

SUNDAY, 18 September	
08:15 - 08:30	Registration desk open all day from 08:15h
18:00 - 18:30	Conference opening (18:00h) Speakers: Alfonso Valencia and Niklas Blomberg
18:30 - 19:00	Conference opening Keynote talk César Hidalgo (University of Toulouse, France) How humans judge machines Chair: Alfonso Valencia
19:00 - 19:30	
19:30 - 20:00	
20:00 - 20:30	
20:30 - 21:00	Welcome cocktail
21:00 - 21:30	
21:30 - 22:00	
22:00 - 22:30	

MONDAY, 19 September			
08:00 - 08:30 Registration desk open all day			
08:30 - 09:00 Welcome and announcements (08:45h)			
09:00 - 09:30 Keynote talk Raúl Rabadán (Columbia University, USA) Some mysteries about microbes and cancer Chair: Niklas Blomberg			
09:30 - 10:00			
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	ELIXIR (Session #01) Chair: Katharina Heil	GENOMES (Session #02) Chair: Toni Gabaldón	SYSTEMS (Session #03) Chair: Patrick Aloy
10:00 - 11:00	<p>ELIXIR talk Identifying resources and exploring synergies between the ELIXIR 3D-Bioinfo, proteomics and IDP communities • Authors: Emmanuel Levy, Christine Orengo, Nathalie Reuter, Sameer Velankar, Shoshana Wodak, Norman Davey, Zsuzsa Dosztanyi, Damiano Piovesan, Silvio Tosatto, Eva Csoz, Julien Marcoux, Lennart Martens, Pathmanaban Ramasamy, Juan Antonio Vizcaino, Massimiliano Bonomi, <u>Wim Vranken</u></p> <p>ELIXIR talk Using the IDP-KG to enable IDPcentral information on submission • Authors: Alasdair Gray, Ivan Mičetić, <u>Alexander Monzon</u> and Damiano Piovesan</p> <p>ELIXIR talk AHOJ: rapid, tailored search and retrieval of apo and holo protein structures • Authors: <u>Christos P. Feidakis</u>, Radoslav Krivak, David Hoksza and Marian Novotny</p>	<p>Proceeding talk SALAI-Net: Species-Agnostic Local Ancestry Inference Network • Authors: <u>Benet Oriol Sabat</u>, Daniel Mas Montserrat, Xavier Giro-i-Nieto and Alexander Ioannidis</p> <p>Proceeding talk Improving Bacterial Genome Assembly Using a Test of Strand Orientation • Authors: <u>Grant Greenberg</u> and Ilan Shomorony</p> <p>Highlight talk plots: Visualising structural similarities and rearrangements between multiple genomes • Authors: <u>Manish Goel</u> and Korbinian Schneeberger</p>	<p>Proceeding talk MERRIN: METabolic Regulation Rule INference from time series data • Authors: <u>Kerian Thuillier</u>, Caroline Baroukh, Alexander Bockmayr, Ludovic Cottret, Loïc Paulevé and Anne Siegel</p> <p>Proceeding talk Small compound-based direct cell conversion with combinatorial optimization of pathway regulations • Authors: Toru Nakamura, <u>Michio Iwata</u>, Momoko Hamano, Ryohei Eguchi, Jun-Ichi Takeshita and Yoshihiro Yamanishi</p> <p>Proceeding talk Design centering enables robustness screening of pattern formation models • Authors: <u>Anastasia Solomatina</u>, Alice Cezanne, Yannis Kalaidzidis, Marino Zerial and Ivo F. Sbalzarini</p>
11:00 - 11:30 Coffee break and Exhibition			
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	ELIXIR (Session #04) Chair: Katharina Heil	DATA (Session #05) Chair: Peter Maccallaum	PROTEINS (Session #06) Chair: Mark Wass
