

THEME / TRACK: DATA

Poster #	EasyChair ID	Presenting Author	Authors	Title	Topic
P_Ap001	368	Mahmoud Elhefnawi	Elsayed Hegazy, M. Omar Fares and Mahmoud Elhefnawi	Comparative Analysis of Corynebacterium pseudotuberculosis Genomes and association with their hosts	Application
P_Ap002	373	Meryl Vila Nova	Meryl Vila Nova, Kevin La, Arnaud Felten, Kevin Durimel, Philippe Bessieres, Michel-Yves Mistou, Mahendra Mariadassou and Nicolas Radomski	Host adaptations of Salmonella enterica subsp. enterica serovars deciphered by the first Genome Wide Association Study implementing accessory genes and coregenome variants	Application
P_Ap003	378	Diana Larisa Roman	Diana Larisa Roman, Marin Roman, Vasile Ostafe and Adriana Isvoran	A computational assessment of the biological effects of some parabens	Application
P_Ap004	380	Abiel Roche-Lima	Abiel Roche-Lima, Jovaniel Rodríguez, Karla Claudio, Kelvin Carrasquillo-Carrión, Brenda Nieves, Steven Massey and Jorge Duconge	Computational Tools for Ancestry Analysis In Hispanics	Application
P_Ap005	386	Anil Kumar	Anil Kumar, Aleksandr Ianevsky, Alexander Kolmonov and Tero Aittokallio	INTASS: a novel approach for synergy scoring incorporating inhibition and toxicities due to drug pair	Application
P_Ap006	391	Nikolay Kulemin	Nikolay Kulemin, Alexey Gorbachev, Vladimir Naumov, Sergey Popov and Anastasiya Gubina	Zenome Platform - a unique infrastructure for storing and processing of genetic data based on the blockchain	Application
P_Ap007	406	Zainab Usman	Zainab Usman, Michael Roggendorf and Dimitrij Frishman	Absence of mutations in the HBsAg "a" determinant during REP 2139 therapy validates serum HBsAg reductions observed in the REP 102 protocol	Application
P_Ap008	436	Diana Low	Diana Low, Pierre Alexis Vincent Goy and Ernesto Guccione	SPLINTER : Splicing Interpreter of Transcripts	Application
P_Ap009	438	Berfu Büyüköz	Hakime Öztürk, Mehmet Aziz Yirik, Efe Ercetin, Berfu Büyüköz, Kutlu Ö. Ülgen, Arzucan Ozgur and Elif Ozkirimli	PLITool: Protein-Ligand Interactions Tool	Application
P_Ap010	440	Raphaëlle Lesage	Raphaëlle Lesage, Johan Kerkhofs and Liesbet Geris	Computational Modelling to Integrate Complex Knowledge Underlying Endochondral Ossification and Help Identifying Intervention Targets	Application
P_Ap011	444	Leonidas Souliotis	Leonidas Souliotis and Christopher Quince	Binning metagenomic contigs using Dirichlet process mixtures	Application
P_Ap012	447	Luca Beltrame	Luca Beltrame, Lara Paracchini, Enrica Calura, Paolo Martini, Robert Fruscio, Lorenzo Ceppi, Maurizio D'Incalci, Chiara Romualdi and Sergio Marchini	Genomic and transcriptomic variant detection in advanced ovarian cancer through longitudinal surgeries	Application
P_Ap013	461	Jong Cheol Yoon	Jong Cheol Yoon, Gunhwan Ko and Byungwook Lee	SSV: Apache Spark-Based NGS Analyzer for Big Data of Predicting Genomic Structure Variations	Application
P_Ap014	473	Vasyl Hurmach	Vasyl Hurmach, Maxim Platonov, Dmytro Kovalskyy, Olexander Boyko and Nouri Neamati	Search of a new selective inhibitors of the HIV-1 integrase-LEDGF/p75 interaction	Application
P_Ap015	477	Leonhard Heizinger	Leonhard Heizinger and Rainer Merkl	ShortID: Translating sequence identifiers to acronyms based on phylogenetic and environmental properties	Application
P_Ap016	478	Kristina Heyn	Kristina Heyn and Rainer Merkl	Sequence selection by FitS4ASR alleviates ancestral sequence reconstruction as exemplified for geranylgeranylgeranyl phosphate synthase	Application
P_Ap017	482	Euna Jeong	Euna Jeong and Sukjoon Yoon	Identification of tumor-specific cell surface transcriptome markers for advanced cancer therapies	Application
P_Ap018	492	Marius Wöste	Marius Wöste and Martin Dugas	VIPER: a web application for rapid expert review of variant calls	Application
P_Ap019	498	Panagiotis Moulos	Panagiotis Moulos	recoup: Advanced Next Generation Sequencing Signal Visualization	Application
P_Ap020	500	Panagiotis Moulos	Panagiotis Moulos, Antonis Giakountis and Pantelis Hatzis	SeqCVIBE: Interactive Data Exploration, Analysis, Visualization and Genome Browsing of RNA-Seq Data	Application
P_Ap021	503	Pemra Ozbek Sarica	Onur Serçinoğlu and Pemra Ozbek Sarica	gRINN: Software for Analysis of MD Simulations in the Context of Amino Acid Interaction Energies and Network Analysis	Application
P_Ap022	504	Pemra Ozbek Sarica	Murat Aydıncal, Onur Serçinoğlu and Pemra Ozbek Sarica	Development of a web-based tool for network analysis of protein structures	Application
P_Ap023	506	Chao-Chun Chuang	Chao-Chun Chuang, Chang-Wei Yeh, Yu-Tai Wang, Nan-Yow Chen and Chia-Lee Yang	A novel approach for automatically deploying the developed bioinformatics tools and workflows in HPC	Application
P_Ap024	512	Giancarlo Russo	Giancarlo Russo, Andrea Salzmänn and Cordula Haas	Deciphering body fluids-derived stains through their gene expression profile and microbial composition	Application
P_Ap025	518	Mahdi Heydari	Mahdi Heydari, Giles Miclotte and Jan Fostier	BrownieAligner: Accurate Alignment of Illumina Sequencing Data to de Bruijn Graphs	Application
P_Ap026	528	Salvatore Cosentino	Salvatore Cosentino and Wataru Iwasaki	SonicParanoid: fast, accurate, and easy orthology inference	Application
P_Ap027	537	Sanna Abrahamsson	Sanna Abrahamsson, Marcela Davila, Anna Rohlin and Frida Eiengård	Pψfinder: Identification of novel Pψ in DNA sequencing data	Application

P_Ap028	539	Serena Dotolo	Serena Dotolo, Angelo Facchiano and Alessandro Pandini	Detection of the impairment of allosteric regulation in Sirtuin2 proteins through molecular dynamics and residue coevolution analysis	Application
P_Ap029	555	Qiang Fu	Qiang Fu, Bert Bogaerts, Raf Winand, Julien Van Braekel, Cyril Barbezange, Veronik Hutse, Isabelle Thomas, Steven Van Gucht, Sigrid De Keersmaecker, Nancy Roosens and Kevin Vanneste	Development of a bioinformatics pipeline for the routine analysis of Influenza whole genome sequencing data	Application
P_Ap030	568	Gunhwan Ko	Gunhwan Ko, Jong Cheol Yoon and Byungwook Lee	SKY-QC: A tool for quality control and trimming of sequencing data with high-speed file transfer	Application
P_Ap031	575	Katarzyna Hooks	Katarzyna Hooks, Jérôme Audoux, Anne-Aurélié Raymond, Amani Ghousein, Hélène Fazli, Sarah Lesjean, Laurence Brugières, Monique Fabre, Anne Rullier, Marie-Annick Buendia, Thérèse Commes and Christophe Grosset	Regulatory RNA hubs in hepatoblastoma	Application
P_Ap032	580	Wen Chen	Wen Chen, Manuel Zahariev, Sarah Hambleton, Cobus M. Visagie and C. André Lévesque	Design and application of cluster signatures in metagenomics survey	Application
P_Ap033	586	Kerem Wainer Katsir	Kerem Wainer Katsir and Michal Linal	Identifying cell doublets from single cell sequencing using allele-specific expression	Application
P_Ap034	597	Nikolaos Papadopoulos	Nikolaos Papadopoulos, Rodrigo Gonzalo Parra and Johannes Soeding	MERLOT and PROSST! Reconstructing and modelling differentiation lineage trees for single-cell RNAseq experiments	Application
P_Ap035	598	Shu-Hwa Chen	Shu-Hwa Chen, Chieh-Hwa Lin, Zhe-Ren Hsu, I-Hsuan Lu and Chung-Yen Lin	EV_CNN: A web application for Enterovirus Genotyping in Deep learning	Application
P_Ap036	641	Manuel Holtgrewe	Manuel Holtgrewe, Eric Blanc, Clemenens Messerschmidt, Nina Thiessen and Dieter Beule	CNVetti – robust, efficient, and versatile clinical CNV calling from HTS data	Application
P_Ap037	645	Ali Burak Ünal	Ali Burak Ünal and Nico Pfeifer	Privacy-preserving computation of a sequence kernel in secure multiparty computation with precision medicine application for HIV-infected patients	Application
P_Ap038	646	Mugdha Srivastava	Mugdha Srivastava, Shishir K Gupta and Thomas Dandekar	Identification of genes under positive selection in fungal pathogen <i>Aspergillus fumigatus</i> reveals evolutionary strategies to adapt to diverse environments	Application
P_Ap039	647	Shishir K Gupta	Shishir K Gupta, Mugdha Srivastava, Elena Bencurova and Thomas Dandekar	Elementary Flux Modes Analysis through scalable subnetwork definition reveals how <i>Aspergillus fumigatus</i> modulates its metabolic strategy under human dendritic cells	Application
P_Ap040	659	David Dylus	David Dylus, Christophe Dessimoz, Panu Artimo, Severine Duvaud, Andrey Solovyev, Joseph Trafford, Heinz Stockinger and Ioannidis Vassiliou	Phylo.io v2.0: Improved visual and interactive global and local tree comparison	Application
P_Ap041	671	Junehawk Lee	Junehawk Lee, Yongseong Cho, Seongyeol Park and Seok Jong Yu	PedInspector: a toolset for checking integrity between the pedigree annotation and the familial whole genome sequence data set	Application
P_Ap042	673	Emma Sims	Emma Sims, Andrew Thompson and Fady Mohareb	Development of a food quality and safety risk management system, using cloud computing, big data and data science	Application
P_Ap043	674	Andrea Griioni	Andrea Griioni, Grazia Fazio, Vojtech Bystry, Silvia Rigamonti, Andrea Biondi and Giovanni Cazzaniga	BreakingPoint: a Purpose-Built Tool to Identify Fusion Genes from Target Capture NGS for Acute Lymphoblastic Leukaemia Clinical Diagnosis	Application
P_Ap044	679	Dries Decap	Dries Decap, Pascal Costanza, Charlotte Herzeel and Jan Fostier	Exploring big data frameworks for WGS variant calling	Application
P_Ap045	680	Jean-Marc Schwartz	Chuan Fu Yap, Manuel Garcia-Albornoz, Andrew Jarnuczak, Simon Hubbard and Jean-Marc Schwartz	GRaPe 2.0: Accelerating the construction of kinetic models for cell metabolism	Application
P_Ap046	682	Çiğdem Ak	Çiğdem Ak, Önder Ergönül and Mehmet Gönen	Modeling spatiotemporal dynamics of infectious diseases using structured Gaussian processes	Application
P_Ap047	691	Chi-Hwan Choi	Chi-Hwan Choi, Min-Kyu Park and Jeongsu Oh	IMDG-BLAST: BLAST based on In-Memory Data Grid in the cloud environment	Application
P_Ap048	706	Holger Fröhlich	Benjamin Engelhardt, Maik Kschischo and Holger Fröhlich	A Data Science Approach to Find Sources of Errors in Mathematical Models in Systems Biology	Application
P_Ap049	707	Ewelina Sowka	Ewelina Sowka, Andrew Thompson and Fady Mohareb	NextGenPhenomics: a novel approach to phenotype detection	Application
P_Ap050	714	Milot Mirdita	Milot Mirdita, Martin Steinegger and Johannes Söding	MMseqs2 app and server for interactive and fast sequence similarity searches	Application
P_Ap051	722	Stefan Rödiger	Stefan Rödiger, Michal Burdukiewicz, Andrej-Nikolai Spiess and Konstantin Blagodatskikh	Standardized exchange of qPCR data via the RDML package	Application
P_Ap052	732	Petros Kountouris	Petros Kountouris, Coralea Stephanou, Stella Tamana, Carsten Werner Lederer and Marina Kleanthous	ITHANET: An information and database community portal for haemoglobinopathies	Application
P_Ap053	744	Akrishta Sahay	Akrishta Sahay, Meemansa Sood, Reagon Karki, Akrishta Sahay, Holger Froehlich and Martin Hofmann-Apitius	Towards Enabling Virtual Clinical Studies with Longitudinal Bayesian Network Modeling	Application
P_Ap054	748	Adriana Toutoudaki	Adriana Toutoudaki, Kim Brugger and Stephen Abbs	ClicS(Clinical Cancer Signatures): making cancer mutational signature analysis available in a clinical environment	Application
P_Ap055	749	Vishnu K. Sharma	Vishnu K. Sharma and Prasad V. Bharatam	Identification of novel, selective Inhibitors of LdDHFR Enzyme using Computer Aided Drug Design Approaches	Application

P_Ap056	763	Christophe Bécavin	Christophe Bécavin, Pierre Lechat and Nicolas Maillet	Build your own multi-omics website with BACNET	Application
P_Ap057	764	Daniele Capocéfalo	Daniele Capocéfalo, Mauro Truglio, Ferenc Jordan and Tommaso Mazza	Unraveling the complexity of molecular networks with Pyntacle	Application
P_Ap058	766	Carlos Menor	Carlos Menor, David Seide, Robert Nica, Mariana Monteiro, Alejandro Rocamonde, Francisco Salavert and Stefan Götz	Functional Genomics Analysis of Newly Sequenced Genomes From Scratch with Blast2GO	Application
P_Ap059	774	Amin Ardehshirdavani	Amin Ardehshirdavani, Masoud Zamani Esteki, Daniel Alcaide, Heleen Masset, Alejandro Sifrim, Parveen Kumar, Nathalie Brison, Niels Van der Aa, Eftychia Dimitriadou, Koen Theunis, Hilde Peeters, Jan Aerts, Joris Vermeesch, Thierry Voet and Yves Moreau	HiVA: a web platform for haplotyping and copy number analysis of single-cell genomes and mosaicism detection in bulk DNA	Application
P_Ap060	785	Dong-Jun Lee	Dong-Jun Lee, Do-Wan Kim, Jae-Hyeon Oh, Tae-Ho Lee and Dong-Wook Kim	An integrated SNP mining and utilization pipeline system construction for genome sequencing data analysis	Application
P_Ap061	797	Sergey Petrov	Sergey Petrov, Leonid Uroshlev, Artem Kasyanov and Vsevolod Makeev	GenGTools: software for alignment of reads to variance graph.	Application
P_Ap062	801	Toshiaki Katayama	Toshiaki Katayama and Shuichi Kawashima	TogoGenome, TogoStanza and TogoVar: application of the modularized semantic genome database	Application
P_Ap063	807	Yumi Kawamura	Yumi Kawamura and Ryo Yoshida	Statistical modeling and inference of the rate of RNA polymerase II elongation by total RNA sequencing	Application
P_Ap064	814	Verena Heinrich	Verena Heinrich, Anna Ramisch and Martin Vingron	Differential Analysis of Regulatory Elements Based on ChIP-seq Data	Application
P_Ap065	824	Stella Tamana	Stella Tamana, Petros Kountouris, Paola Bianchi, Rafaella Colombatti, Victoria Gutierrez Valle, Beatrice Gulbis, Marina Kleanthous and Maria del Mar Mañá Pereira	RADeep: The Rare Anaemia Disorders European Epidemiological Platform	Application
P_Ap066	838	Chris Fotis	Chris Fotis, Asier Antoranz and Leonidas Alexopoulos	Prediction of human protein secretion from its amino acid sequence via a machine learning algorithm	Application
P_Ap067	839	William Newell	William Newell, Daniel Zerbino and Open Targets Consortium	Assignment of SNPs to genes for Open Targets using public genetics and functional genomics data	Application
P_Ap068	850	Yassen Assenov	Pavlo Lutsik, Reka Toth, Christoph Plass and Yassen Assenov	Benchmarking Project of Bisulfite Sequencing Workflows	Application
P_Ap069	857	Bo Gao	Bo Gao, Qingyao Huang and Michael Baudis	segment_liftover : a Python tool to convert segments between genome assemblies	Application
P_Ap070	860	Minh Duc Cao	Minh Duc Cao, Umut Eser, Michael Meyer, Zhizhuo Zhang and Jonathan Rothberg	Deep learning model to improve speed and accuracy of genome assembly	Application
P_Ap071	862	Ruben Sanchez-Garcia	Ruben Sanchez-Garcia, Carlos Oscar Sánchez Sorzano, Jose M. Carazo and Joan Segura	Boosting Partner-Specific Protein-Protein Interface prediction with BIPSPI	Application
P_Ap072	869	Maya Polishchuk	Maya Polishchuk, Inbal Paz, Zohar Yakhini and Yael Mandel-Gutfreund	SMARTIV: Web server for combined sequence and structure de-novo RNA motif discovery	Application
P_Ap073	875	Davide Cirillo	Davide Cirillo, Dario Garcia-Gasulla, Ulises Cortés and Alfonso Valencia	Graph Analytics for phenome-genome association inference	Application
P_Ap074	876	Francesc Muyas	Francesc Muyas, Mattia Bosio and Stephan Ossowski	Allele Balance Bias Identifies Systematic Genotyping Errors and False Disease Associations	Application
P_Ap075	885	Antonio Fabregat	Antonio Fabregat, Konstantinos Sidiropoulos, Guilherme Viteri, Pascual Lorente, Lincoln Stein, Peter D'Eustachio, Guanming Wu and Henning Hermjakob	Reactome graph database	Application
P_Ap076	886	Zhizhuo Zhang	Zhizhuo Zhang, Umut Eser, Minh Duc Cao and Jonathan Rothberg	Re-inventing Pairwise Sequence Alignment using Fully Differentiable Deep Recurrent Neural-network	Application
P_Ap077	887	Konstantinos Sidiropoulos	Konstantinos Sidiropoulos, Pascual Lorente, Guilherme Viteri, Lincoln Stein, Peter D'Eustachio, Guanming Wu, Henning Hermjakob and Antonio Fabregat	Reactome multiscale pathway visualisation	Application
P_Ap078	891	Mattia Bosio	Mattia Bosio, Alfonso Valencia and Salvador Capella-Gutiérrez	Improving RNA-Seq variant calling characterization and interpretation within RD-connect consortium	Application
P_Ap079	892	Pascual Lorente	Pascual Lorente, Konstantinos Sidiropoulos, Chuang Deng, Guilherme Viteri, Lincoln Stein, Peter D'Eustachio, Guanming Wu, Henning Hermjakob and Antonio Fabregat	Reactome Analysis PDF reports	Application
P_Ap080	893	Umut Eser	Umut Eser, Zhizhuo Zhang, Michael Meyer and Jonathan Rothberg	Functional Annotation of Genes Through Integration of Disparate Data Sources with Deep Learning	Application
P_Ap081	895	Chetna Tyagi	Chetna Tyagi, Tamás Marik, András Szekeres, Csaba Vágvolgyi, László Kredics and Ferenc Ötvös	Tripleurin XIII: peptide folding dynamics using accelerated molecular dynamics	Application
P_Ap082	896	Guilherme Viteri	Guilherme Viteri, Cristoffer Sevilla, Antonio Fabregat, Konstantinos Sidiropoulos, Lincoln Stein, Peter D'Eustachio, Guanming Wu and Henning Hermjakob	Reactome icon library	Application
P_Ap083	906	Haris Zafeiropoulos	Haris Zafeiropoulos, Katerina Vasileiadou, Viet Ha Quoc, Christos Arvanitidis, Pantelis Topalis, Christina Pavloudi and Evangelos Pafilis	P.E.M.A.: a Pipeline for Environmental DNA Metabarcoding Analysis	Application
P_Ap084	934	Mayla Abraham	Mayla Abraham, Marcos Catanho, Antonio Basilio, Fernando Alvarez, Luisa Berna, Luiza Pereira, Patrícia Cuervo and Claudia Levy	Identification, characterization, and annotation of pseudogenes and investigation of their biological roles in trypanosomatids pathogenic to humans	Application

