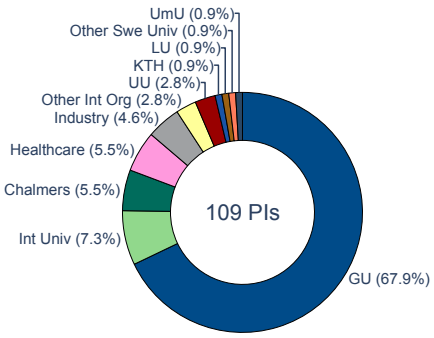
Users 2021



Users 2022



Users 2023



- *Education: 30 courses/workshops/conferences 2021–2023*
- *Training: 28 users trained one-on-one 2021–2023*

[1] Statistics include all activities at IMT Gothenburg, of which SciLifeLab-supported services in CAT are one part.

Integrated Microscopy Technologies Stockholm

Read more: Webpage, Publications Database

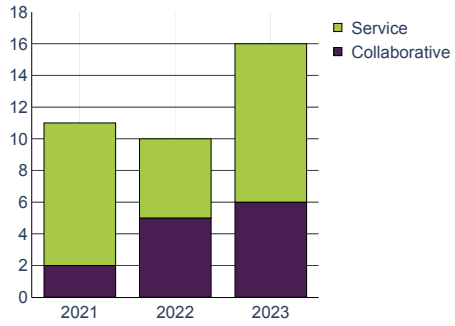
Basic Information

HU: Hans Blom
Host University: KTH
SciLifeLab unit since: 2013
FTEs: 4.2
PSD: Hjalmar Brismar

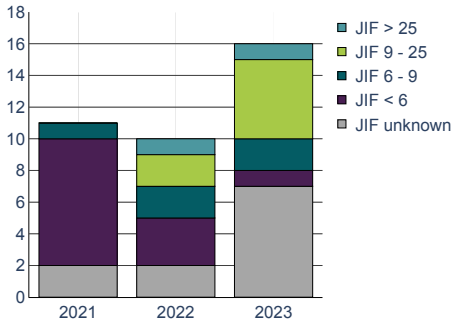
Funding 2023 (kSEK)

SciLifeLab: 3500
Other: 9160
User Fees: 1100

Publications by category

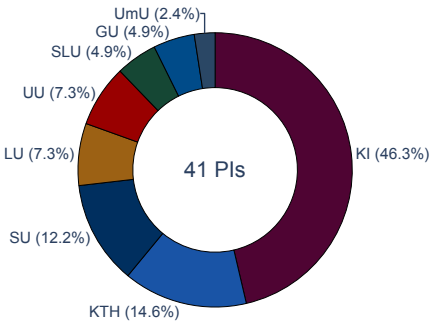


Publications by JIF

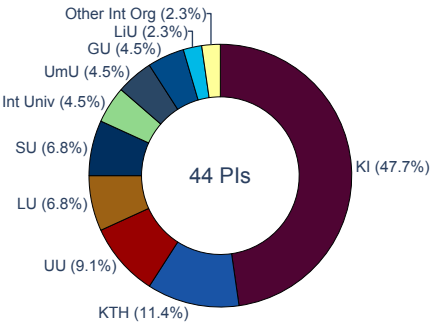


No. of Tech Dev Publications 2021 - 2023: 6

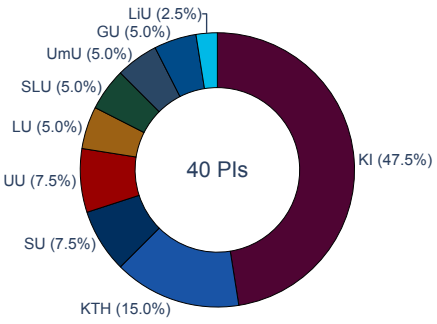
Users 2021



Users 2022



Users 2023



- *Education: 27 courses/workshops/conferences 2021–2023*
- *Training: 203 users trained one-on-one 2021–2023*

Integrated Microscopy Technologies Umeå [1]

Read more: Webpage, Publications Database

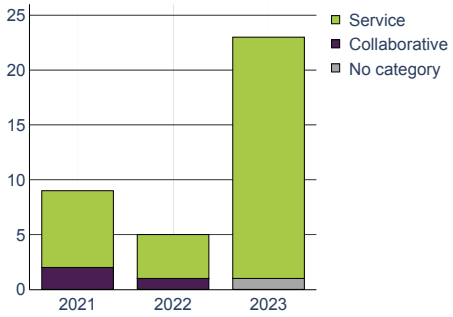
Basic Information

HU: Sara Henriksson
Host University: UmU
SciLifeLab unit since: 2021
FTEs: 2.5
PSD: Linda Sandblad, Richard Lundmark

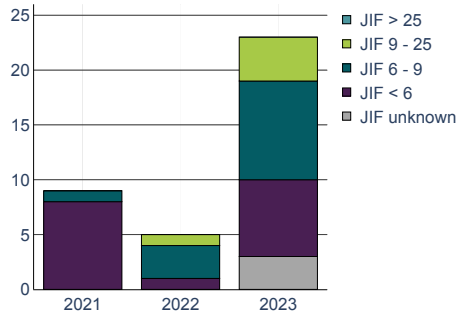
Funding 2023 (kSEK)

SciLifeLab: 1500
Other: 900
User Fees: 757

Publications by category

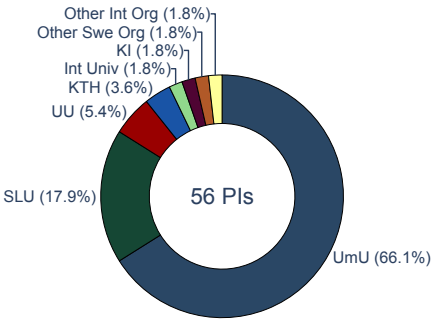


Publications by JIF

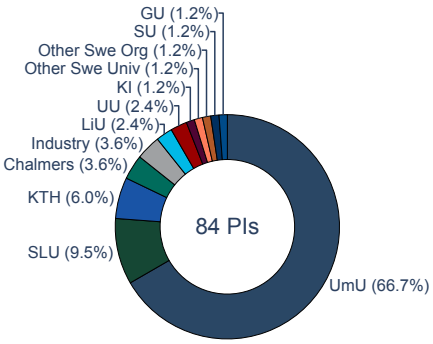


No. of Tech Dev Publications 2021 - 2023: 1
SciLifeLab Technology (FIB-SEM)-Specific Publications 2021–2023: 3

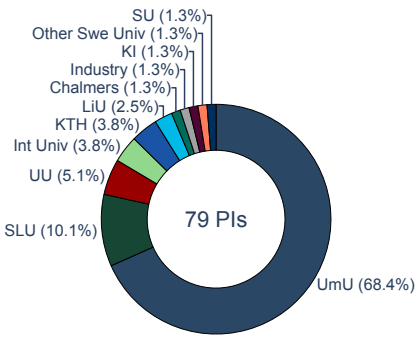
Users 2021



Users 2022



Users 2023



- *Education: 10 courses/workshops/conferences 2021–2023*
- *Training: 12 users trained one-on-one 2021–2023*

[1] Statistics include all activities at IMT Umeå, of which SciLifeLab-supported services in FIB-SEM are one part

User fee models

IMT works on a fee-for-service model:

- *Academic users*: Based on microscope running costs (spare parts, service contracts, lab rent etc.)
- *Industrial users*: Full cost model that in addition to the academic user fee also includes instrument depreciation, staff salaries, overheads and VAT.

Co-authorship on publications is not required or expected. The intellectual property belongs to users, with exceptions agreed upon mutually. While IMT maintains close user interaction, ownership of scientific projects remains solely with the users.

Scientific environments and synergies

IMT contributes to regional, national, and European scientific support via the National Microscopy Infrastructure (NMI), the Bridging Nordic Microscopy Infrastructure (BNMI), and the Euro-Bioimaging-ERIC infrastructures.

- ALM: Close interaction with several Campus Solna research groups for development of advanced imaging, e.g., SciLifeLab fellows Ilaria Testa (doi.org/10.7554/eLife.73114), Erdinc Sezgin (doi.org/10.1098/rsob.220175) and Simon Elsässer (doi.org/10.1002/cbic.202100399), Prof. Hjalmar Brismar (doi.org/10.1111/acel.13649), Prof. Björn Önfelt (doi.org/10.1126/scisignal.abe2740),.
- CCI-CAT: Close collaboration with research groups at Sahlgrenska University Hospital, University of Gothenburg, Chalmers University of Technology and local biotech and pharma industry: Prof. Henrik Zetterberg and Jörg, Hanrieder (doi.org/10.1089/brain.2022.0047), Michael Kurczy and Prof. Andrew Ewing (doi.org/10.1021/acs.analchem.2c02675), Prof. Roger Bagge (doi.org/10.1002/jev2.12380), Prof. Florian Gruber (submitted), among other researcher groups, which all play key roles in advanced knowledge transfer.
- UCEM-FIB-SEM: Close collaboration with users at UmU: Lars-Anders Carlson (WCMM fellow), Linda Sandblad (SciLifeLab group leader), Barbara Sixt, Oliver Billker, Prof. Staffan Bohm who all are frequent users of both the IMT unit and of the local facility as such. Local cross-facility users are essential for competence development in the facility. The local users benefit from staff that have a deeper understanding in their projects and can help with several biological questions at one place. The facility in return make use of their samples for cross-disciplinary method developments.

Plans for development including new technologies/service offerings 2025–2028

The opportunities presented by new and innovative microscopy techniques in the life sciences are strong, and the expectations of the user community for the IMT services are correspondingly high. IMT has close collaboration with both academic and industrial developers of microscopy, the broad user base of NMI is here an important asset. Specific plans for development:

- *ALM:* Extend core technology services with nanoscale MINFLUX microscopy, and multispot-single-molecule-dynamics microscopy. Increase the capacity to support more users with ultra-fast sub-cellular resolution lattice light-sheet microscopy. Develop capacity for correlative super-resolution light and cryo-electron microscopy.
- *CCI-CAT:* Development and implementation of new workflows for CAT, by integrating multi-beam scanning electron microscopy, X-rays, MALDI-IMS and NanoSIMS. Develop smart microscopy and machine learning methods to automate the time-consuming steps and to increase the image acquisition speed in array tomography, both for LM and EM. Develop improved management of big data for processing and visualization.
- *UCEM-FIB-SEM:* Develop the sample preparation techniques at the facility with a focus on high pressure freezing and freeze substitution, which are techniques that give superior preservation and resolution of the sample. A long-term plan is to implement MicroCT as a complementary technique for targeted localization of the area of interest.
- *Joint IMT:* Establishing support for correlated multi-modal multi-unit microscopy. Developping workflows for providing users with consultation and training on experimental design that includes sample preparation for correlated microscopy, multi-unit image acquisition and multimodal data processing and analysis.
- *Extended technologies/services:* The proposed integration of chemical imaging (NanoSIMS), and volumetric light microscopy with tissue clearing (LBIC/Lighsheet network), will enable IMT to serve a broader user base with imaging in the field of molecular life sciences.

Plans for data handling and analysis 2025–2028

To realize the full potential of the expert imaging services at IMT, the nodes support the users also in general data management, primary data analysis and transfer of large data sets. All data generated in IMT is compatible with FAIR principles and include the full metadata: microscope parameters, experimental data, method descriptions, sample preparation and image analysis. Users are supported in making the data open in public repositories.

Data handling and support has so far been done independently at each node without coordinated support from the Data Center. During 2025-2028 we request that the Data Centre prioritize relevant support for imaging data and that an Open Microscopy Environment (OME, openmicroscopy.org) is implemented for the all of SciLifeLab.

IMT has a specific need for support from the Data Center to host a central OME database server (OMERO), including an open and public image data repository (IDR). This will provide a uniform and more efficient image data access and data transfer for users and will also support efforts in making imaging data available for wider (re)use. OME is based on open standards with open APIs for integration with remote image analysis and provides user-friendly interfaces for remote and platform independent access, including tools for interaction and analysis of images and image data.

IMT is responsible for handling and storing all image data in a users project during its execution. When the project is finished, data and the responsibility for long-term storage is transferred to the user. IMT supports users in making the data publicly available in external repositories or directly in the proposed SciLifeLab open access IDR.

Current bottlenecks

Meeting users demand

All IMT facilities operate at high capacity. User access is in general not a bottleneck, obviously correlated to number of staff scientists and instrumentation up-time availability.

FIB-SEM users have experienced relative long waiting time for service (months), due to that the FIB-SEM is a shared resource with the Cryo-EM unit (making cryo lamellas).

IMT experience some limitation in the capacity to assist users in 3D image processing and visualization. New software and tools for segmentation are emerging, especially based on AI and deep learning, however facility staff has experienced some limitations in capacity to assist users in these rapidly developing methods.

Data generated to be efficiently shared/transformed to knowledge, publications, and translations

Advanced microscopy includes interactive handling and processing of large datasets. Current bottlenecks include:

- the previously used OMERO image server is not operational after Data Center failed to maintain it
- the support for sharing data needs to be improved
- fast access to a unified data storage is needed

Adressing these items

Data handling issues will be addressed by establishing a central Open Microscope Environment (OME) data system. This requires allocation of Data Center resources to establish relevant competence and support for image data.

Adressing the capacity for advanced visualization and AI analysis of image data relies in part on the above, that data can efficiently be transferred, and on close collaboration with the bioimage informatics facility in NBIS and with DDLS research groups. Additionally, collaboration and support from the Euro-Bioimaging-ERIC Image Data Services (eurobioimaging.eu/data), will be pursued.

Concerning volumeEM access and up-time, our plan is to resolve this within the coming year by an upgrade of our instruments.

NBIS – current support and needs for 2025–2028

- *Current support*: Advanced image analysis is supported by the BioImage Informatics Facility (BIIF). Collaboration via Call4Help sessions provides support for image analysis in user projects. Co-organization of courses and workshops in image analysis aimed at both facility users and staff.
- *Needed support*: Increased need for quantitative single-molecule image analysis; development of workflows for data analysis in cellular 3D volume electron microscopy and correlated multimodal imaging. We propose an integrated DDLS and NBIS staff support to establish AI tools for correlation and visualization directly in the data collection workflow.

Data Centre – current support and needs for 2025–2028

- *Current support*: Access to administrative tools, Publications database, Project portal, Access to fast local storage at Campus Solna, subscription to Protocols.io.
- *Needed support*: prioritize resources for scientific data support with focus on infrastructure facilities. For IMT a priority is to establish Open Microscope Environment (OME) support for all facilities and users at SciLifeLab including an open access IDR. Establish fast data transfer and access to storage for online data processing. Establish workflows for access to national high-performance/GPU computing.
- *We suggest* that staff at Data Center are embedded in the data generating facilities, to build competence and better serve the users of SciLifeLab with a more appropriate development of data services. Increasing the Data Centre support to imaging facilities with data management, including data repository services is needed.

Current and planned SciLifeLab collaborations

- *with other SciLifeLab units/platforms*: IMT collaborates with the BIIF facility (NBIS) for advanced image analysis. Nanoscale and 3D volumetric imaging are synergistic with the ISB and Spatial Biology platforms. Collaborative inter-facility/platform development projects have been initiated with national and SFO SciLifeLab funding for: correlative super-resolution light and cryo-electron microscopy; correlative 3D transcriptome and proteome analysis; 3D volume electron microscopy processing and analysis.
- *with SciLifeLab capabilities PM, PB and PLP*: Precision medicine and planetary biology capabilities benefit from the capacity to decipher molecular biology in true 3D context at the IMT nodes. A facility spin-off company pursue 3D nanoscale kidney diagnostics (magnephy.com) that can in the future also service PM digital pathology of other organs, including cancer diagnostics.

Collaboration with industry, healthcare, and other organizations

Industry users

Several SMEs as well as larger pharmaceutical companies benefit from access to advanced microscopy support, e.g., AstraZeneca, Mölnlycke Health Care AB, Nanoxis Consulting AB, Mycorena, VERIGRAFT AB, EnginZyme, Clockwinder Therapeutics.

Industry collaborations

Several leading imaging companies, e.g., Carl Zeiss Microscopy, Leica Microsystems, Bruker Corporation, Thermo Fisher Scientific, and smaller companies such as Phase Focus Limited, Andor Technology Ltd, Spectra-Physics, DELMIC BV and Abberior Instruments GmbH, use our nodes as demo/test sites as well as following our developments/services. Further collaborations include developing and testing new imaging instruments and assays, e.g., DELMIC BV integrated light and electron microscopy in one system, and SECOM (Prof. Jacob P. Hoogenboom). The ALM and CCI-CAT nodes are *Lab@Location* partners to Carl Zeiss since 2015.

Healthcare

IMT has strong collaboration with the healthcare regions in Stockholm, Umeå and Gothenburg, giving support to many clinical research groups. IMT staff scientists participate in the healthcare innovation development at the Stockholm MedTechLabs hub, and lead the optical 3D kidney pathology program (medtechlabs.se/research/research-projects). Important as well is the creation of the European consortium, *Big mUltimodal hIgh-resolution Brain atLas Data Management*, as part of the NanoWorldMap consortium (nanoworldmaps.eu) and the Human Brain Connectome Project (Forschungszentrum Jülich, EBRAINS).

IMT is also participating in two health and well-being Horizon Europe funded projects through the Euro-Bioimaging that give support for transnational access to infrastructures for research: ISIDORe – Integrated Services for Infectious Disease Outbreak and canSERV - providing Cutting Edge Cancer Research Services Across Europe.

Current and planned training

- ALM: Between 2021-2023 the facility supported and offered 15 microscopy courses (9 PhD, 3 MSc and 3 BSc level) and 12 workshops in nanoscale microscopy, single molecule dynamics, volumetric imaging, and sample preparation (clearing/expansion). For 2025-2028 we plan for a similar volume of training.
- CCI-CAT: During 2021-2023 the facility supported and offered 9 PhD courses in microscopy and image analysis; 10 specialized courses on correlative imaging, image analysis and innovation and engagement with industry; 6 workshops on correlative multimodal imaging, smart microscopy, image analysis, sample preparation for electron microscopy and remote facility operations; 5 conferences on correlative multimodal imaging and advanced microscopy. For 2025-2028 we plan a similar volume of training.
- UCEM-FIB-SEM: The FIB-SEM node has together with the local facility organized 9 PhD courses giving a total 120 users training in electron microscopy and sample preparation. The facility has also co-organized a workshop on correlative light and electron microscopy and continuously gives one-on-one training for all steps involved in the FIB-SEM imaging process. For 2025-2028 we plan a similar volume of training.

E12 Lund University Biomaging Centre/LSFM Network

Current funding, expertise, technologies, and services offered

Lund University Bioimaging Centre (LBIC), established in 2008, supports medical imaging (MRI and PET/SPECT), electron microscopy (EM) and light microscopy (LM, including light-sheet fluorescence microscopy (LSFM) and optical clearing) on regional and national levels. Currently, the light-sheet services available at LBIC are covered by 0.3 FTE staff (Dr. Sebastian Wasserstrom: 0.1 FTE, Dr. John Stegmayr: 0.1 FTE and Dr. Nils Norlin: 0.1 FTE). Staff is funded by the medical faculty.

Strategic investments and recruitments have since 2020 focused on extending services in 3D light-sheet microscopy and multiple tissue clearing techniques. Installed platforms such as a M2 Life Airy beam Aurora light-sheet, a Miltenyi Biotech Blaze light-sheet, and a Life Canvas Technologies Epoxy-based SmartBatch for automated optical clearing, form a strong technology base. Competence expertise such as recruitment of Dr. John Stegmayr with 5+ years of experience in optical clearing and light-sheet imaging and Dr. Nils Norlin with 10+ years of experience in light-sheet development (at Umeå University, EMBL, Karolinska Institutet) furthermore extend service support.

The light-sheet platforms (Aurora 75% open access & Blaze 50% open access) and the high-throughput clearing system will be offered for national usage, supported by Dr. John Stegmayr and Dr. Nils Norlin through the 0.5 FTE SciLifeLab support in the suggested LSFM/Clearing network.

Scientific environment

LBIC offers an open access imaging environment not limited to the faculty of medicine or Lund University. With more than 400 research groups spread around three campuses the faculty of medicine support a broad breadth of experimental basic research, clinical research, and health sciences. Moreover, LBIC has a strong collaboration with the Centre for Translational Genomics (CTG) at the faculty of medicine in Lund providing supporting workflows for spatial transcriptomics and single-cell NGS.

In the field of 3D imaging, LBIC has close ties and scientific collaborations with leading research groups that develop and implement whole organ clearing methods and light-sheet imaging, e.g. Wallenberg Center of Molecular Medicine (WCMM) fellows Iben Lundgaard and Darcy Wagner. The above listed light-sheet systems were further purchased with joint grants from the Olle Enqvist foundation (PI Dr. Iben Lundgaard), the LMK foundation (LBIC), the Crafoord foundation (Dr. John Stegmayr) and ERC (PI Dr. Darcy Wagner). The optical clearing equipment was purchased with a grant from the Carl Tesdorpf foundation (Dr. John Stegmayr).

In addition, Dr. Nils Norlin has recently received support (in total >4MSEK by VR, the Crafoord foundation, and the IngaBritt and Arne Lundbergs foundation etc.) for 3D imaging development, custom light-sheet microscopy hardware, and for multiplexed (mRNA, protein) 3D tissue imaging.

The collaborative and rooted interactions in 3D imaging forms a strong scientific base, with opportunities for innovations and implementations of light microscopy of large samples.

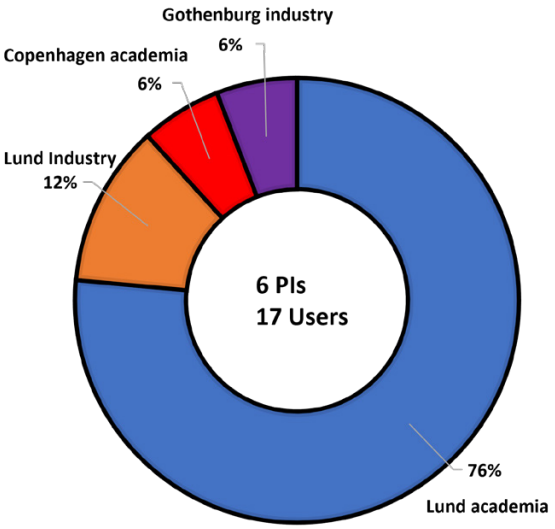


Figure 8. LBIC light-sheet project distribution 2020-2023

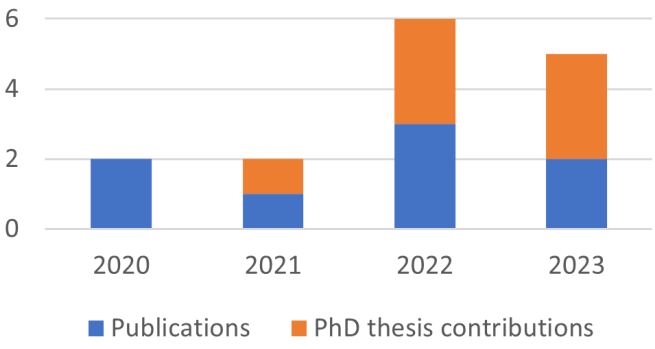


Figure 9. LBIC light-sheet publications by category

User base (current and expected 2025–2028)

Current numbers of light-sheet users and geographical distribution: Lund, 5 research groups (13 physical users) and 2 Industry users (Asgard Therapeutics and Truly labs); Gothenburg, 1 Industry user (Astra Zeneca); Copenhagen, 1 research group. In total 17 users.

Current user fees: microscopy usage 400 SEK/h; optical clearing 1250 SEK/sample chemical fee; image analysis/visualisation 150 SEK/h; general staff support: 650 SEK/h.

Scaling up user services with light-sheet imaging and clearing support is presently limited by staff availability (i.e., supported funding). A significant user-base growth of 2-3 times is expected with a 770 kSEK annual SciLifeLab network funding in 2025-2028.

Complementarity and synergistic opportunities within and across SciLifeLab platforms

Formation of extended and complementary services in light-sheet microscopy and tissue clearing support allow supporting a growing demand nationally. Visualizing biology in true 3D content drives for example next generation precision medicine capabilities with imaging of whole tumour biopsies.

Implementation of optical clearing and analysis pipelines developed at individual nodes or in collaboration between the nodes will be a key outcome from the network and benefit SciLifeLab users nationally. Regarding user-support access, the national SciLifeLab booking and data handling infrastructures, will facilitate open access and availability of the integrated equipment at LBIC.

Moreover, with complementary technology systems and affiliated staff expertise, synergetic opportunities for innovations and implementations are at hand. Specifically, our network has an overarching goal of supporting technology and application development for 3D transcriptome and proteome analysis to benefit the Swedish research community.

A project focused on development of multiplexed 3D tissue imaging for transcriptome and proteome analysis is already initiated at Campus Solna (led by Mats Nilsson, SU, and Hjalmar Brismar, KTH/KI). Expanding and leveraging combined network expertise and equipment available in Stockholm and Lund could shorten the project lead time, as well as allow an earlier innovative national user-service support.

Plans for organizing and operating the network

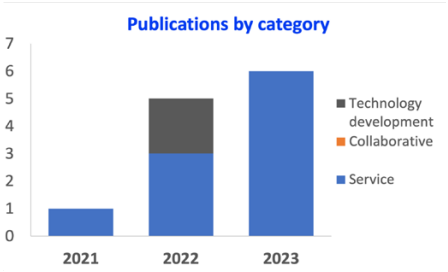
LBIC staff will handle user requests, method development/implementation and teaching within the SciLifeLab framework and communicate regularly within the network (monthly meetings). Evaluation and planning will also be done together in the network with support from the IMT management.

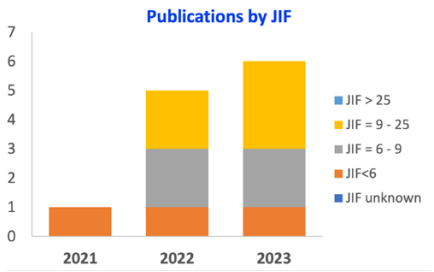
Operational support for the LBIC node in Lund is here applied for, providing complementary technology support and affiliated staff expertise. Into our national LSFM network we will also integrate knowledge transfer and interactions with microscopy facilities and researchers also at Gothenburg and Umeå Universities.

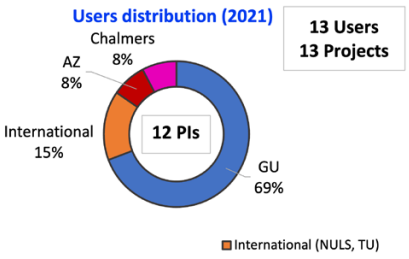
E13 NanoSIMS

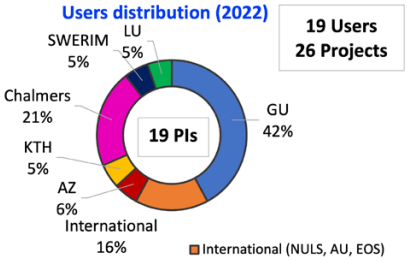
NanoSIMS Facility at Gothenburg (NFG)

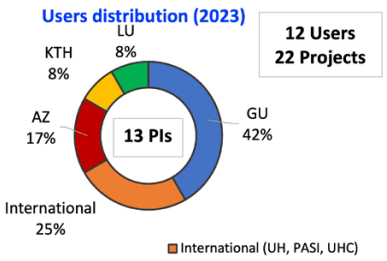
Funding 2023 (in kSEK)
SciLifeLab: 0
Total: 1692











Current technologies and services offered

- CAMECA nanoscale secondary ion mass spectrometry (NanoSIMS) imaging system to analyse samples at the nanoscale spatial resolution (down to 50 nm) for metal ions, inorganic and organic materials, and biomolecules such as metabolites, lipids, peptides, and proteins.
- Consultancy on experimental design, sample preparation, image acquisition and data processing and analysis support.
- Training on the basic operation of NanoSIMS for routine measurements. Training on the data processing and analysis in 2D and 3D images, using CAMECA image analysis software and ImageJ.

New technologies and services 2025-2028

- Support and perform sample preparation for NanoSIMS in connection with the service at the Centre for Cellular Imaging (CCI), part of the IMT unit in Gothenburg.
- Consultancy and support on NanoSIMS applications in pharmaceutical research and industry.

Scientific environment

The NFG was founded in 2015 with the mandate to secure the access of the nanoscale mass spectrometry imaging technology to researchers in Sweden, having surpassed this by serving all Nordics. Currently, the NFG has initiated a second 5-year agreement with AstraZeneca to host the NanoSIMS instrument on site as a part of the open innovation ecosystem called the AstraZeneca BioVentureHub, which provides unprecedented collaborations between academic research and pharmaceutical development and applications. The NanoSIMS is a unique secondary ion nanoprobe in the Nordics, with capabilities to measure elemental, isotopic, inorganic, organic to biomolecular distributions in all kinds of samples with excellent sensitivity (ppm), 2D/3D imaging can be performed with excellent spatial resolution (~ 50 nm laterally, 10 nm axially). The NFG has unparalleled expertise in high resolution mass spectrometry imaging and absolute quantification of concentration with NanoSIMS - developed in our facility, as well as development of new standards for NanoSIMS and SIMS. The success of the absolute quantification allows us to be the first team in the world capable of assessing the true accumulation of drugs at subcellular level, which is critical for design of therapeutics. Correlative multimodal imaging has been also developed and implemented in a close collaboration with the CCI in Gothenburg, facilitating a correlation of NanoSIMS with electron and light microscopy. This has been integrated into a total workflow which can be easily applied in various fields from life sciences to material characterization, and into the drug discovery pipeline in applied research and the pharmaceutical industry.

The NFG is associated closely with all the expert competence in mass spectrometry and multimodal imaging located in Gothenburg, specifically Prof. Andrew Ewing, GU, scientific advisor; Prof. John Fletcher, GU; Dr. Michael Kurczy, AstraZeneca, members of the local scientific committee; Dr. Elias Ranjbari, GU, NanoSIMS engineer, and Dr. Nhu Phan, GU, director of NFG. The NFG plays as an active interface between innovative and methodological developments in academia, the NanoSIMS company (CAMECA), and applications in industry, environment, and healthcare. The NFG has secured a collaboration contract with CAMECA and AstraZeneca on development of new pharmaceutical applications, and new NanoSIMS product

sharing (standards, software and technologies for imaging acquisition and processing), which promotes the visibility of the NFG in international conferences sponsored by CAMECA. We are also very active in networking with other national and international expertise, outreaching to scientists within and outside Gothenburg with the aim to introduce NanoSIMS to the broader community and encourage collaborations. Since 2022, we have organised a *Mass Spectrometry Imaging Webinar series*, for which, every month, a national or international expert of SIMS imaging is invited to give a talk to scientists within and outside Gothenburg. The facility always pushes to offer the most competent and reliable service, from consultation in experimental design, training, to total service in sample preparation, image acquisition and data mining, ensuring the highest quality of data obtained for each project in various fields.

User base (current and expected 2025–2028)

The NFG currently works on a fee-for-service model with 4 types of user fees: internal academic users (GU), external academic users, industrial users, and frequent users. We have successfully attracted users from many different fields, ranging from metabolism, microbiology, pharmaceuticals, marine science, palaeontology and origin of life, and material science. A large fraction of the users are academic, especially external users which contributes significantly to the annual income of the facility over 2021-2023. The NFG also obtains a large fraction of frequent users offering prior commitment to user time providing a stable annual income. It is also noted that the number of international users from Norway, Finland, and Denmark has increased constantly from 15% in 2021 to 25% in 2023, as proof of our recognition in the Nordic region. The industrial users contribute only a minor fraction, however, with our effort to push the NanoSIMS applications to pharmaceuticals, it is expected that this user category

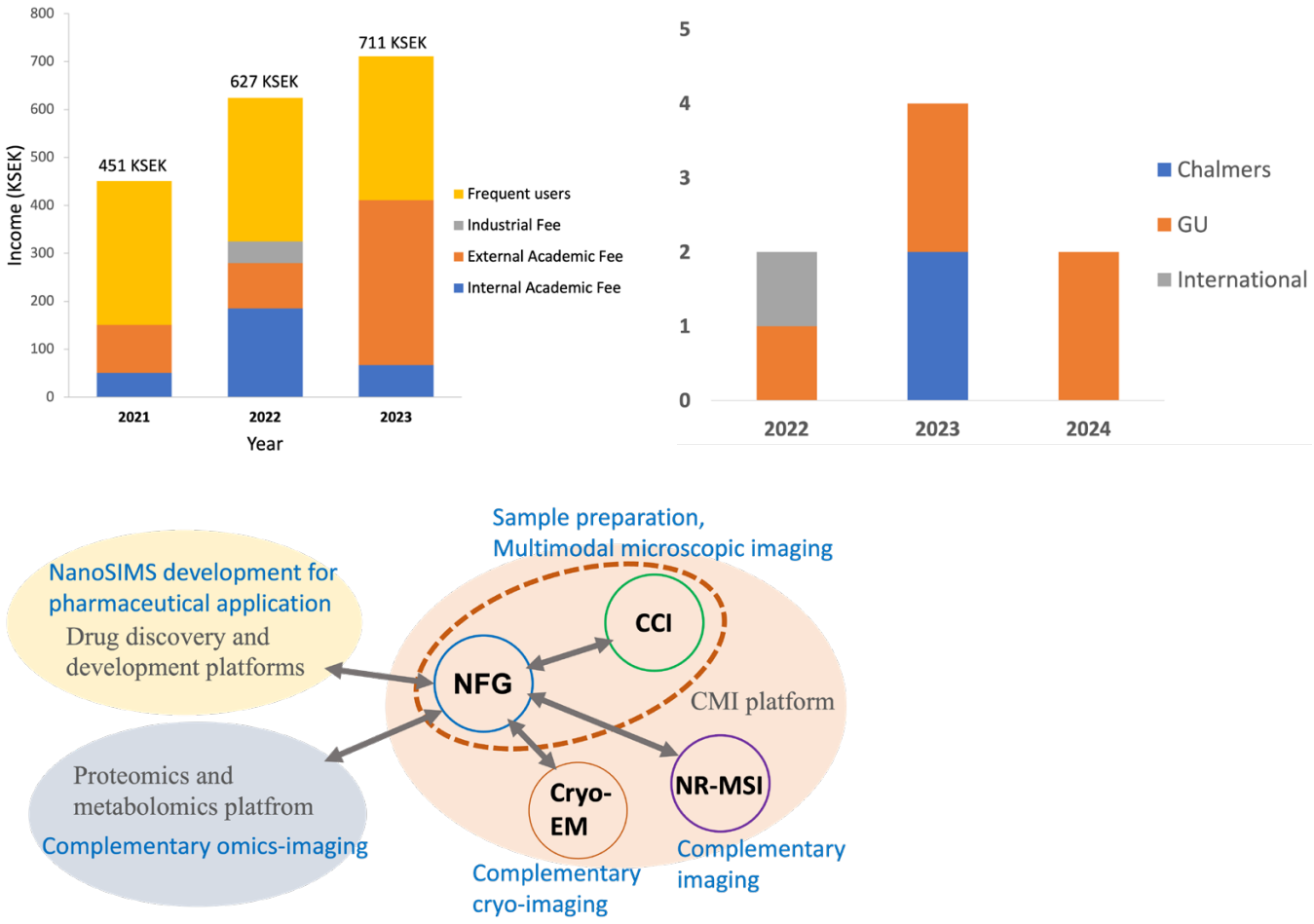


Figure 10. Annual income from NanoSIMS users 2021-2023 (top left). Number of completed PhD theses using NanoSIMS at NFG 2021-2024 (top right). Collaborations within SciLifeLab infrastructure (bottom).

will increase in the upcoming years. Among academic users, a large number are PhD students, whose NanoSIMS work is critically evaluated in the form of PhD theses. We now suggest to include NanoSIMS technology in the IMT-Gothenburg node of the CMI Platform to provide the Swedish research environment with access and support to world class mass spectrometry imaging in life science research.

Complementarity and synergistic opportunities within and across SciLifeLab platforms

The integration of the NanoSIMS as a service of the SciLifeLab CMI Platform from the IMT-Gothenburg node provides great potential strengthened partnership with the CCI, enabling better coordination in experimental planning and execution from the sample preparation, image acquisition with NanoSIMS or with electron and light microscopy modalities if needed, data processing to speed up the project progress. Moreover, this opens new opportunities for collaborations with other SciLifeLab units, such as the cryo-EM and NR-MSI, and across platforms, such as the proteomics and metabolomics, drug discovery and development platforms, in synergistic projects at the national and European level. Complementary expertise and instrumental resources among SciLifeLab infrastructures are expected to be highly valuable.

Plans for incorporation of the operations into the platform

The NFG has already implemented protocols and workflow (e.g. sample prep, data processing and analysis) together with the IMT-Gothenburg node. The NFG will participate in meetings within the CMI platform to introduce NanoSIMS technology and our service as well as to learn about other units for potential collaborations. This will help to connect our users with other units based on the needs of their projects. NFG will announce the monthly SIMS imaging webinars to the platform to promote applications and collaborations using NanoSIMS. Finally, cooperations with other SciLifeLab units will be improved to ensure the workflow and realiability for user access and support, training, sample preparation, sample storage and shipment for researchers across Sweden.

Budget request

Platform Strategic Budget

The general platform-centric budget, including support for the Platform Director and Coordination Officer, is described in detail in the Platform strategic budget table. It includes costs for advanced platform workshops to disseminate awareness and expertise related to Platform technologies, particularly the most recent acquisitions and services developed in-house. In 2023 we ran an advanced workshop in CAT at the Gothenburg node; similarly, we are organizing a workshop in FIB-SEM applications at the Umeå node in 2024. During the 2025–2028 budget cycle, we will offer workshops on novel CLEM approaches, nanoSIMS, as well as clearing and expansion methods coupled with light-sheet imaging. All these programs involve expert international instructors, whose visits also enrich our local environments and staff networks. We also budget for one platform retreat per year, ideally in combination with the workshop, for the staff of the different nodes to meet, interact and brainstorm. In light of compelling opportunities in the field of machine learning coupled with CMI technologies, the Platform also asks for support for an FTE to develop AI-driven image analysis projects. Optimally, this staff member would be co-funded by another platform with shared interests, such as NBIS, ISB, Spatial Biology, DDD or others.

Cryo-EM Unit funding

The Cryo-EM Unit currently supports a large volume of users and activities mainly for structure determination of protein-protein and protein-nucleic acid complexes by single-particle analysis. The unit was established thanks to support from the Knut and Alice Wallenberg (KAW) Foundation, the Erling Persson Foundation, the Kempe Foundation, SciLifeLab, Stockholm and Umeå Universities. Funding from the Foundations allows the Unit to provide affordable access to all users in Sweden, the Nordics and some from other EU countries. This support, combined with open and transparent operations, have made Cryo-EM a truly national infrastructure. Funding for instrument upgrades and development have also been increasingly secured, and the Heads of Unit and Scientific Directors are committed to continued fund-raising to support novel implementations. These efforts are needed to keep the SciLifeLab Cryo-EM Unit at the technological forefront. The current major financial challenge to the Unit is represented by service maintenance costs for the high-end cryo-electron microscopes. As the original grants from the Foundations are ending, maintaining affordable costs for users is becoming challenging. User fees have been raised, but it is not sustainable to raise them much further; it will not be possible to sustain cryo-EM operations fully on academic user fees. The Unit has worked hard to increase the usage from industrial users, which pay the full cost of operations, but income from industrial usage is unpredictable. In the new proposed Unit budgets (see tables for Cryo-EM in Stockholm and Umeå), an additional 3M SEK/year support (total for the two nodes) is required from SciLifelab to co-fund service maintenance costs for the microscopes (not the full expected service cost).

The Cryo-EM Unit asks also for continued support to the National CryoScreeNET to co-fund cryo-EM personnel at Gothenburg, Lund and Uppsala univerisities. Some money will be available, on a project-base request from users, to facilitate microscope access at the Karolinska cryo-EM facility.

The Cryo-EM Unit is also seeking, upon repeated interest shown by users, for SciLifeLab support to Mass Photometry access. Refeyn mass photometry instruments are now available at both Cryo-EM nodes (Stockholm and Umeå). To enable this service, a support for 0.5 FTE at each of the two nodes during the 2025–2028 cycle is requested. The Unit has been successful in securing SciLifeLab Instrument grants during the 2021–2024 cycle to acquire a CLEM system and a Glacios microscope, for which depreciation costs, shown in the budget table, will be paid over 10 years (including 2025–2028).

To potentiate cryo-ET and *in situ* (in cell) structural biology using cryo-EM, the Unit will require substantial additional fundings. Although not included in the current budget, the Unit continues to explore opportunities to co-fund larger upgrades such as cryo-FIB with both SciLifeLab and the host universities, pending support raised from other funding sources.

Integrated Microscopy Technologies Unit funding

Requested budget contributions from SciLifeLab correspond to parts of the total budget needed running costs and FTE salaries for each unit (representing a good balance with funding from external sources, university co-funding, and user fee income).

ALM (IMT-Stockholm) seeks continued support for 3 FTEs to serve SciLifeLab users in super-resolution microscopy (ExM, SIM, STED, SMLM etc.), single-molecule dynamics (FCS, STED-FCS, FRET-FCS etc.) and high-resolution volumetric imaging (light sheet, clearing). The budget includes running costs related to extension of the core technology services at ALM with nanoscale MINFLUX microscopy, multispot-single-molecule-dynamics microscopy, and ultra-fast sub-cellular resolution lattice light-sheet microscopy during 2025–2028. Financial support to cover increasing service and maintenance costs for advanced instrumentation is also included. Management support to coordinate the proposed national light-sheet/clearing screening network (eventually to include Lund, Gothenburg, Stockholm and Umeå) is also part of the IMT Unit budget. External and host university (internal) funding supports 1.2 FTE and 82% of advanced instrumentation costs at the Unit.

CAT (IMT-Gothenburg) seeks continued support for 1 FTE to serve SciLifeLab users with correlative array technologies, i.e. combinations of light and electron microscopy for correlative volumetric imaging including specific sample preparation and advanced analysis. Funding also covers running costs and some service and maintenance of instruments. External and host university (internal) funding supports 1 FTE and 85% of advanced instrumentation costs at the unit.

FIB-SEM (IMT-Umeå) seeks continued support for 1 FTE to serve SciLifeLab users with access to lamella FIB-SEM sample preparation and nano-volumetric imaging technology. Funding also covers running costs. External and host university (internal) funding supports 80% of advanced instrumentation costs at the unit.

LBIC (clearing/lightsheet microscopy network, to be incorporated into IMT) seeks initialization funding for 0.5 FTE to support increased access to light-sheet imaging and advanced clearing methods in the proposed national network. External and host university (internal) funding supports 0.3 FTE and 100% of advanced instrumentation costs.

NanoSIMS seeks initialization funding for 1 FTE to provide nanoscale mass spectrometry imaging technology services to SciLifeLab users, with development of dedicated protocols and analysis support, including multimodal imaging accessibility. External and host university (internal) funding supports 100% of advanced instrumentation costs.