11:30 - 12:30	<p>ELIXIR talk Open source genome-scale metabolic models: why and how • Authors: <u>Mihail Anton</u>, Barbara Szomolay and Vitor A P Martins dos Santos</p> <p>ELIXIR talk Genome-wide metabolic annotation for Methanocaldococcus (Methanococcus) jannaschii, the first member of the Archaea to be sequenced a quarter of a century ago • Authors: <u>Ismini Baltasavia</u>, George Stamoulos, Konstantinos Tziavara, Alexandros Dermaris, Ioannis Iliopoulos, Ron Caspi, Peter D. Karp, Nikos C. Kyrpides, Christos A. Ouzounis</p> <p>ELIXIR talk Rare disease specific FAIR Maturity Indicators • Authors: <u>Núria Queralt Rosinach</u>, Rajaram Kaliyaperumal, Annika Jacobsen, Mark Wilkinson, Marc Hanauer, Marco Roos</p>	<p>Proceeding talk Linking cells across single-cell modalities by synergistic matching of neighborhood structure • Authors: <u>Borislav Hristov</u>, Jeffrey Bilmes and William Noble</p> <p>Highlight talk Marker-based annotation and integration of large scale single-cell transcriptomics data on a laptop • Authors: <u>Sikander Hayat</u>, Yang Xu, Simon Baumgart, Christian Stegmann, Rafael Kramann and Rachel Patton McCord</p> <p>Highlight talk Polymact: exploring functional relations among common human genetic variants • Authors: <u>Samuel Valentini</u>, Francesco Gandolfi, Mattia Carolo, Davide Dalfovo, Lara Pozza and Alessandro Romanel</p>	<p>Highlight talk TITAN: T-cell receptor specificity prediction with bimodal attention networks • Authors: <u>Anna Weber</u>, Jannis Born and Maria Rodriguez Martinez</p> <p>Highlight talk Online predictions for protein biophysical features and their conservation • Authors: <u>Wim Vranken</u>, Luciano Kagami and Adrian Diaz</p> <p>Proceeding talk Group-walk, a rigorous approach to group-wise false discovery rate analysis by target-decoy competition • Authors: <u>Jack Freestone</u>, Temana Short, William Stafford Noble and Uri Keich</p>
12:30 - 13:00 Lunch, Exhibition and Poster viewing			
13:00 - 13:30 Lunch, Exhibition and Poster viewing			
13:30 - 14:00 Lunch, Exhibition and Poster viewing			
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	SYSTEMS (Session #07) Chair: Patrick Aloy	GENES (Session #08) Chair: Artemis Hatzigeorgiou	APPLICATIONS (Session #09) Chair: Javier De Las Rivas

14:00 - 15:00	<p>Proceeding talk PILSL: pairwise interaction learning-based graph neural network for synthetic lethality prediction in human cancers Authors: Xin Liu, Jiale Yu, Siyu Tao, Beiyuan Yang, Shike Wang, Lin Wang, Fang Bai and Jie Zheng</p> <p>Highlight talk Interpretable systems biomarkers predict response to immune-checkpoint inhibitors Authors: Óscar Lapuente-Santana, Maisa van Genderen, Peter Hilbers, Francesca Finotello and Federica Eduati</p> <p>Highlight talk Comprehensive prediction of robust synthetic lethality between paralog pairs in cancer cell lines Authors: Barbara De Kegel, Niall Quinn, Nicola Thompson, David Adams and Colm Ryan</p>	<p>Proceeding talk NSF4SL: negative-sample-free contrastive learning for ranking synthetic lethal partner genes in human cancers Authors: Shike Wang, Yimiao Feng, Xin Liu, Yong Liu, Min Wu and Jie Zheng</p> <p>Proceeding talk Efficient Permutation-based Genome-wide Association Studies for Normal and Skewed Phenotypic Distributions Authors: Maura John, Markus Ankenbrand, Carolin Artmann, Jan Freudenthal, Arthur Korte and Dominik Grimm</p> <p>Highlight talk Analysis of eukaryotic lincRNA sequences indicates signatures of hindered translation linked to selection pressure Authors: Anneke Bruemmer, Rene Dreos, Ana Claudia Marques and Sven Bergmann</p>	<p>Applications talk A cloud based resource to manage, access and explore omics datasets in multiuser environments Authors: Mario Looso, Philipp Goymann, Franz Ziegengest, Carsten Kuenne, Daniel Spothelfer, Noah Knoppik and Jasmin Walter</p> <p>Applications talk Introducing X-Omics, the central multi-omics data integration and AI modeling platform for biomarker data at Merck Author: Sven-Eric Schelhorn</p> <p>Applications talk Global biodata resources: challenges to long-term sustainability of a crucial data infrastructure Authors: Guy Cochrane and Chuck Cook</p>
