#	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	**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
3	**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 continually collated, 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
4	**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
5	**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				data standards	software development	imaging, microscopy		bioinformatics research	computational biology	cell biology
6	**Henning Hermjakob - EMBL-EBI, Hinxton** The Molecular Networks team provides curated databases for network biology (IntAct, Reactome, BioModels), as well as the pan-EBI data discovery infrastructure indexing more than five billion data objects. We are aiming to optimise our resources through advanced visualisation and integration of AI technologies for curation support and data discovery.	X				AI and machine learning	data science and big data			bioinformatics research	disease modelling	network biology
7	**Maria Martin - EMBL-EBI, Hinxton** Our work focuses on developing technologies for the delivery of scalable and robust data infrastructures for protein data (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. We are interested in applying AI/ML and large language models to text summarization, search enginees and software development.	X				AI and machine learning	bioinformatics	data management		bioinformatics research	computational biology	
8	**Santiago Rompani - EMBL Rome** Previously, the Gross group has done extensive work on quantifying animal behavior, while the Rompani group is supporting the ML approaches to analyse such data. We seek to develop a new pipeline that allows various groups that quantify video-recorded animal behavior using novel machine learning approaches to dramatically accelerate the extraction of behavioral motifs from data.	X				AI and machine learning	data science and big data	software development		computational biology	epigenetics	neurobiology
9	**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. BioStudies acquires data via a variety of routes, both pre- and post-publication. We are looking to extend our infrastructure and apply data harmonisation methods to support new, emerging fields with a particular interest in human health and environmental exposures.	X				data management	software development			computational biology	bioinformatics	
10	**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	

11	**Oliver Stegle - EMBL Heidelberg** Our laboratory develops innovative computational technologies for making genomic data resources accessible to pan-European analysis using federated data infrastructures coupled with privacy-preserving algorithms. This project seeks to advance genome data services and infrastructures to make them “AI ready”, permitting to train large-scale machine learning models on major European genome data initiatives from research and health care. We seek to deploy these advances to bring together data from multiple European cohorts to tackle key questions in human ecosystems services and research.	X				AI and machine learning	bioinformatics	data science and big data		bioinformatics research	computational biology	genome biology
12	**Alejandro Torres-Sánchez - EMBL Barcelona** Our group develops mathematical models and computer codes to investigate the self-organisation of cells and tissues, e. g., ias, based on finite element approaches. Currently, we are focusing on making these tools available to people without computational expertise such as experimentalists working in cell and tissue-biology labs.	X				computational modelling	software development	high performance computing		biophysics	developmental biology	tissue biology
13	**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 on their background. In the context of data integration, this would involve different data types such as gene and protein expression information (in collaboration with the Expression Atlas team), post-translational modifications (collaboration with UniProt), and (meta)proteomics data and (meta)genomics sequences (Ensembl, MGnify, proteogenomics approaches). Additionally, support in PRIDE for additional proteomics data types (e.g. top down proteomics, non-mass spectrometry methods) is also an important topic for our future work.	X				bioinformatics	data science and big data	software development		bioinformatics research	computational biology	Proteomics
14	**Andrew Yates - EMBL-EBI, Hinxton** My team provides services to genomic researchers around the world developing and deploying systems for the interpretation and interrogation of annotated genomes. I co-wrote the refget and variation representation standards within GA4GH and more recently have been working to redevelop the Ensembl infrastructure to further scale towards the challenges of working with biodiversity and pangenome data.	X				bioinformatics	data management	software development		genome biology	computational biology	
15	**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
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	**Clement Blanchet - EMBL Hamburg** Our team specializes in providing comprehensive support for small angle X-ray scattering (SAXS) experiments, including experimental design, setup, data collection, analysis, and interpretation. With a strong focus on advancing new scattering methods, such as time-resolved and high-throughput SAXS, we actively develop the SAXS beamline, including its sample environments, and refine data reduction and analysis methods. As a fellow, you'll have the opportunity to participate in diverse activities aligned with your interests, encompassing experimental development, computational analysis, and contributing to our dynamic research environment.	X		X		AI and machine learning	computational modelling	data science and big data		bioinformatics research	biophysics	structural biology
19	**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
20	**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
21	**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
22	**Christoph Müller - EMBL Heidelberg** Our group is pioneering the use of single-particle cryo-EM in the drug discovery process. Through the ARISE program we plan to develop a stable workflow for the high-throughput screening of ligand binding to drug targets by single-particle cryo-EM. Critical elements of the workflow comprise sample tracking throughout the workflow, automated EM grid dispensing, automated cryo-EM sample evaluation and HTP processing.	X		X	X	automation	data management	imaging, microscopy		biophysics	drug design	structural biology
23	**Gergely Papp - EMBL Grenoble** Over the two past decades, the instrumentation team has developed instruments for neutron and x-ray scattering experiments with constant objectives of supporting the most challenging structural biology experiments and making the instruments available to the scientific community worldwide through services provided by synchrotron beamlines and high throughput crystallization facilities. As an example, our CrystalDirect automated harvesting technology is used at ALPX, an EMBL spinoff company (https://www.embl.org/news/lab-matters/alpx/), which provides MX services for drug design. Relying on patent applications, and technology transfers, most of the instruments used in Macromolecular Crystallography are commercialized worldwide (CrystalDirect™ automatic crystal harvester, HC-Lab crystal Humidity Controller, MD2S and MD3 X-ray Micro diffractometer families, BioSAXS sample changers). A similar strategy is being developed for our automated Cryo-EM sample grids preparation system.	X		X	X	automation	image analysis	software development		drug design	structural biology	
24	**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 which started in Spring 2023.	X		X	X	automation	imaging, microscopy	software development		cell biology		

