Scientific Programme

Monday, 09 September 2019

[BC]2 Session , University of Basel Seminarraum 106

09:00 - 16:00   **T1: Using the Ensembl REST APIs to programmatically access genomic data**

Room Seminarraum 106 Overview The Ensembl project provides a comprehensive and integrated source of annotation of genome sequences, including genes, genetic variation, features that regulate gene expression, homologues and alignments. These data are accessible programmatically in a language agnostic manner via the Ensembl REST APIs. Scripting against public databases like Ensembl facilitates quick retrieval of valuable data in your preferred format or can be integrated into pipelines for data analysis. This tutorial is aimed at researchers and developers interested in exploring Ensembl beyond the website. The workshop covers how to use the Ensembl REST APIs, including understanding the major endpoints and how to write scripts to call them. Feedback from previous courses •"Wish I had taken the course long time ago. Didn't know before how good and powerful APIs are!" API workshop, EMBL-EBI, January 2016 •"I really enjoyed the course, and the ENSEMBL API will become a very relevant part of my toolset." API workshop, Cambridge, December 2013 Audience and requirements The tutorial is aimed at bioinformatics and wet-lab researchers who use genomic data and would like to use scripting to access these data directly, including integrating into pipelines. This is a hands-on training course and participants will need to bring a laptop with WiFi enabled in order to take part. Participants must be able to code in Python, Perl or R. The training will utilise Jupyter Notebooks hosted by Microsoft Azure – to use these all participants will need to have a free Microsoft Account. Maximum participants: 20

Organiser: Astrid Gall (Ensembl Outreach Team, EMBL-EBI, United Kingdom)

09:00 - 09:45	**Introduction to ensembl and its data types**
09:45 - 10:30	**Overview of the ensembl REST API**
10:30 - 11:00	**Tea/Coffee Break**
11:00 - 11:45	**Accessing GET queries with the ensembl REST API**
11:45 - 12:30	**Decoding json; other content types**
12:30 - 13:30	**Lunch**
13:30 - 14:30	**Chaining REST queries together**
14:30 - 15:30	**Accessing POST queries with the ensembl REST API**
15:30 - 16:00	**Rate-limiting**

Scientific Programme

[BC]2 Session , University of Basel Seminarraum 107

09:00 - 16:00   **T2: Genomic epidemiology and phylodynamics with Nextstrain**

Room Seminarrraum 107 Overview Mutations that accumulate in pathogen genome sequences contain information on the pathogen's evolutionary history and allow us to reconstruct patterns of transmission. Since sequencing capacity and surveillance has increased by orders of magnitude in recent years, data sharing, timely analysis, and dissemination of results has become crucial for harnessing the power of genomics in public health. Nextstrain is an open-source project for phylodynamic analysis, data integration, and visualization of large data sets of viral and bacterial pathogens. Nextstrain can analyse thousands of sequences within minutes and visualizes the results using an interactive browser-based interface (see Fig. 1). This interface can be used locally on the user's computer or shared on the internet. Audience and requirements The workshop is targeted to users with basic bioinformatic knowledge that want to use the Nextstrain pipeline to analyse and visualize their own data. The workshop would be split into a morning session covering background, the structure and use of Nextstrain tools, and tutorials using example data, and an afternoon session where users analyse their own data. Participants would be expected to bring their own laptops. Nextstrain is extensively tested on Linux, MacOS, and Windows 10 with Linux Subsystem and can be installed via conda and npm.

Maximum participants: 23

Organiser: Emma Hodcroft (Biozentrum University of Basel & SIB Swiss Institute of Bioinformatics, Basel, Switzerland)
Organiser: Richard Neher (Biozentrum University of Basel & SIB Swiss Institute of Bioinformatics, Basel, Switzerland)

09:00 - 10:00   **Basics of genomic epidemiology and phylogenetics**

10:00 - 11:00   **The Nextstrain interface and interactive visualization**

11:00 - 12:00   **From input to output: analysis pipelines using snakemake and augur**

12:00 - 13:00   **Conducting phylodynamic analysis using treetime**

13:00 - 14:00   **Interactive, step-by-step tutorials for viral and bacterial pathogens**

14:00 - 15:00   **Cleaning and formatting your data**

15:00 - 15:30   **Assembling a data-set specific snakefile**

15:30 - 16:00   **Visualization locally and online**

	[BC]2 Session , University of Basel Regenzimmer 111
09:00 - 16:30	**T3: Introduction to machine learning: opportunities for advancing omics data analysis**

Room Regenzimmer 111 Overview Machine learning has emerged as a discipline that enables computers to assist humans in making sense of large and complex data sets. With the drop-in cost of sequencing technologies, large amounts of omics data are being generated and made accessible to researchers. Analysing these complex high-volume data is not trivial and the use of classical tools cannot explore their full potential. Machine learning can thus be very useful in mining large omics datasets to uncover new insights that can advance the field of medicine and improve health care. The aim of this tutorial is to introduce participants to the Machine learning (ML) taxonomy and common machine learning algorithms. The tutorial will cover the methods being used to analyse different omics data sets by providing a practical context through the use of basic but widely used R and Python libraries. The tutorial will comprise a number of hands on exercises and challenges, where the participants will acquire a first understanding of the standard ML processes as well as the practical skills in applying them on familiar problems and publicly available real-world data sets. Learning objectives •Understand the ML taxonomy and the commonly used machine learning algorithms for analysing "omics" data •Understand differences between ML algorithms categories and to which kind of problem they can be applied •Understand different applications of ML in different -omics studies •Use some basic, widely used Python and R packages for ML •Interpret and visualize the results obtained from ML analyses on omics datasets •Apply the ML techniques to analyse their own datasets Audience and requirements This introductory tutorial is aimed towards bioinformaticians (graduate students and researchers) familiar with different omics data technologies that are interested in applying machine learning to analyse them. Prerequisites •Previous experience in Bioinformatics analysis •Familiarity with any programming language (especially R) is preferable but not necessary Maximum participants: 30

Organiser: Amel Ghouila (Institut Pasteur de Tunis, H3ABioNet, Tunisia)
Organiser: Fotis Psomopoulos (INAB|CERTH ELIXIR-GR, Certh, Greece)

09:00 - 09:15	**Tutorial introduction, get to know each other and, setup**
	Part I: Background
09:15 - 10:45	**Introduction to ML / DM: Data mining / machine learning basic concepts / taxonomy of ML and examples of algorithms / deep learning overview**
10:45 - 11:00	**break**
11:00 - 12:30	**Applications of ML in bioinformatics: examples of different ML/DM techniques that can be applied to different NGS data analysis pipelines / how to choose the right ML technique**
12:30 - 13:15	**break**
13:15 - 14:45	**Loading and exploring omics data: what is exploratory data analysis (EDA) and why is it useful? Unsupervised learning how could unsupervised learning be used to analyze omics data?**
	Part II: Hands-on
14:45 - 15:00	**break**

15:00 - 16:30	**Supervised learning I: classification how could supervised learning be used to analyze omics data? Supervised learning II: regression what if the target variable is numerical rather than categorical?**

Closing, discussion and resource sharing

[BC]2 Session , University of Basel Hörsaal 117

09:00 - 16:00   ## T4: Interpretability for deep learning models in computational biology

Room Hörsaal 117 Overview The recent application of deep neural networks to long-standing problems such as the prediction of functional DNA sequences, the inference of protein-protein interactions or the detection of cancer cells in histopathology images has brought a break-through in performance and prediction power. However, high accuracy often comes at the price of loss of interpretability, i.e. many of these models are built as black-boxes that fail to provide new biological insights. This tutorial focuses on illustrating some of the recent advancements in the field of Interpretable Artificial Intelligence. We will show how explainable, smaller models can achieve similar levels of performance than cumbersome ones, while shedding light on the underlying biological principles driving model decisions. We will demonstrate how to build and extract knowledge using interpretable approaches in two different domains of computational biology, (1) the functional analysis of raw DNA sequencing data and (2) drug sensitivity prediction models. The choice of these two applications is motivated by the availability of adequately large datasets that can support deep learning (DL) approaches and by their high relevance for personalized medicine. We will exploit both publicly available deep learning models as well as in-house developed models. Learning objectives The tutorial is aimed to strike the right balance between theoretical input and practical exercises. The tutorial has been designed to provide the participants not only with the theory behind DL and interpretability, but also to offer a set of frameworks, tools and real-life examples that they can implement in their own projects. Specifically, the participants will acquire/refresh basic knowledge on DL models for CB by both a brief technical introduction and a showcase of established models for specific practical applications. Next, several techniques to enhance model interpretability will be explored. In a first case study, a multimodal drug sensitivity prediction model will be introduced and discussed with an emphasis on neural attention mechanism that identify genes and molecular substructures that drove the model decision. Secondly, the problem of predicting transcription factor binding sites from raw DNA sequences will be utilized to demonstrate applications of various interpretability techniques, followed by an evaluation and comparison Audience and requirements This course is designed for everyone who would like to learn the basics of interpretability techniques for deep learning. The tutorial will provide a brief introduction to key concepts in deep learning, before exploring recent developments in the field of interpretability. Participants who want to participate in the hands-on exercises should bring a laptop and should have a basic programming knowledge of Python and shell scripting. All the material for the lectures and hands-on exercises will be available prior the day of the tutorial for download. Maximum participants: 83

Organiser: Jannis Born (Zurich Research Laboratory, Zurich, Switzerland)
Organiser: An-Phi Nguyen (Switzerland)
Organiser: Ali Oskooei (Zurich Research Laboratory, Zurich, Switzerland)

Scientific Programme

09:00 - 09:45	**Introduction to deep learning: Deep learning: What, why, how deep? Activation and cost functions, backpropagation, regularization, optimization.**
09:45 - 10:30	**Common deep learning models: Multi-layer perceptron (MLP); auto-enconders (AE); convolutional neural networks (CNN); recurrent neural networks (RNN).**
10:30 - 10:45	**Coffee break**
10:45 - 12:00	**Interpretability in deep learning:local versus global methods; A few techniques for interpretability: (1) perturbation-based approaches, (2) attention mechanisms, (3) LIME, (4) surrogate models.**
12:00 - 13:00	**Lunch break**
13:00 - 14:15	**Drug sensitivity prediction through deep learning and data integration (hands-on exercise): Introduction to deep learning models for drug prediction; attention mechanisms to identify genes and structural components relevant for the classification.**
14:15 - 14:30	**Coffee break**
14:30 - 16:00	**Interpretability for genomic deep learning models (Hands-on exercise): Prediction of transcription factor binding sites using CNNs, generation of explanations behind the predictions, evaluation of different methods for interpretability.**

[BC]2 Session , University of Basel Seminarraum 104

09:00 - 16:00	**T5: Bioinformatics pipelines for the analysis of viral NGS data**

Room Seminarrraum 104 Overview Viruses are both important models for evolutionary biology and causes of severe infectious diseases, thus representing major public health and economic concern. Viral genetics based on next-generation sequencing (NGS) of viral genomes is now the method of choice for analysing the diversity of intra- and inter-host virus populations, including epidemiological studies and individual treatment optimization in clinical virology. To support the computational analysis of viral NGS data, we have developed V-pipe, a bioinformatics pipeline that integrates various computational tools. It is freely available at https://cbg-ethz.github.io/V-pipe. It enables the reproducible analysis of genomic diversity in intra-host virus populations, including quality control, read alignment, and inference of viral genomic diversity on the level of single-nucleotide variants and viral haplotypes. V-pipe uses the workflow management system Snakemake to determine the order in which the steps of the specified pipeline are executed and checks that the output files are produced. It has a modular and extensible architecture. Users can design their own fully reproducible and transparent pipelines. Developers can test their own tools in a defined environment and help establishing best practices for virus research and clinical diagnostics. This tutorial provides the conceptual basis for analysing viral NGS data and hands-on training on mastering and extending workflows implemented in V-pipe. The purpose of this tutorial is to enable participants to leverage V-pipe to analyse virus sequencing data in production settings, including genomics research and clinical diagnostics. Learning objectives •Understanding the general computational concepts behind the most important processing steps and selected software tools implementing them •Using V-pipe as a practical implementation of those concepts •Performing quality control of input sequencing data •Setting up a robust workflow to map reads, call variants, and reconstruct haplotypes •Use of V-pipe as a benchmarking platform •Extending and customizing V-pipe Audience and requirements The tutorial is accessible to anyone with a Bachelor degree in life sciences, bioinformatics or equivalent, including biomedical scientists with additional (self-)training in bioinformatics. The main target audience of the tutorial are scientists who analyse virus sequencing data either in basic research or clinical settings, e.g., bioinformaticians embedded in clinical research groups, staff of bioinformatics core units, etc. As V-pipe is an open platform, which includes benchmarking capabilities, this tutorial is also of interest to developers who want to test their own tools or integrate those into the pipeline. Both the general concepts and V-pipe are of more general interest to researchers and practitioners, who wish to analyse the genomic diversity of a sample in a reproducible and streamlined manner. Prerequisites •Basic UNIX command line, such as provided in SIB's UNIX fundamentals e-learning module. •Basic knowledge of common sequencing data file formats. •To simplify organization, we will provide virtual machine images ahead of the tutorial. All participants should bring a laptop and make sure they can run the virtual machine on it. •A laptop with at least 10 GB free on hard disk and 4 GB of RAM. Maximum participants: 20

Organiser: Niko Beerenwinkel (ETH Zurich & SIB, Zurich, Switzerland)
Organiser: Susana Posada Céspedes (ETHZ, Zurich, Switzerland)
Organiser: Ivan Topolsky (Swiss Federal Institute of Technology Zurich (ETHZ) & SIB Swiss Institute of Bioinformatics, Zurich, Switzerland)

Session 1 - Methodological background I (talks)

09:00 - 09:15	**Introduction**

Scientific Programme

09:15 - 09:45	**Data quality control and cleaning, sequencing error characteristics of relevant platforms**
09:45 - 10:15	**Read alignment artefacts and common pitfalls**
10:15 - 10:30	**Coffee break**
	Session 2 - Methodological background II (talks)
10:30 - 11:00	**Principles of variant calling and allele frequency estimation**
11:00 - 11:30	**Methods for haplotype reconstruction**
11:30 - 12:00	**Design and usage of the V-pipe framework**
12:00 - 13:00	**Lunch**
	Session 3 - Basic workflows (hands-on)
13:00 - 13:25	**"Hello V-pipe" - create your first workflow**
13:25 - 13:50	**Analysis of example data from HIV sequencing**
13:50 - 14:15	**Result visualization and interpretation**
14:15 - 14:30	**Coffee break**
	Session 4 - Advanced workflows (hands-on)
14:30 - 15:00	**Parameter tuning and customization**
15:00 - 15:30	**V-pipe as a benchmarking platform**
15:30 - 16:00	**Extending V-pipe with your own tools**

[BC]2 Session , University of Basel Seminarraum 119

09:00 - 16:00	**T7: Analysis of multi-sample multi-condition scRNA-seq datasets**