15:00 - 15:30	Coffee break and Exhibition		
15:30 - 16:30	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	PROTEINS (Session #10) Chair: Mark Wass	GENOMES (Session #11) Chair: Toni Gabaldón	APPLICATIONS (Session #12) Chair: Javier De Las Rivas
	<p>Highlight talk PDBe-KB: collaboratively defining the biological context of structural data Author: Preeti Choudhary</p> <p>Proceeding talk APPRIS Principal Isoforms and MANE Select Transcripts Define Reference Splice Variants Authors: Fernando Pozo Ocampo, Laura Martinez Gomez, Jose Manuel Rodriguez, Jesús Vázquez and Michael Tress</p> <p>Highlight talk AlphaFold Protein Structure Database: massively expanding the structural coverage of protein-sequence space with high-accuracy models Authors: Mihaly Varadi, Sameer Velankar, Stephen Anyango, Mandar Deshpande, Sreenath Nair, Cindy Natassia, Galabina Yordanova, David Yuan, Oana Stroe, Gemma Wood, Agata Laydon, Augustin Zidek, Tim Green, Kathryn Tunyasuvunakool, Stig Petersen, John Jumper, Ellen Clancy, Richard Green, Ankur Vora, Mira Lutfi, Michael Figurnov, Andrew Cowie, Nicole Hobbs, Pushmeet Kohli, Gerard Kleywegt, Ewan Birney and Demis Hassabis</p>	<p>Proceeding talk 3CAC: improving the classification of phages and plasmids in metagenomic assemblies using assembly graphs Authors: Lianrong Pu and Ron Shamir</p> <p>Highlight talk A global metagenomic map of urban microbiomes and antimicrobial resistance Authors: Alina Frolova, David Danko, Daniela Bezdán, Christopher E. Mason and The International Consortium Metasub</p> <p>Highlight talk Unlocking capacities of genomics for the COVID-19 response and future pandemics Authors: Sergei Mangul, Karishma Chhugani, Sergey Knyazev, Varuni Sarwal, Ram Ayyala, Angela Lu and Adam Smith</p>	<p>Applications talk Open Targets: A Platform for Biological Data Integration Author: Irene Lopez Santiago</p> <p>Sponsored talk by Vaticle Building Biomedical Knowledge Graphs for In-Silico Drug Discovery Authors: Tomás Sabat</p> <p>Applications talk Scalable In-memory paradigm for genomics data processing Authors: Ritesh Krishna, Vadim Elisseev and Laura-Jayne Gardiner</p>
16:30 - 17:00	Keynote talk		
17:00 - 17:30	<p>Ana T. Freitas (INESC-ID/IST Technical University of Lisbon, Portugal) Personalized medicine in the era of artificial intelligence</p> <p>Chair: Fátima Sánchez-Cabo</p>		
17:30 - 18:00	Monday Poster session and Exhibition		
18:00 - 18:30			
18:30 - 19:00			
19:00 - 19:30			

TUESDAY, 20 September			
08:00 - 08:30	Registration desk open all day		
08:30 - 09:00	Welcome and announcements (08:45h)		
09:00 - 09:30	Keynote talk		
09:30 - 10:00	<p>Maria Rodriguez-Martínez (IBM Research Europe, Switzerland) Interpretable deep learning for cancer personalized medicine</p> <p>Chair: Fátima Al-Shahrour</p>		
10:00 - 11:00	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	ELIXIR (Session #13) Chair: Katharina Heil	PROTEINS (2) + GENES (1) (Session #14) Chair: Mark Wass	SYSTEMS (2) + DATA (1) (Session #15) Chair: Anaïs Baudot
