#	Group	Broad technology fields groups are working on				Technology fields			Life Science fields		
		computational engineering and data sciences	molecular biotechnology	mechanical engineering	imaging and optical engineering						
1	**Alex Bateman - EMBL-EBI, Hinxton** My group provides a wide range of world leading resources for protein and non-coding RNA sequence and families (InterPro, Pfam, RNAcentral & Rfam). We are particularly interested in applying modern ML/AI approaches to enhance our resources.	x				AI and machine learning	bioinformatics	data management	bioinformatics research	computational biology	structural biology
2	**Peer Bork - EMBL Heidelberg** The main focus of the Bork group is to gain insights into the functioning of biological systems and their evolution by comparative analysis and integration of complex molecular data. We are developing and maintaining widely used web services and resources on (meta)genomics and function prediction. The current focus is planetary biology, including global microbial sampling and analysis, with challenges in (meta)data organisation, integration, and visualization.	x				bioinformatics	data science and big data	data integration	computational biology	planetary biology	microbiology
3	**Sarah Dyer - EMBL-EBI, Hinxton** The Non-vertebrate Genomics team is part of the Ensembl project providing access to integrated genomic data sets for Plants and invertebrate Metazoa. We also have joint projects with VeuPathDB, WormBase and the Alliance of Genomic Resources. Our focus is on delivering data and tools to support our user communities, with a focus on agriculture and supporting host, vector and parasite research.	x				bioinformatics	software development		computational biology	genome biology	agriculture
4	**Robert Finn - EMBL-EBI, Hinxton** My group focuses on the analysis of the microbes found within the environment or associated with a host organism, such as humans or plants. DNA sequencing technologies have revolutionised modern molecular biology, facilitating large-scale sequencing of microbial genomes. However, concomitant with the data deluge, there is an urgent need to develop robust computational frameworks that enable these genomes to be rapidly and continuallycollated, compared, and functionally annotated. Capturing this biodiversity and presenting quality reference datasets enables biologists to gain a greater understanding of evolutionary biology and the adaptations microbes have made to enable them to survive in diverse environments.	x				data science and big data	software development	bioinformatics	computational biology	genome biology	planetary biology
5	**Tudor Groza - EMBL EBI, Hinxton** The Phenomics team develops state of the art data acquisition and integration services to support advances in computational phenotyping for rare and complex disorders. Currently, it focuses on two unique large-scale knowledge bases: the International Mouse Phenotyping Consortium and the Patient-Derived Cancer Models (PDCM) repository. The former is the only initiative that provides a systematic framework to produce standardised phenotype data for model organisms and underpins critical insights into understanding the phenotypic consequences of variants, the essentiality of genes and the contribution of genes to diseases, hence enabling downstream functional follow up. The latter provides a standardised and unified entry point for research and clinical communities to search and compare PDCM models and their associated data including frequently mutated genes, diagnoses, drug treatments and sequence data. Future endeavours of the team include building automated pipelines for disease models and phenotype trajectories. From a technical perspective, the team sits at the intersection of ontologies (mouse and human phenotypes), statistical analysis, large-scale parallelisation (Hadoop) and production-level environments (Java, React, MongoDB, Kubernetes).	x				data management	data science and big data	software development	disease modelling	computational phenotyping	
6	**Peter Harrison - EMBL-EBI, Hinxton** The genome analysis team develops state-of-the-art cloud-based data analysis and portal infrastructure to coordinate, analyse, enrich, and present the wealth of genomic data arising from global agricultural and biodiversity projects. This includes projects such as the Earth Biogenome Project (https://www.earthbiogenome.org/), a moonshot for biology, that aims to sequence all of Earths eukaryotic life within ten years. We are seeking projects that utilise cutting edge cloud data engineering to design and develop analysis, visualisation and data management infrastructure at significant data scale. This could include development in the areas of pangenomics, single cell atlases, cloud-based interactive analysis platforms and 'omic data visualisation. Data analysis platforms and portals are crucial services to enable and accelerate global agricultural and biodiversity research, tackling key societal issues of food security, climate change and biodiversity loss. The fellow would join a vibrant and highly professional group of software engineers and bioinformaticians, contributing both new and to existing services fostering a detailed understanding of cloud DevOps, user-led design, open science, and FAIR data management.	x				data management	data science and big data	software development	bioinformatics research	computational biology	genome biology