Room Seminarrraum 119 Overview Single-cell RNA-sequencing (scRNA-seq) has quickly become an empowering technology to characterize the transcriptomes of individual cells. Most early analyses of differential expression (DE) in scRNA-seq data have aimed at identifying differences between cell types, and thus are focused on finding markers for cell sub-populations (experimental units are cells). There is now an emergence of multi-sample multi-condition scRNA-seq datasets where the goal is to make sample-level inferences (experimental units are samples), with 100s to 1000s of cells measured per replicate. To tackle such complex experimental designs, so-called differential state (DS) analysis follows cell types across a set of samples (e.g., individuals) and experimental conditions (e.g. treatments), in order to identify cell-type specific responses, i.e., changes in cell state. DS analysis: i) should be able to detect "diluted" changes that only affect a single cell type or a subset of cell types; and, ii) is orthogonal to clustering or cell type assignment. Furthermore, cell-type level DE analysis is arguably more interpretable and biologically meaningful. While there is an opportunity here to leverage existing robust bulk RNA-seq frameworks, by first aggregating single cells into "pseudo-bulk" data at the sub-population level, many new questions arise: How does one track subpopulations across patients (e.g. in the presence of batch effects)? Do we lose information by aggregating (i.e. is it better to model the single-cell data directly)? How do we do normalization when using pseudo-bulks? An extensive workflow for DS analysis in CyTOF data has been established, along with a set of visualisations and differential testing methods, and has been applied to predict cell-type specific responses to immunotherapy. An analogous approach has been applied in the context of scRNA-seq to uncover cell-type specific responses of lupus patients to INF-beta stimulation. However, while there have been comprehensive comparisons of DE analysis methods for scRNA-seq data, an analysis framework for sample-level DE analysis of scRNA-seq data has not been established yet. Learning objectives In this tutorial, we will introduce participants to R-based scRNA-seq analysis workflows that are tailored to complex experimental designs. Upon completion, attendees should have become familiar with: •basic pre-processing steps (e.g., filtering and normalisation) •exploring and evaluating different clusterings •identifying cluster-specific marker genes to aid in assigning cell populations •aggregation of single-cell to pseudo-bulk data •DS analysis to detect cell-type specific changes across conditions •DA analysis to detect differences in cell-type frequencies across conditions •how to visualise and explore differential testing results Audience and requirements Intermediate knowledge of R. Personal laptop with WiFi connection, and latest versions of R, Rstudio and various Bioconductor packages pre-installed. Maximum participants: 30

Organiser: Helena L. Crowell (Zurich, Switzerland)
Organiser: Pierre-Luc Germain (UZH and Laboratory of Systems Neuroscience,, Zurich, Switzerland)
Organiser: Mark D. Robinson (UZH, Zurich, Switzerland)

09:00 - 10:30	**Introduction, motivation, and historical/theoretical background**
10:30 - 11:00	**Coffee break**
11:00 - 12:30	**Session 1: pre-processing & clustering**
12:30 - 13:30	**Lunch**
13:30 - 14:30	**Session 2: DA/S analysis; visualisation and exploration of results**

14:30 - 15:30	**Session 3: Do-it-yourself application**
15:30 - 16:00	**Closing discussion: Q&A, current state/future directions of the field**

[BC]2 Session , University of Basel Hörsaal 115

09:00 - 16:00 **WS1: EMBO young investigator workshop on evolutionary and computational biology**

Room Hörsaal 115 Overview The goal of this workshop is to foster exchanges on cutting-edge research topics in evolutionary and computational biology. Current and past EMBO Young Investigators & Installation Grantees will give short talks, interspersed by ample time for discussion. To foster exchanges and interactivity among the participants, attendance to the workshop will be capped at 20 participants (including speakers) - with priority given to early-career researchers aspiring to progress toward independence. The workshop will include a roundtable discussion on raising the profile of evolutionary and computational biology within the EMBO Young Investigator Programme, as these areas are currently underrepresented in the programme. Potential prospective applicants to the programme are particularly encouraged to join the workshop. Speakers •Claudia Bank, Gulbenkian Institute, Portugal •Christophe Dessimoz, University of Lausanne, Switzerland •Santiago F. Elena, Spanish National Research Council, Valencia, Spain •Manuel Irimia, CRG Barcelona, Spain •Anna Karnkowska, University of Warsaw, Poland •Tomas Marques Bonet, Universitat Pompeu Fabra, Barcelona, Spain •Giulia Rancati, A*Star, Singapore •Christian Schlötterer, Vetmeduni Vienna, Austria •Joanna Sułkowska, University of Warsaw, Poland •Dario Valenzano, Max Planck Institute for Biology of Ageing, Cologne, German Maximum participants: approx. 20. Application procedure To apply for this workshop, please submit a brief statement on your career stage, why you would like to participate, and what you are expecting from the workshop using the following application form. Important dates •Submission opening date: 17 March, 2019 •Extended submission deadline: 12 June , 2019, 23:59 CET •Notification of acceptance: 19 June, 2019

Organiser: Christophe Dessimoz (University of Lausanne, Lausanne, Switzerland)
Organiser: Manuel Irimia (CRG Barcelon, Barcelona, Spain)
Organiser: Giulia Rancati (A*Star, Singapore, Singapore)

09:00 - 10:20	**Session 1**
10:20 - 10:50	**Coffee break**
10:50 - 12:05	**Session 2**
12:05 - 13:20	**Lunch**
13:20 - 14:35	**Session 3**
14:35 - 15:00	**Coffee break**
15:00 - 16:00	**Session 4, including a round table**

[BC]2 Session , University of Basel Hörsaal 116

09:00 - 16:15	**WS2: Annotation and curation of computational models in biology**

Room Hörsaal 116 Motivation, goals and scope The fast accumulation of biological data calls for more systematic approaches for their integration, analysis and exploitation. The generation of novel, relevant hypotheses from this enormous quantity of data remains challenging. Logical models have long been used to answer a variety of questions regarding the dynamical behaviours of regulatory networks. As the number of published logical models increases, there is a pressing need for proper model annotation, referencing and curation in community-supported and standardised formats. In this context, organised by members of the Consortium for Logical Models and Tools (CoLoMoTo – http://colomoto.org) and of the Computational Modeling of Biological Systems Community of Special Interest (COSI) of the International Society for Computational Biology (ISCB) (SysMod - https://sysmod.info/), this workshop aims to review and connect different ongoing projects, bringing together people from different communities involved in modelling and annotation of molecular biological entities, interactions, pathways and models. Speakers Several experts on data annotation, model curation, and community standard development are invited. In addition, a call for abstract submissions will be issued (see details below). •Martin Kuiper, Norwegian University of Science and Technology, NO, •Denis Thieffry IBENS, Paris, FR •Rahuman S. Malik Sheriff, Project Leader (BioModels), EMBL-EBI, London, UK •Cristina Casals, UniProtKB/ Swiss-Prot Biocurator, SIB, Geneva, CH •Paul Thomas – GO, (LEGO/Noctua), USC, USA, tentative

Selected abstracts

Abstract submissions for oral presentations should be sent to the following addresses anna.niaraki[at]univ-evry.fr, thelikar2[at]unl.edu, Laurence.Calzone[at]curie.fr, with the indication: [BC]2_2019 Workshop Submission. There will be no poster sessions. Abstracts should include title, author affiliation and contact information and a summary of the work that should not exceed 800 words. In an effort to maintain a balanced women to men ratio, female candidates are strongly encouraged to apply. Important dates: Submission Opening date: April 20, 2019 Submission Deadline (abstract): June 28, 2019 Notification: July 10, 2018 Workshop Date: September 9th, 2019

Organiser: Laurence Calzone (Institut Curie/U900, INSERM/Mines ParisTech, Paris, France)
Organiser: Tomas Helikar (University of Nebraska, Nebraska–Lincol, United States)
Organiser: Anna Niarakis (UEVE, Univ Paris-Saclay, Paris, France)

09:00 - 09:10	**Welcome and introduction to the workshop**
	Session 1 - Data/model curation and annotation and available repositories Chair:Denis Thieffry, Anna Niarakis
09:10 - 09:30	**Martin Kuiper: Towards a curation platform for causal interaction statements**
09:30 - 09:50	**Marek Ostaszewski: BioKB and MINERVA: a workflow for curation and quick prototyping of annotated knowledge repositories**
09:50 - 10:10	**Sheriff Malik: Curation and annotation of models in BioModels repository promotes reproducibility and reusability**
10:10 - 10:30	**Cristina Casals: SysVasc Prior Knowledge Network: An example of biocuration for Boolean modelling**

Scientific Programme

10:30 - 11:00	**Coffee break / tea break**
	Session 2 - Community standards development and interoperability/reusability – Chair Ioannis Xenarios – Laurence Calzone
11:00 - 11:20	**Denis Thieffry: Computational verification of large logical models - application to the prediction of T cell response to checkpoint inhibitors**
11:20 - 11:40	**Tom Freeman: A graphical and computational model of the renal mammalian circadian clock**
11:40 - 12:00	**Paul Thomas: Gene Ontology Causal Activity Modeling**
12:00 - 12:20	**Anna Niarakis + Vidisha Singh: Automated inference of annotated Boolean models from molecular interaction maps using CaSQ**
12:20 - 12:30	**Wrap up of morning sessions**
12:30 - 13:30	**Lunch break with coffee fix**
13:30 - 14:00	**Round table – Discussion and Exchanges**
	Session 3 – Tools (I) Chair: Julio Saez Rodriguez
14:00 - 14:20	**Tomas Helikar: Cell Collective**
14:20 - 14:40	**Laurence Calzone + Gaultier Stoll: MaBoSS ecosystem**
14:40 - 15:00	**Vasundra Touré: The Minimum Information about a Molecular Interaction Causal Statement (MI2CAST): a guideline for the management of molecular causal interaction**
	Session 4 – Tools (II) Chair: Tomas Helikar
15:00 - 15:20	**Julio Saez Rodriguez: CellNOpt**
15:20 - 15:40	**Aurélien Naldi: The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks**
15:40 - 16:00	**Eugenia Oshurko: KAMIStudio**

EMBO Session, Town Hall (Rathaus)

16:45 - 18:00	**Welcome and Opening lecture**

Chair: Michael N Hall (Basel, Switzerland)

16:45 - 17:00	**Welcome** Lukas Engelberger (Basel Stadt, Basel, Switzerland)
17:00 - 18:00	**Climate crisis: how much can we bear?** Thomas Stocker (University of Bern, Bern, Switzerland)

Networking event, Town Hall (Rathaus)

18:00 - 19:00	**Welcome reception**

Scientific Programme

Tuesday, 10 September 2019

Joint Session, Montreal

09:00 - 09:45   **Keynote lecture 1: Kari Stefánsson**

Chair: Geneviève Almouzni (Institut Curie, Research Center UMR 3664 CNRS, Paris Cedex 05, France)

09:00 - 09:45   **Genetics of common diseases**
Kári Stefánsson (deCODE Genetics, Reykjavik, Iceland)

Job Fair, Job Fair

09:45 - 17:00   **European Job Fair @ BASEL LIFE**

[BC]2 Session , Montreal

10:00 - 11:45   **[BC]2 Plenary session 1: Single-cell data**

Chair: Manfred Claassen (ETH Zurich & SIB, Zurich, Switzerland)
Chair: Mark D. Robinson (UZH, Zurich, Switzerland)

10:00 - 10:45   **Joint analysis of heterogeneous single-cell dataset collections**
Peter Kharchenko (Harvard Medical School, Boston, United States)

10:45 - 11:05   **Uncertainty quantification in multivariate mixed models for mass cytometry data**
Christof Seiler (Maastricht University, Maastricht, Netherlands)

11:05 - 11:25   **Psupertime: supervised pseudotime inference for single cell RNA-seq data with sequential labels**
Will Macnair (University of Zurich, Zurich, Switzerland)

11:25 - 11:45   **Hyperbolic geometry as a tool for analysis of complex hierarchies from single-cell data**
Anna Klimovskaia (Facebook AI Research, Paris, France)

EMBO Session, Singapore

10:00 - 11:45   **EMBO Plenary session 1: Microbiome as a driver of health and disease**

Chair: Yasmine Belkaïd (NIAID/NIH, Bethesda, United States)

10:00 - 10:25   **Host micro biome interactions in health and disease**
Eran Elinav (Weizmann Institute of Science, Rehovot, Israel)

Scientific Programme

10:25 - 10:50	**Microglia at the crossroads of brain circuits and microbiota**
	Sonia Garel (PSL Research University, Paris, France)
10:50 - 11:15	**Small molecules from the human microbiota**
	Michael A. Fischbach (UCSF, San Francisco, United States)
11:15 - 11:40	**Microbiota control of tissue immunity and repair**
	Yasmine Belkaïd (NIAID/NIH, Bethesda, United States)

Innovation Forum, Sydney

10:00 - 11:00   **Aging and drug discovery and AI**

In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.

Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)
Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)

10:00 - 10:20	**Exploiting aging pathways to extend healthspan**
	Brian Kennedy (Singapore, Singapore)
10:20 - 10:40	**Mitochondrial metabolic checkpoint, stem cell aging and rejuvenation**
	Danica Chen (University of California, Berkeley, United States)
10:40 - 11:00	**"Translational geroscience: a new paradigm for 21st century medicine"**
	Matt Kaeberlein (U of Washington, Washington, United States)

Scientific Programme

	Innovation Forum, Rio
10:00 - 11:00	**Peptide therapeutics**

The framework of the BASEL LIFE, we will host the "Peptide Therapeutics Forum 2019" for 2 days on September 10, and 11. Similar to previous events, presentations highlight important new insights regarding the drug discovery of peptides including examples for successful development. The first day is dedicated to topics to be addressed more early during peptide optimization, and the second day focuses more on issues related to later-stage development. As in the past, this event is thought to disseminate information on latest news in the broad field of therapeutic peptides and to enable networking of interested parties from academia and industries.

Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

10:00 - 10:30	**New Trends in Clinical Development of Peptide Therapeutics**
10:30 - 11:00	**Optimization of the lipopeptide arylomycin natural product into Gram-negative antibiotics**
	Michael Koehler (Genentech Research & Early Development, San Francisco, United States)

	Innovation Forum, Samarkand
10:00 - 11:00	**Biotherapeutics - Making complex biologics accessible**

Disruptive innovations are driving future biotherapeutics to become more personalized, cost-effective and efficacious. The biotherapeutics are shifting from classical monoclonal antibodies towards more complex modalities, such as engineered antibodies, multi-specific antibodies, cell and gene therapies. The 2019 biotherapeutics forum discusses technology trends and developments required to progress current and future drug modalities from concepts to the market.

Chair: Stefan Weigand (Roche, Basel, Switzerland)
Chair: René Assenberg (Janssen Biologics, Leiden, Netherlands)

10:00 - 10:30	**Fusion proteins: design principles and consequences for manufacturing**
	Stefan Schmidt (Bioatrium, Visp, Switzerland)
10:30 - 11:00	**Master checkpoint Cbl-b inhibition: ambulatory siRNA-based autologous cell therapy for cancer**
	Anderson Gaweco (Apeiron, Vienna, Austria)

Scientific Programme

	Innovation Forum, Osaka
10:00 - 11:00	**Advances in 3R**

The principles of 3Rs will celebrate their 60 years old in 2019. They were originally proposed in the book "The principles of humane experimental technique", published in 1959 by Russell and Burch. The concept of the three Rs addresses the Replacement, Reduction and Refinement of animal experimentation. Fortunately, we have come a long way in 60 years. Nowadays, many scientific and technological advances facilitate the use of alternative methods in research. Also, scientific knowledge can lead to improved design of animal studies, which can potentially reduce the numbers of used animal and the severity of the interventions (animal suffering). Moreover, specific bodies, like the 3RCC (Swiss 3R competence centre: https://swiss3rcc.org/) strongly promote education, research, dissemination and application of 3Rs. In this session, we will focus on the current status and applications of the 3R-principles in industrial and academic research. We will address the uses of alternatives to animal experimentation in drug discovery research for pharmacological and toxicological characterization of potential drugs. The session will also touch upon the relevance of animal experimentation for the detection of human-relevant effects.

Chair: Chantra Eskes (3RCC, Bern, Switzerland)
Chair: Laura Suter-Dick (University of Applied Sciences and Arts Northwestern Switzerland, Muttenz, Switzerland)

10:00 - 10:10	**Introduction**
	Chantra Eskes (3RCC, Bern, Switzerland)

10:10 - 10:35	**Making better use of non-animal approaches in science**
	Maurice Whelan (European Commission Joint Research Centre (JRC), Ispra, Italy)

10:35 - 11:00	**iPSC-derived BrainSpheres: 21th century tools for human brain disease modelling and neurotoxicology testing**
	David Pamies (University of Lausanne, Lausanne, Switzerland)

	Poster , San Francisco
10:15 - 18:30	**Poster exhibition**

Scientific Programme

Innovation Forum, Sydney

11:30 - 12:30 **Aging and drug discovery and AI**

In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.

Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)
Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)

11:30 - 11:50 **Rejuvenation biotechnology: why age may soon cease to mean aging**

Aubrey de Grey (AgeX / SENS Research Foundation, London, United Kingdom)

11:50 - 12:10 **Translational Strategies to Prevent Sarcopenia through Targeted Cellular Nutrition**

Jerome Feige (Nestle Research, Lausanne, Switzerland)

12:10 - 12:30 **C/EBPβ transcription factors in health- and lifespan determination**

Cornelis F. Calkhoven (European Institute for the Biology of Ageing (ERIBA), University of Groningen, Groningen, Netherlands)

Innovation Forum, Rio

11:30 - 12:30 **Peptide therapeutics**

The framework of the BASEL LIFE, we will host the "Peptide Therapeutics Forum 2019" for 2 days on September 10, and 11. Similar to previous events, presentations highlight important new insights regarding the drug discovery of peptides including examples for successful development. The first day is dedicated to topics to be addressed more early during peptide optimization, and the second day focuses more on issues related to later-stage development. As in the past, this event is thought to disseminate information on latest news in the broad field of therapeutic peptides and to enable networking of interested parties from academia and industries.

Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

11:30 - 12:00 **Activation of the Hippo pathway via targeting of transcription factor TEAD using designed tertiary protein structure mimetics**

Hélène Adihou (Astra Zeneca, Dortmund, Germany)

12:00 - 12:30 **Elimination of Aβ oligomers by the orally available anti-prionic all-D-peptide PRI-002 reverses cognition deficits and decelerates neurodegeneration**

Dieter Willbold (Heinrich-Heine-Universität Düsseldorf, Jülich, Germany)

Innovation Forum, Samarkand

11:30 - 12:30   **Biotherapeutics - Making complex biologics accessible**

Disruptive innovations are driving future biotherapeutics to become more personalized, cost-effective and efficacious. The biotherapeutics are shifting from classical monoclonal antibodies towards more complex modalities, such as engineered antibodies, multi-specific antibodies, cell and gene therapies. The 2019 biotherapeutics forum discusses technology trends and developments required to progress current and future drug modalities from concepts to the market.

Chair: Stefan Weigand (Roche, Basel, Switzerland)
Chair: René Assenberg (Janssen Biologics, Leiden, Netherlands)

11:30 - 12:00   **Challenges in CMC development of bispecific antibodies from DNA to FIH studies using the DuoBody technology**

Christian Cimander (GenMab, Copenhagen, Denmark)

12:00 - 12:30   **Gene therapy CMC**

Diane Blumenthal (Spark Therapeutics, Philadelphia, United States)

Innovation Forum, Osaka

11:30 - 12:30   **Advances in 3R**

The principles of 3Rs will celebrate their 60 years old in 2019. They were originally proposed in the book "The principles of humane experimental technique", published in 1959 by Russell and Burch. The concept of the three Rs addresses the Replacement, Reduction and Refinement of animal experimentation. Fortunately, we have come a long way in 60 years. Nowadays, many scientific and technological advances facilitate the use of alternative methods in research. Also, scientific knowledge can lead to improved design of animal studies, which can potentially reduce the numbers of used animal and the severity of the interventions (animal suffering). Moreover, specific bodies, like the 3RCC (Swiss 3R competence centre: https://swiss3rcc.org/) strongly promote education, research, dissemination and application of 3Rs. In this session, we will focus on the current status and applications of the 3R-principles in industrial and academic research. We will address the uses of alternatives to animal experimentation in drug discovery research for pharmacological and toxicological characterization of potential drugs. The session will also touch upon the relevance of animal experimentation for the detection of human-relevant effects.

Chair: Chantra Eskes (3RCC, Bern, Switzerland)
Chair: Laura Suter-Dick (University of Applied Sciences and Arts Northwestern Switzerland, Muttenz, Switzerland)

11:30 - 11:55   **Non-clinical models to predict toxicities of immunotherapies in patients**

Ekaterina Breous-Nystrom (F. Hoffmann-La Roche, Basel, Switzerland)

11:55 - 12:20   **1 culture of care in an industrial setting**

Thomas Bertelsen (Novo Nordisk, Malov, Denmark)

12:20 - 12:30   **Concluding remarks**

Laura Suter-Dick (University of Applied Sciences and Arts Northwestern Switzerland, Muttenz, Switzerland)

Scientific Programme

Job Fair, Rio

12:45 - 13:45	**Workshop European Job Fair: Take the Bull by the Horns: What you can do to take steps to a fulfilling career in science**

I have a PhD, now what? How can I find out what I like? It's never too late to start thinking about career plans. This presentation is designed to inspire one to seek information and connections that will help chart a course for a happy and long-term career in science. Will address many aspects of science life including relationship building, skill building, diversity and work/life balance issues.

Chair: Joanne Kamens (Executive Director Addgene, Switzerland, Switzerland)

MipTec / Industry related session, Samarkand

12:45 - 13:45	**Industry Symposium: Life-science research in microgravity**
	Supported by SpacePharma S.A

Chair: Martin Aebi (SpacePharma S.A, Switzerland)

12:45 - 13:00	**Welcome - Introduction to Space 4.0**
	Martin Aebi (SpacePharma S.A, Switzerland)
13:00 - 13:15	**To infinity and beyond… the adventures of a bioengineered kidney chip onboard the international space station**
	Catherine Yeung (University of Washington School of Pharmacy, United States)
13:15 - 13:30	**Microgravity effects on human serum albumin binding properties**
	Alessandra Di-Masi (Roma Tre University, Italy)
13:30 - 13:45	**Crystallization of proteins and small molecules in micro-gravity**
	Guy Samburski (SpacePharma Ltd, Israel)

[BC]2 Session , Montreal

13:15 - 15:00	**[BC]2 Plenary session 2: Evolutionary medicine**

Chair: Anna-Sapfo Malaspinas (University of Lausanne & SIB, Lausanne, Switzerland)
Chair: Richard Neher (Biozentrum University of Basel & SIB Swiss Institute of Bioinformatics, Basel, Switzerland)

13:15 - 14:00	**Predicting antibiotic resistance**
	Roy Kishony (Israel Institute of Technology, Israel)
14:00 - 14:20	**The next step for Nextstrain: tracking pathogen evolution and transmission**
	Emma Hodcroft (Biozentrum University of Basel & SIB Swiss Institute of Bioinformatics, Basel, Switzerland)

14:20 - 14:40	**Comparative genomics of 1600 species reveals new insights regarding "superpowers", breast cancer, and genetic diseases**
	Yuval Tabach (The Hebrew University-Hadassah Medical School, Jerusalem, Israel)
14:40 - 15:00	**How pairwise coevolutionary models capture the collective residue variability in proteins**
	Pierre Barrat-Charlaix (University of Basel & Swiss Institute of Bioinformatics, Basel, Switzerland)

EMBO Session, Singapore

13:15 - 15:00	**EMBO Plenary session 2: The emergence of infectious diseases**
	Chair: Elena A. Levashina (Vector Biology Unit Max Planck Institute for Infection Biology, Berlin, Germany)
13:15 - 13:40	**Digital Epidemiology**
	Marcel Salathé (School of Life Sciences, School of Computer and Communication Sciences, Geneve, Switzerland)
13:40 - 14:05	**Experimental and computational approaches for manipulating virus evolution and population dynamics**
	Marco Vignuzzi (Institut Pasteur, Paris, France)
14:05 - 14:30	**Microevolution of malaria vectors**
	Elena A. Levashina (Vector Biology Unit Max Planck Institute for Infection Biology, Berlin, Germany)
14:30 - 14:55	**Antimicrobial resistance, a threat for our planet as big as climate change, and the role of vaccines**
	Rino Rappuoli (Italy)

Innovation Forum, Sydney

14:00 - 15:00	**Aging and drug discovery and AI**
	In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.
	Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)
	Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)

Scientific Programme

14:00 - 14:20	**Drivers of neurotoxicity in prion diseases**
	Adriano Aguzzi (University of Zurich, Zurich, Switzerland)
14:20 - 14:40	**Autophagy and neurodegeneration**
	David Rubinsztein (Cambridge, Cambridge, United Kingdom)
14:40 - 15:00	**Convergent mechanisms of longevity**
	Adam Antebi (Max Planck, Cologne, Germany)

Innovation Forum, Rio

14:00 - 15:00   **Peptide therapeutics**

The framework of the BASEL LIFE, we will host the "Peptide Therapeutics Forum 2019" for 2 days on September 10, and 11. Similar to previous events, presentations highlight important new insights regarding the drug discovery of peptides including examples for successful development. The first day is dedicated to topics to be addressed more early during peptide optimization, and the second day focuses more on issues related to later-stage development. As in the past, this event is thought to disseminate information on latest news in the broad field of therapeutic peptides and to enable networking of interested parties from academia and industries.

Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

14:00 - 15:00	**Plenary Lecture: The chemical evolution of endocrine hormones**
	Richard DiMarchi (University of Indiana, Bloomington, United States)

Innovation Forum, Samarkand

14:00 - 15:00   **Biotherapeutics - Making complex biologics accessible**

Disruptive innovations are driving future biotherapeutics to become more personalized, cost-effective and efficacious. The biotherapeutics are shifting from classical monoclonal antibodies towards more complex modalities, such as engineered antibodies, multi-specific antibodies, cell and gene therapies. The 2019 biotherapeutics forum discusses technology trends and developments required to progress current and future drug modalities from concepts to the market.

Chair: Stefan Weigand (Roche, Basel, Switzerland)
Chair: René Assenberg (Janssen Biologics, Leiden, Netherlands)

14:00 - 14:30	**Co-expression of IgG-like bispecifics for efficient manufacturing**
	Michael Bardroff (Novartis, Basel, Switzerland)
14:30 - 15:00	**mRNA as a platform technology ideally suited for individualised therapeutics**
	Andreas Kuhn (BioNtech, Mainz, Germany)

Scientific Programme

	Innovation Forum, Osaka
14:00 - 15:00	**Antibiotic resistance**

Antimicrobial resistance has become a major threat to public health. Inappropriate use of antibiotics had and still has a major effect on resistance evolution. Rapid diagnostics of the pathogen and determination of its antimicrobial susceptibility will be one strategy for more effective antibiotics treatments as well as for epidemiological surveillance of resistant pathogens. Also, new insights in antibiotics resistance mechanisms can support the development of new antimicrobials. In this session, the speakers will focus on both the latest advances in antimicrobial diagnostics and the pathogen's resistance mechanisms.

Chair: Eric Kübler (FHNW, Muttenz, Switzerland)
Chair: Jürg Dreier (Basilea Pharmaceutica Ltd, Basel, Switzerland)

14:00 - 14:30 **Flip-flopping antibiotic-resistance to fight tuberculosis**
Alain Baulard (University of Lille, Lille, France)

14:30 - 15:00 **Next-generation aminoglycoside antibiotics demonstrate superior efficacy against superbugs and improved drug safety**
Sven Hobbie (Juvabis AG, Switzerland)

Joint Session, Montreal
15:30 - 16:30 **EMBO & [BC]2 Flash talks**

Chair: Sven Bergmann (University of Lausanne & SIB, Lausanne, Switzerland)
Chair: Philippe Bucher (EPFL & SIB, Lausanne, Switzerland)

15:30 - 15:32 **P01** **A simple and flexible computational framework for inferring sources of heterogeneity from single-cell dynamics**
Lekshmi Dharmarajan* (Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland)

15:32 - 15:34 **P02** **Deciphering the role of Nrf2-related glutathione pathways in malignant cancer cells**
Agathe Morand (University of Basel, Basel, Switzerland)

15:34 - 15:36 **P03** **Realizing Waddington's metaphor: Inferring regulatory landscapes from single-cell gene expression data**
Jeremie Breda (Universitaet Basel, Basel, Switzerland)

15:36 - 15:38 **P04** **MDR to preXDR to XDR tuberculosis: whole genome sequencing reveals several different evolutionary strategies**
Serej Ley (Swiss Tropical and Public Health Institute, Basel, Switzerland)

15:38 - 15:40 **P05** **Representation learning of disease associated cell subsets from single-cell RNA sequencing data**
Nicolas Ochsner (ETH Zurich / Institute of Molecular Systems Biology, Zurich, Switzerland)

15:40 - 15:42 **P06** **HABP4 is required for colon tumorigenesis in the murine colitis-associated carcinoma model**
Talita Diniz Melo Hanchuk (Unicamp, Campinas, Brazil)

15:42 - 15:44	**P07**	**The challenges of annotation and integration of scRNA-Seq into Bgee**
		Sara Fonseca Costa (University of Lausanne, Lausanne, Switzerland)
15:44 - 15:46	**P08**	**Discovery of potent anthranilic acid derivatives for the treatment of chronic inflammation**
		Madhwi Ojha (Banasthali Vidyapith, Niwai, India)
15:46 - 15:48	**P09**	**An alignment-free method for predicting phenotypes of sequenced bacterial isolates**
		Maido Remm (University of Tartu, Tartu, Estonia)
15:48 - 15:50	**P10**	**Gut microbiota, neuropsychometric test scores and neuroimaging differentiate cognitive impairment in Parkinson's disease**
		Suleyman Yildirim (Istanbul Medipol University / International School of Medicine, Istanbul, Turkey)
15:50 - 15:52	**P11**	**Leveraging correlated risks to increase power in Genome-Wide Association Studies**
		Ninon Mounier (University Center for Primary Care and Public Health, Lausanne, Switzerland)
15:52 - 15:54	**P12**	**Non-parametric modeling of state shifts in microbial communities**
		Ville Laitinen (Turku University, Turku, Finland)
15:54 - 15:56	**P13**	**Insights into lung microbiome dysbiosis in patients with active pulmonary tuberculosis: a nested case-control study**
		Monica R. Ticlla (Swiss Tropical and Public Health Institute, Basel, Switzerland)
15:56 - 15:58	**P14**	**Codon bias in lincRNAs: a mechanism to prevent translation?**
		Anneke Brümmer (University of Lausanne, Lausanne, Switzerland)
15:58 - 16:00	**P15**	**Tracking bacterial pathogens in the regime of fast horizontal gene transfer**
		Nicholas Noll (Universitaet Basel, Basel, Switzerland)
16:00 - 16:02	**P16**	**Deep motif deconvolution of HLA-II peptidomes for robust class II epitope predictions**
		Julien Racle (University of Lausanne, Lausanne, Switzerland)
16:02 - 16:04	**P17**	**Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis**
		Van Du T. Tran (SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland)
16:04 - 16:06	**P18**	**Characterisation of wild-type Von Hippel-Lindau ccRCC with the application of both a bottom-up and a top-down multi-omic integrative approach**
		Aashil A Batavia (University Hospital Zurich, Zurich, Switzerland)
16:06 - 16:08	**P19**	**PCTAIRE1 kinase overcomes PolST induced mitotic arrest and cell death**
		Qaaifah Gillani (University of Kashmir, Srinagar, India)
16:08 - 16:10	**P20**	**Cracking the HCC code - a multi-OMICS study of liver cancer to understand its development and therapy response**
		Eva Dazert (Biozentrum / University of Basel, Basel, Switzerland)

16:10 - 16:12	P21	**shortRNA: a flexible framework for the analysis of short RNA sequencing data**
		Deepak K Tanwar (Statistical Bioinformatics Group, Swiss Institute of Bioinformatics, Zürich, Switzerland)
16:12 - 16:14	P22	**Explore a new ligand binding site of G protein-coupled receptors**
		Shuguang Yuan (Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, Shenzhen, China)
16:14 - 16:16	P23	**A national infrastructure network to enable secure biomedical data processing: the BioMedIT project**
		Martin Fox (SIB Swiss Institute of Bioinformatics, Personalized Health Informatics Group, Lausanne, Switzerland)
16:16 - 16:18	P24	**A bioinformatic workflow to enable species assignment directly from metagenetic sequencing**
		Tsering Wüthrich (University of Bern, Bern, Switzerland)
16:18 - 16:20	P25	**SwissTargetPrediction: web tool update and large-scale evaluation of protein target prediction for bioactive small molecules**
		Antoine Daina (SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland)
16:20 - 16:22	P26	**LEMMI: a live evaluation of computational methods for metagenome investigation**
		Mathieu Seppey (University of Geneva, Geneva, Switzerland)
16:22 - 16:24	P27	**Microbial population in fluctuating environments, how the size influences the strategy**
		Athos Fiori (Universitaet Basel, Basel, Switzerland)
16:24 - 16:26	P28	**Molecular and functional characterization of papillary renal cell carcinoma**
		Silvia Angori (University Hospital Zurich, Zurich, Switzerland)
16:26 - 16:28	P29	**Characterization of kinase activities inferred by phosphoproteomics in myeloid cell lines treated with targeting compounds for the identification of driving and bypassing oncogenic signaling pathways**
		Mahmoud Hallal (University of Bern, Bern, Switzerland)
16:28 - 16:30	P30	**Loss of hexokinase 2 causes insulin resistance**
		Mitsugu Shimobayashi (University of Basel, Basel, Switzerland)

Innovation Forum, Sydney

15:30 - 16:30	**Aging and drug discovery and AI**

In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.

Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)
Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)

15:30 - 15:50	**Impact of food perception on proteostasis & aging**

Thorsten Hoppe (University of Cologne, Cologne, Germany)

15:50 - 16:10	**The art of decision-making by stem cells in the aging brain**

Ana Martin-Villalba (German Cancer Research Center (DKFZ), Heidelberg, Germany)

16:10 - 16:30	**Power and benefit of selective phosphatase inhibition for neurodegenerative diseases**

Anne Bertolotti (Cambridge Biomedical Campus, Cambridge, United Kingdom)

Innovation Forum, Rio

15:30 - 17:00	**Peptide therapeutics**

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Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

15:30 - 16:00	**Peptide platforms for therapy and imaging: the first total synthesis of amanitin for ADCs and one-step 18F-labeling PET-oncology**

David Perrin (University of British Columbia, Vancouver, Canada)

16:00 - 16:30	**Orally active short chemokine antagonist peptides for pain, stroke, and neurodegeneration**

Michael Ruff (Creative BioPeptides, Montreal, United States)

16:30 - 17:00	**Strategies for efficient, optimized high throughput solid phase peptide synthesis of challenging peptides**
	Andrew Kennedy (Gyros Protein Technologies, Uppsala, Sweden)

Innovation Forum, Samarkand

15:30 - 16:30	# Biotherapeutics - Making complex biologics accessible

Disruptive innovations are driving future biotherapeutics to become more personalized, cost-effective and efficacious. The biotherapeutics are shifting from classical monoclonal antibodies towards more complex modalities, such as engineered antibodies, multi-specific antibodies, cell and gene therapies. The 2019 biotherapeutics forum discusses technology trends and developments required to progress current and future drug modalities from concepts to the market.

Chair: Stefan Weigand (Roche, Basel, Switzerland)
Chair: René Assenberg (Janssen Biologics, Leiden, Netherlands)

15:30 - 16:00	**CMC opportunities and challenges in bringing new, complex modalities to the patient**
	Iedo Beeksma (Janssen Pharmaceuticals, Leiden, Netherlands)
16:00 - 16:30	**Audience Q&A with the speakers**

Innovation Forum, Osaka

15:30 - 16:30	# Antibiotic resistance

Antimicrobial resistance has become a major threat to public health. Inappropriate use of antibiotics had and still has a major effect on resistance evolution. Rapid diagnostics of the pathogen and determination of its antimicrobial susceptibility will be one strategy for more effective antibiotics treatments as well as for epidemiological surveillance of resistant pathogens. Also, new insights in antibiotics resistance mechanisms can support the development of new antimicrobials. In this session, the speakers will focus on both the latest advances in antimicrobial diagnostics and the pathogen's resistance mechanisms.

Chair: Eric Kübler (FHNW, Muttenz, Switzerland)
Chair: Jürg Dreier (Basilea Pharmaceutica Ltd, Basel, Switzerland)

15:30 - 16:00	**Emerging antibiotic resistance in Gram negatives and their rapid diagnostic**
	Patrice Nordmann (University of Fribourg, Fribourg, Switzerland)
16:00 - 16:30	**Improving early detection of AMR in a global context - the roles of diagnostics and OneHealth**
	Daniel Paris (Swiss Tropical Institute, Basel, Switzerland)

Joint Session, Montreal

16:30 - 17:45	# SIB Bioinformatics Awards

16:30 - 16:55	**SIB Early Career Bioinformatician Award**
16:55 - 17:20	**SIB Best Swiss Bioinformatics Graduate Paper Award**
17:20 - 17:45	**SIB Bioinformatics Resource Innovation Award**

Joint Session, Singapore

16:30 - 17:30 **Louis-Jeantet Prize lecture**

Chair: Paul Nurse (The Francis Crick Institute, London, United Kingdom)

16:30 - 17:00 **Advanced genetic engineering of hematopoiesis to treat human diseases**

Luigi Naldini (San Raffaele Telethon Institute for Gene Therapy, Milan, Italy)

17:00 - 17:30 **Restoring Vision**

Botond Roska (Institute of Molecular and Clinical Ophthalmology Basel (IOB), Basel, Switzerland)

Networking event, San Francisco

17:30 - 18:30 **Networking event & Poster session for EMBO and [BC]2 Presenters**

Chair: Sven Bergmann (University of Lausanne & SIB, Lausanne, Switzerland)
Chair: Philippe Bucher (EPFL & SIB, Lausanne, Switzerland)

Poster (P01-P30) - EMBO & [BC]2 Flash talks

P01 **A simple and flexible computational framework for inferring sources of heterogeneity from single-cell dynamics**

Lekshmi Dharmarajan* (Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland)

P02 **Deciphering the role of Nrf2-related glutathione pathways in malignant cancer cells**

Agathe Morand (University of Basel, Basel, Switzerland)

P03 **Realizing Waddington's metaphor: Inferring regulatory landscapes from single-cell gene expression data**

Jeremie Breda (Universitaet Basel, Basel, Switzerland)

P04 **MDR to preXDR to XDR tuberculosis: whole genome sequencing reveals several different evolutionary strategies**

Serej Ley (Swiss Tropical and Public Health Institute, Basel, Switzerland)

P05 **Representation learning of disease associated cell subsets from single-cell RNA sequencing data**

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P06	**HABP4 is required for colon tumorigenesis in the murine colitis-associated carcinoma model**
	Talita Diniz Melo Hanchuk (Unicamp, Campinas, Brazil)

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	Maido Remm (University of Tartu, Tartu, Estonia)

P10	**Gut microbiota, neuropsychometric test scores and neuroimaging differentiate cognitive impairment in Parkinson's disease**
	Suleyman Yildirim (Istanbul Medipol University / International School of Medicine, Istanbul, Turkey)

P11	**Leveraging correlated risks to increase power in Genome-Wide Association Studies**
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P18	**Characterisation of wild-type Von Hippel-Lindau ccRCC with the application of both a bottom-up and a top-down multi-omic integrative approach**
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P19	**PCTAIRE1 kinase overcomes PolST induced mitotic arrest and cell death**
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P20	**Cracking the HCC code - a multi-OMICS study of liver cancer to understand its development and therapy response**
	Eva Dazert (Biozentrum / University of Basel, Basel, Switzerland)
P21	**shortRNA: a flexible framework for the analysis of short RNA sequencing data**
	Deepak K Tanwar (Statistical Bioinformatics Group, Swiss Institute of Bioinformatics, Zürich, Switzerland)
P22	**Explore a new ligand binding site of G protein-coupled receptors**
	Shuguang Yuan (Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, Shenzhen, China)
P23	**A national infrastructure network to enable secure biomedical data processing: the BioMedIT project**
	Martin Fox (SIB Swiss Institute of Bioinformatics, Personalized Health Informatics Group, Lausanne, Switzerland)
P24	**A bioinformatic workflow to enable species assignment directly from metagenetic sequencing**
	Tsering Wüthrich (University of Bern, Bern, Switzerland)
P25	**SwissTargetPrediction: web tool update and large-scale evaluation of protein target prediction for bioactive small molecules**
	Antoine Daina (SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland)
P26	**LEMMI: a live evaluation of computational methods for metagenome investigation**
	Mathieu Seppey (University of Geneva, Geneva, Switzerland)
P27	**Microbial population in fluctuating environments, how the size influences the strategy**
	Athos Fiori (Universitaet Basel, Basel, Switzerland)
P28	**Molecular and functional characterization of papillary renal cell carcinoma**
	Silvia Angori (University Hospital Zurich, Zurich, Switzerland)
P29	**Characterization of kinase activities inferred by phosphoproteomics in myeloid cell lines treated with targeting compounds for the identification of driving and bypassing oncogenic signaling pathways**
	Mahmoud Hallal (University of Bern, Bern, Switzerland)
P30	**Loss of hexokinase 2 causes insulin resistance**
	Mitsugu Shimobayashi (University of Basel, Basel, Switzerland)
	EMBO Microbiome as a driver of health and disease
P31	**Arsenic disturbs the gut microbiome of a disadvantaged community in Nepal**
	Samendra Sherchan (Tulane University, New Orleans, United States)
P32	**Are metagenomic data sufficiently informative to robustly predict inflammatory bowel disease status?**
	Lusine Khachatryan (Philip Morris International R&D, Neuchatel, Switzerland)

Scientific Programme

P33	**Cluster partitions and fitness landscapes of the Drosophila fly microbiome**
	Lisa Lamberti (ETH Zurich, Basel, Switzerland)

[BC]2 Single-cell data

P34	**Copy number phylogenetics for single cells**
	Mustafa Anil Tuncel (ETH Zurich, Basel, Switzerland)
P36	**Machine learning-aided single-cell transcriptomics of HAdV-infected cells**
	Anthony Petkidis (University of Zurich / Institute of Molecular Life Sciences, Zurich, Switzerland)
P37	**Bayesian nonparametric clustering of single-cell mutational profiles**
	Nico Borgsmüller (ETH Zürich, Basel, Switzerland)
P38	**A probabilistic model for clustering scRNAseq data**
	Pascal Grobecker (University of Basel & Swiss Institute of Bioinformatics, Basel, Switzerland)
P39	**Multi-omics analysis in real time using SCfind**
	Jimmy Tsz Hang Lee (Wellcome Sanger Institute, Hinxton, United Kingdom)
P40	**Combined unsupervised clustering and anomaly detection to identify disease associated rare cell populations**
	Madeleine Suffiotti (Lausanne University Hospital, Lausanne, Switzerland)
P41	**A network-based approach for visualization and simplification of single-cell RNA sequencing data**
	Mariia O. Bilous (University of Lausanne, Lausanne, Switzerland)
P42	**rCASC: reproducible classification analysis of single cell sequencing data**
	Raffaele Calogero (University of Torino, Torino, Italy)
P43	**Single-cell transcriptomics in unravelling the cellular diversity and molecular signature that govern anti-tumour functions of myeloid cells in vivo**
	Marta Bica (Instituto de Medicina Molecular João Lobo Antunes, Lisboa, Portugal)
P44	**Variations on a single-cell RNAseq pipeline: benchmarks from filtering to clustering**
	Pierre-Luc Germain (UZH and Laboratory of Systems Neuroscience,, Zurich, Switzerland)
P45	**Benchmarking confounder removal tools for scRNA-Seq data**
	Ruben Chazarra - Gil (Wellcome Sanger Institute, Hinxton, Cambridshire, United Kingdom)
P179	**Phototoxicity in live cell imaging: the evil within**
	Hugo Moreno (Nanolive SA, Ecublens, Switzerland)

EMBO The emergence of infectious diseases

P46	**Effect of rabies virus infection on expression levels of Parvalbumin and secretagogin genes in the brains of rabies infected mice**
	Brenda Kanu (Ahmadu Bello University, Zaria, Nigeria)

P47	**Effect of rabies virus infection on the expression levels of calbindin D28k and calretinin in mouse brain**
	George Chibuike Korie (Ahmadu Bello University, Zaria, Nigeria)
P48	**Insilico profiling and structural insights to understand impact of SNPs in pfact transporter protein by MD simulation approach**
	Rahila Sardar (ICGEB, New Delhi, India)
P49	**Investigation of HIV transmission dynamics among young women engaged in sex work in Mombasa, Kenya**
	Michael Becker (Public Health Agency of Canada, Winnipeg, Canada)
P50	**Novel Rhabdovirus and an almost complete drain fly transcriptome recovered from two independent contaminations in clinical metagenomic samples**
	Francisco Brito (University of Geneva, Geneva, Switzerland)
P51	**Non-invasive monitoring of drug action: exploring new assay designs for Chagas' disease in vitro drug discovery**
	Anna Frieda Fesser (Swiss Tropical & Public Health Institute, Basel, Switzerland)
	[BC]2 Evolutionary medicine
P52	**Predicting tumour evolution using cancer progression models**
	Ramon Diaz-Uriarte (Universidad Autonoma de Madrid, Madrid, Spain)
P53	**Genetic simulation with frequency-dependent fitness to examine the role of genetic constraints, mutator genes, and population size on cancer cooperation and competition and their effects on tumour progression**
	Ramon Diaz-Uriarte (Universidad Autonoma de Madrid, Madrid, Spain)
P54	**A diversity study of the Epstein-Barr Virus (EBV) in HIV-infected patients**
	Alexis Loetscher (University of Geneva, Geneva, Switzerland)
P55	**Discovery of a newly evolved pneumococcal Serotype 6F in Switzerland**
	Oluwaseun Oyewole (Institute for Infectious Diseases, University of Bern, Bern, Switzerland)
P56	**Building an automated continuous culture device to study drug resistance evolution in bacteria**
	Eric Ulrich (Biozentrum, 4056, Switzerland)
	EMBO Chronic inflammation: the common denominator of post-modern pathologies
P57	**Static stretch affects the pro- inflammatory response of type II alveolar epithelial cells**
	Jorge Miguel Ferreira (Medical Carl Gustav Carus Universiy, Dresden, Germany)
P58	**Circulating miR-1246 in the progression of chronic obstructive pulmonary disease (COPD) in patients from the BODE cohort**
	Sara Estefania Cazorla-Rivero (Hospital Universitario N/S de Candelaria, Santa Cruz de Tenerife, Spain)

P59	**Trifostigmanoside I, an active constituent from sweet potato, restores the function of MUC-2 and tight junctions through PKC α/β to maintain intestinal barrier function**
	Amna Parveen (Gachon University, Incheon, Korea, Republic of)
P60	**Role of NLRP3 inflammasome in sterile cardiovascular disease**
	Fumitake Kawanishi (Toyama Prefectutal University, Imizu, Japan)
P180	**The pro-inflammatory mediators adenosine and hyaluronan modulate lung fibrosis and pulmonary hypertension in combined pulmonary fibrosis and emphysema (CPFE)**
	Harry Karmouty Quintana (University of Texas Health Science Center at Houston, Houston, United States)

[BC]2 Clinical population genomics

P61	**Integrating variant frequencies in neXtProt for a better representation of the human proteome**
	Alain Gateau (CALIPHO group, SIB Swiss Institute of Bioinformatics, Zürich, Switzerland)
P62	**Genetic diversity of Mycobacterium tuberculosis from extensively drug-resistant patients from Georgia**
	Tatjana Meyer (Swiss Tropical and Public Health Institute, Basel, Switzerland)
P63	**Transcriptome analysis describing immunity and metabolism genes in peripheral blood mononuclear cells of cervical cancer patients to Senegal**
	Moussa Ndiaye (University Cheikh Anta Diop of Dakar, Dakar, Senegal)
P64	**Identifying genetic modifiers of prion disease**
	Jiang-An Yin (University of Zurich, Zurich, Switzerland)
P65	**An enhanced workflow for variant interpretation in UniProtKB/Swiss-Prot improves consistency and reuse in ClinVar**
	Anne Estreicher (SIB Swiss Institute of Bioinformatics, Geneva, Switzerland)

EMBO Regenerative medicine

P66	**CD34+ cells in liver with myogenic potential**
	Bipasha Bose (Yenepoya Research Centre, Mangalore, India)
P67	**Possible therapeutic roles of diet-regulated gene expressions during brain aging using zebrafish**
	Begün Erbaba (Bilkent University, Ankara, Turkey)
P68	**A novel approach in stem cell therapy for alzheimer's animal model**
	Mehdi Mehdizadeh (Cellular and Molecular Research Center, Department of Anatomy, Faculty of Advanced Technologies in Medicine, Iran University of Medical Sciences, Tehran, Iran, Tehran, Iran, Islamic Republic of)