P_Ap085	939	Asier Antoranz	Asier Antoranz, Leonidas Alexopoulos, Theodoros Sakellaropoulos, Julio Saez-Rodriguez, Sushrut Waikar and Benjamin Humphreys	Integration of multi-omics data with biological models for biomarker discovery in Chronic Kidney Disease	Application
P_Ap086	940	Susana Arbas	Susana Arbas, Shaman Narayanasamy, Malte Herold, Laura A. Lebrun, Tony Lam, Cedric Laczny, Nathan D. Hicks, Lance B. Price, John D. Gillette, James M. Schupp, Paul S. Keim, Karoline Faust, Yuzhen Ye, Patrick May, Emilie E.L. Muller and Paul Wilmes	A multi-omic view of invasive genetic elements and their linked prokaryotic population dynamics within a mixed microbial community	Application
P_Ap087	943	Tomi Suomi	Tomi Suomi, Fatemeh Seyednasrollah, Maria Jaakkola, Thomas Faux and Laura Elo	Reproducibility-optimized statistical testing for omics studies	Application
P_Ap088	945	Meltem Eda Ömür	Meltem Eda Ömür, Kayra Kösoğlu, Özlem Keskin Özkaya and Attila Gürsoy	Computational Investigation of K-RAS4B Homodimer Complexes and Interactions	Application
P_Ap089	952	Costas Bouyioukos	Mohamed Elati and Costas Bouyioukos	3D transcription map. A package to analyse associations between transcriptomics and 3D genomics.	Application
P_Ap090	961	Pijush Das	Pijush Das, Dr. Susanta Roychoudhury and Dr. Sucheta Tripathy	sigFeature: Significant feature selection using SVM-RFE & t-statistic	Application
P_Ap091	976	Benjamin Hitz	Benjamin Hitz, Esther Chan, Ulugbek Baymuradov, Idan Gabdank, Jason Hilton, J Seth Strattan, Weiwei Zhong, Yunhai Luo, Phillip Adenekan, Zachary Myers, Keenan Graham, Otto Jolanki, Forrest Tanaka, Stuart Miyasato and Mike Cherry	The Encyclopedia of DNA elements (ENCODE): 2018 Update.	Application
P_Ap092	986	Sombeet Sahu	Sombeet Sahu, Manimozhi Manivannan, Maurizio Pellegrino, Sebastian Treusch, Keith Jones and Anup Parikh	Methods for Identifying Tumor Heterogeneity and Rare Subclones in Single Cell DNA Sequence Data	Application
P_Ap093	987	Josef Moser	Josef Moser and Alexandra Graf	BioPytainer: Easy workflow development with BioContainers for Python.	Application
P_Ap094	990	Charles E. Chapple	Christos Kopanos, Vasilis Tsiolkas, Alexandros Kouris, Charles E. Chapple, Monica Albarca Aguilera, Richard Meyer and Andreas Massouras	VarSome: The Human Genomic Variant Search Engine	Application
P_Ap095	991	Sumaiya Nazeen	Sumaiya Nazeen and Bonnie Berger	Carnelian: alignment-free functional binning and abundance estimation of metagenomic reads	Application
P_Ap096	994	Faiz Khan	Faiz Khan	Identification of Diagnostic and Therapeutic Markers in Tumor Invasion using Logic-based Modeling	Application
P_Ap097	997	Ahmed Allam	Ahmed Allam, George Thoma and Michael Krauthammer	Neural networks versus Logistic regression for 30 days all-cause readmission prediction	Application
P_Ap098	1000	Thomas Bukur	Thomas Bukur, Jos de Graaf and Ugur Sahin	Virus gene expression profiles in human primary tumors enable stratification of patients with distinct overall survival	Application
P_Ap099	1001	Jorge Roel-Touris	Jorge Roel-Touris, Charleen G. Don, Joao P.G.L.M. Rodrigues and Alexandre M.J.J. Bonvin	Less is more: Coarse-grained protein-protein docking in HADDOCK	Application
P_Ap100	1006	Tomasz Magdziarz	Tomasz Magdziarz, Karolina Mitusińska, Agata Raczyńska, Maria Bzówka and Artur Góra	AQUA-DUCT: beyond geometry-based methods for protein tunnels and cavity exploration	Application
P_Ap101	1011	Martial Sankar	Martial Sankar, Petra Baumgartner, Julien Dorier, George Coukos, Ioannis Xenarios, Alexandre Harari and Nicolas Guex	Application of MEGAClust for multi-parameters CYTOMETRY – based clinical studies.	Application
P_Ap102	1014	Alexey Samosyuk	Alexey Samosyuk, Ilya Kurochkin, Dmitri Pervouchine and Dmitriy Papatsenko	CellPI: unsupervised processing of mouse and human single-cell RNA-seq data	Application
P_Ap103	1017	Athanasios Alexiou	Athanasios Alexiou, Dimitrios Zisis, Ioannis Kavakiotis, Dimitra Karagkouni and Artemis Hatzigeorgiou	Automated MicroRNA NGS Analysis Pipeline: From pre-process to quantification	Application

THEME / TRACK: DATA

Poster #	EasyChair ID	Presenting.Author	Authors	Title	Topic
P_Da001	39	Delphine Steinbach	Delphine Steinbach, Alice Beaugrand, Yannick De-Oliveira, Stéphane Nicolas, Delphine Madur, Cyril Bauland, Laurence Moreau and Alain Charcosset	ThaliaDB, a tool for data management and genetic diversity data exploration	Data
P_Da002	83	R. Gonzalo Parra	Maria I. Freiburger, A. Brenda Guzovsky, Diego U. Ferreira and R. Gonzalo Parra	Energetic conflicts in catalytic sites of protein enzymes	Data
P_Da003	201	Tair Shauli	Tair Shauli, Nadav Brandes and Michal Linial	A Human-Specific Amino Acid Substitution Matrix	Data
P_Da004	206	Stefan Janssen	Stefan Janssen, Daniel McDonald, Antonio Gonzalez, Jose Navas Molina, Lingjing Jiang, Zechnjang Zech Xu, Kevin Winker, Deborah M Kado, Eric Orwoll, Mark Manary, Siavash Mirarab and Rob Knight	Phylogenetic placement of exact amplicon sequences improves associations with clinical information	Data
P_Da005	223	Alisher Ikramov	Fatima Adilova and Alisher Ikramov	Effectiveness of Modelability Index	Data

P_Da006	244	Nabi Nge	Nabi Nge and Colin Sutherland	Does the time of occurrence of Pfcsp T cell epitope haplotype in a population affect the distribution pattern of predominant haplotypes within specific subpopulations in a high transmission location?	Data
P_Da007	367	Mohamed Hamed Fahmy	Mohamed Hamed Fahmy, Yvonne Saara Gladbach, Sarah Fischer and Georg Fuellen	Towards Precision Medicine in Leukaemia; Challenges and Computational Approaches to Overcome	Data
P_Da008	375	Aurelien Dugourd	Aurelien Dugourd and Julio Saez-Rodriguez	Multi-omic functional analysis to predict metabolic enzyme, kinases and transcription factor activity changes.	Data
P_Da009	379	Ömer An	Ömer An, Kar-Tong Tan, Ying Li, Jia Li, Chan-Shuo Wu, Yang Liu, Siqin Zhou, Bin Zhang, Xi Ren and Henry Yang	CSI NGS Portal: An Online Platform for Automated NGS Data Analysis and Sharing	Data
P_Da010	381	Sarah MCGarrity	Sarah MCGarrity, Þóra Björg Sigmarðóttir, Óttar Rólfsson and Ólafur Eysteinn Sigurjónsson	Using metabolic modelling to improve osteogenic differentiation	Data
P_Da011	393	Aikaterini Polyzou	Aikaterini Polyzou, Indre Piragyte, Thomas Clapes, Stylianos Lefkopoulos, Ramon Klein-Geltnik, Na Yin, Pierre Cauchy, Lheanna Klaeyle, Xavier Langa Oliva, Cora Beckmann, Marcin Wlodarski, Dominic Van Essen, Angelika Rambold, Friedrich G. Kapp, Marina Mione, Jörg Büscher, Erika Pearce, Alexander Polyzos and Eirini Trompouki	A metabolic interplay coordinated by HLX regulates myeloid differentiation	Data
P_Da012	400	Athanasios Dimitriadis	Athanasios Dimitriadis, Dimitra Dafou, Eirini Kanata, Konstantinos Ksanthopoulos and Theodoros Sklaviadis	META-ANALYSIS OF RNA-SEQUENCING DATA SUPPORTS DISTINCT REGULATION OF RNA EDITING IN ALZHEIMER'S DISEASE PATIENTS	Data
P_Da013	409	Alessandro Vitriolo	Alessandro Vitriolo, Pierre-Luc Germain, Giuseppe D'Agostino, Michele Gabriele, Sebastiano Trattaro, Matteo Zanella, Ludovico Rizzuti and Giuseppe Testa	Neurodevelopmental disorders share modules of transcriptional dysregulation explaining brain- and craniofacial-development associated phenotypes	Data
P_Da014	441	Arjun Baghela	Arjun Baghela, Erin Gill, Amy Lee and Robert Ew Hancock	Machine Learning Approaches to Classify Patients Progressing to Sepsis	Data
P_Da015	443	Daniele Parisi	Daniele Parisi, Yves Moreau and Michael Schroeder	Structure-based drug target interaction prediction for drug repositioning	Data
P_Da016	449	Kai Kang	Kai Kang, Qian Meng, Igor Shats, David Umbach and Leping Li	A novel computational deconvolution method for extracting cell-type-specific information using bulk RNA-seq data	Data
P_Da017	452	Emanuel Weitschek	Fabrizio Celli, Fabio Cumbo and Emanuel Weitschek	Classification of large DNA methylation datasets for identifying cancer drivers	Data
P_Da018	453	Gregor Sturm	Gregor Sturm and Tatsiana Aneichyk	Benchmarking methods for estimating immune cell abundance from bulk RNA-sequencing data	Data
P_Da019	454	Nicolas Alcaraz	Nicolas Alcaraz and Robin Andersson	Predicting and elucidating transcriptional activity from sequence with Deep Learning	Data
P_Da020	460	Jan Fehmi Sayilgan	Jan Fehmi Sayilgan, Türkan Haliloğlu and Mehmet Gönen	Protein dynamics analysis reveals that missense mutations in cancer-related genes appear frequently on hinge-neighboring residues	Data
P_Da021	465	Artur Yakimovich	Artur Yakimovich and Jason Mercer	DeepInfectome: Convolutional Neural Network Approach to Systems Biology Dataset Rediscovery	Data
P_Da022	471	Marielena Georgaki	Marielena Georgaki, Christina Koutsothanassis and Panagiotis Moulos	Evaluation of Multiple Variant Calling Algorithms Using Simulated and Real Whole Genome Sequencing Data	Data
P_Da023	475	Gamze Gursoy	Gamze Gursoy, Arif Harmanci, Molly Green, Fabio Navarro and Mark Gerstein	Quantification of private information leakage and privacy-preserving file formats for functional genomics data	Data
P_Da024	479	Elisa Micarelli	Elisa Micarelli, Alberto Calderone, Andrea Cerquone Perpetuini, Marco Rosina, Luisa Castagnoli and Gianni Cesareni	A predictive model to infer drug similarity by integrating eight different chemical features	Data
P_Da025	481	Marta Interlandi	Marta Interlandi and Martin Dugas	Cell type classification in single-cell RNA sequencing: Review of methods	Data
P_Da026	486	Angela Lopez-Del Rio	Angela Lopez-Del Rio, David Vidal, Alfons Nonell-Canals and Alexandre Perera-Lluna	A sequence-based deep learning proteochemometrics model for binding affinity prediction	Data
P_Da027	487	Susana Vinga	Eunice Carrasquinha, Marta B. Lopes, André Veríssimo, Sandra Casimiro, Niko Beerwinkel and Susana Vinga	Ensemble outlier detection in cancer gene expression data	Data
P_Da028	489	Andreas Weidemann	Andreas Weidemann, Maja Rey, Ulrike Wittig and Wolfgang Müller	SABIO-RK – a curated database for reaction kinetics	Data
P_Da029	490	Thilde Terkelsen	Thilde Terkelsen, Pavel Gromov, Anders Krogh, Irina Gromova and Elena Papaleo	Integrative Molecular Profiling of Breast Tumour Interstitial Fluid - Towards Targetable Biomarkers in Blood.	Data
P_Da030	491	Sivarajan Karunanithi	Sivarajan Karunanithi and Marcel Schulz	Cell type specific prediction of monoallelically expressed genes from human epigenomes	Data
P_Da031	499	Kalliopi Markopoulou	Kalliopi Markopoulou, Pantelis Hatzis and Panagiotis Moulos	Investigating the Discriminative Potential of Long non-coding RNAs in Cancer Using Dimensionality Reduction on RNA-Seq Data	Data
P_Da032	502	Theresia Conrad	Theresia Conrad, Olaf Knimeyer, Sebastian G. Henkel, Thomas Krüger, Derek J. Mattern, Vito Valiante, Reinhard Guthke, Ilse D. Jacobsen, Axel A. Brakhage, Sebastian Vlaic and Jörg Linde	Integration of multilevel omics data based on the identification of regulatory modules	Data
P_Da033	505	Yvonne Saara Gladbach	Yvonne Saara Gladbach, Claudia Maletzki and Mohamed Hamed Fahmy	Towards precision medicine: Finding cellular vaccination in MLH1-/- mice mimicking colorectal tumor patients.	Data
P_Da034	507	Michal Linial	Nadav Brandes, Nathan Linial and Michal Linial	Modeling Functional Genetic Alteration in Cancer Reveals New Candidate Driver Genes	Data
P_Da035	516	Luis Cristobal Monraz Gomez	Luis Cristobal Monraz Gomez, Jean-Marie Ravel, Emmanuel Barillot, Andrei Zinoviyev and Inna Kuperstein	Comprehensive signaling network of regulated cell death: comparison of cell death modes in Alzheimer's neurodegenerative disease and cancer	Data
P_Da036	519	Alina Bazarova	Alina Bazarova, Conrad Nieduszynski and Nigel Burroughs	Bayesian inference of DNA origin firing time distributions, origin interference and licensing probabilities from NGS data	Data

