INTERNATIONAL EVALUATION OF THE SCILIFELAB INFRASTRUCTURE

# Report from the International Evaluation Committee (IEC)

## 2024

SciLifeLab

# Foreword from the IEC

Dear Reader,

We were tasked with evaluating and reviewing the SciLifeLab Infrastructure program. While this process is common, SciLifeLab itself is anything but ordinary. What began as a Swedish flagship project has evolved into the European benchmark for national research infrastructures in life sciences.

This national program, offering equal access to ten multi-unit and decentralized platforms spread across Sweden, is truly unique. With 500 FTEs and a total funding of 980 MSEK (2023, *Figure 11* Infrastructure report), the significance and importance of this operation for the local research community cannot be overstated.

In total, we were asked to evaluate 23 independent entities and provide our general feedback on three new cross-facility capabilities (Personalized Medicine, Planetary Biology, Pandemic Laboratory Preparedness), the centralized Data Centre, the Training hub and future budgets. Given the breadth and depth of SciLifeLab's infrastructure, the review process was divided into several stages: (1) a virtual introduction, (2) pre-evaluation of the written Infrastructure report, (3) an onsite visit, and (4) our subsequent written evaluation report.

The on-site visit, at the heart of this process, allowed us to interact directly with all stakeholders. This format was essential for our discussions, internal calibration, and ultimately for writing this report. Our mission was to assess whether SciLifeLab's funding was utilized effectively, generating the desired impact for the national research community.

Our role was to provide an external reference frame on all aspects of SciLifeLab's operations. Specifically, we were tasked with grading (A) the relevance and impact of current technologies, (B) the current performance, and (C) the strategic significance and impact of developmental plans (2025–2028) for each entity.

Each entity was graded using key criteria outlined in the Terms and Conditions for Funding, provided in Appendix II. Grades were assigned during the pre-evaluation phase and onsite after each presentation. The process was consensual, with expert opinions provided and subsequently discussed and challenged by all IEC members. To ensure accuracy in assessing relative rather than absolute grades and to avoid any potential biases, we recalibrated Grade C at the conclusion of our onsite visit.

Our focus was on identifying specific issues within entities and common challenges across them. We considered an in-depth analysis of every entity beyond the scope of our evaluation. While our view may differ from the local user base, reflecting its national relevance, we believe that balancing both international excellence and national relevance is essential for maximizing the impact of SciLifeLab's funding.

We hope that our input will contribute to shaping SciLifeLab's continued success.

Enjoy reading,

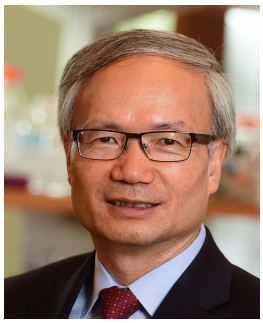
*Daniele Soroldoni on behalf of the IEC 2024*

# International Evaluation Committee

**Daniele Soroldoni (Chair)**
Vienna BioCenter Core Facilities, Austria

**Elisa May (Co-Chair)**
German Cancer Research Center (DKFZ), Germany

**Melinda Duer**
University of Cambridge, UK



**Haian Fu**
Emory University School of Medicine, USA

**Alain van Gool**
Radboud University Medical Center, EATRIS, Netherlands

**Stefanie M. Hauck**
Helmholtz Munich, Germany

**Florian Jug**
Human Technopole, Italy

**Donald C. Lo**
European Infrastructure for Translational Medicine, (REMEDi4ALL), EATRIS, Netherlands

**Janna Saarela**
NCMM Center for Molecular Medicine Oslo, Norway

**Olli Silvennoinen**
Biocenter Finland, Finland

**Nicole Soranzo**
Human Technopole, Italy

**Sharon Wolf**
Weizmann Institute, Israel

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

# Contents

# Overall Feedback on the SciLifeLab Infrastructure

Outstanding research requires exceptional management. Managing a decentralized operation is inherently challenging, but doing so at a national level without legal entity status is a heroic achievement. To this end, the IEC can only emphasize that it is difficult to envision a governance and operation model that is more effective at this scale. The professionalism demonstrated in the preparation and organization of the evaluation, as well as the quality of the provided materials, reflects on the management excellence of the entire organization. Before delving into the evaluation of individual entities, we would like to highlight some key aspects and recommendations that are applicable across multiple entities.

## From data to discoveries

While there is a general acknowledgement of the significance of data-driven life sciences, there is a pressing need for targeted strategies to address this requirement. There must be a better appreciation of data value, utilization and lifetime across most platforms. This appreciation needs to start at the top management and be central to all future developmental plans at the platform level until it becomes intrinsic to SciLifeLab's routine operations. Naturally, the focus of many platforms is on technology development and quality of data production. The actual use of data is often an afterthought rather than part of the overall, strategic plan. This cultural change needs to be flagged to all researchers too whenever they access platform resources. To meet these needs, SciLifeLab should explore strategies for embedding computational experts at the platform or unit level. Simultaneously, these embedded experts require a bridging framework linking them with centralized data services provided by NBIS, the Data Centre, or any other dedicated structure. This integration should be seamless to minimize friction and foster synergies. To underscore the importance of data utilization, we suggest refining the existing Good Infrastructure Practices. Data production should prioritize reproducibility, adherence to FAIR principles, and traceability, while seamlessly integrating with data utilization. Formal incorporation of data-specific metrics, such as the quantity of annotated/curated data deposited under FAIR access, into the key evaluation criteria (Terms & Conditions for funding) may exert a significant steering effect.

## Emergent properties of cross-facility workflows

Emergent properties cannot be predicted or explained by examining individual parts in isolation but instead emerge from the collective behaviour of systems such as research organizations. They often exhibit novel characteristics or behaviours that are not present at the level of the individual components, illustrating the idea that the whole is greater than the sum of its parts (1 + 1 = 3). SciLifeLab acknowledges this concept and has implemented a platform-centric organization structure to enhance interdisciplinary collaborations and facilitate cross-facility workflows. The IEC recognizes efforts to strengthen this approach through new Capabilities designed to serve as a nexus between different platforms and units. However, while these capabilities may provide cohesion, we assert that they alone cannot drive the necessary shift in mindset and foster a culture of synergy from the top down throughout the organization, ultimately permeating the research community. This cultural transformation could be facilitated by central funding to stimulate dedicated events and proof-of-concept studies. Additionally, implementing organizational tools such as unique identifiers for sample/request submissions could enhance transparency and encourage transversal use of platforms. Strategic developmental plans should include concrete examples for collaborations and optimizing cross-facility workflows.

## Bridging the gap to healthcare and industry researchers

SciLifeLab aims to provide access to state-of-the-art technologies for researchers across academia, industry, and healthcare sectors. However, there is a noticeable gap in reaching users outside the academic/clinical research communities, particularly in healthcare and industry. While missing industry users may be subject to missing outreach activities, the failure to attract more healthcare users appears to be more systematic. The IEC acknowledges the challenges posed by the fragmented healthcare system and advocates for measures to bridge the obvious gap between academia and healthcare. It is crucial for existing and future clinical platforms to thrive by closing this systematic disparity. New capabilities, like Precision Medicine, must also prioritize addressing this issue to ensure ongoing progress and targeting the right audience. Collaboration between SciLifeLab and healthcare decision-makers is essential to implement

technologies effectively in clinical care, particularly in achieving precision medicine goals. Joint activities and co-funding initiatives between SciLifeLab and healthcare entities should be established to drive progress in specific areas. Furthermore, a re-evaluation of instrument ownership in clinical platforms is needed to prioritize goal-oriented strategies over mere instrument ownership.

## Translating scientific visions into operational strategies

SciLifeLab has clear governance, but decision-making is inherently difficult in a scientific operation of this size and complexity. We propose that achieving the appropriate balance between generic and platform-specific metrics could facilitate this process. Effectively blending scientific and financial considerations across various organizational levels is crucial for making sustainable budgetary decisions and enhancing cost awareness among academic researchers. Merely assessing investment costs or individual platforms in isolation can be misleading and may inadvertently favour already established platforms over smaller, potentially more innovative ones.

## Staff retention and career development

In absence of a clear career progression, retaining high-quality staff scientists across SciLifeLab platforms appears to be challenging. This is a common problem across research infrastructures. To address this issue, some platforms implemented specific programs for staff scientist career development already. We suggest centralizing and facilitating these individual staff development initiatives, ensuring they are uniformly implemented across all platforms. These proposed initiatives include offering training programs such as the Core Facility Leadership and Management Course, providing travel grants for staff scientists without access to travel budgets to enhance their international profile, and establishing mini-sabbatical programs for staff scientists to visit and train at other facilities.

# Genomics Platform

## E1 Genomics

**Grade A** – Current technologies (1–9): **9**

**Grade B** – Performance 2021–2023 (1–9): **7–8**

**Grade C** – Development plans 2025–2028 (1–9): **6**

### Motivation and feedback

NGI (National Genomics Infrastructure) emphasizes inclusivity and adaptability in its operations, accommodating diverse research needs. It strategically allocates its workforce, with 36% focused on critical areas like sequencing and governance. NGI's annual performance is impressive, engaging 500 PIs and executing over 1,000 projects, processing 90,000 samples, and publishing 250+ research outputs. Project coordinators ensure scientific rigor, and NGI stays innovative by adopting new methodologies.

Despite market changes, NGI maintains an optimistic outlook but faces challenges in interfacing with clinical genomics and lacks a sustainable cost model. Questions raised include workflow management, adherence to standards, project balance, and clarity on services. NGI aims to improve data management, enhance societal impact, expand its industrial user base, and collaborate with biobanks.

### Recommendations for 2025–2028

- Address complacency: NGI should anticipate changes and remain agile to stay competitive.
- Integrate multi-omics: incorporating multi-omics approaches will enhance research depth and breadth.
- Develop sustainable cost model: NGI needs a balanced cost model for financial resilience.
- Clarify Clinical Genomics interface: define pathways for better collaboration with clinical partners.
- Improve data management: enhance data traceability and usability through better metadata annotation.
- Enhance societal impact: engage stakeholders for greater societal relevance and support.
- Increase industrial user base: forge partnerships to drive innovation and commercialization.
- Strengthen biobank collaborations: collaborate with biobanks for sample quality assurance and enrichment of research materials.

### Extended feedback

Considering the scientific impact and operational scale of NGI, we deem it appropriate to provide an extensive feedback section. This feedback is intended to offer a comprehensive evaluation of NGI by the IEC. If needed, the IEC has the option to merge the executive and extended feedback sections for consolidation.

NGI places significant emphasis on accommodating a wide spectrum of capabilities within its operations, catering to the diverse needs arising from a broad range of input samples. This approach underscores NGI's commitment to inclusivity and adaptability, ensuring that researchers across various domains can leverage its services effectively. In terms of resource allocation, NGI strategically distributes its Full-Time Equivalent (FTE) workforce, with a notable portion, approximately 36%, dedicated to critical areas such as short-read sequencing, governance structure maintenance, and oversight from its international Scientific Advisory Board (SAB). This distribution reflects NGI's concerted efforts to uphold operational efficiency while simultaneously fostering a conducive environment for innovation and governance.

NGI's annual performance metrics are indeed impressive, serving as a testament to its impactful contributions to the scientific community. Engaging with a substantial cohort of 500 Principal Investigators (PIs) annually and executing over 1,000 projects highlights the breadth and depth of NGI's reach. Moreover, the processing of over 90,000 samples coupled with the publication of 250 or more research outputs underscores NGI's pivotal role in driving scientific progress and knowledge dissemination.

Integral to NGI's operational framework are its project coordinators, who serve as linchpins in maintaining scientific rigor and quality assurance. Beyond administrative duties, these coordinators provide essential scientific gatekeeping and consultancy services, ensuring that projects adhere to the highest standards of integrity and methodology.

NGI's proactive stance towards innovation is evident through its early adoption of new commercial methodologies. By staying abreast of emerging trends and technologies, NGI demonstrates its commitment to remaining at the forefront of scientific advancements, thereby enhancing the quality and relevance of its services.

Despite the emergence of new players in the short-read sequencing market, NGI's outlook remains surprisingly

optimistic. This resilience speaks to NGI's confidence in its capabilities and its ability to navigate competitive landscapes while staying true to its mission and values.

However, challenges persist, particularly concerning NGI's interface with clinical genomics. The extent to which NGI collaborates and integrates with clinical genomics initiatives is currently unclear, highlighting a potential area for improvement in enhancing interdisciplinary cooperation and service delivery.

Moreover, the absence of a sustainable cost model poses a significant challenge to NGI's long-term viability and financial stability. Addressing this issue is paramount to ensure that NGI can continue to deliver high-quality services while effectively managing operational costs and resources.