[BC]2 Systems biology of disease

P69	**Development of the multiscale model of germinal center B cell differentiation**
	Bhavesh Soni (IBM research Lab Zurich, Rüschlikon, Zurich, Switzerland)

P70	**Suppression of 1-deoxydihydroceramide production protects against protein aggregation and anoxia injury**
	J. Thomas Hannich (Geneva University, Geneva, Switzerland)

P71	**A service for the automated creation of genome-scale metabolic network model from a microbial genome**
	Sébastien Moretti (SIB, Lausanne, Switzerland)

P72	**BioModels parameters: a resource to search and access parameters from published systems models**
	Rahuman S Malik Sheriff (European Bioinformatics Institute (EMBL-EBI), European Molecular Biology Laboratory,, Cambridge, United Kingdom)

P73	**An in-silico approach to explore the evolutionary signatures of host pathogen interactions**
	Aranyak Goswami (Bose Institute, kolkata, India)

P74	**Major improvements in the reconciliation of metabolites and biochemical reactions to ease metabolic network reconstruction**
	Sébastien Moretti (SIB, Lausanne, Switzerland)

P181	**Investigating the prevalence of anaemia in rural gambia, in relation to levels of zinc protoporphyrin, haemoglobin and haptoglobin (phenotype and genotype)**
	Ebrima Bah (MRC Unit The Gambia at the London School of Hygiene and Tropical Medicine, Banjul, Gambia)

EMBO Computational biology, artificial intelligence, machine learning in precision medicine

P75	**Discovery, estimation and prediction analysis using a Bayesian survival model for complex diseases**
	Sven Erik Ojavee (University of Lausanne, Lausanne, Switzerland)

P76	**In silico approach of jack bean as DPP1V inhibitory activity**
	Andriati Ningrum (UGM, Yogyakarta, Indonesia)

P77	**In silico approach of collagen from tuna fish by-product as ACE inhibitor**
	Andriati Ningrum (UGM, Yogyakarta, Indonesia)

P78	**Diagnostics and correction of batch effects in large-scale proteomics studies**
	Chloe H. Lee (ETH Zurich, Zurich, Switzerland)

P79	**Homopolymers in mycobacterium tuberculosis: a source for rapid adaptation?**
	Michaela Zwyer (Swiss Tropical and Public Health Institute, Basel, Switzerland)

P80	**Assessing cancer heterogeneity among cancer types**
	Paula Carrio Cordo (University of Zurich, Zurich, Switzerland)

P81	**Facilitating collection of literature for personalized cancer treatments**
	Emilie Pasche (Swiss Institute of Bioinformatics, Geneva, Switzerland)

P82	**Identification of potential inhibitors targeting cholinesterase: an in silico and in vitro approach**
	Manish Kumar Tripathi (Department of Pharmaceutical Engineering & Technology, Varanasi, India)
P83	**Unconventional cell cycle modeling: a vision from third angle**
	Mustafa Pasha (Lincoln University, Lincoln, New Zealand)
P84	**A machine learning based algorithm for deciphering complex chemical structures of secondary metabolites by genome mining**
	Priyesh Prateek Agrawal (National Institute of Immunology, New Delhi, India)
P85	**Hierarchical ensemble methods for ontology-based predictions in computational biology and precision medicine**
	Marco Notaro (Università degli Studi di Milano, Milano, Italy)
P86	**A pipeline for characterization of possible ncRNA homologs in BLAST output**
	Marek Schwarz (Institute of Microbiology of the CAS, v. v. i., Prague, Czech Republic)
P182	**HumanGEM: the generic genome-scale metabolic model of Homo sapiens**
	Hao Wang (Chalmers University of Technology, Gothenburg, Sweden)
P183	**Structure-function relationships of high-density lipoprotein in type 2 diabetes and coronary heart disease**
	Mathias Cardner (ETH Zurich, Basel, Switzerland)
	[BC]2 Multi-level data Integration
P87	**Haplotype based expression quantitative Trait Loci mapping**
	Robin Hofmeister (University of Lausanne, Lausanne, Switzerland)
P88	**Molecular basis of gene regulatory variation in human adipose stromal cells**
	Daniel Alpern (EPFL, Lausanne, Switzerland)
P89	**Protein-wide simulations to drive the design of new therapies from multi-omics data**
	Attila Csikász-Nagy (Pázmány Péter Catholic University, Budapest, Hungary)
P90	**Integrating expression data into metabolome-wide GWAS identifies genes involved in the modulation of the metabolite concentration**
	Reyhan Sonmez Flitman (UNIL, Lausanne, Switzerland)
P91	**Remote and local services to search and visualize reactions and metabolites from the Rhea databases**
	Parit Bansal (Swiss Institute of Bioinformatics, Geneva, Switzerland)
P92	**Identifying a good animal model for age-related muscle loss in humans**
	Anastasiya Börsch (University of Basel & Swiss Institute of Bioinformatics, Basel, Switzerland)
P93	**Cancer cell lines in focus: somatic copy number variation and germline variation**
	Qingyao Huang (University of Zurich, Zurich, Switzerland)

P94	**Rhea, an expert curated resource of biochemical reactions with SPARQL endpoint**
	Alan Bridge (Swiss-Prot group, SIB Swiss Institute of Bioinformatics, Geneva, Switzerland)
P95	**Representing the human metabolome in UniProtKB using Rhea**
	Lionel Breuza (SIB - Swiss Institute of Bioinformatics, Geneva, Switzerland)
	EMBO Genetic diseases: genome and epigenome
P96	**A novel MASP1 gene mutation causes 3MC1 syndrome in the first reported Egyptian family**
	AmiraA Nabil Khalaf (Medical Research Institite, Alexandria, Egypt)
P97	**Transcriptional regulators which are induced in HCC affect deregulation of central catabolism**
	Sujin Park (Biozentrum Univ. of Basel, Basel, Switzerland)
P98	**Role of mTOR in regulating DLK1-DIO3 cluster miRNAs**
	Dritan Liko (University of Basel, Basel, Switzerland)
P99	**ER and mitochondrial stress in liver cancer cells**
	Amandine Thomas (Biozentrum / University of Basel, Basel, Switzerland)
P100	**Conditional estimation of the contribution of genomic regions and functional annotations to common complex disease**
	Marion Patxot (University of Lausanne, Lausanne, Switzerland)
P101	**An evolutionarily conserved mechanism of translation regulation by TORC1**
	Sunil Shetty (Biozentrum Univ. of Basel, Basel, Switzerland)
P102	**Interactome profiling of mTOR signalling**
	Wenxiang Fu (University of Basel, Basel, Switzerland)
P103	**Role of the transcription factor TCF3 in HCC progression**
	Stefania Battaglioni (Biozentrum, University of Basel, Basel, Switzerland)
P184	**Cysteine oxidation triggers phase separation of the tumour suppressor p16INK4A**
	Loes van Dam (UMC Utrecht Center for Molecular Medicine, Utrecht, Netherlands)
P185	**Epigenetic modification associated with type II interferon gamma in challenge virus standard (CVS) strain and Nigerian street rabies virus (SRV) infected mice**
	Maryam Abdulazeez (African Centre of Excellence for Neglected Tropical Diseases and Forensic Biotechnology, Ahmadu Bello University Centre, Zaria, Nigeria)
P186	**Analysis of DNA methylation patterns and epigenetic drug response of acute myeloid leukemia**
	Ralitsa Langova (German Cancer Research Center (DKFZ), Heidelberg, Germany)
	[BC]2 Others
P104	**CRUNCH: completely automated analysis of ChIP-seq data**
	Mikhail Pachkov (Universitaet Basel, Basel, Switzerland)

P105   **Deciphering the landscape of phosphorylated HLA-I ligands**

Marthe Solleder (University of Lausanne, Lausanne, Switzerland)

P106   **Inferring RNA-binding sites, motifs and regulation from CLIP data with RCRUNCH**

Maria Katsantoni (University of Basel & Swiss Institute of Bioinformatics, Basel, Switzerland)

P107   **PolyASite 2.0: a comprehensive atlas of RNA 3' ends**

Christina Janina Herrmann (Biozentrum, University of Basel, Basel, Switzerland)

P108   **ViraMiner: deep learning for identifying viral genomes in human samples**

Zurab Bzhalava (Karolinska Institutet, Stockholm, Sweden)

P109   **Crunch-mara: modeling gene regulation on DNA Level**

Anne Krämer (Universitaet Basel, Basel, Switzerland)

P110   **Protein histidine phosphorylation - a novel target in cancer therapy?**

Markus Linder (University of Basel, Basel, Switzerland)

P111   **A deep learning framework to score cancer cell proliferation and oncolytic virus efficacy in 3D tumor models**

Fanny Georgi (University of Zurich / Institute of Molecular Life Sciences, Zurich, Switzerland)

P112   **sparql.uniprot.org: moving past search for research**

Jerven Bolleman (SIB Swiss Institute of Bioinformatics, Geneve, Switzerland)

P114   **ReSequenceR: simulating more realistic high-throughput sequencing data**

Stephan Schmeing (Universität Zürich, Zürich, Switzerland)

P115   **UniLectin, a knowledge-base of carbohydrate-binding proteins**

François Bonnardel (UniGe, Geneva, Switzerland)

P116   **Swiss-PO. A new web tool to help predicting mutation pathogenicity for precision oncology**

Fanny Krebs (University of Lausanne, Epalinges, Switzerland)

P117   **Supporting structure prediction method development with continuous automated model eEvaluatiOn (CAMEO)**

Juergen Haas (SIB - Swiss Institute of Bioinformatics and Biozentrum, University of Basel, Basel, Switzerland)

P118   **Studies on the interaction of rotavirus non-structural proteins NSP5, NSP2 with host cellular factors and their role in virus replication**

Varsha Tandra (Indian Institute of Science, Bangalore, Bangalore, India)

P119   **Minimisation of surface energy drives apical epithelial organisation and gives rise to Lewis' law**

Marco Kokic (ETH Zurich, Basel, Switzerland)

P120   **α-Synuclein aggregation and amyloid formation in Parkinson´s disease nucleates through liquid-liquid phase separation**

Soumik Ray (Indian Institute of Technology Mumbai, Mumbai, India)

P121   **γ-enolase as a marker of resistance to syrosingopine-metformin therapy for cancer**

Don Benjamin (Biozentrum, University of Basel, Basel, Switzerland)

P122   **Kinetic analysis of the minimal model to describe metabolic oscillations in Bacillus subtilis biofilms**

Ravindra Garde (Friedrich-Schiller Univerity, Jena, Germany)

P123   **Optimised nitrogen fixing bacteria: a whole cell modelling approach**

Leanne Massie (Imperial College London, London, United Kingdom)

P124   **Biomedical big data analysis and management on secure research platforms**

Diana Coman Schmid (Scientific IT Services ETH, Zurich, Sweden)

P125   **Design and development of potential acetylcholinesterase and BACE-1 inhibitors for the treatment of Alzheimer's disease**

Avanish Tripathi (Indian Institute of Technology BHU, Varanasi, India)

P126   **HLA-I 9-mer peptides exhibit a preference for helical topologies in the source proteins1**

Marta A. S. Perez (University of Lausanne, Lausanne, Switzerland)

P127   **SWISS-MODEL: homology modelling of protein structures and complexes**

Gerardo Tauriello (SIB Swiss Institute of Bioinformatics & Biozentrum, University of Basel, Basel, Switzerland)

P128   **Minimum error calibration and normalization for copy number analysis**

Bo Gao (University of Zurich, Zurich, Switzerland)

P129   **User experience (UX) at the SIB swiss institute of bioinformatics**

Chiara Gabella (SIB, Lausanne, Switzerland)

P130   **Kinetic properties of rhodanese from African locust bean seeds (Parkia biglobosa)**

Leonard Ehigie (Ladoke Akintola University of Technology, Ogbomoso, Nigeria)

P131   **Genome-wide association study in Japanese cohort identifies variants near amylase genes associated with serum amylase level**

Zannatun Nayema (Kanazawa University, Kanazawa, Japan)

P132   **Computational exploration to design and synthesise N-benzylpiperidines as multifunctional therapeutics to treat Alzheimer's disease**

Piyoosh Sharma (Indian Institute of Technology BHU, Varanasi, India)

P133   **Complete genome sequencing and molecular characterization of a rabies virus isolated from trade dogs in Plateau State, Nigeria**

Grace Kia (Faculty of Veterinary Medicine, Ahmadu Bello University Zaria, Nigeria, Zaria, Nigeria)

P134   **Krini: data analysis in the cloud**

Alexander Kanitz (University of Basel & Swiss Institute of Bioinformatics, Basel, Switzerland)

P135   **Fruit of Lycium barbarum displays neurotrophic, neuritogeneis and anti-neuroinflammatory activities In-vitro**

Zahra Khan (Gachon Institute of Pharmaceutical Science, Gachon University, Incheon, Korea, Republic of)

P136   **SWITCH edu-ID based login into SSH servers**

Heinz Stockinger (SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland)

EMBO Tissue regeneration, organoids without borders

P137   **Sodium fluoride induced skeletal muscle changes: muscle hypertrophy versus muscle atrophy and signaling mechanisms**

Sudheer Shenoy P (Yenepoya University, Mangalore, India)

P138   **Searching for robust Turing patterns using discrete models**

Thomas Leyshon (Imperial College London, London, United Kingdom)

P187   **Human broncho-alveolar epithelial cells from normal and diseased lungs maintain progenitor status and form organoids**

Harry Karmouty Quintana (University of Texas Health Science Center at Houston, Houston, United States)

Scientific Programme

Wednesday, 11 September 2019

	[BC]2 Session , Montreal
09:00 - 09:45	**[BC]2 Keynote lecture**

Chair: Erik van Nimwegen (University of Basel & SIB, Switzerland)
Chair: Niko Beerenwinkel (ETH Zurich & SIB, Zurich, Switzerland)

09:00 - 09:45   **Hidden variables: quantifying our uncertainties in the analyses of human microbiome data**

Susan Holmes (Stanford University, Stanford, United States)

	EMBO Session, Singapore
09:00 - 09:45	**Keynote lecture 2: Michal Schwartz**

Chair: Caetano Reis e Sousa (Immunobiology Laboratory The Francis Crick Institute, London, United Kingdom)

09:00 - 09:45   **Empowering the immune system to combat Alzheimer's disease and dementia; a key role of myeloid cells**

Michal Schwartz (Weizmann Institute of Science, Rehovot, Israel)

	[BC]2 Session , Montreal
10:00 - 11:45	**[BC]2 Plenary session 3: Clinical population genomics**

Chair: Zoltán Kutalik (CHUV, University of Lausanne & SIB, Lausanne, Switzerland)
Chair: Matthew Robinson (University of Lausanne & SIB, Lausanne, Switzerland)

10:00 - 10:45   **From GWAS to function: interpreting GWAS results in biological context**

Danielle Posthuma (Vrije Universiteit (VU) Amsterdam & VU University Medical Center Amsterdam (VU), Amsterdam, Netherlands)

10:45 - 11:05   **Integrative haplotype estimation with sub-linear complexity**

Olivier Delaneau (University of Lausanne, Lausanne, Switzerland)

11:05 - 11:25   **Simultaneous estimation of heritability, genetic confounding, and bi-directional causal effect from GWAS summary statistics**

Liza Darrous (University Center for Primary Care and Public Health, Lausanne, Switzerland)

11:25 - 11:45   **Bayesian inference for large human medical genetic datasets**

Daniel Trejo-Banõs * (University of Lausanne, Lausanne, Switzerland)

Scientific Programme

EMBO Session, Singapore

10:00 - 11:45 **EMBO Plenary session 3: EMBO Molecular Medicine Anniversary Lecture and Awards**

Chair: Philippe Sansonetti (France)

10:00 - 10:40 **A new way to look at Alzheimer's disease: the cellular phase**

Bart de Strooper (VIB Center for Brain & Disease Research, Leuven, Belgium)

EMM 10th anniversary awards for posters and one speaker per topical session

10:40 - 10:50 **Integrated stress response remodels macrophage immune-metabolism to propagate chronic inflammation and atherosclerosis**

Ebru Erbay (Cedars-Sinai Medical Center, Los Angeles, United States)

10:50 - 11:00 **Detecting the mutational signature of homologous recombination deficiency in clinical samples**

Doga C. Gulhan (Harvard Medical School, Boston, United States)

11:00 - 11:10 **Suppression of arginine catabolism promotes liver cancer**

Dirk Mossmann (Biozentrum, University of Basel, Basel, Switzerland)

11:10 - 11:20 **Penile microbiota of heterosexual black South African men and analysis of abundances of bacteria associated with HIV risk**

Harris Onywera (University of Cape Town, Cape Town, South Africa)

11:20 - 11:30 **Vitamin D modulates macrophage polarization and ER stress in lung inflammation and injury targeting miR-34a/Sirt1 axis**

Mansoor Syed (Jamia Millia Islamia, New Delhi, India)

11:30 - 11:45 **Awards**

Innovation Forum, Sydney

10:00 - 11:00 **Aging and drug discovery and AI**

In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.

Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)
Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)

10:00 - 10:20 **Mechanisms of intracellular DNA sensing through the cGAS-STING pathway**

Andrea Ablasser (EPFL, Lausanne, Switzerland)

10:20 - 10:40   **Pandomics: a drug discovery tool for aging and oncology**
Ivan Ozerov (Insilico Medicine, Hong Kong, China)

10:40 - 11:00   **From longevity signatures to longevity interventions**
Vadim Gladyshev (Harvard Medical School, Boston, United States)

Innovation Forum, Rio

10:00 - 11:00   Peptide therapeutics

The framework of the BASEL LIFE, we will host the "Peptide Therapeutics Forum 2019" for 2 days on September 10, and 11. Similar to previous events, presentations highlight important new insights regarding the drug discovery of peptides including examples for successful development. The first day is dedicated to topics to be addressed more early during peptide optimization, and the second day focuses more on issues related to later-stage development. As in the past, this event is thought to disseminate information on latest news in the broad field of therapeutic peptides and to enable networking of interested parties from academia and industries.

Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

10:00 - 10:30   **Exotic side chain-to-side-chain cyclization modes in octreotide analogs for tumor pretargeting**
Anna Maria Papini (University of Florence, Florence, Italy)

10:30 - 11:00   **Peptide-based radiopharmaceuticals for cancer imaging and therapy Agonist or Antagonist? Does it really matter?**
Melpomeni Fani (University Hospital Basel, Basel, Switzerland)

Innovation Forum, Samarkand

10:00 - 11:00   Microfluidics and microenvironment

CSEM, the Molecular Evolution Lab of the University of Basel, and the cluster Toolpoint for Lab Science join forces to organize the 2nd Basel Microfluidics and Microenvironment Forum at BASEL LIFE. As in the previous year, the forum will focus on the preparation of microphysiological systems in a microenvironment for boosting the relevance of in-vitro assays towards in-vivo outcome. This includes developments related to organ or model organism on a chip, droplet microfluidics or bioprinting. Newest technological developments and critical insights from the end users will come together at this forum. The forum brings together scientists, entrepreneurs and managers in these fields, from both industry and academia, to exchange ideas and to promote innovation applicable to bio-pharmaceutical development.

Chair: Marc Creus (University of Basel, Basel, Switzerland)
Chair: Helmut Knapp (CSEM, Alpnach, Switzerland)
Chair: Vincent Revol (CSEM, Switzerland)

10:00 - 10:10	**Introduction**
	Marc Creus (University of Basel, Basel, Switzerland)
	Helmut Knapp (CSEM, Alpnach, Switzerland)
	Vincent Revol (CSEM, Switzerland)
10:10 - 10:35	**Organ-on-a-Chip systems: Integrated microphysiological platforms recapitulating complex human biology**
	Peter Loskill (Fraunhofer Institute for Interfacial Engineering and Biotechnology IGB, Stuttgart, Germany)
10:35 - 11:00	**Tissue engineering of functional human skeletal muscle models for drug screening using 3D bioprinting**
	Hansjörg Keller (Novartis Institutes for BioMedical Research, Basel, Switzerland)

Innovation Forum, Osaka

10:00 - 11:00   Innovating in healthcare - global health data sharing

Healthcare is facing an uncertain future. People are living longer, costs are rising and patients are demanding a different experience. The cost to discover new medicines is skyrocketing, and efficacy of these treatments is regularly being questions by reimbursement authorities. The future of healthcare is focusing on Precision Medicine to decrease costs and increase efficacy. Precision medicine utilizes the patient's health data to define a personalized signature for individualized treatment. But what the field lacks to move forward significantly is access to sufficient data to elucidate signatures of states of human health. The ability to exchange genome and other health data can have multiple benefits to advance healthcare. Stakeholders in the healthcare ecosystem, like academics, pharmaceutical corporations, insurers, and governments, can get population molecular data to develop health care programs (new drugs, reimbursement models, national programs). Patients can get preventative healthcare based on diagnosis of biomarkers that might predispose them to disease. New business models can be developed based on needs of rare diseases communities, for example. Leading to overall better health, lower costs, increased productivity and longevity.

Chair: Bhupinder Bhullar (Swiss Vault, Basel, Switzerland)
Chair: Thomas Brenzikofer (DayOne Initiative BaselArea, Basel, Switzerland)

10:00 - 10:15	**Introduction**
	Thomas Brenzikofer (DayOne Initiative BaselArea, Basel, Switzerland)
10:15 - 10:45	**The 100,000 genomes project and beyond: mainstreaming genome medicine in the UK National Health Service as a model for use of patient data for both clinical care and research**
	Tim Hubbard (Genomics England, London, United Kingdom)
10:45 - 11:00	**Q&A**

Poster , San Francisco

10:15 - 16:45   Poster exhibition

Innovation Forum, Sydney

11:30 - 12:30   Aging and drug discovery and AI

In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.

Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)
Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)

11:30 - 11:50   **Protecting the Aging Genome**

Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)

11:50 - 12:10   **How to obtain an indication that targets health span**

Nir Barzilai (Albert Einstein, New York, United States)

12:10 - 12:20   **Is anti-aging drug discovery becoming a reality**

Alexey Moskalev (Engelhardt Institute of Molecular Biology, Moscow, Russian Federation)

12:20 - 12:30   **Identification and application of gene expression signatures associated with lifespan extension**

Alexander Tyshkovskiy (Harvard Medical School, Boston, United States)

Innovation Forum, Rio

11:30 - 12:30   Peptide therapeutics

The framework of the BASEL LIFE, we will host the "Peptide Therapeutics Forum 2019" for 2 days on September 10, and 11. Similar to previous events, presentations highlight important new insights regarding the drug discovery of peptides including examples for successful development. The first day is dedicated to topics to be addressed more early during peptide optimization, and the second day focuses more on issues related to later-stage development. As in the past, this event is thought to disseminate information on latest news in the broad field of therapeutic peptides and to enable networking of interested parties from academia and industries.

Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

11:30 - 12:00   **Vancomycin regains effectiveness for resistant bacteria by conjugation to cationic peptides**

Walter Mier (University of Heidelberg, Heidelberg, Germany)

12:00 - 12:30	**Peptide discovery at protagonist therapeutics: A platform yielding multiple clinical candidates**
	Mark Smythe (Protagonist, Newark, CA, United States)

Innovation Forum, Samarkand

11:30 - 12:30	# Microfluidics and microenvironment

CSEM, the Molecular Evolution Lab of the University of Basel, and the cluster Toolpoint for Lab Science join forces to organize the 2nd Basel Microfluidics and Microenvironment Forum at BASEL LIFE. As in the previous year, the forum will focus on the preparation of microphysiological systems in a microenvironment for boosting the relevance of in-vitro assays towards in-vivo outcome. This includes developments related to organ or model organism on a chip, droplet microfluidics or bioprinting. Newest technological developments and critical insights from the end users will come together at this forum. The forum brings together scientists, entrepreneurs and managers in these fields, from both industry and academia, to exchange ideas and to promote innovation applicable to bio-pharmaceutical development.

Chair: Marc Creus (University of Basel, Basel, Switzerland)
Chair: Helmut Knapp (CSEM, Alpnach, Switzerland)
Chair: Vincent Revol (CSEM, Switzerland)

11:30 - 11:50	**Parallelized long-term monitoring of 3D tissues**
	Oliver Frey (Insphero, Schlieren, Switzerland)
11:50 - 12:10	**Next generation cell culture: enhancing tissue complexity in perfused microfluidic chips**
	Paul Vulto (Mimetas, Leiden, Netherlands)
12:10 - 12:30	**BI/OND: Versatile Organ-on-Chip Platform**
	Nikolas Gaio (Delft, Netherlands)

Innovation Forum, Osaka

11:30 - 12:30   **Innovating in healthcare - global health data sharing**

Healthcare is facing an uncertain future. People are living longer, costs are rising and patients are demanding a different experience. The cost to discover new medicines is skyrocketing, and efficacy of these treatments is regularly being questions by reimbursement authorities. The future of healthcare is focusing on Precision Medicine to decrease costs and increase efficacy. Precision medicine utilizes the patient's health data to define a personalized signature for individualized treatment. But what the field lacks to move forward significantly is access to sufficient data to elucidate signatures of states of human health. The ability to exchange genome and other health data can have multiple benefits to advance healthcare. Stakeholders in the healthcare ecosystem, like academics, pharmaceutical corporations, insurers, and governments, can get population molecular data to develop health care programs (new drugs, reimbursement models, national programs). Patients can get preventative healthcare based on diagnosis of biomarkers that might predispose them to disease. New business models can be developed based on needs of rare diseases communities, for example. Leading to overall better health, lower costs, increased productivity and longevity.

Chair: Bhupinder Bhullar (Swiss Vault, Basel, Switzerland)
Chair: Thomas Brenzikofer (DayOne Initiative BaselArea, Basel, Switzerland)

11:30 - 11:35   **Managing the global data deluge**

Bhupinder Bhullar (Swiss Vault, Basel, Switzerland)

11:35 - 11:45   **How SPHN is making data sharing possible**

Katrin Crameri (SPHN, Basel, Switzerland)

11:45 - 11:55   **New innovations and business models based on distributed ledger technologies**

Markus Stauffiger (4eyes, Basel, Switzerland)

11:55 - 12:05   **Titanium Trust Report: psychological perspectives on artificial intelligence and trust**

Marisa Tschopp (SCIP.cH, Zurich, Switzerland)

12:05 - 12:30   **Round Table Discussion**

Bhupinder Bhullar (Swiss Vault, Basel, Switzerland)
Katrin Crameri (SPHN, Basel, Switzerland)
Markus Stauffiger (4eyes, Basel, Switzerland)
Marisa Tschopp (SCIP.cH, Zurich, Switzerland)

MipTec / Industry related session, Rio

12:45 - 13:45   **MipTec 2019 - Workshop - Life-science research in microgravity**

Supported by SpacePharma S.A

Chair: Martin Aebi (SpacePharma S.A, Switzerland)

12:45 - 12:50   **Welcome - Introduction**

Martin Aebi (SpacePharma S.A, Switzerland)

12:50 - 13:00	**How microgravity affects chemical and biological processes**
	Guy Samburski (SpacePharma Ltd, Israel)
13:00 - 13:10	**What can research in space contribute to science on earth**
	Yair Glick (Spacepharma Inc, Israel)
13:10 - 13:25	**Discussion**

MipTec / Industry related session, Samarkand

12:45 - 13:45   **Industry Symposium: Label-free 3D Live Cell Imaging in Drug Discovery: Introducing the CX-A, saying good bye to phototoxicity and end point assays**

Supported by Nanolive

Nanolive provides high quality live cell images, label-free and in 3D, for these reasons this imaging technique is well suited for testing the effects of drugs on cell's morphological and sub-cellular organisation. To further support drug discovery applications we have developed our new automated system, the CX-A, which we are showing for the first time at MipTec / Basel Life. We will further report on recent imaging experiments where we perform a range of perturbations with various drugs in long-term time-lapse approaches. Demonstrating the practicality of the technology in a drug testing context. These experiments provide stunning video of cells evolving in a perturbed or unperturbed context. This process demonstrated that automatizing our technology should be a advantage for laboratories, both in time, cost, and the new unperturbed biological insight observed. Providing not only the possibility to evaluate drugs in prospective steps but to parallelise the process of drug effect evaluation with non-invasive, label-free power. We can now show that it is possible to use Nanolive Imaging technology for automatized drug effect evaluation in multi-well setup.

Chair: Hugo Moreno (Nanolive SA, Ecublens, Switzerland)
Chair: Alex Jones (Switzerland)

Scientific Programme

MipTec / Industry related session, Osaka

12:45 - 13:45	**Industry Symposium: Superresolution meets High Content Screening - IXplore spinSR and scanR AI**

Supported by OLYMPUS Schweiz

Research and clinical system solutions As a leading supplier of life science microscope systems for professional use, Olympus microscopy solutions are an integral part of scientific practice in the fields of biology and medicine and are extensively used in clinical, wet lab, research and education applications. From microscopes for training and routine tasks to high-end system solutions in the fields of life science, there is a system for every need. The product line is complemented by innovative laboratory equipment for cellular research applications and the new all-in-one microscopes that offer user engagement at all levels. Product lines •High-end Laser Scanning Microscopes •Screening Stations and Imaging Systems •Standard Research Microscopes •Imaging Software •Microscopy Cameras

Chair: Andrea Rackow (OLYMPUS, Germany)

12:45 - 13:25	**Superresolution meets high content screening - IXplore spinSR and scanR AI**
	Daniel Bemmerl (OLYMPUS SOFT IMAGING SOLUTIONS GmbH, Germany)
13:25 - 13:45	**Drug discovery: single cell injection and extraction - cytosurge**
	Pablo Doerig (Switzerland)

[BC]2 Session , Montreal

13:15 - 15:00	**[BC]2 Plenary session 4: Systems biology of disease**

Chair: Mihaela Zavolan (University of Basel & SIB, Basel, Switzerland)

13:15 - 14:00	**Cellular and clonal dynamics in humoral immunity**
	Thomas Kepler (Boston University School of Medicine, Boston, United States)
14:00 - 14:20	**An ab-initio derivation of the Drosophila gap gene system from an optimization principle**
	Gasper Tkacik (IST Austria, Klosterneuburg, Austria)
14:20 - 14:40	**Deciphering HLA-I motifs across HLA peptidomes improves epitope predictions and reveals novel properties of HLA-I molecules**
	David Gfeller (University of Lausanne, Lausanne, Switzerland)
14:40 - 15:00	**Automated inference of Boolean dynamics from molecular interaction maps. Application on rheumatoid arthritis**
	Anna Niarakis (UEVE, Univ Paris-Saclay, Paris, France)

Scientific Programme

	EMBO Session, Singapore
13:15 - 15:00	**EMBO Plenary session 4: Chronic inflammation: The common denominator of post-modern pathologies**
	Chair: Alberto Mantovani (Istituto Clinico Humanitas, Milan, Italy)
13:15 - 13:40	**Trained immunity: potential target in immune-mediated diseases**
	Mihai G. Netea (Radboud University Medical Center, Nijmegen, Netherlands)
13:40 - 13:50	**Neuronal regulation of innate lymphocytes**
	Henrique Veiga-Fernandes (Centro Champalimaud, Lisbon, Portugal)
13:50 - 14:15	**T cell metabolism in infection and cancer**
	Erika Pearce (Max Planck Institute for Immunobiology and Epigenetics, Freiburg, Germany)
14:15 - 14:35	**Molecular pathways linking innate immunity, inflammation and cancer**
	Alberto Mantovani (Istituto Clinico Humanitas, Milan, Italy)

	Innovation Forum, Sydney
14:00 - 15:00	**Aging and drug discovery and AI**
	In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.
	Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark) Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)
14:00 - 14:20	**Targeting of stem cell niche produced Notum increases repair of old tissue**
	Pekka Katajisto (University of Helsinki, Helsinki, Finland)
14:20 - 14:40	**Making aging biology part of drug development**
	Martin Borch Jensen (Gordian Biotechnology, San Francisco, United States)
14:40 - 15:00	**Panel discussion**

Scientific Programme

	Innovation Forum, Rio
14:00 - 15:00	**Peptide therapeutics**

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Chair: Thomas Vorherr (Novartis, Basel, Switzerland)
Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

14:00 - 14:30	**Synthetic disulfide-rich peptide manufacturing at Ambiopharm Inc.**
	Mike Pennington (AmbioPharm, North Augusta, SC, United States)

14:30 - 15:00	**A new green solvent for solid phase peptide synthesis**
	Jon Collins (CEM, Matthews, NC, United States)

	Innovation Forum, Samarkand
14:00 - 15:00	**Microfluidics and microenvironment**

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Chair: Helmut Knapp (CSEM, Alpnach, Switzerland)
Chair: Vincent Revol (CSEM, Switzerland)

14:00 - 14:20	**Microfluidic cell cultivation and analysis**
	Petra Dittrich (ETHZ Basel, Department of Biosystems Science and Engineering, Basel, Switzerland)

14:20 - 14:40	**3D Cell Culture for Discovery of Prostate Cancer Biomarkers for Liquid Biopsy Diagnostics**
	Chris Millan (CellSpring, Schlieren, Switzerland)

14:40 - 15:00	**Applying Multi-Organ-Chip technology in safety and efficacy testing: how far have we come?**
	Reyk Horland (TissUse, Berlin, Germany)

Scientific Programme

	Innovation Forum, Osaka
14:00 - 15:00	**Innovating in healthcare - global health data sharing**

Healthcare is facing an uncertain future. People are living longer, costs are rising and patients are demanding a different experience. The cost to discover new medicines is skyrocketing, and efficacy of these treatments is regularly being questions by reimbursement authorities. The future of healthcare is focusing on Precision Medicine to decrease costs and increase efficacy. Precision medicine utilizes the patient's health data to define a personalized signature for individualized treatment. But what the field lacks to move forward significantly is access to sufficient data to elucidate signatures of states of human health. The ability to exchange genome and other health data can have multiple benefits to advance healthcare. Stakeholders in the healthcare ecosystem, like academics, pharmaceutical corporations, insurers, and governments, can get population molecular data to develop health care programs (new drugs, reimbursement models, national programs). Patients can get preventative healthcare based on diagnosis of biomarkers that might predispose them to disease. New business models can be developed based on needs of rare diseases communities, for example. Leading to overall better health, lower costs, increased productivity and longevity.