7	**Matthew Hartley - EMBL-EBI, Hinxton** I have worked at the interface between computational BioImaging technology development and service provision for the last decade. Over that time, I have developed novel image analysis algorithms tools and pipelines as well as image data management software. I now lead the BioImage Archive (BIA), which provides services to the global BioImaging community. We work on image archival, visualisation, file formats, data models and data compression as well as AI and machine learning application to large image datasets. We provide services to life sciences researchers wishing to archive their image data across the world. Scientists using the BIA ecosystem number in the hundreds.	x			x	data standards	software development	imaging, microscopy	bioinformatics research	computational biology	cell biology

8	**Wolfgang Huber - EMBL-Heidelberg** The Huber group develops open-source scientific software esp. in the areas of single cell omics, spatial omics, large-scale CRISPR and drug screens, and other high-throughput assays of modern biology. They are a core contributor to the Bioconductor project, the largest biological data science software project in the world (https: //www.bioconductor.org, Huber et al. Nat. Meth. 2015 DOI: 10.1038/nmeth.3252), which supports developers with essential software infrastructures such as data containers and I/O, tools for continuous integration and testing, and with a platform for publicly distributing, supporting and maintaining their software. Specific interests are also in robustification and life-cycle management of research software, interoperability and APIs, virtualization and containerization, software usability, scientific developer support, platform integration (e.g. between R, Julia, Python), interactive dashboards, living papers, reproducible research and open science.	x				AI and machine learning	bioinformatics	software development	computational biology	cancer biology	genetics
9	**Maria Martin - EMBL-EBI, Hinxton** Our work focuses on developing technologies for the delivery of scalable and robust data infrastructures for protein data (SQL and NoSQL databases, programming languages, Graph Knowledgebases, Apache Lucene and Solr search engines, clustering algorithms) as well as developing novel data mining methods for protein function prediction and large-scale data analysis. The team use Deep Learning algorithms for extracting knowledge from biological data and recommendation systems.	x				AI and machine learning	bioinformatics	data management	bioinformatics research	computational biology	
10	**Ellen McDonagh - EMBL-EBI, Hinxton** In the past, I worked closely with bioinformaticians, developers, scientific curators and clinicians to create an open source crowdsourcing knowledgebase for rare disease gene evaluation, which is utilised within a genome analysis service at Genomics England for patient diagnosis with the NHS, as well as by researchers and clinicians worldwide. In my current role, the open source Open Targets Platform and Genetics Portal and provide aggregated data, visualisations and tools to inform evidence-based prioritisation of targets and therapeutic hypothesis generation for drug discovery for external and internal scientists worldwide.	x				bioinformatics	data management	data science and big data	disease modelling	drug design	genome biology
11	**Ugis Sarkans - EMBL-EBI, Hinxton** Our team builds and maintains the BioStudies database - a resource that facilitates transparent, reproducible science by aggregating and publishing all outputs of a scientific study. This can include pointers to components of data in specialised community resources, as well as data that do not belong anywhere else. BioStudies acquires data via a variety of routes, both pre- and post-publication. The main challenge for us is to find the right balance between the generic nature of this infrastructructure necessary to support a wide variety of users on one hand, and the ability to adjust the system to the specific needs of a particular user community, project, or data type on the other hand.	x				data management	software development		computational biology	bioinformatics	
12	**Thomas Schneider - EMBL Hamburg** EMBL Hamburg is operating synchrotron beamlines for macromolecular crystallography for several, decades. Currently, we are using radiation from PETRA III for which an upgrade to the next generation synchrotron technology is in the planning. For making synchrotron radiation usable for scientific user community we are constantly developing software for controlling high-rate and high-volume data acquisition, automated sample handling, data flows and data evaluation. A large part of this work takes place in international consortia.	x				software development			biophysics	structural biology	
13	**Sameer Velankar - EMBL-EBI, Hinxton** We develop and deliver world leading data resources including Protein Data Bank, PDBe Knowledge Base and AlphaFold Database.Our work is focused on developing a scalable, state-of-the-art, integrated data management and delivery infrastructure for structural biology data (SQL databases, programming languages, Graph Knowledgebases, Apache Lucene and Solr search engines, clustering algorithms). We are keen on deploying machine learning and AI approaches for deriving knowledge from our integrated structural biology knowledge base. Our technology development work also involves better information retrieval and ranking systems and multiscale structural data visualisation tools (https://github.com/molstar) to enable scientific research in both academic and industry settings.	x				AI and machine learning	data science and big data	Information retrieval & relevance ranking	bioinformatics research	structural biology	translational research