P_Da037	524	Dmitry Ravcheev	Dmitry Ravcheev, Almut Heinken, Federico Baldini, Laurent Heirendt, Ronan Fleming and Ines Thiele	Personalized modeling of the human gut microbiome reveals distinct deconjugation and biotransformation of bile acid for healthy and IBD individuals	Data
P_Da038	526	Edward De Brouwer	Edward De Brouwer, Jaak Simm, Adam Arany and Yves Moreau	Tensor factorization for longitudinal data with missing values	Data
P_Da039	532	Marcela Davila	Marcela Davila, Jelena Milosevic, John Inge Johnsen and Per Kogner	TC-Hunter: Identifying insertion sites of a transgenic construct within its host	Data
P_Da040	533	Sebastian Salentin	Florian Kaiser, Sebastian Bittrich, Sebastian Salentin, Christoph Leberecht, V. Joachim Haupt, Sarah Krautwurst, Michael Schroeder and Dirk Labudde	Evidence for ancient bidirectional coding of aminoacyl tRNA synthetases: Backbone Brackets and Arginine Tweezers	Data
P_Da041	535	Janet Piñero	Janet Piñero, Abel Gonzalez-Perez, Emre Guney, Joaquim Aguirre-Plans, Ferran Sanz, Baldo Oliva and Laura I. Furlong	Network, transcriptomic and genomic characterization of genes relevant for drug response	Data
P_Da042	538	Charlotte Nachtgeael	Charlotte Nachtgeael, Sofia Papadimitriou, Nassim Versbraegen, Guillaume Smits and Tom Lenaerts	First insights into the oligogenic potential of DDD patients	Data
P_Da043	540	Max von Kleist	Maureen Smith, Redmond Smyth, Roland Marquet and Max von Kleist	High-throughput characterization of RNA function at single site resolution from mutational interference mapping experiments (MIME)	Data
P_Da044	542	Pashupati P. Mishra	Pashupati P. Mishra, Leo-Pekka Lyytikäinen, Mika Kähönen, Olli T. Raitakari, Reijo Laaksonen and Terho Lehtimäki	Ceramides improve accuracy in prediction of preclinical atherosclerosis	Data
P_Da045	547	Sofia Papadimitriou	Sofia Papadimitriou, Andrea Gazzo, Nassim Versbraegen, Charlotte Nachtgeael, Jan Aerts, Yves Moreau, Sonia Van Dooren, Ann Nowé, Guillaume Smits and Tom Lenaerts	Towards a multivariate pathogenicity assessment: developing predictive methods for disease-causing digenic variant combinations	Data
P_Da046	549	François Bucchini	François Bucchini, Michiel Van Bel and Klaas Vandepoele	Functional and taxonomic analysis of de novo transcriptomes with TRAPID 2.0	Data
P_Da047	550	Christian Wiwie	Christian Wiwie, Richard Röttger and Jan Baumbach	A Knowledge Base for Cluster Studies: The ClustEval Store	Data
P_Da048	551	Linda Grob	Linda Grob, Franziska Singer, Anja Irmisch, Nora Toussaint, Jochen Singer, Thomas Thurnherr, Niko Beerenwinkel, Mitchell Levesque, Reinhard Dummer, Luca Quagliata, Sacha Rothschild, Andreas Wicki, Christian Beisel and Daniel Stekhoven	The Swiss Molecular Tumor Board: Comprehensive Molecular Cancer Diagnostics in the Clinics	Data
P_Da049	552	Alessandra Dal Molin	Alessandra Dal Molin, Giacomo Baruzzo, Ilaria Patuzzi and Barbara Di Camillo	Exploring single-cell RNA-seq data: a survey on sparsity and multimodality.	Data
P_Da050	553	Mihaly Varadi	Mihaly Varadi, Christine Orengo, Michael Sternberg, Janet Thornton and Sameer Velankar	PDB-KB.org: A new community-driven knowledge base resource integrating macromolecular structures with their biological context	Data
P_Da051	558	Christian Wünsch	Christian Wünsch and Martin Dugas	REST based annotation and filtering of Next-Generation Sequencing variant lists with integration into standard office tools	Data
P_Da052	562	Carlos Salort Sanchez	Carlos Salort Sanchez, Jan Baumbach and Marga Martin Sanchez	Big Data applied to gestational diabetes	Data
P_Da053	569	Nassim Versbraegen	Nassim Versbraegen, Aziz Fouche, Sofia Papadimitriou, Charlotte Nachtgeael, Guillaume Smits and Tom Lenaerts	Identification and characterisation of bi-locus diseases	Data
P_Da054	574	Shalu Jhanwar	Shalu Jhanwar, Jens Stolte, Jonas Malkmus, Aimeé Zuniga and Rolf Zeller	Cross-species Analysis Reveal Regulatory Loci Underlying Limb Diversity	Data
P_Da055	576	Andrea Garofoli	Andrea Garofoli, Hesam Montazeri, Viola Paradiso, Luigi M. Terracciano, Salvatore Piscuoglio and Charlotte K. Y. Ng	PipelT: Stand-alone Singularity container for somatic variant calling on the Ion Torrent platform	Data
P_Da056	587	Katarina Truvé	Katarina Truvé, Keiko Funo, Hans Ågren, Toshima Parris, Dzeneta Vizlin Hodzic, Susanne Salmela and Sebastian Illes	Integration of Data Sources and Omics to Identify Susceptibility Variants for Bipolar Disorder	Data
P_Da057	589	Takács Kristóf	Takács Kristóf, Varga Bálint and Grolmusz Vince	PDB_Amyloid: A new program for amyloid segment identification	Data
P_Da058	590	Raik Otto	Raik Otto, Christine Sers, Pamela Riemer, Carsten Groetzinger and Ulf Leser	DECO: DECOvolution of neuroendocrine expression signatures determines cell-subtype compositions of patient-derived endocrine cancer samples and elucidates their etiology	Data
P_Da059	591	Kiyoto Ito	Kiyoto Ito, Michihiro Araki, Taizo Hanai, Tomokazu Shirai, Kenji Tsuge and Shizu Takeda	Artificial Intelligence Technologies Extracting Design Knowledge for Creation of Highly Productive Microorganisms	Data
P_Da060	605	Alexia Giannoula	Alexia Giannoula, Emilio Centeno, Ferran Sanz and Laura I. Furlong	Temporal comorbidity analysis of disease trajectories using semantic, genetic and phenotypic similarities: an application to prostate cancer	Data
P_Da061	607	Line Mærsk Staunstrup	Line Mærsk Staunstrup, Morten Karsdal, Jørn Wulff Helge, Søren Brunak and Cecilie Liv Bager	General obesity and body fat distribution in relation to chronic disease burden in postmenopausal women	Data
P_Da062	610	Tunca Dogan	Tunca Dogan	HPO2GO: Prediction of Human Phenotype Ontology Term Associations for Proteins Using Cross Ontology Annotation Co-occurrences	Data
P_Da063	615	Maria Masid	Maria Masid, Vikash Pandey and Vassily Hatzimanikatis	Studying cancer cells phenotypes integrating omics data in human reduced genome-scale metabolic models	Data
P_Da064	617	Dimitrios Zisis	Dimitrios Zisis, Pawel Krajewski, Iris Hovel, Maïke Stam and Blaise Weber	Comparison of computational methods for 4C-seq NGS data analysis in different species	Data
P_Da065	618	Rayees Rahman	Rayees Rahman, Peter Ung and Avner Schlessinger	Redefining the Protein Kinase Conformational Space with Machine Learning	Data
P_Da066	622	Duong Vu	Duong Vu, Sonja Georgievska, Szanislo Szoke, Arnold Kuzniar and Vincent Robert	fMLC: Fast Multi-Level Clustering and Visualization of Large Molecular Datasets	Data
P_Da067	626	Laura Cantini	Laura Cantini, Ulybek Kairov, Aurélien de Reyniès, Emmanuel Barillot, Francois Radvanyi and Andrei Zinovyev	Stabilized Independent Component Analysis outperforms other methods in finding reproducible signals in tumoral transcriptomes	Data
P_Da068	631	Konstantina Vennou	Konstantina Vennou, Panagiota Kontou and Pantelis Bagos	An approach for multiple outcome meta-analysis of microarray data	Data
P_Da069	632	Ioannis A. Tamposis	Ioannis A. Tamposis, Konstantinos Tsirigos, Margarita C. Theodoropoulou, Panagiota Kontou and Pantelis Bagos	Semi-supervised learning of Hidden Markov Models for biological sequence analysis	Data
P_Da070	634	Ahmet Süreyya Rifaioğlu	Ahmet Süreyya Rifaioğlu, Tunca Dogan, Ömer Sinan Saraç, Tulin Ersahin, Rabie Saidi, Volkan Atalay, Maria Martin and Rengul Atalay	Large-scale automated function prediction of protein sequences and an experimental case study validation on PTEN transcript variants	Data

P_Da071	637	Despoina Kalfakakou	Despoina Kalfakakou, Florentia Fostira, Paraskevi Apostolou, Myrto Papamentzelopoulou, Andromachi Vagena, Angeliki Delimitsou, Ioannis Vlachos, Drakoulis Yannoukakos and Irene Konstantopoulou	CanVaS: Documenting genetic variation among cancer patients in Greece	Data
P_Da072	638	Onur Dereli	Onur Dereli, Ceyda Oğuz and Mehmet Gönen	Path2Surv: Pathway/gene set-based survival analysis using multiple kernel learning	Data
P_Da073	639	Elena Ocheredko	Elena Ocheredko, Dmitry Penzar and Sergey Spirin	Machine learning approach to prediction of quality of phylogenetic inference	Data
P_Da074	642	Manolis Maragkakis	Fadia Ibrahim, Manolis Maragkakis, Panagiotis Alexiou and Zissimos Mourelatos	Ribothrypsis, a novel process of canonical mRNA decay, and its implications	Data
P_Da075	651	Malvika Sudhakar	Malvika Sudhakar, Karthik Raman and Raghunathan Rengaswamy	Novel ratio-metric features enable the identification of new driver genes across cancer types	Data
P_Da076	653	Teerna Bhattacharyya	Teerna Bhattacharyya, Pritha Ghosh, Oommen K. Mathew and Ramanathan Sowdhamini	PASS2 version 6: a database of structure-based sequence alignments of protein domain superfamilies in accordance with SCOPe	Data
P_Da077	656	Vitor C. Piro	Vitor C. Piro, Temesgen H. Dadi, Enrico Seiler, Knut Reinert and Bernhard Y. Renard	ganon: fast indexing and classification of metagenomic sequences against huge databases	Data
P_Da078	661	Arezou Rahimi	Arezou Rahimi and Mehmet Gönen	Discriminating early- and late-stage cancers using multiple kernel learning on gene sets	Data
P_Da079	662	Alexey Stukalov	Alexey Stukalov, Philipp Hubel and Andreas Pichlmair	Chasing the Infected Proteome: System-wide Analysis of Virus-Induced Changes to Protein Synthesis and Degradation	Data
P_Da080	663	Eric Bach	Eric Bach, Céline Brouard, Juho Rousu, Sandor Szedmak and Sebastian Böcker	Liquid-Chromatography Retention Order Prediction for Metabolite Identification	Data
P_Da081	666	Neetika Nath	Neetika Nath, Till Ittermann, Henry Völzke and Lars Kaderali	Using random forest to predict thyroid disease – an example from the Study of Health in Pomerania	Data
P_Da082	670	Dmitry Ivankov	Laura Avino, Natalya Bogatyreva, Fyodor Kondrashov and Dmitry Ivankov	Finding epistasis in high-throughput experimental data	Data
P_Da083	683	Christine Jandrasits	Christine Jandrasits, Stefan Kröger, Walter Haas and Bernhard Renard	Pan-genome mapping and pairwise SNP-distance improve detection of Mycobacterium tuberculosis transmission clusters	Data
P_Da084	686	Maryam Ghareghani	Maryam Ghareghani, David Porubsky, Ashley Sanders, Sascha Meiers, Evan Eichler, Jan Korbel and Tobias Marschall	Strand-seq Enables Reliable Separation of Long Reads by Chromosome via Expectation Maximization	Data
P_Da085	687	Anna Katsiki	Anna Katsiki, Pantelis Karatzas, Alexandros Georgakilas and Constantinos Vorgias	DExplore: an online tool for detecting differentially expressed genes from mRNA microarray experiments	Data
P_Da086	688	Sudhir Kumar	Sudhir Kumar and Sayaka Miura	CloneFinder: Predicting clone genotypes from tumor bulk sequencing of multiple samples	Data
P_Da087	689	Ana Moya-Beltrán	Ana Moya-Beltrán, Camila Rojas and Raquel Quatrini	Cryptic diversity and genus delimitation of the prokaryotes in the genomic era: Acidithiobacillus species complex as study case.	Data
P_Da088	698	Naveen Kumar	Naveen Kumar and Todd Taylor	Knowledge discovery using semantic annotation with iCLIKVAL	Data
P_Da089	705	Mark Wilkinson	Beatriz García-Jiménez, Tomas de la Rosa and Mark Wilkinson	MDPbiome: microbiome engineering through prescriptive perturbations	Data
P_Da090	711	Chirag Jain	Chirag Jain, Sergey Koren, Alexander Dilthey, Adam Phillippy and Srinivas Aluru	A Fast Adaptive Algorithm for Computing Whole-Genome Homology Maps	Data
P_Da091	718	Sebastian Roskosch	Sebastian Roskosch, Bjarni Halldórsson and Birte Kehr	PopDel: Population-scale detection of genomic deletions	Data
P_Da092	720	Dimitris Manatakis	Dimitrios Manatakis, Vineet Raghu and Panayiotis Benos	piMGM: Incorporating Multi-Source Priors in Mixed Graphical Models for Learning Disease Networks	Data
P_Da093	721	Francisco Issotta	Francisco Issotta, Camila Rojas and Raquel Quatrini	Benchmarking of taxonomy assignment methods for metagenomic analysis using acidic microbiomes as test case	Data
P_Da094	725	Yaxuan Wang	Yaxuan Wang and Luay Nakhleh	Towards an Accurate and Efficient Heuristic for Species/Gene Tree Co-estimation	Data
P_Da095	735	Sunjoo Bang	Sunjoo Bang, Sang Joon Son and Hyunjung Shin	Min-cut on disease pathway for target protein identification	Data
P_Da096	736	Mehmet Akdel	Mehmet Akdel and Dick de Ridder	Signal-based optical map alignment and assembly	Data
P_Da097	738	Anna Ershova	Anna Ershova, Marina Khachatryan, Ivan Rusinov, Anna Karyagina, Sergei Spirin and Andrei Alexeevski	Restriction-Modification systems sharing in microbial community	Data
P_Da098	739	Anna Karyagina	Eugene Baulin, Olga Zanegina, Anna Karyagina, Andrei Alexeevski and Sergei Spirin	New automated classification of DNA-protein complexes in Nucleic acids – Protein Interaction Database	Data
P_Da099	740	Petr Nazarov	Petr Nazarov, Tony Kaoma, Aranud Muller, Katharina Baum, Sang-Yoon Kim, Gunnar Dittmar and Francisco Azuaje	Multi-omics data integration using parallel consensus independent component analysis	Data
P_Da100	741	Marina Khachatryan	Marina Khachatryan, Anna Ershova, Ivan Rusinov, Anna Karyagina, Sergei Spirin and Andrei Alexeevski	Distribution of Restriction-Modification systems in microbiomes of Tara Ocean project	Data
P_Da101	743	Aneta Sawikowska	Aneta Sawikowska, Anna Piasecka, Piotr Kachlicki and Pawel Krajewski	Computational peak deconvolution in chromatographic data by clustering and by functional data analysis	Data
P_Da102	746	Fernando Pozo	Fernando Pozo and Michael Tress	Machine Learning algorithm predicts the functional importance of potential Alternative Splicing isoforms	Data
P_Da103	747	Jakub M. Bartoszewicz	Jakub M. Bartoszewicz, Anja Seidel and Bernhard Y. Renard	Interpretable neural networks predict pathogenicity from short DNA reads	Data
P_Da104	752	Neetika Nath	Neetika Nath	Is lipid mass spectrometry measurement enough to predict lipid classes?	Data
P_Da105	755	Nurcan Tuncbag	Nurcan Tuncbag, Esra Sinoplu and Rengul Cetin-Atalay	Modeling of undefined off-target effects of drugs by computational systems biology methods and in vivo validation in hepatocellular carcinoma	Data
P_Da106	761	Gleb Goussarov	Gleb Goussarov, Ilse Cleenwerck, Mohamed Mysara, Natalie Leys, Peter Vandamme and Pieter Monsieurs	On the potential of short oligonucleotide frequencies for bacterial genome analysis	Data

P_Da107	762	Luciano Giaco'	Luciano Giaco', Elena Belloni, Elena Marino, Cristian Mauro, Matteo Dal Molin, Irene Feroce, Loris Bernard and Pier Giuseppe Pelicci	Variants significance by network in breast cancer predisposition	Data
P_Da108	767	Fabian Kern	Florian Schmidt, Fabian Kern and Marcel Schulz	Integrative prediction of gene expression with chromatin accessibility and conformation data	Data
P_Da109	770	Rania Hassan	Rania Hassan, Nourhan Abu-Shahba, Marwa Mahmoud and Mahmoud El-Hefnawi	Bioinformatics meta-analysis of tumor suppressor microRNA in hepatic cancer stem cells	Data
P_Da110	771	Ivan Rusinov	Ivan Rusinov, Anna Ershova, Anna Karyagina, Sergey Spirin and Andrei Alexeevski	Different families of Type II restriction endonucleases unequally induce recognition site avoidance in both bacteria and bacteriophages	Data
P_Da111	777	Evangelos Pafilis	Evangelos Pafilis, Manimozhiyan Arumugam and Lars Juhl Jensen	Text-mining-based interpretation of microbiome data	Data
P_Da112	778	Dong-Gi Lee	Dong-Gi Lee, Myungjun Kim, Sunghong Park and Hyunjung Shin	Causal Disease Chains from Various Biomedical data	Data
P_Da113	780	Declan Bennett	Declan Bennett, Dylan Spalding, Cristina Y. Gonzalez, Jorge Izquierdo, Zhicheng Liu, Selvakumar Kamatchinathan and Thomas Keane	AMP-Type 2 Diabetes Knowledge Portal	Data
P_Da114	790	Sabeur Aridhi	Seyed Ziaeddin Alborzi, Sabeur Aridhi, David Ritchie and Marie-Dominique Devignes	PPI DomainMiner: predicting domain-domain interactions from protein-protein interactions using tripartite graph modeling and vector similarity	Data
P_Da115	793	Martin Schwersensky	Martin Schwersensky, Fabrizio Pucci and Marianne Rooman	Exploring protein stability - evolution relationships to improve rational protein design methods	Data
P_Da116	798	Yao-Zhong Zhang	Yao-Zhong Zhang, Seiya Imoto, Satoru Miyano and Rui Yamaguchi	Modeling the correlation between read count and nucleotide sequence in NGS data within the framework of neural networks	Data
P_Da117	799	Alexander Monzon	Martín González Buitrón, Alexander Monzón, Silvina Fornasari and Gustavo Parisi	Conformational diversity in RNAs	Data
P_Da118	802	Yonghyun Nam	Yonghyun Nam, Jong Ho Jhee, Junhee Cho, Ji-Hyun Lee and Hyunjung Shin	Immune Disease Gene Ranker	Data
P_Da119	806	Hyunjung Shin	Junhee Cho, Yonghyun Nam and Hyunjung Shin	Prediction for orphan drugs using the hierarchical structure of biomedical networks	Data
P_Da120	808	Manli Yang	Manli Yang, Caroline Genco, Paola Massari, Thomas Rudel and Thomas Dandekar	Neisseria gonorrhoeae (GC) and Chlamydia trachomatis (CT) co-infection in human: Comparison of gene expression analysis pipelines and combined results including metagenomic analysis	Data
P_Da121	811	Moritz Hess	Moritz Hess, Stefan Lenz and Harald Binder	Using independent training data to improve the learning of immune cell infiltration patterns with deep learning techniques	Data
P_Da122	812	Tarcisio Fedrizzi	Tarcisio Fedrizzi, Davide Prandi, Alessio Locallo and Francesca Demichelis	Refined copy number analysis uncovers aggressive phenotypes in human tumors	Data
P_Da123	813	Atakan Yuksel	Atakan Yuksel, Hakime Ozturk, Arzucan Ozgur and Elif Ozkirimli	Use of Dimension Based Input Representation and LSTM in Biomedical Relation Extraction	Data
P_Da124	817	Lydia Giannakou	Lydia Giannakou, Erasmia Rouka, Eleftherios Papazoglou, Rajesh Jagirdar, Georgios Vavougiou, Konstantinos Gourgoulis, Chrissi Hatzoglou, Evgeniy Solenov and Sotiros Zarogiannis	Bioinformatic analysis of OCLN gene and protein and its differential expression in human cancers.	Data
P_Da125	818	Daphne Ezer	Daphne Ezer and Joseph Keir	Selection of time points for costly experiments: a comparison between human intuition and computer-aided experimental design	Data
P_Da126	819	Aleksandra Galitsyna	Aleksandra Galitsyna, Vlada Zakharova, Ekaterina Khrameeva, Sergey Razin, Mikhail Gelfand and Sergey Ulyanov	Single-cell Hi-C data analysis of Drosophila melanogaster	Data
P_Da127	820	Matteo Manica	Matteo Manica, Joris Cadow, Roland Mathis and Maria Rodriguez Martinez	PIMKL: Pathway Induced Multiple Kernel Learning	Data
P_Da128	821	Erasmia Rouka	Erasmia Rouka, Vassilios Liakopoulos, Konstantinos Gourgoulis, Chrissi Hatzoglou and Sotiros Zarogiannis	In-Silico analysis of the CLDN16 gene and protein: prediction of subcellular localization to mitochondria	Data
P_Da129	822	Barbara Martinelli	Barbara Martinelli, Pilib Ó Broin, John Grealley and Cathal Seoighe	MHap: Maximum likelihood inference of methylation haplotypes	Data
P_Da130	827	Tobias Frisch	Tobias Frisch, Jonatan Gøttke, Richard Röttger, Qihua Tan and Jan Baumbach	DIMmer – Discovery of Differentially Methylated Regions in Epigenome-Wide Association Study (EWAS) data	Data
P_Da131	829	Mikel Hernaez	Mikel Hernaez and Olivier Gevaert	Comparison of single gene and module-based methods for modeling gene regulatory networks	Data
P_Da132	834	Ernesto Luis Aparicio Puerta	Ernesto Luis Aparicio Puerta, David Jaspez, Juan Antonio Marchal, Danijela Koppers-Laic and Michael Hackenberg	Systematic reanalysis of small RNA-seq data from healthy patients reveals little agreement among liquid biopsy studies	Data
P_Da133	836	David P. Kreil	Paweł P. Łabaj and David P. Kreil	Assessing targetted RNA-seq for onco capture panels	Data
P_Da134	845	Michal Kolář	Michal Kolář, Veronika Živicová, Peter Gál, Alžběta Mířková, Herbert Kaltner, Hynek Strnad, Jana Šachová, Miluše Hradilová, Martin Chovanec, Hans-Joachim Gabius, Karel Smetana Jr. and Zdeněk Fik	Detection of distinct changes in gene-expression profiles in specimens of tumours and transition zones of tenascin-positive/-negative head and neck squamous cell carcinoma	Data
P_Da135	847	Bishnu Sarker	Bishnu Sarker, David Ritchie and Sabeur Aridhi	GrAPFI: Graph Based Inference for Automatic Protein Function Annotation	Data
P_Da136	851	Sucharita Dey	Sucharita Dey, David Ritchie and Emmanuel Levy	PDB-wide Identification of Biological Assemblies from Conserved Quaternary Structure Geometry	Data
P_Da137	854	Loredana Ciaccia	Loredana Ciaccia, Maria Angela Diroma, Claudio Lo Giudice, Bruno Fosso, Anita Annese, Italia Aiello, Caterina Manzari, Anna Maria D'Erchia, Graziano Pesole and Ernesto Picardi	Genome-wide RNA editing analysis in human neurological disorders	Data
P_Da138	855	Maria Angela Diroma	Maria Angela Diroma, Annarita Oranger, Anita Annese, Caterina Manzari, Marina Roberti, Francesco Bruni, Paola Loguercio Polosa, Ernesto Picardi, Anna Maria D'Erchia and Graziano Pesole	No evidence of mtDNA methylation by real-time direct Nanopore sequencing	Data
P_Da139	856	Claudio Lo Giudice	Claudio Lo Giudice, Luigi Mansi, Graziano Pesole and Ernesto Picardi	Detecting A-to-I RNA editing signatures in long RNA-Seq reads	Data