### *Questions raised and ensuing discussion*

1. **Management of workflows among distributed lab infrastructure:** One of the key challenges facing NGI is the effective management of workflows across its distributed laboratory infrastructure. Ensuring seamless coordination and communication between different facilities and teams is essential to optimize operational efficiency and resource utilization.
2. **Adherence to ISO standards for all samples:** Maintaining adherence to ISO standards for sample processing is crucial to uphold quality control and data integrity. Ensuring compliance with these standards not only enhances the reliability of NGI's services but also instills confidence among researchers and stakeholders regarding the validity of results.
3. **Balance between large-scale and smaller-scale projects:** Striking a balance between large-scale, high-impact projects and smaller-scale initiatives is pivotal for NGI to cater to diverse research needs while maximizing its overall impact. This entails careful resource allocation and project prioritization to ensure equitable support for both types of endeavors.
4. **Percentage of services available commercially at similar or lower cost/turnaround:** Assessing the competitiveness of NGI's services in terms of cost and turnaround time compared to commercial alternatives is essential for maintaining relevance and attractiveness to researchers and clients. Identifying areas where NGI can offer comparable or superior value proposition is critical for sustaining its market position.
5. **Phasing out services commercially available:** Deciding on the phased discontinuation of services that are readily available commercially requires careful consideration of factors such as demand, cost-effectiveness, and strategic alignment with NGI's core objectives. Clear communication and stakeholder engagement are essential to navigate this transition smoothly.
6. **Distinction between NGI and Clinical Genomics platform:** Clarifying the distinction between NGI and the Clinical Genomics platform is imperative to avoid overlap in services and responsibilities while maximizing synergy and collaboration between the two entities. Clearly defining their respective roles and areas of specialization is essential for enhancing operational efficiency and service delivery.
7. **Interaction with other units for environmental monitoring:** Collaborating within NGI and across the organization for environmental monitoring initiatives presents an opportunity to leverage collective expertise and resources towards addressing pressing environmental challenges. Establishing seamless communication channels and interdisciplinary cooperation is essential for realizing synergistic outcomes.
8. **Cost-effectiveness of units and services:** Evaluating the cost-effectiveness of NGI's units and services is essential to ensure optimal resource allocation and financial sustainability. Conducting thorough cost-benefit analyses and implementing efficiency measures can help identify areas for improvement and optimization.
9. **Vision for multi-omics advancement:** Articulating a clear vision for advancing multi-omics research is essential for guiding NGI's strategic direction and investment priorities. This entails identifying emerging trends, technological innovations, and research opportunities in the multi-omics space and aligning organizational efforts accordingly.
10. **Opening NGI open lab to other units:** Exploring the possibility of opening NGI's open lab to other units presents an opportunity to foster collaboration, resource sharing, and knowledge exchange within the organization. Assessing the feasibility, benefits, and potential challenges of such an initiative is essential for informed decision-making.
11. **Co-publication number across platforms:** Monitoring and analysing the co-publication number across different platforms can provide valuable insights into the effectiveness of collaborations and partnerships facilitated by NGI. Tracking this metric over time can help evaluate the impact of NGI's services and identify opportunities for enhancing collaborative efforts.
12. **Data management lacking experimental metadata annotation:** Effective data management is essential for ensuring the integrity and usability of research outcomes. However, a notable gap exists in NGI's current practices regarding the annotation of experimental metadata. Addressing this deficiency is crucial to enhance data traceability, reproducibility, and interoperability, ultimately bolstering the reliability and value of NGI's services.

13. **High-value project meetings with coordinators:** The convening of high-value project meetings with coordinators reflects NGI's commitment to fostering collaborative partnerships and ensuring the successful execution of research initiatives. These meetings serve as forums for aligning project objectives, addressing challenges, and optimizing resource allocation, thereby enhancing project outcomes and stakeholder satisfaction.
14. **Strategy for societal impact and cost-effectiveness considerations:** Formulating a robust strategy for maximizing societal impact while simultaneously ensuring cost-effectiveness is paramount for NGI's long-term sustainability and relevance. Balancing societal priorities with fiscal constraints requires a comprehensive approach that encompasses stakeholder engagement, resource optimization, and strategic investment in high-impact initiatives.
15. **Challenges in interfacing with other landscape players:** NGI faces significant challenges in effectively interfacing with other stakeholders and entities within the broader genomics landscape. Overcoming barriers such as divergent priorities, communication gaps, and competitive dynamics requires proactive engagement, collaboration frameworks, and a shared commitment to advancing common goals.
16. **Work in progress for cross-platform pipelines and sample preparation:** Ongoing efforts to develop cross-platform pipelines and streamline sample preparation processes are indicative of NGI's commitment to innovation and operational excellence. These initiatives aim to enhance workflow efficiency, data integration, and research reproducibility, ultimately advancing NGI's capabilities and service offerings.
17. **Decision against single-cell sorting:** NGI's decision against single-cell sorting reflects a strategic choice informed by factors such as resource constraints, technological feasibility, and alignment with organizational priorities. While single-cell analysis holds promise for advancing scientific understanding, NGI's decision underscores the importance of prioritizing initiatives that offer the greatest value and impact within existing constraints.
18. **Consumables to user fees ratio at 75%, room for improvement:** Evaluating NGI's consumables to user fees ratio reveals an opportunity for optimization and resource management. Achieving a more favourable ratio necessitates initiatives such as bulk purchasing, waste reduction strategies, and pricing adjustments, all aimed at enhancing cost efficiency and financial sustainability.
19. **Phasing out considering Illumina patents expiration:** The impending expiration of Illumina patents presents both challenges and opportunities for NGI. Phasing out certain services or technologies affected by patent constraints requires careful strategic planning to mitigate potential disruptions while leveraging the opportunity to explore alternative solutions, innovate, and adapt to evolving market dynamics.
20. **Challenges with outsourcing due to regulatory issues and lack of commercial providers:** NGI faces hurdles in outsourcing certain aspects of its operations due to regulatory complexities and limited availability of commercial providers. Overcoming these challenges necessitates proactive engagement with regulatory authorities, fostering partnerships with reliable vendors, and exploring in-house alternatives where feasible.
21. **Recommendations to focus on cutting-edge technologies and increase industrial user base:** NGI's recommendations to prioritize cutting-edge technologies and expand its industrial user base align with its mission to drive innovation and maximize societal impact. Leveraging emerging technologies and engaging industrial partners not only enhances NGI's competitive advantage but also accelerates the translation of research into real-world applications and commercialization opportunities.
22. **Distinction between NGI and SciLifeLab, potential collaboration with biobanks:** Clarifying the distinction between NGI and SciLifeLab and exploring potential collaborations with biobanks offer avenues for synergistic partnerships and resource sharing. Establishing clear delineations of roles and responsibilities between NGI and SciLifeLab enhances operational efficiency, while collaboration with biobanks enriches NGI's sample repository and facilitates access to valuable research materials for scientific investigations.

*Extended recommendations for 2025–2028*

- **Address complacency with the status quo and prepare for upcoming genomics space changes:** It's imperative for NGI to recognize and confront any complacency within its operational framework to stay agile and responsive in the face of evolving genomics landscape dynamics. Proactively anticipating and adapting to emerging trends, technologies, and scientific paradigms ensures NGI remains at the forefront of innovation and maintains its competitive edge.
- **Integrate multi-omics better into operations:** The integration of multi-omics approaches into NGI's operations holds immense potential for unlocking new insights and driving synergies across various research disciplines. By leveraging complementary omics data sets, NGI can offer more comprehensive and holistic analyses, enhancing the depth and breadth of its service offerings and empowering researchers to explore complex biological phenomena with greater precision and accuracy.
- **Develop a sustainable cost model:** Establishing a sustainable cost model is essential for ensuring NGI's long-term viability and financial resilience. By optimizing resource allocation, streamlining operational processes, and implementing efficient cost management strategies, NGI can achieve a balance between financial sustainability and service quality, thereby enhancing its capacity to deliver impactful research solutions while maximizing value for stakeholders.
- **Clarify the interface with Clinical Genomics:** Clarifying the interface with Clinical Genomics is crucial for enhancing collaboration and synergy between NGI and clinical research initiatives. By delineating clear pathways for engagement, communication, and data sharing between NGI and clinical partners, NGI can better align its services with clinical research needs, accelerate translational research efforts, and facilitate the integration of genomic data into clinical practice for improved patient outcomes.
- **Improve data management with experimental metadata annotation:** Improving data management practices by enhancing experimental metadata annotation is essential for ensuring the integrity, reproducibility, and usability of research data generated by NGI. By implementing standardized metadata annotation protocols and robust data curation workflows, NGI can enhance data traceability, facilitate data integration and analysis, and promote open science principles, ultimately fostering greater transparency, collaboration, and knowledge sharing within the scientific community.
- **Enhance societal impact strategies and outreach actions:** Enhancing societal impact strategies and outreach actions is critical for maximizing the relevance and reach of NGI's research endeavors. By actively engaging with diverse stakeholders, including policymakers, industry partners, patient advocacy groups, and the public, NGI can ensure its research efforts address pressing societal challenges, contribute to evidence-based decision-making, and foster broader societal awareness and support for genomics research and innovation.
- **Increase industrial user base and focus on cutting-edge technologies:** Expanding NGI's industrial user base and prioritizing investment in cutting-edge technologies are key strategies for driving innovation and accelerating the translation of research discoveries into real-world applications and commercialization opportunities. By forging strategic partnerships with industry stakeholders, fostering technology transfer initiatives, and investing in state-of-the-art infrastructure and expertise, NGI can catalyse the development of novel genomic tools, diagnostics, and therapies that address unmet medical needs and create tangible societal impact.
- **Strengthen collaborations with biobanks and other cohorts for sample quality assurance:** Strengthening collaborations with biobanks and other cohorts is essential for ensuring sample quality assurance and enhancing the robustness and reliability of NGI's research outputs. By leveraging biobank partnerships and engaging with diverse research cohorts, NGI can access high-quality, well-characterized sample collections, implement rigorous sample handling and processing protocols, and validate research findings across multiple cohorts, thereby enhancing the reproducibility, generalizability, and translational potential of its research efforts.

# Clinical Genomics Platform

## E2 Clinical Genomics

**Grade A** – Current technologies (1–9): **7**

**Grade B** – Performance 2021–2023 (1–9): **6**

**Grade C** – Development plans 2025–2028 (1–9): **5**

### Motivation and feedback

Clinical Genomics (CG) stands as a nationally unparalleled distributed infrastructure, establishing its presence in all university hospitals affiliated with medical faculties. The platform collaborates with healthcare, playing a pivotal role alongside its key partner, Genome Medicine Sweden, in providing genomics-based services for both translational and clinical research endeavours. Moreover, it facilitates the implementation of new genomics-driven diagnostics into the healthcare system. While the initiative to support clinical trials is underway, it has yet to yield a substantial number of industry-funded projects.

CG has grown into the largest platform in terms of staffing, including a diverse array of expertise ranging from laboratory and sequencing to bioinformatics and clinical practices. With a notable portion of its budget sustained by user fees (64%), CG receives additional support from regional universities, healthcare institutions, and SciLifeLab. Over recent years, there has been an increase in both number of users and number of projects, prompting the development of tailored services to meet the evolving demands of translational and clinical research. This concerted effort has culminated in the production of 306 publications between 2021 and 2023, significantly contributing to the body of medical knowledge, clinical applications, and the advancement of precision medicine. However, one third of the services provided during 2021–2023 have been related to SARS-CoV2 pandemic, which are unlikely to continue in the post-pandemic era.

Assays co-developed with healthcare have been implemented in diagnostics, and the Stockholm unit has developed a close collaboration crossing the challenging border between research and healthcare, exemplified by joint infrastructure utilization, appointments, and personnel transfers. However, this cohesion has not been uniformly replicated across all nodes, resulting in redundant infrastructure both locally and nationally. Despite the expectation for escalating demand for healthcare-related services, the proportion of healthcare users has remained stagnant, while academic users from Lund and Gothenburg universities have surged to nearly 50%. This shift raises questions regarding the optimal allocation of resources and the potential underutilization of existing, more cost-effective infrastructure. Thus, there remains a need for clearer coordination with NGI to mitigate service overlap and ensure efficient resource utilization.

Furthermore, CG actively engages with national and international networks, projects, and data infrastructures to enhance service quality, staff training, and knowledge dissemination. Praiseworthy efforts are underway to establish a unified framework for data storage, annotation, and FAIR compliance across all nodes, spearheaded by a recently appointed research data manager. Collaboration with key entities such as the Data Centre and NBIS aims to bolster analytics capabilities and expand data analysis capacities. Additionally, partnerships with the Training Hub and NBIS facilitate staff training and contribute to university education initiatives. CG has also a prominent role in supporting Precision Medicine and Pandemic Laboratory Preparedness capabilities.

Looking ahead, CG plans to advance its technology development focus on long-read sequencing, multi-omics, epigenetics, ultra-sensitive tumour variant detection, metagenomics, and data analytics. The aim to continue driving quality improvements in clinical diagnostics (e.g., long-read sequencing) and cost reduction is commendable. CG's new technology development initiatives are guided by internal working groups and the scientific advisory board. Clinical priorities are defined within the platform by a limited number of medical doctors. Formal processes for technology evaluation and decision-making are areas ripe for improvement within the framework of CG.

## Recommendations for 2025–2028

Early transitioning of genomics technologies to extended clinical use is a critical success measure for the Clinical Genomics platform. This can be best achieved through joint definition of clinical priorities, teamwork, and shared use of expertise and infrastructure between SciLifeLab nodes and healthcare. As the clinical laboratories have acquired high-throughput sequencing instruments for producing diagnostic services, clearer division of tasks, better collaboration, and avoidance of duplication between CG, NGI and healthcare are needed to ensure cost-efficiency.

- Clarify operational roles of CG, NGI, and healthcare laboratories to delineate operational areas and eliminate redundant overlaps. CG should concentrate on translating technologies into clinical applications, including clinical research, translational projects, and clinical trials. All large-scale sequencing efforts, including retrospective studies involving large population or patient cohorts, should leverage cost-effective processes and capacity of NGI.
- Foster collaboration between CG and NGI in exploring and validating new technologies for clinical use. Centralizing adaptation and validation processes for clinical application within CG, while providing support for distribution within the CG network through comprehensive training, laboratory visits, and ring tests, can streamline the transition process.
- Facilitate the transition of novel technologies to healthcare settings by jointly defining clinical priorities, conducting formal Health Technology Assessments to evaluate likely utility and cost-benefit, and securing funding from both healthcare and SciLifeLab. This approach encourages active healthcare involvement in strategic discussions and co-publications.
- Expand the scope of assessing clinical priorities by engaging a broader community of clinical experts, extending beyond clinical genetics. Establishing a more formalized process for identifying and prioritizing clinical needs can enhance decision-making and resource allocation.
- Prioritize Collaborative Infrastructure Sharing: Emphasize the "Stockholm model" of collaborative infrastructure and expertise sharing between SciLifeLab and healthcare in innovation projects aimed at developing technologies to address clinical needs. This collaborative approach fosters efficiency and maximizes resource utilization.
- Encourage researcher-driven collaboration projects between CG and other SciLifeLab platforms (experimental and computational structural biology and chemical genomics) aiming to translate clinical genomics diagnoses into therapeutic interventions beyond patient stratification for clinical trials, potentially including novel variant targeting and individualized therapeutic interventions, like N = 1 antisense oligonucleotides (ASOs). This interdisciplinary approach holds promise for advancing precision medicine initiatives.