Chair: Bhupinder Bhullar (Swiss Vault, Basel, Switzerland)
Chair: Thomas Brenzikofer (DayOne Initiative BaselArea, Basel, Switzerland)

14:00 - 14:10	**Lyfegen. The next generation of data and value driven healthcare**
	Nico Mros (Lyfegen HealthTech AG, Switzerland)
14:10 - 14:20	**GeneLook a mobile application to manage your DNA form the palm of your hand**
	Daniel Gutierrez (Genelook, Basel, Switzerland)
14:20 - 14:30	**The Healthbank Model**
	Reto Schegg (Healthbank, Luzern, Switzerland)
14:30 - 14:40	**Panel Discussion**
	Nico Mros (Lyfegen HealthTech AG, Switzerland) Daniel Gutierrez (Genelook, Basel, Switzerland) Reto Schegg (Healthbank, Luzern, Switzerland) Enkelejda Miho (FHNW, Muttenz, Switzerland)

	[BC]2 Session , Montreal
15:30 - 17:15	**[BC]2 Plenary session 5: Multi-level data integration**
	Chair: Karsten Borgwardt (ETH Zurich & SIB, Zurich, Switzerland) Chair: Julia Vogt (University of Basel & SIB, Basel, Switzerland)
15:30 - 16:15	**Bayesian matrix factorization and deep learning data fusion for drug-target interaction prediction.**
	Yves Moreau (KU Leuven, Leuven, Belgium)
16:15 - 16:35	**The molecular basis and genetic control of local gene co-expression**
	Diogo M. Ribeiro (University of Lausanne, Lausanne, Switzerland)

| 16:35 - 16:55 | **Automated analysis of large-scale NMR data generates metabolomic signatures and links them to candidate metabolites** |
| | Bita Khalili (UNIL, Lausanne, Switzerland) |

| 16:55 - 17:15 | **Exploring neXtProt data and beyond: a SPARQLing solution** |
| | Monique Zahn (SIB Swiss Institute of Bioinformatics, Geneva, Switzerland) |

EMBO Session, Singapore

| **15:30 - 17:15** | **EMBO Plenary session 5: Regenerative medicine** |
| | Chair: Alain Fischer (Institut Imagine, Paris, France) |

| 15:30 - 15:55 | **Mendelian genetics of autoimmunity** |
| | Alain Fischer (Institut Imagine, Paris, France) |

| 15:55 - 16:20 | **Human type I interferonopathies** |
| | Yanick J. Crow (MRC Institute of Genetics & Molecular Medicine, Edinburgh, United Kingdom) |

| 16:20 - 16:45 | **Cellular heterogeneity in cardiovascular repair and aging** |
| | Stefanie Dimmeler (Centre for Molecular Medicine, Frankfurt , Germany) |

| 16:45 - 17:10 | **Epigenetic regulation in development, aging and disease** |
| | Rudolf Jaenisch (Whitehead Institute for Biomedical Research and Department of Biology, MIT, Cambridge MA, United States) |

Innovation Forum, Rio

15:30 - 17:00	**Peptide therapeutics**
	The framework of the BASEL LIFE, we will host the "Peptide Therapeutics Forum 2019" for 2 days on September 10, and 11. Similar to previous events, presentations highlight important new insights regarding the drug discovery of peptides including examples for successful development. The first day is dedicated to topics to be addressed more early during peptide optimization, and the second day focuses more on issues related to later-stage development. As in the past, this event is thought to disseminate information on latest news in the broad field of therapeutic peptides and to enable networking of interested parties from academia and industries.
	Chair: Thomas Vorherr (Novartis, Basel, Switzerland) Chair: Roderich Süssmuth (Technical University Berlin, Berlin, Germany)

| 15:30 - 16:00 | **Synthetic immune system engagers target cancer cells and prevent tumor formation** |
| | Christian Becker (University of Vienna, Vienna, Austria) |

| 16:00 - 16:30 | **Discovery and clinical development of an inhaled cyclic peptide elastase inhibitor for the treatment of cystic fibrosis** |
| | Marc Thommen (Santhera Pharmaceuticals (Switzerland) Ltd, Pratteln, Switzerland) |

| 16:30 - 17:00 | **Peptide solubility and synthesis** |
| | John Offer (The Francis Crick Institute, London, United Kingdom) |

Innovation Forum, Samarkand

| 15:30 - 16:30 | **Microfluidics and microenvironment** |

CSEM, the Molecular Evolution Lab of the University of Basel, and the cluster Toolpoint for Lab Science join forces to organize the 2nd Basel Microfluidics and Microenvironment Forum at BASEL LIFE. As in the previous year, the forum will focus on the preparation of microphysiological systems in a microenvironment for boosting the relevance of in-vitro assays towards in-vivo outcome. This includes developments related to organ or model organism on a chip, droplet microfluidics or bioprinting. Newest technological developments and critical insights from the end users will come together at this forum. The forum brings together scientists, entrepreneurs and managers in these fields, from both industry and academia, to exchange ideas and to promote innovation applicable to bio-pharmaceutical development.

Chair: Marc Creus (University of Basel, Basel, Switzerland)
Chair: Helmut Knapp (CSEM, Alpnach, Switzerland)
Chair: Vincent Revol (CSEM, Switzerland)

| 15:30 - 15:55 | **Applications of renal and cardiovascular models in drug discovery** |
| | Stefan Platz (AstraZeneca, United Kingdom) |

| 15:55 - 16:20 | **Case studies for the characterisation of chemical metabolism in a microphysiological system combining skin and liver organ models** |
| | Jochen Kühnl (Beiersdorf AG, Hamburg, Germany) |

Innovation Forum, Osaka

| 15:30 - 16:30 | **Innovating in healthcare - global health data sharing** |

Healthcare is facing an uncertain future. People are living longer, costs are rising and patients are demanding a different experience. The cost to discover new medicines is skyrocketing, and efficacy of these treatments is regularly being questions by reimbursement authorities. The future of healthcare is focusing on Precision Medicine to decrease costs and increase efficacy. Precision medicine utilizes the patient's health data to define a personalized signature for individualized treatment. But what the field lacks to move forward significantly is access to sufficient data to elucidate signatures of states of human health. The ability to exchange genome and other health data can have multiple benefits to advance healthcare. Stakeholders in the healthcare ecosystem, like academics, pharmaceutical corporations, insurers, and governments, can get population molecular data to develop health care programs (new drugs, reimbursement models, national programs). Patients can get preventative healthcare based on diagnosis of biomarkers that might predispose them to disease. New business models can be developed based on needs of rare diseases communities, for example. Leading to overall better health, lower costs, increased productivity and longevity.

Chair: Bhupinder Bhullar (Swiss Vault, Basel, Switzerland)
Chair: Thomas Brenzikofer (DayOne Initiative BaselArea, Basel, Switzerland)

15:30 - 15:40		**Innovating in healthcare - global health data sharing - patient perspective**
		Philipp do Canto (Public Sector Law, Zurich, Switzerland)
15:40 - 15:50		**Health Insurer perspective**
		Nicolas Loeillot (Groupe Mutuel, Martigny, Switzerland)
15:50 - 16:00		**Pharma perspective**
		Miro Venturi (F. Hoffman la Roche, Basel, Switzerland)
16:00 - 16:10		**Panel Discussion**
		Philipp do Canto (Public Sector Law, Zurich, Switzerland)
		Nicolas Loeillot (Groupe Mutuel, Martigny, Switzerland)
		Miro Venturi (F. Hoffman la Roche, Basel, Switzerland)
		Tim Hubbard (Genomics England, London, United Kingdom)

Innovation Forum, San Francisco

16:45 - 17:45 **Innovation Forums Poster session**

Advances in 3R

P139 **Identification of novel microbial P450s as drug-metabolizing enzymes**
Lisa Marie Schmitz (TU Dortmund University, Dortmund, Germany)

P140 **Nrf2/KEAP1 reporter human 3D epidermal model**
Bruno Guy Henri Filippi (ZHAW, Waedenswil, Switzerland)

Aging,drug discovery & Artificial Intelligence

P141 **In-silico protein-wide models predicts effect of Metformin in murine liver cells**
Simone Rizzetto (Cytocast Ltd., Vecsés, Hungary)

P142 **Lamin A/C promotes DNA base excision repair**
Scott Maynard (Danish Cancer Society Research Center, Copenhagen, Denmark)

P143 **Nsun5 in ribosome function and mammalian healthy lifespan**
Lisa Liendl (University of Natural Resources and Life Sciences, Vienna, Vienna, Austria)

P144 **Discovery of MYST1 small-molecule inhibitors as epigenetic tools of gene regulation**
Anastasiia Gryniukova (Bienta/Enamine Ltd., Kyiv, Ukraine)

P145 **Development of a RORγ-CoAP interaction assay based on TR-FRET suitable for HTS**
Huiping Huang (Axxam S.p.A., Bresso, Italy)

P146 **XFEL-based serial femtosecond crystallography in drug discovery**
Alexey Mishin (Research center for molecular mechanisms of aging and age-related diseases, Moscow Institute of Physics and Technology, Dolgoprudny, Russian Federation)

P147	**From a new premature aging disorder towards aging mechanisms**
	Daniela Bakula (University of Copenhagen, Copenhagen, Denmark)

P149	**Leveraging NAD+ signalling as a treatment pathway for age-related metabolic dysfunction**
	Brenna Osborne (University of Copenhagen, Copenhagen N, Denmark)

P150	**Targeting aging with deep learned drugs**
	Garik Mkrtchyan (University of Copenhagen, Copenhagen, Denmark)

P151	**The Dlk1-Dio3 miRNA cluster plays a crucial role in skeletal muscle aging by targeting Smad4**
	KI-SUN Kwon (KRIBB Aging Research Center, Daejeon, Korea, Republic of)

P152	**Text mining pathology reports and machine learning for aging knowledge discovery**
	Michael Ben Ezra (University of Copenhagen, Copenhagen, Denmark)

P153	**An effort to build an in vitro high-throughput screening for seizure liability based on calcium oscillation of human iPS-derived dopaminergic neurons with astrocyte**
	Sunao Hisada (Hamamatsu Photonics, Hamamatsu City, Japan)

P154	**Engineer the DNA damage that drives senescence**
	Guido Keijzers (University of Copenhagen, Copenhagen, Denmark)

P155	**Recombinant expression and assay development for Ghrelin O-acyltransferase (GOAT) to support a hit discovery program based on high-throughput screening**
	Huiping Huang (Axxam S.p.A., Bresso, Italy)

P156	**Neuropathological changes in the PDAPP transgenic mouse model of Alzheimer disease**
	Hamed Omidi (Azad university of Tehran/Olom Tahghyghat, Tehran, Iran, Islamic Republic of)

P157	**A chemical language based approach for the prediction of protein - ligand binding affinity**
	Elif Ozkirimli (Bogaziçi University, Istanbul, Turkey)

P158	**CNOT6 affects genome stability by regulating mismatch repair**
	Peng Song (University of Copenhagen, Copenhagen, Denmark)

P159	**Pharmacokinetic parameters may vary in different mice strains after a single dose of drugs**
	Yuliia Holota (Bienta/Enamine Ltd., Kyiv, Ukraine)

P160	**Deciphering the interplay between hypoxia and DNA metabolism in aging**
	Amanuel Teklu (University of Copenhagen, Copenhagen, Denmark)

P161	**Ketogenic diet to delay brain aging in Cockayne syndrome**
	Tulika Tulika (University of Copenhagen, Copenhagen, Denmark)

P162	**Glycation extent of hemoglobin (HbA1c) might reflect biological age**
	Urs Nydegger (University of Bern, Liebefeld, Switzerland)

P163   **Deep learning of histopathology to understand age-related disease**
Indra Heckenbach (University of Copenhagen, Copenhagen, Denmark)

P164   **Modelling the collective migration of neural crest cells with multi-agent reinforcement learning**
Koki Shimada (University College London, London, United Kingdom)

Antibiotic resistance

P165   **Investigating treatment response of patients with confirmed drug-resistant tuberculosis in an HIV-1-endemic population in Western Kenya**
Clement Shiluli (Maseno University, Kisumu, Kenya)

P166   **The impact of Fluoroquinolone-resistance mutations on the rates of further drug-resistance acquisition in Mycobacterium tuberculosis**
Rhastin A. D. Castro (Swiss Tropical and Public Health Institute, Basel, Switzerland)

Biotherapeutics

P167   **Flow induced dispersion analysis (FIDA) for size-based characterization of proteins and protein interactions under native conditions**
Morten E. Pedersen (FIDA-tech aps, Copenhagen, Denmark)

P168   **A novel tool for the treatment of peripheral demyelinating neuropathies**
Anna Henzi (University of Zurich, Zurich, Switzerland)

P169   **Rational design of neuroprotective antibodies against the prion protein by phage display**
Assunta Senatore (University of Zuich, Zurich, Switzerland)

P170   **The smart DNA-based biosensor as a new method for mRNA in vitro detection**
Ekaterina A Bryushkova (Shemyakin and Ovchinnikov Institute, Moscow, Russian Federation)

Cellular allergy

Genome editing (CRISPR/Cas9) in drug discovery

P172   **Construction of a multiplexed CRISPRi knockdown library in mycobacteria**
Kristin Winkler (SAMRC/NHLS/UCT Molecular Mycobacteriology Research Unit, DST/NRF Centre of Excellence for Biomedical TB Research, Division of Medical Microbiology, Department of Pathology, University of Cape Town, Cape Town, South Africa)

Microfluidics and microenvironment

P173   **Use of a human urothelial organoid model for pre-clinical validation of novel ultrasound-activated microbubbles in the treatment of chronic urinary tract infection**
Harry Horsley (University College London, London, United Kingdom)

Peptide therapeutics

P174   **High throughput discovery of novel peptides with biological function**
Francesca Billwiller (Orbit Discovery Ltd, Oxford, United Kingdom)