P_Da140	861	Gaëlle Lefort	Gaëlle Lefort, Laurence Liaubet, Cécile Canlet, Nathalie Vialaneix and Rémi Servien	ASICS: a new R package for identification and quantification of metabolites in complex 1D 1H NMR spectra	Data
P_Da141	866	David Nieuwenhuijse	David Nieuwenhuijse, Bas Oude Munnink, My Phan and Marion Koopmans	Viral sequence classification using deep learning algorithms	Data
P_Da142	870	Soufiane Mourragui	Soufiane Mourragui, Marco Loog, Marcel Jt Reinders and Lodewyk Fa Wessels	Domain adaptation to transfer predictors of drug response from cell lines to tumors	Data
P_Da143	882	Romain Groux	Romain Groux, Onur Tidin and Philipp Bucher	A K-means implementation to cluster genomic (and time lapse) data	Data
P_Da144	888	Anton I. Petrov	Anton I. Petrov, Blake Sweeney, Boris Burkov, Rob Finn, Alex Bateman and Rnacentral Consortium	RNAcentral: The unified database of ncRNA sequences with comprehensive genomic mapping and improved quality controls	Data
P_Da145	890	Sidney Walker	Sidney Walker, Julia Eckenberger, Marcus Claesson and Susan Joyce	Gut Microbiota is correlated with Bile Acids and Body Mass Index in Inflammatory Bowel Disease	Data
P_Da146	897	Anastasios Nentidis	Anastasios Nentidis, Konstantinos Bougiatiotis, Anastasia Krithara and Georgios Paliouras	Semantic integration of disease-specific knowledge	Data
P_Da147	898	Ioanna Kalvari	Ioanna Kalvari, Joanna Argasinska, Eric Nawrocki, Anton Petrov, Rob Finn and Alex Bateman	Rfam: The transition to a genome-centric sequence database	Data
P_Da148	907	Ricardo Arcila	Leyla Jael García Castro, Ricardo Arcila, Alasdair Gray and Bioschemas Community	Bioschemas, structured data on your web pages	Data
P_Da149	911	Sean Bankier	Sean Bankier, Tom Michoel, Filippo Menolacina, Brian Walker, Lingfei Wang, Andrew Crawford and Johan Björkregren	Cortisol Responsive Gene Networks in Cardiovascular Disease	Data
P_Da150	913	Vincenzo Lagani	Christina Chatzipantasiou, Vincenzo Lagani, Maria Markaki, Olav Toai Duc Nguyen, Robin Mjelle, Ioannis Tsamardinos and Oluf Dimitri Roe	Metabolomics signature in serum months to years before thoracic cancer: A HUNT study	Data
P_Da151	914	Gosia Golda	Gosia Golda, Lara Bossini-Castillo, Natalia Kunowska, Dafni Glinos, Paweł Łabaj and Gosia Trynka	Model for pre-sequencing quality control of ATAC-seq libraries	Data
P_Da152	915	Maria Stella de Biase	Maria Stella de Biase, Florian Markowitz, Bruce Ponder, Roland Schwarz and Robert Rintoul	Assessing the potential of nasal swabs as an alternative to bronchoscopy for early diagnosis of lung cancer	Data
P_Da153	916	Gopal Peddinti	Outi Koivistoinen and Gopal Peddinti	PlasmidDB: a data management system for strains and plasmids	Data
P_Da154	921	Daniel Sanchez Taltavull	Daniel Sanchez Taltavull	Bayesian Correlation Analysis for single-cell RNA-seq data	Data
P_Da155	922	Henning Hermjakob	Yasset Perez-Riverol, Andrey Zorin, Gaurhari Dass and Henning Hermjakob	Quantifying the impact of public omics data	Data
P_Da156	927	Shalaw Sallah	Shalaw Sallah	Use of homology modelling in clinical interpretation of variant pathogenicity: CACNA1F as an exemplar	Data
P_Da157	930	Meric Kinali	Meric Kinali, Ebru Bilget Guven, Mehmet Ozturk, Rengul Cetin Atalay and Aybar C. Acar	Leveraging the Human Kinome for Prediction of Anticancer Agent Cytotoxicity	Data
P_Da158	932	Dilip Durai	Mikko Rautiainen, Dilip Durai, Jonathan Göke, Marcel Schulz and Tobias Marschall	Aeron: Graph-based alignment and quantification of long reads to the transcriptome	Data
P_Da159	948	Gustavo Parisi	Martin Nicolas Salas, Gustavo Parisi, Marcia Hasenahuer, Silvina Maria Fornasari and Alex Monzon	Disease related and neutral variants in human proteins in ordered, disordered and order-disorder transition regions.	Data
P_Da160	951	Nikos Perdikopanis	Nikos Perdikopanis, Antonis Giannakakis, Ioannis Kavakiotis and Artemis Hatzigeorgiou	DIANA sORF: An algorithm for small coding ORFs identification	Data
P_Da161	955	Evangelos Bellos	Evangelos Bellos, Vanessa Sancho-Shimizu, Chenxi Zhou, Michael Levin and Lachlan Coin	Deep Learning techniques for accurate detection of Identity by Descent in sequencing datasets with high error rates	Data
P_Da162	958	Lukeman Shittu	Lukeman Shittu, Abiodun Jinadu, Remilekun Shittu and Solomon Shittu	Pharmacophore-Based Virtual Screening and Molecular Docking of Novel Inhibitors for HCV NS5B RNA-Dependent RNA Polymerase Enzyme from Crude Sesame Essential Oil.	Data
P_Da163	959	Bo Zeng	Bo Zeng	Properties and prediction of homotypic transmembrane helix-helix interfaces	Data
P_Da164	960	Veit Schwämmle	Veit Schwämmle and Ole N Jensen	VSCLust: Feature-based variance-sensitive clustering of omics data	Data
P_Da165	963	Giorgos Skoufos	Giorgos Skoufos, Joseph Paulson, Fatemeh Almodaresi, Robert Patro, Artemis G. Hatzigeorgiou and Ioannis S. Vlachos	AGAMEMNON: an Accurate metagEnomic And METatranscriptoMic quantification analysis suite	Data
P_Da166	964	Nikos Perdikopanis	Nikos Perdikopanis, Georgios Georgakilas, Ioannis Vlachos, Maria Paraskevopoulou, Peter Yang, Yuhong Zhang, Aris Economides and Artemis Hatzigeorgiou	MicroRNA Transcription Start Site (TSS) identification Using Machine Learning, enable the establishment of genome-wide maps of TF::miRNA interactions.	Data
P_Da167	968	Gal Dinstag	Gal Dinstag and Ron Shamir	Personalized prioritization of cancer driver mutations	Data
P_Da168	972	Boleslaw Karwowski	Boleslaw Karwowski	Influence of (5'R/S) 5'8-cyclo-2'-deoxyAdenosine and 7,8-dihydro-8-oxo-2'-deoxyGuanosine on radical cation formation in ds-DNA. The theoretical approach.	Data
P_Da169	973	Linnea Axelsson	Linnea Axelsson, Christian Blau and Erik Lindahl	Mining structural information from Cryo-EM densities	Data
P_Da170	983	Miroslava Cuperlovic-Culf	Miroslava Cuperlovic-Culf, Will Costain, Nam Huan Khieu, Junzhuo Huang, Nabil Belacel, Balu Chakravarthy, Kerry Rennie and Brian Green	Metabolomics analysis and computational modeling for determination of significant processes in Alzheimer disease development and diagnosis	Data
P_Da171	988	Susanne Kirchen	Susanne Kirchen, Dheeraj Bobbili and Patrick May	Variant annotation pipeline for the identification of splice-altering SNVs	Data
P_Da172	989	Arvind Sundaram	Pål Marius Bjørnstad and Arvind Sundaram	De novo identification of well hopping fragments in Illumina patterned flow cells using suprdUPr	Data
P_Da173	996	Margaretha Veltman	Margaretha Veltman, Jae Choi, Michael Purugganan and Eric Schranz	Origins and geographic diversification of African rice (<i>Oryza glaberrima</i>)	Data
P_Da174	1002	Laura Jenniches	Laura Jenniches, Alexander Westermann and Lars Barquist	Statistical modeling of complex sequencing experiments with Stan	Data
P_Da175	1005	Maria Kousi	Maria Kousi, Carles Boix, Hansruedi Mathys, Li-Huei Tsai and Manolis Kellis	Leveraging single-cell RNA-seq to infer cell type-specific somatic mutations and mosaicism in Alzheimer's disease.	Data
P_Da176	1010	Oleg Shpynov	Oleg Shpynov, Aleksei Dievskii, Roman Chernyatchik, Evgeny Kurbatsky, Petr Tsurinov and Maxim Artyomov	Semi-supervised peak calling solution	Data
P_Da177	1015	Aleksandra Gruca	Aleksandra Gruca, Roman Jaksik, Łukasz Wróbel and Marek Sikora	Integration of heterogeneous multi-omics data to determine the prognostic markers in Acute Lymphoblastic Leukemia	Data
P_Da178	1020	Hongyu Miao	Hongyu Miao	Statistical Time-Frequency Analysis of Nonstationary Time Series	Data

THEME / TRACK: ELIXIR

Poster #	EasyChair ID	Presenting Author	Authors	Title	Topic
P_EI001	376	Rachel Drysdale	Rachel Drysdale	The ELIXIR Data Platform	ELIXIR
P_EI002	384	John Hancock	John Hancock and Gary Saunders	The ELIXIR Communities	ELIXIR
P_EI003	394	Torsten Schwede	Christine Orengo, Bohdan Schneider, Torsten Schwede, Joel L. Sussman, Janet M. Thornton, Sameer Velankar and Shoshana Wodak	Coordination of Structural bioinformatics Activities across Europe	ELIXIR
P_EI004	424	Jennifer Harrow	Jennifer Harrow	Exploring the ELIXIR Tools Platform	ELIXIR
P_EI005	425	Sirarat Sarntivijai	Sirarat Sarntivijai	ELIXIR: Interoperability with a FAIR Purpose	ELIXIR
P_EI006	428	Sayoni Das	Sayoni Das, Natalie Dawson, Ian Sillitoe and Christine Orengo	Integrating Protein Structure Data and Functional Site Data from CATH and Other Resources to Aid Analysis of Human Genetic Variations Linked to Diseases	ELIXIR
P_EI007	445	Haleh Chizari	Haleh Chizari, Amin Ardehshirdavani and Yves Moreau	PhenBook: Userfriendly interface for phenotyping	ELIXIR
P_EI008	448	Kim T Gurwitz	Kim T Gurwitz, Louisa Bellis, Sarah L Morgan and Gabriella Rustici	Developing a framework to assess the quality and impact of bioinformatics training across ELIXIR	ELIXIR
P_EI009	493	Enio Gjerga	Enio Gjerga, Julio Saez Rodriguez and Aurelien Dugourd	Efficient training of logic models to mass spectrometry phosphoproteomics data with Integer Linear Programming	ELIXIR
P_EI010	571	Marek Schwarz	Marek Schwarz, Jiří Vohradský and Josef Pánek	Automated pipeline to characterize possible ncRNA homologs in BLAST output	ELIXIR
P_EI011	572	Foivos Gypas	Foivos Gypas, Alexander Kanitz, Christina Herrmann, Edim Zdralovic, Marcel Luckeneder, Patrick Keller, Jessica Koeberle, Jonas Schurr and Mihaela Zavolan	Krini: A modern web application for the analysis of sequencing data	ELIXIR
P_EI012	573	Malo Le Boulch	Malo Le Boulch, Sylvie Combes and Géraldine Pascal	MACADAM a user-friendly MetAbolic pATHway DATabase for complex Microbial community function analysis	ELIXIR
P_EI013	584	Gurnoor Singh	Arnold Kuzniar, Gurnoor Singh, Carlos Martinez Ortiz, Richard Visser and Richard Finkers	Linked Data Platform for Plant Breeding & Genomics	ELIXIR
P_EI014	588	Panos Bravakos	Panos Bravakos, Christos Christakis, Kleoniki Keklikoglou, Christos Arvanitidis, Artemis Hatzigeorgiou, Maria Klappa, Evangelos Pafilis and Georgios Kotoulas	The Elixir-Greece Marine Biology joint research activity and the LifeWatch Greece microCT vLab	ELIXIR
P_EI015	690	Mahmoud Elhefnawi	Nourhan Abu-Shahba, Elsayed Hegazy, Tarek A. A. Moussa and Mahmoud Elhefnawi	A Comprehensive Meta-analysis of MicroRNA Expression Data from Liver Cancer	ELIXIR
P_EI016	781	Gianvito Urgese	Gianvito Urgese, Orazio Scicolone, Emanuele Parisi, Santa Di Cataldo, Enrico Macii and Elisa Ficarra	BioSeq-Zip: a tool for collapsing recurrent reads in high throughput sequencing datasets	ELIXIR
P_EI017	844	Salvador Capella-Gutiérrez	Salvador Capella-Gutiérrez, Juergen Haas, Vicky Sundesha, Dmitry Repchevsky, Miguel Madrid-Mencia, Javier Garrayo, Victor Fernández-Rodríguez, Laia Codó, José María Fernández González, Analia Lourenco, Josep Ll Gelpi and Alfonso Valencia	OpenEBench. The ELIXIR platform for benchmarking.	ELIXIR
P_EI018	863	Matthias Lange	Daniel Arend, Astrid Junker, Uwe Scholz and Matthias Lange	From FAIRer data do faster discovery - using ELIXIR and de.NBI infrastructure to serve comprehensive plant research data	ELIXIR
P_EI019	864	Uzma Saqib	Uzma Saqib	Drug repositioning as an effective therapy for Protease-Activated Receptor-2 inhibition	ELIXIR
P_EI020	865	Mirza Baig	Mirza Baig	Heterotrimeric complex of p38 MAPK, PKCδ, and TIRAP is required for AP1 mediated inflammatory response.	ELIXIR
P_EI021	867	Joel Hedlund	Antti Pursula, Joel Hedlund, Niclas Jareborg, Johanna Kaunisvaara, Abdulrahman Azab and Ali Syed	Tryggve – Nordic collaboration on sensitive data	ELIXIR
P_EI022	868	Anjali Shrivastava	Anjali Shrivastava, Noemi Del Toro Ayllon, Pablo Porras Millan, Margaret Duesbury, Livia Peretto, Sandra Orchard and Henning Hermjakob	IMEx Mutations Data Set	ELIXIR
P_EI023	873	Joan Segura	Joan Segura, Ruben Sanchez-Garcia, Carlos Oscar Sánchez Sorzano and Jose Maria Carazo	3DBIONOTES crossing genomics, proteomics and interactomics	ELIXIR
P_EI024	879	Jan Jelinek	Jan Jelinek and Josef Panek	cpPredictor: Webserver for template-based prediction of RNA secondary structure	ELIXIR
P_EI025	883	Christine Stansberg	Kidane Tekle, Sveinung Gundersen, Kjetil Klepper, Lars Ailo Bongo, Inge Alexander Raknes, Xiayi Li, Wei Zhang, Christian Andretta, Teshome Mulugeta, Matúš Kalaš, Morten Rye, Erik Hjerde, Jeevan Anthony Karloss Samy, Ghislain Fornous, Abdulrahman Azab, Dag Inge Våge, Eivind Hovig, Nils Peder Willassen, Finn Drablos, Ståle Nygård, Kjell Petersen, Inge Jonassen and Christine Stansberg	The Norwegian e-infrastructure for Life Sciences (NeLS)	ELIXIR
P_EI026	919	Roland Krause	Pinar Alper, Regina Becker, Venkata Satagopam, Valentin Groues, Jacek Lebioda, Yohan Jarosz, Christophe Trefois, Roland Krause, Sandrine Munoz and Reinhard Schneider	DAISY – a Data Information System for GDPR compliance	ELIXIR
P_EI027	923	Mateusz Kuzak	Mateusz Kuzak, Jennifer Harrow, Rafael C Jimenez, Paula Martinez, Fotis Psomopoulos, Radka Svobodová Vařeková and Allegra Via	Lesson development for Open Source Software best practices adoption	ELIXIR
P_EI028	924	Venkata Satagopam	Venkata Satagopam, Christophe Trefois, Wei Gu, Roland Krause, Pinar Alper, Valentin Groues, Yohan Jarosz, Jacek Lebioda, Noua Toukourou, Dietlind Gerloff, Regina Becker and Reinhard Schneider	ELIXIR-LU : Giving life to data	ELIXIR