# E3 SiMSen-Seq

**Grade C** – Development plans 2025–2028 (1–9): **3**

*Please be aware that we only evaluated the developmental plans, as this unit is new and not yet integrated into SciLifeLab. We assigned a very low score to this entity due to the unclear demand and the possibility of user bias.*

## Motivation and feedback

The SiMSen-Seq unit at the University of Gothenburg (GU) exhibits a commendable focus on ultrasensitive sequencing applications, covering a breadth of expertise in DNA/RNA analysis, liquid biopsy handling, pre-analytics, and data analysis. Operating within the Translational Genomics Platform (TGP), the unit has made significant strides, evidenced by its contributions to over 60 research articles, 4 patent applications, and the establishment of 2 start-up companies. Additionally, the unit has engaged in partnerships with over 30 projects, showcasing its collaborative nature and commitment to advancing genomic research.

The core technology, developed through collaboration between GU and Boston University, holds promise for a wide array of applications and demonstrates potential for clinical impact, particularly in liquid biopsy analysis. This technology aligns with the evolving landscape of genomics, where liquid biopsies offer opportunities for enhanced diagnostics, treatment design, surveillance, and preventative health measures. The integration of SiMSen-Seq services into the CG Gothenburg initiative marks a pivotal step towards incorporating cutting-edge technologies into patient care, including personalised medicine.

However, to ensure continued relevance and effectiveness, it is imperative for the unit to maintain flexibility and openness to incorporating emerging liquid biopsy technologies. While SiMSen-Seq serves as a foundation, ongoing evaluation of alternative methodologies will be vital to adapt to advancements and potential superior solutions. This necessitates a proactive approach towards assessing the technological landscape and readiness to embrace innovations that may arise from external sources.

Moreover, the unit should formulate strategies to extend its reach beyond local boundaries and engage with the wider national user community. Facilitating the introduction of SiMSen-Seq technology into healthcare settings requires thoughtful planning and collaboration with relevant stakeholders. By fostering partnerships with academic institutions, national networks, and healthcare providers, the unit can facilitate the adoption of its technology and amplify its impact on patient care nationwide.

In summary, while the SiMSen-Seq unit has made commendable progress and holds promise for transformative contributions to genomic research and healthcare, continued vigilance, adaptability, and strategic outreach efforts will be crucial to maximising its potential and ensuring sustained relevance in an ever-evolving landscape.

## Recommendations for 2025–2028

The addition of the SiMSen-Seq to the platform will be a key type of platform growth that CG needs to undergo to stay current in not just research but delivering diagnostics and care (including PM) to patients.

It will be important, however, to continually evaluate and be prepared to onboard other liquid biopsy technologies as they may be developed elsewhere and not be tied solely to SiMSen-Seq just because the technology was invented at GU. The unit would be strengthened by continuous technology landscape assessment and agility in adopting new technologies as they become relevant and/or superior.

As an integrated SciLifeLab infrastructure, the unit should develop a comprehensive roadmap for 2025–2028 including:

- Implementation model for scale-up of services and implementation of platform.
- Outreach activities to national user community, including the healthcare sector.
- Training activities to support the users in high-quality sample collection and processing. as well as in data management and analysis.
- Forecast for continued technology development.

# Clinical Proteomics and Immunology

## Feedback and recommendations to the platform

The Clinical Proteomics and Immunology platform currently encompasses two affinity proteomics units (Uppsala, Stockholm) and two mass spec-based units (Gothenburg, Stockholm), with plans to establish a new SciLifeLab entity for mass spec-based Clinical Proteomics in Lund, Gothenburg, and Stockholm. Overall, the platform boasts a state-of-the-art methods and instrument portfolio, attracting a well-balanced user base both nationally and internationally. Notably, the platform has successfully analysed nearly all Swedish cohorts to date, totalling over 400,000 samples, marking a significant achievement.

However, the primary challenge now is transitioning these methods from research and development to clinical application. To achieve this goal, several efforts are required:

- Inclusion of clinicians and healthcare professionals in strategic project planning.
- Prioritization of projects based on clinical needs.
- Standardization and promotion of platform access across hospitals.
- Potential harmonization of patient consent procedures across hospitals to encompass all technologies.
- Urgent pursuit of accreditation and ISO certification.

Another crucial aspect to address is the distribution of projects and samples across the platform's various locations. Potential competition between locations should be avoided and resolved through a clear access plan. Additionally, rather than focusing on building entities around instruments, a purpose-built access model should be developed and implemented. For instance, the utilization of sensitive new timsTOF SCP instruments could facilitate the profiling of precious yet limited biopsy samples from clinics, with potential collaboration with the spatial proteomics group within SciLifeLab.

The platform generates vast amounts of data, particularly with the introduction of six additional mass spectrometers, projecting an additional capacity of approximately 100,000 samples per year. This necessitates substantial computational and storage resources, as well as innovative approaches to transform raw data into meaningful omics insights. Moreover, integrating other omics data from the same patients or probands is essential to advance towards personalized medicine.

# E4 Affinity-Based Proteomics

**Grade A** – Current technologies (1–9): **9**

**Grade B** – Performance 2021–2023 (1–9): **9**

**Grade C** – Development plans 2025–2028 (1–9): **6**

## Motivation and feedback

The affinity-based proteomics program encompasses two units, offering a world leading toolbox for precision medicine research. These units integrate individual phenotyping through multiplex protein profiling and quantification realized on cutting edge technology. They serve as both national and international reference laboratories, catering to the analysis needs of large population studies and diverse research disciplines. In 2023, they supported 146 principal investigators (doubled since 2019), contributing to around 80 publications, with a sound proportion of high impact papers.

Exceptional visibility and productivity: ranked highest among all SciLifeLab entities regarding publications per full-time equivalent (FTE) employee (16.6). Impressive financial sustainability attained through a user fee cost model, with *Affinity Proteomics Stockholm* covering 73% and *Affinity Proteomics Uppsala* covering 87% of expenses, leading among all entities. *Autoimmunity and Serology Profiling*, though with a lower coverage of 22%, still maintains an average ranking across all entities. The user base is well dispersed across Sweden's academic institutions, with notable representation from industry partners (up to 10%). Internationally acknowledged, with 5–17% of principal investigators originating from overseas. Demonstrating exceptionally high sample throughput, the units have effectively screened numerous large Swedish and international cohorts. They engage in close collaboration with prominent research groups to pioneer new assays, methods, and technologies, capitalizing on unique reagent resources from endeavors like the Human Protein Atlas. The units notably made significant impacts during the COVID-19 pandemic by detecting antibodies in dry blood spots.

Future plans involve enhanced integration of affinity-based technologies with mass spec-based technologies to better capitalize the complementarity of proteins detectable by either technology. Enhanced biomarker discovery is complemented by a variety of state-of-the art methods for targeted validation in low multiplex methods achieving absolute quantification and assessment of key performance characteristics for clinical assays. Certification and accreditation (SWEDAC, ISO17025) as well as SOP under CLSI and EMA guidelines are planned. A unique portfolio strength is the analysis of body fluids as well as breath from microsampling devices which enable home sampling and thus reach out to the general population and offer opportunities to better longitudinal data in a non-clinical context. Additionally new affinity-based methods with even larger (> 11000 proteins) or more sensitive detection ranges are planned to be integrated (Somalogics, Alamar).

A strategy to bridge the gap towards healthcare is missing (see also general feedback) and the unit suffers from a lack in data analysis support. Due to limited capacity, data analysis is currently in the hands of the users/PIs which implies fragmented solutions. More support is needed to unify data analysis especially in the clinical research context where central data analysis under unified protocols is highly wanted to enable large-scale data integration and biomarker discovery across larger cohorts.

## Recommendations for 2025–2028

- Dedicated support for data utilization is needed, it should be tightly connected to the platform rather than to the single users to ensure streamlined and effective data analysis pipelines.
- Integrate other omics from the same patients/probands towards multi-omics datasets.

# E5 MS-Based Proteomics

**Grade A** – Current technologies (1–9): **9**

**Grade B** – Performance 2021–2023 (1–9): **6**

**Grade C** – Development plans 2025–2028 (1–9): **7**

## Motivation and feedback

The CPI platform presently comprises two MS-based proteomics units: Global Proteomics and Proteogenomics (GPP), and Glycoproteomics and MS Proteomics (GMP). These units offer a diverse array of MS-based services to projects spanning various biological and biomedical research fields nationwide. They provide world-class support for specialized applications in glycoproteomics, glycomics, and proteogenomics. Equipped with state-of-the-art instrumentation, including the latest highly sensitive mass spectrometers recently acquired and installed, both units boast international competitiveness. Their extensive expertise coverage is poised to catalyse the development of new techniques in the field.

The units served 130 PIs in 2023, half of which were from local universities, and contributed to an average of 23 publications per year in 2021–2023, including high impact papers. The units have witnessed stable user numbers for GMP and increasing users for GPP. Approximately 20% of the costs are covered by user fees, indicating room for improvement, although this level still compares favourably on average. Both units maintain close ties with the local research community and are actively engaged in national and international networks and collaborative projects. The method repertoire of both units is extensive, presenting considerable challenges due to the diverse nature of MS-based proteomics. This complexity arises from the need for project-specific adjustments throughout the entire process, spanning from sample preparation and analysis to data interpretation.

Future plans involve the incorporation of cutting-edge instrumentation that promises enhanced resolution, mass accuracy, and sensitivity at unprecedented speeds. Additionally, new instruments tailored for single-cell analysis, automation to manage large cohorts, and AI-based tools for data analysis are on the agenda. These advancements will facilitate progress in critical areas where minimal human input material, such as rare cell populations, is utilized for discovery purposes and guiding clinical applications, particularly in neoantigen identification. Furthermore, the units aim to broaden their portfolio to encompass post-translational modification analysis, linking PTM modulation to mechanisms of action to propel functional proteomics forward. In pursuit of better identification rates in MS data, novel search algorithms for proteogenomics and de novo sequencing will be developed, harnessing the potential of AI. Similarly, AI tools will be devised to address the current challenge of glycan structure prediction, thus overcoming existing bottlenecks in this field.

Although these plans are highly motivated, the resources available to implement them appear insufficient. The projects are diverse, each presenting unique challenges that necessitate meticulous planning, consume significant resources, and entail extensive data analysis. Given that MS technology generates vast quantities of data, establishing a centralized and harmonized data analysis pipeline is crucial for effectively harnessing biological and clinical insights from these datasets in a sustainable manner. See also general feedback on this point. It also remains unclear how the distribution of clinical samples between these two entities and the clinical proteomics (E6) is envisioned.

## Recommendations for 2025–2028

- Expand on national broadcast of capabilities of this platform. Also here a central registration of patients/samples would probably inspire the usage.
- Increase connection and interaction with other MS-based platforms/units within SciLifeLab, e.g. Spatial Proteomics, cross-distribute users according to best fits.
- Ideally all samples have a unified consent. This could be driven as a central initiative through SciLifeLab.
- Much more support needed from DC for developing raw data analyses pipelines for the platform, instead of doing that in a fragmented fashion for each single user.

# E6 Clinical Mass Spectrometry Facility

**Grade C** – Development plans 2025–2028 (1–9): **3**

*Please note: Our low grade reflects the lack of clarity in the developmental plans. The actual demand, the strategy to bridge the gap with healthcare, and the management of prospective data remain unclear to the IEC.*

## Motivation and feedback

This proposed addition to the Clinical Proteomics and Immunology platform spans across Lund, Gothenburg, and Stockholm, aiming to spearhead clinical MS research and implementation. Its vision is to advance precision medicine by generating molecular phenotypes using MS-generated proteomics data, complementing affinity data. The unit has secured funds for substantial investments in automation and state-of-the-art instrumentation capable of analysing approximately up to 100,000 clinical samples annually. However, it has failed in securing funds for operational costs (personnel) and establishing data analysis pipelines (infrastructure, personnel). More importantly, it remains unclear how the (systemic) gap between (clinical) research labs and healthcare can be bridged.

## Recommendations for 2025–2028

- Develop a mature concept for data management and data utilization. It seems that there is currently no concept for data analysis in place. The potential data output from this machine park at maximum capacity is substantial, necessitating a completely new approach to data storage utilization and post-analysis procedures.
- Consider reallocating or sharing instruments with other SciLifeLab units, as the capacity far exceeds the current and projected usage from the clinics. Shared, local proteomics instrument parks may help to increase instrument usage and maximize the impact of funding. Three of the six new machines (timsTOF SCPs) are specifically designed to analyse low sample inputs with high sensitivity, yet they quickly reach saturation with highly abundant proteins. Consequently, scarce biopsy material or samples from spatial proteomics would be best analysed on these machines. We recommend a better integration of cross-facility workflows and a more collaborative approach across various proteomics units across SciLifeLab.
- Include clinicians and regional healthcare organizations into the strategic planning, develop a translational plan with co-design, co-prioritization and co-development of clinical test with the healthcare sites.
- Prioritize ISO certification and accreditation.
- Harmonize sample tracking to enable structured post-acquisition analyses (also repeated analyses as tools improve and additional questions arise).
- Integrate other omics on the same samples (metabolomics, epigenetics, spatial omics, genetics) and create added value from multi-omics analyses.
- Capitalize on the complementarity of affinity-based proteomics and MS-based proteomics and develop a joint data analysis plan.

# Metabolomics Platform

## E7 Metabolomics

**Grade A** – Current technologies (1–9): **6–7**

**Grade B** – Performance 2021–2023 (1–9): **8**

**Grade C** – Development plans 2025–2028 (1–9): **8**

### Motivation and feedback

The Metabolomics platform is a relatively small part of SciLifeLab, regarding FTEs and allocated budgets. Yet, it provides a strong add-on technology to the other biomedical technologies as it adds another layer of data to better understand biology. Particularly the intrinsic ability of metabolomics to determine the outcomes of metabolism as predicted by genomic variations and suggested by proteomic changes form a crucial aspect of system biology approaches. In addition, the power of fluxomics analyses to quantitate dynamic metabolomic changes in time provides insight in biological pathways that cannot be given by other platforms. For this to happen, two things are needed: 1. a fit-for-purpose metabolomics technology platform that delivers metabolomics data to its users, and 2. a computational workflow that enables the combination of metabolomics data with other data. With this in mind, the metabolomics platform was assessed.