	<p>From integrated COVID-19 data to integrated pathogen data analysis</p> <p>Title: Setting the scene: Beyond COVID-19 - European preparedness for infectious disease outbreaks Speaker: Katharina Lauer (ELIXIR)</p> <p>Title: Pathogen Data Sharing and Workflows at the ENA Speaker: Colman O'Cathail (EBI/COVID19 Data Portal)</p> <p>Title: Using COVID-19 data genomics and sharing to set a new future standard Speaker: Bas Oude Munnink (Erasmus MC/VEO)</p> <p>Title: Fully transparent viral genomics data analysis and sharing for everyone using public infrastructure</p>	<p>Proceeding talk Genes: Improved NSGA-II algorithms for multi-objective biomarker discovery Authors: Luca Cattelan and Vittorio Fortino</p> <p>Proceeding talk Proteins: DistilProtBert: A distilled protein language model used to distinguish between real proteins and their randomly shuffled counterparts Authors: Yaron Geffen, Yanay Ofran and Ron Unger</p>	<p>Highlight talk Data: The AIMe registry for artificial intelligence in biomedical research Authors: Julian Matschinske, Nicolas Alcaraz, Arriel Benis, Gerda Cristal Villalba Silva, Martin Golebiewski, Dominik G. Grimm, Lukas Heumos, Tim Kacprowski, Olga Lazareva, Markus List, Zakaria Louadi, Josch Pauling, Nico Pfeifer, Richard Röttger, Veit Schwämmle, Kristel Van Steen, Gregor Sturm, Alberto Traverso, Martíela Vaz de Freitas, Leonard Wee, Nina Wenke, Massimiliano Zanin, Olga Zolotareva, Jan Baumbach and David B. Blumenthal</p> <p>Proceeding talk Systems: DrDimont: Explainable drug response prediction from differential analysis of multi-omics networks Authors: Pauline Hiort, Julian Hugo, Justus Zeinert, Nataníel Müller, Spoothi Kashyap, Jagath C. Rajapakse, Francisco Azuaje, Bernhard Y. Renard and Katharina Baum</p>

	<p>snaring for everyone using public infrastructure</p> <ul style="list-style-type: none"> • Speaker: Wolfgang Maier (Universitaet Freiburg/Galaxy) <p>> Discussion</p>	<p>Highlight talk Proteins: The clinical importance of tandem exon duplication-derived substitutions</p> <ul style="list-style-type: none"> • Authors: Laura Martinez Gomez, Fernando Pozo Ocampo, Thomas Walsh, Federico Abascal and Michael Tress 	<p>Proceeding talk Systems: GNN-SubNet: disease subnetwork detection with explainable Graph Neural Networks</p> <ul style="list-style-type: none"> • Authors: Bastian Pfeifer, Anna Saranti and Andreas Holzinger
11:00 - 11:30	Coffee break and Exhibition		
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	<p>ELIXIR (Session #16) Chair: Katharina Heil</p>	<p>DATA (Session #17) Chair: Josep Lluís Gelpí</p>	<p>PROTEINS (Session #18) Chair: Mark Wass</p>
11:30 - 12:30	<p>ELIXIR talk The ELIXIR Machine Learning Focus Group: achievements and the road ahead</p> <ul style="list-style-type: none"> • Speakers: Silvio Tosatto, Fotis Psomopoulos <p>ELIXIR talk The ELIXIR Biodiversity Community - "Biodiversity data" aims and challenges</p> <ul style="list-style-type: none"> • Speakers: Toni Gabaldón, Josephine Burgin, Robert Waterhouse <p>ELIXIR talk Federated EGA (title TBC)</p> <ul style="list-style-type: none"> • Speaker: Jordi Rambal 	<p>Proceeding talk SimBu: Bias-aware simulation of bulk RNA-seq data with variable cell type composition</p> <ul style="list-style-type: none"> • Authors: Alexander Dietrich, Gregor Sturm, Lorenzo Merotto, Federico Marini, Francesca Finotello and Markus List <p>Proceeding talk Detecting DNA of novel fungal pathogens using ResNets and a curated fungi-hosts data collection</p> <ul style="list-style-type: none"> • Authors: Jakub M Bartoszewicz, Ferdous Nasri, Melania Nowicka and Bernhard Y Renard <p>Highlight talk Discovering cell types using manifold learning and enhanced visualization of single-cell RNA-Seq data</p> <ul style="list-style-type: none"> • Authors: Akram Vasignizaker, Saiteja Danda and Luis Rueda 	<p>Proceeding talk Insights into performance evaluation of compound-protein interaction prediction methods</p> <ul style="list-style-type: none"> • Authors: Adiba Yaseen, Imran Amin, Naeem