P_EI029	941	Olga Krebs	Olga Krebs, Finn Bacall, Martin Golebiewski, Hadas Leonov, Stuart Owen, Natalie Stanford, Alan Williams, Ulrikeg Wittig, Katherine Wolstencroft, Bernd Rinn, Jacky Snoep, Wolfgang Müller and Carole Goble	FAIRDOMHub for Findable, Accessible, Interoperable, and Reusable Research Data.	ELIXIR
P_EI030	942	Irene Liampa	Irene Liampa, Hector - Xavier de Lastic, Eleftherios Pilalis and Aristotelis Chatziioannou	Development of an integrated functional network analysis and composite signature derivation pipeline for ncRNAs RNA-seq data	ELIXIR
P_EI031	966	Alexandros Dimopoulos	Alexandros Dimopoulos and Martin Reczko	Integrated web resource usage monitoring	ELIXIR
P_EI032	967	Michaela Nekardova	Michaela Nekardova, Lada Biedermannova, Jiri Cerny and Bohdan Schneider	Ordered Hydration Sites around Dinucleotide Conformational Classes NtC	ELIXIR
P_EI033	969	Kalaivani Paramasivan	Kalaivani Paramasivan and Sarma Mutturi	Genome-scale model based target prediction for improvement of terpenoid precursors in <i>Saccharomyces cerevisiae</i>	ELIXIR
P_EI034	970	Peder Worning	Peder Worning, Heidi Gumpert and Henrik Westh	The contaminated genome	ELIXIR
P_EI035	995	Bengt Persson	Bengt Persson, Mikael Borg, Henrik Lantz, Niclas Jareborg, Jonas Hagberg, Jessica Lindvall, Fredrik Levander, Kalle von Feilitzen, Per Oksvold, Johan Viklund, Frederic Haziza, Andreas Kähäri, Nanjiang Shu, Pontus Freyhult, Jacques Dainat, Mahesh Binzer-Panchal, Lucile Soler, Yvonne Kallberg, Leslie Copley, Martin Norling and Anders Larsson	Elixir-SE	ELIXIR

THEME / TRACK: GENES

Poster #	EasyChair ID	Presenting Author	Authors	Title	Topic
P_Ge001	219	Chul Kim	Chul Kim, Boseok Seong and Yunji Jang	Identification of epigenetic recovery factor from medicinal-herb (<i>Descurainia sophia</i>) treated asthma based on multi-omics approach	Genes
P_Ge002	392	Panagiotis Mokos	Panagiotis Mokos, Fotis Psomopoulos, Chrysanthi Ainali, Anagnostis Argiriou, Alexandra Charalampidou, Paschalis Korosoglou, George Mosialos, Margarita Hadzopoulou-Cladaras and Dimitra Dafou	A network-structured prognostic model robustly predicts overall survival of hepatocellular carcinoma patients	Genes
P_Ge003	396	Morten Rye	Morten Rye, Helena Bertilsson, Maria Andersen, Kjersti Rise, Tone Bathen, Finn Drablos and May-Britt Tessem	Computational minimization of tissue confounding shows that cholesterol synthesis pathway genes in prostate cancer are transcriptionally downregulated.	Genes
P_Ge004	399	Mikael Andersen	Julian Brandl and Mikael Andersen	Reconstruction of the <i>Aspergillus niger</i> metabolic network	Genes
P_Ge005	433	ChantrioInt-Andreas Kapourani	ChantrioInt-Andreas Kapourani and Guido Sanguinetti	Melissa: Bayesian clustering and imputation of single cell methylomes	Genes
P_Ge006	435	Nuriye Özlem Özcan Şimşek	Nuriye Özlem Özcan Şimşek, Arzucan Özgür and Fikret Gürgen	Analysis of Data Representation Techniques and Machine Learning Methods on Variant Calls for Classification of Cancer Types	Genes
P_Ge007	455	Agnieszka Chetkowska	Agnieszka Chetkowska and Marek Żywicki	rnaSMART - tool for identification of Structural Motifs Across RNA Transcripts	Genes
P_Ge008	458	Kamil Khafizov	Kamil Khafizov, Andrey Ayginin, Alina Matsvay, Ekaterina Pimkina, Anna Speranskaya, Marina Safonova, Ilya Artyushin, Vladimir Dedkov and German Shipulin	Detection and identification of viral RNA in biological samples using next-generation sequencing	Genes
P_Ge009	459	Martin Treppner	Martin Treppner and Harald Binder	Boltzmann Encoded Adversarial Machines for Simulating Single Cell RNA-seq Data	Genes
P_Ge010	464	Cristina M. Osuna-Cruz	Cristina M. Osuna-Cruz, Emmelien Vancaester, Petra Bulankova, Gust Bilcke, Bram Verhelst, Atle M. Bones, Wim Vyverman, Lieven De Veylder and Klaas Vandepoele	Genome assembly, gene annotation and expression analysis of the diatom <i>Seminavis robusta</i> .	Genes
P_Ge011	466	Elisa Mariella	Elisa Mariella, Elena Grassi, Mattia Forneris, Federico Marotta, Alessandro Lussana, Marika Catapano, Ivan Molineris and Paolo Provero	A functional strategy to characterize expression Quantitative Trait Loci	Genes
P_Ge012	494	Alberto Meseguer	Oriol Fornes, Alberto Meseguer, Jaume Bonet and Baldo Oliva	Prediction of transcription factor binding by structural modeling	Genes
P_Ge013	501	Rodrigo Santibáñez	Rodrigo Santibáñez, Daniel Garrido and Alberto J.M. Martin	Automatic Rule-Based Model Reconstruction and Model Calibration of a Gene Regulatory Network	Genes
P_Ge014	510	Maria Elkjær	Maria Elkjær, Tobias Frisch, Mark Burton, Torben Kruse, Mads Thomassen, Richard Reynolds, Jan Baumbach and Zsolt Illes	Lesion Evolution and Fate in Progressive Multiple Sclerosis Patients	Genes
P_Ge015	511	Davide Cittaro	Paolo Provero, Dejan Lazarevic and Davide Cittaro	Somatic mutability in cancer predicts the phenotypic relevance of germline mutations	Genes
P_Ge016	515	Josephine Daub	Josephine Daub, Saman Amini, Frank Holstege and Patrick Kemmeren	Genetic interactions in childhood cancer	Genes
P_Ge017	525	Paolo Martini	Paolo Martini, Enrica Calura, Monica Chiogna and Chiara Romualdi	Gaining power from multi-omic data integration and pathway topology: improvement of prognostic gene module identification	Genes
P_Ge018	529	Anne-Christin Hauschild	Anne-Christin Hauschild, Malgorzata Maciukiewicz, Victoria Marshe, Igor Jurisica and Daniel J. Müller	Systems biology approach to evaluate genetic factors of antidepressant treatment outcome in major depressive disorder	Genes
P_Ge019	544	Katerina Boufea	Katerina Boufea and Nizar Batada	scID: matching single cell RNA-seq data to gene signatures on an individual cell level	Genes
P_Ge020	548	Alexander G. B. Grønning	Alexander G. B. Grønning, Christian Wiwie and Jan Baumbach	Convolutional neural network for cis-regulatory module detection.	Genes

P_Ge021	559	Marina Petkovic	Marina Petkovic, Thomas Watkins, Charles Swanton and Roland Schwarz	Reconstructing the evolutionary history of cancer from allele-specific copy-number profiles	Genes
P_Ge022	560	Joshua Backman	Joshua Backman, Nilanjana Banerjee and Colm O'Dushlaine	Leveraging correlation in a biobank-scale cohort: New insights from DiscovEHR	Genes
P_Ge023	564	Lise Pomiès	Lise Pomiès, Louise Gody, Charlotte Penouilh-Suzette, Nicolas Langlade, Brigitte Mangin and Simon de Givry	Building artificial genetical genomic dataset to optimize the choice of gene regulatory network inference methods	Genes
P_Ge024	567	Anastasia Filia	Anastasia Filia, George Bertsis, Nikolaos Panousis, Emmanouil Dermizakis and Dimitrios Boumpas	Biomarkers for the activity of Systemic Lupus Erythematosus using RNA sequencing and machine learning techniques	Genes
P_Ge025	570	Maria Katsantoni	Maria Katsantoni, Alexander Kanitz, Erik van Nimwegen and Mihaela Zavolan	Inferring RNA-binding sites, motifs and regulation from CLIP data with RCRUNCH	Genes
P_Ge026	578	Floriane Noel	Paula Michea, Floriane Noel, Eve Zakine, Urszula Czerwinska, Philemon Sirven, Omar Abouzid, Christel Goudot, Alix Scholer-Dahirel, Anne Vincent-Salomon, Fabien Reyat, Sebastian Amigorena, Maude Guillot-Delost, Elodie Segura and Vassili Soumelis	Analysis of dendritic cells subsets transcriptional reprogramming in the breast-cancer microenvironment	Genes
P_Ge027	596	Insong Koh	Hyoen Kang, Kiejung Park and Insong Koh	Identification of Korean specific gastric cancer predisposing genes based on whole genome sequences of Korean patients	Genes
P_Ge028	599	Serdar Bozdog	Banabithi Bose and Serdar Bozdog	Copy Number-Derived microRNA-Gene Interactions in Cancer	Genes
P_Ge029	613	Nikolaos Vakirlis	Nikolaos Vakirlis, Anne-Ruxandra Carvunis and Aoife McLysaght	Homology, sequence divergence and the origin of new genes	Genes
P_Ge030	614	Martin Burkert	Martin Burkert, Uwe Ohler and Roland F Schwarz	Sensitive mapping of regulatory variation in neuroblastoma tumor genomes	Genes
P_Ge031	621	Florian Schmidt	Florian Schmidt, Alexander Marx, Markus List, Jilles Vreeken, Jonathan Göke and Marcel Schulz	Integrative analysis of epigenetics data defines promoter-enhancer interactions.	Genes
P_Ge032	625	Sutapa Datta	Sutapa Datta and Rajgopal Srinivasan	A novel scoring scheme for predicting health status of an individual based on the genome data	Genes
P_Ge033	627	Tammi Vesth	Tammi Vesth, Inge Kjærboelling, Jane L. Nybo, Sebastian Theobald, Jens Frisvad, Scott Baker and Mikael Rørdam Andersen	Immense diversity found in secondary metabolite gene clusters in filamentous fungi and bacteria using comparative genomics	Genes
P_Ge034	629	Anna Pacinkova	Anna Pacinkova and Vlad Popovici	Cross-platform gene expression signature for microsatellite instability in colon and gastric cancers	Genes
P_Ge035	648	Jose Mg Izarzugaza	Jose Mg Izarzugaza and Søren Brunak	Defects in Calcium Signalling Cause Congenital Heart Disease	Genes
P_Ge036	649	Ilan Ben-Bassat	Ilan Ben-Bassat, Benny Chor and Yaron Orenstein	A Deep Learning Approach for Learning Intrinsic Protein-RNA Binding Preferences	Genes
P_Ge037	658	Roberta Bosotti	Giovanni Carapezza, Carlo Cusi, Ettore Rizzo, Laura Radrizzani, Sebastiano Di Bella, Alessio Somaschini, Rosita Lupi, Margherita Mutarelli, Vincenzo Nigro, Diego Di Bernardo, Paolo Magni, Antonella Isacchi and Roberta Bosotti	KING-REX: a custom end-to-end solution for kinome gene expression profiling	Genes
P_Ge038	660	Sofie Demeyer	Sofie Demeyer, Marlies Vanden Bempt, Charles de Bock and Jan Cools	Cooperative enhancer activation by TLX1 and STAT5 drives leukemia development in NUP214-ABL1/TLX1-positive T-cell acute lymphoblastic leukemia	Genes
P_Ge039	664	Shohag Barman	Shohag Barman and Yung-Keun Kwon	A Boolean Network Inference from Time-Series Gene Expression Data Using a Genetic Algorithm	Genes
P_Ge040	667	Patricia Sieber	Patricia Sieber, Matthias Platzer and Stefan Schuster	The definition of open reading frame revisited	Genes
P_Ge041	668	Julia Varga	Julia Varga and Gábor E. Tusnády	Effect of alternative splicing on human transmembrane protein topology	Genes
P_Ge042	669	Sylvain Foissac	Camille Mestre, Sarah Djebali, Thomas Faraut, Nathalie Vialaneix, Andrea Rau, Cédric Cabau, Matthias Zytnicki, David Robelin, Thomas Derrien, Hervé Acloque, Sandrine Lagarrigue, Elisabetta Giuffra and Sylvain Foissac	Integrative analyses of chromosome conformation, chromatin accessibility and gene expression in human and livestock genomes	Genes
P_Ge043	684	Denis Moshensky	Denis Moshensky and Andrey Alexeevski	CAN ESSENTIAL GENES BE ENCODED BY LONG ANTIPARALLEL OPEN READING FRAMES IN PROKARYOTIC GENOMES?	Genes
P_Ge044	712	Panayiotis Benos	Lucas Dos Santos and Panayiotis Benos	mirSNPEffect: A binding-energy based algorithm for measuring SNP effects in miRNA binding	Genes
P_Ge045	715	Mahsa Ghanbari	Mahsa Ghanbari and Uwe Ohler	A multitask and multimodal deep neural network for characterizing RNA binding protein target preferences	Genes
P_Ge046	724	Dowan Kim	Dowan Kim	Transcriptome analysis and Differential Gene Expression of two papaver herbs	Genes
P_Ge047	733	Daniil Wiebe	Daniil Wiebe, Viktoria Mironova and Nadezhda Omelyanchuk	Auxin regulates functional gene groups in a fold-change-specific manner in Arabidopsis thaliana roots	Genes
P_Ge048	737	Arlin Keo	Arlin Keo, Ahmed Mahfouz, Gillian Bonvicini, Angela Ingrassia, Johan Marinus, Jean-Pascal Meneboo, Celine Villenet, Martin Figeac, Eugénie Mutez, Thomas Comptdaer, Vincenzo Bonifati, Marie-Christine Chartier-Harlin, Wilma van de Berg, Jacobus van Hilten and Marcel Reinders	Brain-wide differences in gene expression and selective vulnerability to Parkinson's disease	Genes
P_Ge049	750	Gnanavel Mutharasu	Gnanavel Mutharasu and Matti Nykter	Cloud computing pipeline for detecting gene-fusion events in human cancers	Genes
P_Ge050	768	Julien Lagarde	Julien Lagarde, Silvia Carbonell, Barbara Uszczynska-Ratajczak, Adam Frankish, Rory Johnson and Roderic Guigo	Towards a complete atlas of long noncoding RNAs in human and mouse	Genes
P_Ge051	779	Xiaokang Zhang	Xiaokang Zhang and Inge Jonassen	EFSIS – Ensemble Feature Selection Integrating Stability	Genes
P_Ge052	784	Warren W. Kretschmar	Warren W. Kretschmar, Shirin Akhter, Veronika Nordal, Nicolas Delhomme, Nathaniel R. Street, Ove Nilsson, Olof Emanuelsson and Jens F. Sundström	Novel transcriptome assembly method identifies novel MADS-box isoforms during early bud development in Picea abies	Genes
P_Ge053	789	Alex Warwick Vesztrocy	Alex Warwick Vesztrocy, Christophe Dessimoz and Henning Redestig	Prioritising Candidate Genes Causing QTL using Hierarchical Orthologous Groups	Genes

P_Ge054	805	Eleftherios Pilalis	Eleftherios Pilalis and Aristotelis Chatziioannou	A cloud computational platform for discovery of bioactive compounds against neurodegenerative disorders	Genes
P_Ge055	815	Rishi Das Roy	Rishi Das Roy, Outi Hallikas, Elodie Renvoise and Jukka Jernvall	DELocal: Chromosomal co-occurrence of genes of dissimilar functions allow improved identification of differentially expressed genes	Genes
P_Ge056	823	Rajesh Jagirdar	Rajesh Jagirdar, Vijay Bhaskar Ciriium, Eleftherios Papazoglou, Erasmia Rouka, Ram Podicheti, Chrissi Hatzoglou, Konstantinos Gourgouliannis and Sotirios Zarogiannis	RAG recombinase and DNA sequence dependant interactors promote recurrent gene fusions in solid tumors	Genes
P_Ge057	825	Frances Pearl	Hanadi Baieisa, Sarah Wooller, Chris Richardson and Frances Pearl	Predicting loss of function and gain of function driver missense mutations in cancer	Genes
P_Ge058	826	Sergio Picart-Armada	Sergio Picart-Armada, Wesley K. Thompson, Alfonso Buil and Alexandre Perera-Lluna	A tissue-specific network-based pathway enrichment technique and application to GWAS data	Genes
P_Ge059	830	Gwenneg Kerdivel	Gwenneg Kerdivel, Jérôme Bertherat, Guillaume Assié and Valentina Boeva	Deciphering the role of epigenetic modifications in aggressiveness of adrenocortical carcinoma	Genes
P_Ge060	833	Dan Deblasio	Dan Deblasio and Carl Kingsford	Automatically eliminating errors induced by suboptimal parameter choices in transcript assembly	Genes
P_Ge061	835	Georgios Tsaousis	Georgios Tsaousis, Dimitrios Fotiou, Eirini Papadopoulou and George Nasioulas	Tumor Mutational Burden (TMB) and Neoantigen Load (NAL) estimation model using targeted Next Generation Sequencing (NGS) gene panels	Genes
P_Ge062	841	Lélia Polit	Lélia Polit, Sebastian Gregoricchio, Michaela Esposito, Christel Guillouf and Valentina Boeva	Epigenetic landscape in the neighborhood of binding sites of the pioneer transcription factor Spi1/PU.1 affects the efficiency of Spi1/PU.1 regulation of gene expression	Genes
P_Ge063	846	Wim Cuypers	Wim Cuypers, Gordon Dougan, Jan Jacobs, Pieter Meysman, Kris Laukens, Stijn Deborgraeve and Sandra Van Puyvelde	Comparative genomics of Salmonella Concord from the Horn of Africa reveals genomic signatures related to high resistance and virulence.	Genes
P_Ge064	852	Irina Poverennaya	Irina Poverennaya and Nadezhda Potapova	Search for intron sliding in Mammals.	Genes
P_Ge065	859	Remi Momo	Remi Momo, Natasa Przulj and Noel Malod-Dognin	Prognostic significance of HOX gene expression in breast cancer	Genes
P_Ge066	894	Paweł Mackiewicz	Paweł Mackiewicz, Adam D. Urantówka and Aleksandra Krocak	Efficiency of tree constructed methods and mitochondrial markers on inferring phylogenetic relationships in the example of parrots	Genes
P_Ge067	901	Georgios Bikos	Georgios Bikos, Anastasios Nentidis, Apostolos Malatras, William Duddy and Georgios Paliouras	Discovery of Functional Associations in Duchenne Muscular Dystrophy	Genes
P_Ge068	917	Olga Ivanova	Olga Ivanova, Alexander Mazein, Irina Balaur, Ludovic Roy, Bertrand De Meulder and Charles Auffray	Towards generating AsthmaMap Activity Flow	Genes
P_Ge069	920	María Markaki	Michail Tsagris, Maria Markaki, Kleio Maria Verrou Verrou, Zacharias Papadovasilakis and Ioannis Tsamardinos	Efficient and Accurate Feature Selection with the R Package MXM	Genes
P_Ge070	938	Jan Grau	Jens Keilwagen, Frank Hartung, Michael Paulini, Sven O. Twardziok and Jan Grau	Improving homology-based gene prediction using intron position conservation and RNA-seq data	Genes
P_Ge071	956	Dimitra Karagkouni	Dimitra Karagkouni, Maria D Paraskevopoulou, Ioannis S Vlachos, Spyros Tastsoglou, Serafeim Chatzopoulos, Ioannis Kavakiotis, Thanasis Vergoulis, Theodore Dalamagas and Artemis G Hatzigeorgiou	Indexing experimentally supported interactions of microRNAs with coding and non-coding transcripts	Genes
P_Ge072	957	Maria D Paraskevopoulou	Maria D Paraskevopoulou, Dimitra Karagkouni, Ioannis S Vlachos, Spyros Tastsoglou and Artemis G Hatzigeorgiou	Super Learning offers new insights in CLIP-Seq guided identification of functional miRNA interactions	Genes
P_Ge073	978	Francisco Callejas	Francisco Callejas, Nuria Gironès and Manuel Fresno	Assembly and analysis of the circular mitochondrial DNA of Trypanosoma cruzi, a neglected human pathogen.	Genes
P_Ge074	982	Christopher Penfold	Christopher Penfold, Anastasiya Sybirna, John Reid, Yun Huang, Lorenz Wernisch, Murray Grant, Zoubin Ghahramani and Azim Surani	Nonparametric Bayesian inference of transcriptional branching and recombination identifies regulators of early germ cell development	Genes
P_Ge075	1009	Atul Sethi	Atul Sethi, Milan Obradovic, Ryoko Okamoto, Christian Biesel, Michael Stadler and Mohamed Bentires-Alij	Single cell RNA sequencing reveals heterogeneity and pre-existing chemo-resistant cells in breast cancer	Genes
P_Ge076	1013	Dimitra Sarantopoulou	Dimitra Sarantopoulou, Emanuela Ricciotti, Nicholas Lahens, Soon Yew Tang, Damien Lekkas, Xiaofeng S. Guo, George Paschos, Jonathan Schug, Garret Fitzgerald, Allan I. Pack and Gregory Grant	Comparative analysis of library preparation methods for strand-specificity and high amplification	Genes
P_Ge077	1016	Ali Oghabian	Ali Oghabian and Mikko J. Frilander	Applying IntERest (Intron-Exon Retention Estimator) for intron retention level estimation and differential intron retention analysis	Genes