The currently chosen approaches of the metabolomics platform seem comparable as being done by others in the metabolomics field. The application of targeted and untargeted metabolite and lipid profiling for small projects of which part if scaled up to population screening is logical. The inclusion of fluxomics within the metabolomics platform is good. To fully appreciate the technological status of the metabolomics platform, details on analytical technologies (particularly on equipment and automation) and data processing workflows are needed but missing in the report.

The current computational workflows seem focused on the metabolomics data itself, to ensure and increase data reliability and robust datasets. Collaboration with the Proteomics Core Facility and the Wallenberg Laboratory as part of the Swedish National Infrastructure for Biological Mass Spectrometry is mentioned, but not to what extent data is combined in multi-omics data sets.

The current staffing of the platforms seems small for a platform that aims to support researchers for national impact. Particularly as the metabolomics platform is focusing on biomedical research and planetary biology, which are different research fields with potential for impact in both. The user base and output seem appropriate for the size of the platform. The users of the Swedish Metabolomics Centre are spread over several institutes which on a positive note indicates its potential for local impact and user increase, and at the same time provides a challenge for maintaining and expanding close interaction with users.

### Recommendations for 2025–2028

Four focus areas are mentioned: 1. Target panels, 2. Fluxomics and identification, 3. Data handling and analysis, 4. Training and collaborations with industry. These are good and logical directions. Several comments and suggestions can be made here:

- Target panels are most likely the most direct way to produce impact in biomedical research, as researchers can interrogate specific pathways by analysis of such panels in their systems. Collaboration with the Wishart group is good, as he also collaborates with others in the world with similar intentions, thus improving the metabolomics field at large. Here, we would recommend classifying the panels in an attractive manner to align with the needs of the users, and thereby also distinguish from panels being offered by other metabolomics core facilities in the world.
- Fluxomics is a good expansion of traditional metabolomics approaches. The report details little on the development of specific fluxomics approaches to interrogate enzymatic pathways that are needed by researchers. We recommend a more user-driven approach to build the catalogue of fluxomics expertise and methods.
- A further focus on identification of unknown metabolites is key and well recognised by the platform. However, the approaches to identify unknowns are described to a limited extent. The open access database of MS/MS data can and should be combined with similar initiatives in the metabolomics field, e.g. through the global Metabolomics Society. We recommend a more intense focus on building libraries, measuring standards, comparing retention times, etc, in close collaboration with the metabolomics field. We also recommend investigating the added value of other methods other than MS/MS, such as ion mobility scanning and infrared spectroscopy.
- For scaling up, automation in the lab and in data processing is key. Lab automation will improve data quality and reproducibility while on the longer run reduce hands needed to generate data. Automated data workflows will improve standardization in data reports, aiming at improved quality control by the platform and FAIRification of data at-source. We would also rec-

ommend applying DL/ML methods to improve peak annotation. The intentions to improve computational development are well appreciated, but we would recommend improving lab automation as well.

- Metabolomics data can be quite complex to interpret for non-expert users. Good attention is paid to data handling and analysis. Particularly the integration of multi-omics and multi-modal data has strong potential in increasing the impact of metabolomics data. The creation of a computational metabolomics support group and improved contextualization of data are good plans. We believe the metabolomics platform can and should be more ambitious in this and would recommend both teaming up with other SciLifeLab facilities to integrate omics data and adding more staff to develop the computational part of the platform.
- Interaction with other platforms should be increased to improve and facilitate operational and technical workflows, and to produce multi-platform data. For instance, interact with the chemical biology platform by doing metabolomics analyses in organoids as a single profile and in time series to measure response. Also, the aim to set-up microsampling is similar as in the proteomics platform, providing a good starting point for synergy.

# E8 Exposomics

**Grade C** – Development plans 2025–2028 (1–9): **3**

*Please note: Our low score is attributed to the lack of clarity in the provided information and does not accurately represent the entity's true disruptive potential. With further enhancements, such as the development of a draft 4-year plan with clear objectives (as outlined below), this entity would likely receive a significantly higher score.*

## Motivation and feedback

The Exposomics unit is a recent addition to SciLifeLab and currently limited to one PI and 2 FTE staff. The potential of exposomics analysis is strong as it provides a highly complementary data component in precision health and medicine. However, the approach and user base is quite different from other SciLifeLab units, as exposomics generates real-world data on exposure of human populations (cohorts) to environmental compounds over time and as such supports environmental and health researchers. To deliver on this potential, it cannot be done at small scale but with sufficient focus and manpower to do it well. Moreover, similar exposomics platforms are set-up in other countries, e.g. Exposome-NL in the Netherlands, and organized in the European Scientific Research Infrastructure IRENE. As such, the IEC did not evaluate the exposomics as a typical platform, yet encouraged the initiative.

## Recommendations for 2025–2028

We recommend the following:

- Define a thorough 4-year strategic direction and aim. Include defining a niche in the Swedish and international landscape that serves the national need and synergizes with international exposomics platforms. Include an initial focus of research and technology development, e.g. on toxin exposure, and develop this well before broadening the scope to other exposome challenges.
- Based on this strategic direction, define the adequate size and composition of the unit to reach these objectives. Include a significant amount of data scientists, as linking exposomic data to epidemiological data, demographic distributions of disease, toxicology assessments, and data from other platforms is critical to achieve impact and build the base for success.
- Then define the proper analytical technologies (equipment and automation), data workflows (automation) and future developments needed, also with respect to international comparable initiatives.
- Install an International Advisory Board to help in making these decisions.

# Spatial Biology Platform

## E9 Spatial Biology

**Grade A** – Current technologies (1–9): **9**

**Grade B** – Performance 2021–2023 (1–9): **9**

**Grade C** – Development plans 2025–2028 (1–9): **4–5**

*Please note: Our low rating for C is meant to highlight the need for developmental plans to address barriers to entry and make this emerging technology more accessible to a national user base. This low rating does not reflect on the disruptive potential of this platform.*

### Motivation and feedback

The platform has been operational since 2021 and provides state-of-the-art commercial and in-house technologies and services on spatial transcriptomics, in situ sequencing, proteomics and MS. Operates at UU, KTH and SU and has a functional governance structure including an extended Platform Management Group with representation from Bioinformatics, Genomics and Data Centre providing connections to other SciLifeLab platforms. The platform is harnessing the great potential of this emerging field and obtained additional external funding (30 MSEK) from VR. The real strength of the platform is the extensive expertise in their leaders and staff that has created close connections to industry, both leading manufacturers and SMEs and the platform serves as beta tester for new instruments and methods. The platform shows quite moderate publication numbers but > 50% in high quality JFI > 9 journals and the impetus in development is shown in a high number of technology development and collaborative papers. The user base has gradually increased to current ~ 100, mainly in human and mouse models, but plans are to extend the services in clinical and precision medicine, pandemic preparedness and planetary health on non-model organisms. Data management and analysis is a bottleneck, and the platform favours the current embedded NBIS model but suggests increasing the resource from 1 to 3 FTEs. The platoform is connected to several international programs including Human Protein Atlas, Human Developmental Cell Atlas and several EU funded projects as well as Elixir and Euro Bioimaging ESFRIs. The IEC supports the platform suggestion to change its name to Spatial Omics.

To enhance its impact, the platform could strengthen its connections with other units or platforms like affinity-based proteomics and metabolomics. Additionally, efforts to optimize cost recovery are necessary, as the current rate stands at 25%, with significant variations among units. Despite the potential of its technologies, the user base remains relatively small, indicating a need for expanded outreach. The current level of cost recovery suggests that prices are heavily subsidized. Therefore, the relatively small user base cannot be solely attributed to the elevated costs of spatial workflows. Moving forward, the platform should carefully strategize its future plans, focusing on integrating multiple omics technologies and updating relevant instrumentation. Importantly, these plans should consider how to balance resources used to implement new vs resources used to lower the barrier to entry for existing workflows. The latter is crucial to facilitate implementation in clinical settings and broaden its capabilities, cost reduction and increased throughput are essential considerations.

### Recommendations for 2025–2028

- Refine the platform's vision. The platform has a high strategic importance for SciLifeLab. To this end, we recommend assessing and refine the platform's mission that can be translated into a sustainable strategy and operation.
- Tap into cross-platform collaboration opportunities, e.g. liaison with affinity-based proteomics in development of in situ interaction assays.
- Actively reach out to demonstrate the capabilities of the technologies and possibilities in question settings.
- Refine data management and improve data utilization for users. Consider how DDLS could be involved.
- Fine-tune rapid technological development towards more high-throughput assays and cost-efficient services that would serve better clinical applications, capabilities and specific fields such as digital pathology.
- Consider benchmarking with relevant international units such as Vanderbilt in the US.

# Cellular and Molecular Imaging

## Feedback and recommendations to the platform

CMI is a very well-functioning platform. Management meets regularly from across the units, and also meets regularly with the ISB platform management. They have highly developed outreach to users (mainly Cryo-EM) with drop-in and zoom sessions for users. Particularly, the Cryo-EM unit has embedded an NBIS staff scientist who sits physically in the Cryo-EM unit and is intimately acquainted with the special needs of the Cryo-EM workflows. Such models should be adopted across the entire CMI platform, indeed across SciLifeLab infrastructure platforms in general. A major weakness across platforms has been the lack of bioinformatics and computational analysis support, and the Cryo-EM unit could be a model for excellent partnership.

Many of the units in CMI face hardship with data management. A suggestion is to also form tight partnership with the Data Centre in the sense of earmarking specific Data Centre staff who will be particularly in tune with the needs of CMI units.

Altogether the CMI offers a diverse array of imaging modalities, most of which are truly cutting edge.

It is highly recommended for CMI to form strong ties with the Spatial Biology platform, in light of the suggested addition of the nanoSIMS unit. Indeed, at first it appears to be a more natural fit for nanoSIMS to be incorporated into the Spatial Biology unit. However, in consideration of the fact that the nanoSIMS is situated in Gothenburg at the site of the CAT unit, and sample preparation methods are the same for both technologies, the imaging modalities can complement each other in a natural way at this site.

There is a CMI budget request for an intra-platform pilot project to work on a kidney sample with all the units participating. A comprehensive plan and subsequent report would be beneficial not only for the platform participants, but also for users to see how such results can be achieved with such an integrated approach.

# E10 Cryo-EM

**Grade A** – Current technologies (1–9): **9**

**Grade B** – Performance 2021–2023 (1–9): **9**

**Grade C** – Development plans 2025–2028 (1–9): **6**

## Motivation and feedback

The Cryo-EM unit provides top-notch service and education to users. They provide every 2 weeks both drop-in appointments, and zoom meetings with users, to provide support and a network for users to help each other. Their performance and support have been made stronger by the addition of the CryoScreeNET service, allowing researchers at universities without high-end microscopes to be able to perform cryo-EM research. They support around 120 research groups, many of them working independently.

The service for "single particle analysis" (SPA) for protein structure elucidation is very mature at this point. The unit wants now to focus on expanding their cryo-tomography capabilities. To this end, a cryo-light microscope for correlative light-electron microscopy (CLEM) will be installed in Stockholm soon, a capability which also exists in Umeå.

To grow the community of cryo-tomography users will require active outreach to cell biologists, and there should be an outreach plan in place. This would ideally be coordinated with the CAT and FIB-SEM units, thus presenting a spectrum of 3D imaging modalities offered to cell biologists, each with their core strengths and limitations.

The clear bottleneck for expanding tomography services is the lack of a cryoFIB-SEM instrument dedicated to cryoFIB lamella production. There is a budget request for such an instrument in the Stockholm unit, but ideally such dedicated instruments would be installed in both locations. Currently in Umea, the FIB-SEM is shared with IMT (E11) for Volume imaging of plastic sections.

The Cryo-EM unit currently runs at a loss, due to the expensive maintenance costs for the instruments. There should be a sustainable plan for budgeting this unit, whether or not it can balance costs with income, considering that increasing user fees at some point would make the service not attractive to users, who can potentially apply for services outside Sweden.

The Cryo-EM unit has an NBIS staff member embedded in their unit, and this gives them a real advantage in serving their users with robust computational support.

This model should be adopted for the other units in CMI and indeed in other SciLifeLab platforms, as needed.

This is altogether an excellent unit, run professionally and clearly looking forward.

## Recommendations for 2025–2028

- A well-constructed plan for outreach to cell biologists in Sweden, as part of the expansion of cryo-tomography services.
- We recommend planning for acquiring a new cryoFIB-SEM for lamella production at both the Umea and Stockholm sites, although the budget request is only for Stockholm.
- Budgeting and user fees are an issue - a comprehensive plan for a sustainable budget is needed in light of foreseeable instrument maintenance charges.
- A stronger association with the Data Centre is clearly needed. The needs of data storage, manipulation and access are a continuing issue.

# E11 Integrated Microscopy Technologies

**Grade A** – Current technologies (1–9): **8**

**Grade B** – Performance 2021–2023 (1–9): **7**

**Grade C** – Development plans 2025–2028 (1–9): **6**

## Motivation and feedback

The three units that make up IMT are quite different in their current performance parameters. The reported infographics and numbers are not the same, so it is difficult to understand how many SciLifeLab users are being served vs. local users. It appears that the ALM serves a large user base, while the CAT and FIB-SEM have pretty small numbers of SciLifeLab users. They only joined in 2021, so this is part of the issue. But in the meantime, their user base is quite local and the publication output is small, especially for non-local users.

These are cutting-edge and difficult technologies to master and require sustained committed involvement by staff members throughout a project's lifetime.

The units are not requesting more FTEs, but this may pose a problem if the ALM, CAT and FIB-SEM units have more demand. Indeed, they do need to expand their user base beyond local users.

Since many projects coming to these units are intensive, long-term projects, there needs to be a clear and transparent path for selection of projects, in case of overcapacity, with clear criteria of acceptance for potential unit users.