14	**Juan Antonio Vizcaíno, EMBL-EBI, Hinxton** Improving PRIDE's functionality as the world-leading proteomics data repository, and the integration of proteomics data with other omics data types are two key aspects for the team in the near future. This offers the possibility for the fellow to work in different topics (e.g. data analysis, data visualisation, infrastructure, data management practises, etc), depending their background. In the context of data integration, this would involve different data types such as gene and protein expression information (together with Expression Atlas), post-translational modifications (UniProt), and (meta)proteomics data and (meta)genomics sequences (Ensembl, MGnify). Additionally, support in PRIDE for additional proteomics data types (e.g. top down proteomics, non-mass spectrometry methods) is also a key aspect in our future work.	x				bioinformatics	data science and big data	software development	bioinformatics research	computational biology	Proteomics
15	**Maria Garcia Alai - EMBL Hamburg** The SPC facility supports external and internal researchers carrying out structure determination experiments and has a strong track record in the development and implementation of new technologies and methods to precisely determine the stability, shape and size of different biomolecules and biomolecular assemblies. We develop our own software for the data analysis of biophysical interactions such as Kinetic analysis, Time resolved conformational changes, Analysis of thermal stability data beyond a simple melting temperature analysis, Ligand screening and Processing of spectral data	x	x			bioinformatics	chemistry and chemical biology	computational modelling	bioinformatics research	biophysics	structural biology

16	**Matthias Wilmanns - EMBL Hamburg** Our group employs an integrated structural biology approach using X-ray based methods, single particle cryo-electron microscopy, biophysical methods and integrative modelling approaches for large protein complexes. Our structures provide rich opportunities to discover function from structure, where many of them aim to resolve mechanisms relevant for infection processes. In the coming years we aim to generate a multidisciplinary metabolomics/structure service platform for determination of turnover mechanisms of specific drugs or prodrugs by different microorganisms. The platform will include establishment of a pipeline for high resolution structures of selected protein-drug complexes in microorganisms, and in-vitro analysis of the enzymatic processing of specific drugs by microorganisms. The platform will thus integrate technologies in structural biology and metabolomics, complemented by microbial genetics and biochemistry, defining the required skill set of the developer we are looking for. All data generated will be stored a common data base, as a basis for further improving the integration of procedures. The platform will be useful to both future internal EMBL projects specifically from selected transversal themes (especially microbiome, infection, planetary biology) and for our external user community working on drug discovery in industry and academia. This work will build on our previous and ongoing work with Michael Zimmermann research group (EMBL Heidelberg). Previously we jointly discovered a mycobacterial drug target by a combined structure-based and metabolomics approach to be associated with an unexpected catalytic function, when Michael was working as graduate student at the ETH Zurich (Ehebauer, Zimmermann et al, 2015). In an ongoing pilot project with Michael's research group at EMBL, we have initiated a structure-based functional drug transformation project of selected microbiome targets with evidence for specific drug turnover, but lacking any mechanistic insight into the underlying process. At the present stage, the project connects high-resolution structural biology with biochemical and metabolomic approaches, including in vitro enzymology, as well as ex vivo and in vivo functional assays. In a first step, we determine the high-resolution structures of these targets, coupled by the identification of specific substrates suitable for turnover, including established drugs that are processed by these targets. Part of this analysis is the quantitative measurement of binding affinities, as a prerequisite for structure-based binding studies. As binding in enzymatic reactions is generally weak this may require, depending on the specific target, intervention with the active site topography to strengthen binding and to avoid rapid turnover, which would prevent structure-based ligand binding studies as well. Subsequent protein target ligand structures provide then the basis for mechanistic investigation of the turnover mechanism for specific drugs or prodrugs. In a future perspective this knowledge could be further exploited either by protein engineering e.g. using directed evolution approaches or by medicinal chemistry approaches for rational modification and improvement of established drugs. In addition, as this concept is not limited to the characterisation of drug transformation it could be similarly applicable to other metabolites susceptible to microbial enzyme catalysis such as nutrients or environmental toxins.	x	x			automation	chemistry and chemical biology	data management	biophysics	drug design	structural biology