Table 1. Cellular and Molecular Imaging – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Intra-platform pilot project	1 250				
Advanced intra-platform workshops		300	300	300	300
Retreat	200	250	250	250	250
Data analysis inter-platform collaborations (shared FTEs for machine learning of molecular and cellular images, e.g. BeyondFold	100	1 000	1 000	1 000	1 000
Platform Director	150	150	150	150	150
Platform Coordination Officer	200	200	200	200	200
Sum costs (kSEK):	**1 900**	**1 900**	**1 900**	**1 900**	**1 900**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*1 900*	*1 900*	*1 900*	*1 900*	*1 900*
Sum revenues (kSEK):	**1 900**	**1 900**	**1 900**	**1 900**	**1 900**

Table 2a. Cryo-EM Stockholm Budget

Costs	2024	2025	2026	2027	2028
Personnel 4.5 FTEs (2024) -> 4.5 FTEs (2025–2028)	6 021	6 232	6 450	6 676	6 909
Persomel 0.5 FTE Mass Photometer	-	500	500	500	500
Operations	1 725	2 000	2 000	2 000	2 000
Premises	2 548	2 675	2 809	2 950	3 097
Instrument depreciations	13 705	13 600	8 200	7 700	7 700
Instrument service costs	5 926	7 000	8 000	9 000	10 000
Investment for new capabilities (cryoFIB for in situ structural biology) [1]		4 500	4 500	4 500	4 500
Sum costs (kSEK):	**29 925**	**36 507**	**32 459**	**33 325**	**34 706**

Revenues	2024	2025	2026	2027	2028
SciLifeLab core funding (current and requested 2025–2028)	*5 046*	*6 750*	*6 750*	*6 750*	*6 750*
SciLifeLab funding (requested 2025–2028) Mass photometry		*500*	*500*	*500*	*500*
SciLifeLab instrument grants (current and requested 2025–2028)	*1 293*	*800*	*800*	*800*	*800*
University co-funding	3 087	1 000	1 000	1 000	1 000
KAW funding	13 162	12 500	8 500	8 500	6 000
SSF	952	952	952	952	
Erling Perssons Stiftelsen	2 678	2 678			
User fees	3 700	3 700	3 700	3 700	3 700
New required fundings for keeping current state-of-the-art operations [2]		3 126	5 756	6 623	11 456
New funding required for expansion to new capabilities (*in situ* structural biology) [1]		4 500	4 500	4 500	4 500
Sum revenues (kSEK):	**29 918**	**36 506**	**32 458**	**33 325**	**34 706**

[1] This is the rough estimation for the expansion towards cryo-ET for subtomogram averaging and in situ structural biology at the Stockholm node. The Unit aims at acquiring an Aquilos 2, Hydra or Arctis cryo-FIB-SEM to make it possible for all users to have new opportunity for cryo-ET projects. In addition to the main cryo-FIB microscopes, ancillary instrumentation, such as high-pressure freezer, and access to a nearby cell lab, have been considered. Investment costs are depreciated over 10 years.

[2] This is the amount required for the maintenance of the current cryo-EM operations. The Unit is in the process of holding conversations with both SciLifeLab and Stockholm University for support.

Table 2b . Cryo-EM Umeå Budget

Costs	2024	2025	2026	2027	2028
Personnel 2,5 FTEs (2024) -> 2,5 FTEs (2025–2028)	3 500	3 553	3 606	3 660	3 715
Operations	5 493	5 603	5 715	5 829	5 945
Premises	1 089	1 110	1 132	1 155	1 178
Instrument depreciations, estimation, and partial deposit of depreciation funding	8 022	7 000	5 000	3 500	3 500
Sum costs (kSEK):	**18 103**	**17 265**	**15 453**	**14 144**	**14 338**

Revenues	2024	2025	2026	2027	2028
SciLifeLab core funding (current and requested 2025–2028)	*4 779*	*4 375*	*4 375*	*4 375*	*4 375*
SciLifeLab funding (requested 2025–2028) Mass photometry		*500*	*500*	*500*	*500*
SciLifeLab funding (requested 2025–2028) cryo-EM service		*1 300*	*1 300*	*1 300*	*1 300*
KAW instrument service funding	1 500				
SciLifeLab funding expensive instruments, cryo-EM screening	*1 000*	*1 000*	*1 000*		
Funding KAW cryoNET, until 2022	183				
Funding KAW cryoNET, until 2026	1 000	1 000	1 000	1 000	1 000
University co-funding (Umeå KBC)	2 800	2 800	2 800	2 800	2 800
Tek NAT Kempe depreciation (EBL Physics)	380	380	380	380	380
SSF depreciations	300	300	300	300	300
UmU KAW co-funding	1 000	250	250	250	250
Kempe (previously Glacios-Selectris-Falcon4i)	1 500	1 500			
VR-RFI equipment funding	2 000	2 000			
Periodization of depreciation	586	360	2 048	1 739	1 933
User fees	**1 075**	**1 500**	**1 500**	**1 500**	**1 500**
Sum revenues (kSEK):	**18 103**	**17 265**	**15 453**	**14 144**	**14 338**

Table 2c. CryoScreeNET Budget

Costs	2024	2025	2026	2027	2028
Personnel 1.5 FTEs (2024) -> 1.5 (2025–2028)*	2 328	2 328	2 328	2 328	2 328
Project-base support		270	270	270	270
Sum costs (kSEK):	**2 328**	**2 598**	**2 598**	**2 598**	**2 598**

Revenues	2024	2025	2026	2027	2028
SciLifeLab CryoScreeNET personnel funding (current and requested 2025–2028) [1]	*2 328*	*2 328*	*2 328*	*2 328*	*2 328*
SciLifeLab CryoScreeNET project funding (current and requested 2025–2028)		*270*	*270*	*270*	*270*
Sum revenues (kSEK):	**2 328**	**2 598**	**2 598**	**2 598**	**2 598**

[1] Host universities (GU, UU and LU) fund the remaining FTE cost

Table 3a. Integrated Microscopy Technologies Gothenburg Budget [1]

Costs	2024	2025	2026	2027	2028
Personnel 7,5 FTEs (2024) -> 7,5 FTEs (2025–2028)	8 180	8 343	8 509	8 679	8 852
Operations	2 650	2 703	2 757	2 812	2 868
Premises	1 500	1 530	1 560	1 590	1 620
Instrument depreciations	4 500	4 000	3 700	3 700	2 500
Sum costs (kSEK):	**16 830**	**16 576**	**16 526**	**16 781**	**15 840**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding CAT (current and requested 2025–2028)	*1 550*	*1 580*	*1 610*	*1 640*	*1 670*
Founding from host University (infrastructure support: Sahlgrenska Academy)	*4 900*	*4 900*	*4 900*	*4 900*	*4 900*
University co-funding	3 350	3 000	3 000	3 000	3 000
Founding VR (NMI)	1 500	950	950	950	950
Founding SSF	2 750	2 750	2 750	2 750	1 500
EU Funding H2020	375	375			
User fees	2 500	2 500	2 600	2 800	3 000
Sum revenues (kSEK):	**16 925**	**16 055**	**15 810**	**16 040**	**15 020**

[1] Budget includes all activities of the CCI core facility, of which SciLifeLab-supported services in CAT are one part

Table 3b. Integrated Microscopy Technologies Stockholm Budget

Costs	2024	2025	2026	2027	2028
Personnel 4 FTEs (2024) -> 4 FTE (2025–2028)	4 653	4 746	4 841	4 938	5 037
Operations	782	1 167	1 167	1 167	1 167
Premises	1 057	1 089	1 122	1 156	1 191
Instrument depreciations	8 890	8 700	7 100	3 100	0
Other (STED laser service)	0	250	250	250	250
Sum costs (kSEK):	**15 382**	**15 952**	**14 480**	**10 611**	**7 645**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 620*	*4 250*	*4 250*	*4 250*	*4 250*
SciLifeLab Infrastructure (MINFLUX)	*1 600*	*1 600*	*1 600*	*1 600*	
KTH Infrastructure (Light Sheet)	190				
KTH Infrastructure (Lattice Light Sheet)	1 600	1 600			
KTH Infrastructure (AIRY2)	1 000	1 000	1 000		
KTH Infrastructure (MINFLUX)	1 500	1 500	1 500	1 500	
Funding agency VR-RFI (Elyra7)	3 000	3 000	3 000		
Funding agency VR-RFI (NMI)	1 000	1 000	1 000	1 000	1 000
Faculty co-funding	1 000	1 000	1 000	1 000	1 000
User fees	872	1 000	1 000	1 000	1 000
Sum revenues (kSEK):	**15 382**	**15 950**	**14 350**	**10 350**	**7 250**

Table 3c. Integrated Microscopy Technologies Umeå Budget [1]

Costs	2024	2025	2026	2027	2028
Personnel 2,5 FTEs (2024) -> 2,5 FTEs (2025–2028)	3 500	3 553	3 606	3 660	3 715
Operations	2 354	2 354	2 354	2 354	2 354
Premises	467	476	485	495	505
Instrument depreciations, estimation, and partly deposit of depreciation funding	1 839	1 839	200	200	200
Sum costs (kSEK):	**8 160**	**8 221**	**6 645**	**6 709**	**6 774**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*1 552*	*1 600*	*1 600*	*1 600*	*1 600*
SciLifeLab instrument funding, IMT sample preparation/FIB	*667*	*667*	*667*		
SciLifeLab platform technology development	448				
University co-funding (Umeå KBC)	1 200	1 200	1 200	1 200	1 200
SSF personal costs	1 350	1 350	1 350	1 350	1 350
Periodization of operations	1 031	732	328	1 059	1 124
Periodization of depreciation	1 172	1 172			
User fees	740	1 500	1 500	1 500	1 500
Sum revenues (kSEK):	**8 160**	**8 221**	**6 645**	**6 709**	**6 774**

[1] Budget includes activities of the UCEM core facility (excluding cryo-EM), of which SciLifeLab-supported services in FIB-SEM are one part

Table 3d. Lund University Biomaging Centre – LSFM Network Node Budget

Costs	2024	2025	2026	2027	2028
Personnel 0,3 FTEs (2024) -> 1 FTEs (2025–2028)	326	1 088	1 132	1 178	1 225
Service contracts	60	62	63	65	66
Premises	184	190	195	201	207
Instrument depreciations	444	222	-	-	-
Sum costs (kSEK):	**1 014**	**1 561**	**1 390**	**1 443**	**1 499**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	-	*770*	*770*	*770*	*770*
University co-funding	-	*702*	*519*	*559*	*602*
User fees	91	89	101	114	127
Sum revenues (kSEK):	**91**	**1 561**	**1 391**	**1 444**	**1 499**

Table 3e. NanoSIMS Budget

Costs	2024	2025	2026	2027	2028
Personnel 1 FTEs (2024) -> 1.5 FTEs (2025–2028) (NanoSIMS engineer, sample prep)	1 200	1 800	1 800	1 850	1 850
Operations	380	750	750	800	800
Premises	330	330	330	330	330
Instrument depreciations	60	60	50	50	40
Other (Travels, consumables)	100	100	100	100	100
Sum costs (kSEK):	**2 070**	**3 040**	**3 030**	**3 130**	**3 120**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)		*1 500*	*1 500*	*1 500*	*1 500*
University co-funding		*450*	*450*	*450*	*450*
Department of Chemistry and Molecular Biology	500	-	-	-	-
Co-funding on premise by AstraZeneca	100	100	100	100	100
User fees	800	1 100	1 150	1 150	1 200
Sum revenues (kSEK):	**1 400**	**3 150**	**3 200**	**3 200**	**3 300**



Swedish NMR Centre Unit in Umeå. Photo: Mikael Wallerstedt

Integrated Structural Biology Platform

Basic Information

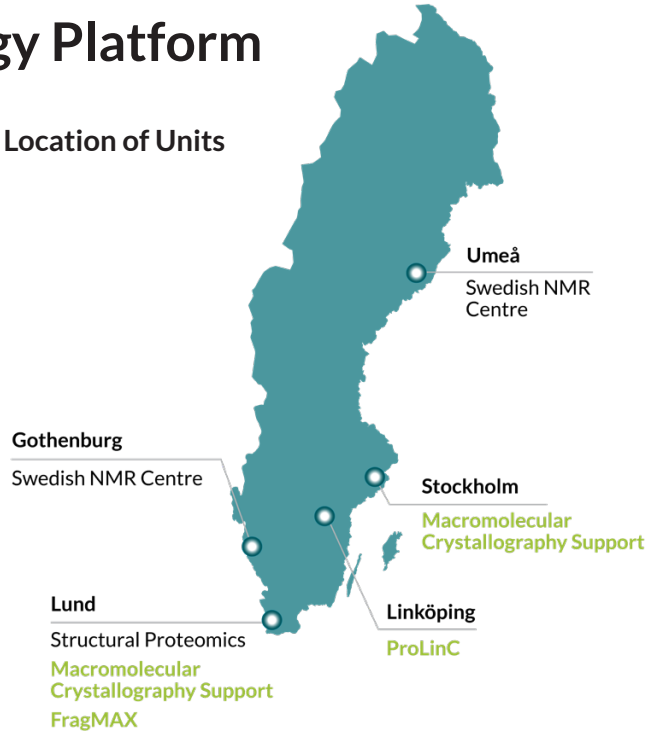
Platform Director: Göran Karlsson, University of Gothenburg

Platform Coordination Officer: Cecilia Persson, University of Gothenburg

Platform vision: Towards *in-situ* structural biology – understanding cellular processes on a molecular level in a native environment

Platform mission: Provide access to state-of-the-art instrumentation and expert support for structural biology in an integrated fashion

Location of Units

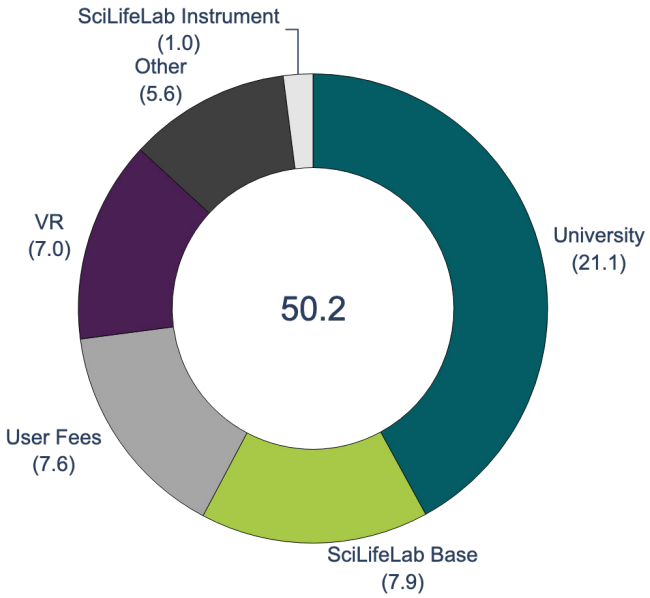


SciLifeLab Funding

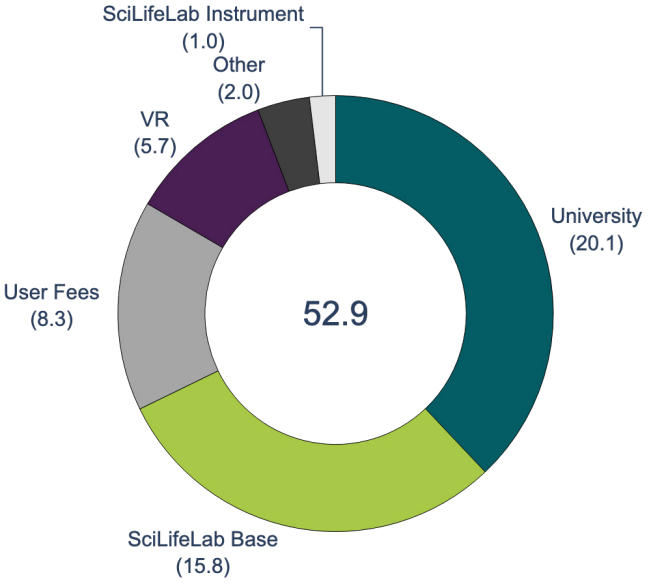
Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Structural Proteomics	2.6	2.6
Swedish NMR Centre	4.8	6.8
Macromolecular Crystallography Support and FragMAX*	0.0	4.1
ProLinC*	0.0	1.2
Platform Strategic Funding	0.6	1.2
Total SciLifeLab Funding	**7.9**	**15.8**

*Proposed to be included in the platform

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E14 Integrated Structural Biology

The Integrated Structural Biology (ISB) platform coordinates major technologies for structural biology with advanced support for the benefit of life science research in Sweden. Our aim is to provide expert support and state-of-the-art instrumentation in an integrated fashion to describe the structure and dynamics of macromolecular systems. ISB addresses e.g. how molecular machines work, delineates mechanistic aspects of molecular signaling and contributes to the understanding of disease, whereas detailed description of drug-protein interactions forms the basis for efficient drug development. The integration of different but complementary cutting-edge techniques warrants expert knowledge and support. Cross platform interactions and collaboration between units are key characteristics of the 2025-2028 ISB platform.

The ISB platform 2025-2028 comprises the Swedish NMR Centre (SNC) and the Structural Proteomics (SP) unit and the new units ProLinC, for biophysical characterization, and the FragMAX/MX unit, for macromolecular protein crystallography and crystallography-based fragment screening. The Cryo-EM unit is virtually associated to the ISB platform, and part of the ISB platform management group (PMG), and there is a close collaboration with NBIS. The ISB platform will maintain close connection to other relevant stakeholders (e.g. MAX IV, ESS, the research infrastructure Protein Production Sweden (PPS), InfraLife, LINXS) and coordinate SciLifeLab ISB activities (*Figure* 1).

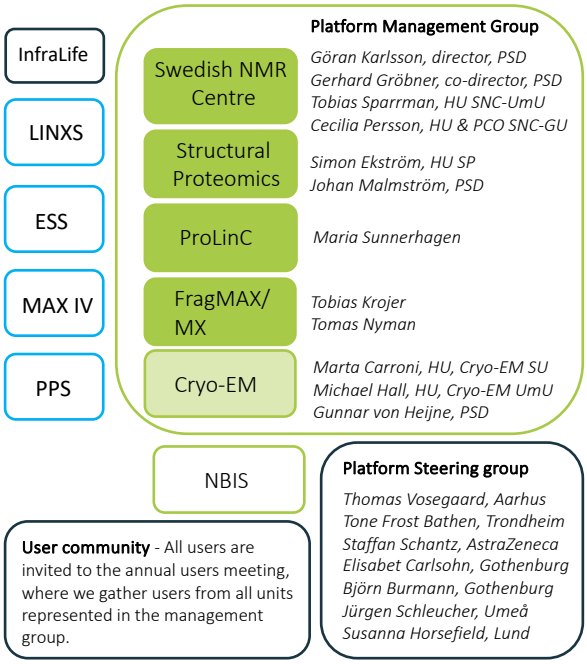


Figure 1. Organogram of the ISB platform.

Overall platform development and key achievements 2021–2024

The ISB platform was formed in 2021 by joining SNC, part of SciLifeLab since 2016 with the new Structural Proteomics (SP) unit. Organizationally, the two units formed the core of the platform. The Cryo-EM unit, part of SciLifeLab since 2016, was virtually associated to the ISB and in all practical aspects equal to SNC and SP. A mission for the new platform was to coordinate the service area Integrated Structural Biology in collaboration with Cryo-EM, MAX IV, ESS, the national protein production network (PPS), InfraLife and other relevant stakeholders in the extended ISB platform.

The ISB management group (PMG) meets every three weeks to handle SciLifeLab related matters. The extended PMG meets every 6 to 12 weeks to discuss ISB development and inform about ongoing activities and upcoming events. The entire ISB platform also meets IRL once per year for operations and strategy planning.

Joint platform key achievements include the ISB course, the annual ISB users meeting, organizing a series reach-out activities including an ISB session at the SweProt meeting, initating a platform staff visitors program to enhance intra-platform technology knowledge and administrating the expensive equipment support program. Three years into operation, the ISB platform organized the third annual users meeting (Dec 6, 2023) in Stockholm. The third meeting attracted ca 60 participants and featured presentations from users of the extended ISB platform.

The two-week ISB course was first organized in 2022. InfraLife coordinated activities and unit participation from SP, SNC and CryoEM in addition to MAX IV, ESS, PPS and ProLinC. The hands-on ISB course traversed through Sweden, starting in Lund, stopping over in Gothenburg to finally finish in Stockholm. In 2023, the course was organized by the ISB platform as a compact two-day web-based event. Plans for the 2024 two-week course (Sep 2-13), open to users outside Sweden, are in progress. The course evaluation is available at infralife.se/infralife-integrated-structural-biology-course-evaluation-and-future-plans.

The ISB platform expensive equipment program has been instrumental for the continuous development of the platform. The program co-funded an NMR console and cryoprobe upgrade (SNC-GU), an NMR console and the first 3.2 mm cryo-MAS probe (SNC-UmU) and the robotic automated sample preparation MS front-end equipment at SP. The development of the platform is illustrated in *Figure* 2.

Infographics: Statistics and Metrics for Integrated Structural Biology Units

Structural Proteomics

Read more: Webpage, Publications Database

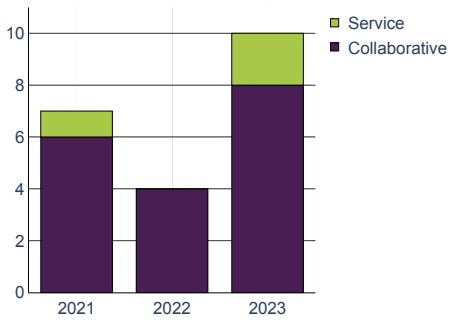
Basic Information

HU: Simon Ekström
Host University: LU
SciLifeLab unit since: 2021
FTEs: 3
PSD: Johan Malmström

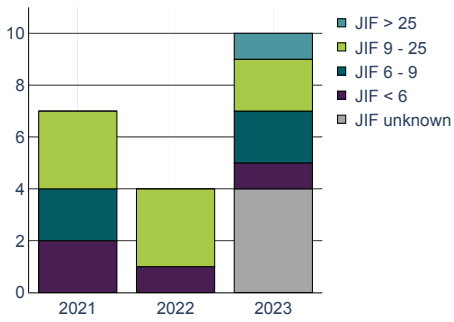
Funding 2023 (kSEK)

SciLifeLab: 2500
Other: 2681
User Fees: 450

Publications by category

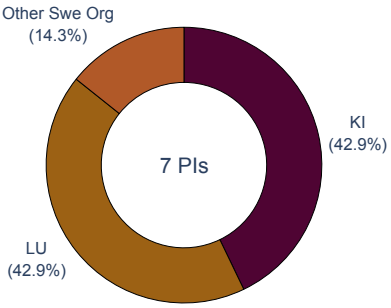


Publications by JIF

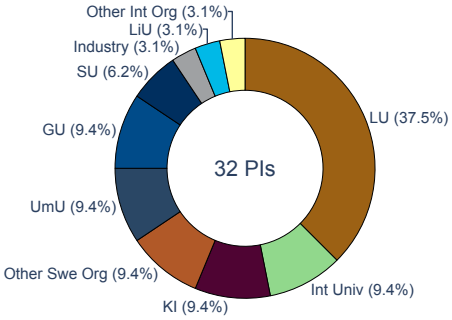


No. of Tech Dev Publications 2021 - 2023: 3

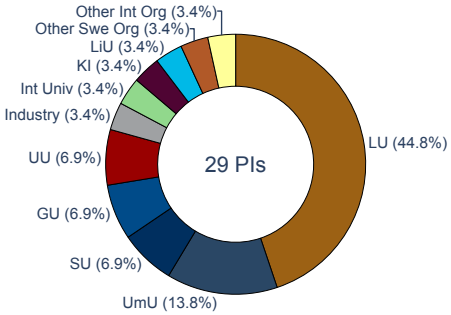
Users 2021



Users 2022



Users 2023



Swedish NMR Centre

Read more: Webpage, Publications Database

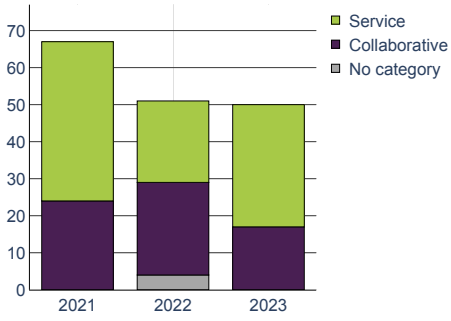
Basic Information

HU: Cecilia Persson, Tobias Sparrman
Host University: GU, UmU
SciLifeLab unit since: 2016
FTEs: 13.2
PSD: Göran Karlsson, Gerhard Gröbner

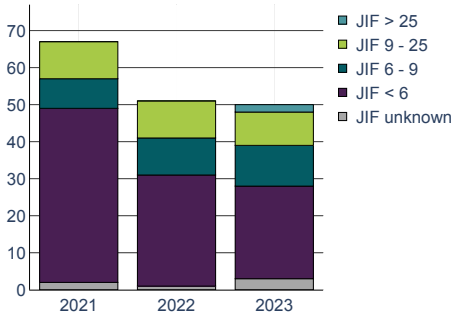
Funding 2023 (kSEK)

SciLifeLab: 4600
Other: 17015
User Fees: 3490

Publications by category

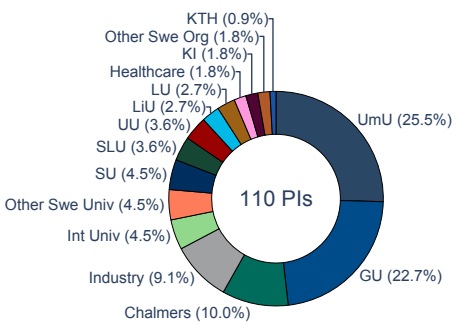


Publications by JIF

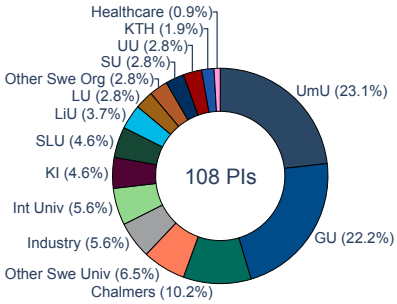


No. of Tech Dev Publications 2021 - 2023: 3

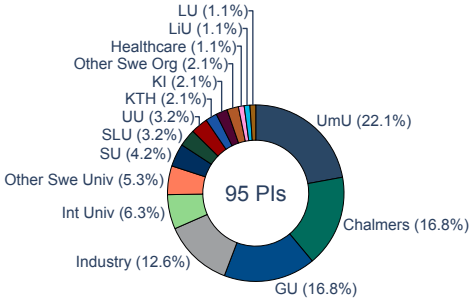
Users 2021



Users 2022



Users 2023



- *BeyondFold – TDP together with NBIS on how to exploit AlphaFold for protein dynamics*

Overall platform plans 2025–2028

In the protein data bank (PDB), few deposits are the result of ISB multi-technology use. Yet the ISB approach is required to go beyond the current understanding where biomolecules often are regarded as static and isolated. From ISB, we can obtain a deeper understanding of functional biomolecular dynamics and interactions in large systems, and, in some cases, will be able to describe structural features inside a cellular environment. This is of outmost importance, since molecular characteristics (e.g. conformational sampling, dynamics, complex formation, folding state, reaction kinetics, chemical equilibrium) in a crowded cellular environment can be vastly different from that in an isolated environment at pH 7.

The platform development plans include expansion of the current organization as shown in *Figure* 4, *increasing from two to four units* and with Cryo-EM virtually associated. In this context, it should be noticed that the units of the ISB platform are not only operating within SciLifeLab. The different ISB units are already functional in their respective capacity, e.g. as part of a national (SP, SNC) or international (SNC, ProLinC) research infrastructure network and FragMAX is part of MAX IV. For specific details on new technology, methodology development and support for SNC and SP, *vide infra*. The new units FragMAX/MX and ProLinC are described below.

The ISB platform plans for 2025-2028 precipitates into the following actions, which are addressed below:

- Introduce a *coordinator function* to promote the ISB aspect of projects
- Establish *project pipelines* for seamless integrations and optimal use of all technologies
- *Add new technologies* to the ISB platform, specifically a biophysical characterization unit (ProLinC) and support for macromolecular crystallography (MX)

ISB project coordinator

All units within the ISB platform have multiple funding sources and are to serve their users to the best of their capability and towards different research infrastructure networks. This *smorgasbord* of techniques (illustrated in *Figure* 3) has a huge value to the users and is also unique to Sweden, being in the forefront globally when it comes to infrastructure. Successful structural biology projects, however, depend on more than one technology and even though this is easy to grasp, it is not easy for the individual user to first identify and then find the complementary techniques that puts the gold lining to a project. Technically and competence wise, all units are constantly developing (see separate sections) but for the inexperienced user, we believe that a well worth strategic development in 2025-2028 is to introduce the function of an ISB project coordinator. Besides that, we are facing the fact that with the planned development, the ISB platform will double in size, we also believe it to be of great value for the field if we can offer additional support and guidance between units. And for the unexperienced structural biology user, this is pivotal.

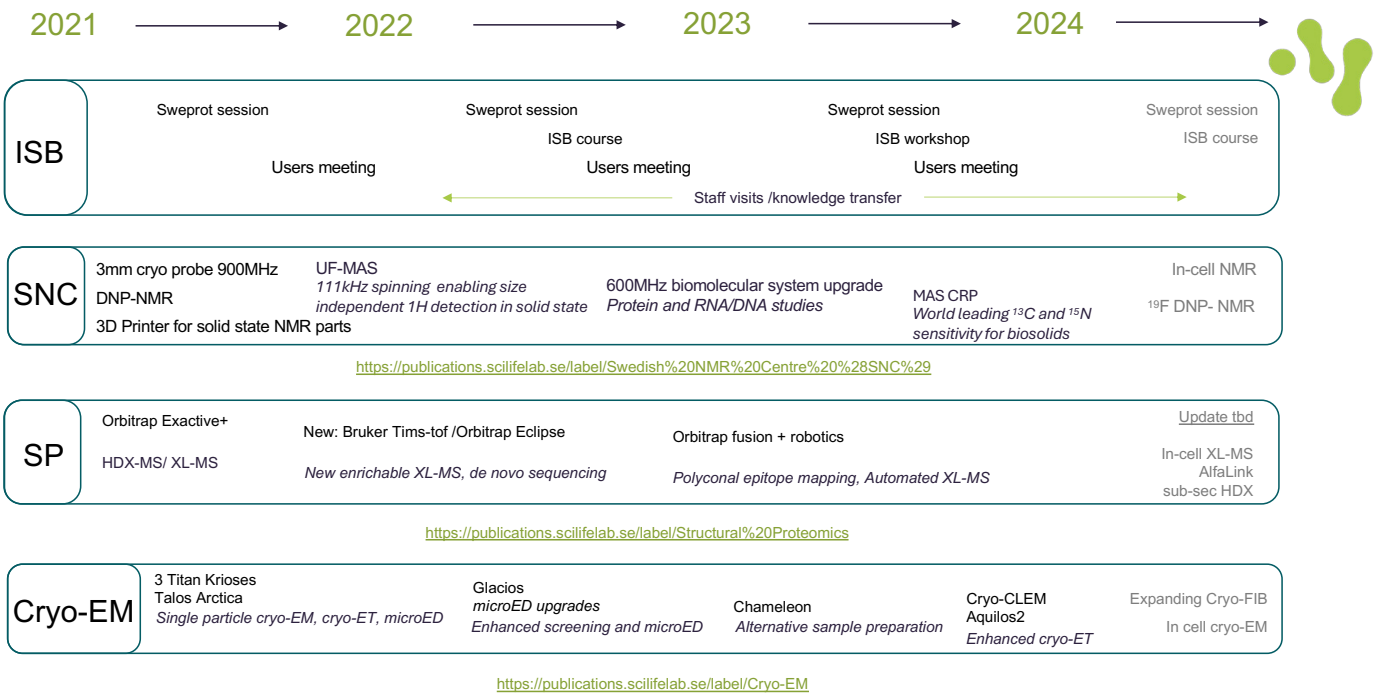


Figure 2. ISB platform work and technology development for the individual units 2021-2024

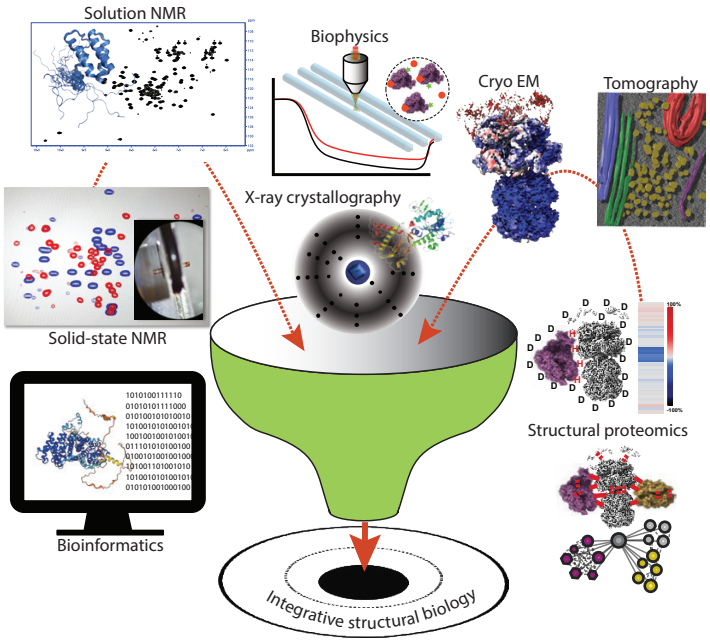


Figure 3. After expansion, the ISB platform will provide all key technologies for integrated structural biology in combination with advanced expertise and support throughout the ISB process, and in collaboration with advanced bioinformatics support.

Project pipeline in the future ISB platform – how to integrate multiple technologies

Our future strategic development to offer users guidance that goes beyond the individual techniques, is described in the above section 'ISB project coordinator'. This also aligns well with our platform vision - towards in-situ structural biology – where we anticipate the scientific questions to arise in new and vastly different systems. Whole cells (plant or animal) or tissue. This is already feasible to some extent within current platform units, but the biological systems to study are difficult and enhanced collaboration between units is required. Integration of ISB technologies spans from biophysical characterization to structural techniques such as cross-linking mass spectrometry (XL-MS), proton/deuterium exchange mass spectrometry (HDX), NMR, crystallography, and Cryo-EM. Protein expression is a prerequisite for any ISB project and ISB collaborates closely with PPS, e.g. SNC is the host unit for the cell-free protein expression offered within PPS.

Biophysical characterization

A prerequisite for successful and efficient structural and dynamic studies of a protein is basic knowledge regarding which conditions are required for its study, such as folding, monodispersity and stability, and how to steer this by buffer conditioning. Studies of protein complexes require knowledge of affinities and stoichiometry, where intrinsically disordered and/or unstable proteins/complexes need special attention. It is of great value to have the ProLinC unit for sample optimization, enabling close discussions and optimizing protocols towards specific downstream methods. ProLinC offers facile supported access to the above and will therefore be a crucial part of ISB projects.

XL-MS and HDX

Mass spectrometry (MS) plays a crucial role in modern structural biology, offering valuable complimentary insights into the molecular dynamics of interactions and structure. MS offers advantages in the ability to work with in-solution conditions using small volume samples spanning protein size ranges from 1-1000 of kDa. In addition to cross-linking (XL-MS) and hydrogen deuterium exchange mass spectrometry (HDX-MS), other important MS techniques are provided for the community on request, e.g. affinity purification, *de novo* sequencing and intact MS. With continued development, further services such as native MS will be made available. The strong synergies between structural proteomics and the technologies offered by the ISB platform offer unique possibilities to leverage science.

NMR

NMR provides dynamics information over a wide time range, adding another layer of key information to structure data from e.g. X-ray crystallography, Cryo-EM or AlphaFold. For protein liquid-liquid phase separation, weakly structured proteins and IDPs, NMR is the only method that provides structural information on the atomic level. Ultra-Fast Magic Angle Spinning NMR (UF-MAS) is probably the most interesting development in NMR-based structural biology in recent years. It allows the study of macromolecules irrespective of size, while retaining the unique dynamical information, one of the hall marks of NMR.

MX support and FragMAX

Macromolecular crystallography has matured to the point where it can be made available to scientists beyond the traditional structural biology community. LP3, PSF and FragMAX are three existing research infrastructures that offer an array of protein crystallography services. We propose adding them to the ISB platform and making their services available to non-expert users through SciLifeLab. LP3 and PSF will contribute their expertise ranging from protein crystallization to structure determination as MX support, whereas FragMAX will specifically support structure-based *compound development* efforts at the CBCS/CBGE platform.

Cryo-EM

Cryo-EM has in the past ten years emerged as a powerful tool in the field of structural biology, enabling routine structure determination of sample types previously considered challenging by other methods such as membrane proteins, large assemblies and low abundant complexes prepared from endogenous sources. The field of electron microscopy, and therefore also the SciLifeLab Cryo-EM unit, is currently moving rapidly towards *in situ* structural biology applications, where focused-ion-beam SEM coupled to Cryo-electron tomography (Cryo-ET) is expected to be one of the main driving forces behind this development. In understanding these complex systems,

the integration of Cryo-ET data with other methods such as NMR, XL-MS and MX will be critical. Furthermore Cryo-EM can be utilized for micro crystal electron diffraction, complementing MX for challenging cases where crystal size is limited to the nano scale.

Cross-platform developments

We will continue to develop and expand all the different cross-platform interactions that where established during 2021-2024. We expect an increased interest in the use of AlphaFold within ISB. The advent of AlphaFold 2.0 (AF) does not mean the end to structural biology. Instead, it represents a new era, further enabling hypothesis-driven structural biology. AF typically generates a static structural model of a monomeric protein. But to what extent can AF predict e.g. protein conformational dynamics? In the joint (NBIS, CMI and ISB) technology development project "BeyondFold" tweaking AF code and varying the MSA input generated thousands of slightly different structures that were compared with experimental NMR relaxation dynamics data (biorxiv.org/cgi/content/short/2024.02.01.578365v1). A relevant question to address is how additional experimental input can be integrated in AF in the coming years. ISB, CMI and NBIS together fund an FTE during 2024 for continuation of the BeyondFold project.

CBGE/CBCS

Together with the unit for chemical biology (CBCS) at the Chemical Biology and Genome Engineering (CBGE) platform we propose to strengthen the services in fragment based screening and structural based drug/compound design. Based on the fragment libraries provided by CBCS, we suggest to build a common pipeline using the available techniques at our platform (FragMAX, SNC, ProLinC) to identify hit fragments. CBCS expertise in computational and medicinal chemistry, and the use of "SAR by catalog" strategies will efficiently expand the hit fragments. The expanded hits can then be validated using complimentary biophysical techniques, e.g. SPR and further evaluated in biological activity assays provided by CBCS. For a description of current FragMAX operations, techniques, and expertise as well as future plans as an ISB platform, please see the annex.

A summary of ISB and cross platform activities can be seen in *Figure* 4.

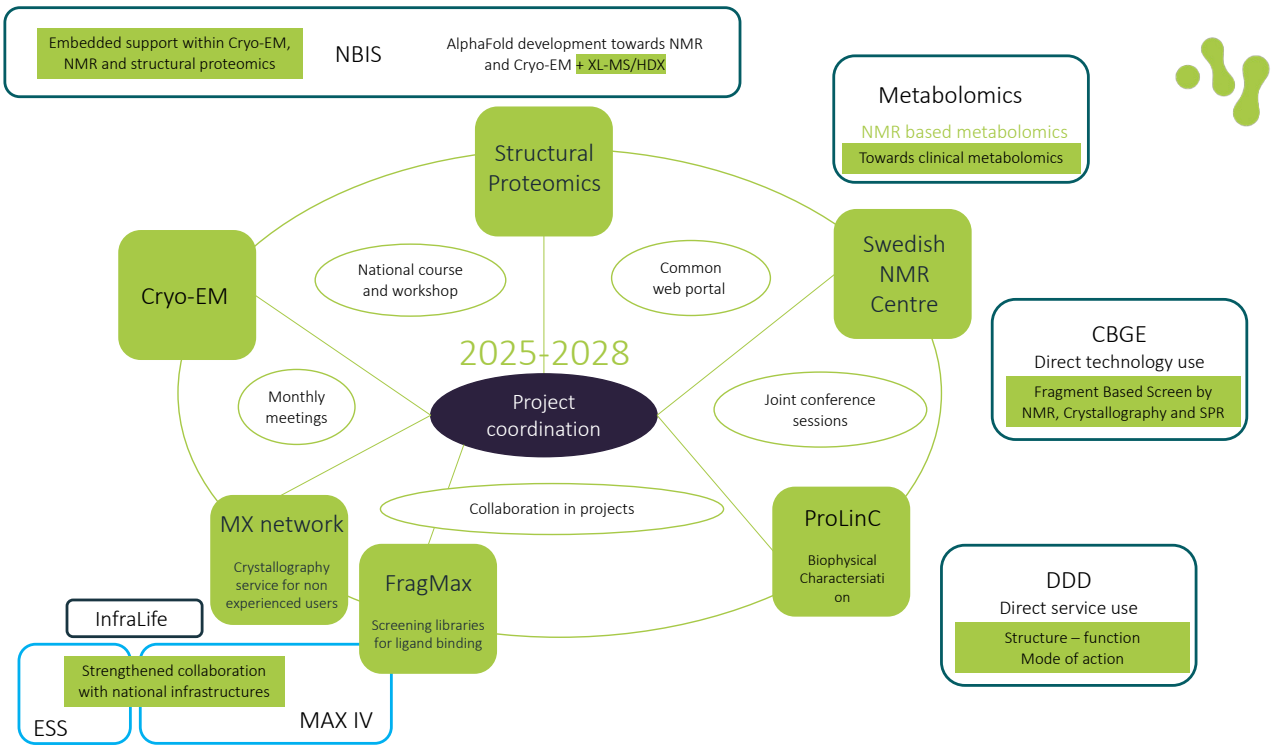


Figure 4. Several units within the platform provide expertise relevant to other SciLifeLab platforms or units, in particular the metabolomics platform where SNC offers state-of-the-art NMR-based metabolomics, and the CBCS unit of the CBGE platform, where FragMAX, SNC and ProLinC jointly provide access to a unique pipeline for Fragment Based Screen.

The Swedish NMR Centre

The Swedish NMR Centre (SNC) provides access to unique instrumentation and advanced support for NMR based integrated structural biology. Structure determination, interaction studies, conformational sampling and molecular dynamics over wide time scales is offered using advanced solution NMR methodology and new developments in solid state NMR technology. NMR has wide-spread use also in materials science, small molecules NMR, metabolomics, and fragment-based screen (FBS). Metabolomics and FBS are flavors of NMR that help SNC contribute to cross-platform activities with the Metabolomics and CBGE platform. SNC operates through the two nodes at University of Gothenburg (GU) and Umeå University (UmU).

SNC provides leading expertise and unique instrumentation in structural biology and has contributed to the NMR development in data acquisition (NUS, Targeted Acquisition) and use of e.g. artificial intelligence (AI) in data processing and analysis. SNC is also active in the current development in NMR crystallography and ^{19}F DNP-NMR. SNC offers access to ten (10) NMR spectrometers with dedicated unique probes. Five magnets operating between 700 MHz and 900 MHz are complemented by three 600 MHz magnets, a 500 MHz magnet and a 400 MHz DNP-NMR system. The most recent probe acquirements include the first commercial 600 MHz 3.2 mm cryo-MAS probe (2023) and the first 400 MHz HFX DNP-NMR probe (2024). Most magnets are equipped with cryogenic probes for highest sensitivity and several magnets are equipped with peripheral high-capacity automatic sample changers (*Table* 1). Peripheral equipment includes the Bruker InsightCell 2 system (installed 2023) which enables days-long NMR acquisition on living cells or flow through experiments. The system has been tested on two different magnets at SNC-GU with procaryotic cells. The combination of available cryogenic probes with the Insight Cell systems enables both ^{19}F detection and ^{31}P detection in addition to the other biologically relevant nuclei ^{1}H,^{13}C and ^{15}N.