Akhter, Asa Ben-Hur and Fayyaz Ul Amir Afsar Minhas <p>Proceeding talk Cross-Modality and Self-Supervised Protein Embedding for Compound-Protein Affinity and Contact Prediction</p> <ul style="list-style-type: none"> • Authors: Yuning You and Yang Shen <p>Highlight talk Missense variants in human ACE2 strongly affect binding to SARS-CoV-2 Spike providing a mechanism for ACE2 mediated genetic risk in Covid-19: A case study in affinity predictions of interface variants</p> <ul style="list-style-type: none"> • Authors: Stuart A. MacGowan, Michael I. Barton, Mikhail Kutuzov, Omer Dushek, P. Anton van der Merwe and Geoffrey J. Barton
12:30 - 13:00	Lunch, Exhibition and Poster viewing		
13:00 - 13:30	<p>Birds of a Feather [12:45h - 13:45h, Margaret O. Dayhoff] Sex and Gender Biases in Technology and Artificial Intelligence Organised by Bioinfo4Women; Chair: R. Gonzalo Parra</p>		
13:30 - 14:00	Lunch, Exhibition and Poster viewing		
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	<p>ELIXIR meets Latin America (Session #19) Chair: José María Carazo</p>	<p>GENOMES (Session #20) Chair: Toni Gabaldón</p>	<p>Institutional talks (Session #21) Chair: Salvador Capella-Gutierrez</p>
14:00 - 15:00	<p>Welcome and Introduction</p> <ul style="list-style-type: none"> • Speakers: José María Carazo and Andrew Smith <p>ELIXIR Europe: overview and opportunities</p> <ul style="list-style-type: none"> • Author: Andrew Smith <p>Development and evolution of Bioinformatics Societies in Latin America: A2B2C (Argentina), AB3C (Brasil), BIOCANET (Costa Rica & Panama), BioNetMX (Mexico), SC2B2 (Colombia), SCB (Chile), SPB2C (Peru) and SOIBIO (Iberoamerica)</p> <ul style="list-style-type: none"> • Author: Javier De Las Rivas and Consortium Representatives Of Seven Bioinformatics National Societies From Latin-America And Soibio <p>AB3C</p> <ul style="list-style-type: none"> • Author: Marcelo Brandão <p>Creating paths for the development and application of bioinformatics in Mexico</p> <ul style="list-style-type: none"> • Authors: Irma Martínez-Flores, Shirley Alquicira-Hernández and Alejandra Eugenia Medina-Rivera <p>Bioinformatics in Argentina: The first 10+3 years of A2B2C</p> <ul style="list-style-type: none"> • Authors: Nicolas Palopoli, Lucia Chemes, Georgina Stegmayer, Elin Teppa, Diego Bustos, Cristina Marino-Buslje, Flavio Spetale and Sebastián Fernández Alberti 	<p>Proceeding talk Discovering Significant Evolutionary Trajectories in Cancer Phylogenies</p> <ul style="list-style-type: none"> • Authors: Leonardo Pellegrina and Fabio Vandin <p>Highlight talk Towards a metagenomics machine learning interpretable model for understanding the transition from adenoma to colorectal cancer</p> <ul style="list-style-type: none"> • Authors: Carlos Sánchez-Casimiro-Soriguer, Carlos Loucera, María Peña-chilet and Joaquín Dopazo <p>Highlight talk Higher order genetic interactions switch cancer genes from two-hit to one-hit drivers</p> <ul style="list-style-type: none"> • Authors: Solip Park, Fran Supek and Ben Lehner 	<p>Institutional talk The Spanish Supercomputing Network (RES): HPC and Data Resources for a scientific revolution</p> <ul style="list-style-type: none"> • Authors: Infrastructure Access Policy Unit - Barcelona Supercomputing Center, Oriol Pineda and Alberto A. Gómez <p>Institutional talk Ersilia, a hub of open-source AI/ML models for drug discovery and global health</p> <ul style="list-style-type: none"> • Authors: Gemma Turon and Miquel Duran-Frigola <p>Institutional talk The Bioinfo4Women Programme: towards gender equity and diversity in science</p> <ul style="list-style-type: none"> • Authors: Alba Jene-Sanz, María José Rementería, Eva Alloza and Àtia Cortés