17	**Michael Zimmermann - EMBL Heidelberg** In combination with EMBL's Chemical Biology Core Facility (CBCF) our laboratory combines high-throughput screening and computational approaches to develop tools and pipelines to investigate the mutual interactions between environmental contaminants and biological systems. In this context we are currently establishing a platform available to EMBL and Non-EMBL researchers that involves chemical libraries, screening pipelines together with computational tools, software, and data resources that will enable integrative analyses of the impact of environmental toxins on organisms at the molecular level.	x	x			chemistry and chemical biology	data science and big data	software development	computational biology		
18	**Josan Marquez - EMBL Grenoble** Our Team has pioneered the development of Online Crystallography; fully automated protein-to structure pipelines integrating crystallization, synchrotron data collection and crystallographic data analysis into continuous workflows operated via the web. These pipelines are currently used by hundreds of scientists worldwide and are based on the CrystalDirect technologies and CRIMS software, which we have contributed to develop. Recently, we have implemented a fully automated pipeline for ligand and fragment screening to support structure guided drug design. EMBL Grenoble is co-located with the European Synchrotron Radiation Facility (ESRF) in Grenoble, which produces some of the world's most brilliant X-ray beams worldwide. EMBL and ESRF jointly operate six crystallography beamlines one of which is the fully automated MASSIF-1 whose operation is highly integrated with the operations at EMBL's HTX Lab. Our interdisciplinary team offers opportunities for scientists, engineers and software developers to work in one of the leading infrastructures for structural biology within the areas of protein crystallography, drug desing, automation, and large-scale scientific data management and analysis. Currently, we are particularly interested in profiles in structural biology or computer science orientated towards one or several of the following areas: fragment screening, structure guided drug design, cloud computing, machine learning and artificial intelligence.	x	x			AI and machine learning	chemistry and chemical biology	data management data science and big data	drug design	structural biology	translational research
19	**Sebastian Eustermann - EMBL Heidelberg** The Eustermann lab studies the molecular landscape of chromatin to understand the principles underlying expression and maintenance of genomic information in eukaryotes. The core technologies used in the group are recombinant production of large human chromatin complexes followed by cryo-electron microscopy analysis in order to visualize the atomic structures. As mammalian cell expression and purification of protein complexes still forms a bottleneck not only in structural biology but also in many other scientific fields, we are trying to develop novel and more efficient approaches. To do so, we collaborate with the EMBL Protein Expression and Purification Core Facility joining both the method development and the process optimisation. Once the workflows are sufficiently robust and reproducible, they can be implemented into the service provision platform of the facility, which is accessible for both internal and external researchers.		x			(bio)chemical engineering	chemistry and chemical biology	recombinant protein production	biophysics	structural biology	biochemistry/protein engineering

20	**Mikhail Savitski- EMBL Heidelberg** Savitski group is closely linked to the Proteomics core facility, with Mikhael Savitski leading both the facility and the group. Infrastructure in the Proteomics Core Facility is centred around state-of-the-art mass spectrometry for MS and LC-MSMS experiments. This is complemented by chromatographic and electrophoretic systems for protein and peptide separation. The research team uses and develops stability proteomics for understanding the phenomenon of aggregation and disaggregation, cell phenotyping, and detection of protein interactions with drugs, metabolites, DNA and RNA. In future we plan to work on characterization of protein complexes from cell lysates without extensive purification. Currently protein crosslinking is established for highly purified complexes at the EMBL proteomics core facility and is widely used. However, pioneering work has shown that cross linking of proteins in complex mixtures is possible. Here it would be very beneficial to combine sample fractionation approaches that can separate complexes and reduce sample complexity with protein cross linking in order to deduce structural information. Such technology development would enable systematic characterization of protein complexes without the need of in-depth purification. A robust implementation of this workflow would greatly accelerate unbiased protein complex characterization and the resulting service would appeal to a large number of EMBL groups interested in protein complexes and protein interactions as well as the broader scientific community in Europe. In particular, as science moves beyond model organisms such an unbiased technology will accelerate greatly functional characterization of ecologically important, but so far understudied species. To be able to do this, we will need to establish complementary fractionation techniques for fractionation of whole cell samples of different sources (prokaryotic and eukaryotic cells) and implement crosslinking mass spectrometry in the medium complexity samples collected from the different fractions. With this line of future research, we aim to strenthen our expertise in development of instrument methods, mass spectrometry and optimization and development of biochemical (fractionation, crosslinking) approaches.		x			chemistry and chemical biology			molecular biology	biotechnology	biophysics