The capacity of the helium recovery system at SNC-GU was increased in 2023 to recover all helium during normal operations and top-up. In 2023, 7 600 L of helium were liquefied on-site, for the benefit of the environment and the economy. Liquefier installation at the SNC-UmU is planned in 2025.

SNC offers services in form of access and support on all levels. Advanced users can request remote access, whereas less experienced users are offered support for experimental design and set-up, data acquisition and downstream analysis.

SNC has 12 highly qualified staff scientists, all with PhD titles, covering a broad range of expertise. Two of these work integrated with CBCS and PPS. Staff turnover is inevitable – staff scientists have moved on, e.g. to academic careers or positions as application experts in industry and have been replaced by new co-workers. Swedish universities cannot compete with salaries but are competitive in offering permanent staff scientist positions and an attractive working environment. In this context, the research infrastructure environment provides rich opportunities for competence development through varying degrees of challenging scientific problems and complexity in user projects or in technology development.

Table 1. NMR instrumentation at SNC

Location	Field	Specific use	Sample changer	Type
Gothenburg	400 MHz DNP-NMR	Co-owned by AstraZeneca and used for drug development		*Solid state*
Umeå	500MHz	HR-MAS for metabolomics on tissues, CP-MAS with automation for solids characterisation	Yes, with cooling	*Solid state*
Gothenburg	600 MHz	IVDr for metabolomics	Yes, with cooling	*Liquid state*
Gothenburg	600 MHz	Walkup system for organic chemists *Uniqeness*: 31P	Yes, with cooling	*Liquid state*
Umeå	600MHz	Cryo-MAS probe with superior sensitivity for biosolid, 5mm BBO cryo probe for broad range of nuclei	No Yes, with cooling	*Solid state* *Liquid state*
Gothenburg	700 MHz	Possibility to run 19F and 1H correlated experiments	Yes	*Liquid state*
Gothenburg	800 MHz	3mm TCI cryo probe with superior sensitivity	Yes, with cooling	*Liquid state*
Gothenburg	800 MHz	5mm TCO cryo probe with world leading 13C sensitivity	Yes	*Liquid state*
Umeå	850MHz	UF-MAS probe for 1H detection in solid state, 5mm DUL cryo probe for world leading 2H sensitivity, 5mm TCI cryo probe	No Yes Yes	*Solid state* *Liquid state*
Gothenburg	900MHz	3mm TCI cryo probe with superior sensitivity	No	*Liquid state*

The current user base (ca 100 PIs, 150 projects annually) has been stable with small variations. Important to note is that the number of publications with high impact factor has increased. In the coming years, we expect an increase as a result of a larger focus on ISB and possibilities for inside-cell NMR. We also anticipate an increased interest in metabolomics and FBS applications. Both nodes of SNC have stable strong local user bases combined with national users from all major Swedish universities. RISE and FOI are reoccurring users in Umeå while Gothenburg has a close collaboration with AstraZeneca and also provides access to SMEs and regional health care.

Continuous access is offered to expert users on submission of a standard application form (nmraccess.se), followed by a feasibility and SOP check. A call system will be applied for projects requesting extensive or advanced support, including ISB projects. Both feasibility (including control of SOP and test samples) and scientific quality will be reviewed by an expert panel.

A user fee model based on actual running costs (including rent but excluding depreciation) is applied. A set fee per sample is applied in metabolomics projects, based on the principle of actual running costs. A reduced fee can be applied provided that the project aligns with e.g. tech development or competence development projects.

The scientific environment at SNC comprises four PIs directly associated to the SNC (Karlsson, Director SNC-GU, Orekhov SNC-GU, Gröbner, Director SNC-UmU, Schleucher, SNC-UmU), two PIs (Burmann, GU, Wolf-Watz, UmU) and one adjunct professor at SNC-GU (Schantz, AstraZeneca) confer a broad expertise in NMR including structural biology in solution and solid state, relaxation, dynamics, metabolomics and DNP-NMR.

SNC-GU coordinates the national research infrastructure SwedNMR which includes local NMR core facilities at all Swedish universities. SNC-GU is also part of the EU Horizon 2020-supported research infrastructures PANACEA and R-NMR. Relevant publications are e.g.

- Unambiguous Tracking of Protein Phosphorylation by Fast High-Resolution FOSY NMR(2021) DOI: 10.1002/anie.202102758
- Atomic-level structure determination of amorphous molecular solids by NMR (2023) DOI: 10.1038/s41467-023-40853-2
- Targeting the Main Protease (Mpro, nsp5) by Growth of Fragment Scaffolds Exploiting Structure-Based Methodologies (2024) DOI: 10.1021/acschembio.3c00720
- Insights into the evolution of enzymatic specificity and catalysis: From Asgard archaea to human adenylate kinases. (2022) DOI: 10.1126/sciadv.abm4089
- Neutron reflectometry and NMR spectroscopy of full-length Bcl-2 protein reveal its membrane localization and conformation. (2021) DOI: 10.1038/s42003-021-02032-1

Development 2025-2028

A new level of analytical and structural methodology for small and/or complex solid and semi-solid bio-samples has become available by installing two cutting-edge solid-state NMR probes; the first ultrafast magic angle spinning (UF MAS up to 111kHz) probe in Sweden enabling sensitive ^{1}H detection in solids requiring only sub milligram sample amounts, and the first commercial MAS bio-solids cryoprobe worldwide for ^{13}C or ^{15}N detection from complex samples like biomembranes or even whole living cells at room/relevant temperature. The cryo-MAS together with the UF MAS and the DNP-NMR systems open completely new avenues in structural biology and life science, including inside cell NMR and in-situ structural biology. Investment plans include a 0.4 mm UF MAS probe.

The DNP-NMR technology boosts sensitivity manifold and addresses new user groups, e.g. for the study of nucleic acids in living cells or pharmaceutical industry where "NMR crystallography" is a game changer in studies of the active pharmaceutical ingredient (API). The DNP-NMR system, complemented with the first probe for ^{19}F DNP, a development project together with Bruker within PANACEA, gives new possibilities for e.g. the study of protein-ligand interaction inside cells.

All this has to be seen in the light of an increasing user demand for small but complex samples and advanced NMR experiments.

NMR provides dynamics information complementing the static picture provided by x-ray and Cryo-EM. Methyl group ^{13}C labeling is the preferred approach for the study of very large systems and molecular complexes using either liquid or solid state NMR. The methodology is available but requires expertise and unique instrumentation for efficient use and will be fully supported at SNC.

By making this unique top-level infrastructure, together with expert support, available at the national level, SNC creates new opportunities for breakthroughs in research and technology, in everything from structural biology to precision medicine.

SNC contributes strongly to the metabolomics platform. GU Metabolomics activity focuses on biofluids, with human serum, plasma and urine being the major matrices. One spectrometer is dedicated to delivering the highly standardized targeted Bruker In Vitro Diagnostics for research (IVDr) panel of metabolites, lipoprotein profile and composite inflammation markers for human serum and plasma. In addition, high field cryoprobe-equipped

spectrometers are used in less standardized matrices, e.g. microbial or insect extracts. The typical project workflow is to a large degree automated with an unbroken cold chain from sample prep to spectrometer sample changer. SNC-UmU focuses on MAS solid state metabolomics on solids and tissue samples. The NMR-based clinical metabolomics is strongly connected to the *Precision Medicine (PM)* capability.

For 2024-2026, active development in metabolomics methodology at SNC-GU is focused on extending current biobank sample quality assessment (doi.org/10.26434/chemrxiv-2024-5ppgz), sample preparation and analysis of highly variable matrices i.e. urine; doi.org/10.26434/chemrxiv-2023-8bmjg-v3, (*Figure* 5) and assessing new generation blood microsampling devices for metabolomics. Furthermore, we suggest developing 0.7 mm UF MAS NMR for metabolic profiling of tiny medical biopsies: ^{1}H, ^{13}C and ^{31}P -profiling is possible while reducing the NMR signal contribution from not relevant tissue around the small tissue part of interest (e.g. small prostate cancer loci, brain AD biopsies).

With regard to the *Planetary Biology (PB)* capability, we suggest to develop and apply solid-state NMR towards soil fertility (especially third world), green biology and environmental challenges, and new materials to combat climate change (e.g. battery/solar cell material, smart material etc.)

Plans for data handling and analysis 2025–2028 including how to make data open and FAIR. NMR based structure biology is a mature technique. Format and depositories for NMR data (bmrb) and structural data (PDBe) are well established and operate in compliance with FAIR principles. The same applies for data obtained in FBS through ELIXIR. Handling of Metabolomics data is generally regulated by the GDPR. We envision discussions on how to distribute anonymized data together with the SciLifeLab data centre.

Lack of analytical support for ISB has been a major bottle neck at SNC during 2021-2024. Locally embedded NBIS support, as already implemented at the Cryo-EM unit, focusing on the use of NMR data in structural biology and inclusion of AI in NMR is required. Such embedded support together with the ISB project coordinator function, already described, would greatly enhance the capability of SNC.

User training is continuously provided either on request or as part of projects. SNC has organized an annual international workshop for PhD and postdocs in NMR-based structural biology since 2008.

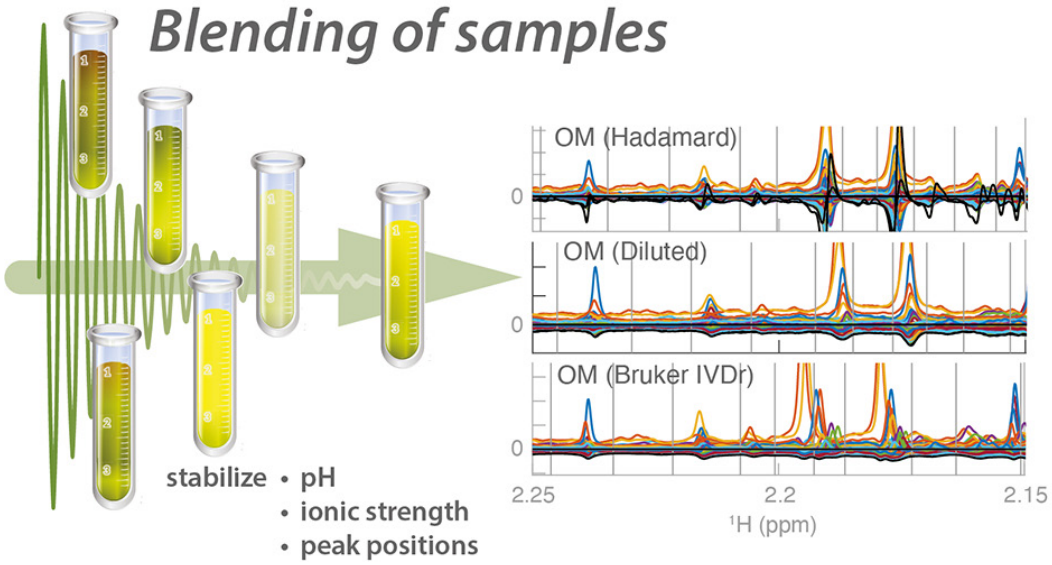


Figure 5. Blending of samples improves NMR metabolomics data quality in complex matrices.

Structural Proteomics

The structural proteomics unit (SP) at Lund University provides access to *cutting-edge equipment and expertise*, for analysis of protein interactions and conformational dynamics. The unit provides full service for all aspects of structural proteomics, including project planning, sample preparation, data collection and data analysis. Hydrogen Deuterium Exchange (HDX-MS), Crosslinking Mass Spectrometry (XL-MS) and *de novo* sequencing services are well established and available to all users.

The unit has a total of 3 FTEs, *2 PhD staff scientist and 1 professor* all with 20 years of experience in the field. In addition, we have 1 staff scientist with a master's in molecular biotechnology engineering and one part time bioinformatician. We offer a unique competence development for our staff, unfortunately this also makes them highly attractive for the pharmaceutical industry. Together with the Lund Node SciLifeLab director, were we have 2 seats (SP and BioMS) on the management board, we are now pushing for the implementation of a career ladder and access to university courses for our infrastructure staff, this will be very beneficial for keeping and attracting competent and younger talent.

The SP unit became a part of the SciLifeLab, ISB platform in June 2021. Access to the SciLifeLab network has been a *major milestone for our unit* and the open and dynamic collaboration with all different stakeholders involved in the ISB platform has been extremely beneficial, as the SP *user base increased from < 10/year (before 2021) to >30 projects/year*, also the amount national users has increased. During the period 2021-2023 we have seen a big overall improvement in the quality of publications from our user base, as well as the size and scope of projects. Through participation in the ISB platform a number of scientific and developmental milestones could be achieved during the current funding period (2021-2024), spanning both methods and instruments (*Figure 2*). This has facilitated our ability to support the science community, during the covid pandemic the SP unit could respond very quickly and provide antibody epitope mapping services. Over 30 antibody epitopes on the spike protein were mapped for 3 different projects with lead times < 1 month/project, resulting in several publications; doi.org/10.1016/j.immuni.2022.12.005, doi.org/10.1126/sciadv.abm0220, doi.org/10.3389/fimmu.2021.808932

Based on the current demand we foresee a continued increase in our user base for the period 2025-2028. A key driver to an increased userbase will be the many synergies available within the ISB environment. This will be addressed by developing even more integrated service offerings, together with our ISB (and affiliated) partners, and advertise these to the Swedish research community through the SciLifeLab network.

Each project is evaluated and prioritized according to preset criteria: feasibility, relevance, national importance and considers potential synergies with other infrastructure units or partners. This ensures fairness and the flexibility to meet societal demands.

The user fee cost model in the field of structural biology is complicated as many services are quite subsidized or even free (e.g. synchrotron beamtime) and currently SP implement a similar model as Cryo-EM where the user pays a fixed heavily subsidised price/day, covering approximately 20% of our yearly budget. It is foreseeable that during 2025-2028 the cost for data analysis might have to be increased or in some cases redirected to NBIS.

The unit is part of the *national infrastructure for biological mass spectrometry* (*BioMS*) that is coordinated from LU and funded by the Swedish Research Council. SP is co-localized with 3 other mass spectrometry groups (>20 MS instruments at site) at the biomedical center in Lund with 3 directly associated PI's. We also collaborate with key players from the structural biology, infection medicine and genomics research community of which many are situated in neighboring corridors. This ensures a dynamic cutting-edge environment with many opportunities for development of novel services. As an example, one of our successful projects during 2023 came from the research environment at Clinical Genomics (LU) and went to antibody production and evaluation of functional assays at the SciLifeLab, DDD platform. Subsequently SP contributed to the project by deducing the specific Ab epitopes related to mode of action (the results are now patented by a startup company, Lead Biologics). Other examples from the local environment in the publications below;

- A human monoclonal antibody bivalently binding two different epitopes in streptococcal M protein mediates immune function, doi.org/10.15252/emmm.202216208
- Pseudouridine-modified tRNA fragments repress aberrant protein synthesis and predict leukaemic progression in myelodysplastic syndrome, doi.org/10.1038/s41556-022-00852-9
- (p)ppGpp controls stringent factors by exploiting antagonistic allosteric coupling between catalytic domains, doi.org/10.1016/j.molcel.2021.07.026

For 2025-2028, *the unit will develop* several new and improved services. The development of new services will be targeted to 1) meet the demand of the scientific community and 2) be focused on services that benefit the integrative aspect off the platform. We will 2024-2025 establish one of the first automated front-end sample preparation platforms for XL-MS worldwide. This has the potential to greatly improve and expand

the use of XL-MS e.g., facilitate Cryo-EM and NMR structural elucidation of large protein complexes, as well as enable dynamic studies from controlled time course experiments. This development will then be further refined and connected to the in-situ structural biology scheme of the ISB platform over the period 2025-2028. We will also develop *workflow/pipelines for new services related to analysis* of; intact/native protein, antibody-drug conjugates, optimization of protein constructs for X-ray crystallography, oligomerization state of proteins and stoichiometry of complexes prior to analysis with Cryo-EM and other structural biology techniques (*Figure 6*).

A data analysis and IT handling framework developed by BioMS is in place as of 2022. This system automatically fetches generated data from instruments and provides workflows for analysis and reports. While heavily geared towards clinical proteomics, we have during 2023 started implementation of analysis pipelines for structural proteomics. It is desirable that the ISB platform can get access to NBIS resources for development of novel analysis solutions, e.g. to ensure that all our users can get access to AlphaFold solutions and assistance with MD simulations based on integrative data acquired at different ISB units and associated partners. Considering the current access to modern lab automation and state of the art instrumentation we could probably generate at least 50% more data, the *through-put limiting step* is in data analysis and reporting to our projects. This will be addressed in the period 2024-2028 by internal development and in collaboration with NBIS (candidate unit LU-fold, would strengthen this immensely) to implement data analysis and report generation pipelines that can free up staff hours for experimental work. From experience within clinical proteomics, it is apparent that machine learning can be very efficient and powerful for analysis of MS data, and efforts are underway to translate this to structural proteomics.

In this respect it will also be beneficial to investigate how data integration from different techniques could improve knowledge generation for our (ISB) joint projects.

Collaboration with healthcare and other organizations. Structure-function relationships is fundamental for understanding disease and mode of action for any treatment. SP's local environment means that we have a close natural connections to the clinical research, e.g. through BioMS(LU) and we receive partial funding from Region Skåne. We have had quite a few projects that originate from the clinical side of infection medicine and immunology. During 2021-2023 we have also performed research contract projects for small start-ups, and analysis services for other governmental agencies (FOI, SMILE). These collaborations are of major importance for us and will hopefully increase with additional outreach efforts and improvements to the legal framework associated.

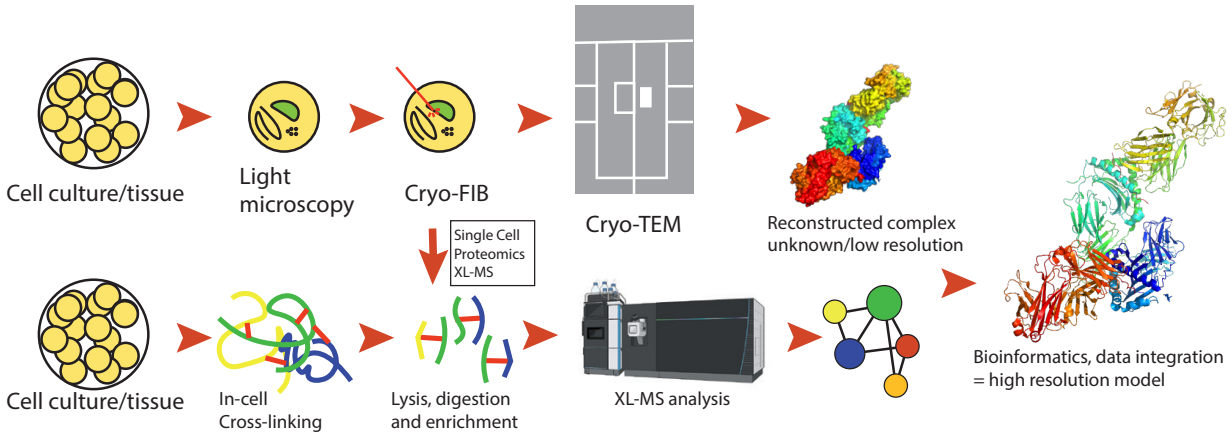


Figure 6. New pipeline in Structural Proteomics envisioned to complement *in-situ* studies with CryoEM/NMR.

E15 Macromolecular Crystallography Support and FragMAX

Expertise, technologies, and services offered / Competence/background of staff and plans for keeping/attracting competent staff scientists

LP3, PSF (Macromolecular Crystallography Support – MX) and FragMAX are three existing research infrastructures that offer an array of protein crystallography services to their user communities. We propose adding them to the ISB platform to coordinate their activities and make their services available to non-expert users through SciLifeLab. LP3 and PSF will contribute their expertise ranging from protein crystallization to structure determination, whereas FragMAX will specifically support X-ray based compound screening efforts at the CBCS/CBGE platform.

For MX, the services include crystallization screening and optimization, synchrotron data collection (e.g. at MAX IV), structure determination, and data deposition to the Protein Data Bank (PDB). Deposition at the PDB *makes data open and FAIR* and is mandatory for any publication – the same applies also for FragMAX (*Figure 1*). For MX support we propose a *unit of two facilities* with long-track record in MX service and support: LP3 (Protein Production Platform, Lund, LU, lu.se/lp3) and PSF (Protein Science Facility, Stockholm, KI, ki.se/en/research/protein-science-core-facility-psf. Both units are *fully equipped* for high-throughput MX services for protein and protein-ligand complexes, including lipid cubic phase MX for membrane proteins and their current services are described on the respective homepages. LP3 and FragMAX share laboratory space and equipment, and LP3 aids FragMAX with protein crystallisation experiments. Moreover, LP3 offers services and support in *neutron macromolecular crystallography* (NMX). PSF offers HTP crystal *imaging systems with web-interface* and access to sample mail-in SAXS *services and data analysis* via Diamond Light Source. Having all these techniques and expertise available cannot be done at one node but requires a unit with complementary technologies for a joint effort. Additionally, two nodes in MX support ensure continued service in case of instrument failures or staff absence. We have staff in place with long experience in MX and services for non-expert users. Together, the units are staffed with 2.3 FTEs, equaling 2.65 MSEK per year. In addition, equipment worth many millions, running costs, rent and user fees represent further counter-financing.

FragMAX provides X-ray fragment screening and high-throughput protein-ligand X-ray structure determination services at the BioMAX beamline at MAX IV Laboratory. This is accomplished through innovative workflows, automated X-ray data collection, robotics, a data management system, and high-performance computing. The facility can be accessed by academic and industrial user groups through the MAX IV user program and Industrial Relations Office, respectively. However, prospective users need to have expertise in protein crystallography since they need to provide a suitable crystal system and are responsible for final structure refinement, PDB deposition and dissemination. The facility is funded through the BioMAX operational budget and employs 2 FTEs to support the growing academic and industrial user program.

To keep and attract staff, we will 1) Push for the development of new career tracks for infrastructure personnel within host universities and at a national level. 2) Work for our services to be sustainable on long-term basis. 3.) Maintain close contact with the academic research community as well as national and international infrastructures in the field to ensure recruitment of highly qualified personnel scientists when necessary and provide in general a supporting and stimulating work environment.

User base (current and expected 2025–2028)

In 2022-2023 we counted about 20 service projects yearly for non-experts. LP3 also supported all FragMAX campaigns 2023. Going forward we expect at least 30 *projects* 2025 with the number growing as the awareness of this service will spread. In addition, we provide instrument access and user training to around 20 groups per year. FragMAX completed 12 projects in 2023. Two-thirds of the projects were from academia and one-third from industrial users. Sweden and Scandinavia accounted for 80% of FragMAX users (e.g. LU, SU, FOI). FragMAX plans to increase throughput by 50% in 2024 and aims to reach up to 20 projects per year by 2028.

Procedure for prioritization of projects

Here will be a difference if a user wants MX support or to access the FragMAX screening platform. For MX support, projects in synergy with other technologies within the ISB platform or aiming for downstream use of FragMAX will be given priority. Other than that, priority is based on first come first served. Projects are checked for feasibility and in the case of lacking capacity will be prioritized by the MX management group for scientific value. Applications aiming at later using FragMAX will be given priority.

FragMAX will remain accessible to expert users through the MAX IV user program, but we will allocate enough beamtime for collaborative FragMAX/CBCS projects. Since these projects require a significant amount of medicinal and computational chemistry support by the CBCS unit within the CBGE platform, it is therefore recommended to use the same prioritization process for fragment-based projects that is already in place at CBCS. This includes a twice-yearly project support call in which potential users submit an application, which is then evaluated by an external project prioritization committee. The primary evaluation criteria are scientific impact and

novelty of the project proposal. Based on the resulting priority, resources will be allocated from FragMAX and CBCS to carry out the project jointly.

User fee model

User fees must cover at least running and material costs and any further costs are subsidized. In our budget, we propose to cover about 20% of the total costs with user fees. User fees will be harmonized between both facilities in MX support. Non-academic users pay full cost coverage. Non-academics have access to crystallization services but all requests for beamtime at MAX IV and other synchrotron facilities must be negotiated with the respective industrial liaison office. FragMAX, in line with other European screening centers, does currently not charge academic users for facility access and beam time. MAX IV will continue to provide beamtime free-of-charge for academic users as an in-kind contribution to the planned unit, but given the extended support provided to CBCS projects, fees will be applied using the CBCS costing model. Industrial users need to access FragMAX through the MAX IV industrial relations office and are not eligible to apply directly via SciLifeLab.

Scientific environment / collaboration with industry, healthcare, and other organizations

Both MX-support platforms provide laboratories, equipment, and workforce to the national infrastructure Protein Production Sweden (PPS). LP3 provides laboratories, equipment, and workforce to FragMAX MAX IV and ESS ERIC. PSF manages the PReSTO project being incorporated into the NBiS platform.

Other scientific connections and synergies

National: Lund University Pandemics and Alertness Collaboration, Swedish NMR center, SciLifeLab node Lund, Cryo-EM Sweden, CBCS, DDD.

International: EATRIS, P4EU, DeuNet, Diamond Light Source, ESRF, DESY, BESSY. FragMAX has shared PhD students with Jens Carlsson (UU) and Pål Stenmark (SU). It has a long-standing partnership with Nick Pearce (SciLifeLab DDLS Fellow at Linköping University) and cooperates with other European X-ray fragment screening centres and the European Protein Data Bank (PDBe). All three platforms also works with Swedish and international companies.

Examples of joint publications e.g.

LP3, FragMAX, ESS

- doi.org/10.1016/j.jsb.2018.12.009
- doi.org/10.3390/ijms21197375
- doi.org/10.1039/D1CB00135C

PSF, BioMAX, PReSTO:

- doi.org/10.3390/ijms2408753
- doi.org/10.3389/fmicb.2023.1216799

Complementarity and synergistic opportunities within and across SciLifeLab platforms

With 10^4 crystal structures added yearly to the PDB, crystallography remains the leading method for achieving structural information on proteins and their interactions. Adding MX support and FragMAX to the ISB platform would allow its users to reach all structural biology technologies from a single access point at SciLifeLab with coordinated use of multiple techniques as needed. This will allow for a better integration of SciLifeLab and MAX IV Laboratory, two of Sweden's largest research infrastructures, ensure that resources are optimally allocated and advanced instrumentation is available to a broad spectrum of scientist, as well as offering new training opportunities for the next generation of researchers. The increased use of micro-crystals in emerging technologies such as MicroED, XFEL, and SSX further underlines the strength and development possibilities of MX within the ISB platform. The PSF-MX facility collaborates in microED projects with Cryo-EM facilities at SciLifeLab, KI, and SU. MX will continue to contribute to the Pandemic Laboratory Preparedness (PLP) capability as was done dring Covid-19 pandemic where both facilities contributed to solving structures of SARS-CoV-2 proteins. LP3 is a local unit in the SciLifeLab Lund node and will closely work together with its other units. PSF will have a leading role in involving PReSTO in NBIS from 2024, provides MX services to EUbOPEN, SciLifeLab CBCS/DDD projects, and collaborates with the Cryo-EM node in Stockholm.

The proximity of MX support and FragMAX will create the opportunity to develop flexible access models that take advantage of new methods developed at MAX IV and support non-expert FragMAX users that are not requiring advanced chemical biology support from CBCS. Further, FragMAX and SNC provide complementary fragment screening and validation services that are fundamental to chemical tool development. Having both methods accessible through a single access point will be a unique constellation. Further, improved coordination with biophysical methods at ProLinC will extend the available biophysical toolbox for researchers.

Plans for development including new technologies/service offerings 2025–2028

Within MX support, this includes detection of microcrystals smaller than 1 µm for microED and MicroMAX, for which an application of a Formulatrix SONICC imager is prepared, and further development of

methods for NMX. FragMAX will develop new screening modalities that take advantage of the new technical abilities of the MicroMAX beamline.

Current bottlenecks

National SciLifeLab usage will require additional staff of 1 FTE each per site in Lund and Stockholm (2 in total) for MX support and 1 FTE for FragMAX.

Training offers

We contribute to undergraduate and graduate teaching and do user training at instruments. This will continue, as well as contributions to ISB courses/PhD schools and PRISMAS PhD program.

Plans for organizing and incorporating the operation into the platform

Establishment of a joint management group for MX support consisting of Dr. W. Knecht, Dr. M. Moche, and Dr. T. Nyman. They will engage in regular meetings with Dr. T. Krojer in an extended management group for the Macromolecular Crystallography (MX) Support and FragMAX as a whole.

In contrast to MX support which offers broad crystallographic support to anybody, FragMAX will serve as a structural biology support node for CBCS/CBGE projects within SciLifeLab, while remaining available to academic and industrial users through the MAX IV user program (see above). FragMAX will provide CBCS scientists with end-to-end structural biology support and deliver 3-D information on protein-ligand interactions. There will be a regular scientific exchange between scientists from the two platforms and shared usage of laboratory information systems for streamlined flow of information. The unit does not require any additional development or investment; however, it needs an additional staff member (1 FTE) who will oversee all steps from feasibility assessment to purified protein sourcing, crystallization, crystallographic compound screening, and structure refinement. Additionally, FragMAX will collaborate closely with the MX support node to improve access to MAX IV via the existing Block Allocation Group system, which includes use of the FragMAX facility.

Budget

Funding of 3 FTE is necessary, as stated under bottlenecks above for national service and development activities. For MX, additional operational costs will be fully covered by user fees, which we expect to cover approx. 20 % of total costs. More information on page 198.

Concluding remarks

In summary, the proposed MX support & FragMAX infrastructure will be

1. unique and cutting-edge – there is no other academic facility offering national MX services with a multitude of techniques, including X-ray aided fragment screening in Sweden.
2. accessible and relevant to many national users with focus on non-expert users.
3. highly synergistic with other strategic research and infrastructure initiatives.
4. embedded in excellent research environments.
5. utilizing the best expertise available.

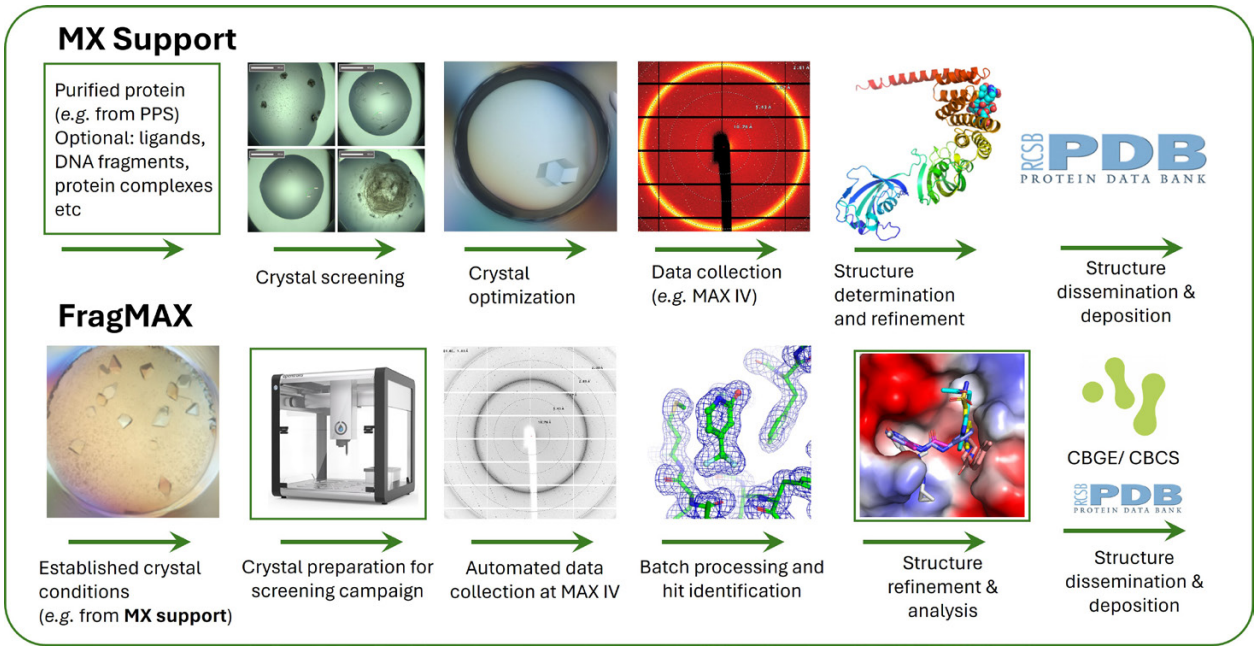


Figure 1. The work flow of services offered by MX Support / FragMAX. The unit provides a uniquely strong, cutting edge, broad service in macromolecular crystallography and screening.

E16 ProLinC

Current operations – funding, expertise, technologies and services offered

ProLinC (Protein folding and Ligand Interaction Core Facility at Linköping University) (liu.se/en/research/prolinc) is currently operating as the LiU core facility for biophysics as well as Swedish node in the Horizon-2020 Molecular-Scale Biophysics Infrastructure MOSBRI (mosbri.eu/partners/). ProLinC offers a dedicated biophysics facility with staff scientist support, making it possible for SciLifeLab users to fully explore their protein/complex properties and refine conditions for downstream applications as part of the ISB pipeline described above, as well as explore the nature and dynamics of its interactions. The facility is jointly funded by user fees and LiU central support. Through MOSBRI, ProLinC offers transnational access (TNA) as well as joint research activities (JRAs) in protein/peptide molecular studies and its applications within cancer, regenerative medicine and neurodegenerative and infectious diseases. When needed, our research environment allows for sample preparation and analysis according to Biosafety level 3 (BSL-3).

To enable structural characterization of high-complexity and difficult-to-target samples, carefully designed biophysical characterization is of essence. Integrating ProLinC into SciLifeLab will thereby open up ISB resources to novel users, who may be new to Structural Biology but need such data to expand scientific frontiers in their field. Where structural data is already available, ProLinC support will add functional data related to interactions, dynamics and stability, as well as enhance the use of other ISB structural nodes such as FragMAX and Structural Proteomics. Supported by VR, ProLinC has developed biophysical maturation strategies for biomedical projects intended for neutron and x-ray scattering, and will establish this further in collaboration with ESS, an ISB external stakeholder.

ProLinC provides added value to SciLifeLab by facile one-stop access to complementary and advanced biophysical techniques jointly with experts in their use, which creates unmatched sample and experiment synergies. In the same lab, ProLinC holds a near-complete set of instrumentation for the biophysical analysis of proteins and their interactions, which enables parallel investigation of essential properties such as oligomerisation, interactions, stability and conformational change, with complementary verification by at least two independent methods (*Figure 1*). Several of our instruments offer the possibility to screen many conditions and/or libraries with little sample consumption.

As a SciLifeLab service, ProLinC will offer user-performed expert-supported access to SPR, CD, SEC-MALS, DLS, ITC, DSC, nanoDSF, MST and fluorescence (microscopes, plate readers, fluorimeters). Access includes expert advice on instrument setup and data analysis as well as instrument training as defined by MOSBRI, with same user fees as for LiU users. Access to Benchtop SAXS (low intensity beam for radiation-sensitive samples), AUC, Stopped-Flow and the BSL-3 facility will only be available for selected cases and under expert guidance. ProLinC at LiU also houses two NMR spectrometers (Bruker 500 MHz, Bruker 600 MHz with cryoprobe and IVDr) which can currently be made accessible via SwedNMR for specific cases (joint analysis with biophysics, BSL-3 proteins). Mail-in access will be available at extra cost depending on staff availability.

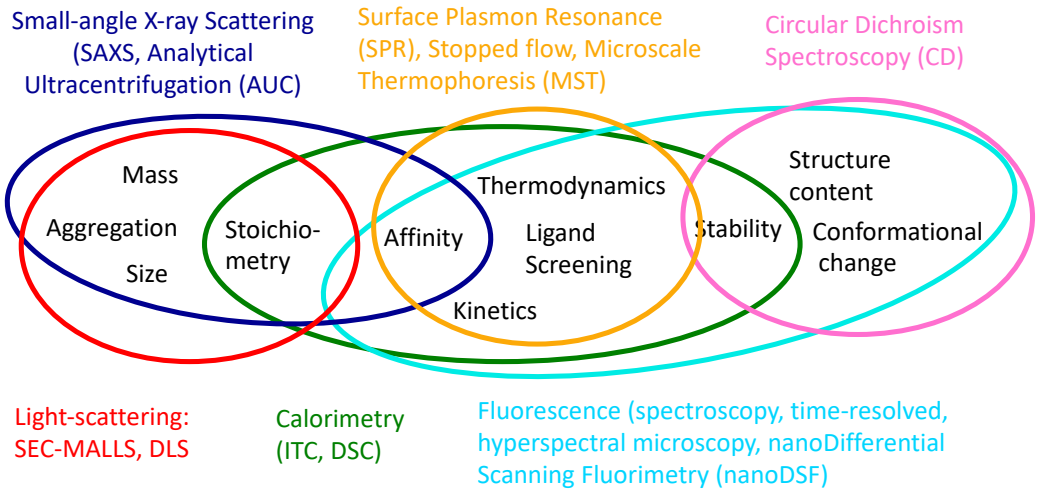


Figure 1. Biophysical techniques and expertise offered at ProLinC. Each technique area is indicated with color, with corresponding circles encompassing major biophysical properties that they can address. For detailed description of instrumentation, please see the ProLinC home page.

Scientific environment

ProLinC holds 5 affiliated expert PIs with grants of excellence (VR, CF, ERC and more) in Protein Science, Chemistry and/or Applied Physics at the LiU Technical Faculty (Daniel Aili, Eleonore von Castelmur, Per Hammarström, Peter Nilsson, Maria Sunnerhagen). ProLinC is a core facility for Life Science at LiU, with close links to LiU interdisciplinary strategy areas Cancer and Neuro, LiU Wallenberg Centre for Molecular Medicine (WCMM) with a medical technology profile, and LiU technical faculty profile area Life Science Technology (an aspiring "VR profilområde"). Through its users, ProLinC staff and experts collaborate with over 60 PIs in medicine, science and technology in Sweden and abroad. In international competition with >65 European core facilities, ProLinC gained its position as the Swedish infrastructure node in the Institut Pasteur-run MOSBRI infrastructure in 2022 and collaborates closely with its 13 nodes (mosbri.eu), as well as with corresponding biophysics facilities in Toronto (SickKids SBC facility) and Cambridge to provide excellence in instrumentation, management and user support (*Figure* 2). ProLinC full-time staff and Facility Manager Dean Derbyshire is an expert in biophysics and structural biology with both academic (PhD Cambridge University, postdoc MRC/LMB Cambridge) and industry background (15+ years in Medivir, UK and Stockholm) is well suited to cater to ISB and SciLifeLab user needs.

User base (current and expected 2025–2028)

During 2021-2023, ProLinC has hosted >200 research users. Out of these, LiU users from 16 PI groups included 101 PhD students, postdocs or researchers and »50 MSc Diploma students. Furthermore, we hosted external guided research users (1-2/group) from 21 Swedish PI groups (LU (3 groups), OrU(2), LTU (2), KI (5), KTH (2), Chalmers (1), GU (1), UU (1)) and abroad (U of Toronto (2), NTU Trondheim (1) and IRB Barcelona (1)). Added to this we hosted 11 MOSBRI users (each user stayed for 1-4 weeks and two came for repeat visits), and 6 users within four biotech contracts. Based on this external interest, we expect a >30% research user increase over 2025-2028 as a SciLifeLab node, counting both on-site users and mail-in projects (*Figure* 3).

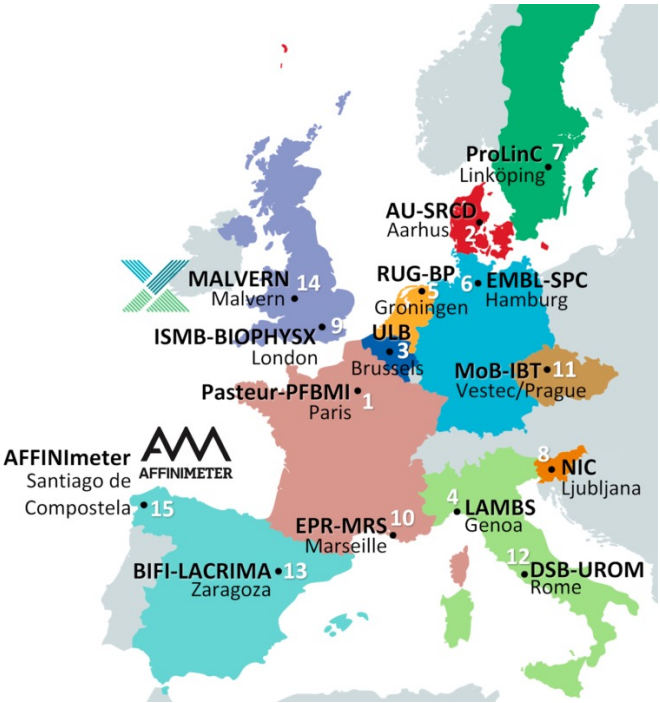


Figure 2. MOSBRI organization. The geography of the thirteen academic nodes of MOSBRI and the two company nodes. Multi-technique biophysics nodes include Pasteur-PFBMI (project leader), ProLinC, ISBM-BiophysX at Birkbeck, MoB-IBT in Prague, and EMBL-SPC in Hamburg located at the PetraIII syncrotron.

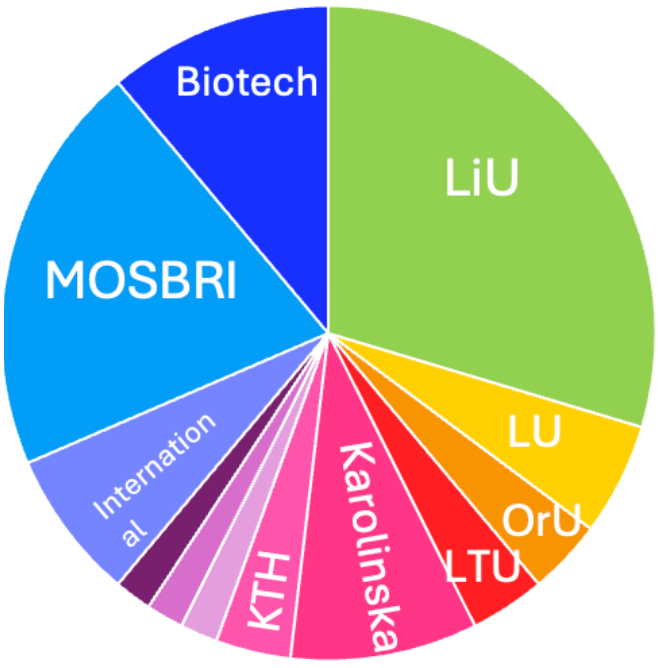


Figure 3. Distribution of PI groups using ProLinC. During 2021-2023, ProLinC was used by 52 PI groups and six companies as detailed in the main text; unlabeled sectors correspond to UU, GU and Chalmers with one PI user group each. Each PI group contributes equally to the diagram irrespective of size, users or number of visits.