15:00 - 15:30	Coffee break and Exhibition		
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	<p>ELIXIR meets Latin America (Session #22) Chair: José María Carazo</p>	<p>DATA (Session #23) Chair: Josep Lluís Gelpí</p>	<p>APPLICATIONS (Session #24) Chair: Jaime Huerta-Cepas</p>
15:30 - 16:30	<p>Research data management (RDM) in ELIXIR and insight into the RDM Toolkit</p> <ul style="list-style-type: none"> • Authors: Frederik Coppens and Carole Goble <p>ELIXIR Training activities and opportunities for engagement</p> <ul style="list-style-type: none"> • Author: Katharina Heil, Jessica Lindvall and Fotis E Psomopoulos 	<p>Proceeding talk Exploiting Pretrained Biochemical Language Models for Targeted Drug Design</p> <ul style="list-style-type: none"> • Authors: Gökçe Uludağın, Arzucan Özgür, Elif Özkırmıli, Kutlu Ülgen and Nilgün Karali <p>Highlight talk Scaling up oligogenic diseases research with OLIDA: the Oligogenic Diseases Database</p> <ul style="list-style-type: none"> • Authors: Barbara Gravel, Charlotte Nachtgaeel, Arnau Dillen, Guillaume Smits, Ann Nowé, Sofia Papadimitriou and Tom Lenaerts 	<p>Applications talk Bioinformatics methods for the analysis of rare-disease patient data – applications for target discovery and obtaining phenotype associations</p> <ul style="list-style-type: none"> • Authors: Elena Rojano, James Perkins, Fernando Moreno Jabato, José Córdoba-Caballero, Elena Diaz-Santiago, Federico García-Criado, Florencio Pazos, Pedro Seoane and Juan Ranea <p>Applications talk AI microbiome-based recommendation system for improving soil health with bio-stimulants</p> <ul style="list-style-type: none"> • Authors: Beatriz García-Jiménez, Sam Röttjers, Diego Rodríguez-de-Prado and Alberto Acedo

	> Open discussion	Highlight talk PharmacDB 2.0: improving scalability and transparency of in vitro pharmacogenomics analysis • Authors: Nikta Feizi, Sisira Kadambat Nair, Petr Smirnov , Gangesh Beri, Christopher Eeles, Parinaz Nasr Esfahani, Minoru Nakano, Denis Tkachuk, Anthony Mammoliti, Evgeniya Goroberts, Arvind Singh Mer, Eva Lin, Yihong Yu, Scott Martin, Marc Hafner and Benjamin Haibe-Kains	Applications talk Whole-genome sequencing analysis of food enzyme products reveals contaminations with genetically modified microorganism of related origin • Authors: Jolien D'Aes , Marie-Alice Fraiture, Bert Bogaerts, Sigrid C.J. De Keersmaecker, Nancy H.C. Roosens and Kevin Vanneste
16:30 - 17:00	Keynote talk		
17:00 - 17:30	Graciela Gonzalez-Hernandez (Cedars-Sinai Medical Center (USA)) Mining for Digital Epidemiology: Overcoming the Challenges of Real World Data Chair: Salvador Capella-Gutierrez		
17:30 - 18:00	Tuesday Poster session and Exhibition		
18:00 - 18:30			
18:30 - 19:00			
19:00 - 19:30			
19:30 - 20:00			
20:00 - 20:30	Conference dinner		
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23:00 - 23:30			
23:30 - 00:00			

WEDNESDAY, 21 September			
08:00 - 08:30	Registration desk open all day from 8:00h		
08:30 - 09:00	Welcome and announcements 8:45h		
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	CLIMATE CRISIS AND HEALTH (Session #25) Chair: Ana Conesa	DATA (Session #26) Chair: Josep Llull Gelpí	APPLICATIONS (Session #27) Chair: Anaïs Baudot