21	**Kim Remans - EMBL Heidelberg** The EMBL Protein Expression and Purification Core Facility offers services regarding recombinant protein production and biophysical characterisation to both internal and external researchers. The main technologies that are being used in our group are protein expression in bacteria, insect and mammalian cells, protein purification using an array of chromatographic techniques and various biophysical characterisation methods suitable for protein quality control and interaction studies. We work closely with life science researchers of a large variety of backgrounds, such as structural biologists, cell biologists, developmental and genome biologists, immunologists and medical researchers. As such, we have established a broad expertise in handling many different types of biological projects, each with their own specific requirements and challenges. To facilitate our work, we are also active in the development of more efficient reagents, workflows and technologies, which we then aim to make available to the scientific community through our service platform.		x			automation	(bio)chemical engineering	recombinant protein production	biophysicy/ biochemistry	biotechnology	
22	**Andrew McCarthy - EMBL Grenoble** The McCarthy team is composed of engineers and scientists who provide operational and user support on seven high brilliance X-ray based structural biology beamlines with proven expertise in developing automated data collection instruments and methods in collaboration with our colleagues at the European Synchrotron Radiation Facility (ESRF). We will continue to optimise data collection protocols and analyses methods as well as develop and expand the experimental instruments and techniques currently available in order to realise the scientific potential of the recently completed ESRF-Extremely Brilliant Source upgrade for the European structural biology community.	x		x		automation	chemistry and chemical biology	data management software development	biophysics	drug design	structural biology
23	**Justin Crocker - EMBL Heidelberg** Our group builds automation and robotics pipelines for high-throughput developmental biology. We build experimental frameworks that will serve as platforms for future research by allowing a broader community of users to build, execute, and share similar technologies.			x		automation	microfluidics	robotics	biotechnology	developmental biology	Planetary biology
24	**Jan Korbel - EMBL Heidelberg** Dr. Korbel has contributed key experimental and computational methods for structural variation characterization to the field some of which have become the standard methodologies used in genetics and disease biology, such as the development of paired-end mapping, which Science Magazine considered as one of the scientific breakthroughs of the year 2007. Recently, we developed the scTRIP method (for single cell tri-channel processing) which – for the first time - enables the scalable and direct detection of SVs including de novo SV formation processes in single cells, and as such can be used to obtain insights into important pathomechanisms acting in human tissues. Currently, we are sharing this technology with collaborators within international research studies, but the amount of collaborative sharing we can purse in a pure research setting has become a limitation – which in our view will necessitate to provide the technique as a service. We currently see exponential growth of the use of Strand-seq, with 10 laboratories having used the technique this year in collaboration with us (until ~18 months ago all the Strand-seq publications came from only a single lab) and a strong upwards trend with many new expressions of interest, as a number of applications from comprehensive single cell sequencing of genetic variation to single cell multi-omics and haplotype-resolved genomic assemblies (see above) have been described by us and some of our collaborators. In July 2020, Jan Korbel took on the role of Head of Data Science at EMBL Heidelberg, and this position will have both a research and a service remit.			x		automation	chemistry and chemical biology		computational biology	genome biology	translational research

25	**Vikas Trivedi - EMBL Barcelona** Trained as an engineer (focus: mechanical engineering and bioengineering), I switched to optics and instrumentation during my PhD where I developed 2- photon light sheet imaging based methods for deep and fast imaging. Current technological focus of my group is development of novel embryonic organoids and high-throughput, long term monitoring of such in vitro systems and therefore demands automated systems for protocol optimization and molecular characterization through staining, all of which can be provided as services to labs both within and outside EMBL as well as in industry.			x		automation	high-precision mechanics	robotics	biotechnology	translational research	Tissue engineering
26	**Anna Kreshuk - EMBL Heidelberg** Kreshuk Lab develops novel machine learning-based methods for microscopy image analysis, in collaboration with both internal and external scientists. To make such methods accessible to scientists without computational expertise, we also develop and maintain the ilastik software, used by thousands of biologists all over the world.	x			x	AI and machine learning	image analysis	software development	cell biology	developmental biology	structural biology