Plans for organizing and incorporating the operation into the ISB platform

ProLinC is already a stand-alone biophysics infrastructure which facilitates its integration into the ISB platform. Well-established setups for user fees, project screening, user support, instrument booking and data reporting are in place, as are ProLinC Director, Facility manager, Management group, Steering group and Scientific Advisory Board. ProLinC takes part in monthly MOSBRI steering group meetings and is an external stakeholder in the SciLifeLab ISB since 2022. With increased SciLifeLab use, additional technical staff will need to be recruited as successfully done in the ISB StructProt/HDX facility at LU. Based on user demands, we foresee a need for novel instrument investments on the 1-5 MSEK scale, where SciLifeLab contributions will be applied for in separate calls.

To engage SciLifeLab users, and to demonstrate applicability of ProLinC within and beyond the ISB platform, we have prepared *novel user pipeline offers* (below), focusing on lines of investigation tailored to facilitate/enable the investigation of novel "difficult" targets by structural biology methods.

Protein quality control and buffer conditioning:

- monodispersity, folding, stability: extensive conditions screen w DLS and nanoDSF
- SEC-MALS, CD, DSC follow-up for selected conditions

Protein-ligand/peptide interaction: *affinities*, *stochiometry*

- MST and/or SPR (tailor-made surfaces available)
- Sample-dependent follow-up: ITC, fluorescence, CD, if needed AUC or SAXS
- Solution ligand affinity screening by SPR towards user-provided, CBCS, SNC and/or FragMAX libraries

Unstable protein characterization: IDPs, aggregating and/or unstable proteins/complexes

- fibrillation kinetics (fluorescence spectro/microscopy (hyperspectral, confocal, FLIM))
- multi-technique small-volume assays (nanoDSF, MST, DLS, SPR)
- direct sample transfer to structural characterization accessible within the ISB platform
- safety lab sample prep for proteinaceous pathogens (prions/amyloids) to selected users.

Complementarity and synergistic opportunities within and across SciLifeLab platforms

In a wider SciLifeLab context, ProLinC will be able to enhance studies at CBCS/CBGE by appropriate sample conditioning and small- molecule interaction affinity/stability screening, support Cryo-EM and ISB structure platform with protein control specifically dedicated to their needs and extend DDD biophysical and affinity screening using complementary methodologies. ProLinC is already supporting scientists active in in Precision Medicine, Pandemic Laboratory Preparedness and Planetary Biology (non-biomedical research) and collaborates with DDLS fellow Nicholas Pierce and Claudio Mirabello (DDLS) to provide essential data for AI-based protein structure and docking.

Taken together, integrating ProLinC as a unit will increase synergy and complementarity within and between SciLifeLab platforms, engage external stakeholders, attract novel users and further enable existing ones. Thereby, ProLinC will contribute to increasing the scientific value of the investigations pursued at SciLifeLab and, consequently, its overall impact on science and society as a whole.

Budget request

The different units of the ISB platform are already functional entities with documented track record of user support, providing access to unique instrumentation and excellent support. This is reflected in the budgets for the individual units, with running costs and FTE salaries. The contribution requested from SciLifeLab corresponds to a fraction of the total budget of each unit, and at the same time represents a good balance between university co-funding, funding from other external sources and user fees income. The strategic platform budget and budget for each unit is briefly commented below.

Platform Strategic Budget

The costs for the platform director and the coordination officer are described here. Together with 0.4 FTE for the ISB project coordinator function. This is a key function for the ISB platform in order to reach above serendipitous multi-technology application in user projects. The operations costs (350 kSEK) reflect the platform expansion with the ProLinC and the FragMAX/MX units; Operations costs cover e.g. platform strategy and operations meetings. Staff exchange between units has been successful in 2021-2024 and will continue 2025-2028. The cross-platform methodology knowledge is key for the successful platform development. Costs related to interactions with users, i.e. for the annuals user's meeting and the ISB session at the yearly SweProt meeting are included in the platforms operations.

Swedish NMR Centre

SNC receives support from external funding agencies in addition to a substantial university co-funding. The current funding scheme from the Swedish Research Council is guaranteed until 2026. The SciLifeLab unit funding 2024, 4 761 kSEK, accounts for 4 FTEs (of a total of 12 active FTEs at the unit). For the period 2025-2028 we request a unit funding of 6 760 kSEK, an increase equivalent to 1.5 FTEs. The increase is required to adapt to e.g. changes in OH costs and co-funding models. Funding of expensive equipment, 1 020 SEK, covers part of the depreciation for new probes and consoles. This funding is shown as constant for the period since investment in new equipment is under discussion. The total funding from SciLifeLab corresponds to 30% of the unit budget.

Structural Proteomics

BioMS recently received renewed funding from VR for the period 2025-2028. The projected SP budget is balanced for the period 2025-2028. The equivalent of two FTEs is requested from SciLifeLab.

Macromolecular Crystallography Support and FragMAX

LP3 has a budget until the end of 2026. The actual expected revenues until end of 2026 are presented. For 2027 and 2028 the assumption of continued support at the 2026 level is made. Salaries are calculated with a yearly increase of 3 %. The budget for whole LP3 is presented, currently (2024) 1.3 FTE out of this whole pot is allocated to support crystallography – see also below in MX support under Plans. For the proposed national MX support/service within ISB, LP3 requests SciLifeLab funding corresponding to 1 FTE 2025-2028.

PSF as a whole involves protein production, protein characterization, and MX. PSF is funded by the Karolinska Institutet and VR (for protein produciton within the national infrastructure PPS) and has in total 5 FTEs of which ~1 supports the MX platform. The VR funding runs until 2026. During 2024 PSF receives temporary funding of 0.3 FTE as project manager for the PReSTO project. For the proposed national MX support/service within ISB, PSF requests SciLifeLab funding corresponding to 1 FTE 2025-2028.

FragMAX is funded by the BioMAX beamline budget at MAX IV Laboratory. The budget includes 2 FTEs to support the academic and industrial user programmes, as well as to manage and develop the platform. FragMAX receives additional support from BioMAX personnel to ensure beamline readiness. Hence, the planned extended support for CBCS-related projects requires 1 additional FTE and a contribution for consumables. The cost of consumables will be recovered through user fees.

ProLinC

ProLinC and the biophysical characterization requires funding for one FTE. The unit costs are covered together with university co-funding and user fees.

Table 1. Integrated Structural Biology – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Platform Director	150	150	150	150	150
Platform Coordination Officer	200	200	200	200	200
Personnel 0 FTEs (2024) -> 0.40FTEs (2025–2028)	-	500	500	500	500
Operations	250	350	350	350	350
Sum costs (kSEK):	**600**	**1 200**	**1 200**	**1 200**	**1 200**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*600*	*1 200*	*1 200*	*1 200*	*1 200*
Sum revenues (kSEK):	**600**	**1 200**	**1 200**	**1 200**	**1 200**

Table 2. Structural Proteomics Budget

Costs	2024	2025	2026	2027	2028
Personnel 3 FTEs (2024) -> 3 FTEs (2025–2028)	3 181	3 300	3 430	3 560	3 560
Operations	1 200	1 500	1 500	1 600	1 600
Premises	320	350	350	350	350
Instrument depreciations	1 841	1 841	1 841	2 200	2 200
Sum costs (kSEK):	**6 542**	**6 991**	**7 121**	**7 710**	**7 710**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*2 588*	*2 588*	*2 588*	*2 588*	*2 588*
University co-funding	1 150	1 500	1 500	2 000	2 000
The Swedish research council (BioMS)	2 000	2 000	2 000	2 000	2 000
User fees	800	800	1 000	1 000	1 000
Sum revenues (kSEK):	**6 538**	**6 888**	**7 088**	**7 588**	**7 588**

Table 3. Swedish NMR Centre Budget

Costs	2024	2025	2026	2027	2028
Personnel 12 FTEs (2024) -> 12 FTEs (2025–2028)	11 232	12 100	12 100	12 100	12 100
Operations	6 230	6 230	6 230	6 230	6 230
Premises	3 810	3 810	3 810	3 810	3 810
Instrument depreciations	3 214	3 214	3 300	3 300	3 300
Sum costs (kSEK):	**24 486**	**25 354**	**25 440**	**25 440**	**25 440**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*4 761*	*6 760*	*6 760*	*6 760*	*6 760*
SciLifeLab instrument grant	1 020	1 020	1 020	1 020	1 020
University co-funding	12 199	11 050	11 050	11 050	11 050
The Swedish research council	2 414	2 414	2 414	2 414	2 414
EU	480	500			
User fees	3 600	3 600	4 200	4 200	4 200
Sum revenues (kSEK):	**24 474**	**25 344**	**25 444**	**25 444**	**25 444**

Table 4. Macromolecular Crystallography Support-LP3 Budget

Costs [1]	2024	2025	2026	2027	2028
Personnel 5,8 FTEs (2024) -> 6,8 FTEs (2025–2028)	7 100	8 259	8 689	8 950	9 218
Operations	1 200	1 400	1 470	1 544	1 621
Premises					
Instrument depreciations	150	150	150	150	150
Sum costs (kSEK):	**8 450**	**9 809**	**10 309**	**10 643**	**10 989**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)		1 200	1 236	1 273	1 311
VR	2 453	2 467	2 498	2 500	2 500
LU	4 459	4 459	4 459	4 500	4 500
User fees	1 700	1 950	2 145	2 360	2 595
Sum revenues (kSEK):	**8 612**	**10 076**	**10 338**	**10 633**	**10 907**

[1] All inclusive LU overhead except depreciations

Table 5. Macromolecular Crystallography Support-PSF Budget

Costs [1]	2024	2025	2026	2027	2028
Personnel 1 FTE (2024) -> 2 FTE (2025-2028)	1 200	2 400	2 472	2 546	2 623
Operations	400	500	600	600	600
Premises	500	500	500	500	500
Instrument depreciations	-	-	-	-	-
Sum costs (kSEK):	**2 100**	**3 400**	**3 572**	**3 646**	**3 723**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	-	1 200	1 236	1 273	1 311
University co-funding	1 200	1 600	1 536	1 573	1 611
SciLifeLab NBIS (30% project manager PReSTO 2024)	400				
User fees MX services	500	600	800	800	800
Sum revenues (kSEK):	2 100	3 400	3 572	3 646	3 723

[1] Costs include OH

Table 6. FragMAX Budget

Costs	2024	2025	2026	2027	2028
Personnel 1,5 FTEs (2024) -> 3 FTEs (2025–2028) 100%	1 726	3 290	3 355	3 421	3 489
Operations	230	350	370	390	410
Premises	769	1 384	1 409	1 435	1 462
Sum costs (kSEK):	**2 724**	**5 024**	**5 134**	**5 246**	**5 360**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)		1 605	1 583	1 562	1 542
University co-funding	2 201	3 219	3 301	3 384	3 468
User fees		200	250	300	350
Sum revenues (kSEK):	**2 201**	**5 024**	**5 134**	**5 246**	**5 360**

Table 7. ProLinC Budget

Costs	2024	2025	2026	2027	2028
Personnel X FTEs (2024) -> X FTEs (2025–2028)	758	1 500	1 600	1 700	1 800
Operations	550	650	600	700	750
Premises (covered by OH)	196	323	330	360	383
Instrument depreciations	900	900	800	900	900
OH	317	465	660	720	765
Sum costs (kSEK):	**2 721**	**3 838**	**3 990**	**4 380**	**4 598**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)		1 200	1 200	1 200	1 200
University co-funding	1 000	1 000	1 000	1 000	1 000
LiU user fees	600	625	650	675	700
Other academic user fees	260	338	400	425	450
Industry user fees	250	300	350	400	450
Horizon2020 MOSBRI [1]	600	400			
MOSBRI follow-up			400	700	800
Sum revenues (kSEK):	**2 710**	**3 863**	**4 000**	**4 400**	**4 600**

[1] Aug 2021-July 2025; only TNA-related part
[2] Calls not yet announced





Chemical Biology Consortium Sweden (CBCS) Unit in Umeå. Photo: Mikael Wallerstedt

Chemical Biology and Genome Engineering Platform

Basic Information

Platform Director: Anna-Lena Gustavsson, Karolinska Institutet

Platform Co-Director: Bernhard Schmierer, Karolinska Institutet

Platform Coordination Officer: Bernhard Schmierer, Karolinska Institutet

Platform vision: Empower transformative breakthroughs in life science and human health by co-developing and guiding projects from unbiased discovery to detailed mechanistic insight

Platform mission: Deliver cutting-edge services in chemical biology, chemical proteomics, and CRISPR technology to explore the function of biological systems through chemical and genetic perturbation

Location of Units

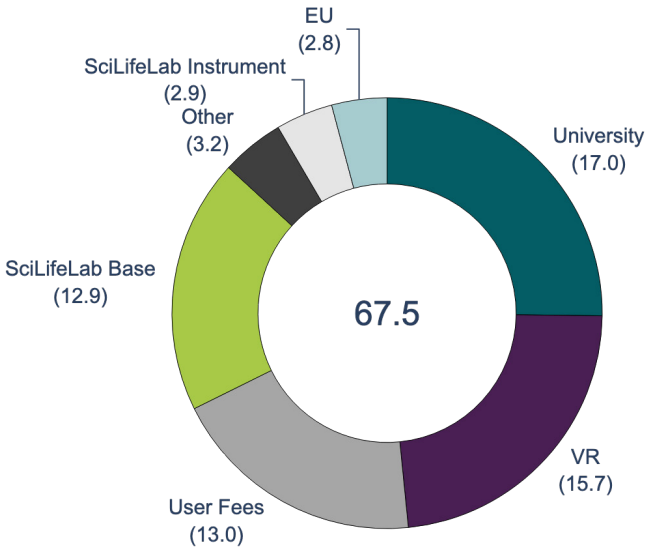


SciLifeLab Funding

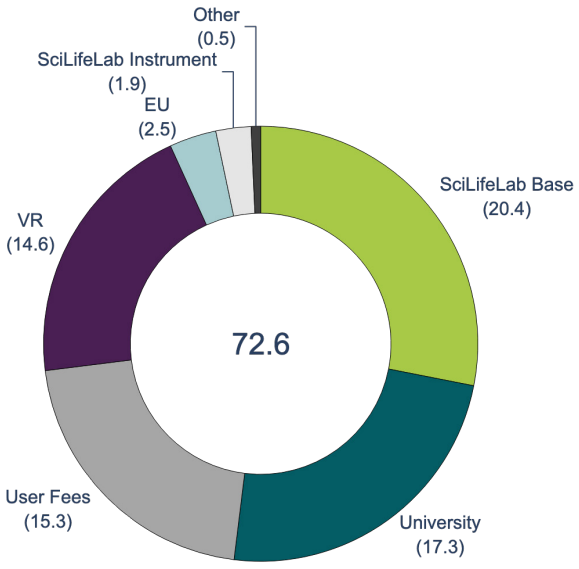
Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Chemical Biology Consortium Sweden	6.2	7.2
Chemical Proteomics	2.6	3.6
CRISPR Functional Genomics	3.3	4.5
Automated Patch Clamp Profiling – CBCS LiU node*	0.0	0.5
Morphological Profiling – CBCS UU node*	0.0	1.0
Cell and Gene Therapy Core*	0.0	2.5
Platform Strategic Funding	*0.8*	*1.1*
Total SciLifeLab Funding	**12.9**	**20.4**

*Proposed to be included in the platform

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E17 Chemical Biology and Genome Engineering

What we do

Positioned as a cutting-edge research hub, CBGE specializes in chemical biology, chemical proteomics, and CRISPR technologies, integrating these disciplines through collaborative endeavors. By perturbing biological systems for investigative and innovation purposes, the platform acts as a catalyst for basic research, precision medicine, and planetary biology. Noteworthy examples include the identification and validation of novel disease pathways and the initiation of drug discovery efforts, with applications extending beyond human health. The platform has been purposely built to provide seamless access to both genetic and small molecule-based tools for various research objectives. Additionally, CBGE offers the necessary technology and expertise to provide detailed mechanistic insights at a molecular level. It is only through such comprehensive understanding that discoveries can effectively deliver innovation for the benefit of society.

The possibility to choose the most appropriate tool for each biological perturbation experiment is the norm in our operations, whether this means interference on a genetic, transcriptional or protein level. We recognize how academic and industry standards continuously evolve – and that complementary use of tools is required to thoroughly address a biological question. In our vocabulary we talk about "targets" – commonly equating to the specific DNA, RNA or protein molecule we aim to identify or perturb. Examples include the use of CRISPR to specifically introduce a disease-driving mutation in a human gene and then assessing whether this perturbation changes the response to known small molecule-based inhibitors. Scientific advancement now requires the use of such improved reagents and complementary technology for proper confirmation of new findings. This is where the integration of the three complementary platform units *Chemical Biology Consortium Sweden* (CBCS), *Chemical Proteomics* (*ChemProt*) and CRISPR *Functional Genomics* (*CFG*) comes into play. Collectively, the units create the possibility to generate relevant models, apply these for identification of bioactive molecules within compound libraries, and assess whether the observed events represent what we set out to achieve, or whether they are the consequence of modulating multiple unintended biological pathways. Notably, this combination of CBGE methodologies and offerings is commonly available within pharmaceutical industry, but not in academia, and CBGE's service is unique within Europe.

Platform organization

With 24 FTEs, CBCS is the largest unit. CBCS is also a national infrastructure funded by the Swedish Research Council (Vetenskapsrådet, VR) and since 2022 has expanded from its two main nodes at KI and UmU to four additional nodes (UU, GU, LU, LiU). Staff expertise ranges from biochemistry and cell biology to medicinal and computational chemistry - many with PhD's and/or experience from the pharmaceutical industry and international academic screening labs. *ChemProt unit* is co-funded as a national infrastructure by VR's BioMS initiative and has five staff scientists (four PhD level) combining expertise in general and chemical proteomics, LC-MS engineering, sample preparation and data analysis. *CFG unit* employs five PhD-level scientists with postdoctoral experience in functional genomics and molecular cell biology, as well as one MSc-level scientist.

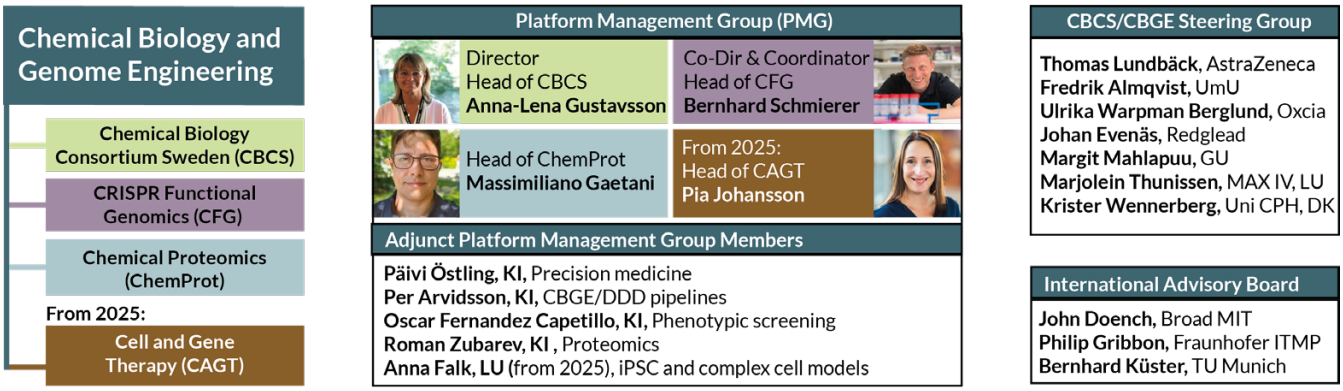


Figure 1. Platform organization and governance. The platform consists of three units, the Chemical Biology Consortium Sweden (CBCS), CRISPR Functional Genomics (CFG) and Chemical Proteomics (ChemProt). From 2025 onwards, inclusion of a fourth unit, a LU core facility, the Cell and Gene Therapy Core (CAGT), is proposed. The platform is managed by a Platform Management Group supported by an International Advisory Board and a National Platform Steering Group. The Steering Group can take decisive action for the VR-funded CBCS unit; its role for the platform level is advisory.

Infographics: Statistics and Metrics for Chemical Biology and Genome Engineering Units

Chemical Biology Consortium Sweden

Read more: Webpage, Publications Database

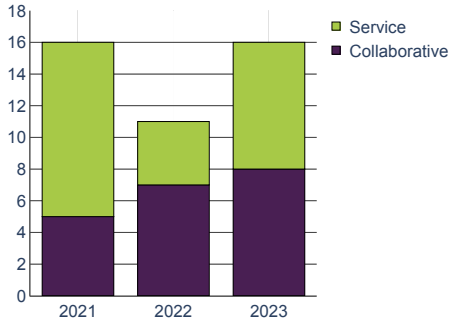
Basic Information

HU: Anna-Lena Gustavsson, Stina Berglund Fick
Host University: KI, UmU, GU, LiU, LU, UU
SciLifeLab unit since: 2013
FTEs: 24
PSD: Erik Chorell

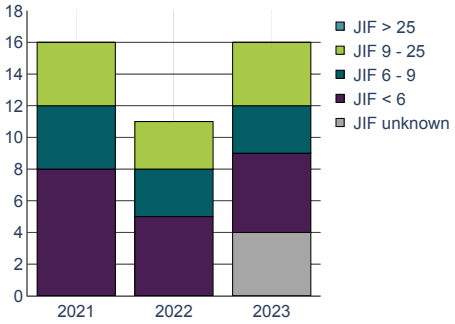
Funding 2023 (kSEK)

SciLifeLab: 6000
Other: 24025
User Fees: 6000

Publications by category

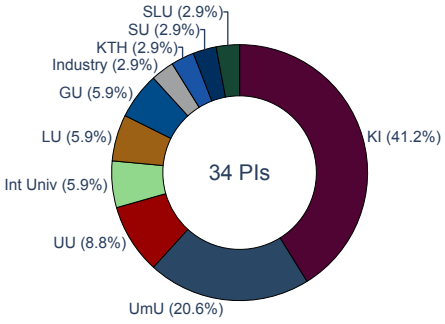


Publications by JIF

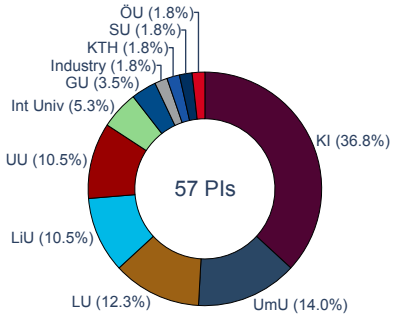


No. of Tech Dev Publications 2021 - 2023: 1

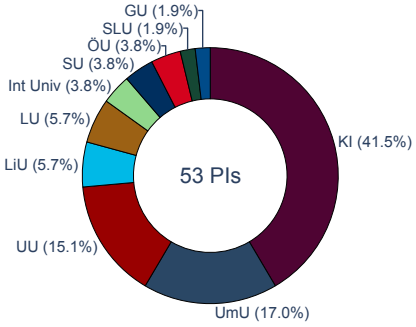
Users 2021



Users 2022



Users 2023



Chemical Proteomics

Read more: Webpage, Publications Database

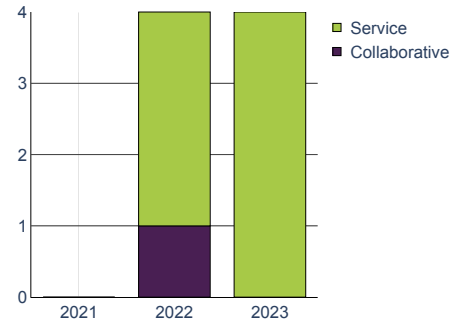
Basic Information

HU: Massimiliano Gaetani
Host University: KI
SciLifeLab unit since: 2017
FTEs: 4.5
PSD: Roman Zubarev

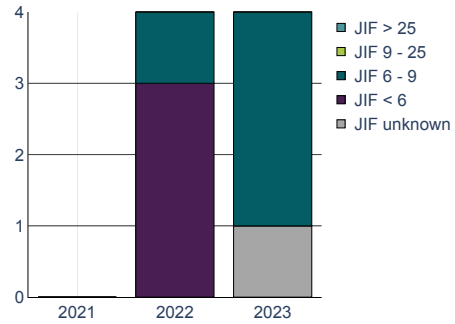
Funding 2023 (kSEK)

SciLifeLab: 2500
Other: 5368
User Fees: 2794

Publications by category

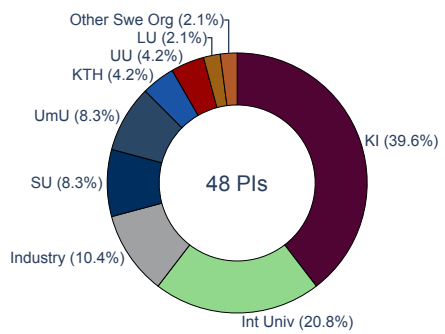


Publications by JIF

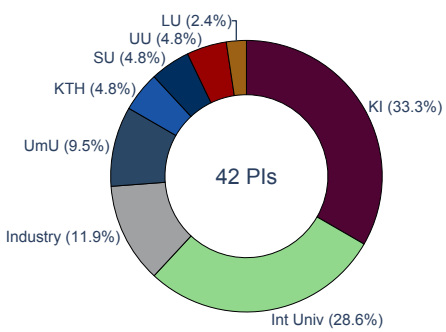


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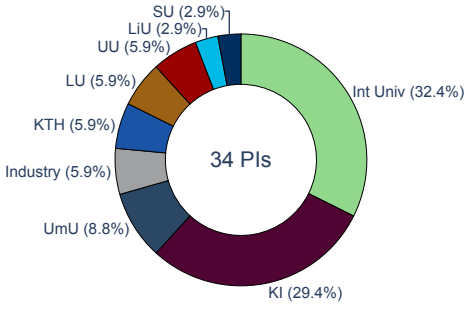
Users 2021



Users 2022



Users 2023



CRISPR Functional Genomics

Read more: Webpage, Publications Database

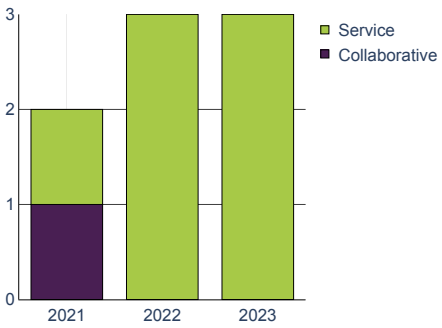
Basic Information

HU: Bernhard Schmierer
Host University: KI
SciLifeLab unit since: 2017
FTEs: 7

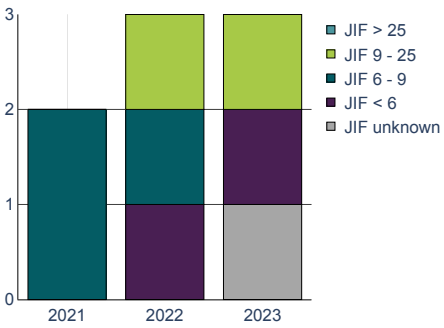
Funding 2023 (kSEK)

SciLifeLab: 3200
Other: 700
User Fees: 3000

Publications by category

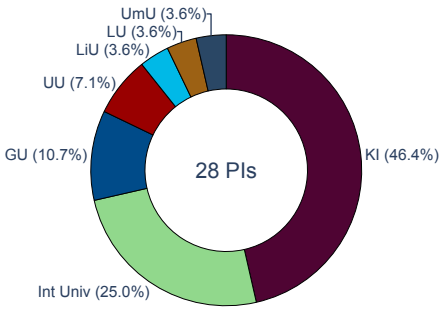


Publications by JIF

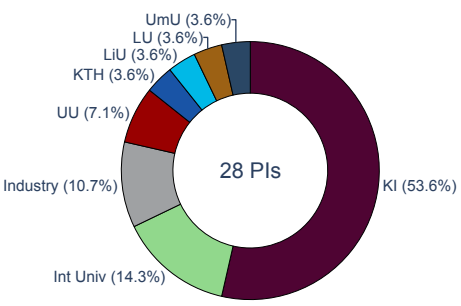


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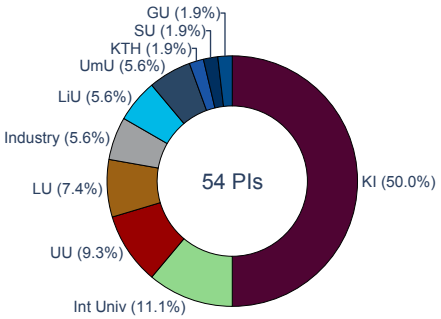
Users 2021



Users 2022



Users 2023



Chemical Biology Consortium Sweden (CBCS)

Expertise, technologies, and services

CBCS strives to act as a catalyst for research groups in Sweden to explore biology using small molecules. Currently, CBCS has two SciLifeLab-supported nodes at KI and UmU, both offering assay development, high throughput screening (HTS), and enabling chemistry. The KI node houses the Compound Center, which stores and manages ~350,000 small molecules. We have started to expand our services to disease and compound profiling, infectious pathogen screening, virtual screening, and automated patch clamp profiling. Several nodes also offer open access to automation and instrumentation.

User base

Current users (around 50 PIs per year) come from all major Swedish universities, although KI is heavily represented, and most users are active in the field of biomedicine. User interest in CBCS services has grown steadily, especially in our new service offerings. We foresee an increase in the overall user base as the new nodes and associated services have just launched their activities. We also expect new users referred by EU-OPENSCREEN, a large European infrastructure consortium, with CBCS as the Swedish national node. Compound Center fulfills around 500 compound requests per year, and supports Drug Discovery & Development (DDD) platform with compound logistics and storage.

Scientific environment and collaborations

All CBCS nodes are in active research environments, with many nodes co-localized with research groups. CBCS-UmU is strongly connected to the research community at the Umeå Centre for Microbial Research (UCMR). The CBCS KI node is part of several larger EU-funded projects including REMEDi4ALL, and an associated partner of EUbOPEN. Several nodes have contributed to successful grant applications with Swedish researchers. Most recently the KI node was part of a granted EIC Pathfinder application led by Filipe Pereira, LU, which is an extension of a previous screening project. CBCS has a collaboration agreement with AstraZeneca (AZ) that enables CBCS users to access AZ's phenotypic screening collection for target identification. This has been successfully applied in five screens since 2018. CBCS also interacts with Swedish Biotechs, such as Sprint and Pelago. CBCS has a strong international network. Both CBCS-KI and UmU as approved EU-OPENSCREEN partner sites for screening and medicinal chemistry. In addition we draw on expertise from our platform advisor, Phil Gribbon, Fraunhofer ITMP, Hamburg.

Current training and plans for 2025–2028

CBCS provides an online course in basic HTS and we continuously train users in our labs. CBCS personnel contribute with lectures in organic/medicinal chemistry and chemical biology, as well as with demonstrations of screening automation. CBCS co-organizes a PhD course in cancer drug discovery. We usually have several students a year performing summer work or Master's projects in our labs. CBCS contributes regularly to co-organizing scientific meetings (e.g., ELRIG Cell-based Screening, and the European Chemical Biology Symposium).

Table 1. Example projects, methodologies and output

Service type	Model type	Project description	Comments	Publications
Assay dev & screening	target-based	biochemical strategy to NUDT15 inhibitors	malachite green readout, screened diversity set	s41589-020-0592-z
Assay dev & screening	phenotypic	targeting Glioma using iPSC models	viability readout, screened both known drugs and diversity set; current platform MOA project	MS in preparation
Assay dev & screening	phenotypic	Co-culture of pancreatic cancer cells with cancer associated fibroblasts	imaged based assay, screened both known drugs and diversity set, current platform MOA project	10.1101/2022.03.11.483991v1
Assay dev & screening	plant-based phenotypic	tobacco BY-2 cells reporter assay for autophagic flux	dual-luciferase assay, screened focused set, followed by structure based virtual screen and target-based full screen	10.1104/pp.19.00647
Computational chemistry	virtual; binding mode prediction	docking studies to LarS	docking of hit compounds; basis for the virtual screening of commercial space	10.3389/fmolb.2023.1264773
Enabling chemistry	synthetic chemistry	synthesis of tool compounds	new compounds for TRAST spectroscopy	10.1088/2050-6120/acfb59
Disease profiling	phenotypic	Breast cancer patient-derived cells	Concentration-response testing of clinically relevant drugs	10.1073/pnas.2209856120

Data handling

Data from all CBCS nodes is stored in a MySQL database hosted by SUNET. The CBCS user agreement stipulates the conditions for publication of results, ensuring open access. In addition, CBCS aims at assisting users to deposit curated data in interoperable formats in data repositories (such as ChEMBL). We are striving for reference datasets and annotated datasets comprising images from e.g., phenotypic screens, which we want to deposit in open access repositories, such as FigShare from the Data Centre at SciLifeLab.

Current bottlenecks

Address chemical biology and drug repurposing in advanced cellular models. With the increased interest from user to screen and profile compounds in relevant model system, including iPSC organoids, and patient-derived material, rather than in cell lines we see need to enhance our capabilities and expertise to ensure the optimal support of user projects.

Resources in chemoinformatics. With the launch of virtual screening services, we see an increase demand for resources that we cannot currently meet. In addition, there are increasing amounts of publicly available data that can be used to complement our internal findings. Here, we see a need for the development of tailored ML and AI workflows and in the future, we anticipate the need for specific large language models for CBCS internal use, as well as for users. This also includes improved chemoinformatics for hit to lead activities, and the alignment of these to future services with the offerings from the ISB platform.

Support of data-driven strategies for MoA and drug repurposing. Both drug repurposing and MoA studies can leverage publicly available datasets or integration of existing multimodal datasets. CBCS currently cannot effectively provide these resources.

Publication delay. Analysis of our project portfolio (since 2010) shows that it takes on average 5 years from project start to publication. These long lead times make calculating impact and KPIs challenging.

Plans for development including new technologies and service offerings 2025–2028

CBCS suggests expanding the screening and profiling repertoire at the node in UU and LiU. These are formally nodes in the VR-funded infrastructure, which do not currently receive SciLifeLab funding. This is discussed in the separate section below.

In addition, CBCS has identified the following areas for development to positively impact the quality and reproducibility of user projects:

1) *Enabling chemical biology studies in advanced cellular models.* This includes increased use of genome engineering, iPSC and patient-derived models for phenotypic screening, profiling and validation studies, and improved readouts for complex cell systems, such as high content imaging. This has the potential to provide high quality chemical starting points for users. To implement this we will work closely with CFG and CAGT, as well as the precision medicine capability.

2) *Strengthening chemoinformatics from hit to lead.* With the recent advances in virtual libraries and "SAR by catalogue", we aim to strengthen our resources in virtual screening and predictive modeling. This will not only enable us to meet user demand in virtual screening, but also generate AI-driven predictive models for future projects. We see there is a major opportunity to join forces with the Integrated Structural Biology (ISB) platform (the Swedish NMR Center, the proposed new units ProLinC and FragMAX) to provide improved workflows from hit to lead in fragment-based screens with chemoinformatic and chemistry support. Two pilot projects are ongoing, and we will build on these studies.

3) *Data-driven strategies for MoA elucidation and drug (re) positioning.* We see that there is a need to provide users with more efficient, data-driven methods for mechanism of action and drug repurposing studies. Here, we will develop improved workflows for analyzing data from curated compound sets, integrating multimodal data, and implementing AI solutions. We envision that the resources in 2 and 3 could come from one additional FTE with a bioinformatic/chemoinformatic background.

Chemical Proteomics (ChemProt)

Expertise, technologies, and services

ChemProt supports projects in target deconvolution and MoA elucidation, most commonly downstream of phenotypic screening or other phenotype-based assay. ChemProt offers orthogonal technologies using unbiased, deep, and high throughput proteomics on lysates, intact cells, tissues, or bodily fluids. Unlike other methodologies that rely on cellular responses over extended periods, chemical proteomics identify drug-specific interactions and mechanisms in the first hour of treatment.

The most requested service today is the Proteome Integral Solubility Alteration (PISA) assay recently developed by ChemProt. ChemProt has continuously improved and optimized PISA to integrate it with other proteomics profiling methods and to allow miniaturization of cellular models down to those used in precision medicine (primary cells, iPSCs, organoids, etc). Regarding throughput and sensitivity, the PISA assay is one of the most effective technologies for target deconvolution, allowing detection and quantification of solubility changes of up to 10,000 proteins across several biological replicates. ChemProt offers optimized experimental design for PISA-based target deconvolution, allowing inclusion of many experimental conditions, such as different compound concentrations, treatment times and cell models, as well as compound analogues in statistically relevant number of biological replicates. ChemProt provides full support for data analysis and visualization, including publication quality figures. Tailored PISA workflows are optimized for identifying enzyme protein substrates. ChemProt is one of two Swedish nodes for Hydrogen/Deuterium Exchange Mass Spectrometry (HDX-MS), and has the most advanced and fully automated technological platform for optimal control of time and temperature, with extreme reproducibility and sensitivity. HDX-MS maps and characterizes binding sites not only in protein-small molecule interactions, but also in protein-protein, and protein-peptide interactions (e.g. for antibody epitope and paratope mapping). Moreover, HDX-MS is applied to monitor conformational changes and to study the effects of mutations and misfolding, as well as for biosimilar characterization.

Table 1. Services offered at ChemProt

Service	Application
Proteome Integral Solubility Alteration (PISA)	Solubility changes upon compound treatment
Time-resolved expression proteomics	On its own or integrated with PISA (total versus soluble amount of protein)
Expression proteomics combined with FITExP or ProTargetMiner database analysis	Compare expression changes with known proteome signatures of anticancer molecules
High throughput RedOx Proteomics	RedOx changes in Cys-peptides and proteins
Affinity-proteomics with engineered probes	Identification of interactions using chemically engineered probes
Analysis of post-translational modifications	phosphoproteomics, etc.
FT-IsoR-MS for isotope composition	biomedicine, archaeology, environmental biology
Hydrogen/Deuterium exchange Mass Spectrometry (HDX-MS)	Binding site mapping and characterization of drug-target or protein-protein interactions

User base

The ChemProt unit supports 30-40 users per year, depending on the size of the projects. A similar trend is expected in the coming years. ChemProt uses are served on a first-come first-served basis, where industrial users are charged full cost and have lower priority compared to academia.

Scientific environment and collaborations

ChemProt closely collaborates with the research group of the unit's Scientific Director, Roman Zubarev, KI. Some of ChemProt's staff are shared with this research group, and methods developed are directly adapted by ChemProt and rolled out as new services. ChemProt has many collaborative projects with international universities in, amongst others, the US, Canada, China, Netherlands, UK and Germany. As part of the National Infrastructure for Biological MS (BioMS), ChemProt is in regular contact with other MS labs in this consortium (KI, LU, Chalmers and GU). Within SciLifeLab, ChemProt has strong interactions with other MS-based units at the CPI, ISB, and Metabolomics platforms. A recently procured new generation MS instrument with the unique integration of Orbitrap and TOF technologies for increased sensitivity, proteome depth and high throughput, is a joint investment with the CPI Platform.

Current training offerings and plan for 2025–2028

ChemProt co-organizes the annual Janeiro-na-Madeira International School of Proteomics and participates in teaching within and outside KI by giving lectures. ChemProt trains both local and international PhD students for instance within the ALLODD project, a collaboration between 13 academic and industrial organizations with the aim to train a new generation of scientists to exploit the concept of allostery in drug design. Special training is offered to expert MS users for using instruments, and to other researchers for sample processing.

Current bottlenecks

ChemProt provides a range of powerful technologies for target deconvolution, which are often applied in combination. The integration of data obtained from different orthogonal proteomic methods remains challenging, and on-site expertise is needed, but not currently available. From 2025, ChemProt is facing a decrease of BioMS funding by around 1.3 MSEK, which makes recruitment of on-site expertise challenging.

Plans for development including new technologies/service offerings 2025–2028

ChemProt is continuously expanding the range of services and is currently developing 1) a new method for target identification and binding site identification based on partial digestion of proteins; 2) affinity/activity-based chemical proteomics with probes engineered at CBCS 3) hybrid temperature and solvent-PISA; and 4) PISA and PISA-Express workflows for protein degraders such as PROTAC's. A special emphasis will be placed on single cell chemical proteomics for drug target engagement in single cells and single cell proteomics compound profiling by expression proteomics; as well as on contributing to the platform's joint compound profiling efforts by high throughput expression proteomics. Conditional to funding, a staff scientist with bioinformatic expertise will be recruited to develop methods for integration of data obtained within the unit, but also in other units of the platform.

Data handling

All data is stored on KI servers, as raw file and analyzed data. Full data analysis and reports are provided, shared with the PIs by email or using "Nextcloud". This tool is limited, and discussions with the Data Centre regarding adoption of SciLifeLab's Data Delivery System have been initiated. Raw data is stored on the server for at least five years and is uploaded to data repositories by ChemProt upon publication.

CRISPR Functional Genomics (CFG)

Expertise, technologies, and services

The CFG unit focuses on CRISPR-based, massively parallel genetic perturbations and on precision genome engineering in cell lines. Established in 2017, the unit's initial focus was on genome-wide, pooled CRISPR-Cas9 loss-of-function screens with barcoded guide libraries, an in-house development. Since the unit's inception, the range of services has diversified, and now includes:

- Creation of pooled, barcoded sgRNA libraries (100 – 150K guides), from design to lentivirus
- Creation of stable Cas9/Cas12/Cas13 expressing cell lines (lentivirus, piggybac)
- Genome-wide/custom CRISPR-Cas9 KO, inhibition and activation screens for protein coding genes, miRNAs, lncRNAs, and regulatory genetic elements
- Multi-guide synthetic lethality screens with Cas12a and RNA targeting screens with Cas13d
- Pooled screens with single-cell RNASeq readout
- Scanning mutagenesis with base-editors

From 2019-2022, CFG had dedicated KI core facility funding to perform precision gene-editing in cell lines. From 2023, these services are offered nationally under the SciLifeLab umbrella and are reported as such, which explains the increase in users in 2023. In precision gene-editing, CFG offers the following services in cell lines and embryonic stem cells (from strategy design to verified clonal cell lines):

- Knock-outs and deletions to study gene function and validate drug targets
- Creation of functional or pathogenic variants (point mutations, etc).
- Reporter cell lines for chemical or genetic screens (endogenous tagging by knocking in e.g. GFP, luciferase, inducible degrons, etc.)
- Strategy and reagent design for animal model generation

CFG's expertise is unique in Europe, and there is no other academic center which provides a comparable range of services or offers similarly advanced screening technology.

User base

In the screening space, CFG supports 20-25 unique research groups annually. Precision editing adds another 20-30 smaller projects per year. Demand has been stable at a high level over the last few years and is expected to remain comparable also in the future. Most users come from Swedish universities, but also from DK, NO, NL, UK, CZ, ES, IT, CH, US and from industry. The proportion of projects from KI has been decreasing thanks to active outreach, but is still high, reflecting the large number of research groups at KI working in relevant fields.