THEME / TRACK: GENOME

Poster #	EasyChair ID	Presenting_Author	Authors	Title	Topic
P_Go001	204	Siyu Liu	Siyu Liu	Genome-wide characterization of 5-hydroxymethylcytosine in head and neck cancers by HPV status	Genome
P_Go002	370	German Demidov	German Demidov and Stephan Ossowski	ClinCNV: novel method for large-scale CNV and CNA discovery	Genome

P_Go003	374	Jaume Sastre	Jaume Sastre, Emidio Capriotti, Emilia Amengual, Victor Asensio, Damià Heine and Jairo Rocha	Epistatic SNP Pairs with a Significant Subset of Subjects in Lung Cancer	Genome
P_Go004	383	Kalyani Dhusia	Kalyani Dhusia, Ankush Bansal, Tirathraj Singh and Pramod Ramteke	Genome wide analysis of <i>Serratia marcescens</i> unraveled the key regulatory mechanisms in antibiotics resistance	Genome
P_Go005	403	Ulrike Löber	Ulrike Löber, David E. Alquezar-Planas, Pin Cui and Alex D. Greenwood	SIP - Sonication inverse PCR	Genome
P_Go006	430	Manish Goel	Manish Goel, Hequan Sun, Wen-Biao Jiao and Korbinian Schneeberger	Identification of structural rearrangements within whole-genome assemblies using Synteny and Rearrangement Identifier - SyRI	Genome
P_Go007	432	Marc Sturm	Marc Sturm and Christopher Schroeder	ngs-bits - Short-read sequencing tools	Genome
P_Go008	442	Piotr Kopeć	Piotr Kopeć and Wojciech M. Karłowski	Detection of single nucleotide variability of pre-mRNA G-quadruplexes using plant WGS datasets	Genome
P_Go009	446	Anshupa Sahu	Anshupa Sahu and Ho Ryun Chung	EPIGENE: an EPIgenomic based tissue-specific GENE annotation	Genome
P_Go010	450	Satoshi Ito	Satoshi Ito, Masaaki Yadome and Satoru Miyano	Virtual Grid Engine: A pseudo grid engine on MPI parallel environments	Genome
P_Go011	457	Tobias Rausch	Tobias Rausch, Markus Fritz, Vladimir Benes and Andreas Untergasser	GEAR: The Genome Analysis Server gear.embl.de	Genome
P_Go012	462	Sarah Sandmann	Sarah Sandmann, Tasneem Khanam, Katrin Reutter, Birgit Burkhardt and Martin Dugas	A Novel Algorithm for CNV Calling in Matched WES Data	Genome
P_Go013	463	Nav. Krishnamoorthy	Navaneethakrishnan Krishnamoorthy and Sahar Da'as	Structure-functional relationship of disease-causing mutations in cMyBP-C: Impact on phenotypes of hypertrophic cardiomyopathy	Genome
P_Go014	469	Ron Huebler	Ron Huebler, Felix M Key, Christina Warinner, Kirsten Bos, Johannes Krause and Alexander Herbig	HOPS: A pipeline for screening archaeological remains for pathogen DNA	Genome
P_Go015	470	Lea Meunier	Lea Meunier, Sandrine Imbeaud, Julien Calderaro, Sandra Rebouissou, Gabrielle Couchy, Alexis Laurent, Jean-Frédéric Blanc, Jean-Charles Nault, Paulette Bioulac-Sage, Jessica Zucman-Rossi and Eric Letouzé	Independent component analysis of DNA methylation signatures in hepatocellular carcinoma	Genome
P_Go016	474	Leonidas Salichos	Leonidas Salichos, William Meyerson, Jonathan Warrell and Mark Gerstein	Estimating positive growth and driver effects in 994 single tumors from bulk sequencing data	Genome
P_Go017	476	Jasleen Grewal	Jasleen Grewal and Steven Jones	Inferring biological programs from cancer transcriptomes using Bayesian modelling	Genome
P_Go018	485	Enrica Calura	Enrica Calura, Paolo Martini, Luca Beltrame, Sergio Marchini, Maurizio D'Incalci, Sampsa Hautaniemi and Chiara Romualdi	A multi-omics pathway analysis for an actionable understanding of high-grade serous epithelial ovarian cancer	Genome
P_Go019	497	Annika Bürger	Annika Bürger and Martin Dugas	Linear and non-linear association analysis of genomic ranges annotations	Genome
P_Go020	508	Laura Mannarino	Laura Mannarino, Ilaria Craparotta, Sara Ballabio, Roberta Frapolli, Ezia Bello, Marta Barisella, Paolo Casali, Silvana Pilotti, Sergio Marchini, Luca Beltrame and Maurizio D'Incalci	The use of a commercial reference for matched somatic variant calling is responsible for a high rate of false positive calls on patient-derived xenograft models	Genome
P_Go021	514	Edgars Celms	Peteris Rucevskis, Martins Opmanis, Paulis Kikusts, Edgars Celms, Lelde Lace, Gatis Melkus, Juris Viksna and Dace Ruklisa	Predicting functionally related modules in promoter capture Hi-C data	Genome
P_Go022	517	Giles Miclotte	Giles Miclotte, Pieter Audenaert and Jan Fostier	Hybrid long read error correction using inexact seeds and flow graphs	Genome
P_Go023	520	Athena Sklias	Athena Sklias and Zdenko Herceg	DNA methylation-wide changes by estrogen hormones in breast cancer	Genome
P_Go024	527	Hyeonun Bang	Hyeonun Bang, Hyeongu Kang and Jung Kyoony Choi	Alternative splicing in normal tissues as a primary risk factor for breast cancer	Genome
P_Go025	530	Mikyung Je	Mikyung Je, Myeongji Cho, Hyeon S. Son and Hyeon Kim	Sequence analysis and characterization of the polynucleotides	Genome
P_Go026	531	Myeongji Cho	Myeongji Cho, Mikyung Je, Hyeon Kim and Hyeon Seok Son	Analysis of the sequence and structure of receptor proteins conferring species differences in viral infections	Genome
P_Go027	534	Marko Verce	Marko Verce, Luc De Vuyst and Stefan Weckx	Comparative genomics of <i>Lactobacillus fermentum</i> suggests specialisation for different ecological niches	Genome
P_Go028	536	Carolin Walter	Carolin Walter, Daniel Schuetzmann, Frank Rosenbauer and Martin Dugas	Benchmarking of 4C-seq pipelines based on real and simulated data	Genome
P_Go029	541	Gaurav Sablok	Gaurav Sablok, Xiaolan He, Mari Miranto, Elina Peltomaa, Robin Sleith, Kenneth Karol, Charles Delwiche, Neil Bell, Lars Paulin, Peter Poczai and Jaakko Hyvönen	Plastomics of embryophyte <i>Blasia pusilla</i> and charophycean <i>Coleochaete orbicularis</i>	Genome
P_Go030	561	Marta Adinolfi	Marta Adinolfi, Marco Pietrosanto, Gabriele Ausiello, Fabrizio Ferrè and Manuela Helmer-Citterich	String-based encoding for RNA secondary structure for sequence-structure alignment and motifs discovery	Genome
P_Go031	566	Erle Holgersen	Erle Holgersen, Olivia Leavy, Olivia Fletcher, Frank Dudbridge and Syed Haider	CHICane: A statistical method for identifying Capture Hi-C interactions	Genome
P_Go032	595	Tomas Vinar	Eduard Batmendijn, Broňa Brejová and Tomas Vinar	Identification of SNPs in Raw Signals from MinION	Genome
P_Go033	616	Nina Baumgarten	Nina Baumgarten, Florian Schmidt and Marcel H. Schulz	Domain Information improves motif enrichment analysis for CHIP-seq data	Genome
P_Go034	624	Marjorie Mersch	Marjorie Mersch, Frédérique Pitel, Sylvain Foissac, Sophie Leroux, Céline Noirot, Diane Esquerré, Laure Frésard, Sandrine Lagarrigue, Sarah Djebali-Quelen, Mireille Morisson, David Gourichon, Gérald Salin and Vincent Coustham	Integrative analysis of WGBS and RNA-seq data in chicken	Genome
P_Go035	633	Wataru Iwasaki	Sira Sriswasdi, Ching-Chia Yang and Wataru Iwasaki	Generalist species drive microbial dispersion and evolution.	Genome
P_Go036	635	Pouya Baniyadi	Pouya Baniyadi	Applications of Combinatorial Optimization in DNA-Assembly	Genome
P_Go037	643	Pau Erola	Pau Erola, Johan L M Björkegren and Tom Michoel	Model-based clustering of multi-tissue gene expression data	Genome
P_Go038	644	Xinan Holly Yang	Zhezhen Wang, John Cunningham and Xinan Yang	CisPi: an RNA-based score for disclosing disease-associated lincRNAs	Genome
P_Go039	654	Tobias P. Loka	Tobias P. Loka, Simon H. Tausch, Martin S. Lindner, Piotr W. Dabrowski, Benjamin Strauch, Jakob M. Schulze, Aleksandar Radonić, Andreas Nitsche and Bernhard Y. Renard	Analyzing Illumina NGS data while the sequencer is running	Genome
P_Go040	655	Matteo Togninalli	Matteo Togninalli, Damian Roqueiro, Copdgene Investigators and Karsten Borgwardt	Accurate and Adaptive Imputation of Summary Statistics in Mixed-Ethnicity Cohorts	Genome
P_Go041	675	Sayaka Miura	Sayaka Miura, Sudhir Kumar, Louise Huuki, Tiffany Buturla, Tracy Vu and Karen Gomez	BEAM: Computational enhancement of single-cell sequences for inferring tumor evolution	Genome

P_Go042	676	Lesley Sitter	Lesley Sitter, Travis Glare and Mark Hurst	Evolutionary divergence of the insect disease-encoding Serratia plasmid pADAP	Genome
P_Go043	677	Katrine Højholt Iversen	Katrine Højholt Iversen, Louise Hesselbjerg Rasmussen, Jens Jørgen Christensen, Christian Salgård Jensen, Xiaohui Chen Nielsen, Rimtas Dargis, Claus Moser, Flemming Schönning Rosenvinge, Ulrik Stenz Justesen, Oksana Lukjancenko, Kosai Al-Nakeeb and Simon Rasmussen	Streptococcus sanguinis and Streptococcus gordonii: prediction of virulence potential using a comparative analysis of functional domains	Genome
P_Go044	678	Natalia Valdes	Natalia Valdes, Joselin Rojas, Mick Parra, Claudia Zapata and Mario Tello	Characterization and isolation of the microbiota of resistant salmonids versus susceptible to Flavobacterium psychrophilum and comparison with the effect produced by antibiotics.	Genome
P_Go045	694	Dirk Walther	Laura Perlaza and Dirk Walther	A genome-wide scan for correlated mutations detects macromolecular and chromatin loop interactions in Arabidopsis thaliana.	Genome
P_Go046	713	Christoforos Nikolaou	Vassilis Ntassis, Nikolaos Panousis, Emmanouil Dermizakis, Dimitrios Boumpas, George Bertias and Christoforos Nikolaou	Topological coordination of gene expression in the peripheral blood of Systemic Lupus Erythematosus (SLE) patients	Genome
P_Go047	719	Svetlana Shabalina	Svetlana Shabalina	ESTIMATION OF NUCLEOTIDE SELECTION PRESSURE IN BACTERIAL GENOMES IMPROVES SMALL RNA TARGET PREDICTION	Genome
P_Go048	726	Ho Yong Chung	Ho Yong Chung, Kikwang Oh, Jong-Young Lee, Kwangmin Kim, Hyunbae Lee, Hyunseok Lee and Junhyung Park	Establishment of database and network analysis platform of fruit softening related genes	Genome
P_Go049	727	Zhixun Zhao	Hui Peng, Yi Zheng, Zhixun Zhao, Tao Liu and Jinyan Li	Recognition of CRISPR/Cas9 off-target sites through ensemble learning of uneven mismatch distributions	Genome
P_Go050	728	Tom Mokveld	Tom Mokveld, Jasper Linthorst, Zaid Al-Ars and Marcel Reinders	CHOP: Haplotype-aware path indexing in population graphs	Genome
P_Go051	734	Jakob Nissen	Jakob Nissen and Simon Rasmussen	Variational Autoencoder for Metagenomic Binning	Genome
P_Go052	745	Samuel Valentini	Samuel Valentini, Tarcisio Fedrizzi, Francesca Demichelis and Alessandro Romanel	PaCBAM: fast and scalable NGS processing	Genome
P_Go053	754	Christoforos Nikolaou	Stylianos Mavropoulos Papoudas and Christoforos Nikolaou	Locating Domains of Focal Deregulation from Gene Expression Data	Genome
P_Go054	782	Andrei Alexeevski	Andrei Alexeevski and Lidia Smirenina	Comparison of non-local evolutionary events in 80 prokaryotic species using nucleotide pangenomes	Genome
P_Go055	794	Maria Samsonova	Elena Plekhanova, Sergey Nuzhdin, Lev Utkin and Maria Samsonova	Prediction of deleterious mutations with Transfer learning	Genome
P_Go056	803	Yuki Kuriya	Yuki Kuriya, Akira Ohyama, Tomokazu Shirai and Michihiro Araki	Validation and prediction accuracy improvement with experimental data on reconstructed metabolic model for bioproductions	Genome
P_Go057	816	Tu Le	Tu Le and Hidetoshi Saze	Learning genetic determinants of plant epigenome by convolutional neural network	Genome
P_Go058	831	Xabier Calle Sanchez	Xabier Calle Sanchez and Thomas Werge	DeepCNV: A method based on Recurrent Neural Networks (RNN) for predicting CNVs using SNP array data.	Genome
P_Go059	837	Sarah O. Fischer	Sarah O. Fischer, Mohamed Hamed and Georg Fuellen	A radiogenomic approach for better stratification of Lung cancer patients	Genome
P_Go060	842	Fatemeh Behjati Ardakani	Fatemeh Behjati Ardakani, Kathrin Kattler, Karl Nordstrom, Sarah Fuchs, Florian Schmidt, Tobias Heinen, Jonas Fischer, Joern Walter and Marcel Schulz	Cell to task: A multi-task-learning approach towards predicting single cell RNA-seq	Genome
P_Go061	843	Ali Kishk	Ali Kishk, Mohamed El-Hadidi and Karim Amer	Short reads amplicon classification using convolutional neural network	Genome
P_Go062	849	Alex Salazar	Alex Salazar and Thomas Abeel	Approximate, simultaneous comparison of microbial genome architectures via syntenic anchoring of quiver representations	Genome
P_Go063	871	Paschalis Natsidis	Paschalis Natsidis, Pavlos Pavlidis, Tsigenopoulos Costas and Tereza Manousaki	A PHYLOGENOMIC PERSPECTIVE ON SPARIDAE (TELEOSTEI: SPARIFORMES) POSITIONING WITHIN THE TREE OF TELEOSTS: CHALLENGES AND NEW INSIGHTS	Genome
P_Go064	872	Małgorzata Wnętrzak	Małgorzata Wnętrzak, Paweł Błażej and Paweł Mackiewicz	Studying robustness of the standard genetic code to various types of mutations	Genome
P_Go065	877	Christine Anyansi	Christine Anyansi and Thomas Abeel	Classification of mixed Mycobacterium tuberculosis infections from WGS data	Genome
P_Go066	878	Birte Kehr	Birte Kehr	Barcode correction for linked-read sequencing data	Genome
P_Go067	881	Elina Koletou	Elina Koletou, Maria Anna Rapsomaniki, Maria Gabrani, Peter Wild and Maria Rodríguez Martínez	Compression of genomic data by Dictionary Learning to characterise Prostate Cancer heterogeneity	Genome
P_Go068	902	Georgia Kontogianni	Georgia Kontogianni, Olga Papadodima, Irene Liampa, Hector Xavier de Lastic, Ilias Maglogiannis and Aristotelis Chatziioannou	Development of a classification system for the translational analysis of cancer genomic and imaging data for melanoma prognosis	Genome
P_Go069	904	Dorota Mackiewicz	Dorota Mackiewicz, Małgorzata Wnętrzak, Paweł Błażej and Paweł Mackiewicz	Optimization of the standard genetic code in terms of to three codon positions using an evolutionary algorithm	Genome
P_Go070	909	Panagiotis Agioutantis	Panagiotis Agioutantis, Vasilios Kotsikoris, Fragiskos N. Kolisis and Heleni Loutrari	RNA-seq data analysis reveals target genes and mechanisms of epigallocatechin gallate and fisetin on stimulated human hepatocellular carcinoma cells	Genome
P_Go071	918	Diya Sen	Diya Sen, Ramesh Vetukuri and Laura Grenville Briggs	New insights into pathogenicity of the emerging tropical pathogen: Phytophthora colocasiae on taro	Genome
P_Go072	946	Alena van Bömmel	Alena van Bömmel and Martin Vingron	Statistical inference for comparison of ChIP-seq genomic experiments	Genome
P_Go073	962	Spyros Tastsoglou	Joanna E Handzlik, Spyros Tastsoglou, Ioannis Vlachos and Artemis Hatzigeorgiou	Manatee: detection and quantification of small ncRNAs from next-generation sequencing data	Genome
P_Go074	974	Areej Alsheikh-Hussain	Areej Alsheikh-Hussain, Nouri Ben Zakour, Andrew Barnes and Scott Beatson	Insertion Sequence elements are drivers of diversification in the broad host range aquatic pathogen Streptococcus iniae	Genome
P_Go075	980	Greta Romano	Greta Romano, Elisa Genuardi, Elvio Amparore, Simone Ferrero, Marco Beccuti and Francesca Cordero	HASHCLONE: A NEW BIOINFORMATICS SUITE TO QUANTIFY MINIMAL RESIDUAL DISEASE BY NEXT-GENERATION SEQUENCING IN B-CELL LYMPHOMA	Genome