25	**Sinem Saka - EMBL Heidelberg** We are interested in spatial biology and bridging high-end imaging of phenotypes with omics depth profiling of the molecular make-up. Using DNA nanotechnology, we have previously developed super-resolution, multiplexed imaging and spatial omics methods to address the limitations in the field. We aim to expand our spatial omics approaches futher into higher resolution and 3D implementations (including high-throughput light-sheet microscopy, expansion microscopy and tisuse clearing), which will be unique and of high value to many groups at EMBL and beyond to investigate the heterogeneous ecosystem of disease models and tissues (thick tissue slices, whole embryos or organisms, organoids, organs, xenografts) spanning studies in cancer, neuroscience, developmental biology, microbiome and exposome. We also strive to increase the community access to these kind of methods by implementiang automated workflows for staining, imaging (fluidic/microflidic labeling both on and off the microscope stage or adaptive feedback microscopy pipelines) and data analysis. Furthermore, we are interested in implementing hypersectal multiplexing, compressed sensing, and DNA-barcoding approaches to create next-generation single-cell and spatial-omics technologies in collaboration with both medical/clinical partners and industial partners like Leica and GSK. We work closely with many EMBL core facilities and platforms including ALMF and GenTechDev Open Lab and share know-how and instrument access with other Heidelberg institutions within the MULTI-SPACE intiative. Through the ARISE program, we have multiple opportunities to join our interdisciplinary team and contibute to method development, automation, optical/fluidic instrument customization, experimental design, workflow optimization and data analysis.		X		X	image analysis	imaging, microscopy	microfluidics	Omics technologies	developmental biology	genome biology	tissue biology
26	**Simone Matei - 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
27	**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	image analysis	imaging, microscopy	microfluidics	bioinformatics research	biophysics	cell biology
28	**Kristina Djinovic Carugo - EMBL Grenoble** We intend to employ the principles of Design of Experiment (DoE), which allow to determine how input parameters influence each other to produce output for streamlining and expediting cryo-EM grid preparation, by selectively testing parameters and more efficiently optimising the conditions to generate data-collection quality grids. The developed approach will be made available as an important part of the EasyGrid instrument's external service for the automated preparation of cryo-EM/ET grids, as well as to internal users.				X	automation	software development	cryo-EM/ET		biophysics	structural biology	
29	**Elizabeth Duke - EMBL Hamburg** HiTT is an X-ray imaging pipeline that has been established on the EMBL beamline P14 using the infrastructure designed for macromolecular crystallography. We are now taking the next steps of offering HiTT as a user facility at the beamline. In parallel with establishing a user program in biological X-ray imaging here in Hamburg we are also extending the scope of HiTT to allow imaging data to be collected from a wider variety of samples.				X	image analysis	imaging, microscopy	software development		tissue imaging	histology	medical imaging
30	**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
31	**Cornelius Gross - EMBL Rome** We have worked closely with the Prevedel group to apply innovative deep brain imaging technologies for use in behavioral circuit neuroscience applications. Via the ARISE programme we are looking to recruit outstanding postdoctoral fellows who are committed to focusing on technology that can be taken up and used successfully by the wider behavioral neuroscience community. Following the model we have used in the past collaborating with the Prevedel Group to adapt novel three photon microscopy and adaptive optics approaches to in vivo deep brain imaging in mice, we expect the ARISE fellow to push the boundaries of novel deep brain imaging technologies, adapt and establish them for use in living animals, and develop them for distribution to the wider behavioral neuroscience field.				X	image analysis	imaging, microscopy	optical instruments development		neurobiology		
32	**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

33	**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	
The following group and team leaders are open to collaborating with others and acting as an advisor to ARISE fellows where a good fit is found and a different group and team leader is the main supervisor.												
34	**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
35	**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