Scientific environment and collaborations

CFG is embedded in an exceptionally strong research environment in Biomedicum. As a stand-alone infrastructure, CFG is not affiliated with a research group, however holds its own VR project grant 2024-2026 to optimize nanoparticle-based delivery of the CRISPR machinery (collab. with Molly Stevens, KI and Oxford). CFG is a collaborator in four other granted projects from VR (2020, 2022, 2 x 2023), and one from the Norwegian Cancer Society (2023), underscoring the added value CFG creates. CFG regularly interacts with other SciLifeLab platforms: CFG has a pipeline together with ESCG for pooled CRISPR screens with single-cell transcriptomic readout, which is increasingly requested by users. In collaboration with Mats Nilsson's lab at SciLifeLab/SU, we are developing a novel method for pooled optical CRISPR screening based on sgRNA detection by hybridization rather than in situ guide sequencing (*Figure* 2, left). Once established, the ISS unit in the Spatial Omics platform will be instrumental in rolling out pooled optical CRISPR screens in 3D models and tissues as a new joint service. CFG sequences pooled CRISPR screens and other amplicons at NGI, and NBIS has helped create CFG's data reporting pipeline for pooled screens. Last but not least, CFG is establishing a pipeline

Table 1. Project examples to illustrate the range of CRISPR screens performed at CFG

Screening modality	Example project
lncRNAs	CRISPR-I/A for ~20,000 lncRNAs in prostate/breast/blood cancer
Non-coding elements	CRISPR-I on open chromatin regions, 120K guides in untransformed cells
RNA targeting	Cas13d screen to identify targetable loci in the SARS-CoV-2 genome
Synthetic interactions	Cas12a dual guide screen, 155 x 155 genes, 112K guide combos
3D models	Genome-wide CRISPR-KO screen in pancreatic organoids
Primary cells	miRNA-targeting CRISPR-KO screen in primary human keratinocytes

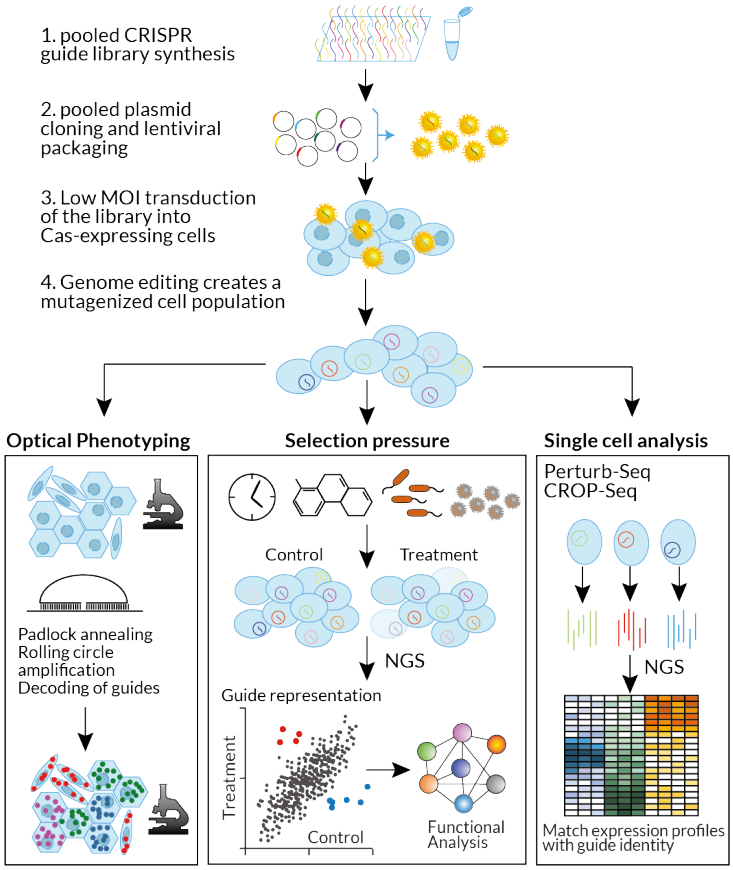


Figure 2. Pooled genetic screening modalities offered at CFG. By stably inserting one guide per cell into Cas-expressing cells, a mutagenized cell population is established. The integrated guide is used as a flag to read out a cell's perturbation.

Bottom middle. Standard pooled screen, where a selection pressure enriches for certain guides and depletes other guides from the population. Bottom left. Microscopic cell phenotyping and readout of guides directly on the microscopy slide by hybridization-based detection (in development in collab. with Mats Nilsson, SU).

Bottom right. Single cell readout of guide and transcriptome (Perturb-Seq, CROP-Seq). Collaboration with the Eukaryotic Single Cell Genomics unit (ESCG).

with DDD for the creation of custom HiBiT-based reporter cell lines for testing of protein degraders.

CFG's advanced technological know-how is also highlighted by a collaboration agreement with the AstraZeneca/Cancer Research Horizons Functional Genomics Centre (FGC) in Cambridge, UK for exchange of tools, protocols and data analysis pipelines. CFG acts as a testbed for gene-editing analysis kits developed by the local start-up Countagen AB, and for long ssDNA HDR templates for Moligo AB. CFG has created custom guide libraries for MOMA Therapeutics, Boston, US and is currently discussing a large screening project with Novo Nordisk. CFG regularly exchanges experiences with other academic core facilities in DK, BE, NL and UK, and is part of the EU-funded REMEDi4ALL initiative to accelerate drug repurposing, the EU COST action GenE-HumDi (Genome Editing for the treatment of Human Disease), and an international academy/industry network on CRISPR screening. Through CFG's advisor, John Doench, Broad MIT, we have our finger on the pulse of the latest developments.

Current training and plans for 2025–2028

The unit participates in graduate teaching (MSc and PhD-level) with lectures and lab project mentoring. In the last four years, CFG has hosted two Erasmus exchange students and five visiting scientists from SE, NL, BE and DK. In May 2023, CFG organized "CRISPR as a research tool", a two-day conference with top international speakers and more than 150 participants from all over Europe, including many PhD students, which hopefully will become a recurring event. In addition to this "reportable" teaching activities, CFG teaches and advises graduate students and researchers on a daily basis. These activities will continue during the next funding cycle.

Current bottlenecks

Funding for precision editing. General demand for precision editing services is high, and the expertise at CFG is crucial for the entire CBGE platform for model system generation. There is currently no dedicated funding for these services, which is increasingly problematic.

Publication delay. CFG contributes to the initial steps of a research project, either by performing a genetic screen for unbiased discovery, or by creating a cellular model system for research. Five years delay between data delivery and publication is common, and the number of publications reflects CFG's impact prior to 2019, when the unit had only 3 FTE's. Publications are thus expected to increase steeply in the coming years, as more projects initiated with support by CFG reach maturity.

Plans for development including new technologies/service offerings 2025–2028

In 2024, CFG will roll out a new screening service, base-editing scanning mutagenesis, for studying protein-protein or protein/drug interactions. Briefly, a gene of interest is tiled with a CRISPR guide library, and guide-proximal mutations are introduced by base-editors. The effect of these mutations can then be assessed in a workflow analogous to conventional pooled CRISPR screens. The method has been established at CFG including unpublished improvements, and we hope this will become a powerful genetic complement to biophysical binding site mapping. We will also complete implementation of optical pooled screens together with the In Situ Sequencing unit at the Spatial Omics Platform and Mats Nilsson's lab at SU, which will enable us to execute pooled screens in tissues and 3D models. For transcriptomic profiling of small compounds, which CFG will implement to complement the platform's MoA elucidation, please see the platform

section. Retaining and further developing CFG's expertise in precision gene editing is a major priority.

Data handling

Screening data created at CFG (< 1 TB/year) is non-sensitive and is stored in a "small storage" project at Uppmax, and as a local copy on a KI resource. A copy of raw data and analyzed data is delivered to the client at the completion of the project. All other data, as well as lab books are stored at a backed-up remote server at KI and the Electronic Lab Notebook (ELN). Data is delivered to clients using the webexport functionality of Uppmax. A formal data management plan is in development.

Platform development and key achievements 2021 – 2024

CBGE has established and applied multi-disciplinary pipelines in MoA elucidation. Selection of therapeutically relevant targets is a challenging task even for pharmaceutical industry, as witnessed by high clinical attrition, and even more so for academic researchers with limited resources. The same applies for thorough Mechanism-of-Action (MoA) elucidation, particularly for compounds where the molecular targets are yet to be defined. These challenges contrast with DDD's requirement for a deep understanding of a small molecule's MoA prior to further development and funneling into the innovation system. To help bridge this obvious gap, the CBGE platform was joined by the ChemProt unit in 2021, adding proteomics methods to the already existing chemical and genetic methods. By delivering orthogonal high-throughput datasets for data-driven discovery, the platform is now able to connect phenotypic effects with targets and molecular mechanisms, pushing MoA projects significantly further.

These positive developments are largely due to a recurring CBGE call for projects that can benefit from the contribution of all three units. The intent was to establish working routines between units while delivering more comprehensive data packages and improve publication quality. We refer to these projects as "Platform Pipeline Projects" (PPPs). In executing PPPs, the platform has gained valuable experience in collaborating, integrating and interpreting data. Four PPPs have hitherto been successfully concluded. One example is a project aimed at identification of novel therapeutic targets in medulloblastoma. CBCS identified a compound series that selectively kills iPSC-derived, malignant neuroepithelial stem cells, and ChemProt experiments and CRISPR screens converged on a biosynthetic pathway for the likely target of one of the compounds. Follow-up is now ongoing in the researcher's own lab.

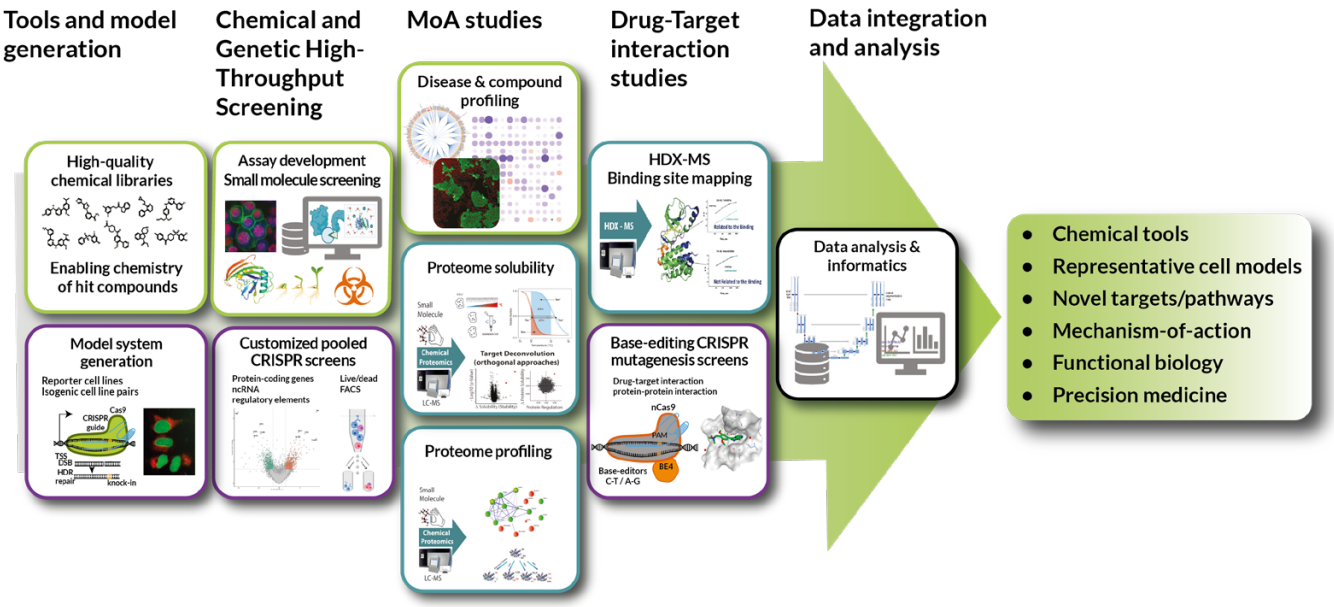


Figure 3. Combining chemical, genetic and proteomic workflows into discovery pipelines. Services from the individual units can be flexibly combined according to project needs. The chemical tools and cellular model systems created through our services can be used in chemical or genetic screens, which are followed up by MoA studies and characterization of drug-target interaction. Platform output ranges from chemical tools and representative cell models to identification of novel targets, active compounds, and insight into their MoA.

CBGE contributes to all SciLifeLab capabilities. Platform services are well-aligned with the SciLifeLab capabilities: CBCS is establishing drug libraries and automated screening methods for functional precision medicine, helped equip the BSL3 lab at KI for screening, enabling screening projects relevant to the pandemic laboratory preparedness capability, and has several ongoing and concluded projects outside of human health, supporting the planetary biology capability. ChemProt adopts, optimizes, and develops methods for miniaturization to better support projects in the precision medicine field with often limited material. Development of single cell chemical proteomics for target engagement will be a further milestone in this space. CFG contributes to precision medicine by creating disease-representative model systems by creating isogenic cell line pairs. Screening for cell-type specific vulnerabilities is another example. By creating fish reporter cell lines for environmental toxicology testing, CFG contributes to planetary biology, and by screening for SARS-CoV2 infectability, as well as SARS-CoV2 vulnerabilities, the unit has contributed to pandemic preparedness.

CBGE is a crucial node in the SciLifeLab infrastructure. The platform is tightly embedded in the SciLifeLab infrastructure, which is described in detail in the unit sections. CBGE has established a particularly strong alliance with DDD. The co-localization of these platforms allows the upholding of a strong infrastructure at SciLifeLab Campus Solna, where they share knowledge, lab space and equipment. Operations are intentionally kept separate to safe-guard support for basic research at CBGE, while DDD is strictly focused on the development of potential drug candidates. This setup has afforded several success stories that started within CBCS and matured at DDD before exit. Historically, about 50% of small molecule projects at DDD originated from CBCS. DDD in turn ensures that CBGE projects with a potential therapeutic application have a path towards commercialization

Platform plans for 2025-2028

To expand our cutting-edge services, meet upcoming demand, and diversify our toolboxes in target discovery and MoA elucidation, CBGE has identified four key areas that need strengthening: iPSCs and iPSC derived model systems; data rich compound profiling for MoA; drug repurposing as a cheaper and faster alternative; and fragment-based screening:

iPSCs, iPSC-derivatives and CRISPR-edited cell lines as models for chemical and genetic screening and hit evaluation. Most chemical and genetic screens at CBGE are currently performed in cancer cell lines, with few exceptions in primary cells and iPSC-derived models. Relevant models such as endogenous reporter cell lines, disease-recapturing models with purposefully introduced genetic changes, as well as iPSCs and iPSC-derived models are crucial for many phenotypic screening projects. CFG's precision gene editing capability covers this need in cell lines. To apply CBGE's toolbox to disease areas other than oncology however, inclusion of iPSCs and iPSC-derived model systems is desirable, and we propose to include a specialized new unit, the "Cell and Gene Therapy Core" at Lund Stem Cell Center (see below for details).

Data rich compound and disease profiling. *Morphological profiling* by Cell Painting is already implemented at CBCS-UU, but needs strengthening to contribute sustainably to high-content chemical screening and MoA elucidation. *Transcriptional profiling* of small molecules is not currently on offer, but will be implemented as a service at CFG, based on existing pipelines at NGI. The method will complement chemical proteomics and expression proteomics, to distinguish whether compound effects are transcriptional or post-transcriptional, and will be a valuable complement to morphological profiling, creating even richer, multi-modal datasets.

Drug repurposing is attracting considerable interest due to significantly reduced cost and accelerated time lines compared to *de novo* drug discovery (e.g. EU initiatives REMEDi4ALL, which the platform is part of, and RePo4EU). We propose to provide profiling of curated drug libraries in advanced disease models (e.g. primary cells, iPSCs, organoids, tumor spheroids) using high content imaging including cell painting. These services can uncover the functional taxonomy of a disease, connect disease characteristics with drug response, and identify effective drugs for specific patient groups. To best leverage our data and incorporate public datasets, the platform will increase chemoinformatics resources at CBCS for artificial intelligence and machine learning.

Fragment-based screening. Together with the ISB platform, CBGE proposes to strengthen services for fragment-based screening. We will build a pipeline starting from biophysical screening hits (SPR, NMR, X-ray, etc.) to improve "SAR by catalog" strategies. This will enable efficient exploration of the commercially available chemical space (in the order of 10^{10} structures), expanding hit fragments with the expertise of medicinal and computational chemists at CBCS.

Implementing these four key technologies will further align the platform offerings with SciLifeLab's precision medicine capability, strengthen interactions with the ISB platform, researchers at UU and LU, as well as at Max IV, and will allow CBGE to provide even more comprehensive services.

E18 Morphological Profiling and Automated Patch Clamp Profiling

To expand technologies within CBCS, we seek to support two specialized services existing at CBCS nodes: *Morphological profiling* at CBCS Uppsala, and *Automated Patch Clamp profiling* (APC) at CBCS Linköping. Both nodes are supported by VR and their host universities, are fully operational and and strategically aligned with CBCS. Our ambition is to qualify these as SciLifeLab nodes to secure long-term operations.

Morphological profiling

The CBCS-UU node became part of CBCS in 2022. The node specializes in large-scale Cell Painting for morphological profiling of cells (Phenomics), which is typically applied to compound profiling, disease modeling, mechanism of action (MoA) elucidation, and drug discovery/repurposing. The node currently offers compound profiling, disease modeling and screening services. In-house reference datasets provide insights into compound MoA. Since 2022, 12 users from UU, KI, SLU and UmU have been supported. Increased interest in these technologies and datasets qualified the node to receive UU SciLifeLab bridge funding for 2024, and growth to 25-45 users is expected in 2025-28. The CBCS-UU node is located at the Biomedical Centre (BMC) and is part of the Pharmaceutical Bioinformatics group headed by Ola Spjuth, who is also Head of AI at Data Center. The node is the only morphological profiling facility in Sweden. Funded by KAW-SciLifeLab COVID-19 research program, CBCS developed a method based on morphological profiling for efficient and rapid antiviral drug repurposing, highlighting the power of the approach and its relevance to the pandemic preparedness capability. Methods for cell painting on primary patient material are being developed, supporting the precision medicine capability. The billions of data points created per experiment are managed and analyzed on modern e-infrastructure with in-house developed data-driven methods. The node anticipates strong interaction with DDLS fellows, and will both provide infrastructure and procedures, as well as data for AI models.

Electrophysiology

CBCS-LiU became part of CBCS in 2022 and has one 48 well automated patch clamp instrument - the first high-throughput electrophysiology equipment available to the Swedish research community. One full-time senior APC electrophysiologist is dedicated to this equipment (funded by VR, LiU, and Elinder lab). Another scientist is responsible for the cell lines used (funded by user fees). CBCS-LiU offers all types of electrophysiological investigations possible on cell lines expressing specific ion channels, both voltage and ligand gated, and including drug screening and cardiac safety. Since instrument installation, CBCS-LiU has supported eight projects with users from four different universities. In September 2024, the node will arrange a two-day international ion channel conference (expecting 120-140 participants) with one session dedicated to APC and our CBCS unit. CBCS-LiU has an active list of 120 PIs in Sweden, who have shown interest in using APC technology and services in Linköping. The APC equipment is located at one of the strongest ion channel communities in Europe, with four independent research groups. Many ion channels, such as hERG, are known liabilities in drug discovery and need to be carefully monitored during lead optimization, thus creating synergies between CBCS-LiU and the DDD platform.

E19 Cell and Gene Therapy Core

Expertise, technologies, and services

The CAGT core is located at the Lund Stem Cell Centre at LU and provides nationally unique services (*Figure* 4). The unit was established in 2022 and has four technical staff managed by Head of Unit, Pia Johansson, and the Scientific Director, Anna Falk. CAGT is currently funded by LU and user fees.

Induced pluripotent stem cells (iPSCs) are used for drug development, diagnostics, tissue regeneration, and cell therapy, and have become an unprecedented resource for modelling of human disease (*Figure* 5). However, iPSCs are highly sensitive cells prone to pluripotency drift and genetic instability and require standard operating procedures

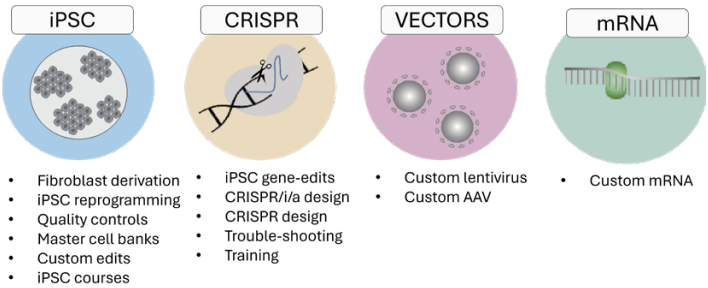


Figure 4. Services of the Cell and Gene Therapy Core.

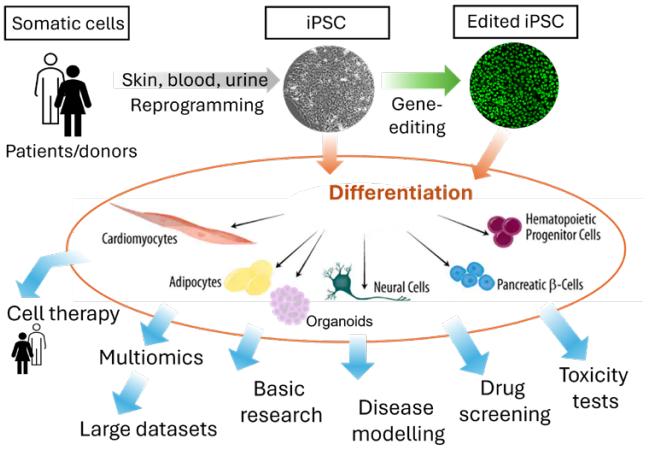


Figure 5. Reprogramming and application potential of iPSC, which provide unlimited starting material for deriving any human cell type for research or cell therapy.

and stringent quality control (*Figure* 6). The potential of the iPSC field expanded even further with CRISPR/Cas9-mediated gene-editing. The CAGT core offers several types of precision gene-editing; such as mutation insertion & correction, large deletions, gene knock-outs, gene reporters, protein tags and more. However, due to the sensitivity of the iPSCs, additional considerations are needed compared to other cell types before delivering the product to the customer.

User base and scientific environment

The CAGT core is currently (2023/2024) providing services to more than 45 distinct research groups, primarily to local researchers. At Lund Stem Cell Centre, CAGT is surrounded by >40 research groups, all studying different aspects of stem cell biology. CAGT receives scientific input and expertise from its local Scientific Advisory Group, consisting of three local PIs with extensive expertise, who support the core with expertise and advice on how to best align the services with the evolving needs of the community. Frequent interaction with Anna Falk's team boosts core development through method sharing, discussions and collaboration. The CAGT Core is also in connection with a novel iPSC based pre-GMP facility (in development), and is member in the COST-funded iPSC-core network CorEuStem (Pia Johansson is a work package co-leader) to ensure that the facility stays state-of-the art.

Complementarity and synergistic opportunities for CAGT in SciLifeLab

iPSC models have significant potential in diseases such as neurodegeneration, cardiovascular disease, liver disease, etc. To harness this potential, chemical or genetic screens in iPSCs and derivatives require professional support in creating, differentiating, and quality controlling these

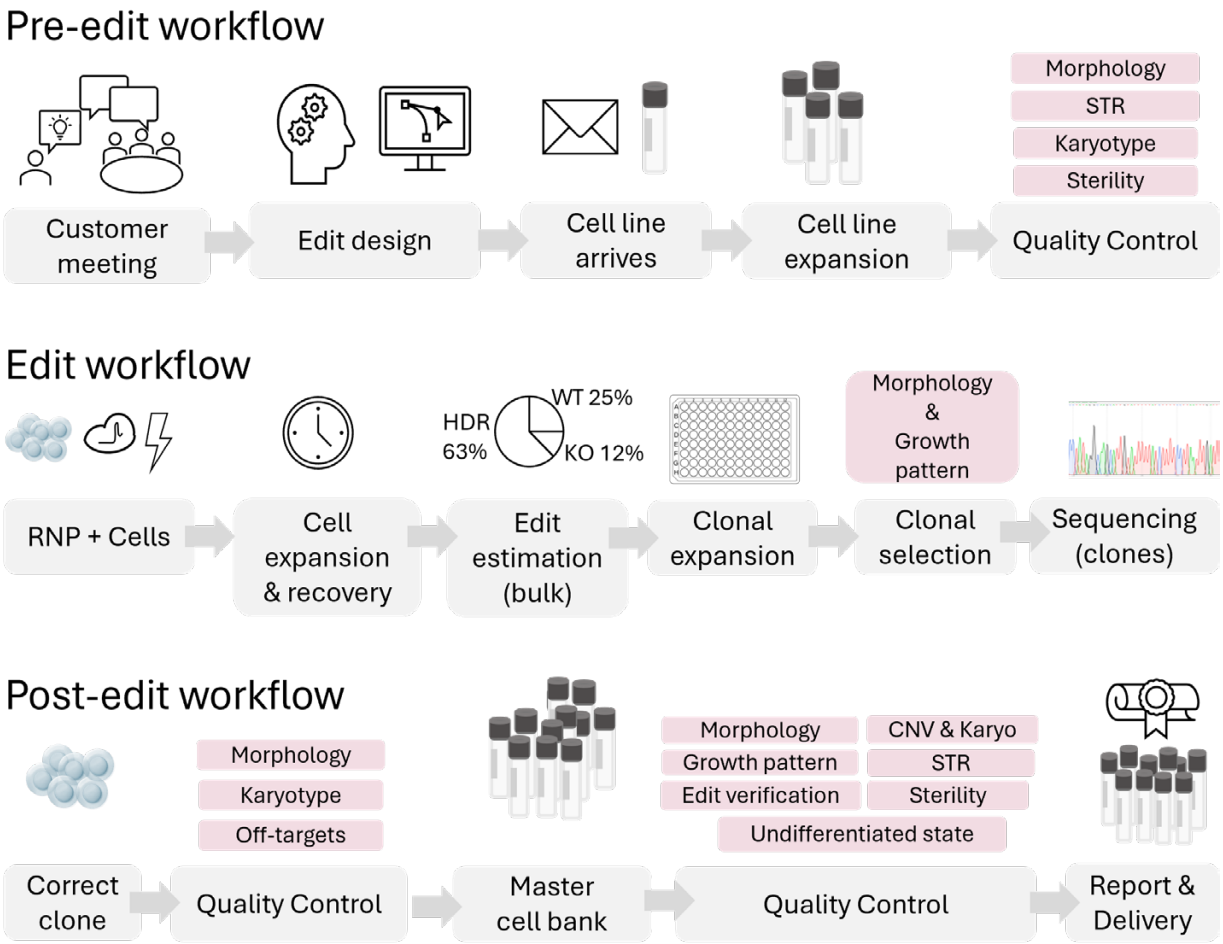


Figure 6. Example of a standardized workflow, here of a custom gene-edit in human iPSCs. All pink boxes indicate expertise-driven quality control checkpoints.

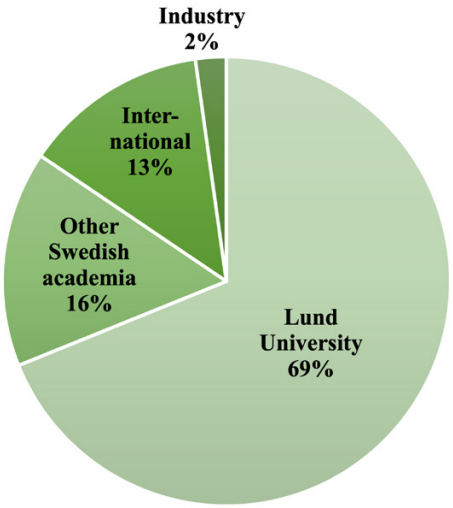


Figure 7. The CAGT userbase 2023.

models. Only then can the advantages of iPSC models outweigh their potential disadvantages, such as batch-to-batch variability, challenging culture, and relatively high cost. CRISPR editing of iPSCs, either to correct mutations in patient-derived iPSCs, or to recreate mutations in healthy donor-derived iPSCs, creates isogenic cell lines, i.e. cell lines that differ only by one or a few purposefully introduced mutation(s). Such isogenic iPSC cell line pairs can be further differentiated into iPSC-derived models (neurons, cardiomyocytes, hepatocytes, etc) and are invaluable tools for studying drug response and toxicity, individual responses to treatment, and disease modeling. A reliable and reproducible source of iPSCs is of crucial importance to the research performed in these cells, as is continuous quality control. A national infrastructure standardizing iPSCs would greatly benefit reproducible research in the field of stem cells and regenerative medicine in Sweden.

Relationship between SciLifeLab and ATMP initiatives

The anticipated transformative impact of Advanced Therapy Medical Products (ATMPs) on healthcare is reflected by recent funding initiatives by VR, Vinnova and other players. SciLifeLab is not currently active in this field. Taking some of CAGT's services into SciLifeLab would establish a first synapse with the Swedish ATMP community and prepare the ground for a possible later extension of SciLifeLab's precision medicine capability towards cell- and gene therapies. To which extent the CBGE platform should become involved in a potential connection with the ATMP field remains to be seen, however from a current perspective, the platform has no ambition or expertise to move into this space. Any efforts towards GMP or pre-GMP production of cell- and gene therapies are currently outside the scope of the platform.

Plans for incorporation of CAGT into the CBGE platform

CBGE brings together model cell line generation in cancer cell lines with chemical and genetic screens and a range of technologies for target discovery and mechanism-of-action elucidation. The CBGE platform envisages three concrete contributions of CAGT:

1. the generation and QC of iPSCs, gene-edited iPSCs, and isogenic iPSC pairs for chemical and genetic screening campaigns (precision medicine, drug discovery)
2. Differentiation of iPSCs into disease-relevant models for studying drug effects (mechanism of action, drug repurposing, target validation)
3. Providing high-titer lentiviral and AAV-based library viruses for in vivo CRISPR screens

Already now, the CAGT Core has several customers who are clinical scientists with access to patient material for reprogramming to iPSC, and/or CRISPR edits and quality control. Inclusion of CAGT services into the platform would strengthen the platform's relevance to clinicians and healthcare. CFG and CAGT are complementary, with CFG's precision gene editing focusing on cell lines, and CAGT limiting itself to iPSCs. The two units have already collaborated and referred customers to each other. CFG used to have a common pipeline with the Karolinska iPSC core, which, prior to its closure in 2023, was headed by CAGT's scientific director, Anna Falk. Re-establishing this collaboration between two national units would greatly benefit the research community.

SWOT analysis for a CBGE platform with CAGT on board

Strengths

- Access to patient-derived cells and isogenic cell lines for chemical/genetic screens and MoA
- Ideal complement to CFG services at a competitive centre for stem cell research

Weaknesses

- Cost and labour intensity of iPSC/iPSC-derived models
- Distance Lund – Stockholm problematic

Opportunities

- Transformative potential for the precision medicine capability
- Link SciLifeLab to the ATMP community
- New disease areas for CBGE services
- Strong representation for CBGE in Lund

Threats

- Dilution of funding
- Number of potential projects with relevance to the platform might be small

Budget request

Platform Strategic Budget

The platform obtains 450 KSEK p.a. from SciLifeLab. These funds have been used to support our platform pipeline projects (PPP's), and for fostering interactions within the platform. Additionally, 350 KSEK are obtained as a salary contribution for Platform Director Anna-Lena Gustavsson and Platform Coordinator Bernhard Schmierer. From 2025, we will continue to use the funds for cross-unit projects, but we ask 300 KSEK extra to task NBIS with the creation of pipelines for the analysis of our multi-modal data, which is currently a real bottleneck for the platform.

Chemical Biology Consortium Sweden (CBCS, including Morphological Profiling and Automated Patch Clamp Profiling)

CBCS is funded as a national infrastructure by VR until the end of 2026. A new pre-application has been sent to VR as an "inventory of need" in 2023, which is a prerequisite to be considered in the next funding round starting 2027. Increased base funding from SciLifeLab is needed to meet user demand for virtual screening, predictive AI models for drug discovery, including leveraging public data, improved informatics for drug repurposing and MoA studies, as well as chemoinformatics pipelines specific to fragment-based screening and structure-based drug design projects stemming from the ISB platform (FragMAX), see suggested platform and unit development plans above. This can be achieved by one additional FTE at CBCS-KI to strengthen the chemoinformatics/ML/AI competence. Additional funds are requested to establish one FTE at the morphological profiling unit at UU, and 0.5 FTE at the Electrophysiology Facility at LiU. These CBCS nodes and their unique expertise and equipment are suggested to become SciLifeLab funded nodes within CBCS.

CRISPR Functional Genomics (CFG)

Increased base funding from SciLifeLab is needed to maintain expertise and cover support for precision genome engineering and model system generation, which is not currently funded. From 2019-2021, CFG was funded with 1.5 MSEK/annum as a KI core facility for precision editing. CFG now offers these services nationally under the SciLifeLab umbrella, but without dedicated funding. A new call for core facility funding has been published by KI, and CFG will apply with its entire service portfolio, precision editing and genetic screening. If obtained, funding is unlikely to exceed 1.5 MSEK p.a. (2025-2028), and an increase of SciLifeLab base funding is requested to secure continued operation and avoid loss of critical mass and expertise.

Chemical Proteomics (ChemProt)

As described in the unit specific bottlenecks above, an increased base funding from SciLifeLab is requested to remain fully operational and address the multi-modal data integration. Further, this will cover the set-up of services in single cell chemical proteomics, described in the unit development plans.

Cell and Gene Therapy Core (CAGT)

The requested funds will be used to establish two FTEs to cover platform-relevant services at the national level.

Table 1. Chemical Biology and Genome Engineering – Platform Strategic Budget

Costs	2024	2025	2026	2027	2028
Platform Pipeline Project call	400	400	400	400	400
Salary PCO and PD	350	400	400	400	400
Data analysis and integration support by NBIS	-	250	250	250	250
Platform integration (retreats and networking)	50	50	50	50	50
Sum costs (kSEK):	**800**	**1 100**	**1 100**	**1 100**	**1 100**

Revenues	2024	2025	2026	2027	2028
Platform Strategic Funding	*450*	*700*	*700*	*700*	*700*
PCO and PD salary contribution	350	400	400	400	400
Sum revenues (kSEK):	**800**	**1 100**	**1 100**	**1 100**	**1 100**

Table 2. Chemical Biology Consortium Sweden (CBCS) (Including Morphological Profiling and Automated Patch Clamp Profiling) Budget

Costs	2024	2025	2026	2027	2028
Personnel 24 FTEs (2024) -> 25 FTEs (2025–2028)	24 188	25 000	25 500	26 000	26 500
Personnel morphological profiling UU -> 1 FTE		800	820	840	860
Electrophysiology -> 0.5 FTE LiU		400	410	420	430
Operations	7 358	7 800	7 800	7 800	7 800
Premises	2 847	2 900	2 900	3 000	3 100
Instrument depreciations	4 330	4 330	4 000	4 000	4 000
Sum costs (kSEK):	**38 723**	**41 230**	**41 430**	**42 060**	**42 690**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*6 200*	*7 200*	*7 200*	*7 200*	*7 200*
SciLifeLab funding (requested 2025–2028) CBCS-LiU		*500*	*500*	*500*	*500*
SciLifeLab funding (requested 2025–2028) CBCS -UU		*1 000*	*1 000*	*1 000*	*1 000*
University co-funding (KI, UmU, LU,LiU, UU, GU)	9 200	9 200	9 200	9 200	9 200
VR	13 100	13 100	13 100	13 100	13 100
SciLifeLab expensive instrument fund	1 750	1 750	1 750	1 750	1 750
EU funding (R4A; Impulse, RE-SYNC)	2 500	2 500	2 500	2 500	2 500
User fees	6 000	6 300	6 600	6 900	7 400
Sum revenues (kSEK):	**38 750**	**41 550**	**41 850**	**42 150**	**42 650**

Table 3. Chemical Proteomics (ChemProt) Budget

Costs	2024	2025	2026	2027	2028
Personnel 4.85 FTEs (2024) -> 4.85 FTEs (2025–2028)	5 097	5 224	5 355	5 489	5 626
Operations	1 400	1 435	1 471	1 508	1 545
Premises	506	506	506	506	506
Instrument depreciations	3 465	2 036	1 623	1 599	1 222
Other	100	103	105	108	110
Sum costs (kSEK):	**10 568**	**9 304**	**9 060**	**9 209**	**9 010**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*2 588*	*3 600*	*3 600*	*3 600*	*3 600*
VR funding for BioMS	2 568	1 540	1 540	1 540	1 540
KI co-funding for BioMS	1 900	1 610	1 610	1 610	1 610
Approved SciLifeLab Expensive Instrument	750	300	300	-	-
R4All contribution	250				
User fees	2 400	2 400	2 400	2 400	2 400
Sum revenues (kSEK):	**10 456**	**9 450**	**9 450**	**9 150**	**9 150**

Table 4. CRISPR Functional Genomics (CFG) Budget

Costs	2024	2025	2026	2027	2028
Personnel 5.75 FTEs (2024) -> 6 FTEs (2025–2028)	5 240	5 500	5 610	5 722	5 837
Operations	2 400	2 500	2 550	2 600	2 650
Premises	350	350	350	350	350
Instrument depreciations	650	150	150	150	-
Facility management Biomedicum, IT fees	455	480	480	480	480
Sum costs (kSEK):	**9 095**	**8 980**	**9 140**	**9 302**	**9 317**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*3 312*	*4 500*	*4 500*	*4 500*	*4 500*
KI core facility funding 2025-2028 [1]	-	1 500	1 500	1 500	1 500
SciLifeLab instrument funding	400	-	-	-	-
Opening balance	2 900	367	437	347	95
Remedi4All	50	50	50	50	-
User fees	2 800	3 000	3 000	3 000	3 000
Sum revenues (kSEK):	9 462	9 417	9 487	9 397	9 095
Sum revenues (kSEK):	**9 662**	**9 617**	**9 687**	**9 597**	**9 295**

[1] Not decided

Table 5. Cell and Gene Therapy Core (CAGT) Budget

Costs	2024	2025	2026	2027	2028
Personnel 5 FTEs (2024) -> 7 FTEs (2025–2028)	5 700	6 800	7 344	7 564	7 791
Operations	1 600	2 600	2 600	2 700	2 700
Premises	500	600	600	650	700
Instrument depreciations	200	200	200	200	200
Sum costs (kSEK):	**8 000**	**10 200**	**10 744**	**11 114**	**11 391**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)		*2 500*	*2 500*	*2 500*	*2 500*
SFO:Stem Therapy	5 400	4 000	4 000	4 000	4 000
SFO: Multipark	500	500	500	500	500
LU SRA Infrastructure application	300				
Foundation and university grants		500	600	700	700
User fees	1 800	2 700	3 200	3 300	3 600
Sum revenues (kSEK):	**8 000**	**10 200**	**10 800**	**11 000**	**11 300**


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San Francisco, CA 94120



Medicinal Chemistry – Lead Identification Unit in Uppsala. Photo: Mikael Wallerstedt

Drug Discovery and Development Platform

Basic Information

Platform Director: Per Arvidsson, Karolinska Institutet

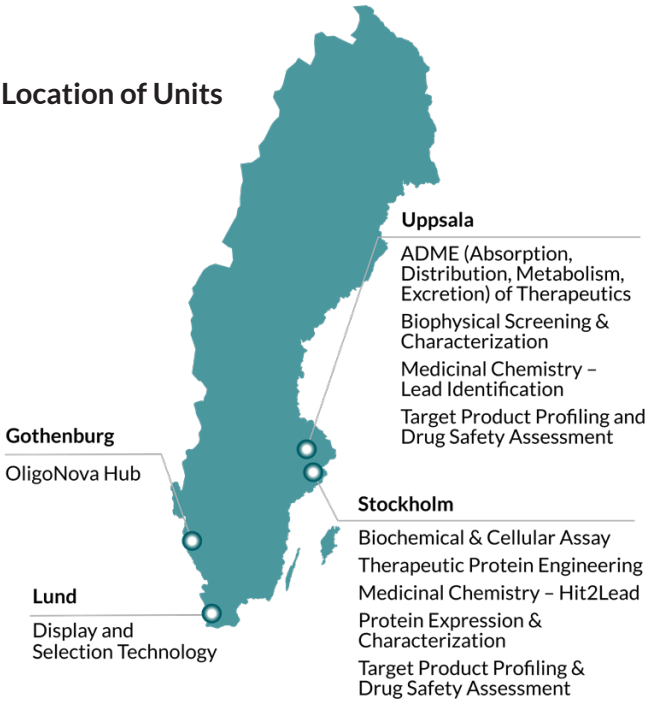
Platform Co-Director: Kristian Sandberg, Uppsala University

Platform Coordination Officer: Rebecka Klintenberg, Uppsala University

Platform vision: that SciLifeLab DDD is recognized as an essential part of the Swedish innovation infrastructure and recognized for delivering high-quality drug discovery programs, which are globally competitive for funding and clinical development.

Platform mission: Turning discoveries into innovations by providing State-of-art drug discovery & development knowledge

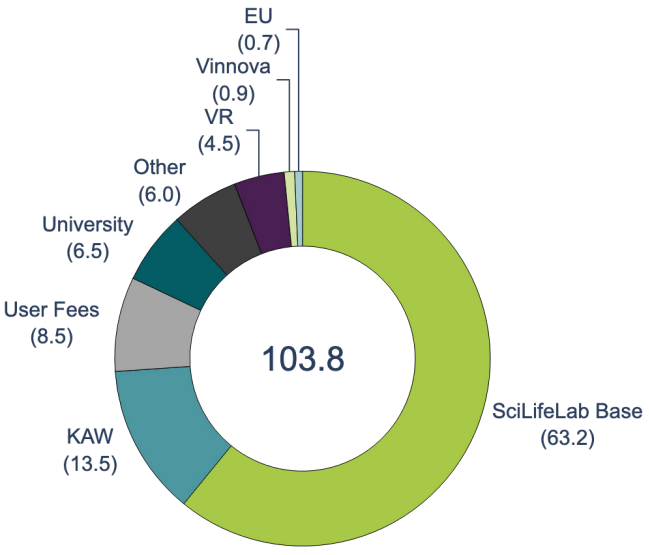
Location of Units



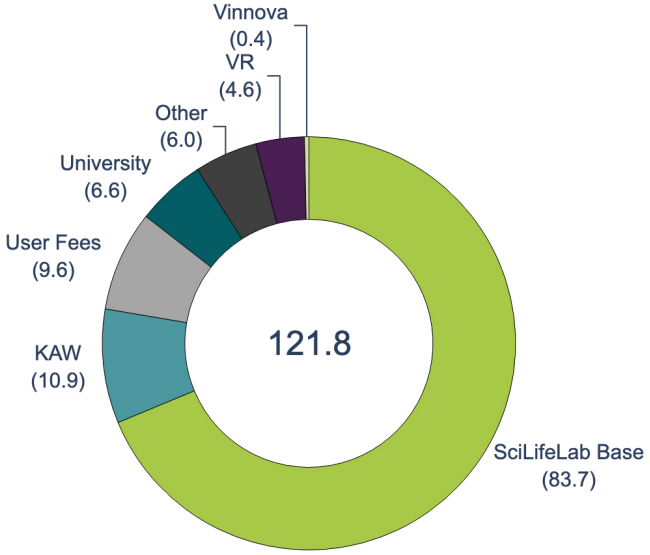
SciLifeLab Funding

Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
SciLifeLab LÄK	59.2	80.2
SciLifeLab NAT	4.0	3.5
Total SciLifeLab Funding	**63.2**	**83.7**

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E20 Drug Discovery and Development

Executive Summary

The Drug Discovery and Development (DDD) platform at SciLifeLab supports innovation by transforming academic research into validated early-stage drug development programs that are globally competitive for further investments. This is achieved by offering an industry-standard drug discovery infrastructure and expertise to academic researchers in Sweden; and, by offering education, training, and expertise in drug discovery to academic scientists and stakeholders within the Swedish innovation system.

