

German Conference on Bioinformatics 2012

Jena, 19-22 September 2012

Conference Program

Joining
Evolution
Networks
Algorithms



Supporters and Sponsors



Leibniz Institute for Age Research
Fritz Lipmann Institute (FLI)



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Welcome

Dear GCB 2012 Attendee,

It is a pleasure to welcome you in Jena, to the German Conference on Bioinformatics 2012. This annual, international conference provides a forum for the presentation of current research in bioinformatics and computational biology. In addition, five satellite workshops place thematic emphasis on diverse aspects of systems biology: "Systems Biology of Aging" organized by J. Sühnel, "Organ-oriented Systems Biology" by D. Driesch and R. Mrowka, "Network Reconstruction and Analysis in Systems Biology" by W. Wiechert and T. Lengauer, "Computational Proteomics and Metabolomics" by S. Böcker, and "Image-based Systems Biology" by M. Figge.

This year we will have 10 highlight papers and 11 regular papers presented at the GCB selected out of 39 submissions. GCB 2012 will also feature keynote presentations by six leading scientists: Claude dePamphilis (Pennsylvania State University, University Park, USA), Oliver Fiehn (University of California, Davis, USA), Arndt von Haeseler (Max F. Perutz Laboratories, Vienna, Austria), Tom Kirkwood (Newcastle University, Newcastle, UK), Erik van Nimwegen (University of Basel, Basel, Switzerland), and Ruth Nussinov (National Cancer Institute, Frederick, USA). With the topics of these talks the meeting indeed succeeded in **'Joining Evolution, Networks, and Algorithms'**, according to this year's conference motto. Additionally, about 95 poster abstracts were accepted for presentation.

The GCB 2012 was organized by the Jena Centre of Bioinformatics (JCB) in cooperation with the German Society for Chemical Engineering and Biotechnology (DECHEMA) and the Society for Biochemistry and Molecular Biology (GBM). GCB 2012 benefited from the voluntary contributions of many members of the supporting scientific institutions and the bioinformatics and computational biology community in Jena. Further, we thank all members of the program committee for their efforts and are very grateful to the participants who present their work. Our special thanks go to the sponsors who supported the conference financially.

We wish you all a great meeting,

Sincerely,
The GCB 2012 Organizers



Fotos: FSU/Fotozentrum

GCB 2012 Organization

Program Chairs

Stefan Schuster
Sebastian Böcker

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Andrew Torda
Martin Vingron
Arndt Von Haeseler
Edgar Wingender
Ralf Zimmer

General Information

Registration/Information/Media Desk:

Opening hours:

- Wednesday, 08:30 – 15:00, Beutenberg Campus
- Wednesday, 18:30 – 21:00, University Main Building
- Thursday-Friday, 8:00 – 17:00, Ernst Abbe Campus
- Saturday, 8:00 – 13:00, Ernst Abbe Campus

Phone number:
(Thu. - Sat.)

+49 (0)3641 941870

Conference Proceedings:

The conference proceedings are published via the Open Access Series in Informatics of Schloss Dagstuhl. Highlights, poster abstracts and proceedings are available online via the conference website (www.gcb2012-jena.de) and on the conference USB stick.

Internet Access:

You can connect to the WLAN using eduroam or via login and password provided in the additional conference material.

Lunch:

During the main conference, lunch will be provided in the different canteens of the university. Please check the conference material for vouchers. For other restaurants, see the enclosed restaurant guide.

Coffee Breaks:

Coffee and snacks will be provided in the foyer.

Speaker Presentation Uploads:

Presentations can be uploaded at the Media Desk in the foyer. Presentations should be uploaded during the session prior to your scheduled talk, at the latest.

Poster Session:

The combined poster session and poster party on Friday gives ample opportunity for discussions in a friendly atmosphere.

- Even numbers: 18:00 – 19:00
- Odd numbers: 19:00 – 20:00

Social Events:

- **Welcome Reception**
Wednesday, 19:00 – 21:00, University Main Building
Enjoy jazzy music and Thuringian barbecue specialties.
- **Guided Walk through Jena's center**
Thursday, start at 18:30 and 20:00 at the historical market.
- **Poster Party**
Friday, 18:00 – 21:00, Ernst Abbe Campus, Foyer

For further information, please contact the Information Desk.