27	**Jan Ellenberg - EMBL Heidelberg** The Ellenberg group develops and applies advanced quantitative imaging methods across scales from single molecules to developing embryos to gain new insights into nuclear architecture and its changes during the cell cycle. We have previously developed and applied methods such as fluorescence correlation spectroscopy (FCS)-calibrated imaging, super-resolution microscopy, correlative light and electron microscopy and light sheet microscopy, and provide training and support in these methods through internal and external scientific, service and industry collaborations. Current interests include the development of the next generation of gentle, yet very high resolution light sheet microscopes suitable for investigating the structure and dynamics of nuclear architecture at the single molecule level in developing mammalian embryos.				x	image analysis	imaging, microscopy	software development	cell biology	developmental biology	genome biology
28	**Thomas Quail - EMBL Heidelberg** The Quail group studies how collections of proteins organize the genome across different length scales, combining quantitative microscopy, biochemistry, cell biology, soft matter physics, and dynamical systems. Mechanistically dissecting these processes in the cell nucleus depends on our ability to image these proteins with high spatial and temporal resolution, which remains challenging. We are currently developing high-throughput, single-molecule imaging approaches to disentangle how individual proteins, enzymes, and genomic loci fluctuate and move in the cell nucleus. In parallel we are developing image analysis pipelines to robustly and accurately extract the physical rules driving these complex spatiotemporal dynamics. Disentangling these physical principles will provide insights into the collective behaviour of diverse processes in the cell nucleus, including transcription, DNA replication, and DNA damage repair.				x	image analysis	imaging, microscopy	microfluidics	biophysics	cell biology	genome biology
29	**Timo Zimmermann - EMBL Heidelberg** In the new EMBL Imaging Centre the Zimmermann Team will provide a wide range of light microscopy instrumentation that is not yet commonly available to external researchers. We also aim to efficiently connect highest resolution LM approaches (including cryo-fluorescence) to the corresponding EM technology offer of the Imaging Centre.				x	image analysis	imaging, microscopy		biophysics	cell biology	
30	**Gergely Papp - EMBL Grenoble** The EMBL Grenoble Instrumentation team develop methods and instruments for Macromolecular X-ray crystallography and Small Angle X-ray Scattering experiments for more than two decades. Furthermore, motivated by the increasing scientific interest in Cryo-Electron Microscopy in the last decade, a project for automated Cryo-EM sample grid preparation and control (EasyGrid) has been conducted. The team is composed of highly motivated mechanical, electronics and software engineers, and is able to design and manufacture in-house high precision, complex scientific instruments. Scientific projects exploiting these machines and pushing them to their limits are essential to keep the activity of the team at the state of the art	x		x	x	automation	image analysis	software development	drug design	structural biology	
31	**Robert Prevedel - EMBL Heidelberg** We are developing advanced optical imaging methods that are based on multi-photon microscopy, active wave-front shaping, photo-acoustics as well as high-resolution spectroscopy. Our aim is to establish our new approaches as disruptive technologies in the life sciences and to further engineer and automate our prototypes for routine service provision.	x		x	x	automation	imaging, microscopy	software development	biophysics	developmental biology	neurobiology
32	**Yannick Schwab -EMBL Heidelberg** The Schwab team, in tight interactions with the Electron Microscopy Core Facility (EMCF), is developing techniques in the field of multimodal correlative imaging, with the main motivation to enable targeted ultrastructural analyses of rare events or cell types in complex biological systems. The ARISE fellowship is a unique opportunity to bridge method development and service provision in that field, with a specific interested to recruit motivated scientists in 2 areas: first, we would like to develop a new software to automate volume correlative light / X-ray and EM; second, we would like to streamline workflows adapted to high throughput EM imaging of plankton cells collected in the field alongside the TREC expedition scheduled to start in Spring 2023.	x		x	x	automation	imaging, microscopy	software development	cell biology		

33	**Simone Mattei - EMBL Heidelberg** Our team is part of the EMBL Imaging Centre, a new service unit with the mission to make the cutting-edge electron and light microscopy technologies available to the scientific international user community, including academically developed methods not yet commercially available. We develop methods and software supporting cryogenic correlative light and electron microscopy (cryo-CLEM) and high-throughput fully automated pipelines to tackle the current challenges in cryo-EM sample preparation and screening.			x	x	automation	image analysis	imaging, microscopy	biophysics	cell biology	structural biology
34	**Rainer Pepperkok - EMBL Heidelberg** The ALMF and Pepperkok Team at EMBL Heidelberg develop and provide a service in advanced light microscopy and image analysis methods to EMBL scientists and external users from and beyond EMBL member states. Currently we are working on projects developing technology to provide a service in spatial multi-omics/phenomics to integrate automated phenotype recognition in complex biological samples by advanced light microscopy and online image analysis to sort the phenotypes for subsequent (single cell) multi-omics analyses.			x	x	automation	imaging, microscopy	microfluidics	bioinformatics research	biophysics	cell biology