P_Go076	981	Giulia Piaggeschi	Giulia Piaggeschi, Nicola Licheri, Silvia Polidoro, Paolo Vineis, Marco Beccuti and Francesca Cordero	Comparison of computational methods for targeted bisulfite sequencing data analysis	Genome
P_Go077	1004	Carine Poussin	Carine Poussin, Nicolas Sierro, Vincenzo Belcastro, James Battey, Stephanie Boue, Elena Scotti, Manuel Peitsch, Nikolai Ivanov and Julia Hoeng	Crowdsourced-benchmarking of computational pipelines for metagenomic taxonomy profiling – the sbv IMPROVER Microbiomics Challenge	Genome
P_Go078	1007	Justin Chu	Justin Chu, Hamid Mohamadi, Jeffrey Tse, Emre Erhan, Ben Vandervalk, Lauren Coombe, Shaun Jackman, Rene Warren and Inanc Birol	Specific and fast alignment-free base pair accurate mapping via multiple spaced seeds and Multi-Index Bloom Filters	Genome

THEME / TRACK: PROTEINS

Poster #	EasyChair ID	Presenting_Author	Authors	Title	Topic
P_Pr001	200	Mindaugas Margelevičius	Mindaugas Margelevičius	Estimating statistical significance of protein profile-profile alignments	Proteins
P_Pr002	242	Yasuhiro Inoue	Yasuhiro Inoue and Riku Ashida	A Method for the Prediction of GPCR-G Protein Coupling Specificity using Deep Neural Networks	Proteins
P_Pr003	372	Hyun Joon Chang	Hyun Joon Chang, Myeongsang Lee and Sungsoo Na	Interface molecular dynamics simulations on designed chimeric hydrophobins to understand the aggregation mechanism	Proteins
P_Pr004	390	Julia Marchetti	Julia Marchetti, Alexander Monzon, Maria Silvana Fornasari, Silvio Tosatto and Gustavo Parisi	Towards biologically meaningful ensembles in disordered proteins	Proteins
P_Pr005	429	Melissa Adasme	Melissa Adasme, Sebastian Salentin, Jörg Heinrich, Joachim Haupt, Yixin Zhang and Michael Schroeder	From malaria to cancer: Computational drug repositioning of amodiaquine using PLIP interaction patterns	Proteins
P_Pr006	431	Hakime Öztürk	Hakime Öztürk, Arzucan Ozgur and Elif Ozkirimli	DeepDTA: Deep Drug-Target Binding Affinity Prediction	Proteins
P_Pr007	437	Gyorgy Abrusan	Gyorgy Abrusan and Joseph Marsh	Ligand binding site structure influences the evolution of protein complex function and topology	Proteins
P_Pr008	467	Maliha Mashkooor	Maliha Mashkooor and Farhat Amin	COMPUTATIONAL MUTAGENESIS OF HETERODIMERIC RECEPTOR COMPLEX OF IFN- λ 3 TO INCREASE ITS THERAPEUTIC POTENTIAL FOR THE TREATMENT OF CARCINOMAS	Proteins
P_Pr009	468	Rodrigo Ochoa	Rodrigo Ochoa, Miguel Soler, Alessandro Laio and Pilar Cossio	Assessing mutation protocols using equilibrium molecular dynamics distributions of protein-peptide complexes	Proteins
P_Pr010	488	Juris Viksna	Mitra Barzine, Alvis Brazma, Edgars Celms, Karlis Cerans, Jyoti Choudhary, Nuno Fonseca, Karlis Freivalds, Fatemeh Ghavidel, Andrew Jarnuczak, Lelde Lace, Darta Rituma and Juris Viksna	An integrated approach to missing data imputation in quantitative proteomics experiments	Proteins
P_Pr011	546	Aram Gyulkhandanyan	Aram Gyulkhandanyan, Nathalie Lagarde, Maria Miteva and Bruno Villoutreix	Assessment of 3D structure-based methods as a complement to existing sequence-based scores for the analysis of protein missense mutations	Proteins
P_Pr012	556	Catherine Mooney	Catherine Mooney, Yandan Zheng, Jialiang Chen, Xuanming Feng, Manaz Kaleel and Gianluca Pollastri	DeepSCLpred: protein subcellular localization prediction by Deep N-to-1 neural networks	Proteins
P_Pr013	557	Andrey Sigorskikh	Andrey Sigorskikh, Dmitry Penzar and Sergei Spirin	Genitor algorithm in phylogenetic reconstruction	Proteins
P_Pr014	577	Tatsuki Kikegawa	Tatsuki Kikegawa and Yuri Mukai	Investigating the localization factors of type II transmembrane protein in secretory pathway	Proteins
P_Pr015	579	Stavros Makrodimitris	Stavros Makrodimitris, Roeland van Ham and Marcel Reinders	Using label-space dimensionality reduction improves protein function prediction	Proteins
P_Pr016	583	Claudia Pareja-Barrueto	Claudia Pareja-Barrueto, Viviana M. Berthoud, Peter J. Minogue, Felipe Villanelo, Eric C. Beyer and Tomas Perez-Acle	Structure-function relationships of human Cx50 hemichannels	Proteins
P_Pr017	585	Jaak Simm	Jaak Simm, Adam Arany, Jörg Wegner, Emmanuel Gustin, Hugo Ceulemans and Yves Moreau	Combining multiple cell-line imaging datasets for protein-ligand activity prediction	Proteins
P_Pr018	592	Daniele Raimondi	Daniele Raimondi, Gabriele Orlando, Yves Moreau and Wim Vranken	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping	Proteins
P_Pr019	593	Adnan Sijoka	Adnan Sijoka	Modelling and predicting allostery and protein flexibility with high throughput rigidity theory-based analysis	Proteins
P_Pr020	594	Typhaine Paysan-Lafosse	Typhaine Paysan-Lafosse, Christine Orengo, Ian Sillitoe, Sameer Velankar and Robert D Finn	Expanding Genome3D and disseminating the structural annotations via InterPro and PDBe	Proteins
P_Pr021	601	Maria-Fernanda Senosain	Maria-Fernanda Senosain, Pierre P. Massion and Jonathan M. Irish	Computational analysis strategies for single-cell mass cytometry data from early lung adenocarcinoma	Proteins
P_Pr022	602	Rivi Verma	Rivi Verma and Shashi B. Pandit	A method to reduce docking solution space for tertiary structure prediction of multi-domain proteins using sphere approximation of domains	Proteins
P_Pr023	606	Rivi Verma	Rivi Verma and Shashi B. Pandit	Understanding structural space of intra protein domain-domain interfaces	Proteins
P_Pr024	608	Giorgos Papanastasiou	Giorgos Papanastasiou, Mark Rodrigues, Rustam Al-Shahi Salman and Gillian Macnaught	Quantitative analysis of 18F-flutemetamol uptake in cerebral amyloid angiopathy using hybrid PET/MR imaging.	Proteins
P_Pr025	609	Sergio M. Marques	Sergio M. Marques, Michele Parrinello, David Bednar and Jiri Damborsky	Computational study of ligand unbinding: application to enzyme engineering	Proteins
P_Pr026	611	Tunca Dogan	Tunca Dogan, Rabie Saidi and Maria Martin	Building a Precise Protein Function Prediction Method: The UniProt Domain Architecture Alignment and Classification (UniProt-DAAC) Example	Proteins

P_Pr027	619	Alexander Monzon	Matías Carletti, Alexander Monzon, Emilio García-Rios, Layla Hirsh, Silvina Fornasari and Gustavo Parisi	Revenant: a database of characterized resurrected proteins.	Proteins
P_Pr028	620	Alexander Monzon	Alexander Monzon, Diego Zea, Cristina Marino-Buslje, Maria Silvina Fornasari and Gustavo Parisi	Conformational space and structural divergence unveils functional change during evolution	Proteins
P_Pr029	630	E. Sila Ozdemir	E. Sila Ozdemir, Hyunbum Jang, Attila Gursoy, Ozlem Keskin, Zhigang Li, David B. Sacks and Ruth Nussinov	Unraveling the molecular mechanism of interactions of the Rho GTPases Cdc42 and Rac1 with the scaffolding protein IQGAP2	Proteins
P_Pr030	650	Maria Gorodetski	Maria Gorodetski and Haim J. Wolfson	PepMatch: Knowledge Based Design of Protein Binding Peptides	Proteins
P_Pr031	657	Natacha Cerisier	Natacha Cerisier, Leslie Regad, Dhoha Triki, Michel Petitjean, Delphine Flatters and Anne-Claude Camproux	Statistical Profiling of One Promiscuous Protein Binding Site: Illustrated by Urokinase Catalytic Domain	Proteins
P_Pr032	665	Andrew Nightingale	Andrew Nightingale, Jie Luo, Peter Mcgarvey, Michele Magrane, Sandra Orchard and Maria Martin	Enabling interpretation of protein variation effects with UniProt	Proteins
P_Pr033	681	Jaume Bonet	Jaume Bonet, Che Yang, Sarah Wehrle, Karen Schriever, Fabian Sesterhenn, Andreas Scheck, Freyr Sverrisson and Bruno Correia	De novo computational design of functional proteins	Proteins
P_Pr034	685	Vasilis Promponas	Stella Tamana and Vasilis Promponas	Dissecting sequence and structural features of compositionally biased regions in the Protein Data Bank	Proteins
P_Pr035	692	Kriti Chopra	Kriti Chopra and Radha Chauhan	Decrypting protein-protein interaction at residue level: A machine learning approach	Proteins
P_Pr036	696	Janani Durairaj	Janani Durairaj, Aalt Dj van Dijk and Dick de Ridder	Structure and Sequence-based Prediction of Sesquiterpene Synthase Cyclization	Proteins
P_Pr037	700	Eleftheria Polychronidou	Eleftheria Polychronidou, Antigoni Avramouli, Maria Psiha and Panayiotis Vlamos	Impact of somatic mutations in the three dimensional structure of proteins related to Alzheimer's disease.	Proteins
P_Pr038	701	Hovakim Grabski	Hovakim Grabski, Lernik Hunanyan, Susanna Tiratsuyan and Hrachik Vardapetyan	Interaction of quercetin with transcriptional regulator LasR of Pseudomonas aeruginosa: Mechanistic insights of the inhibition of virulence through quorum sensing	Proteins
P_Pr039	702	Naama Hurwitz	Naama Hurwitz and Haim J. Wolfson	Pep-Whisperer: Evolution Guided Design of Inhibitory Peptides	Proteins
P_Pr040	703	Eleftheria Polychronidou	Eleftheria Polychronidou, Ilias Kalamaras, Andreas Agathangelidis, Lesley-Ann Sutton, Xiao-Jie Yan, Vasilis Bikos, Anna Vardi, Nicholas Chiorazzi, Chrysoula Belessi, Richard Rosenquist, Paolo Ghia, Kostas Stamatopoulos, Panayiotis Vlamos, Anna Chailyan, Nanna Overby, Paolo Marcatili, Anastasia Hatzidimitriou and Dimitrios Tzovaras	Combination of 3D descriptors and amino acid physicochemical properties lead to highly accurate clustering of IG protein tertiary structures in CLL.	Proteins
P_Pr041	708	Fabrizio Pucci	Fabrizio Pucci and Marianne Rooman	Probing the effect of point mutations on the interactome	Proteins
P_Pr042	709	Deborah Giordano	Deborah Giordano and Angelo Facchiano	Microbial Transglutaminases' structure and their evolution	Proteins
P_Pr043	717	Panagiotis Dimitriou	Panagiotis Dimitriou, Michalis Agathocleous, Vasilis Promponas and Chris Christodoulou	Fast and accurate protein secondary structure prediction using Clockwork Recurrent Neural Networks	Proteins
P_Pr044	729	Miguel Correa Marrero	Miguel Correa Marrero, Richard G.H. Immink, Dick de Ridder and Aalt D.J van Dijk	Simultaneous unsupervised inference of protein-protein contacts and interactions	Proteins
P_Pr045	731	Suryanarayana Seera	Suryanarayana Seera and Hampapathalu Nagarajaram	Computational studies on intrinsically disordered proteins harboring disease causing missense mutations	Proteins
P_Pr046	751	Paul Zierep	Paul Zierep, Adriana Ceci and Stefan Guenther	SSR-viz - a novel software for identification and visualization of subfamily-specific residues	Proteins
P_Pr047	757	Georgia Nasi	Georgia Nasi, Katerina Nastou, Paraskevi Tsiolaki, Zoi Litou and Vassiliki Iconomidou	A repository of amyloidoses and diseases associated with amyloid deposition	Proteins
P_Pr048	758	Michail Batskinis	Michail Batskinis, Katerina Nastou, Zoi Litou, Stavros Hamodrakas and Vassiliki Iconomidou	Pathogenic mutation analysis in human Voltage-Gated Ion Channels and association with Channelopathies	Proteins
P_Pr049	759	Katerina Nastou	Katerina Nastou, Georgios Tsaousis, Stavros Hamodrakas and Vassiliki Iconomidou	Design and construction of a relational database for peripheral membrane proteins from eukaryotic reference proteomes	Proteins
P_Pr050	760	Gift Nuka	Gift Nuka, Matthew Fraser, Siew-Yit Yong, Matthias Blum, Simon Potter, Alex Mitchell and Rob Finn	InterProScan: Improving protein sequence analysis and classification	Proteins
P_Pr051	773	Lucas Machado	Lucas Machado, Marcelo Gomes and Ana Carolina Guimarães	Unveiling the mutational patterns of the HIV-1 Integrase in raltegravir-treated patients using a co-occurrence network	Proteins
P_Pr052	788	Jianyu Li	Jianyu Li and Stefan Günther	Fragment-based in silico drug design for targeting MLL3	Proteins
P_Pr053	791	Neha V. Kalmankar	Neha V. Kalmankar, P. Balaram, Radhika Venkatesan and Ramanathan Sowdhamini	Modeling and Conformational Analysis of Cyclotides, a Class of Macrocyclic Disulfide Bonded Plant Peptides	Proteins
P_Pr054	795	Jiří Vymětal	Jiří Vymětal and Jiří Vondrášek	Computational characterization of two-domain proteins by Markov state modeling: K48-Diubiquitin case.	Proteins
P_Pr055	796	Sherlyn Jemimah	Sherlyn Jemimah and Michael Gromiha	A Computational Study of the Additivity of Binding Free Energy in Protein-Protein Complexes Upon Double Mutation	Proteins
P_Pr056	800	Mayumi Kamada	Mayumi Kamada and Mikito Toda	Detection of differences in protein dynamics caused by genomic variant using wavelet transform	Proteins
P_Pr057	804	Camila Duitama	Camila Duitama and Jorge Bouças	Expansion of the Protein-Protein Interaction network for the set of ageing genes retrieved from AgePy	Proteins
P_Pr058	809	Qingzhen Hou	Qingzhen Hou, Raphaël Bourgeas, Fabrizio Pucci and Marianne Rooman	Computational analysis of the amino acid interactions that promote or decrease protein solubility	Proteins
P_Pr059	810	Jacqueline Schmidt	Jacqueline Schmidt, Rolf Fendel, Benjamin Mordmueller and Nico Pfeifer	Predicting malaria vaccine efficacy from anti-plasmodial antibody profile prior to and under vaccination	Proteins