The FIB-SEM is in demand, but it is also the same instrument that provides cryoFIB lamellae for E10 (Cryo-EM) workflows. There should be a high-profile plan for obtaining an additional FIB-SEM instrument dedicated to producing cryoFIB lamellae, so that the current instrument can be dedicated to FIB-SEM blockface imaging of plastic-embedded samples.

It is impressive that the unit is committed to staff development through a variety of activities, including by being part of the Horizon 2020 RetrainPlus program. Indeed, such programs should be expanded to the entire platform, ideally.

The unit has long term plans for expansion to include micro-CT. This should be encouraged, because micro-CT is a natural correlative partner to FIB-SEM and CAT methodologies. A thorough review of user demand, and indeed an effort to include micro-CT in the CMI pilot project of kidney tissue, would be useful.

## Recommendations for 2025–2028

- Outreach to users outside the local university is needed for the IMT units, especially the CAT and FIB-SEM units, which joined SciLifeLab in 2021, but still are heavily weighted with local users.
- There needs to be a clear and transparent path for selection of projects, in case of overcapacity, with clear criteria of acceptance for potential unit users.
- There is a real need for embedded personnel from the Data Centre, for hosting a central OME database server and public image data repository.
- The units are limited in their ability to help users with 3D image processing, segmentation and visualization. A stronger tie to NBIS, even an embedded member or targeted member who can work with the IMT units to build processing workflows, would be necessary in order to truly allow inexperienced users to reap the benefits of these complex methods.

# E12 Lund University Biomaging Centre/LSFM Network

**Grade C** – Development plans 2025–2028 (1–9): **3**

*Please note: The low grade does not reflect on the potential scientific impact of this technology but rather the ill-defined developmental plans.*

## Motivation and feedback

The Lund University Bioimaging Centre, is being evaluated for its potential to coordinate a national network in Light Sheet Fluorescence Microscopy, aligning with SciLifeLab's initiative to strengthen and integrate national imaging capabilities. LBIC plans to offer access to its light-sheet platforms and high-throughput clearing systems for national usage, featuring tools like a Life Canvas Technologies Epoxy-based SmartBatch for tissue clearing, an M2 Life Airy beam Aurora light-sheet, and a Miltenyi Biotech Blaze light-sheet. These microscopes use advanced technology such as airy beam light paths to enhance imaging depth and clarity, presenting unique advantages that could complement existing SciLifeLab offerings.

However, the implementation details remain unclear. Currently, LBIC's light-sheet services are managed by a small team, and there's a request for an additional 0.5 FTEs from SciLifeLab. The ambiguity in whether the funding is intended for supporting a national LSFM network or simply providing access to instrumentation raises concerns about the feasibility of providing high-quality service with the proposed staff arrangement. Additionally, LBIC's current user base is mostly local, with limited scientific output since 2020, indicating potential gaps in offering relevant services to the broader community. There is an expectation for user base growth, but it is essential to better articulate the unique advantages that would attract users from other institutions, such as the ALM in Stockholm, to utilize the services in Lund.

## Recommendations for 2025–2028

The IEC sees a need for a more defined strategic development plan for LBIC if it is to become an integrated part of the SciLifeLab platforms, ensuring it provides valuable, distinctive services that enhance national bioimaging capabilities. More specifically, the following questions need to be addressed:

- Light sheet data is typically large and can be hard to handle and process. It would be advisable to ask LBIC to also formulate a data utilization strategy. Is this something E12 plans to offer to their users?
- If so, what kinds of analyses and processing routines? If not, are there plans to team up with other platforms so that their analysis offerings can be used by users of LBIC?
- How would the current unit scale its capacity to an increasing national demand?

---

# E13 NanoSIMS

**Grade C** – Development plans 2025–2028 (1–9): **9**

## Motivation and feedback

The incorporation of the NanoSIMS unit is highly recommended. The instrumentation is provided via a partnership with AstraZeneca, who will continue to provide significant funding.

The NanoSIMS provides a unique ability to identify quantitatively chemical content in 3D, and therefore has a natural connection to the Spatial Biology platform (E9). We strongly suggest that the NanoSIMS unit forms a strong connection with Spatial Biology.

The number of users and publication output are small. In 2021 the users were heavily biased towards local PIs but this has improved in 2022 and 2023, even before incorporation into SciLifeLab. A crucial job will be outreach to both the CMI and Spatial Biology users.

Revenue from users seems to be quite high given the small number of users. The budget for this new unit attempts to balance revenue vs costs but it should be kept in mind that if costs are prohibitive, new users will be deterred.

## Recommendations for 2025–2028

- Continue efforts for integration in the CMI platforms (CAT, FIB-SEM and Cryo-EM), as well as with Spatial Biology.
- Outreach to those existing SciLifeLab scientists who are unaware of this service but are already using other types of technologies.
- We recommend incorporation of NanoSIMS into the CMI-wide pilot project of kidney tissue.

# Integrated Structural Biology Platform

## E14 Integrated Structural Biology

**Grade A** – Current technologies (1–9): **7–8**

**Grade B** – Performance 2021–2023 (1–9): **4–5**

**Grade C** – Development plans 2025–2028 (1–9): **5**

### Motivation and feedback

**Swedish NMR Centre (SNC):** SNC has an internationally competitive range of equipment, appropriately distributed across the sites in Umeå and Gothenburg. In particular, DNP, ultra-fast magic-angle spinning, cryo-MAS (cryo for solid samples, as well as cryo-probes for liquids) and the range of magnetic fields from 400 MHz (DNP) through to 900 MHz makes the NMR Centre a highly attractive offering. This is coupled with both breadth and comprehensive experience and expertise in the respective Heads of Units and Platform Scientific Directors. In short, the SNC is in an excellent position to promote and engage in highly impactful, cutting-edge biological and biomedical science research and development, and make significant contributions to the Precision Medicine and Planetary Biology capabilities.

It is therefore disappointing that the numbers of publications attributed to the platform has fallen significantly in the last two years and that the contribution by NMR to some of the publications is relatively small, albeit necessary. However, there has been some truly excellent research represented in these publications, particularly those where NMR spectroscopy is the primary structural tool in the study, highlighting the excellent state-of-the-art equipment and very high calibre of personnel associated with the SNC.

A significant proportion of the outputs in the last three years has been in metabolomics. Despite the ongoing improvements in mass spectrometry (sensitivity and resolution) in this field, NMR still has a vital role to play in metabolomics as evidenced in the metabolic profiling in prostate cancer (Dudka et al. 2023) for instance. Whilst MS requires reference compounds for metabolite identification, $^{1}$H spectra can be relatively accurately predicted and this capability is likely to improve in the future, meaning that NMR can be an increasingly powerful tool in metabolomics as the need to expand the libraries of detectable compounds increases.

**Structural Proteomics (SP):** The SP unit provides cutting-edge equipment and knowhow to directly probe protein-protein interactions. The unit is unique in Sweden and is probably one of only a handful of places where such work can be done worldwide. The data from work at this unit is clearly directly relevant in cryo-EM structure determinations and there is good collaboration between the SP FTEs and those in the Cryo-EM unit, probably aided by the SP FTEs having experience in bioinformatics and IT as well as mass spec and structural biology.

### Recommendations for 2025-2028

**SP:** The plans of the SP unit include further streamlining in the integration of data from their equipment with that from the Cryo-EM unit, clearly highly important. Installation of one of the first automated front-end sample preparation platforms for XL-MS worldwide will expand the unit's ability to assist in structural elucidation of large protein complexes alongside NMR and cryo-EM and can be expected to be particularly insightful in in situ studies. Their identification of data analysis now being the bottleneck is clear and they have excellent plans for collaborative internal and NBIS work to automate data analysis and report generation pipelines, utilizing LU-Fold and machine learning for analysis of MS data. This type of data analysis project needs to be repeated across several platforms, in addition to more streamlined integration of data from different techniques, so it will be important to ensure that lessons learned from it as well as its specific outputs are held more centrally, i.e. with NBIS or the Data Centre, depending on how the Data Centre remit develops.

**SNC:** There is no doubt that NMR spectroscopy has an important and unique role to play in structural biology and in situ structural studies. Integration of NMR data with that from cryo-EM, diffraction methods, and increasingly from bioinformatics and structure prediction tools is clearly essential to gain the level of structural and molecular dynamics insight needed to progress understanding in e.g. signalling mechanisms throughout biology (including plant biology, highly relevant for planetary biology capability), drug mechanisms of action, protein-protein interactions and their disturbance by mutations etc. So, the SNC ambition to contribute to structural biology through NMR-based studies of molecular dynamics is well-founded. Probing the mechanism of action of bacterial adenylate kinases enzyme in a combined solution-state NMR and X-ray diffraction study approach (also utilizing MD simulations) (Tischlik et al, 2023; Verma 2022) is one example of such research conducted under the SciLifeLab roof. Quantification of the distribution of molecular conformations of a Dengue protease by combined solution-state NMR and molecular dynamics calculations to predict the likely dominant conformation of the enzyme's catalytic site (for future drug discovery) is another (Agback et al, 2023); similarly, understanding the mechanism of control of epigenetic modulation by survivin (Jensen et al 2023) (solution-state NMR, biolayer interferometry, SAXS and machine learning analysis of the critical molecular structure/composition features that underpin the hypothesized mechanism). However, there are few other examples from the SciLifeLab 2021–2024 publications and none combining cryo-EM and NMR which has become a valuable structural elucidation combination elsewhere in the world. That is not to say that there are not excellent and beautiful structural studies using NMR

alone in the 2021–2023 publication list, there are. But it is not clear where the research questions that demand integration of NMR with other techniques will come from. The equipment and skilled personnel needed have been in place for several years and it would have been expected that there would by now be increasing appetite for impactful integrated studies would be on a rapidly rising trajectory. However, the publication record does not suggest this is the case.

It is unclear why integrated structural studies and in-cell NMR studies are not more mainstream. The ISB platform identify lack of bioinformatics support behind NMR-based structural studies. They suggest embedded NBIS support focusing on using NMR data in structural biology and use of AI in NMR spectrum analysis. Whilst this will undoubtedly give useful additional support for those engaged in NMR-centric work, it is probably not sufficient to drive cross-platform collaborations which are ultimately what is needed. It would be instructive for the research community if the ISB and Cryo-EM unit collaborate on an illustrative example of how NMR, cryo-EM and structural proteomics can be combined in structure elucidation, similarly to the example already performed by the Cellular and Molecular Imaging platform to demonstrate how multiple imaging methods can be applied to the same sample and the significant increase in information content that arises through data correlation. An example in-cell NMR study may also alert the research community to the potential power of such studies.

The IEC recommends urgent development of a cross-platform roadmap, led by the PDs, for integrated structural and in situ studies as well as NMR-based studies. The roadmap fundamentally needs to address data management and how to develop integrated data analysis tools but also needs to include how to alleviate common barriers, such as the need to have similar sample preparation across analysis techniques to allow meaningful integration of data, the need for robust user-friendly access to in silico trial structure prediction, e.g. LU-Fold, and development of/ support for user-friendly spectral parameter prediction, e.g. ML-approaches, for data fitting processes. The resources needed for integrated studies in the ISB platform can then be more usefully assessed and addressed. It may be that a project coordination person, as requested, will be part of the solution, but at this stage, it is not clear what the ideal qualifications of this person would be.

## E15 Macromolecular Crystallography Support and FragMAX

**Grade C** – Development plans 2025–2028 (1–9): **6**

### Motivation and feedback

The Panel understood that the ISB platform is incomplete without X-ray diffraction and in particular that integrated structural studies could be greatly facilitated by having the existing MX services provided between LP3 (Protein Production Platform, Lund) and PSF (Protein Science Facility, Stockholm, KI) under the SciLifeLab roof. However, until a comprehensive data management and analysis plan is in place for the ISB platform, and more widely in the SciLifeLab portfolio, the incorporation of MX into the ISB platform is unlikely to make significant additional impact, given that the MX service already exists through LP3 and PSF, and FragMAX though LP3 and the proposal seems to be for both facilities to continue running as they currently do.

### Recommendations for 2025–2028

The Panel understood the need to make the MX service accessible to non-expert users, but our understanding is that the unit will run with existing personnel in LP3 and PSF so the possibility for assistance to non-experts is already in place. Thus, our recommendation is that the MX and FragMAX unit is not a high priority for funding but would urge that this position be reconsidered once a roadmap for data management and analysis for integrated structural studies is in place.

## E16 ProLinC

**Grade C** – Development plans 2025–2028 (1–9): **6**

### Motivation and feedback

Whilst the biophysical characterization equipment that would be provided by ProLinC is not internationally or nationally unique, the IEC can see the value of having these mainstream biomolecule characterization facilities in one place, accessible to all.

### Recommendations for 2025–2028

The Panel could not recommend this proposed unit as a priority for funding because similar equipment already exists in e.g. the DDD platform. That being said, the IEC recognizes that the current instrumentation may not always be readily accessible for cross-platform utilization.

# Chemical Biology and Genome Engineering Platform

## E17 Chemical Biology and Genome Engineering

**Grade A** – Current technologies (1–9): **9**

**Grade B** – Performance 2021–2023 (1–9): **9**

**Grade C** – Development plans 2025–2028 (1–9): **7**

### Motivation and feedback

The CBGE platform integrates three cutting edge technologies that offer parallel chemical and genetic perturbation expertise and services to enable investigators to address critical biological questions. It is led by a strong team of experts in respective fields. The CBGE platform offers the state-of-the-art technologies for chemical library access, biochemical and cell-based assay development, HTS/HCS, and enabling chemistry, chemical proteomics, to precision gene editing, with noted weaknesses in the chemical proteomics unit. While individual technology units are powerful and available in a number of academic centres, the integrated operation as one combined platform for the life science community in Sweden is unique and impactful. The combined expertise from three functional units enables investigators to address challenging issues. During the site visit, it became clear that about 60% of the screens involve phenotypic assays, which demand follow-up technologies for target deconvolution and understanding the mode of action studies. Examples were presented to show that CBGE has established functional cross-unit pipelines. This unique integrated platform with both chemical and genetic tools enables ground-breaking basic and translational research. For such a large-scale platform involving multi-sites and multi-technology units and data format, it is challenging to address the data analysis and management issues. The cheminformatics component needs to be further strengthened. Overall, the evaluation team expressed unanimous enthusiasm for the reported impact of the technologies, services, and the expertise of the CBGE platform.