09:00 - 10:00	Invited talk Infectious disease decision-support tools to enhance resilience in climate change hotspots • Speaker: Rachel Lowe Invited talk The Catalan Initiative for the Earth Biogenome Project • Speaker: Montserrat Corominas	Highlight talk Flimma: Federated and privacy-aware medical differential gene expression analysis • Authors: Olga Zolotareva, Reza Nasirigerdeh, Julian Matschinske, Reihaneh Torzadehmahani, Mohammad Bakhtiari , Tobias Frisch, Julian Alexander Späth, David B. Blumenthal, Amir Abbasinejad, Paolo Tieri, Georgios Kaissis, Daniel Rückert, Nina Wenke, Markus List and Jan Baumbach Proceeding talk This is GlycoQL • Authors: Catherine Hayes , Vincenzo Daponte, Julien Mariethoz and Frederique Lisacek Highlight talk Orchestrating and sharing large multimodal data for transparent and reproducible research • Authors: Anthony Mammoliti, Petr Smirnov , Minoru Nakano, Zhaleh Safikhani, Christopher Eeles, Heewon Seo, Sisira Kadambat Nair, Arvind S Mer, Ian Smith, Chantal Ho, Gangesh Beri, Rebecca Kusko, Eva Lin, Yihong Yu, Scott Martin, Marc Hafner and Benjamin Haibe-Kains	Applications talk METALoci, identification of spatial enhancer hubs • Authors: Marc A. Marti-Renom , Irene Mota Gomez-Argente, Juan Antonio Rodriguez Perez and Dario Lupiañez Applications talk Power analysis of cell-type deconvolution across human tissues • Author: Anna Vathrakokouli Pournara , Zhichao Miao and Irene Papatheodorou Applications talk ChiTaH: a fast and accurate tool for identifying known human chimeric sequences from high-throughput sequencing data • Authors: Milana Frenkel-Morgenstern , Rajesh Detroja and Sumit Mukherjee
	Auditorium Anna Tramontano	Room Margaret O. Dayhoff	Room Rosalind Franklin
	CLIMATE CRISIS AND HEALTH (Session #28) Chair: Ana Conesa	GENOMES (Session #29) Chair: Alba Jené-Sanz	APPLICATIONS (Session #30) Chair: Anaïs Baudot
10:00 - 11:00	Invited talk Synergies between climate variation and environmental degradation on malaria in southern Venezuela • Speaker: Isabel Fletcher Invited talk Real-time Genomics for One Health • Speaker: Lara Urban Invited talk Climate-sensitive disease outbreaks in the aftermath of extreme climatic events • Speaker: Tilly Alcayna	Proceeding talk DeepZF: Improved DNA-binding prediction of C2H2-zinc-finger proteins by deep transfer learning • Authors: Sofia Aizenshtein-Gazit and Yaron Orenstein Proceeding talk CRISPRtracrRNA: Robust approach for CRISPR tracrRNA detection • Authors: Alexander Mitrofanov , Marcus Ziemann, Omer Alkhnbashi, Wolfgang Hess and Rolf Backofen Highlight talk Revisiting genetic artifacts on DNA methylation microarrays exposes novel biological implications • Authors: Benjamin Planterose Jiménez , Manfred Kayser and Athina Vidaki	Applications talk A near-full compression of SARS-CoV-2 peptidome using UNIQmin • Authors: Li Chuin Chong and Asif M. Khan Applications talk Cancer patient stratification and molecular mechanism identification using patient clintypes and transcriptomics embeddings • Author: Zongliang Yue, Samuel Bharti, Eric Gong, Radomir Slominski, Thanh Nguyen, Lara Lanov, Christopher Willey and Jake Chen Applications talk Evaluation of machine learning strategies for imaging confirmed prostate cancer recurrence prediction on electronic health records • Authors: Jacqueline Beinecke , Patrick Anders, Tino Schurrat, Dominik Heider, Markus Luster, Damiano Librizzi and Anne-Christin Hauschild
11:00 - 11:30	Coffee break and Exhibition		
11:30 - 12:00	Conference closing Keynote talk Mar Albà (ICREA-IMIM, Spain)		

12:00 - 12:30	The emerging small proteome Chair: Ana Conesa
12:30 - 13:00	Conference closing ceremony Presentation of ECCB/ISMB2023 Awards Final remarks
13:00 - 13:30	Lunch and Exhibition
13:30 - 14:00	