P_Pr060	840	Ioannis Belios	Ioannis Belios, Georgios Eleftheriadis, Thomai Zinoviou, Dimitra Dalampira, Stefanos Giannopoulos, Christina Arvaniti, Anastasia Adamou, Georgios Vavougios and Sotirios Zarogiannis	Bioinformatic analysis of AQP1 molecular mimicry and implications for autoimmune diseases	Proteins
P_Pr061	848	Adam Midlik	Adam Midlik, Ivana Hutarova Varekova, Jan Hutar, Veronika Navratilova, Radka Svobodova Varekova, Jaroslav Koca and Karel Berka	Annotation of protein secondary structure elements for whole protein families	Proteins
P_Pr062	853	François Ancien	François Ancien, Fabrizio Pucci, Maxime Godfroid and Marianne Rooman	Prediction and interpretation of deleterious coding variants in terms of protein structural stability.	Proteins
P_Pr063	884	Joana Pereira	Joana Pereira and Andrei N. Lupas	On The Origins of The First Folded Protein Domains: A Computational Study on The Role of Ancestral Peptide Recombination	Proteins
P_Pr064	903	Marco Salvatore	Marco Salvatore, Per Warholm, Walter Basile, Nanjiang Shu and Arne Elofsson	The SubCons web-server: A user friendly web interface for state-of-the-art subcellular localization prediction	Proteins
P_Pr065	908	Rebecca Wade	Jui-Hung Yuan, Daria Kokh, Stefan Richter and Rebecca Wade	Computational Tools for Exploring Protein Binding Sites and their Dynamics	Proteins
P_Pr066	910	Hovakim Grabski	Hovakim Grabski and Susanna Tiratsuyan	Mechanistic insights of the interaction of taxifolin with transcriptional regulator LasR of Pseudomonas aeruginosa using molecular modeling techniques	Proteins
P_Pr067	912	Erzsébet Fichó	Erzsébet Fichó, László Dobson, Bálint Mészáros and István Simon	Intrinsically disordered proteins: relationship between sequence, structure and function	Proteins
P_Pr068	925	Martin Reczko	Dimitra Panou and Martin Reczko	DeepFoldit - A Deep Reinforcement Neural Net Folding Proteins	Proteins
P_Pr069	928	Rakesh Trivedi	Rakesh Trivedi and Hampapathalu Adimurthy Nagarajaram	Amino acid substitution scoring matrices specific to intrinsically disordered regions in proteins	Proteins
P_Pr070	929	Flavia Corsi	Flavia Corsi, Elodie Laine and Alessandra Carbone	JET2DNA: a tool for accurate prediction of protein-DNA interfaces based on evolutionary information, physico-chemical and geometrical properties.	Proteins
P_Pr071	931	Gabriele Orlando	Gabriele Orlando, Sandra Macedo Ribeiro, Alexandra Olivera Silva and Wim Vranken	Agmata: a single sequence aggregation predictor and its application to Ataxin-3	Proteins
P_Pr072	933	Bhumika Arora	Bhumika Arora, K.V. Venkatesh, Denise Wootten and Patrick Sexton	Improving the prediction of loops and drug binding in GPCR structure models	Proteins
P_Pr073	935	Mohammad Elgamacy	Mohammad Elgamacy, Murray Coles, Patrick Ernst, Hongbo Zhu, Marcus Hartmann, Andreas Plueckthun and Andrei Lupas	De novo protein design through an interface-driven strategy	Proteins
P_Pr074	936	Arumay Pal	Arumay Pal and Yaakov Levy	Structure, Stability and Specificity of the Binding of ssDNA and ssRNA with Proteins	Proteins
P_Pr075	937	Guilherme Bottino	Guilherme Bottino and Leandro Martínez	STATISTICAL METHODS FOR CONSTRAINT SELECTION FROM CROSS-LINKING MASS SPECTROMETRY FOR PROTEIN STRUCTURE DETERMINATION	Proteins
P_Pr076	944	Laura Weidmann	Laura Weidmann, Tjeerd Dijkstra, Oliver Kohlbacher and Andrei Lupas	Homology and Convergence: explaining similarity between natural protein sequences	Proteins
P_Pr077	949	Franco Simonetti	Franco Simonetti, Eloy A Colell, Javier Iserete and Cristina Marino Buslje	MISTIC2: comprehensive server to study coevolution in protein families.	Proteins
P_Pr078	954	Tsukasa Nakamura	Tsukasa Nakamura and Kentaro Tomii	Performance improvement of the method for large-scale structural comparison of protein pockets	Proteins
P_Pr079	965	Yang Shen	Mostafa Karimi and Yang Shen	iCFN: an efficient exact algorithm for multistate protein design	Proteins
P_Pr080	979	Shailesh Kumar Gupta	Shailesh Kumar Gupta, Debashish Kumar Ghosh, Dipti Deshpande and Akash Ranjan	Computational studies to decipher the mechanisms of F334 to L/C mutation(s) associated functional collapse of PDE10A in Chorea disorder: Catalytic loss and Structural instability	Proteins
P_Pr081	985	Shasank Sekhar Swain	Shasank Sekhar Swain, Sudhir Kumar Paidasetty, Rabindra Nath Padhy, Tahziba Hussain and Sanghamitra Pati	A systematic medicinal chemistry based computational approach for development of novel phytochemical-sulfadrag conjugates as prospective anti-MRSA drugs	Proteins
P_Pr082	992	Amresh Prakash	Amresh Prakash	Conformational Dynamics of RNA recognition motifs (RRMs) of TDP-43 Involve in Amyotrophic Lateral Sclerosis	Proteins
P_Pr083	998	Joel Ricci	Joel Ricci, Sergio Aguila and Carlos Brizuela	In silico analysis of Human Papillomavirus E6 protein to identify anti-HPV drugs	Proteins
P_Pr084	999	Panagiotis Koukos	Panagiotis Koukos, Charlotte W. van Noort and Alexandre M.J.J Bonvin	Membrane protein docking with HADDOCK	Proteins
P_Pr085	1012	Georgij Arapidi	Georgij Arapidi, Anatolii Urban, Ivan Butenko, Victoria Shender, Maria Osetrova, Grigori Nos, Olga Ivanova, Tatiana Saveleva, Aleksandr Mitin, Nina Shariva, Margarita Nikonova, Aleksandr Martinov, Elena Ilina, Vadim Ivanov and Vadim Govorun	SEARCH AND INVESTIGATION OF POTENTIAL PEPTIDE AGENTS OF INTERACTION BETWEEN HUMAN ORGANISM AND ITS MICROBIOME	Proteins
P_Pr086	1018	Anna Hadarovich	Anna Hadarovich, Ivan Anishchenko, Alexander Tuzikov, Petras Kundrotas and Ilya Vakser	Gene Ontology in scoring of protein docking	Proteins
P_Pr087	1019	Claudio Mirabello	Claudio Mirabello and Björn Wallner	rawMSA: proper Deep Learning makes protein sequence profiles and feature extraction obsolete	Proteins
P_Pr088		Andre Philipe Vasquez Jimenez	A. P. V. Jimenez, A. F. G. Barrios, J.A.D. Castellanos, A. R. Munoz	Pharmacophore / docking -based virtual screening and deconstruction of natural products to desing and discover novel potential dual CDK2/VEGFR2 type 2 inhibitors	Proteins

THEME / TRACK: SYSTEMS

Poster #	EasyChair ID	Presenting Author	Authors	Title	Topic
P_Sy001	3	Daniela Perry	Daniela Perry and Jeremy Gunawardena	Identification of Non-invasive Cytokine Biomarkers for Polycystic Ovary Syndrome Using Supervised Machine Learning	Systems

P_Sy002	119	Djomangan Adama Ouattara	Djomangan Adama Ouattara, Clémence Joseph, Andrei Bunescu, Joséphine Abi-Ghanem, Kristin Hennig, Emeline Billaud, Xavier Meniche, Mathieu Cyrille and Frédéric Béquet	An automatic platform for Genome-Scale Metabolic Model Reconstruction and Analysis	Systems
P_Sy003	211	Sridhar Hariharaputran	Sridhar Hariharaputran	Repurposing Drugs for Tuberculosis with Semantic Networks	Systems
P_Sy004	215	Sander Rodenburg	Sander Rodenburg, Michael Seidl, Francine Govers and Dick de Ridder	Modelling the metabolism of the Phytophthora infestans - tomato interaction	Systems
P_Sy005	395	Punit Kaur	Punit Kaur and Amit Katiyar	Shared molecular signatures reveal probable links between Endometriosis and Multiple Sclerosis	Systems
P_Sy006	423	Nikolaos Tsiantis	Nikolaos Tsiantis and Julio R. Banga	Inferring metabolic dynamics using optimal control: the role of constraints and trade-offs.	Systems
P_Sy007	434	İlknur Karadeniz	İlknur Karadeniz and Arzucan Özgür	Ontology-based entity normalization using word embeddings	Systems
P_Sy008	439	Jake Alan Pitt	Jake Alan Pitt, Attila Gábor, Julio Saez-Rodriguez and Julio R. Banga	Reduction of logic-based differential equation models improving identifiability	Systems
P_Sy009	451	Joaquim Aguirre-Plans	Joaquim Aguirre-Plans, Alexis Molina, Jordi Mestres, Emre Guney, Narcis Fernandez-Fuentes and Baldo Oliva	DIANA: drug combination prediction using underlying pathways and interaction networks	Systems
P_Sy010	456	Anna Niarakis	Vidisha Singh, Saran Pankaew, Marek Ostaszewski, George D. Kalliolias, Sylvain Soliman, Tomáš Helikar and Anna Niarakis	Executable Disease Networks: Adding dynamics to molecular maps	Systems
P_Sy011	483	Gaëlle Letort	Gaëlle Letort, Arnau Montagud, Gautier Stoll, Randy Heiland, Emmanuel Barillot, Paul Macklin, Andrei Zinovyev and Laurence Calzone	Integrating physical dimension and cell signaling : PhysiBoSS, a multi-scale agent based framework	Systems
P_Sy012	495	Anne Hartebrodt	Anne Hartebrodt, Jan Baumbach and Markus List	A probabilistic pathway enrichment strategy for KeyPathwayMiner	Systems
P_Sy013	496	Justine Rudewicz	Justine Rudewicz, Lindsay S. Cooley, Wilfried Souleyreau, Andreas Bikfalvi and Macha Nikolski	Network-based approach for systems biology in the context of kidney cancer	Systems
P_Sy014	522	Vasiliki Kostiou	Vasiliki Kostiou, Philip Jones and Benjamin Hall	Exploring a spatial Single Progenitor model for the epithelial basal layer	Systems
P_Sy015	523	Laure Talarmain	Laure Talarmain, Daniel Garcia, Carla Martins and Benjamin Hall	Identifying drugging strategies using evolutionary principles in lymphoma mouse model	Systems
P_Sy016	543	Celine Hernandez	Celine Hernandez, Aurélien Naldi, Wassim Abou-Jaoudé, Guillaume Voisinne, Romain Roncagalli, Bernard Malissen, Morgane Thomas-Chollier and Denis Thieffry	Dynamical modelling of T cell co-inhibitory pathways to predict anti-tumour responses to checkpoint inhibitors	Systems
P_Sy017	545	Tim Kacprowski	Tim Kacprowski, Christian Wiwie and Jan Baumbach	Integrating Time-Series Data with Network Enrichment	Systems
P_Sy018	554	Smaragda Dimitrakopoulou	Michael Neidlin, Smaragda Dimitrakopoulou and Leonidas Alexopoulos	Gene set enrichment and co-expression analyses identify overlapping molecular mechanisms in osteoarthritis	Systems
P_Sy019	563	Bhavana Harsha	Bhavana Harsha, Harry Boutselakis, Simon Forbes, Dave Beare, Nidhi Bindal, Chai Yin Kok, Claire Rye, Sally Bamford, Sari Ward, Charlotte Cole, Shicai Wang, Laura Ponting, Ray Stefancsik, Chris Ramshaw, John Tate, Harry Jubb, Zbyslaw Sondka, Sam Thompson, Steve Jupe, Charlie Hathaway, Peter Fish, Celestino Creatore, Mike Stratton and Peter Campbell	DIAS: The COSMIC Data Integration Annotation System	Systems
P_Sy020	581	Gianluca Selvaggio	Gianluca Selvaggio, Archana Pawar, Florence Janody and Claudine Chauyiya	Logical modelling and analysis of cell adhesion properties along Epithelial to Mesenchymal Transition	Systems
P_Sy021	612	Graeme Benstead-Hume	Graeme Benstead-Hume, Xiangrong Chen, Suzi Hopkins, Karen A. Lane, Jessica Downs and Frances M. G. Pearl	Predicting synthetic lethal interactions using conserved patterns in protein interaction networks	Systems
P_Sy022	623	Arnau Montagud	Arnau Montagud, Jonas Béal, Pauline Traynard, Luis Tobalina, Julio Sáez-Rodríguez, Emmanuel Barillot and Laurence Calzone	Patient-specific prostate logical models allow clinical stratification of patients and personalized drug treatment	Systems
P_Sy023	628	Jonas Béal	Jonas Béal, Arnau Montagud, Pauline Traynard, Emmanuel Barillot and Laurence Calzone	Instantiation of Patient-Specific Logical Models With Multi-Omics Data Allows Clinical Stratification of Patients	Systems
P_Sy024	640	Clémence Frioux	Clémence Frioux, Enora Fremy, Camille Trottier and Anne Siegel	Scalable and exhaustive screening of metabolic functions carried out by microbial consortia	Systems
P_Sy025	652	Gayathri Sambamoorthy	Gayathri Sambamoorthy and Karthik Raman	Understanding the evolution of functional redundancy in metabolic networks	Systems
P_Sy026	699	Anastasios Mangelis	Anastasios Mangelis, Ramona Juehlen, Stefanie Hahner, Andreas Schirbel, Peter Dieterich and Graeme Eisenhofer	An in vitro model for evaluation of steroidogenic pathways enzyme kinetics	Systems
P_Sy027	704	Beatriz García-Jiménez	Beatriz García-Jiménez, Jose Luis García and Juan Nogales	FLYCOP: metabolic modeling-based analysis and engineering microbial communities	Systems
P_Sy028	710	Noel Malod-Dognin	Noel Malod-Dognin and Natasa Przulj	Functional geometry of protein-protein interaction networks	Systems
P_Sy029	716	Simone Lederer	Simone Lederer, Tjeerd Dijkstra and Tom Heskes	Additive Dose Response Models: Defining Synergy	Systems
P_Sy030	753	Martin Pirkl	Martin Pirkl and Niko Beerenwinkel	Single cell network analysis with a mixture of Nested Effects Models	Systems
P_Sy031	765	Sam Windels	Sam Windels, Noel Malod-Dognin and Natasa Przulj	Graphlet Laplacians: linking local wiring patterns in network neighbourhoods to biological function	Systems
P_Sy032	769	Delphine Pessoa	Delphine Pessoa and Jorge Carneiro	Making a single product per cell: lessons from V(D)J recombination and X chromosome inactivation.	Systems
P_Sy033	775	Kikwang Oh	Kikwang Oh, Dudekula Db, Ho Yong Chung, Jong-Young Lee, Kwangmin Kim, Hyunbae Lee, Sridhar Srinivasan and Junhyung Park	Genome browser and application system for De-novo genome project	Systems
P_Sy034	776	Ji-Hye Lee	Ji-Hye Lee, Ji-Hye Choi, Taewoon Joo, So Eun Park and Hyun Goo Woo	CGV (Cancer Genome View): A web-service for multiomics cancer genome data retrieval, analyses, and visualization	Systems
P_Sy035	783	Olga Bezudnova	Olga Bezudnova, Ekaterina Guseva, Ivan Rusinov, Anna Ershova, Anna Karyagina, Sergey Spirin and Andrei Alexeevski	Lateral transfer and vertical inheritance of restriction-modification systems	Systems
P_Sy036	828	Myrto Krana	Myrto Krana, Giorgos Papoutsoglou, Yannis Pantazis, Sofia Triantafillou and Ioannis Tsamardinos	Causal discovery limitations in learning molecular interaction networks: An empirical study using linear mechanistic models	Systems

P_Sy037	832	Petronela Buiga	Petronela Buiga, Ari Elson, Lydia Tabernero and Jean-Marc Schwartz	Boolean model analysis of dual specificity phosphatases in resistant breast cancer cell lines	Systems
P_Sy038	858	Anna Hernandez Duran	Anna Hernandez Duran, Kay Grünewald and Maya Topf	Protein-protein interaction network in herpes simplex virus type 1	Systems
P_Sy039	874	Ling Sun	Ling Sun, Therese Lorenz and Alexander Bockmayr	Logical modeling: Inferring structure from dynamics	Systems
P_Sy040	880	Kleio - Maria Verrou	Kleio - Maria Verrou, Georgios Papoutsoglou and Ioannis Tsamardinos	Learning pathway dynamics from single-cell proteomic data	Systems
P_Sy041	905	Kishan K C	Kishan K C, Rui Li, Feng Cui and Anne Haake	Learning topology-preserving embedding for gene interaction networks	Systems
P_Sy042	947	Saikat Banerjee	Saikat Banerjee and Johannes Soeding	Logistic regression in case-control GWAS: Ignored over a decade?	Systems
P_Sy043	953	Tamim Abdelaal	Tamim Abdelaal, Vincent van Unen, Thomas Höllt, Frits Koning, Marcel Reinders and Ahmed Mahfouz	Predicting cell types in single cell mass cytometry data	Systems
P_Sy044	971	Vipin Vijayan	Vipin Vijayan, Dominic Critchlow and Tijana Milenkovic	Alignment of dynamic networks	Systems
P_Sy045	1021	Zaynab Hammoud	Zaynab Hammoud, Frank Kramer	Implementing a multilayer framework for pathway data integration, analysis and visualization	Systems

THEME / TRACK: TRAINING

Poster #	EasyChair ID	Presenting.Author	Authors	Title	Topic
P_Tr001	401	Daniel Wibberg	Daniel Wibberg	The de.NBI training platform	Training
P_Tr002	509	Agnieszka Stańczak	Agnieszka Stańczak, Tomasz Magdziarz and Artur Góra	Short lived ligand-protein interactions – can they control the substrate entry to the buried active site?	Training
P_Tr003	513	Vera Matser	Vera Matser, Rossen Apostolov, Catherine Brooksbank, Adam Carter, Lee Larcombe and Arno Proeme	Implementing a competency-based training strategy for biomolecular researchers with high computational needs	Training
P_Tr004	521	Sarah Wooller	Sarah Wooller, Graeme Benstead-Hume and Frances Pearl	Mutually exclusive 'omic knockouts in TCGA cancer patient data point to candidate synthetic lethal gene pairs.	Training
P_Tr005	565	Werner Veldsman	Werner Veldsman and Jing Qin	Discovering Dysregulated Transcriptional Regulatory Networks in Individual Breast Cancer Patients using Greedy Sparse Learning Algorithms	Training
P_Tr006	600	Vince Grolmusz	Balázs Szalkai, Bálint Varga and Vince Grolmusz	Consensus Connectome Dynamics of the Human Brain	Training
P_Tr007	672	Celia van Gelder	Celia van Gelder and Mateusz Kuzak	FAIR Data Training activities in the Netherlands	Training
P_Tr008	695	Patricia M. Palagi	Celia W.G. van Gelder, Pascal Kahlem, Patricia M. Palagi and Gabriella Rustici	The ELIXIR Training Programme: harmonizing and reinforcing training for life sciences in Europe	Training
P_Tr009	697	Teresa K. Attwood	Teresa K. Attwood, Michelle D. Brazas, Celia W.G. van Gelder and Annette McGrath	GOBLET and the F1000Research Bioinformatics Education and Training Collection	Training
P_Tr010	723	Pedro L Fernandes	Pedro L Fernandes, Nicola Mulder, Allegra Via, Celia van Gelder, Teresa Attwood and The Goblet Learning Education And Training Committee	GOBLET and its role in Bioinformatics Learning, Education & Training	Training
P_Tr011	742	Jianfeng Sun	Jianfeng Sun	Numerical Trajectory Mapping Identifies Dynamic Complex Traits	Training
P_Tr012	756	Jürgen Walther	Jürgen Walther, Adam Hospital, Genis Bayarri and Modesto Orozco	MC_DNA: A web server for the detailed study of the structure and dynamics of DNA and chromatin fibers	Training
P_Tr013	772	Mohd Shamoan Asmat	Mohd Shamoan Asmat and Qayyum Husain	Molecular docking and Characterization studies for unraveling binding interactions of lipase with polypyrrole-methyl anthranilate functionalized "worm-like" titanium dioxide nanocomposite as promising nanobiocatalyst	Training
P_Tr014	786	Cansu Dincer	Cansu Dincer and Nurcan Tuncbag	Structural Modeling of the Patient-Specific Signaling Networks in Glioblastoma	Training
P_Tr015	787	Habibe Cansu Demirel	Habibe Cansu Demirel and Nurcan Tuncbag	Modeling the Tumor Specific Structural Networks by Integrating Alternative Splicing Events	Training
P_Tr016	792	Gökçe Senger	Gökçe Senger and Nurcan Tuncbag	Network Modeling of the Dasatinib Treatment in Glioblastoma Stem Cells by Data Integration	Training
P_Tr017	900	Shifu Chen	Shifu Chen, Yanqing Zhou, Yaru Chen, Hui Wang, Wenting Liao, Tanxiao Huang, Cheng Jin and Renwen Long	Ultra-fast quality control, read filtering and FASTQ data manipulation with fastp	Training
P_Tr018	975	Marcos Caraballo-Ortiz	Marcos Caraballo-Ortiz, Eric Wafula, Prakash Timilsena and Claude Depamphilis	Considerations and challenges building a shallow-level phylogeny in plants using transcriptomes	Training
P_Tr019	977	Ariel Toh	Ariel Toh	Application of bias-variance test to assess complexity of models: initial analysis	Training
P_Tr020	993	Julia Varga	Zsuzsanna Gergely, Julia Varga and Gábor Tusnády	Road to Personalized Medicine: a Bioinformatics Project for High School Students	Training
P_Tr021	1003	Ann Meyer	Ann Meyer, Michelle Brazas and Francis Ouellette	Tracking Workshop Development and Online User Access	Training