The user base of CBCS remains steady throughout the performance evaluation period (2021–2024). CBCS is the largest unit of the platform with 24 FTEs. The chemical biology unit has been expanded from KI and UU to additional four nodes with a broadened user base. The user base appears steady. ChemProt and CFG have smaller footprints with 5 FTEs each, although their technology offerings are cutting edge. The user base for ChemProt seems trending lower from the report (from 48 in 2021 to 34 in 2023). The overall publication productivity is modest.

From the presentation and our own experience with the operation of similar types of chemical biology cores/centres, the success of the platform should be measured by metrics beyond the number of publications. In this case, it is clear that CBGE has been highly active and productive in enabling the advancement of a large number of research projects and enabling other investigators to pursue projects otherwise impossible. In addition, its effort has led to the entry of multiple projects into the DDD pipeline. Evidence for productive collaborations with other platforms, such as DDD, was presented, which is critical for the success of the SciLifeLab. Examples were presented to show how the chemical biology unit worked closed with the chemical proteomics and gene editing units together for target identification from phenotypic screening hits. It illustrates the effective workflow and the close intra-platform collaborations. We rated the performance of CBGE outstanding as a whole (score 9) with noted weaknesses in chemical proteomics.

The proposed platform development plan is sound and impactful, which include technology enhancement for drug repurposing, fragment-based drug screening and virtual screening, compound profiling, and disease model development. In particular, informative disease models, such as iPSC and gene-edited cell lines, are urgently needed with enormous potential to advance biology and therapeutic development. It will not only strengthen the CBGE platform, but also other platforms, like DDD. The fragment-based screening capability is a valuable addition, the impact of which will be enhanced by enabling synthetic and medicinal chemistry. For the proposed fragment-based screens, the Chemical Biology unit recognized the importance of its close collaborations with other platforms with expertise in biophysical, structural biology, and spatial biology technologies and deep engagement with synthetic/medicinal chemists. The chemoinformatics coupled with data science expertise is essential for addressing complex biological questions and for generating novel hypotheses for ground-breaking scientific discoveries. The chemoinformatics and data informatics support should be strengthened during the next phase of the operation. Virtual screening demands the strong support of the high-speed computational infrastructure and intensive synthetic chemistry involvement. As the chemical biology and genetic editing field continue to evolve, future plan should consider cutting edge assay development to support the discovery and utilization of emerging technologies and tools for cross-disciplinary studies.

## Recommendations for 2025–2028

The CBGE platform offers an impressive panel of technology capabilities that has demonstrated its enormous contributions to advancing the mission of SciLifeLab across universities in Sweden. To further elevate its impact, here are some recommended actions:

- Integrated operation of CBGE as a catalyst to advance the mission of SciLifeLab: With the integrated operation, new approaches could be rapidly developed and implemented to address challenging biological issues to provide a competitive edge for the Swedish scientific community. For example, the CRISPR technology, chemoproteomics, and chemical biology approaches could be integrated for the speedy discovery and development of proximity inducing agents, a rapidly rising field in biology and medicine. The development of proximity inducing agents is also a focus of the DDD platform as a future direction, which offers an opportunity for synergistic partnership. Acquisition of fragment libraries for fragment based chemical biology studies adds a new capability to the platform as planned, the success of which requires close collaborations with other units with expertise in biophysical/biochemical assays, structural biology studies, and enabling synthetic chemistry support. The presented examples illustrate the practice of this integrated model, which could be further strengthened with a project management workflow for each project.
- Technology enhancement: To support the proposed new directions, infrastructural support is needed for virtual screening, fragment-based screening, drug repurposing, and compound profiling for target deconvolution and MoA studies. The chemoproteomics capability is a critical component of the platform, which requires significant improvement. For phenotypic screens, target identification is critical that may require technologies beyond PISA as the primary chemoproteomics approach. This is especially important because most of the screens performed by CBGE (60%) are phenotypic screens. Other target ID technologies should be considered and strengthened, which include both affinity-based and activity-based chemoproteomics technologies and other probe-independent target ID approaches. Access to other related technologies, such as Somascan proteome profiling, in NGI, Proteomics and Spatial Biology platforms is encouraged.
- The bioinformatics and data management capabilities should be improved in support of CBGE. It requires the integrated operation with multi- technology platforms, including screenInformatics, chemInformatics, and bioinformatics for data acquisition, analysis, profiling, and data management with the support of computational chemistry.
- Biological and disease model systems with iPSC are expected to have significant impact on gaining biological insights, disease biology, and therapeutic discovery. Interacting with clinicians and members of other units and platforms will enhance its overall performance and its impact.
- A mechanism to effectively promote cross platform collaborations is important for further growth of CBGE and its added values to SciLifeLab. One approach is to use cross-platform co-publications as one parameter for annual evaluation. Enhanced intra-platform interactions and inter-platform collaborations are critical for synergy to elevate the impact of CBGE and SciLifeLab for the broad Swedish scientific community, a defining feature of SciLifeLab.
- Unique KPI for CBGE: For future evaluation of CBGE performance, we recommend that in addition to continued effort for increased joint scientific publications, other metrics for measuring its success should be considered and implemented. These parameters could include the number of scientific projects enabled (enabling PIs), innovative assays developed, powerful chemical or genetic tools developed, breakthrough discoveries made from the chemical and/or genetic perturbations enabled by CBGE, and the effective partnership established with DDD and other platforms, and the number of disclosures/patents filed by supported PIs with contributions from members of CBGE. This performance evaluation recommendation may also be applied to other units including chemoproteomics and CRISPR engineering.
- Expectations for scholarly contributions: In order to further increase the scientific output of CBGE, the pro-active engagement of members of CBGE in selected projects should be encouraged and expected. In addition to offering specialized services to SciLifeLab investigators, CBGE members will provide unique expertise and professional guidance for project enabling AND timely publications. For example, the critical path of each project should include a publication plan from the very beginning. Publications on innovative assays, or conventional assays developed for novel targets/phenotypes, are highly valuable to the scientific community.

# E18 Morphological Profiling and Automated Patch Clamp Profiling

**Grade C** – Development plans 2025–2028 (1–9):
**9** Morphological Profiling
**2** Automated Patch Clamp Profiling

## Motivation and feedback

This entity proposes to integrate two existing specialized services into CBCS: morphological profiling by Cell Painting and automated patch clamping:

Cell-painting has matured into a powerful technology for compound screening and drug discovery and is seen as a very valuable extension of CBCS. Cell Painting is a high-throughput imaging assay in which multiple fluorescent reporters are read out by automated microscopy. Thousands of features can be extracted from these images and aggregated into multidimensional profiles at single-cell resolution. Morphological Profiling is hosted by the CBCS node in Uppsala and is very well positioned to bring this technology to fruition for all of SciLifeLab. Importantly, it is embedded in a bioinformatics group closely linked to the Data Centre (the Head of the Pharmaceutical Bioinformatics is also one of the senior leads of Data Centre), ensuring state-of-the-art e-infrastructure and computational support for data processing, analysis and mining.

Electrophysiology can also be a critical part of target identification and validation, and of MoA elucidation, especially for diseases and disorders involving central and/or the peripheral nervous systems.

## Recommendations for 2025–2028

The IEC recommends including cell painting into SciLifeLab's portfolio. The evaluation panel is highly enthusiastic about the incorporation of the Morphological Profiling technology into the CBGE platform. The cell painting and the related technologies should add significantly to the capabilities for compound profiling and mode of action studies. This component should also be aligned with operations of other related platforms, including Spatial Biology, Imaging, and Genomics platforms. Data analysis is a critical component for such high content screening/profiling technologies.

The addition of electrophysiology support is in principle a strength; however, the automated patch clamp profiling service as proposed seems too limited to be able to provide reliable support to SciLifeLab projects. Key suggestions for improving the concept of the service include:

- Inclusion of manual patch clamping, as typically only not very well differentiated cell lines are amenable to automated patch clamp. As such, with increasing use of patient-derived primary cells and (differentiated) iPSCs, many or most of these will not be suitable for automated patch clamp, but would still be approachable by manual patch clamp.
- The biophysical properties of automated patch clamp technologies are generally quite limiting (especially in terms of frequency response); therefore, findings always need to be validated by manual patch clamp. This includes hERG channel activity for which the gold standard remains manual patch clamping.
- Especially for neuropsychiatric and neuromotor disorders, neural circuit function is often key and not assayable using single-cell electrophysiological techniques. In this context the addition of multi-electrode array platforms should also be considered.
- Finally, synergies of electrophysiological methods with image-based activity measurement technologies needs to be described, notably calcium imaging which can be done manually or with automated imaging systems (e.g. FLIPR-type instruments) which are already available in other cores within the SciLifeLab infrastructure.

# E19 Cell and Gene Therapy Core

**Grade C** – Development plans 2025–2028 (1–9): **5**

*Please note: The IEC considers this entity highly promising but finds a lack of plans for scaling up. The low grade reflects the need for improved planning in this regard.*

## Motivation and feedback

Cell and Gene Therapy core (CAGT) is located at the Lund Stem Cell Centre at LU and provides nationally unique services including iPSC derivation and reprogramming, iPSC gene editing with quality analysis and custom lentivirus/AAV resources. The unit was established in 2022 and is currently serving 45 mainly local research groups. The node is embedded in a strong stem cell research environment. CAGT core would bring in complementary expertise benefiting the CBGE platform, and its role in the preclinical research can open new avenues.

CRISPR-based methods are becoming a mainstay of functional genomics, and this is the focus and strength of this new unit. Indeed, the emphasis this unit has on rigor and reproducibility which has been often lacking in the broader field. This will be one of the most important strengths of this unit in supporting robust chemical genomics as well as drug discovery.

The proposal makes clear that the generation and work-up of iPSCs will be the main contribution to SciLifeLab. In addition, it is noted that the broader focus of the Lund Stem Center in vector design etc. will serve as a "first synapse" to the ATMP space. Looking into the future where therapeutic strategies will routinely incorporate both small molecules as well as ATMPs, this will indeed be a plus.

## Recommendations for 2025–2028

- Include scale up into developmental plans. One area that is not adequately addressed is scale-up, especially for large-scale screening campaigns. While all of the underpinnings of scale-up are well addressed (e.g., master cells banks and quality controls), perhaps at least pilot-scale scale-up studies could be incorporated while acknowledging that the costs of scale-up can be enormous.
- Include alternative/complementary technologies. A broader question here and also for the CFG unit is whether there still is a role of siRNA and ASO technologies e.g., for critical validation of CRISPR results, and to be able to have acute perturbation tools for knockdown for pathway elucidation and to mimic drug intervention. If so, how will these technologies be supported and incorporated into experimental workflows, e.g., by partnering with the OligoNova unit at Goteborg University that is part of the DDD platform?
- Integration into the CBGE platform with validated iPSC models. Quality control of the established iPSC models should be emphasized to enhance the impact of their use.

# Drug Discovery and Development Platform

## E20 Drug Discovery and Development

**Grade A** – Current technologies (1–9): **8**

**Grade B** – Performance 2021–2023 (1–9): **8**

**Grade C** – Development plans 2025–2028 (1–9): **7**

### Motivation and feedback

The DDD platform is designed to directly drive the translation of user research findings towards tangible healthcare outcomes including the development of new drugs and biomarkers. DDD is a distributed platform encompassing 10 units across 6 universities, with central management and the hubs of operations centred at KI and UU. The units cluster around discovery and target validation technologies, medicinal chemistry, ADME, and a new unit focused on oligonucleotide modalities (OligoNova, initiated at GU in 2021 and coming online in 2023). Additional experience and support for nonclinical development not already encompassed within DDD or SciLifeLab can be accessed through external service providers such as RISE for exploratory toxicology and the Testa Centre for pilot-scale biologics manufacturing.

Historically, DDD has mainly supported small molecule therapeutic discovery and early development (the recent addition of DNA-encoded libraries further strengthens these capabilities), and to a lesser extent biologics. DDD also accepts ATMP projects, but as noted full support of ATMP would require substantial expansions of the platform. The addition of the Oligonova unit provides welcome coverage and support for the fast-growing segment of gene-targeted small molecule drugs such as ASOs, especially in the rare and ultra-rare disease space. Now that translation from whole-genome sequencing to first-in-human dosing has been shown to be possible within a year or less, ASO development is becoming one of the fastest paths for clinical translation from basic research findings to patients.

A key strength of the DDD approach is to guide projects through a critical path process that includes major Go/No-go decision points and/or project exit points, such as the Go/No-go Checkpoint 2 (Figure 3 in platform report) after assay development and hit identification and gating towards drug lead candidate generation. This kind of Target Product Profile-directed development and rigor is essential for effective translation and forms the backbone of DDD project process flow.

In sum, the DDD platform spans all the key services and expertise needed for the translation of research findings into tractable drug and biomarker candidates positioned for preclinical development towards regulatory clearance for human studies. As such the services and expertise offered by DDD are key for realizing the healthcare impact of novel therapeutic hypotheses, novel drug and biomarker candidates, and new and cutting-edge drug modalities and discovery and development technologies. There are few if any other examples of such a comprehensive and powerful drug development platform nationally or internationally.

To further increase the healthcare impact of DDD, and to increase the scientific/clinical value of commercial exits, projects would benefit from further service and support towards and even into CTA-directed studies, notably in the areas of dosing and toxicology and safety pharmacology. As such, substantial increases in medicinal chemistry support and in vivo DMPK and safety studies (the latter are not currently offered) should be considered.

Another area of increased focus could be target validation, both in the contexts of elucidating mechanisms-of-action (especially as some 60% of high-throughput screens conducted by CBGE/SciLifeLab have been phenotypic) as well as human target validation. The latter would benefit from more cross-platform interactions, including those focused on non-clinical and clinical genetics, omics, and imaging. In addition, more explicit milestones on reproducibility of key findings (notably in vivo efficacy studies) in an independent lab would increase the scientific robustness and commercial value of DDD projects.