Since its inception ten years ago, DDD has contributed to Sweden's innovation ecosystem by facilitating the formation of multiple new biotech startups and international partnerships. The platform has also actively engaged in pandemic preparedness projects and helped secure funding for several externally funded research programs.

The DDD platform comprises ten formal units distributed across six Swedish universities. The operation is staffed with nearly 50 researchers, many with industrial experience, and engages ten university professors as platform scientific directors. In 2021, the DDD operation was expanded with Oligonova HUB at Gothenburg University (GU) with a special mission to support the development of therapeutic oligonucleotides. In 2022, DDD's international Platform Advisory Board (PAB) helped establish a ten-year strategy for the platform´s long-term development which will increasingly focus on implementing state-of-the-art technologies to support the discovery of therapeutics based on small molecules, antibodies, oligonucleotides, and new modalities. Technology development would greatly benefit from the SciLifeLab PULSE postdoc application. Initiatives to promote translational research at universities, as outlined in the SciLifeLab roadmap in 2023, are identified as another potential avenue for growth.

SciLifeLab DDD's vision is to be an essential component of Sweden's innovation infrastructure that drives advancements in drug discovery and development, fosters collaborations, supports startups, and leads academic-industrial partnerships. Our ambitions in the following period (2025-2028) are to grow collaborations in the Life Science sector and expand our support to the innovation systems. We aim to increase our focus on technology platforms and increase our output of commercial exits to 3 per year.

Background

The mission for SciLifeLab DDD is to successfully turn academic findings into early drug development programs. This is done by combining world-leading biological research with an infrastructure with proven drug discovery competence, standards, and technologies. Our short *mission* statement is therefore: "Turning discoveries into innovations by providing State-of-art drug discovery & development knowledge".

Two major specific objectives are:

1. To provide industry-standard drug discovery services to academic scientists in Sweden that allow their programs to be globally competitive for further (clinical) development.
2. To provide education, training, and expertise in drug discovery to academic scientists and actors in the Swedish innovation system.

Our *vision* is that SciLifeLab DDD is recognized as an essential part of the Swedish innovation infrastructure and recognized for delivering high-quality drug discovery programs, which are globally competitive for funding and clinical development.

DDD was formed to reflect the fact that drug discovery programs are interdisciplinary and require multiple competencies that work together against a common goal. Currently, the DDD platform is staffed with almost 50 researchers, most of them with industrial experience, and engages 10 university professors as platform scientific directors (PSDs), *Figure 1.*

The DDD platform is organized into 10 units distributed to six universities. Since the last IEC review in 2020, one unit has been phased out and two new units at the Oligonova HUB at Gothenburg University (GU) have started. In 2024, we restructured our biologics capabilities by merging two units at the Royal Institute of Technology (KTH) and created a unit at Lund University (LU). The new organization from mid-2024 will have the following expertise:

1. *Therapeutic Protein Engineering* (TPE), KTH Royal Institute of Technology – reorganized 2024 – produce recombinant proteins as antigens or for assays, engineer biological drug modalities through conjugation, half-life extension, etc; engineer cells for protein production. Perform selection campaigns in DNA Encoded Chemical Libraries (DECL).

2. *Display & Selection Technology* (DST), Lund University – reorganized 2024 – plan and exercise selections for biological drug modalities using in-house generated phage-display libraries.

3. *Biochemical and Cellular Assays* (BCA), Stockholm University – responsible for setting up and running primary biochemical and cellular assays for the projects.

4/5. *Two units for medicinal and computational chemistry* (*MCH2L and MCLI*), Stockholm University and Uppsala University – compound synthesis and registration, medical chemistry, computational chemistry, machine learning from DECL selections, etc.

6. *ADME of therapeutics unit*, Uppsala University – supports with in vitro and in vivo data on drug metabolism, pharmacokinetics, and pharmacodynamics, including PKPD and PBPK modeling.

7. *Biophysical Screening and Characterization* (BSC), Uppsala University – supports biophysical and structural studies to demonstrate and understand ligand-to-target interactions.

8. *Target Product Profiling and Drug Safety Assessment* (*TPP&DSA*), Karolinska Institutet, and Uppsala University – gives support to innovation systems and users by preparing projects for entrance and exit from DDD. Provides support for the design of in vivo pharmacological studies to ensure that data of relevance to investors and industry is captured. TPP&DSA also harbors the SciLifeLab DDD office function which allows UU, via a delegation from other host universities, to sign agreements for all of DDD.

9. *Oligonova Biology*, Göteborg University – Bioinformatic design of antisense or siRNA sequences for oligonucleotide projects. Set up and perform cell-based experiments to monitor mRNA and protein knock-down.

10. *Oligonova Chemistry*, Göteborg University – Automated synthesis of modified siRNAs and anti-sense oligonucleotides. Conjugation chemistry for targeted delivery of oligos and other cargo.

An external steering group reviews programs entering the platform and monitors progression biannually. Upon approval of entering the DDD platform, the staff works together with the principal investigator (PI) and associated academic innovation system to add industrial drug discovery quality and expertise to the programs (Figure 2). Importantly, projects that are not accepted are given valuable feedback through the process that raises awareness of the requirements needed for a competitive drug discovery program.

DDD is versatile and has broad competence; drug leads can be either small molecule drugs, human antibodies or proteins, oligonucleotides, or new modalities. Following the Swedish teacher´s exemption law (or Professor´s privilege law), the academic scientist retains all intellectual property rights and ownership of discoveries made during this process. Carefully set exit criteria and the integrated collaboration with the academic innovation support system pave the way for spinouts or partnerships with established pharma or biotech companies.

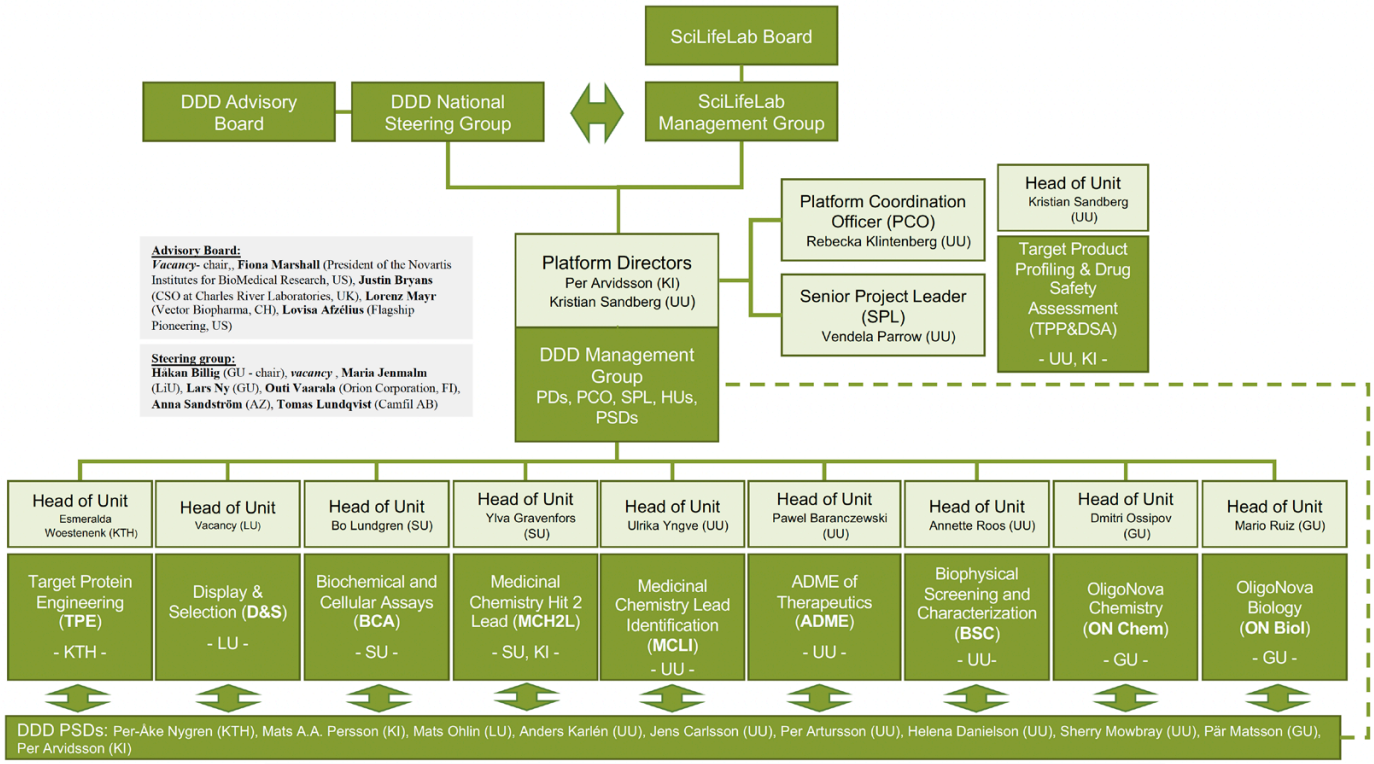


Figure 1. Organization of SciLifeLab Drug Discovery and Development platform. Acronyms are explained in the text.

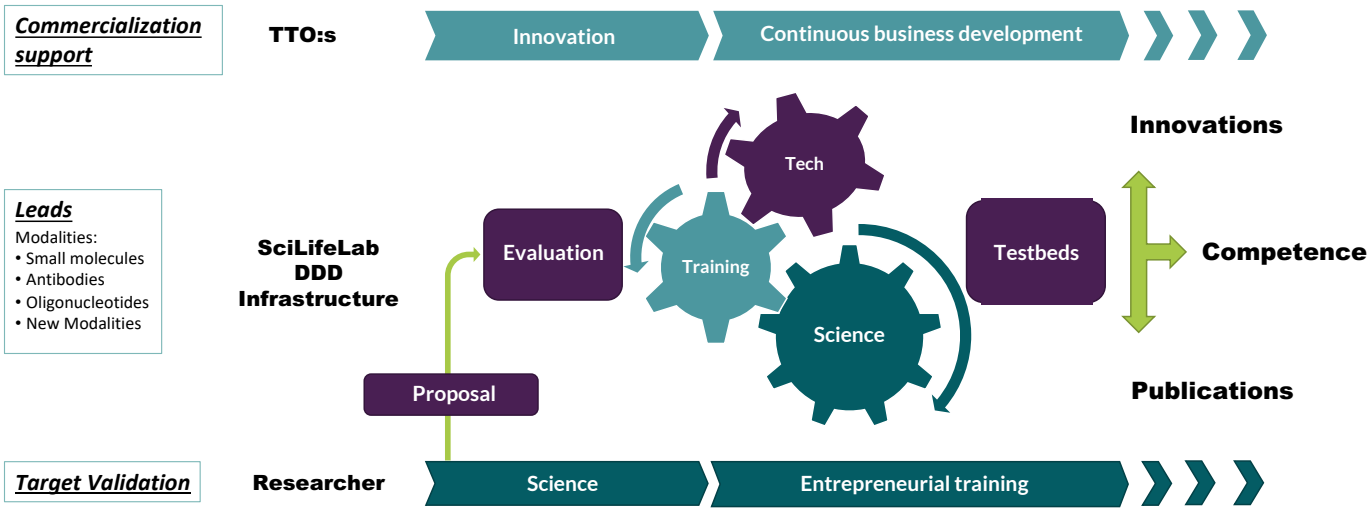


Figure 2. The SciLifeLab DDD program. A Drug Discovery Program at SciLifeLab DDD has three partners: 1) The academic scientific researcher as project owner; 2) the SciLifeLab DDD infrastructure that supports with laboratory support and drug discovery know-how and; 3) the academic innovation systems (innovation offices, incubators, and university holding companies) that can provide commercialization support. The output from a SciLifeLab DDD program is innovative lead compounds as a starting point for preclinical development, patents and scientific publications, and academic scientists trained as entrepreneurs and "drug hunters".

Management

The DDD National Steering Group consists of four representatives from academic research and three representatives from industry/innovation systems (Håkan Billig, GU – chair, Maria Jenmalm, Linköping University, Lars Ny, GU, a vacant university position, Tomas Lundqvist, Camfil AB, Anna Sandström, AstraZeneca, and Outi Vaarala, Orion Pharma, Finland. The steering group meets six times per year and decides on project priorities and strategic directions for the platform. The platform directors (PDs) represent the entire platform and lead the work at DDD. The PDs meet regularly with the SciLifeLab Director and the SciLifeLab Infrastructure Director. The PDs and the chair of the steering group meet the SciLifeLab Board annually.

The DDD International Platform Advisory Board (PAB) meets annually to advise the steering group. Kjetil Taskén (University of Oslo, Norway) was the chair of the PAB until late 2023 when he left this position to become a member of the SciLifeLab International Advisory Board. DDD is currently replacing him. Other members of the DDD PAB are Fiona Marshall (Global Head of Research, Novartis, USA); Justin Bryans (CSO Charles River Laboratories, UK); Lorenz M. Mayr (Vector BioPharma AG, Switzerland) and Lovisa Afzelius (Flagship Pioneering, USA).

The Platform Management Group (MG) meets weekly (hybrid meetings) and consists of the PDs, the Platform Coordination Officer (PCO), the Senior Project Leader (SPL), the Head of Units (HoU), and *ad hoc* the Platform Scientific Directors (PSDs). DDD Project Leaders manage projects run at the platform and are coached by the SPL and individually sponsored by the PDs. The Management Group handles ongoing activities at the platform but also makes decisions on smaller service projects (commissioned research). A data management plan, DMP, has been applied that describes how data produced at the platform is handled.

The procedure for inclusion and prioritization of projects into DDD is described in "DDD Rules of Procedure". Shortly, consultation meetings are held with scientists interested in developing their scientific research into therapeutics. If the idea has a good rationale and if DDD has complementary competence and capacity to support the project a detailed program description is presented to the DDD National Steering Group for prioritization. This documentation is prepared jointly by the principal scientist, DDD personnel, and the associated academic innovation support system, and includes a risk analysis and details plans forward. Alternative tracks to get support by DDD are provided as collaborative projects on technologies and service (commissioned) projects.

New projects and programs and collaborative technology implementation projects in the portfolio are prioritized bi-annually by the DDD National Steering Group. Service projects are decided weekly by the DDD management. More than 80% of DDD funding should be devoted to DDD programs.

Programs run at DDD are highly interactive and each project involves the majority of units at DDD but also units at other platforms and national infrastructures. DDD uses the *SciLifeLab Compound Center* (CC) operated by the CBCS unit within the CBGE platform for handling all synthesized small molecules, preparation of assay-ready plates, and accessing the SciLifeLab compound collection. SciLifeLab

Data Center is supporting with e.g. Anubis, NextCloud, and the DDD Data portal. PK, PKPD, and PBPK studies can be offered in collaboration with the Preclinical Cancer Treatment Center at Uppsala University. Interactions with the various innovations systems in Sweden are maintained during project scouting, in the project work and, supported by the SciLifeLab Innovation coaching and the national hub for SciLifeLab Innovations – Pharma & Biotech in meetings with the academic innovation support systems.

Importantly, the DDD platform promotes the use of additional capabilities inside or outside the SciLifeLab infrastructure. For example, RISE (Research Institutes of Sweden) is a collaborator and is routinely used for discovery toxicology support for DDD programs. Max-IV is used for X-ray structural determination. DDD is running a collaborative project "BRIDGE" together with the infrastructure for pilot-scale biologics manufacturing: Testa Center. Testa Center has also been used by two programs that now have exited DDD. Examples of how DDD engages with other SciLifeLab resources are e.g. NBIS for bio- and chemoinformatic support, Cryo EM-mediated structural determination, Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS) for epitope mapping, global proteomics for evaluating protein degraders, CRISPR facility for engineering reporter cell-lines, etc. ENABLE2, the drug discovery track of the 10-year Swedish initiative to combat antimicrobials is supported in a collaborative service project.

A major impact of SciLifelab DDD is the creation of innovations and new start-ups. This short movie exemplifies the experience of one academic scientist who has developed her idea at DDD and now is running a company approaching clinical trials: Marika Nestor, UU.

Work in collaboration with SciLifeLab DDD also results in publications. An example from 2022 is the publication of inhibitors of SARS CoV2 Mpro identified using a combination of structure-based drug discovery approaches (fragments, X-ray crystallization, screening with surface plasmon resonance (SPR), biochemical methods and pharmacological in vitro and in vivo studies) together with extensive use of in silico methods Luttens et al. JACS 2022 - co-authors from SciLifeLab DDD: Gullberg, Abdurakhmanov, Nekhotiaeva, Lundgren, Gravenfors, Sandberg. Another example from 2023 is that complementarity-determining region clustering may cause CAR-T cell dysfunction Sarén et al. Nature Comm. 2023 - co-authors from SciLifeLab DDD: Andersson, Hofström, Persson.

Swedish academic users of DDD pay for consumables and service costs in DDD programs and DDD service projects. A full cost model is applied for industrial users and international academic scientists.

In addition to running projects, DDD aims to arrange at least two symposia annually. In addition, approximately eight public virtual presentations on the theme "Drug Discovery Seminars" are arranged and announced via SciLifeLab events. News is distributed via an account for DDD on LinkedIn and at the website for SciLifeLab. For internal communication, DDD has a Slack channel and arranges virtual "State of the Platform" meetings monthly. In addition, DDD arranges one off-site meeting for the platform every year and bi-annually kick-off meetings to which the whole platform is invited.

Extensive Key Performance Indicators (KPIs) have been developed by the platform. The most important KPI is the annual number of commercial exits from the platform. The current ambition at DDD is to have two commercial exits from the platform every year. A commercial exit is when a program is licensed by a company or when a PI-founded company gets investments exceeding 30% of the stocks in the company.

Overall Platform developments and key achievements 2021 - 2024

We define developments as major changes in organization, technologies, offerings, or similar, while achievements will focus on major deliverables since 2024.

Major developments 2021-2024

- The unit for In Vitro and Systems Pharmacology (IVSP) at UU was phased out in 2022. The former Head of Unit, Vendela Parrow was recruited to DDD in a new position as Senior Project Leader with special responsibility to develop project leadership skills and interactions with the innovation systems.
- In 2021, KAW, GU, and SciLifeLab decided to fund Oligonova HUB – a national center for therapeutic oligonucleotides to be established at GU with >100M SEK over 8 years. Oligonova HUB became an integrated part of the DDD platform through the formation of two new units at GU: ON_Biol and ON_Chem. After establishing laboratories, procuring infrastructure, and recruiting personnel, the operation became functional in 2023 and is currently supporting 6 therapeutic ON projects.
- To meet future demands for more advanced biologics, we have restructured the units "Human Antibody Therapeutics" and "Protein Expression & Characterization" with the start in 2024. The new organization holds a unit for "Therapeutic Protein Engineering" at KTH, Solna, and a unit for Display & Selection Technologies at LU.
- LU and GU have joined the DDD office agreement that authorizes UU to sign contracts with external parties on behalf of DDD.
- As a result of MG discussions and the mid-term review in 2022, the DDD steering group established key performance indicators for DDD in 2022. These KPIs are divided into "external" KPIs that focus

on sustainability, portfolio, equal terms, societal impact, external communication, partnerships, and adaptation to new technologies. Another set of "internal" KPIs focuses on efficiency, quality, continuous improvement, resources, competence, and internal communication.

- Many co-workers have left for industrial positions, while an even larger number of co-workers have been recruited to meet the increased demand for DDD support. In 2023 alone, we recruited 13 new staff members, meaning that >25% of the total FTE count were new and needed to be onboarded.
- As a result of the Vinnova-funded InnoPharma project, we established SciLifeLab Innovations – Pharma & Biotech in collaboration with SciLifeLab External Relations Office as a vehicle to engage the large life-science community in innovation support.
- The international DDD Platform Advisory Board was established in 2021 and helped to develop a 10-year strategic plan for technology implementation. Four areas, i.e. Machine Learning, Oligonucleotides, Display & Selection technologies, and Proximity-inducing Inducing Agents, were prioritized.
- We have established the DNA Encoded Chemical Libraries (DECL) technology at the platform. The current workflow allows Swedish academic scientists to access libraries containing $>10^{10}$ physical small molecules entitities, and machine learning of experimental out-put, to be combined with virtual screening. This is made possible by collaborations between DDD and other SciLifeLab platforms (NGI), academic scientists (Ulf Landegren, UU; Ola Spjuth, UU; Jens Carlsson, UU; Oscar Verho, UU,) and procurement/collaborations with biotech companies (WuXi Apptec; XChem; Hitgen).
- We have established technologies for the development of protein degraders (Protacs®) in collaboration with academic scientists (Mikael Altun, KI and Helena Danielsson, UU) and industrial partners (Recipharm OnTarget Chemistry). Regular discussions on this topic are also conducted with the CBGE platform and industrial parties like AstraZeneca, RISE, Beactica Therapeutics, and Healthcap.
- We are currently supporting technology implementation in our four strategic areas, machine learning, display & selection, proximity-inducing agents, and oligonucleotides.

Major achievements 2021-2024

- 6 commercial exits have spun out from programs supported by DDD: 1) Sara Mangsbo, UU – Strike Pharma AB; 2) Marene Landström, UmU – MetaCurum Bio-tech AB; 3) Thomas Helleday, KI – One-carbon Therapeutics AB; 4) Marika Nestor, UU – Akiram Therapeutics AB; 5) Thoas Fioretos, LU – Lead Biologics International AB; 6) Jens Carlsson et al. (UU) – international partnering. In addition, one tech-based company was founded based on research done within a DDD program: Mats AA Persson and Daniel X Johansson, KI – AAX Biotech AB. This is an interesting showcase of the accidental impact on work in a DDD program where a biotech company was founded based on technologies developed in a program.
- Two alumni projects have been listed on the Nasdaq First Growth Market: Lipum AB (UmU) and Elicera Therapeutics AB (UU)
- The alumni program that formed Lipum AB advanced their candidate drug into the clinic with positive phase 1 data reported in early 2024
- DDD was actively engaged in three projects for pandemic preparedness (ADAC, spike binders, Mpro inhibitors)
- DDD is currently engaged in the following externally funded programs: VR-funded antibiotics drug research project ENABLE2, Vinnova-funded BRIDGE program, IMI-funded EUbOpen, and Conception programs, JPIAMR-funded MURYXIN program.
- Despite the pandemic, 6 one-day symposia and some 20+ public seminars have been organized. Notably, a virtual 2-half-day event organized in collaboration with the cryoEM unit attracted >700 participants globally (CryoEM in Drug Discovery). During 2024, we will organize two one-day symposia "Aiming for the Clinics" and "Theranostics".
- Inauguration of the OligoNova Hub at AZ BioVenture Hub in Mölndal, April 25th -26th 2022
- The Vinnova-funded project "InnoPharma" was launched in 2021 to develop DDD as the national hub for seamless collaboration within the Swedish innovation systems. As a result, a new model for academic drug discovery emerged. The innovation support system is now a full member of the three-part collaborative programs at DDD (project owner, infrastructure, and innovation support). Another outcome was the establishment of SciLifeLab Innovation Pharma & Biotech which is hosted by the external relations office.

Cumulative achievements of SciLifeLab DDD

Publications claim that 50-90% of academic preclinical biomedical data is non-reproducible. In this context SciLifeLab is seen as a highly valued and independent quality assurance vehicle for academic programs seeking further national funding or being exposed to due diligence by international pharma and VC companies. Figure 3, describes that data generated by DDD is based on validated assays and qualified assured reports. The system of both internal and external (steering group) approved checkpoints assures that the right data is available for decision-making at the right time. Examples include

checkpoints to ensure that validated assays are at hand before starting extensive chemistry programs, input from a DDD "in vivo design team" ensures that relevant pharmacological data are produced in animal experiments in the preclinical proof of concept phase and that an "industry-like" candidate target product profile and commercial plan is created at checkpoint 2 and available upon exit of the program from DDD.

Table I describes the annual attrition of programs at SciLifeLab DDD. The admission rate between the first meetings and the start of program is 12%. The number of programs in the portfolio is currently at a steady level of 16-20 programs. There are 17 commercial exits since 2014 (11 start-ups, 5 licensing and 1 exit when an academic phase 1 and 2 study started).

Table I. Portfolio of DDD programs 2014-2023*

* Portfolio size is the number of DDD programs in the portfolio in December. First meetings is the number of unique project discussions with DDD. preProjects is the number of projects that are accepted to prepare their documentation for the steering group as a potential program. The admission rate is the proportion of programs accepted by the steering in relation to the first meetings. Academic exits are the number of programs that are returned to academic science. Commercial exits are the number of programs that have left DDD for commercial development. # One preProject was withdrawn before presentation to the steering group in years 2018, 2020 2023. Two preProjects were withdrawn in 2019.

Year	Portfolio size	First meetings	preProjects #	Rejected proposals	Admission rate (%)	Academic exits	Commercial exits
2014	4	47	6	1	11	0	1
2015	11	60	7	0	12	0	0
2016	17	56	8	0	14	0	2
2017	16	26	5	2	12	3	3
2018	18	43	9	2	14	3	1
2019	18	31	6	1	7	4	2
2020	17	43	5	1	7	1	2
2021	13	25	2	0	8	2	3
2022	17	35	10	3	20	2	1
2023	20	46	12	3	17	5	2
2014-2023		*412*	*70*	*13*	*12*	*20*	*17*

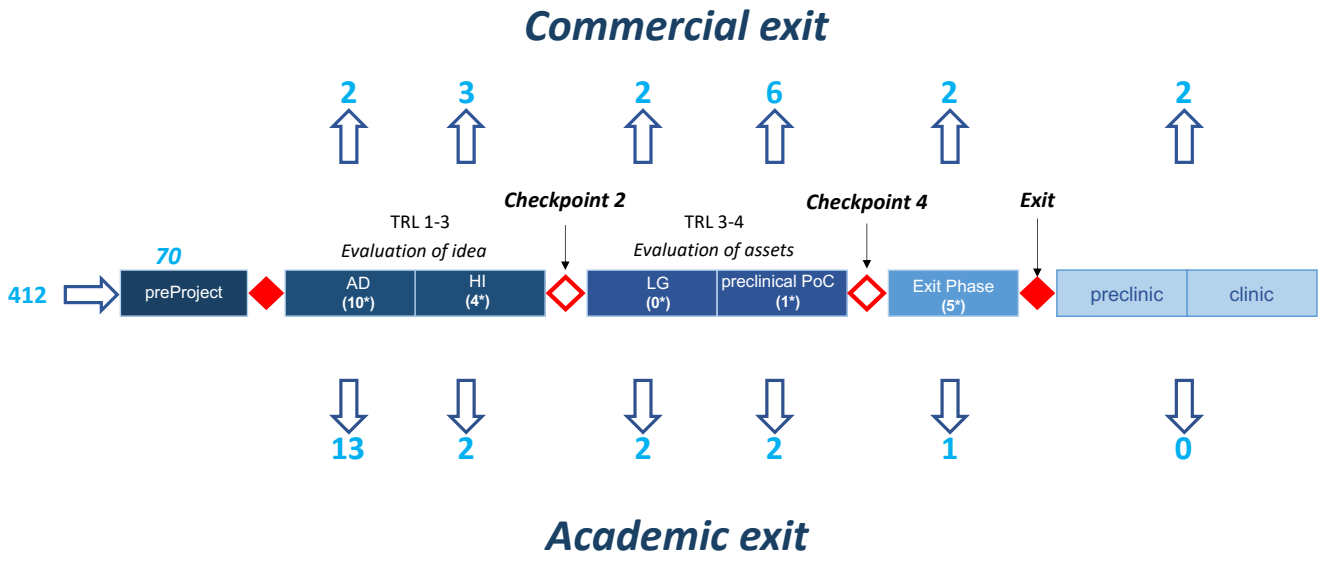


Figure 3. Workflow and cumulative output from SciLifeLab DDD. Academic proposals for drug discovery are processed together with SciLifeLab staff and innovation officers from the academic innovation system. The DDD steering group decides to include the proposal into the DDD project portfolio and when the program can be placed in the exit phase, ready for external investors to move into preclinical development. Data generated by DDD is based on validated assays, developed in the assay development phase (AD). Compounds/protein/oligonucleotides that bind to the target and execute a functional effect are identified in the hit identification phase (HI).

The steering group decides transition over checkpoint 2 based on a candidate drug target profile and a commercialization plan. These documents describe how the hit compounds can be converted to a pharmacologically active lead compound, i.e. a putative drug. In the preclinical proof of concept phase are lead compounds tested for their in vivo activity in pharmacokinetic-pharmacodynamic models. Many of the projects are invalidated in this workflow and returned to academic sciences. Other projects make a commercial exit at an early stage. A commercial exit is when the program is licensed to an external partner or when the academic scientist owns less than 70% of the intellectual property rights of the project.

The figure indicates the number of programs entering the portfolio and when and at what stage the programs left the portfolio. The numbers marked with* indicate the current numbers of programs in the portfolio and in what stage they are.

Infographics: Statistics and Metrics for Platform

Drug Discovery and Development

Read more: Webpage, Publications Database

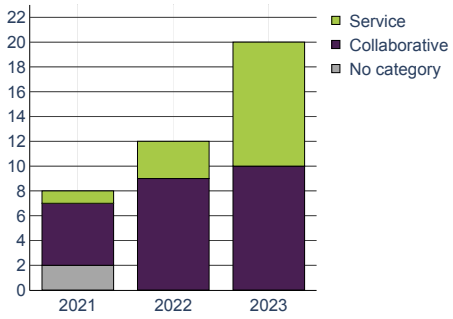
Basic Information

PD: Per Arvidsson
Co-PD: Kristian Sandberg
Host University: KI, KTH, LU, SU, UU, GU
SciLifeLab unit since: 2014
FTEs: 45.9

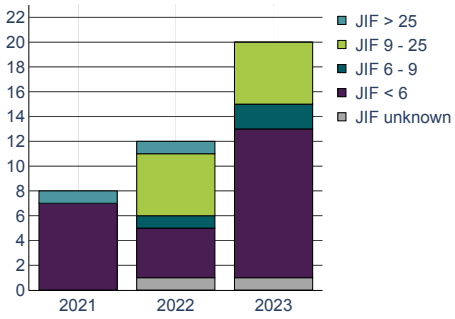
Funding 2023 (kSEK)

SciLifeLab: 57573
Other: 23700
User Fees: 3566

Publications by category

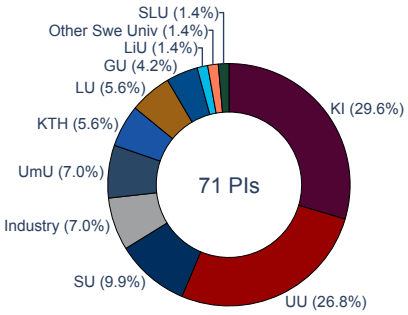


Publications by JIF

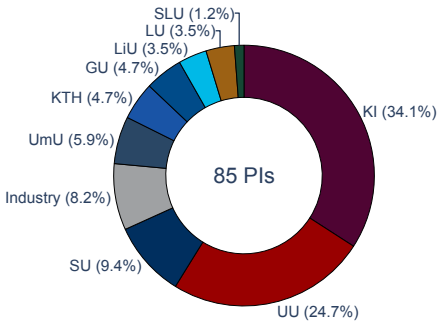


No. of Tech Dev Publications 2021 - 2023: 1

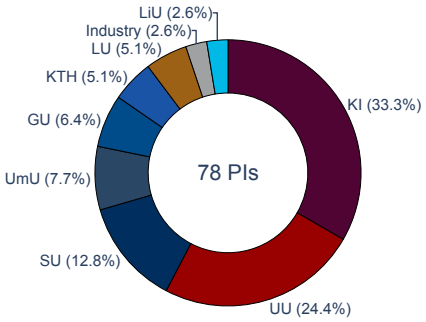
Users 2021



Users 2022



Users 2023



Development plans for DDD 2025–2028

A long-term strategic plan for DDD was developed in discussions with the DDD International Platform Advisory Board (PAB) and was launched in January 2022.

DDD's international PAB points out the following:

- DDD's main competitive advantage is the close alliance with Swedish academic scientists
- The teacher's exemption law is a very important competitive advantage for innovations emerging from Swedish academic research. Universities and innovation agencies should jointly use the teacher's exemption law and find incentives to apply these to the DDD platform operations
- Future therapies will increasingly be based on novel technologies, not new targets. DDD should not include disease focus within the platform, but rather stay focused on technologies
- Stay focused on a few modalities – do not spread resources too thin
- The ability to form strategic partnerships with industry is essential

Technologies

DDD will continue to prioritize large academic programs in four therapeutic modalities: small molecules, antibodies, oligonucleotides, and "new modalities". In support of this, more emphasis will be placed on how to implement state-of-the-art technologies for these modalities. Focus areas for technology implementation are 1) machine learning; 2) oligonucleotides; 3) display and selection technologies and; 4) development of proximity-inducing agents. The integration of therapeutic oligonucleotides as a modality offered by DDD is ongoing. The first oligonucleotide exit is expected around 2025-2026. The output from the SciLifeLab DDD would then be 3 commercial exits per year. The interactions between SciLifeLab DDD and NBIS are expected to increase because of the focus on implementing machine learning tools; build up of DDD internal expertise at the units in Gothenburg (bioinformaticians) and at the units for medicinal chemistry in Stockholm and Uppsala (chemoinformatician/structural biologists). DDD has also committed to support the SciLifeLab PULSE Marie Curie co-fund application for entrepreneurial postdocs with a total of €2,533,000 in kind. Postdocs applying for

the entrepreneurial track will work in one or more of the DDD focus areas for technology implementation together with principal investigators at a Swedish university and an industrial partner. As stated by the PAB, future therapies will increasingly be based on novel technologies, not new targets. DDD therefore plans to prioritize programs with emphasis on new technolo-gy platforms, such as the Sara Mangsbo exit 2021, Strike Pharma AB: About Strike Pharma, Exit info. The increased focus on technologies requires substantial investments in coworkers with specialist competence in these areas. This is considered in the budget proposal for 2025-2028.

Operative model

Starting this year, DDD has modified the operative model for programs. A major change is that the commercialization aspects are brought in earlier in the project since the academic innovation support system is an active partner in the programs. As a result, a commercialization plan is being developed at checkpoint 2 (see *Figure* 3), i.e. at the same time as the pharmacological modality of the future drug is defined in the candidate drug target profile document. The scope of responsibilities for SciLifeLab DDD project leaders therefore increases with the need to coordinate larger and more complex tasks and project teams. We foresee continuous development of leader skills, technical competence, and drug discovery experience. This is considered in the budget proposal for 2025-2028.

Innovation community

DDD will support the work performed by SciLifeLab External Relations in Innovation Coaching and in exposing the national hub for SciLifeLab Innovation – Pharma & Biotech. DDD is also planning for joint actions with research funding organizations for directed funding in prioritized disease areas. A current example of this is the Swedish Research Council-funded initiative on antimicrobial resistance (AMR) in which DDD is supporting the ENABLE2 program and gives priority to antibiotics programs in the DDD portfolio.

Sustainability

Two factors have contributed significantly to the stability of DDD: 1) the earmarked funding from the Government to DDD as an integrated unit with SciLifeLab and 2) the DDD office agreement between the host universities of DDD that makes Uppsala University a legal proxy. Maintaining this basal funding and legal ability is key also for the future.

The PAB underscored the importance of focusing on a few modalities and not spreading resources too thin. DDD supports the initiatives in therapies based on advanced therapy medicinal products (ATMPs). However, DDD does not have the competence or capacity to take the lead in this development because this progress primarily affects the healthcare system and possibly innovations in the MedTech area. If SciLifeLab decides to engage in ATMP, we suggest that a new capability, "Therapeutics", is launched where matters and best practices concerning the discovery of new pharmaceuticals, drug repositioning, and discovery and development of ATMP products could be discussed.

It is currently not clear how DDD could interact efficiently with the SciLifeLab capabilities for precision medicine (PM), pandemic laboratory preparedness (PLP), and planetary biology (PB). Precision medicine is primarily orientated toward clinics and diagnostics, PLP is orientated toward surveillance whereas PB has a broader scope that does not involve the discovery of therapeutics. Likewise, DDD needs to identify synergies with the DDLS initiative, where few (if any) of the recruited fellows are active within the drug discovery area.

As stated by PAB, DDD's main competitive advantage is the close alliance with Swedish academic scientists where the teacher's exemption law is a very important competitive advantage for innovations emerging from Swedish academic research. SciLifeLab DDD (i.e. the host universities) therefore cannot take ownership of inventions made and use this strategy for sustainability. Our strategy is instead to become indispensable for the Swedish innovation system by providing high-quality data that attract investments in the life science sector. A testimony that this strategy may work was the prerequisite that OligoNova were to be integrated within SciLifeLab DDD operations to receive external funding. However, at the same time is it also a sustainability risk to be too dependent on external funding for DDD. The funding to OligoNova and ENABLE2 probably ends in 2027/2028. Again, the strategy is to position SciLifeLab DDD as an attractive partner for future investments.

Competence/background of staff and plans for keeping/attracting competent staff scientists

The gender balance of the workforce at SciLifeLab DDD is 48% females and 52% males. Furthermore, 92% of the staff have a PhD degree or higher. We have successfully recruited a large number of new staff to meet the growing demand for DDD support. However, the recruits often lack relevant industrial experience, which means that we need to develop these skills through internal and external education. As we increase our focus on technology, we recognize the need for substantial investments in staff with specialist competencies in our areas of technology development. To find the best candidates for these positions, we're intensifying our recruitment efforts by co-publishing job openings with SciLifeLab strategic partners, such as EMBL. The SciLifeLab PULSE program is also an investment for keeping and attracting competent staff to the units. This initiative, along with our staffing needs, is factored into our budget proposal for 2025-2028.

Missed opportunities

Our user base is dominated by principal investigators who are well-established at their respective universities. However, many academic projects of high scientific quality and with potential for translational research are not requesting support from SciLifeLab DDD. This probably depends on a lack of entrepreneurial interest from scientists or incentives to take on a drug discovery project that does not promote their scientific career. We are eager to participate in initiatives that can enhance incentives for universities to promote translational research and drug discovery. This could involve career advancement opportunities at the university, exchanging rights of intellectual property against research funding, or other measures. Such initiatives could also appeal to younger scientists with innovative ideas for translational research.

Budget request

SciLifeLab DDD needs to increase the staff with 2 experimentalists/project leaders to maintain our current operations and to give increased support to the innovation system and the increased scope for project management. To support technology platforms initiatives, we need to increase our staff to 4 specialist scientists. Administrative support equaling 1 FTE is required to handle these new collaborations. Finally, the SciLifeLab DDD instrumentation is aging and we need to renew and replace it with new instruments.

There are several uncertainties in the budget. The basal funding of SciLifeLab DDD (SciLifeLab LÄK) relies on Governmental funding based on the upcoming research and innovation bill. Moreover, the agreements between DDD and Uppsala University concerning ENABLE2 (funded by the Swedish Research Council, VR) as well as the strategic funding from Uppsala University (SFO) are signed yearly. Funding to OligoNova from Västra Götaland region (VGR) is decided until December 2024. There is no decision for 2025-2028.

We cannot take the funding for 2025-2028 for granted. The deficit in the budget for year 2024 at DDD (excluding OligoNova) is paid by the surplus from previous years. After accounting for an accumulated surplus during the buildup phase of OligoNova (2021-2023), accumulated deficits for OligoNova at the closing of 2028 are -8.5 MSEK and need to be covered by additional funds.

External funding constitutes approximately 37% of the revenues for the platform (87% for OligoNova during the funding period 2021-2028). SciLifeLab DDD and OligoNova will continue to find new strategic collaborators and funding partners to support translational drug discovery research in Sweden.