P175	**First report of novel unimolecular amylin-adrenomedullin dual agonists**	
	Lisbeth Elster (Gubra, Hørsholm, Denmark)	

P176	**Negative-regulation of gastric proton pump by N-terminal polypeptide of Sonic Hedgehog**	
	Takuto Fujii (University of Toyama, Toyama, Japan)	

P177	**Total synthesis of Cochinmicin I and its role as potent cyclodepsipeptide endothelin antagonist**	
	Romina Schnegotzki (TU Berlin, Berlin, Germany)	

P178	**Towards the development of inhibitors targeting CtIP function in DNA repair**	
	Nour Lydia Mozaffari (University of Zurich, Zurich, Switzerland)	

[BC]2 Session , Montreal

17:15 - 17:30   **[BC]2 Closing remarks**

Scientific Programme

Thursday, 12 September 2019

	Joint Session, Montreal
09:00 - 10:15	**Plenary session 6 (Joint with [BC]2) Computational biology, artificial intelligence and machine learning in precision medicine**
	Chair: Jan O. Korbel (Genome Biology Unit EMBL, Heidelberg, Germany)
09:00 - 09:25	**Machine learning approaches for elucidating complex gene-environment interactions**
	Oliver Stegle (European Bioinformatics Institute, Hinxton, United Kingdom)
09:25 - 09:50	**Understanding chronic blood diseases using millions of electronic health records and single cell genomics**
	Amos Tanay (The Weizmann Institute of Science, Rehovot, Israel)
09:50 - 10:15	**Pinpointing disease-causing regulatory genetic variants by multi-omics and machine learning**
	Julien Gagneur (Fakultät für Informatik Technische Universität München, Garching bei München, Germany)

Innovation Forum, Rio

09:00 - 10:15   **Cellular allergy - Novel strategies for allergy treatment and monitoring**

Allergic reactions are common phenomena during which the immune system overreacts to typically harmless substances from the environment. These hypersensitivities are mostly mediated by IgE antibodies that recognize the allergen and then trigger a cellular reaction that may lead to a severe and possibly lethal anaphylactic shock. This innovation forum at BASEL LIFE 2019 on cellular allergy shall be a platform to present cutting-edge research on cellular allergy and its implication in immunotherapy together with novel in vitro approaches in allergy diagnostics and therapy monitoring. The transition from in vivo oral food challenges or skin-prick tests to in vitro assays based on basophil activation as well as expected FDA clearances of oral immunotherapies are current game changers in allergy diagnostics and treatment. Additionally, the role of IgE directed immunotherapy (Omalizumab, Xolair®) as stand-alone and synergistic treatment will be discussed. Concomitant monitoring of therapy success with ex vivo challenges is expected to alleviate the burden on allergy patients significantly. Deciphering the complex interplay of the allergen and immune cell signalling and hence the understanding of allergy on a cellular and molecular level will shape allergy treatment and diagnosis in the near future. A specific allergic reaction can be mimicked in a test tube by provoking patient-derived basophil cells ex vivo with the appropriate allergens that trigger a PI3 like kinase signalling cascade in these blood cells. This allows its application beyond allergy monitoring as for instance various Bruton's kinase inhibitors, such as Ibrutinib (IMBRUVICA®), which are used to treat various lymphoma and leukemia, could also be applied for therapy of allergy. Therefore, the innovation forum also aims to present novel discoveries in cellular allergy signalling and their exploitation beyond allergy treatment.

Chair: Michael A. Gerspach (BÜHLMANN Laboratories AG, Schönenbuch, Switzerland)
Chair: Christian B. Gerhold (BÜHLMANN Laboratories AG, Schönenbuch, Switzerland)

09:00 - 09:15   **Introduction**

09:15 - 09:45   **Cellular allergy and novel therapy approaches**
Alexander Eggel (Bern, Switzerland)

09:45 - 10:15   **Recent breakthroughs in immunotherapy of allergy**
Wayne Shreffler (Massachusetts General Hospital, Boston, United States)

Innovation Forum, Samarkand

09:00 - 10:30   **Genome editing (CRISPR/Cas9) in drug discovery**

Genome editing technologies allow engineering parts of the genome by removing, adding or altering sections of the DNA Sequence. Recent discovery of the CRISPR/Cas9 system as a technology for genome editing, enables the simplest, quickest and most versatile way of genome editing. CRISPR/Cas9 technology is quickly developing and has already found many applications as a drug discovery tool and even as a potential new therapeutic agent in cellular and gene therapy. This forum focuses on relevant applications of CRISPR/Cas9 for drug discovery such as identification of novel targets through genetic screens, generation of relevant genetic disease models (human cells or animal models) for validation of drug targets and for mechanistic and safety studies. Importantly, current standard practices and perspectives of genome editing in drug discovery will be presented. Furthermore, the forum will show novel applications and discuss future challenges and potential pitfalls of the technology.

Chair: Claas Aiko Meyer (Roche, Basel, Switzerland)
Chair: Filip Roudnicky (Roche, Basel, Switzerland)

09:00 - 09:05   **Indroduction**

Filip Roudnicky (Roche, Basel, Switzerland)
Claas Aiko Meyer (Roche, Basel, Switzerland)

09:05 - 09:35   **Mechanisms of genome editing in human cells**

Jacob Corn (Swiss Federal Institute of Technology, Zürich, Switzerland)

09:35 - 10:05   **Enhancing genome editing with engineered CRISPR Nucleases**

Benjamin Kleinstiver (Harvard University, Boston, United States)

10:05 - 10:30   **Capabilities and caveats of CRISPR-mediated drug modifier screens**

Traver Hart (University of Texas MD Anderson, Houston, United States)

Poster , San Francisco

10:15 - 16:45   **Poster exhibition**

EMBO Session, Montreal

10:45 - 12:30   **EMBO Plenary session 7 - Genetic diseases: genome and epigenome**

Chair: Kristian Helin (Cell Biology Program and Center for Epigenetics Research, Memorial Sloan Kettering Cancer Center (MSKCC), New York, United States)

10:45 - 11:10   **Unraveling the acute stress response in bony vertebrates**

Gérard Karsenty (Columbia University Medical Center, New York, United States)

11:10 - 11:35   **Combined cell and gene therapy for epidermolysis bullosa**

Michele De Luca (Center for Regenerative Medicine, Università degli Studi di Modena e Reggio Emilia, Modena, Italy)

11:35 - 12:00	**Why are diseases tissue-specific? Lessons from mitochondrial diseases**
	Anu Suomalainen (Biomedicum-Helsinki, Stem Cells and Metabolism Research Program, University of Helsinki, Helsinki, Finland)
12:00 - 12:25	**Epigenetics in transcriptional control, development and cancer**
	Kristian Helin (Cell Biology Program and Center for Epigenetics Research, Memorial Sloan Kettering Cancer Center (MSKCC), New York, United States)

Innovation Forum, Sydney

10:45 - 11:45   **Aging and drug discovery and AI**

In this symposium, leaders in the aging, longevity, and drug discovery field will describe the latest progress in the molecular, cellular and organismal basis of aging and the search for interventions. Furthermore, the forum will include opinion leaders in AI to discuss the latest advances of this technology in the biopharmaceutical sector and how this can be applied to interventions. This event intends to bridge academic and commercial research and foster collaborations that will result in practical solutions to one of humanity's most challenging problems: aging. A panel of thought-leaders will give us their cutting edge reports on the latest progress in our quest to extend the healthy lifespan of everyone on the planet. Please join us in this merger of driven scientists and global visionaries in an event that may shape the field in years to come.

Chair: Alex Zhavoronkov (InSilico Medicine, Baltimore, United States)
Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)

10:45 - 11:05	**Deep learning in drug discovery for aging research**
	Quentin Vanhaelen (Insilico Medicine, Hong Kong, China)
11:05 - 11:25	**Combining robotics and AI to produce next generation research data**
	Martin-Immanuel Bittner (Arctoris, Oxford, United Kingdom)
11:25 - 11:45	**Molecule: A novel approach to funding research and development through distributed IP ownership**
	Tyler Golato (Molecule.to, Wildwood, United States)

Innovation Forum, Rio

10:45 - 11:45   **Cellular allergy - Novel strategies for allergy treatment and monitoring**

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10:45 - 11:15   **Molecular and functional differences of anti-IgE antibodies ligelizumab and omalizumab**

Christoph Heusser (NIBR, Basel, Switzerland)

11:15 - 11:45   **Novel approaches for food allergy diagnosis and monitoring of allergen immunotherapy**

Alexandra Santos (King's College, London, United Kingdom)

Scientific Programme

Innovation Forum, Samarkand

10:45 - 11:45   **Genome editing (CRISPR/Cas9) in drug discovery**

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Chair: Claas Aiko Meyer (Roche, Basel, Switzerland)
Chair: Filip Roudnicky (Roche, Basel, Switzerland)

10:45 - 11:15   **Leveraging CRISPR screening for new target discovery**
Scott Martin (Genentech Inc, San Francisco, United States)

11:15 - 11:45   **A fexible, rapid and demand driven CRISPR screening and validation**
Glynn Martin (Horizon Discovery, Cambridge, United Kingdom)

Innovation Forum, Sydney

12:00 - 13:00   **Aging and drug discovery and AI**

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Chair: Morten Scheibye-Knudsen (Center for Healthy Aging, University of Copenhagen, Copenhagen, Denmark)

12:00 - 12:20   **Passing the baton from academia to industry: therapies for thymus regeneration and atherosclerosis reversal**
Reason . (Repair Biotechnologies, Inc., Syracuse, United States)

12:20 - 12:40   **Ketogenic diet to delay brain aging in Cockayne syndrome**
Michael A. Petr (University of Copenhagen, Copenhagen, Denmark)

12:40 - 13:00   **'Retrobiome' as a driver of intrinsic DNA damage in aging**
Andrei Gudkov (Roswell Park Cancer Institute, Buffalo, United States)

Innovation Forum, Rio

12:00 - 13:00   **Cellular allergy - Cellular signalling in allergy and beyond**

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12:00 - 12:10   **How allergens become allergic - the role of the alarmin cytokine IL-33 in allergen sensing**

Jean-Phillipe Girard (Institut de Pharmacologie et de Biologie Structurale (IPBS), Toulouse, France)

12:10 - 12:40   **Orchestrating signalling in allergic inflammation**

Matthias Wymann (University of Basel, Basel, Switzerland)

Scientific Programme

Innovation Forum, Samarkand

12:00 - 13:00 **Genome editing (CRISPR/Cas9) in drug discovery**

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12:00 - 12:20 **Single and combinatorial CRISPR gene perturbations with 3Cs gRNAs**

Manuel Kaulich (Goethe University, Frankfurt, Germany)

12:20 - 12:40 **CRISPR single-cell sequencing: toward functional biology in high throughput**

Christoph Bock (Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria)

12:40 - 13:00 **Genome engineering in T cells**

Lukas Jeker (Univeristy of Basel, Basel, Switzerland)

MipTec / Industry related session, Sydney

13:15 - 14:15   **Industry Symposium: Open Science and/or Compliance – What Future do you Want for Computational Biology?**

Supported by ScienceIndustries Supported by Interpharma Supported by Swiss Biotech Association

The Nagoya Protocol is a supplementary agreement to the Convention on Biological Diversity (CBD), and entered into force in 2014. The Nagoya Protocol is supposed to provide a transparent legal framework for the fair sharing of benefits arising out of the utilization of biological resources, thereby contributing to the conservation and sustainable use of biodiversity. It imposes obligations on all users of biological resources (both academic and industrial) to secure that access to biological resources and benefit sharing are done in full compliance with all applicable Access and Benefit Sharing (ABS) laws. In the international negotiations around the CBD and the Nagoya Protocol, it is currently hotly debated whether also published information on biological resources (subsumed under the term "Digital Sequence Information") should be formally included in the scope of the ABS obligations. This would have far-reaching consequences for research and innovation, and in particular for computational biology. The ambitions of this symposium are: - To present the current "state of affairs", re. the opportunities and risks of the Nagoya Protocol in general, and of the inclusion of "Digital Sequence Information" in the formal scope of ABS obligations - To provide both an academic and an industrial perspective on the potential implications for research and innovation - To trigger interest and engagement in the international debates on the future scope of ABS obligations Speakers: Markus Wyss (DSM) Christin Peters (ZHAW Wädenswil, Group leader Biosystems Technology, Institute of Chemistry and Biotechnology & School of Life Sciences and Facility Management) Within two short presentations, the speakers will provide an academic (Christin Peters) and an industrial (Markus Wyss) perspective on the opportunities and risks of the Nagoya Protocol for life science R&D and innovation with a main focus on Digital Sequence Information. The presentations are followed by an open discussion with the audience.

Chair: Jan Lucht (Switzerland)
Chair: Markus Wyss (Switzerland)
Chair: Christin Peters (ZHAW Wädenswil, Group leader Biosystems Technology, Institute of Chemistry and Biotechnology & School of Life Sciences and Facility Management, Switzerland)

MipTec / Industry related session, Samarkand

13:15 - 14:15   **Industry symposium: Genome Editing**

Supported by Cellecta

EMBO Session, Montreal

13:45 - 15:30   **EMBO Plenary session 8: Tissue regeneration, organoids without borders**

Chair: Sabine Werner (ETH Zurich, Zurich, Switzerland)

13:45 - 14:10	**Fibroblast growth factor: key regulators of epithelial repair and cytoprotection** Sabine Werner (ETH Zurich, Zurich, Switzerland)
14:10 - 14:35	**Self-organization and symmetry breaking in intestinal organoid development** Prisca Liberali (Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland)
14:35 - 15:00	**Single cell analysis of stem cells during development, homeostasis and repair** Cédric Blanpain (Université Libre de Bruxelles, Brussels, Belgium)
15:00 - 15:25	**Building cancer in organoids** Marc van de Wetering (Netherlands)

Innovation Forum, Sydney

14:30 - 15:30   Aging and drug discovery and AI

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14:30 - 14:50	**Study of skin and face features age progression with computer vision methods** Anastasia Georgievskaya (Haut.Ai, Tallinn, Estonia)
14:50 - 15:00	**Conquering Aging: AI Opportunity for the Pharmaceutical Industry** Unmesh Lal (Frost&Sullivan, Germany)
15:00 - 15:30	**Longevity VC panel** Unmesh Lal (Frost&Sullivan, Germany) Cecile Cai (36KR, United States) Michael Antonov (Oculus, San Francisco, United States) Dmitry Kaminsky (Deep Knowledge Ventures, London, United Kingdom) Patrick Burgermeister (Kizoo Technology Capital, Karlsruhe, Germany) Angela Tyrrell (Longevity Leaders, London, United Kingdom)

Innovation Forum, Rio

14:30 - 15:30 **Cellular allergy - Cellular signalling in allergy and beyond**

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14:30 - 15:00 **Application of PI3K-delta inhibitors in allergic asthma**
Augustin Amour (GSK, Stevenage, United Kingdom)

15:00 - 15:30 **Use of BTK inhibitors to prevent cellular and clinical allergic responses**
Bruce Bochner (Northwestern Medicine, Chicago, United States)

Innovation Forum, Samarkand

14:30 - 15:50   **Genome editing (CRISPR/Cas9) in drug discovery**

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14:30 - 14:50   **In vivo genome editing: from disease modeling to screening**

Danilo Maddalo (Novartis Institutes for BioMedical Research Basel, Basel, Switzerland)

14:50 - 15:20   **Novel automation platforms for generating synthetic sgRNA and CRISPR-engineered cells at scale**

Kevin Holden (Synthego Corporation, United States)

15:20 - 15:50   **Quantitative Live-Cellular Assays for Screening Degradation Compounds and their Mechanism of Action**

Richard Somberg (Promega Corporation, Madison, United States)

Joint Session, Montreal

16:00 - 16:45   **Joint Keynote lecture**

Chair: Susan M. Gasser (Friedrich Miescher Institute, Basel, Switzerland)

16:00 - 16:45   **Reimagining medicine: The power of data science and digital technologies**

Vasant Narasimhan (Novartis, Basel, Switzerland)

Joint Session, Montreal

16:45 - 17:00   **Closing address**

Chair: Susan M. Gasser (Friedrich Miescher Institute, Basel, Switzerland)