DDD has been impressively productive especially given its relatively modest size (~ 40 FTEs) and budget (< 80 MSEK in 2024) compared to industrial and other academic or governmental operations (e.g., in the US) with similar remits but considerably larger staffs and budgets. Even so, DDD has managed an average of two commercial exits per year, totalling 17 commercial exits to date since 2014. Four of these exits are in clinical investigation-stage, four are internationally partnered, and 13 have resulted in the establishment of Swedish biotech companies (three listed).

User interest has been consistently strong, with an average of over 40 first meetings with interested users per year over a 10-year period (2014–2023) with an average project admission rate of 12%. In the aggregate admitted projects amount to supporting an average of ~80 PI users per year over the past 3-year period. In fact this is an underestimate of the amount of user engagement and support provided by DDD, as projects are onboarded in a progressive manner, with some 20% of first meetings progressing into "preProjects" for further evaluation and diligence.

An important area will be continued development of key performance indicators (KPIs) for DDD, as customary metrics for academic efforts such as publications and grant funding generally do not pertain to projects in

preclinical development stage. In this context it would be important to formulate intermediate metrics for translational progress on the path towards commercial exits. Examples could include:

- The project review process is done through stages and very interactively with DDD internal experts such that even the almost 90% of applicants who are not accepted nonetheless gain valuable insights into how their projects can become more translatable. Perhaps these insights could be measured in other projects outputs outside of officially onboarded project activities.
- There have been 20 "academic exits" since 2014. Can the continued productivity of these projects be quantified, such as in additional research funding and publications, especially in the clinical setting?
- Can project progress outside of official exits be quantified, such as translation status at entry point vs. current status, even for “failed” projects? Indeed, reasons for project failure are often the most informative and are a key value-add of DDD (e.g., lack of efficacy despite good target coverage/engagement, or on-target toxicity).

One key source of project failures was reported to be lack of entrepreneurial spirit and engagement of project PIs, despite DDD leadership’s effort to pre-empt this issue at project onboarded stage. In fact, this problem is widespread across academic translational efforts worldwide. In the long term, direct outreach to and training of younger scientists (as opposed to PIs)—and beyond the occasional lectures within the established academic curriculum - will surely be important for changing the academic culture in which SciLifeLab is embedded.

Finally, the issue of project ownership will be important to clarify. While the underlying concepts for translational projects do originate from project PIs, substantial additions to the project are made by DDD scientists including novel drug candidate molecules, diagnostics, discovery platforms, and know-how. In many cases DDD scientists will be legal co-inventors of such intellectual property that are captured in patent filings. As such DDD should be a recognized co-owner of DDD projects and have a greater role in the determination of and consent to commercial as well as academic exits. This could reduce the number of project failures as well as premature project exits due to lack of entrepreneurial spirit and experience of the PIs.

DDD leadership have a clear sense of platform strengths and weaknesses and are generally well-positioned to meet future expected needs from the life science user community. For example, to address the limited translational and entrepreneurial experience of user PIs, the establishment of an Innovations Group and entrepreneurial training track are excellent and exciting additions to the platform. It will be good to understand how these new activities can help define optimal exit strategies on a project-by-project basis, for example by collaboratively building target product profiles (TPPs) for each project/asset and contributing to the commercial plan that is part of Checkpoint 2.

Strengthening or rebalancing areas of service in order to optimize value generation in projects should also be considered, with the caveat that drivers of commercial value can vary from year-to-year. Currently, for example, key value drivers are biased towards human target validation and mechanism-of-action, and less towards novel discovery technologies. New chemical and molecular entities at the clinical candidate stage are perennial value drivers. In this case augmenting medicinal chemistry capacity and the strengthening of non-GMP process chemistry and pilot biologics manufacturing could be considered. Collaborations with other external and international initiatives could be leveraged also, such as in early-stage clinical manufacturing infrastructures for ATMPs that are actively being expanded in the UK and Europe.

More explicit description and focus on project management would be helpful. In particular, there is perhaps missing a sense of the assertiveness and aggressiveness usually associated with driving entrepreneurial projects towards value generation, as compared to the provision of discrete a la carte services that are helpful to translational projects in a more general sense.

Finally, how can DDD take more advantage of the Swedish teacher's exemption to generate more value prior to a formal commercial exit? For example, can more access to private investments and industry collaborations be pursued, given that in most other countries such interactions are generally not possible because of institutional ownership of IP generated in the course of the project? Specific examples of such efforts that would generate much more value for DDD exits could include full lead optimisation to clinical lead status, and the development of full CTA-enabling study packages.

## Recommendations for 2025–2028

Although by nature DDD does not need to be right on the cutting edge of all drug discovery and development technologies, it does need to be able to support effective translation of basic research findings towards clinical readiness and the generation of scientific and commercial value. As such DDD should continue to emphasize its strengths (e.g., supporting development of novel therapeutic and diagnostic modalities, exploiting novel mechanisms-of-action) but also seek to support value drivers that may be expensive (e.g., in vivo DMPK and safety studies). Specific recommendations include:

- A major recommendation is for DDD to onboard significantly fewer projects, such that each project can be more substantially supported towards key value inflection points. This in turn will generate great value in commercial exits and be key in supporting long-term sustainability of the DDD platform.
- Development of an explicit AI strategy to incorporate into DDD operations including impact on project onboarding, computational approaches to lead optimization including toxicology and safety pharmacology, and project exit points.
- Emphasize that projects are partnerships rather than simply providing DDD translational services. Current interactions leave too much control over project IP and exits to the user PI and risk premature/suboptimal project exits and unnecessary project failures.
- Establish a dedicated business development unit, including staffing from real-world business professionals with direct experience in drug asset-based transactions and M&A activities in biotech and pharma (not just from MBA and training programs, and not from academic tech transfer offices).

# Bioinformatics Platform

## E21 Bioinformatics

**Grade A** – Current technologies (1–9): **8**

**Grade B** – Performance 2021–2023 (1–9):
**5** (judging from SciLifeLab needs)
**8** (for services NBIS is providing)

**Grade C** – Development plans 2025–2028 (1–9): **3**

### Motivation and feedback

The Bioinformatics platform, designated under the umbrella of National Bioinformatics Infrastructure Sweden (NBIS), provides bioinformatics and data science expertise to the Swedish Life Science community. This platform integrates four critical units: AIDA Data Hub, BioImage Informatics, Support for Computational Resources, and Support Infrastructure and Training. Looking ahead, there is a proposal for further integration of these operations into a cohesive framework with a unified budget starting in 2025.

It is important to note that the platform benefits significantly from SciLifeLab funding — primarily aimed at supporting the users of all SciLifeLab's platforms — NBIS also secures substantial financial support from various other sources, each with its distinct terms and conditions. This diversified funding enhances the platform's capacity to contribute to visible and prestigious European projects. In the context of this evaluation, the utility of these projects appears of limited utility for other SciLifeLab platforms.

When evaluating NBIS as a platform on its own, the provided teaching and national services are useful, the international activity commendable, making NBIS a very visible and active player of undisputable utility. Still, in light of the evolving requirements of the scientific community as a whole, we have identified a noticeable dissatisfaction among other SciLifeLab platforms about availability and support for much needed bioinformatics services.

Regarding planned service extensions, we were tasked to evaluate the potential integration of LU-Fold (Entry 22), which aims to provide cutting-edge support for AlphaFold2 protein structure predictions, and PReSTO (Entry 23), a computational platform designed to advance structural biology.

#### *Key observations*

Our most evident observation is that NBIS is not perceived equally available and useful for all SciLifeLab platforms that would like to receive (and frankly much require) professional computational support for various data storage, data transfer, and data analysis and utilization tasks.

While certain SciLifeLab entities appear content with the support provided by NBIS, others express a sense of insufficiency. Currently, the following areas within the SciLifeLab facilities feel sufficiently supported by NBIS: Cryo-EM and Structural Biology, AI and Deep Learning, AI in medical imaging, Bioimage Analysis, and Spatial -omics, ancient DNA, and drug development. On the other hand, we have noticed that entities E4, E5, E7, E8, E9, E11, and E17 currently seemingly struggle to receive computational support at various levels. The underlying reason for this divergent perception remains unclear to the IEC. We must also note that these platforms deal very differently with the lack of support. Some are very proactive, others very passive. We will allow ourselves to recommend a potential solution below.

Two platforms that do also rely heavily on computational aspects found well working solutions: E1 (Genomics), for example, seem to have hired their own experts. E10 (Cryo-EM), instead, has received funding and support to implement a setup where NBIS staff is permanently seated with them. Some already referred to this model as the "Embedded" Bioinformatics Support Model.

We have received positive feedback about the Embedded Model, and many people we talked to seem to believe that an adequate implementation could be advantageous also for their own platforms.

### Recommendations for 2025–2028

#### *Governance and policy improvements*

We propose to explicitly define the Bioinformatics platform's role in serving not just individual PIs but also other SciLifeLab platforms. This involves establishing a formal mechanism to ensure that NBIS's contributions to the success of other platforms are recognized and supported.

We see value in improving transparency in how projects are selected, prioritized, and funded. Establishing clear guidelines for periodic decision-making meetings, including detailed roles and responsibilities for all stakeholders. This should extend to the board's involvement in strategic decisions, ensuring that everyone is well-informed and engaged in the governance process.

#### *Improving computational support*

In response to the global trend for FAIR data storage, analysis, and tool support, we urge to address the demand noted by other platforms for increased availability and support, e.g. by Adopting an Embedded Bioinformatics Support Model.

We acknowledge that NBIS does already hold a huge amount of relevant computational expertise, and adding more might require making a large entity even larger and potentially harder to efficiently manage. Below, we will propose the adoption of an Embedded Bioinformatics Support Model, but we also have to point out that a continuation and expansion of the training opportunities NBIS offers is equally important. The goal must be to help supported platforms to also teach their staff and users about the computational and analysis aspects that emerge after data is successfully generated.

***Adopt the embedded bioinformatics support model:*** Building on the success of the embedded model seen in platforms like Genomics (E1) and Cryo-EM (E10), we advise extending this model across other platforms that currently suffer from missing computational expertise and support. This approach involves placing NBIS staff directly within these platforms, facilitating immediate and ongoing computational support, thus enhancing the operational synergy between NBIS and other platforms.

We suggest that the funding for such positions should not be seen as a problem for NBIS to solve. Instead, the platforms aiming and improving their storage, analysis, and method and tool development must be given the task of financing these efforts. Whenever this includes the submission of grant proposals, shared authorship of such proposals between NBIS and the respective platform seems to be a natural approach.

***Standardize data management and support across platforms:*** We propose to implement mandatory data management plans for all (investment) projects, ensuring that every platform adheres to standardized procedures for data storage, transfer, and analysis. Such documents should be kept lean but protocol the type, amount, direct utility, and potential utility of the data being created. Depending on the utility, a suitable way of storage and access policy should be suggested and evaluated by suitable entities within NBIS, the Data Centre, and/or SciLifeLab.

### *Implementation strategy and guiding principles*

We suggest aligning the implementation of these recommendations with guiding principles that ensure that data management plans are not only embedded within platforms but also dynamically linked with the bioinformatics support to ensure seamless data integration and analysis.

NBIS is clearly facing a challenge unlike any of the other platforms. Like all the others, it is providing a huge and modern service and training portfolio to a large national user base. Additionally, it is asked to also provide key services to other platforms and is currently criticized for doing too little of it. We believe it is of utmost importance for the SciLifeLab Management to clarify priorities for NBIS, and maybe distinguish the two kinds of support it is requested to provide. While we will continue to refer to NBIS as a single platform, these two aspects could very well also be separated into two SciLifeLab Entities that would work closely together but have a better-defined support mandate.

We understand that an increase of FTEs specifically designated for bioinformatics support across and within platforms is a major funding and implementation challenge. One could consider converting some existing positions to focus more on these important needs. Alternative, new roles tailored to support the specific requirements of different platforms could be created. Still, it must be ensured that NBIS, which is already a very large structure that covers an enormous amount of national and international activities, remains agile and flexible to effectively follow the fast pace of FAIR storage, computation, and AI.

The role of NBIS and the Data Centre are key to meet the evolving needs of the SciLifeLab community. It is paramount that SciLifeLab finds a way to improve data utilization across all platforms to further enhance Sweden's position in the competitive and fast paced international research landscape. Current gaps must be addressed, and NBIS should take an active role in helping to find proactive solutions to prepare SciLifeLab platforms for future challenges and opportunities in bioinformatics, data science, and AI to improve data utilization across data domains.

# E22 LU-Fold

**Grade C** – Development plans 2025–2028 (1–9): **8**

## Motivation and feedback

LU-Fold is proposed to be an extension of the Bioinformatics platform, specifically geared towards supporting users with AlphaFold2 protein structure predictions. AlphaFold2 is an AI-driven approach that predicts the three-dimensional structures of proteins with unprecedented accuracy, currently offering new opportunities to the field of structural biology and the life sciences in general.

The incorporation of LU-Fold into SciLifeLab's services aims to provide state-of-the-art computational resources and expertise to facilitate advanced protein structure analyses. This expansion would enhance the capabilities of the Bioinformatics platform, aligning it with cutting-edge developments in computational biology and supporting a wide range of research applications that require detailed insights into protein structures.

The offered services are cutting-edge, and with E22 being part of the SciLifeLab service portfolio additionally has the advantage of being able to react quickly to future updates and capabilities becoming available.

## Recommendations for 2025–2028

We see value in offering the LU-Fold services as part of the national SciLifeLab platform portfolio and suggest ensuring that updated versions and capabilities are integrated in a timely fashion.

Additionally, we suggest the unit to team-up with the Training Hub and NBIS to incorporate solid training material into suitable courses. The possibilities AlphaFold2 and similar technologies are already capable of offering are likely not understood by all users that could benefit from it in their own research. Hence, we believe it is important to educate and work against “energy barriers” with respect to the uptake of the provided tools and services.

Since LU-Fold is one of the first units that offers cutting edge AI methods and tools, we suggest that other AI services that will become available in the next few years take inspiration from what the LU-Fold team has learned from offering their services.