Table 1. Drug Discovery and Development Platform Budget

Costs	2024	2025	2026	2027	2028
DDD Personnel 40 FTEs (2024) -> 47 FTEs (2025–2028)	38 239	44 931	44 931	44 931	44 931
Operations	13 714	16 000	16 000	16 000	16 000
Premises	5 172	6 827	6 827	6 827	6 827
Instrument depreciations	6 661	11 000	11 000	11 000	11 000
Other	14 118	16 600	16 600	16 600	16 600
Sum DDD (kSEK)	**77 904**	**95 358**	**95 358**	**95 358**	**95 358**
OligoNova					
OligoNova Personnel 10 FTEs (2024) -> 10 FTEs (2025–2028)	9 529	9 780	9 976	10 175	10 379
Operations	8 795	6 923	7 062	7 203	7 347
Premises	1 800	1 800	1 800	2 500	2 500
Instrument depreciations	8 599	9 300	9 300	7 800	3 000
Other	4 634	4 009	4 089	4 171	4 254
Sum OligoNova (kSEK)	**33 357**	**31 812**	**32 227**	**31 849**	**27 480**
Sum costs (kSEK):	**111 261**	**127 170**	**127 585**	**127 207**	**122 838**

Revenues	2024	2025	2026	2027	2028
DDD, excluding OligoNova					
SciLifeLab LÄK funding (current and requested 2025–2028)	*59 224*	*80 224*	*80 224*	*80 224*	*80 224*
SciLifeLab NAT funding (current and requested 2025–2028)	*300*				
Uppsala University (SFO)	2 500	2 700	2 700	2 700	2 700
ENABLE2 (VR)	4 500	4 620	4 620	4 620	4 620
EUbOpen (IMI)	604				
Conception (IMI)	91				
BRIDGE (Vinnova)	930	928	773		
User fees	6 961	7 100	7 242	7 387	7 535
Sum revenues (kSEK):	**75 110**	**95 572**	**95 559**	**94 931**	**95 079**
OligoNova					
SciLifeLab NAT funding (current and requested 2025–2028)	*4 000*	*4 000*	*4 000*	*3 000*	*3 000*
Gothenburg University	4 000	4 000	4 000	3 750	3 750
KAW	13 500	13 500	10 000	10 000	10 000
Carl Bennet	3 000	3 000	3 000	3 000	3 000
VGR	3 000	3 000	3 000	3 000	3 000
User fees	1 500	2 000	2 000	2 500	2 500
Sum revenues (kSEK):	**29 000**	**29 500**	**26 000**	**25 250**	**25 250**
Sum revenues (kSEK):	**104 110**	**125 072**	**121 559**	**120 181**	**120 329**



Support for Computational Resources unit in Uppsala. Photo: Mikael Wallerstedt

Bioinformatics Platform

Basic Information

Platform Director: Bengt Persson, Uppsala University

Platform Co-Director: Björn Nystedt, Uppsala University

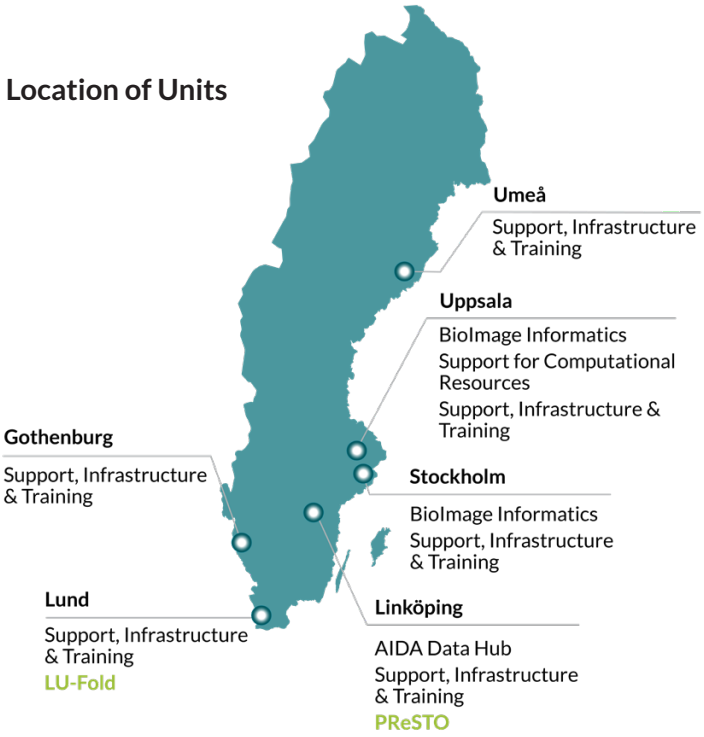
Platform Coordination Officer: Björn Nystedt, Uppsala University

Platform Vision: Enable world-class life science research and maximise scientific and societal impact of collected data

Platform Mission:

- Providing expert knowledge, innovative data integration, advanced training, efficient data publication for open science, and access to high-performance data analysis methods
- Coordinating bioinformatics support within Sweden and making bioinformatics easily accessible for life science researchers
- Swiftly responding to changes in support needs as new techniques are developed and utilised
- Forming the Swedish ELIXIR node and participating in relevant international projects

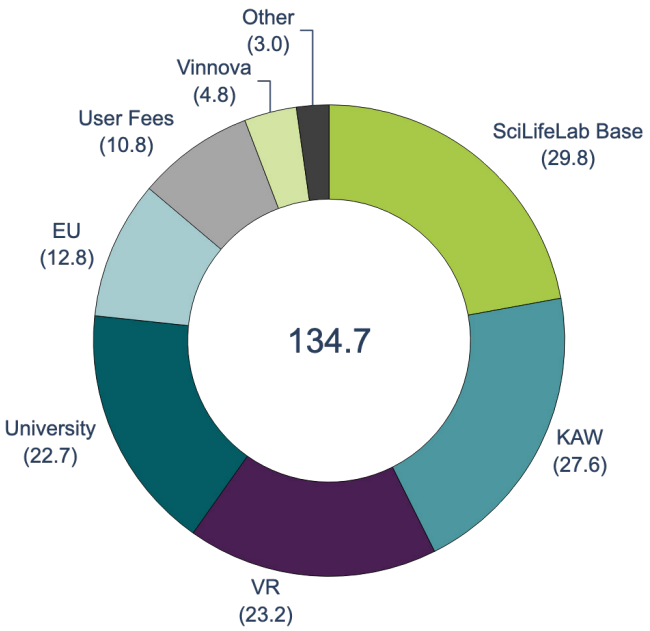
Location of Units



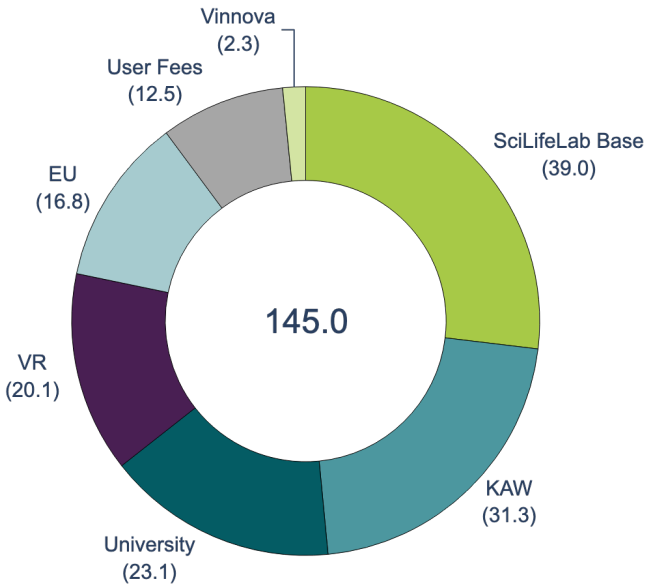
SciLifeLab Funding

Item	SciLifeLab Funding 2024 (MSEK)	Requested Annual SciLifeLab Funding 2025-2028 (MSEK)
Bioinformatics	29.8	34.5
LU-Fold*	0.0	2.1
PReSTO*	0.0	2.5
Total SciLifeLab Funding	**29.8**	**39.1**

Total Funding 2024 (MSEK)



Total Requested/Predicted Annual Funding 2025-2028 (MSEK)



E21 Bioinformatics

Overview of the Bioinformatics Platform

Overall platform development and key achievements 2021–2024

The SciLifeLab Bioinformatics platform, also known as National Bioinformatics Infrastructure Sweden, NBIS, provides the Swedish Life Science community with state-of-the-art expertise in bioinformatics and data science at a level of competence that single research groups are not able to sustain. During 2021–2024, our expertise has broadened to also include image analysis and, as of recently, structural biology. Data integration has remained important for NBIS to glue together the SciLifeLab platforms and other data-producing facilities in Sweden to open up new and exciting research horizons, and our interactions with the other SciLifeLab platforms have been strengthened. With AI, data and training being increasingly important for life science, NBIS has naturally integrated with many central SciLifeLab efforts recently launched, and has also better connected to the public and industrial arena (*Figure 1*). Furthermore, by our membership in the European infrastructure ELIXIR we have in the last four years increased our international engagement to improve access to data and services not available through the national infrastructures. All activities are found at the NBIS SciLifeLab homepage and at nbis.se, as well as in the NBIS Annual Report. A few key achievements 2021–2024 are listed below.

Broadening the scope of bioinformatics support

- About 250 active support projects annually (about 100 new each year).
- About 280 collaborative peer-reviewed publications in 2021–2023.
- Improved collaborations with other SciLifeLab platforms, and new support team structure to align with the SciLifeLab Data-driven Life Science (DDLS) efforts.
- Expanded scope of the support activities by adding the BioImage Informatics unit, AIDA Data Hub competence in AI for medical imaging, and structural biology/protein structure prediction.

Scaling up infrastructure for sensitive data access

Infrastructure projects developed by NBIS and launched for production since 2021:

- FEGA-SE: The Swedish node of the Federated European Genome-phenome Archive, providing secure and legally correct access to sensitive human data.
- DGX-2: Infrastructure for research and innovation in medical imaging diagnostics AI by AIDA Data Hub, including hosting of the SCAPIS data lab.

Infrastructure projects for sensitive data access with major NBIS involvement initiated since 2021:

- GDI: The European infrastructure for genomics data to enable the European 1+ Million Genomes Initiative (1+MG) – an EU DIGITAL project with 25 MSEK to NBIS over 4 years.
- EUCAIM: A sister initiative to GDI in European cancer imaging.
- ASHA: Vinnova-funded data spaces for primary and secondary use of health data in open standards, a sister initiative to the National Genome Platform (NGP) by Genomics Medicine Sweden/Clinical Genomics.

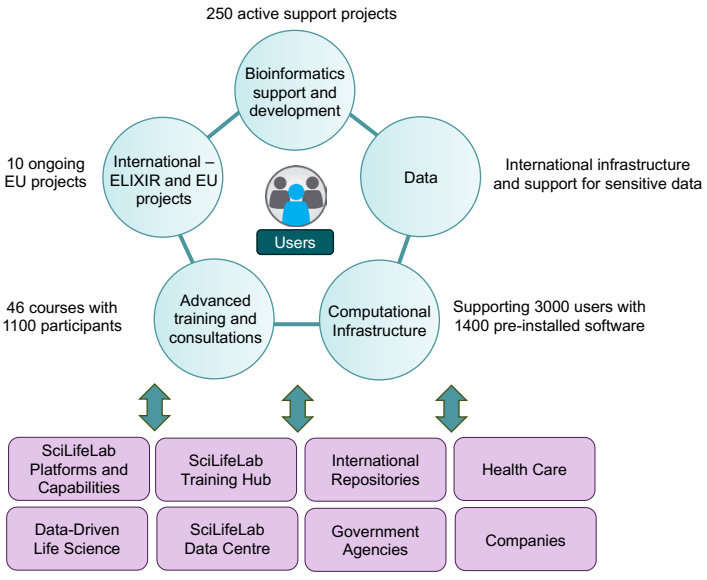


Figure 1. NBIS activities and selected highlights for 2023.

- Bigpicture: The future European infrastructure for digital pathology, a 6-year EU/IMI flagship project with 56 MSEK to NBIS.

Improving data management support and guidance

- Launched the European ELIXIR Research Data Management Community for life science data management professionals (co-chaired by NBIS).
- Launched RDM Guidelines, the support portal for the management of life science research data in Sweden, together with SciLifeLab Data Centre.
- Co-chairing Task Forces within the EOSC Association to advice on the implementation of the European Open Science Cloud (EOSC)
- Co-chairing the Life Science Data Infrastructures Interest Group within the Research Data Alliance (RDA).

Delivering computational infrastructure support for wide user communities

- Helpdesk at the national computational infrastructure, supporting over 3000 active users and about 250 publications annually.
- Installed and/or maintained about 1400 software modules on national compute clusters.
- Launched *PLUPP*, a much improved national pollen data and prognosis framework, developed together with the Swedish Museum of Natural History, for wide societal usage.
- Maintained *MrBayes*, a widely used software with 76 673 citations and more than 1300 installations last year.

Continuing the scale-up of advanced training and consultation

- Gradual increase of the postgraduate training repertoire, now with 46 organised/co-organised national courses with a total of 1100 attendees in 2023.
- Weekly drop-in consultations, and booked one-to-one consultations.
- Continued the Bioinformatics Advisory Mentorship Programme for PhD students.
- Provided international training such as *RaukR summer school in R*, and *Omics integration and Systems Biology workshop for the Chan-Zuckerberg Initiative community.*

Advancing SciLifeLab's international contribution in bioinformatics, data and training

- Co-leads, together with ELIXIR Finland, the construction of the European genomics data infrastructure in the EU project GDI (Genomic Data Infrastructure).
- Participated in 12 EU projects.
- Co-leads the ELIXIR Training Platform and the ELIXIR Research Data Management Community.

Societal impact

NBIS primarily focuses on academic users, but directly and indirectly provides vital societal impact in a number of different areas, as briefly outlined below.

Open Science and FAIR data. NBIS enables access to FAIR data, a key foundation for innovation and research in the public and private domain.

Translational molecular research. NBIS enables important medical and translational molecular research projects of relevance for new diagnostics and treatments, ultimately benefiting patients in Sweden and worldwide.

Medical imaging diagnostics and innovation. AIDA Data Hub provides services in data collection, processing, sharing, and policy support in medical imaging diagnostics, to benefit Swedish patients through clinic-native research and innovation, and adoption of world-leading AI tools.

Forestry, agriculture and fishery. NBIS engages in several research projects on commercially important plants (e.g. spruce, pine, willow, populus) and animals (e.g. chicken, herring, cisco), providing valuable information on population diversity and adaptive traits.

Biodiversity and conservation biology. NBIS is engaged in national and international efforts such as the Biodiversity Genomics Europe and the Swedish pilot of the Earth Biogenome Project, to aid policy decisions for example in sustainable fishery (The Swedish Agency for Marine and Water Management) and species conservation (The Swedish Environmental Protection Agency).

PLUPP – a new pollen prognosis system. Advances the field of aerobiology and public health, enabling researchers and developers to better access and seamlessly incorporate real-time pollen data and forecasts into a wide range of applications.



Figure 2. NBIS Staff at Smådalarö Gård retreat in October 2023

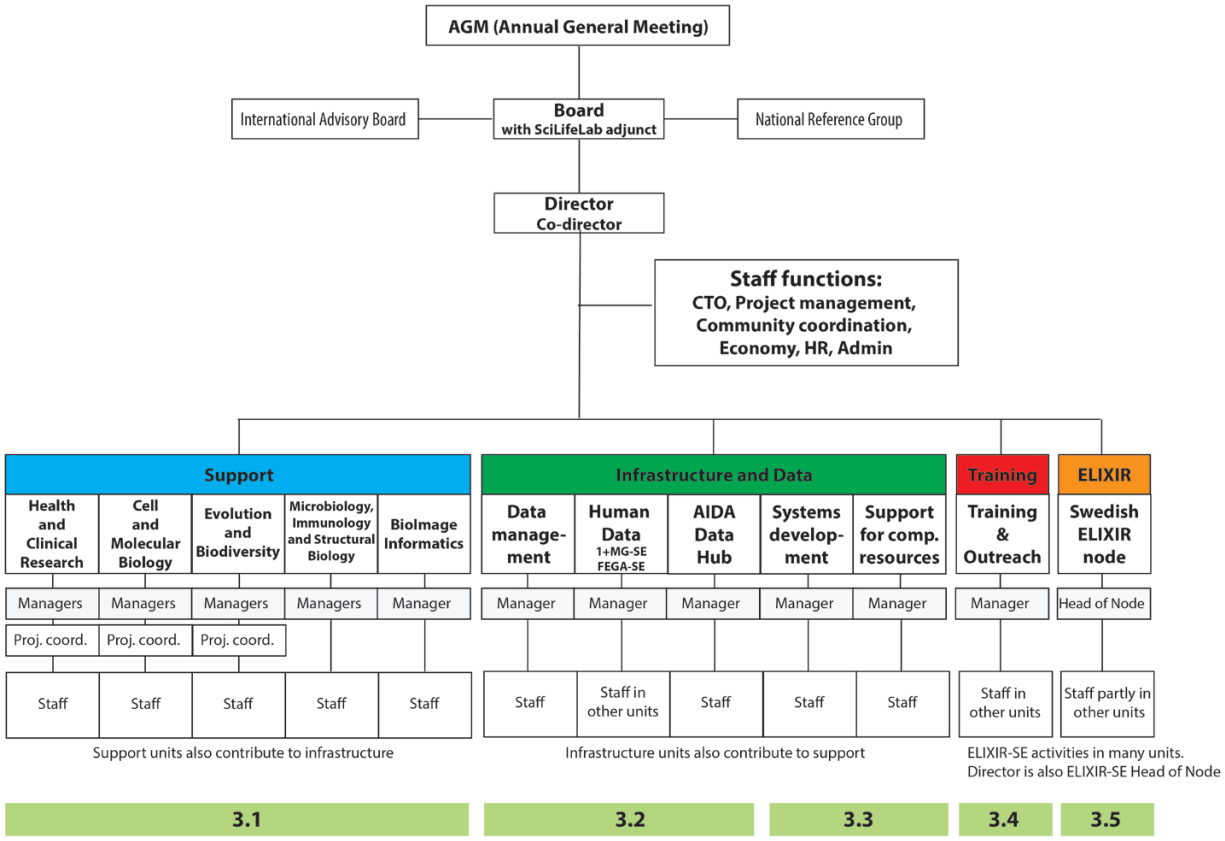


Figure 3. NBIS organisation

Organisation and funding

NBIS is a distributed national infrastructure hosted at Uppsala university, with currently ~120 staff (95 FTE; *Figure* 2) across all 11 partner universities. The operation covers Support, Infrastructure & Data, and Training, for practical reasons organised in a number of teams (*Figure* 3). The light green bars indicate the sections where the activities 2025–2028 are described in detail. Two new activities will be integrated in the current NBIS organisation, LU-Fold will be part of the Support unit and PReSTO will be part of the SCoRe unit. Note that the platform operates as one coherent infrastructure, but during 2021–2024 "BioImage Informatics", "AIDA Data Hub" and "Support for Computational Resources" have been handled as separate units in the SciLifeLab budget and reporting. NBIS is a robust platform with over 15 years of experience of operating national bioinformatics support, infrastructure and training in Sweden, and was incorporated as the SciLifeLab bioinformatics platform in 2013. The main funding sources of NBIS are currently SciLifeLab, VR (the Swedish Research Council), KAW, Universities (11 partners), User fees, and EU projects (including ELIXIR) (*Figure* 4).

Infographics: Statistics and Metrics for Units

Support, Infrastructure and Training

Read more: Webpage, Publications Database

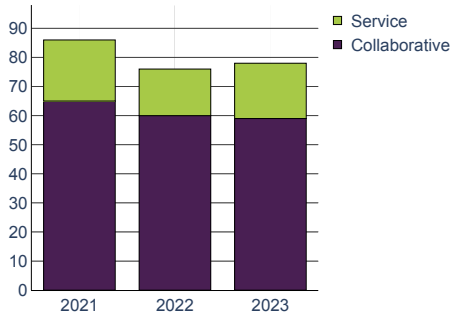
Basic Information

HU: Bengt Persson (Bioinformatics PD) + 9 HUs
Host University: Chalmers, GU, LiU, LU, KI, KTH, NRM, SLU, SU, UmU, UU
SciLifeLab unit since: 2013
FTEs: 79
PSD: Gunnar von Hejine

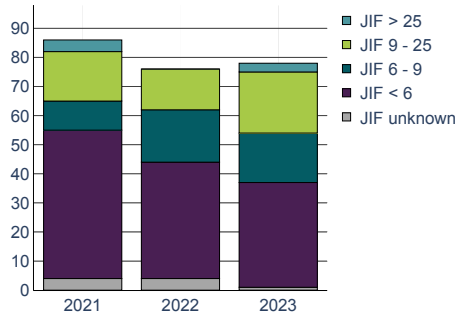
Funding 2023 (kSEK)

SciLifeLab: 18850
Other: 74157
User Fees: 10300

Publications by category

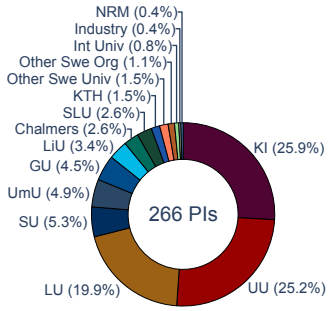


Publications by JIF

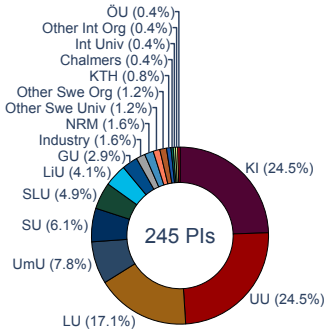


No. of Tech Dev Publications 2021 - 2023: 2

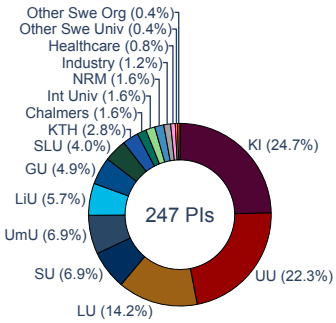
Users 2021



Users 2022



Users 2023



- *During 2023, SIT (together with AIDA DH) participated in 9 EU projects with a total of 17.8 MSEK funding.*
- *During 2023, SIT (and the other three NBIS units) organised and co-organised 46 courses with 1103 participants.*

BioImage Informatics

Read more: Webpage, Publications Database

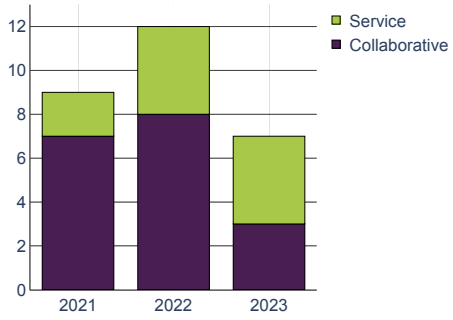
Basic Information

HU: Anna Klemm
Host University: UU, KTH
SciLifeLab unit since: 2016
FTEs: 5.48
PSD: Carolina Wählby, Kevin Smith

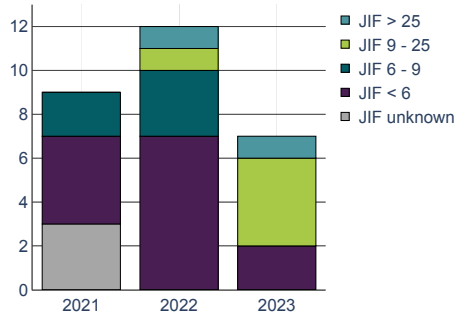
Funding 2023 (kSEK)

SciLifeLab: 3600
Other: 2250
User Fees: 500

Publications by category

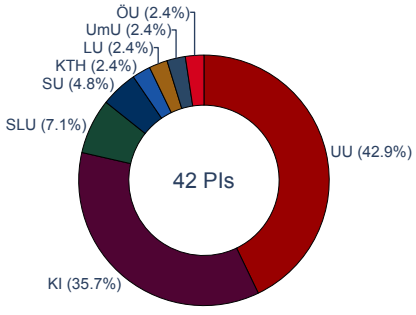


Publications by JIF

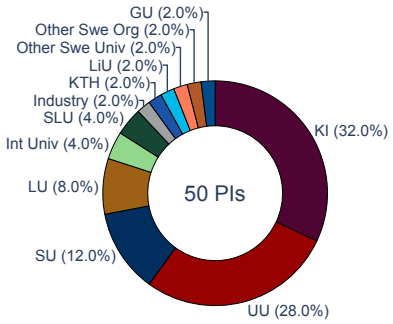


No. of Tech Dev Publications 2021 - 2023: 7

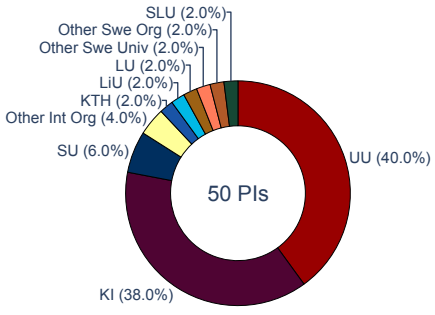
Users 2021



Users 2022



Users 2023



- *17 courses on topics like Deep Learning, Spatial Omics, Digital Pathology + 14000 views on BIIF YouTube channel in 2023*
- *12 contributions to Swedish community events, international conferences and hackathon in 2023*
- *About 3600 TissUUmaps package downloads in 2023*

AIDA Data Hub

Read more: Webpage, Publications Database

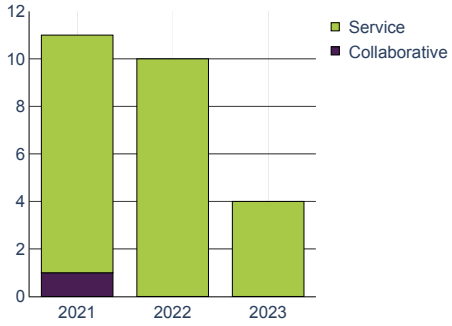
Basic Information

HU: Joel Hedlund
Host University: LiU
SciLifeLab unit since: 2021
FTEs: 7.35
PSD: Claes Lundström

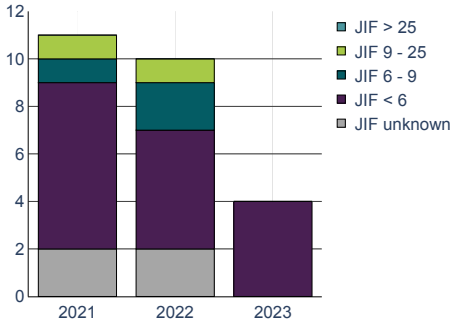
Funding 2023 (kSEK)

SciLifeLab: 3000
Other: 3831
User Fees: 0

Publications by category

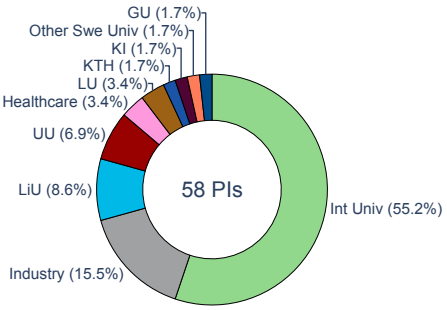


Publications by JIF

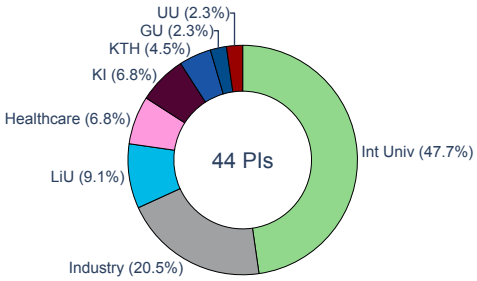


No. of Tech Dev Publications 2021 - 2023: 1

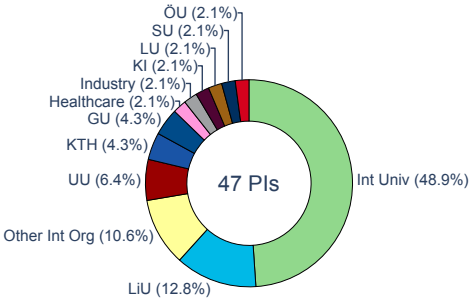
Users 2021



Users 2022



Users 2023



- *Data Sharing*: Countries: 34 (+9), Datasets: 26 (+8) 12.55 TB.
- *AI Support*: 9 projects, 2 training events + 3 planned.

Support for Computational Resources

Read more: Webpage, Publications Database

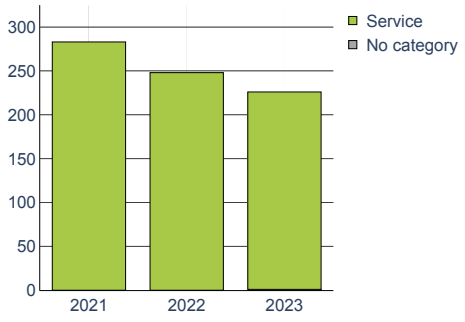
Basic Information

HU: Marcus Lundberg
Host University: UU
SciLifeLab unit since: 2013
FTEs: 5.2

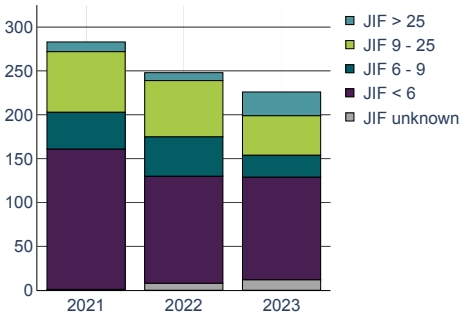
Funding 2023 (kSEK)

SciLifeLab: 3400
Other: 800
User Fees: 0

Publications by category

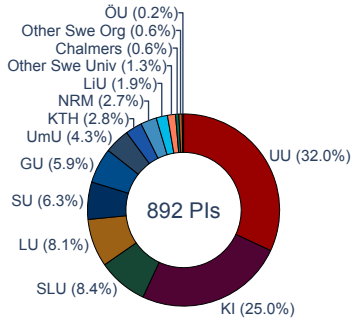


Publications by JIF

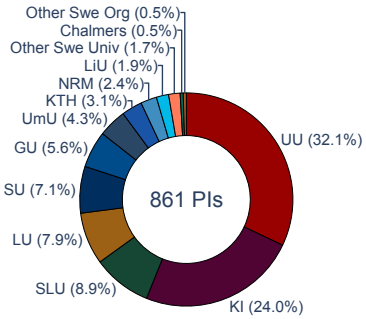


No. of Tech Dev Publications 2021 - 2023: 0

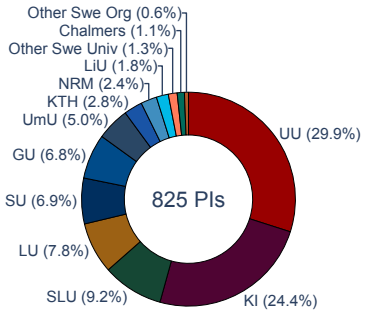
Users 2021



Users 2022



Users 2023



- *1389 software modules*
- *Data in active projects: 4.3 PB of sensitive personal data, 8.2 PB non-sensitive data*
- *PI's with 19 different organisational affiliations, 3633 active users*

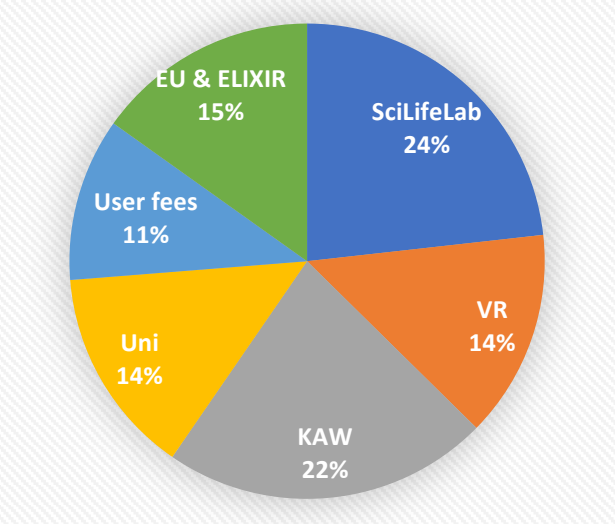


Figure 4. Current NBIS funding

Overall platform plans 2025–2028

Strengthen the role as a key national knowledge-hub

Build and attract competence

NBIS will remain the leading advanced bioinformatics training provider in Sweden, and together with the SciLifeLab Training Hub and the DDLS programme, we will deliver a postgraduate training, consultation and mentoring portfolio of outstanding international quality. In addition to the direct competence impact, this will also market Sweden as a top choice for international recruitments of life science PhD students, post-docs and young researchers in general, offering a leading environment to perform data-driven research. As computational research groups will gradually increase, we will involve them to deliver novel training components, but we envision our staff to remain a key asset for rapid dissemination of knowledge across universities and research domains, and to provide the solid backbone of the national post-graduate bioinformatics training.

Increase international engagement, innovation, and societal services

NBIS is establishing as a robust and trustworthy partner in large international infrastructure, capacity building and resource initiatives, and NBIS forms the Swedish node in the European infrastructure for biological data (ELIXIR). Over the next funding period we will strengthen this development through increased international engagement and funding, and, together with the strong IT infrastructure provided by the Data Centre, even better connect SciLifeLab to the international arena of Open Science, data accessibility, and AI-assisted research and innovation. The public health sector is a key focus of this development with several large projects in genomics, digital pathology, cancer imaging, and rare disease already underway. The Federated European Genome-phenome Archive (FEGA), the European Genomic Data Infrastructure (GDI), Bigpicture, and work by the AIDA Data Hub have put us in a good position to lead also the legal and ethical aspects of this development, to find solutions where health care, academic and private sectors can work together as envisioned in the European Health Data Space (EHDS). Together with the Genomics platform we have also made SciLifeLab a strong European partner in biodiversity, and 2025–2028 we further strengthen our recently established connections to regional, national and international environmental agencies to aid better informed decision making in an era of climate change and rapid biodiversity loss.

Expand in AI-driven competence areas

AI and data-driven life science

AI and large data volumes are transforming life science, and NBIS's role in advanced bioinformatics and data science is thus more crucial than ever. Through permanent staff positions and a dynamic working environment with cutting edge technical and scientific challenges, NBIS has been successful in recruiting leading bioinformaticians, system developers and data stewards. Together with the Data Centre staff, this central hub of competence is a goldmine of knowledge for PhD students, postdocs and other researchers, as they are faced with rapidly emerging opportunities, but also as they meet challenges such as a very fast turnover of new machine learning tools, new requirements for AI result validations, and increased demands on data access. During 2025–2028, NBIS will retain central competence in molecular data analysis, but will also continue to increase efforts in general data science, machine learning and MLOps, and data accessibility questions at the national and international arena, to provide optimal working conditions for researchers in data-driven life science.

Image analysis and digital pathology

Image analysis is a rapidly growing area with huge potential for research and applications. SciLifeLab invested early in this domain thanks to the world-leading Swedish scientists Carolina Wählby (image analysis, UU; recent publications: Pielawski et al., 2023, Chelebian et al., 2024) and Claes Lundström (AI in digital pathology, LiU/Sectra; recent publications: Pocevičiūtė et al., 2024, Lundström and Lindvall, 2023), and they continue to guide our operations as Platform Scientific Directors. We are also collaborating closely with the SciLifeLab Spatial Biology platform, as the merge of image and omics analysis is opening up exciting new research opportunities.

Structural biology including LU-Fold and PReSTO

Thanks to radically improved protein structure prediction methods, structural biology is becoming an integral part of a wide range of biological research projects. With the Platform Scientific Director Gunnar von Heijne (protein bioinformatics, SU; recent publications: Teufel et al., 2022, Mermans et al., 2022), we have already recruited structural bioinformatics experts embedded at the Cryo-EM unit, as well as developed novel approaches to combine experimental data and prediction methods. SciLifeLab is therefore in a perfect position to establish structural biology services in this transformative time at the absolute top international level. To realise this, we see urgent needs to incorporate additional capacities into NBIS, as proposed in the the sections E22 and E23 below. *LU-Fold*, initiated by Assoc. Prof. Gemma Atkinson (LU), provides a very timely opportunity to ramp up our structure prediction capacity with new complementary skills, and connect SciLifeLab with a new and growing community of users. *PReSTO* addresses that the structural biology community increasingly heavily rely on supercomputer resources. PReSTO offers a unique technical framework to make this transformation feasible, to give Swedish and SciLifeLab users a competitive advantage by providing a powerful interface to national high-performance compute resources and a broad repertoire of preinstalled software.

Improve SciLifeLab services by cross-platform initiatives

Increase cross-platform interactions and launch of the NBIS Technology Development Projects

During 2025–2028, NBIS will further strengthen the connections to the other SciLifeLab platforms. Designated NBIS experts are already appointed as main contacts for each platform, to engage in joint user meetings on study design and discuss improved platform interactions in general. NBIS staff are placed at for example the Cellular and Molecular Imaging platform (Stockholm) and Clinical Genomics (Lund) for increased synergies, and a new MS proteomics expert will be embedded at the Clinical Proteomics and Immunology platform. Improved metabolomics support will be achieved through joint recruitment and the establishment of a cross-platform metabolomics computational group with the Metabolomics platform, and other similar initiatives are expected to increase over time.

NBIS is also engaged in a number of joint technology development projects with the other SciLifeLab platforms for improved user services, such as spatial multi-omics processing, AI in structural biology, and metabolomics processing (Table 1). During 2025–2028, we will in collaboration with the SciLifeLab management group scale up and formalise this effort by launching *NBIS Technology Development Projects*, to efficiently identify, prioritise and execute cross-platform projects to provide vital added value for the SciLifeLab user community.

Capabilities

The SciLifeLab capabilities in Precision Medicine (PM) and Planetary Biology (PB) are starting to take shape, and NBIS will be a key partner in both. NBIS is already engaged in the first PM capability project call with providing bioinformatics resources for selected translational projects. NBIS and the Genomics platform currently form the backbone of the PB capability, for example through ongoing national and international efforts in streamlining academic and societal services in biodiversity monitoring and conservation biology, and we foresee for the next funding period a much increased interest in this area. For the Pandemic Laboratory Preparedness (PLP), NBIS will continue to discuss the scope of this capability and to what extent NBIS can take a more prominent role in data access and data analysis, as for example in improved and expanded viral and bacterial waste-water monitoring.

Collaboration with SciLifeLab Data Centre

NBIS interacts closely with the Data Centre, as detailed elsewhere in this report, and will cooperate even more during 2025–2028 as the Data Centre is now significantly expanding within the DDLS programme, for example at the DDLS Data Science Nodes with co-located NBIS and Data Centre staff. The main current collaborative areas are data management, including training activities, provision of NBIS apps and services at Data Centre hardware resources, and services for AIDA Data Hub, where Data Centre operates the AIDA wiki and the AIDA Nextcloud. Coordination between NBIS and Data Centre in AI activities and data access will be increasingly important, with regular coordination meetings planned. In addition, the Data Centre lead is an adjunct member of the NBIS management group, and vice versa, to ensure optimal joint strategic alignment.

Detailed operations and platform plans 2025–2028

Below, we describe our platform operations and plans more in detail, divided into five operational areas, following the organogram from left to right (Figure 3, light green bars at the bottom): 3.1. Bioinformatics Support, 3.2. Data, 3.3. Computational Infrastructure, 3.4. Advanced Training, consultation and outreach, 3.5. International – Swedish ELIXIR node and EU projects. Additional details are found in our Strategic Plan 2024–2028.

Bioinformatics Support (3.1)

There is a global shortage of the advanced bioinformatics and data science competence needed to tackle many life science research questions. NBIS will continue to build on our internationally unique model with distributed national support teams, to upskill the community and to make applied bioinformatics and data science more easily accessible. Our support staff are senior bioinformaticians (many recruited directly from abroad) and count among the best applied bioinformatics experts in Sweden and sometimes among the top in the world in their respective domain. NBIS staff do not drive their own research, but engage in the research questions of Swedish life science researchers according to open and transparent support tracks (see below). With on average more than 10 years post PhD, our 54 support experts represent 21 nationalities, and together hold a staggering 564 working years of senior bioinformatics experience. This unique knowledge hub is key for SciLifeLab to efficiently disseminate bioinformatics skills across Sweden, through deep engagement with PhD students and postdocs in research projects, weekly drop-in online and on site, free consultation meetings, methods and workflow development, a PhD mentoring programme, open seminars, and through a broad and dynamic training catalogue of currently more than 40 annual courses (see Advanced training, Consultation and Outreach below).

Competences

Biological domain knowledge has become more important for our bioinformatics staff, and our support teams comprise competences in all the Research Areas of the SciLifeLab DDLS programme. General skills include classic omics-based bioinformatics, advanced multivariate statistics and data integration, machine learning, data visualisation and robust workflow implementations. We cover established omics areas such as genomics, proteomics and metabolomics, and have in the last decade systematically acted as early adopters and promoters of emerging technologies such as single-cell omics, Olink proteomics, spatial biology, and ancient DNA, very well aligned with the SciLifeLab investments in these areas. The revolution in machine learning/AI is now focusing our competence development and recruitments into new areas, including image analysis, digital pathology, and structural biology. Hence, we are now operating within and across the scope of all the data producing platforms at SciLifeLab.

Projects and user base

NBIS has users from all Swedish major universities, and initiates about 100 new support projects of varying size each year. We are thus actively engaged in data analysis with well over 200 different research groups annually, providing in itself a unique network in Sweden for rapid dissemination of technical knowledge across research groups, universities and domains. About 70% of all projects have SciLifeLab-generated data, with the rest being a mix of projects with only public data, generic workflow and method development projects, smaller pilot projects, and projects with locally produced data. While we occasionally work with research groups with no bioinformatics competence, most times we interact closely with PhD students/postdocs to build community knowledge. Our staff contribute to scientific progress as co-authors of around 280 peer-reviewed research articles across a very wide range of topics in the last three years (2021–2023), as illustrated by just a few recent examples below (additional examples found in our Annual Report for 2023).

The Swedish childhood tumour biobank – To improve paediatric diagnostics and care: NBIS bioinformatics and data management staff have supported The Swedish Childhood Tumour Biobank (BTB), a national infrastructure for tissue samples and genomic data from paediatric patients with central nervous system and other solid tumours. Using blood-derived DNA and methylation profiling we showed potential to enhance diagnostic accuracy, and identified novel driver events. All BTB data are made available at FEGA Sweden (see below) to help impact the clinical care for children with cancer towards improved personalised treatments. (J Transl Med 21:342, 2023).

Novel diagnostic test for metastatic prostate cancer in clinical practice. Together with the Lindberg group (KI) and molecular pathologists at the Karolinska University Hospital, NBIS has developed a novel diagnostic test based on sequencing of circulating tumour DNA in plasma. NBIS staff improved the sensitivity to detect loss of BRCA2, an actionable biomarker which has previously been particularly challenging. The new method is now in clinical use at the Karolinska University Hospital.

Clonal relations in the mouse brain revealed by single-cell and spatial transcriptomics: With the Frisén lab (KI), we have developed a method to simultaneously profile cell phenotypes and clonal relations in vivo, by insertion of DNA barcodes into early progenitors, followed by single-cell RNA-sequencing. In the mouse brain, thousands of clones could be reconstructed, enabling high-throughput reconstruction of cell phenotypes and clonal relations at the single-cell and tissue level in individual animals. (Nat Neurosci 25:285–294, 2022).

A topographic atlas of the human embryonic lung. Using tools co-developed by NBIS, we helped disseminate all spatial data of a topographic atlas defining developmental origins of cell heterogeneity in the human embryonic lung, which was also incorporated in the Human Cell Atlas portal to enable interactive viewing of the developmental lung data. (Nat Cell Biol 25:351–365, 2023).

Metatranscriptomics of Nasopharyngeal Microbiota and Host Distinguish between Pneumonia and Health: Lower respiratory tract infections, including community-acquired pneumonia, are major contributors to morbidity and mortality world-wide especially in children. With the Henriques-Normark's group (KI), we developed a novel ultrasensitive metatranscriptomic pipeline to map the nasopharyngeal microbiota and associated host responses, including a machine learning approach to identify new biomarkers. (Am J Respir Crit Care Med, 206:1564-1567, 2022).

The Tasmanian tiger – The first transcriptional study of an extinct animal: A study on the transcriptional profile of the extinct Tasmanian tiger by the Friedländer and Dalén groups (SU) received a lot of attention in international press, as the first example of sequenced historical RNA recovered from an extinct animal species. NBIS staff contributed with metatranscriptomic analyses designed to authenticate the RNA data from the Tasmanian tiger and explore sources of potential contamination from other organisms. (Genome Res. 33:1299-1316, 2023).

As many different omics data types have become well established in the Swedish research community (much thanks to SciLifeLab) the current trend is towards using large, multi-omics data that require technically advanced, integrative analyses and careful project planning, often including (or only based on) publicly accessible data. This trend is seen across all research areas, in biodiversity projects as well as in projects on complex diseases. We also expect an increase in clinical projects, with a likely focus on data types closer to the disease, such as biomarker arrays, proteomics, metabolomics, metagenomics and registry data. We will therefore further strengthen NBIS guidance and support in data integration, to improve and simplify project planning and data analysis.

Bioimage Informatics (BIIF)

Bioimage Informatics (BIIF) has been part of SciLifeLab since 2013 (initially UU facility, national 2016) and fully integrated with NBIS since 2021, but so far with a separate budget and is therefore specifically outlined in this section.

BIIF provides support and training to perform state-of-the-art analyses on image data using computational methods based on computer vision, machine learning, and bioinformatics. Microscopy data is very heterogeneous, with many specialised tools targeting specific challenges of different imaging modalities. The field has been significantly accelerated by the developments in artificial intelligence, and support projects in 2023 spanned for example the GPU-supported 3D segmentation and spatial analysis of organoids in lightsheet microscopy data, building a deep-learning based segmentation pipeline for complex structures in tissue samples, providing support using pretrained networks through the BioEngine framework, and building an nf-core pipeline for spatial transcriptomics (see also BIIF publication list). BIIF co-develops TissUUmaps, a browser-based spatial omics tool for fast and interactive exploration of millions of data points overlaying a tissue sample. BIIF provides support in publishing data for interactive exploration via the SciLifeLab server (tissuumaps.github.io/gallery). Furthermore, BIIF is regularly involved in advanced technology development projects in close collaboration with the Spatial Biology platform, our AIDA Data Hub unit, and other SciLifeLab researchers, for example supporting the co-registration of multiplexed data sets.

BIIF also contributes importantly to the NBIS training programme, and is engaged in national and international courses such as "Advanced Methods in BioImage Analysis" (EMBO Practical Course), "Neural Nets and Deep Learning" (NBIS), "BioImage Analysis on the cloud" (NEUBIAS/EOSC-Life workshop), and "Imaging based spatial-omics" (EMBL/EMBO). Research support in BioImage analysis is still a young and developing field, and as part of the Chan-Zuckerberg-Initative, Euro-BioImaging and NEUBIAS/GloBIAS initiative, we are actively engaged in shaping this community. BIIF also contributed to the hackathon and symposium of the BioVisionCenter, Zürich – a newly arising centre for bioimage analysis.

Added community value through data, tools, and technology development

In addition to the scientific analysis and interpretations, we aid the projects to publish well-annotated research data in international repositories (cf. Data Management below) and at resources provided by the SciLifeLab Data Centre. To foster open science/reproducible practice, we have revised our user agreement to explicitly require project data and analytic tools to be FAIR, open and reproducible. We also provide data management training to the genomics infrastructure to enhance metadata quality. Data exploring apps and models are made accessible through the Data Centre Serve to catalyse third-party data reuse, and project-specific code is published Open Source. We also derive novel or improved workflows and software in emerging or developing areas, such as cancer genomics (SAREK), Image analysis (TissUUmaps, DEPICTER), genome annotation processing (AGAT), Immunology (IgDiscover), ancient metagenomics (aMeta), conservation biology (GenErode), biodiversity (AmpliSeq) and read trimming (Cutadapt) (see NBIS Tools Page). In the past two years we have ramped up our involvement in joint technology

Table 1. Recent or ongoing joint technology development projects with other SciLifeLab platforms

Collaborating platform(s)	Technology Development
Chemical Biology and Genome Engineering	Chemical Space: In vitro compound screening
Chemical Biology and Genome Engineering	CRISPR data processing
Clinical Genomics	Bioinformatics workflow improvements
Clinical Proteomics and Immunology	Embedded bioinformatician
Drug Discovery and Development	E3 ligases assay development
Integrated Structural Biology / Cellular and Molecular Imaging	BeyondFold: Protein structure prediction
Genomics	Spatial Transcriptomics processing
Metabolomics	MetaboIGNITER: Metabolomics processing
Spatial Biology	Spatial Biology multi-omics integration

developments with the other SciLifeLab platforms for improved user services in for example spatial multi-omics processing, AI improvements in structural biology, and metabolomics processing (*Table* 1). These successful examples have prompted us to scale up and formalise these efforts in the next funding period 2025–2028.

Project prioritisation and support tracks

All projects are screened for scientific and technical feasibility, and we regularly help research groups to improve and complement their studies for optimal scientific value. Support is provided in open and transparent processes in three different tracks to meet different needs and funding constraints.

User fee projects are accepted as first-come-first-serve at 800 SEK/hour, with analyses typically starting within a few weeks from signed contract.

Partner Projects are large projects (typically at least 50% FTE over 2 years) occasionally accepted based on available resources, and charged a standardised salary rate plus 35% overhead costs.

Peer-review projects (WABI) are selected for scientific excellence in open calls by an external review committee appointed by the SciLifeLab DDLS Director, and allocated 500 hours support fully funded by KAW through the DDLS programme. For all Partner Projects and the Peer-review (WABI) projects, extensive involvement in the hands-on data analysis is required by the research group to ensure knowledge transfer.

The total income from user fees has gradually increased over time, indicating better awareness of costs for advanced bioinformatics, and we expect a continued growth of user fees 2025–2028. NBIS services are available also to the private sector on a full cost-recovery basis, currently 1800 SEK/hour. The KAW funding for the Peer-review projects (WABI) will gradually decrease somewhat during 2025–2028 and the volume of this support track will be adjusted accordingly.

Data (3.2)

NBIS is engaged in data management activities regarding Data management and Data publication support and regarding Human data, detailed below.

Data management and Data publication support

The Swedish Government has set a national goal for a transition to open access to research data to be fully implemented by 2026 at the latest, and the National guidelines for Open Science were just published in January 2024. The Swedish Research Council (VR) has been mandated by the government to coordinate this, and NBIS sees as its role to support these efforts, and to be a catalyst for the life science research domain in this transition to open science. The overarching vision for the NBIS data management activities is that Swedish life science researchers apply good data management practices so that the research outputs produced are available to the global research community, and to society at large, according to the principles of Open Science, Reproducible Research, and FAIR (Findable, Accessible, Interoperable, Reusable). Strategically, the NBIS data management efforts focus on three aspects: (1) supporting researchers in making their research data FAIR, (2) training researchers in practices that enable research data FAIRification, and (3) collaboration with national and international stakeholders for capacity building and to provide solutions for researchers. This work is done in close collaboration with the SciLifeLab Data Centre, where the NBIS focus is on the researcher perspective of data management needs, and the Data Centre efforts (mainly) focus on providing some of the technical services to meet those needs.

On the *support* side, NBIS will continue to support and improve the functionality of the Data Management Planning (DMP) online service SciLifeLab Data Stewardship Wizard (DSW), previously established in close collaboration with

the Data Centre. Existing DMP templates support national and international guidelines and are targeted towards the Swedish life science research community, and will be improved as the national and international infrastructure landscape changes, and as the field of data management best practice evolves. The most efficient way to make research data FAIR is by submitting the datasets to trusted international public repositories, especially the Core Deposition Databases (CDDs) identified by ELIXIR and the Global Biodata Coalition. We will continue supporting users in making such submissions. Going forward we will, together with the Data Centre, establish a more formal data brokering role in relation to the CDDs, as well as establishing the necessary brokering services needed for this. In this context, human data is a special focus (see below).

We see a large need for data management *training* and guidelines for Swedish life science researchers. To this end, a data management training and outreach strategy has been developed that outlines the roadmap over the coming years for expanding the training portfolio from the current course offering of basic data management practices with more advanced topics. In collaboration with the SciLifeLab Data Centre we will continue to expand and deepen the content and functionality of the SciLifeLab RDM Guidelines support portal that aims to provide a knowledge hub for the management of life science research data in Sweden.

NBIS will continue to engage and *collaborate* with the key players in the data management field, to take advantage of practices and resources developed by these stakeholders, as well as harmonising activities to follow national and international best practice. For the life science domain at the European level, we will actively contribute to shaping harmonised knowledge management, resources, and training for data management in our engagement in ELIXIR, where we have a leading role in the recently established ELIXIR Research Data Management Community, that also provides a means to leverage those collectively developed resources for the national needs. For more general aspects of data management, outside of the life science domain, we will continue to collaborate with SND (Svensk Nationell Datatjänst) and data management supporting functions at the universities, particularly regarding training and guidance at the national level. At the international level, we will continue our engagement with the Research Data Alliance (RDA) and the EOSC.

Human data – the Swedish node in 1+MG, GDI and FEGA-Sweden

NBIS has since 2011 been engaged in building infrastructure for sensitive human data. The work started in Nordic NeIC collaborations (Tryggve, Tryggve2, and Heilsa), and has intensified and expanded since 2015 with our collaborations within ELIXIR and the Swedish contributions to multiple EU projects.

NBIS takes part in several EU projects on human data. To realise the European member state initiative *1+ Million Genomes* (*1+MG*), we had 2020–2023 the *B1MG* coordination and support action and are now running the implementation project *GDI* (*Genomic Data Infrastructure*; 2022–2027) with a total budget of 40 MEUR. The major part of GDI is the construction of the human genomics data infrastructure, which work is led by NBIS (ELIXIR-SE) together with ELIXIR-FI.

NBIS is constructing a petabyte platform for European digital pathology in the EU IMI 70 MEUR flagship project *Bigpicture*. The platform will enable advanced AI research to improve diagnostics. NBIS receives a total of 56 MSEK over 6 years. Our AIDA DH unit leads the repository infrastructure development, carried out together with our systems development team and ELIXIR-FI.

NBIS is also engaged in the EU project *EUCAIM* for cancer imaging data, especially regarding interoperability with GDI and Bigpicture, and to utilise components from Bigpicture for visualisation of cancer imaging data.

To cater for the needs of publishing human genome sequence data, NBIS has recently launched the Swedish node in the international infrastructure Federated European Genome-phenome Archive (*FEGA*). A helpdesk function to provide data submission support to researchers is in place, and will increase its activities to meet the expected large workload when more human data will be deposited in FEGA Sweden in the coming years. The federated framework with national nodes, where metadata (data about data) are stored centrally, while datasets are stored locally and only accessed with proper agreements, is an elegant solution to allow for international data access within the current legal framework. There is a large unmet need for this type of service in Sweden, and with 1+MG and the coming European Health Data Space (EHDS), expected to be decided by the EU Parliament in April 2024, the importance of these activities as well as the scope will increase.

The data stored in this infrastructure must adhere to international standards that make data discoverable, retrievable, and reusable for the research community. The FEGA and GDI ensure these standards and principles in a way that storage solutions at individual universities cannot.

Human data – AIDA Data Hub

AIDA Data Hub is hosted at the LiU strategic research Center for Medical Image Science and Visualization (CMIV), and primarily directed toward the national AIDA community, providing services and support for AI research and innovation in medical imaging diagnostics.

Services include Sensitive Data Services (SDS) for AI training on sensitive personal medical data, primarily directed to leading edge researchers in medical imaging AI. SDS is host to the AIDA-SCAPIS data lab, where SCAPIS research groups can share and analyse medical imaging data in a trusted research environment. In the coming period, SCAPIS plans to use SDS to facilitate sharing of all SCAPIS imaging data with approved research groups in Sweden. A 15 MSEK v2.0 extension is planned during 2024, based on Bigpicture/GDI technologies. These technologies were originally developed for genetics, and were extended in Bigpicture to also support pathology, and will through SDS 2.0 be further extended to support data from radiology and Open standard Patient Health Records (OpenEHR). SDS 2.0 will introduce a service portfolio priced for sustainability while prioritising scientific impact and incentivising the FAIR data sharing for Open Science that is currently effected through the AIDA Data Hub Dataset Register. The SDS 2.0 extension will continue to serve the AIDA community, and will also support EUCAIM, ASHA, and CMIV, and potentially also further co-funding communities. SDS 2.0 will also be made usable by a wider range of user competence profiles (including clinicians) by providing further modes of access, such as through a locked-down EHDS conformant remote desktop, or through project private SaaS web applications like an open-source or Sectra PACS. In the next period AIDA Data Hub will contribute its SDS experiences to NAISS Arrhenius through its sensitive data procurement group.

AIDA Data Hub also offers advanced support and training in medical imaging diagnostics AI research and innovation. Areas include data sharing and policy, and system design for sensitive data, and since 2023 also advanced research support in AI development. Support has hitherto been provided free of charge; however, a model for user fees will be put in place during 2024 to align with other support functions at SciLifeLab and NBIS.

Computational Infrastructure (3.3)

Systems development

The NBIS systems development unit creates user interfaces and provides support in deploying tools so that they can be used by the entire life science community, and not just by bioinformaticians. The unit is also engaged in international projects for human data and digital pathology (cf. above). Easy-to-use tools that enable researchers to carry out more of the data analysis themselves will help to alleviate the demands for bioinformatics support in the form of consultancy.

Furthermore, the systems developers assist in maintaining and hosting a few major Swedish bioinformatics tools that have been identified as important for the global research community. NBIS provides assistance in the form of software packaging and distribution, hosting, and basic bug fixing in these cases. One example is MrBayes, which is widely used world-wide with 76 673 citations in total, more than 1300 installations last year, and with the software repository cloned 5–20 times per day. Another example is TOPCONS that has completed about 22 million queries from 38883 unique users distributed in 121 countries since Feb. 2015. NBIS is carefully following the development within AI and will adapt our services to match the future demands from new technologies.

Methods and software developed within NBIS are made publicly available to the scientific community through Open Access publication of articles and Open-Source licensing and distribution of software on publicly accessible sites. NBIS maintains public repositories (GitHub) for codes and scripts that are developed by NBIS staff. We have developed and published coding guidelines to aid in developing better software. NBIS staff also participates in the ELIXIR task Software best practices and the recently started EU project ELIXIR-STEERS to make software FAIR.

PLUPP, a new pollen prognosis system, is a collaboration between NBIS and the Swedish Museum of Natural History (NRM), to offer a single, comprehensive platform for pollen data. PLUPP advances the field of aerobiology and public health by a new open API (api.pollenrapporten.se/docs), representing a major upgrade by integrating advanced pollen forecasting functionalities into the NRM's existing PollenDB system. The new platform increases efficiency at NRM, but also enables both researchers and developers to better access and seamlessly incorporate real-time pollen data and forecasts into a wide range of applications.

Support for computational resources – SCoRe

High throughput life science depends on high-performance computers for data processing and bioinformatics analysis. The computer systems (hardware) are provided to researchers primarily by NAISS. However, software provisioning for the community is not in the scope of NAISS and has been an ongoing challenge, not only because of the wide variety of software and the productivity of the community that develops software for genomics and life science research, but also due to the changing landscape of how software is developed, delivered, and used. NBIS supports researchers in the domains of biological sequencing, biological imaging, drug screening, and other life sciences with expertise related to, and support on, high-performance computational and storage resources, as well as cloud resources when that is appropriate.

The SCoRe staff meets researchers in their day-to-day work from the time they start planning their data analysis to the point where papers are published and data are moved out. This makes the unit an effective interface between NBIS and those parts of the research community that do not receive other forms of support, allowing the collection of user needs in for example software or hardware resources or technical training. The SCoRe unit is involved in strategic planning and contributes to bridge NBIS and other SciLifeLab units with NAISS.

For the next years, we expect a continuing high number of projects as well as increasing sizes due to decreasing costs and increased capacity at the Genomics and other SciLifeLab platforms. With the growing power and utility of machine learning methods, we see a trend towards more projects that use AI tools alongside more traditional tools. SCoRe meets this challenge by working more closely with other support providers, as well as by working to increase internal competence in this area.

Advanced training, Consultation and Outreach (3.4)

Advanced training

Advanced training is a key factor to ensure Sweden's scientific competitiveness in the ongoing transformation of biology and medicine into large-scale data driven research. NBIS training activities are dynamic yet well-coordinated efforts built up over more than a decade of experience of delivering national and international courses, a national mentoring programme, and community interactions. NBIS has the mission to provide state-of-the art bioinformatics courses to life scientists within Sweden, and we provide a uniquely ambitious national training catalogue of advanced bioinformatics, data science and data management courses, and our 46 organised/co-organised courses reached more than 1100 participants in 2023 (cf. Annual Report for details). The courses are still oversubscribed, and our training materials are openly available for self-paced learning, at the NBIS and SciLifeLab websites and the ELIXIR TeSS platform.

During 2025–2028, NBIS staff will continue to provide advanced knowledge through continuous development of training materials, and revisions of the course catalogue to encompass emerging areas and techniques as we expand our expertise. NBIS will work in close collaboration with SciLifeLab Training Hub to enable FAIR training materials and standardise training in alignment with the ELIXIR Training platform. Our courses will be offered both nationally, in collaboration with SciLifeLab platforms, sites and computational scientists, and internationally, primarily through collaborations within ELIXIR. We will also continue to develop our strategy to increase interactions with industry in regards to training.

NBIS will continue to deliver PhD mentoring through the Bioinformatics Advisory Mentorship Programme started in 2015, offering PhD students a senior expert as personal advisor for 2 years. Participants are selected in open national calls, and the programme has since it started included more than 120 PhD students across Sweden. Furthermore, NBIS engages in internal capacity building for experts and other staff scientists across Swedish research infrastructures, where knowledge and skills are shared in a peer-to-peer fashion. NBIS will take an active training part in the upcoming DDLS Programme Graduate School, to be launched 2024.

NBIS will continue to have an active role in the ELIXIR Training Platform (co-lead) and contribute to various training activities through our participation in ELIXIR Focus Groups and Communities, including advanced courses on Single-cell omics analysis, Train-the-Trainer, Data science, Biodiversity, Plant sciences, Data management, and Human data. The goal is to provide training to a diverse user base and support the development of the next generation of professionals in bioinformatics, software engineering, and data management. NBIS is also working with the global organisations GOBLET, Australian Biocommons, and NIH to ensure the adequate provision of training to meet the needs of the life science community.

Consultation and Outreach

Consultations on study design and data management planning, and easy access to feedback and advice is a

central mission for NBIS and is offered free of charge. With staff distributed across universities, users can always find local representatives as an entry point, but we also facilitate accessibility in many other ways, including:

- Weekly online (and some on-site) drop-in sessions. These events are popular among users (user survey score: 99.8%; 522 answers) for guidance on experimental and computational design, choice of analysis methods, and feedback on preliminary results.
- Booked one-to-one consultations meetings, easily available at our homepage.
- NBIS technology teams have recently started open seminar series to share their knowledge and experience, for example in AI/machine learning.
- Site visits and presentations at universities, departments and research groups, providing the possibility to meet NBIS staff for discussions and advice.
- Annual symposium open to all, alternating between the NBIS sites.

Our website (nbis.se) is an important communication channel, and we regularly present at relevant conferences and workshops organised by SciLifeLab and others. Presentation material (flyers, leaflets and roll-ups) are produced and continuously updated. As we foresee an increased interest from industry, we have from 2024 assigned a dedicated industry outreach manager to meet this demand and enhance interactions.

International – Swedish ELIXIR node and EU projects (3.5)

NBIS is the Swedish node in the European infrastructure for biological information ELIXIR, and engages in the recently started ELIXIR programme for 2024–2028, NBIS is heavily engaged in human data, user communities, and training.

NBIS participates currently in 10 ongoing EU projects, which will continue through 2026/2027. NBIS contributes with construction of infrastructure for sensitive data (genomics, pathology, and imaging), systems development, bioinformatics analyses (rare diseases, biodiversity), FAIR software, advanced training, and node capacity building. About 10% of our funding is from EU projects (10 ongoing and 2 recently finalised; *Figure* 5).

NBIS had a leading role in the recently finalised ELIXIR-CONVERGE project on harmonising data management for the life sciences across Europe. The project has laid the

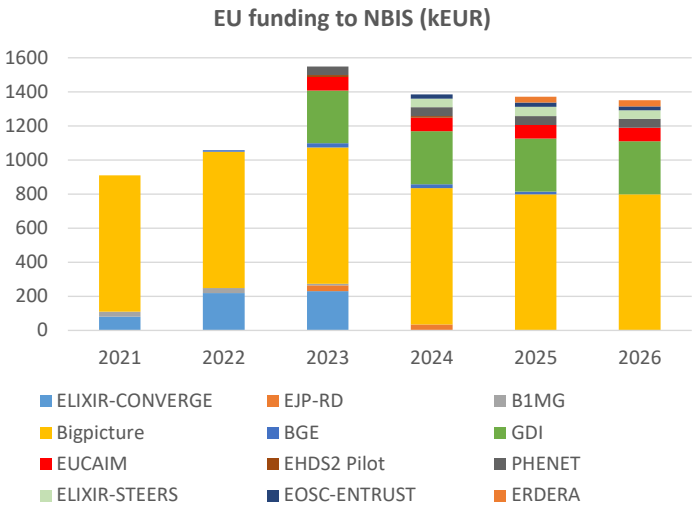


Figure 5. NBIS EU projects

foundations for coherent data management practices by establishing an international network of data stewards, the data management best-practice knowledge-base RDMkit (rdmkit.elixir-europe.org), and data management training resources. The project outputs and coordination of the ELIXIR data management activities will be taken forward in the ELIXIR Research Data Management Community, which is co-lead by the NBIS Data Manager.

Sweden has been active since the start of ELIXIR; Sweden contributes with *Human Protein Atlas* (HPA) and its integration into the ELIXIR landscape. In 2017, HPA was named ELIXIR Core Data Resource, reflecting its fundamental importance to the wider life-science community and the long-term preservation of biological data. Sweden also contributes with the *Metabolic Atlas* (MA), Advanced training (Sweden is currently co-leading the ELIXIR Training Platform), Data Management (Sweden is co-chairing the Research Data Management Community), and much more.

NBIS has regular meetings with the other Nordic ELIXIR nodes and we collaborate in the NeIC Tryggve, Tryggve2, and Heilsa projects, which have been instrumental in establishing infrastructure for sensitive data and the federated human data framework within ELIXIR and beyond.

On the bioimage analysis side, NBIS is engaged in the Chan-Zuckerberg-Initiative (funding of one CZI imaging scientist), Euro-BioImaging (part of the Expert Group on Image Data), Neubias/GloBIAS (member of the steering committee), and the EMBL-SciLifeLab dialogue (co-organiser).

E22 LU-Fold

LU-Fold is a Lund University-based infrastructure supporting researchers with advanced applications of protein structure predictions with AlphaFold2 and AlphaFold-multimer (Jumper et al., 2021; Evans et al., 2021; Nature Methods method of the year 2021). LU-Fold specialises in high-throughput applications to predict novel protein–protein interactions across entire proteomes. This service is urgently needed and is receiving significant interest. While prediction of protein monomers is readily available to all, the high-throughput 'co-folding' services offered by LU-Fold requires specific competences not available in most research groups, and can open up a plethora of new avenues for research questions to be addressed.

LU-Fold started officially in August 2023, based on a rapidly increasing number of collaborative projects initiated by the Atkinson lab (LU). LU-Fold has already helped researchers with a wide variety of different projects, e.g. finding new interactions of virus proteins with the human proteome, predicting various homo-oligomers of soil bacteria cell division proteins and their truncations, discovering binding partners of proteins associated with childhood cancer neuroblastoma, and finding interactions of brain proteins that are associated with neurological disorders. The Atkinson lab regularly uses this approach with great success (as judged by experimental validation) in the discovery of new interactions of bacterial toxins (Ernits et al., 2023). As structural biology is currently growing exponentially, transforming from a niche technology for specialised research groups to an integral part of many (and eventually perhaps most) biological research projects. To establish easy access to advanced expertise in this technology through SciLifeLab's national infrastructure has the potential to greatly advance Swedish life science.

Current operations

Funding

In 2022, Lund University awarded support to establish LU-Fold as a local infrastructure service (ca 1 MSEK annually). User fees are applied in line with the NBIS model with free initial consultation meetings, and hands-on project support charged at 800 SEK/hour. Projects considered to add general long-term value to the LU-Fold services such as setting up specialised databases of human proteins for screening specific subcellular proteomes (most recently a red-blood cell proteome dataset), are charged at reduced or no user fees. LU-Fold is exceptionally good value for money; as long as there are national high-performance computational resources available (for example via NAISS/NSC), the main investment needed is for staff, and no expensive hardware or equipment is required.

Expertise

LU-Fold was initiated by Gemma C. Atkinson, a senior lecturer at Lund University. Gemma has many years of experience in protein bioinformatics, and her lab members are regular users of high throughput AlphaFold-multimer. Gemma has established collaborations with research groups around the world and currently acts as the director of LU-Fold, and as a workshop teacher. The hands-on support of LU-Fold is run by full-time research engineer Dr. Bhanu Chouhan, a former post-doc in the Atkinson lab with extensive experience in AlphaFold-multimer projects. Bhanu consults researchers to plan and advise on their projects, and run analyses. LU-Fold benefits from the additional expertise of two scientific advisors, Prof. Ingemar André and Prof. Mats Ohlin, who were co-applicants on the initial LU infrastructure application.

Technologies and services

The main method used is AlphaFold-multimer, but other related methods are continuously being tested and evaluated, including for example Alpha-crosslink, which allows the incorporation of proteomic crosslinking data (generated by the SciLifeLab structural proteomics unit at LU) to inform constraints on protein-protein interfaces. LU-Fold relies on national research supercomputing infrastructure (e.g. NAISS/NSC). The services provided by LU-Fold include:

- Predicting pairwise binding interactions of a protein of interest with all other proteins in a proteome
- Predicting the structures of all proteins in a proteome (for instance from a newly sequenced genome)
- Predicting higher order structures of larger complexes
- Predicting the effect of mutations and truncations on interactions
- Workshops on using protein structure prediction tools and protein structure visualisation

Consultation and Training

Part of LU-Fold's service is education and training. There is little point providing a researcher with structures of protein complexes if they cannot visualise and interpret the results. LU-Fold therefore provides workshop and drop-in sessions and a range of user guides are planned. In the scope of these workshops researchers are instructed how to use low-throughput structural prediction and comparison methods available online such as Colabfold and FoldSeek. The aim is to open up new low- and high-throughput cutting edge methods to people who have never considered using bioinformatics or structural biology methods before, but for whom use of such methods can be greatly advantageous.

Scientific environment and user base

LU-Fold is physically located at the Medical Faculty of Lund University, but with scientific advisors in two additional faculties (Science and LTH). Notably, LU-Fold has already made connections with researchers running infrastructure at MAX IV, and the SciLifeLab Cryo-EM and Structural Proteomics units in Lund, who see ample opportunities for partnership and knowledge sharing. Established in August 2023, LU-Fold is a very recent infrastructure, but has already handled more than 10 projects, several of which are now being submitted to journals and used in PhD theses. The current user base is mostly at LU, but as of late 2023, LU-Fold is now open to projects from across Sweden, and also part of the international HALRIC consortium (halric.eu).

It has been a challenge to raise awareness of the existence of LU-Fold, something that would be improved by being part of SciLifeLab, and we expect to receive at least 50 project applications annually from 2025 onwards, with a good potential for steady growth as the ease and power of these methods become evident across a wide range of research areas. LU-Fold has so far run one workshop, which was very popular; the 30 places filled up quickly, and there was a waiting list. The plan would be to run similar workshops at least twice annually.

Synergies with SciLifeLab platforms and incorporation into NBIS

LU-Fold has established high-throughput structure prediction competence beyond the traditional use of AlphaFold2 as a reliable and versatile national service. Adding LU-Fold as a SciLifeLab infrastructure would be strategically beneficial for SciLifeLab and for Swedish life science. SciLifeLab/NBIS has recently invested in other AlphaFold2-based services (e.g. Mirabello et al., 2023), and this is a fantastic opportunity to join forces. SciLifeLab funding would secure sustainability and expand to help more researchers across Sweden. With LU-Fold's connections to structural biology, proteomics, genetics, and drug design, there are almost endless opportunities for synergies and integration with other existing SciLifeLab platforms, for both clinical applications and basic biological research. LU-Fold workshops would be expanded through NBIS's well-established training programme and the SciLifeLab Training hub, to reach a wider user-base.

This is a very timely effort, as NBIS is currently broadening scope to include structural biology, in close collaboration with the SciLifeLab Integrated Structural Biology platform and other stakeholders. The LU-fold support and training models are already perfectly aligned with NBIS, and would be seamlessly integrated into the NBIS support teams together with other experts in Cryo-EM and protein structure prediction. G. Atkinson would act as a Platform Scientific Director, adding her unique expertise and network to improve services, but at a much reduced daily administrative burden. For optimal synergies and critical mass, we propose to add two full-time staff to this effort, one located with Atkinson/Chouhan at LU, and one located with NBIS main structure prediction expert (Mirabello) at the strong structure prediction research environment at LiU.

References

1. Jumper, J. *et al.* (2021) *Nature* 596, 583–589
2. Evans, R. *et al.* (2021) bioRxiv doi.org/10.1101/2021.10.04.463034
3. Ernits K, *et al.* (2023) PNAS, 120 e2305393120
4. Mirabello C. *et al.* (2023) bioRxiv doi.org/10.1101/2023.09.20.558579

E23 PReSTO

PReSTO is a ubiquitous structural biology data processing platform deployed at the Swedish national high-performance computer environments. Incorporating PReSTO into SciLifeLab will i) massively simplify data processing for the growing number of SciLifeLab structural biology users, ii) provide essential tools for the SciLifeLab data generating platforms, and iii) help catalyse novel and cross-disciplinary research by integration across stakeholders of Sweden's uniquely strong structural biology infrastructure landscape.

Current operations

PReSTO is a unique compute platform for structural biology, jointly developed over the past 10 years by large-scale structural biology research infrastructures together with staff scientists at the National Supercomputer Centre (NSC) at LiU. This professionally maintained software stack at high-performance compute environments represents a competitive advantage to Swedish structural biology researchers. 3D structure prediction methods including AlphaFold, molecular dynamics simulations, virtual screening methods, and unforeseen AI-derived software to come, will further increase such use of high-performance compute environments, also advanced by the KAW and SciLifeLab Data-Driven Life Science program pushing for novel AI generated applications combined with life science experimental research.

PReSTO is maintained at four national high-performance computer resources (NSC Tetralith and Berzelius, LUNARC Cosmos, and the MAX IV cluster). NSC staff deploy the installations, while a community network of staff and researchers performs software testing, local user documentation, support, and training of fellow scientists. PReSTO has been funded by various grants including MAX IV satellite funding (2015–2017) and VR (2018–2022). Currently, PReSTO is only funded through LiU as an in-kind contribution to MAX IV. Training and support is well established for MAX IV and MX users, but the support pages for Cryo-EM, NMR and other technologies of relevance for SciLifeLab users is yet rudimentary as there is not yet any funding in this direction. NBIS aims to arrange a first PReSTO course for SciLifeLab Cryo-EM users in March 2024, and the SciLifeLab ISB platform will include PReSTO in their Integrated Structural Biology course in September 2024.

Scientific environment

PReSTO has a strong distributed network of researchers to guide the operations, including e.g. Prof. Maria Sunnerhagen (LiU) and Prof. Erik Lindahl (SU). NBIS and the Integrated Structural Biology (ISB) platform will be vital additions to this network, including unit managers and staff such as Dr. Marta Carroni (SU), Dr. Micheal Hall (UmU), Prof. Göran Karlsson (GU), and Dr. Claudio Mirabello (LiU), representing both AI-tools and experimental data processing. The very strong local technical environment at NSC has been recognized by KAW (SuperPOD resource Berzelius, 2021), the Swedish Research Council (National Academic Infrastructure for Supercomputing in Sweden, 2022), and the European High Performance Computing Joint Undertaking (Arrhenius resource, 2023).

User base

The PReSTO project has a broad user base of more than 100 academic members spread across Swedish universities (*Figure 6 and Table 2*), registered through the academic supercomputer centres' access system (SUPR). With data processing being an increasing hurdle for structural biology research groups and with many researchers currently working with suboptimal local solutions, having PReSTO fully incorporated into SciLifeLab would create a great potential for the SciLifeLab user base to rapidly grow. In addition, PReSTO is currently being set up as the main data processing solution for the Cryo-EM units at SciLifeLab and will constitute a key capacity for improved data processing and reproducibility. The Swedish pharmaceutical industry is also a potential beneficiary of PReSTO, although this will require dedicated computing solutions. Infrastructures such as MAX IV, SciLifeLab Cryo-EM and Swedish NMR Centre all have, and aim to increase, industrial access, and MAX IV has already managed tailor-made commercial licence industry agreements.

Complementarity and synergistic opportunities within and across SciLifeLab platforms

Novel laboratory techniques are revolutionising the field of protein structure determination such as Cryo-EM, Serial Synchrotron X-ray crystallography and new applications in NMR, but also thanks to powerful computational prediction tools. SciLifeLab researchers and infrastructures are at the international forefront and leading this development in Sweden, paving the way for a wider use of structural biology across a broad range of research fields. Adding PReSTO to SciLifeLab will ensure an efficient interface for advanced data processing at the Swedish supercomputer centres, and is already being tested as the key framework for the Cryo-EM units, but has so far limited content, documentation, support, and training towards SciLifeLab user groups. The NBIS unit SCoRe is the main SciLifeLab unit serving life science users at the national supercomputer centres, and will ensure a seamless integration of PReSTO into NBIS to serve the SciLifeLab structural biology infrastructures and their user community. With PReSTO already well established at MAX IV, it will also help catalyse the SciLifeLab/MAX IV integration (InfraLife), building on Sweden's uniquely strong and accessible infrastructures in structural biology.

The proposed budget for PReSTO comprises part time activities including one technical project manager reporting to NBIS officials, software staff at the central development hub at Linköping university, and staff maintaining local compute clusters at MAX IV, SciLifeLab Cryo-EM and Swedish NMR Centre. In addition, NBIS and ISB will engage existing bioinformatics and structural biology platform staff as beta testers and to participate in training related to PReSTO outside of the proposed budget. No hardware for running PReSTO is part of this budget.

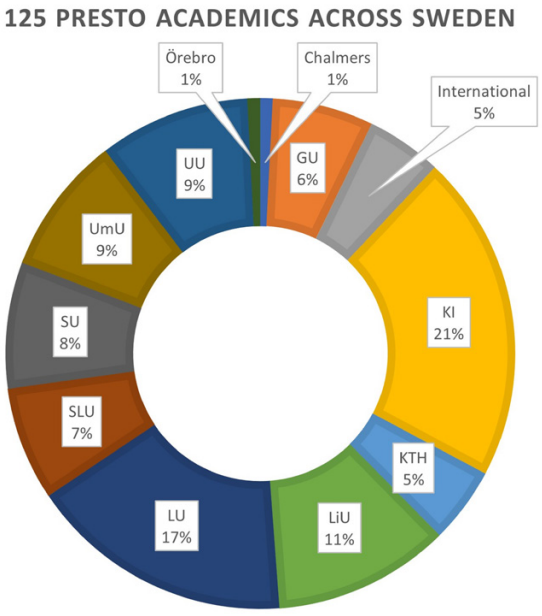


Figure 6. Current PReSTO users are distributed across all larger Swedish Universities.

Category	Number
MX/EM/NMR etc.	36
CryoEM	16
MX	34
NMR	6
SAXS	1
SSX	7
Grand Total	100

Table 2. Number of softwares installed for each structural biology category. Software such as display graphics, software layers and libraries, data format etc. are used by all categories MX/EM/NMR etc.

Budget request

The Bioinformatics platform budget from SciLifeLab will be used to realise the plans described in the text above. In total, 64 staff members (i.e. about half our staff) are entirely or partly financed via the SciLifeLab national budget, predominantly in the following units:

- Bioinformatics support
- BioImage Informatics
- Data management
- Systems development
- AIDA Data Hub
- Support for Computational Resources (SCoRe)
- Training
- Management

The Bioinformatics strategic budget is planned to finance:

- One of the two annual Bioinformatics platform retreats
- Data stewards, including collaboration with Data Centre
- Support at AIDA Data Hub
- Technical Development Activities together with other SciLifeLab platforms

The LU-Fold budget will finance expansion to 3 FTEs for 2025–2028, which is needed to provide the increasing user support:

- 2 FTEs based in Lund
- 1 FTE based in Linköping, to facilitate interactions with research groups in structural bioinformatics at LiU

The PReSTO budget will finance expansion to 2.3 FTEs for 2025–2028, to manage the increased needs from the structural biology community (Cryo-EM, NMR, MAX IV):

- 1.0 FTE for software development and management
- 1.0 FTE for computational development and maintenance for Cryo-EM, NMR and MAX IV
- 0.3 FTE for technical project management

Table 1. Bioinformatics Platform Budget

Costs	2024	2025	2026	2027	2028
Module 1 - Management	10 250	11 830	12 067	12 308	12 554
Module 2A - Bioinformatics support	33 057	31 356	31 983	32 623	33 275
Module 2B - Bioinformatics support (funded by KAW)	35 650	37 458	38 208	38 972	39 751
Module 2C - BioImage Informatics support (BIIF)	5 850	4 200	4 284	4 370	4 457
Module 3A - Data management and data publication	8 660	7 070	7 211	7 356	7 503
Module 3B - Swedish node in 1+MG and EGA-SE	in other modules	10 824	11 040	11 261	11 487
Module 4A - Systems development, tools & infrastructure	17 920	12 360	12 607	12 859	13 117
Module 4B - AIDA Data Hub	10 534	7 570	7 721	7 876	8 033
Module 5 - SCoRe	6 370	5 381	5 489	5 598	5 710
Module 6 - Training and National Networking	in other modules	7 155	7 298	7 444	7 593
Module 7 - International - Swedish ELIXIR node	9 264	6 090	6 212	6 336	6 463
Correction for parental leave (cautiously calculated with 5%)	-6 878	-7 065	-7 206	-7 350	-7 497
Sum costs (kSEK):	**130 677**	**134 230**	**136 914**	**139 653**	**142 446**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	*29 760*	*33 000*	*33 000*	*36 000*	*36 000*
University co-funding	20 142	20 000	21 000	22 000	23 000
Swedish Research Council (VR)	20 000	17 720	19 720	20 720	20 720
KAW	27 600	30 360	30 967	31 587	32 218
EU-project GDI, funding from EU	3 400	3 400	3 400		
EU-project GDI, co-funding from Vinnova	3 400	3 400	3 400		
EU-project Bigpicture	8 000	8 000	8 000		
EU-project EUCAIM, funding from EU	600	600	600		
EU-project EUCAIM, co-funding from Vinnova	600	600	600		
EU project ERDERA, funding from EU		300	300	300	300
Vinnova	838	380	380	380	
Future funding of 1+MG-SE, EGA-SE and Bigpicture				15 000	15 000
ELIXIR and other EU-projects	768	3 000	3 000	3 000	3 000
VR Equipment Grant	1 404	1 404			
VR Biodiversity	1 000				
VR NMI to BIIF	750				
LiU vice-chancellor to AIDA DH	1 000				
CMIV to AIDA DH	1 000				
NeIC	600				
Chan-Zuckerberg	1 000				
User fees	10 500	11 000	11 500	11 500	11 802
Sum revenues (kSEK):	**132 362**	**133 164**	**135 867**	**140 487**	**142 040**

Table 2. LU-Fold Budget

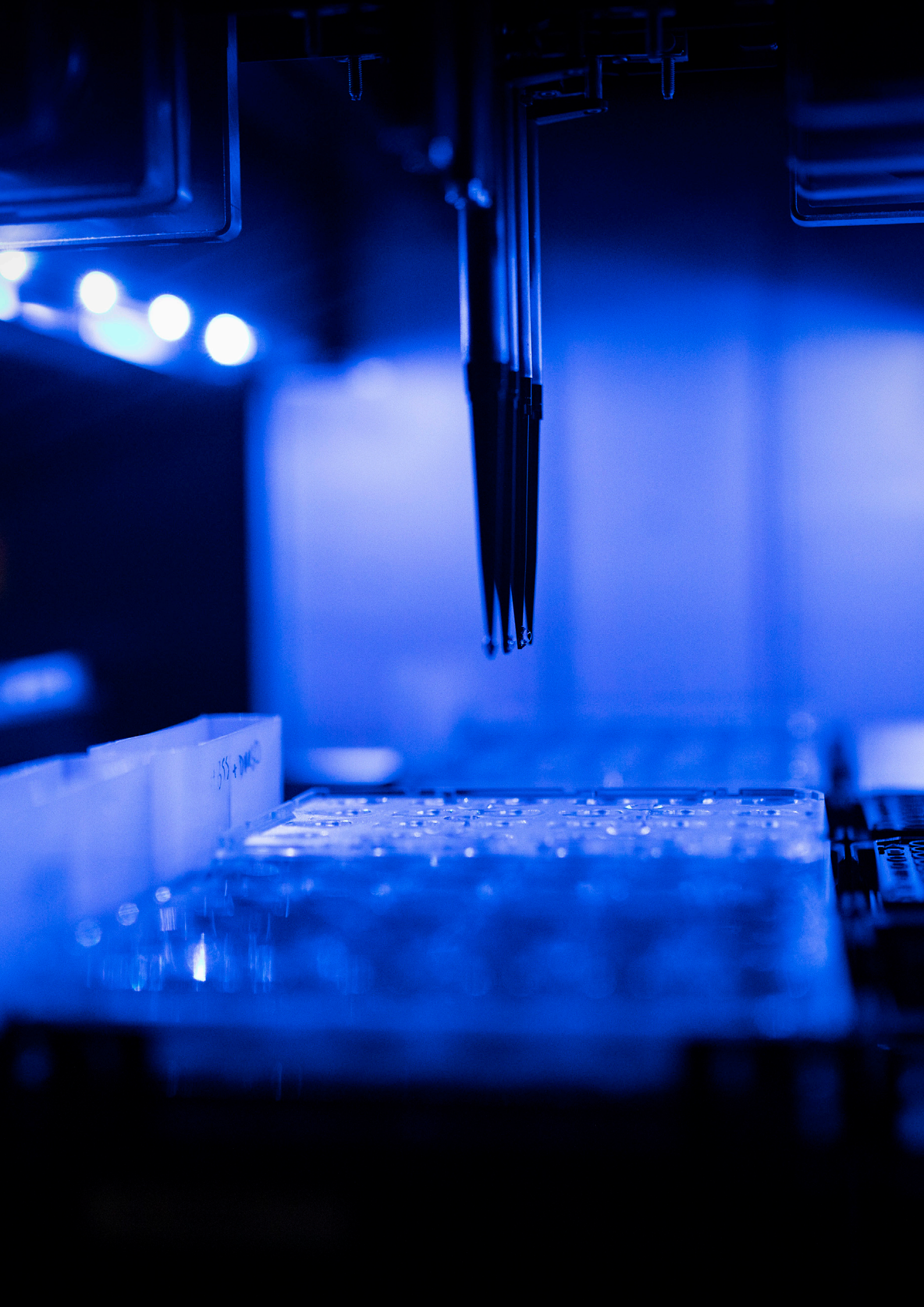
Costs	2024	2025	2026	2027	2028
Personnel 1 FTEs (2024) -> 3 FTEs (2025–2028)	1 200	3 600	3 744	3 888	4 032
Operations	50	150	150	150	150
Premises	50	150	150	150	150
Sum costs (kSEK):	**1 300**	**3 900**	**4 044**	**4 188**	**4 332**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	-	*1 900*	*1 944*	*1 988*	*2 032*
University co-funding (LU)	1 000	1 000	1 000	1 000	1 000
User fees	300	1 000	1 100	1 200	1 300
Sum revenues (kSEK):	**1 300**	**3 900**	**4 044**	**4 188**	**4 332**

Table 3. PReSTO Budget

Costs	2024	2025	2026	2027	2028
Personnel 0.3 FTEs (2024) -> 0.3 FTEs project management (2025–2028)	400	400	416	432	448
Personnel 0.5 FTEs (2024) -> 1.0 FTEs installation@NSC (2025–2028)	600	1 200	1 248	1 296	1 344
Personnel 0.0 FTEs (2024) -> 0.25 FTEs MX/SSX (2025–2028)	-	300	312	324	336
Personnel 0.0 FTEs (2024) -> 0.50 FTEs CryoEM (2025–2028)	-	600	624	648	672
Personnel 0.0 FTEs (2024) -> 0.25 FTEs NMR (2025–2028)	-	300	312	324	336
Operations	-	50	50	50	50
Premises	-	50	50	50	50
Instrument depreciations	-	-	-	-	-
Other	-	-	-	-	-
Sum costs (kSEK):	**1 000**	**2 900**	**3 012**	**3 124**	**3 236**

Revenues	2024	2025	2026	2027	2028
SciLifeLab funding (current and requested 2025–2028)	-	*2 300*	*2 412*	*2 524*	*2 636*
Linköping University co-funding for MAX IV used for PReSTO	600	600	600	600	600
NBIS bridge funding 2024	400	-	-	-	-
Sum revenues (kSEK):	**1 000**	**2 900**	**3 012**	**3 124**	**3 236**



Notes


SciLifeLab