# E23 PReSTO

**Grade C** – Development plans 2025–2028 (1–9): **5**

## Motivation and feedback

PReSTO is envisioned as an addition to the Bioinformatics platform, serving as a computational platform specifically designed for structural biology software. This service aims to support users with a comprehensive suite of tools and resources for modelling and analysing protein structures, potentially integrating with existing computational biology services and enhancing the platform’s capabilities in structural biology.

By including PReSTO, the Bioinformatics platform would be better equipped to support structural biologist with a comprehensive set of tools and thereby reduce the overhead of individual researchers having to find ways to install and run those tools themselves.

PReSTO is already running and providing these services and we understand that the request of integrating it into the NBIS service portfolio is mostly motivated by the desperate need for a more sustained source of funding to keep the service running and maintained.

We believe the provided service is of good quality but remain unsure if a service that is so IT heavy and so little scientific should be cast into a SciLifeLab platform. Instead, we feel that the Data Centre would be the right place to take on the maintenance and expansion of the PReSTO service infrastructure.

## Recommendations for 2025–2028

Throughout this document, we suggest SciLifeLab to give significantly more emphasis on data utilization by strengthening FAIR data storage and analyses. With regards to PReSTO, we suggest to not run it as or within a platform, but instead keep this very important IT infrastructure running in a context closer to IT and the Data Centre.

While PReSTO is currently conceived as a collection of tools for structural biology (also covering the tools for LU-Fold), other data modalities and research directions also require specific tools to be installable and runnable on the available IT infrastructure. Hence, we believe that PReSTO, even if not in the context of a SciLifeLab platform, must receive funding to be continuously provided and its tools regularly evaluated and updated. We also think it would be wise to use the same infrastructure to also provide other tools that will be needed by SciLifeLab platforms and their users.

# Capabilities

## General feedback and recommendations to the capabilities

As mentioned earlier, Capabilities aim to bridge platforms and units, demonstrating a clear vision. While their vision and strategic/political importance are clear, we believe that individual capabilities require refinement of their strategies to catalyse cross-platform activities. The IEC believes that it is essential to clarify whether capabilities primarily function as internal funding bodies, or also as a source of cross-platform communications, and how they intend to avoid becoming an additional administrative layer.

---

## Precision Medicine Capability

As mentioned above, there appears to be a significant divide between (clinical) research and healthcare, with Precision Medicine (PM) holding promise to bridge this gap. However, this was not adequately addressed during the presentation or in the report, leaving observers to question what the intellectual and strategic drivers of the PM initiative are. Furthermore, their definition of a proof-of-concept and measurable success outcomes, such as achieving PM integration across all platforms, seemed vague and overly ambitious.

That said: It will prove beneficial nonetheless, as the questions are urgent, though expectations might be overly optimistic. This initiative will enhance visibility, attract external funding, and potentially establish itself as a leading entity for Precision Medicine on a national scale.

### Recommendations

- Target the right audience: How do they plan to lower the barrier to entry into clinics/healthcare? They should be encouraged to pursue direct engagement with healthcare providers and patients.
- related: Define, brand and sell the USP of this capability to healthcare not research.
- Define clear interfaces or use cases for cross-platform interactions: e.g. How does precision medicine intend to relate and work with DDD?
- Scout for strategic partners and avoid redundancies to PM centres at local universities.

# Planetary Biology Capability

The Planetary Biology (PB) capability was established in 2023 to promote collaboration and efficient use of modern molecular life science approaches in addressing the most pressing questions in environment and society. The mission aligns with EMBL strategy "Molecular to ecosystems" and facilities the use of molecular approaches to address planetary questions. The goal is highly relevant as basic components are universally shared and the modern methodology can allow a paradigm shift in "green biology".

The PB capability is governed by a leadership representing different universities, technologies and spectrum of biology. The funding 3,5 MSEK comes entirely from SciLifeLab but discussions on funding with relevant governmental agencies and ministries as well as with industry have been initiated.

PB has arranged various events to promote and discuss the topic within the disciplines and with SciLifeLab context and wider public. PB has participated in EMBL Trec European level sampling program and is engaged in European reference genome atlas ERGA and biodiversity genome Europe BGE. PB has also conducted a user survey that identified a need for centralized method development and showed the willingness of the community as well as the technology providers to participate in method development.

PB activities have synergy with PLP, One Health and with PM in infection diseases. Related to training activities PB is preparing an online course in advanced genomics in non-model organisms. The future plans involve further workshops/events, engaging with DDLS and DC and act as brokers for bottom-up collaborative projects and development of methods, technologies and data analysis. The plan to provide an open web-based platform for methods on non-model organisms and sample pre-processing seem well founded.

### Point of improvement & Recommendations

PB deals with extremely important but extensive area of science and PB has taken relevant action in this domain and the plans e.g. on sharing of methodology and sampling are clearly needed. However, as the PB covers biology from ecology to evolution and has limited resources, the IEC sees that it would be critical to establish a clear prioritized strategy and action plan, and maybe change the general concept from broker to actor to ensure that the resources will be efficiently used.

The PB topic is of wide global interest and benchmarking to other international institutes e.g. in the Netherlands would be useful for identifying the strengths and opportunities and areas of development of the Swedish activities and possibly find relevant collaborators.

# Pandemic Laboratory Preparedness Capability

From 2021 to 2024, SciLifeLab secured an impressive 130 MSEK of dedicated funding, which is crucial for setting-up its readiness program. During the pandemic, SciLifeLab played a vital role in supporting Sweden with PCR capabilities and other assistance, showcasing an overall vision of pandemic readiness. However, concerns arise regarding the adequacy of the total funding, given the costly nature of these activities. There is a need to balance and ensure sustainable infrastructure for both pandemic and non-pandemic ("peace-times") times. Embedding PLP capabilities in existing platforms or units appears to be a pragmatic approach to the IEC. Questions raised during discussions highlight the importance of addressing gaps in sample logistics, learning from societal impacts, and ensuring a robust supply chain.

# Training Hub

Ensuring high-quality training within its research infrastructure is paramount to fostering scientific advancement in the SciLifeLab community. Therefore, the creation of a Training Hub stands as a logical and necessary step for SciLifeLab's mission. Launched just a year ago, the SciLifeLab Training Hub has already achieved significant milestones: assembling a dedicated team and implementing the central communication platform, the Training Portal. During this brief period, the Hub has organized numerous courses, showcasing the commitment and competence of its leadership. Undoubtedly, the Training Hub is an indispensable component of SciLifeLab, poised to create added value beyond training and contribute to the integration of the SciLifeLab community as a whole.

Moving forward, here are some ideas and recommendations:

- Make a clear distinction between training offers according to their target groups: service USERS and service PROVIDERS.
- USERS: This category largely encompasses courses or training sessions offered by the technology platforms/units and their staff. The intensity and depth of these sessions may vary depending on the operational model of the units: walk-in, open lab-type units typically offer more direct training than full-service, sample-in/data-out facilities. The units are generally best positioned to determine the most effective training methods to optimize technology usage, ensure proper equipment utilization, and maximize resource efficiency. Here, the Training Hub could add value by recommending teaching and training formats, such as webinars and remote-desktop sessions, and providing support to the platforms in implementing these suggestions.
- Bridging between the training hub and the platforms was suggested to occur via an embedded training coordinator. This individual should be a regular staff member who assumes the role of a training consultant and maintains regular communication with the training hub and colleagues at other platforms. Such an individual would firstly be knowledgeable about the technology, which would facilitate acceptance among staff colleagues, and secondly possess teaching talent that could be further developed through interaction with the Training Hub and possibly external entities providing training in pedagogic skills and continuous education. Generally, platform/unit staff may be hesitant to engage in pedagogic education due to their primary mission of staying abreast of technology developments. Introducing this competence in the platforms through a training consultant seems like a more realistic approach.
- PROVIDERS: Training for infrastructure providers should differentiate between technical and soft skills. There are numerous offerings by various scientific organizations for technology and method training. While the Training Hub could play a coordinating role, core staff and leaders are generally well-versed in these opportunities. However, the Hub could offer bursaries to facilitate attendance at courses and conferences (e.g., those provided by EMBL) and thus encourage SciLifeLab infrastructure providers to stay updated in their technology domain.
- Soft skills: Training in management and leadership skills, specifically tailored for infrastructure providers, is not as readily available. The Training Hub could leverage these resources (e.g. German BioImaging, CTLS) and assist in developing courses tailored to the Swedish community, encompassing business and accounting expertise. Additionally, the Training Hub could engage in activities aimed at promoting careers in research infrastructures and assist in defining qualifications and training needs along that trajectory.
- The role of industry: Life science infrastructure relies on equipment, and infrastructure platforms typically maintain longstanding, close collaborations with manufacturers. These partnerships can offer valuable training opportunities for technology application and development, as well as career advancement. This aspect was not mentioned in the presentation. In this regard, the Training Hub could serve as a central contact point for industry, facilitating the organization of connections between SciLifeLab infrastructure members and industry partners. This approach would generate greater leverage to engage industry in training activities.
- Evaluation and quality assessment: The evaluation of infrastructure user trainings should incur minimal overhead. Typically, the metrics utilized in assessing academic training and teaching at universities are ill-suited for infrastructures. In this context, Hub training consultants could collaboratively develop a basic set of metrics that can be shared and compared across SciLifeLab platforms. The dissemination of knowledge, i.e., the potential reach of a particular training offering, should not inherently serve as a quality criterion. Rather, the focus should centre on

the effectiveness of the training in preparing users to utilize the infrastructure proficiently. At times, this efficacy is best achieved through one-on-one sessions. Evaluating effectiveness is not always straightforward: well-prepared users demonstrate proficiency, minimize equipment damage, and achieve high-quality results efficiently. Facilitating the exchange of training best practices among platforms is a valuable approach to enhancing training across the infrastructure and thus improving the quality of the research output. If not yet implemented, the Hub could establish and support a user training exchange forum to facilitate this exchange.

- Overall, the Training Hub holds huge potential to enhance the quality of services provided by the SciLifeLab infrastructure and is progressing effectively toward realizing this potential. The Hub has requested additional funds from SciLifeLab to implement "Training Coordinators" at each site. Undoubtedly, such a role is essential to leverage and maximize the expertise and capacity dispersed throughout the SciLifeLab infrastructure for its benefit. However, there is room for refinement in the concept. One approach could involve the Hub identifying the most critical generic tasks it currently undertakes, such as implementing a searchable training collection or rubric. Subsequently, the Hub could engage platforms and units in discussions, potentially supported by surveys, to pinpoint their most pressing training needs. Identifying common requirements could help establish impactful measures for the entire national infrastructure. Furthermore, introducing training consultancy through a competitive incentive program is another avenue to explore. Under this model, platforms could submit proposals for enhancing their training and fostering connections with other platforms. An embedded consultant could oversee these efforts while also fulfilling part-time platform duties. Such initiatives would not only optimize training but also promote collaboration and innovation across the infrastructure.

# Data Centre

The Data Centre is already key for SciLifeLab operations across all platforms, services, and scientific disciplines. Still, we predict that the importance of the Data Centre continues to grow rapidly, with a well working service portfolio having the potential to improve the productivity for all its users.

Overall, while the Data Centre is recognized for its crucial role within SciLifeLab, there appears to be room for improvement in its structure, resource allocation, strategic direction, and integration with other platforms. Additional support will have to come with additional funding and personnel, but enhancing the aspects the Data Centre can cover is key to support SciLifeLab's transition into a data-driven future effectively.

Since we are not per-se tasked to evaluate the Data Centre, we keep our feedback short, but would like to point at some key aspects we noticed during our limited interactions with Data Centre personnel and users.

- **Steering group:** the absence of a dedicated steering group for the Data Centre with defined representation of all stakeholders appears to be a point of concern. While it was initially viewed as not a significant issue, the suggestion to create a specific group including users from all platforms, representatives from NBIS, and external experts indicates a recognized need for more structured governance and strategic oversight. This group could help in prioritizing and effectively aligning the Data Centre's services with the broader needs and goals of SciLifeLab, particularly with smaller computational teams will be embedded in the diverse facilities of SciLifeLab, as we suggest (see, for example, E21).
- **Support to improve SciLifeLab's data utilization:** throughout this document, we suggest SciLifeLab to embrace a data-driven future where the realized utility of generated data can catch up with its potential. For this goal to manifest, the Data Centre plays a crucial role but is currently missing the right mandate, is underutilized, or under-equipped to fully support the existing and future needs of the platforms. This gap might pertain to the integration and management of large data sets, where SciLifeLab could play a pivotal role in standardizing and enhancing data handling practices nationally as well as internationally.
- **Open source and international collaboration:** the current approach of relying on open-source solutions is positive, but there seems to be an opportunity to expand this by building and/or reinforcing international alliances. Such collaborations could help synchronize technical solutions and perhaps provide a way to leverage external expertise and resources.
- **Source allocation and staffing:** resources allocation in SciLifeLab is complex. To our understanding the Data Centre employs a total of 39 FTE financed through different programs. Only six FTE are financed directly through SciLifeLab funding, raising concerns over whether the staffing at the Data Centre is sufficient to meet the current and future demands of the platforms. In order to ensure improved data utilization throughout all platforms and therefore for all their users, the Data Centre must be adequately staffed, and additional FTEs appear unavoidable.
- **Immediate contributions of the Data Centre:** there is an expectation that the Data Centre could play a more immediate role in areas such as IT systems consolidation, needs assessment, and hosting of solutions. The suggestion to utilize cloud storage and compute providers reflects a practical approach to overcoming current limitations in infrastructure, but also hosting services like PReSTO (E23) appears a task best conducted by the Data Centre.
- **Data safety, GDPR, and ethical concerns:** the mention of data safety and the broader ethical, legal, and societal implications of data management highlights a critical area that requires more attention. Ensuring data safety and compliance with regulations is not only crucial for operational integrity but also for maintaining public trust and the reputation of SciLifeLab. Since data safety and GDPR topics are complex and themselves in motion, we urge SciLifeLab to avoid unnecessary duplication of efforts. Instead of hiring experts in multiple platforms, a centralized model that reaches out to individual platforms, educating the computational experts that work with NBIS and/or the Data Centre along the "Embedded Model" is highly recommended.


SciLifeLab