Conference Venue



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1 - Campus

Ernst-Abbe-Platz

Conference Venue
Poster Party

2 - University Main Building (Universitätshauptgebäude)

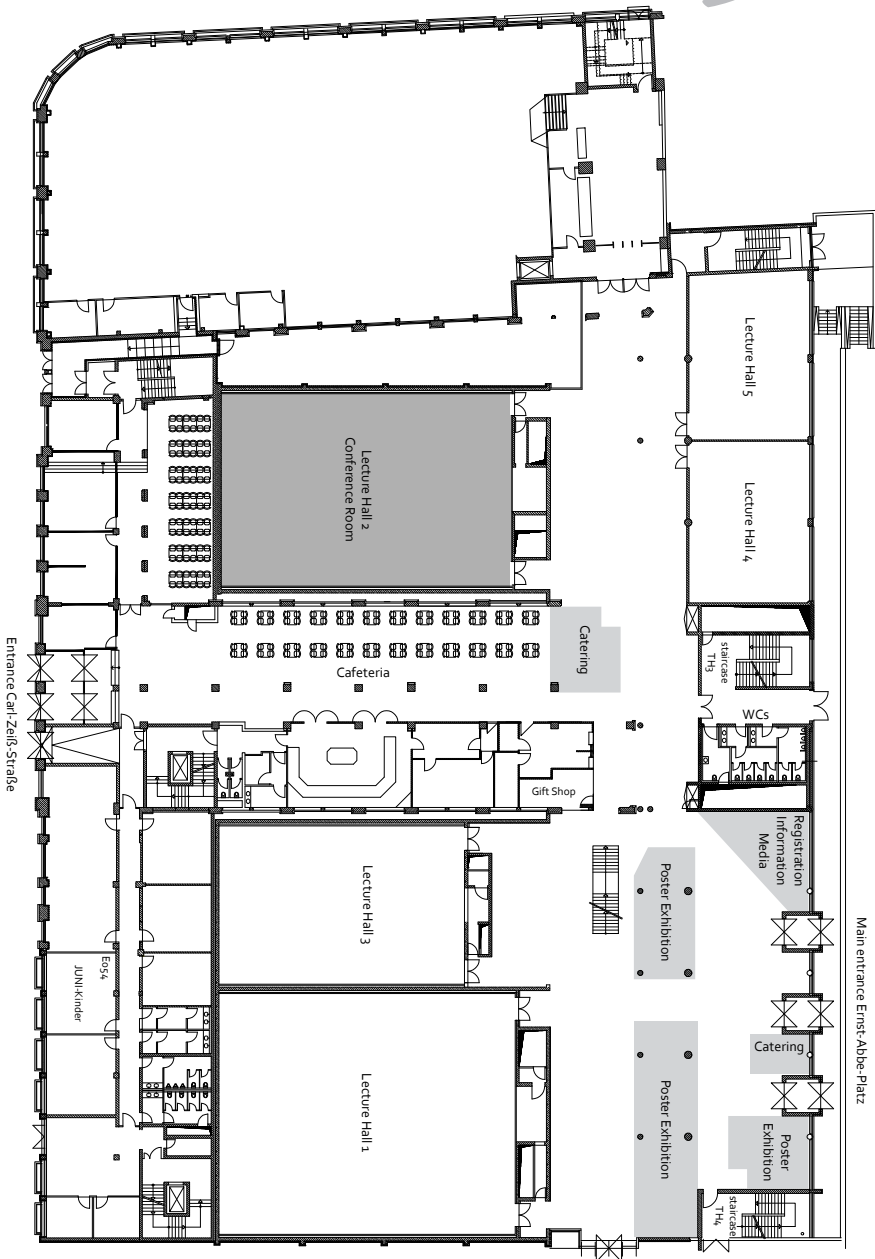
Fürstengraben 1

Welcome Reception

3 - Botanical Garden

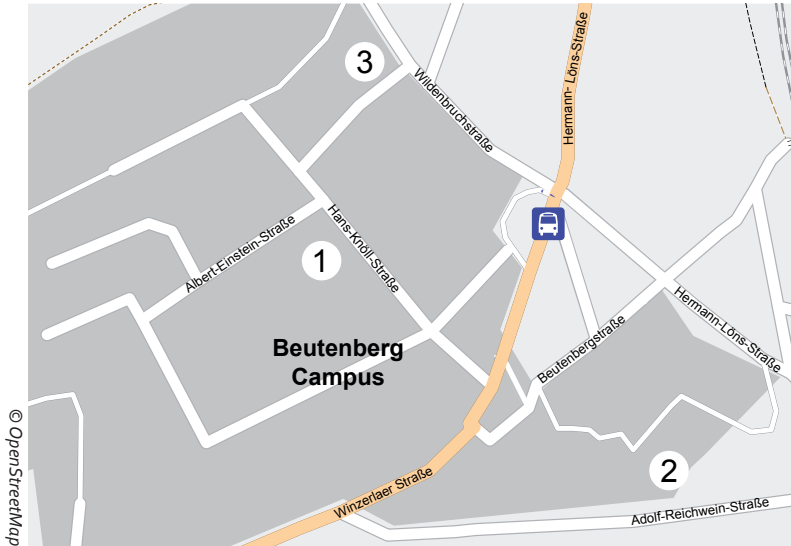
Fürstengraben 26

For a detailed map of the city center with a restaurant guide, see the additional conference material.



Satellite Workshops

Five satellite workshops will take place on 19 September 2012 on Jena's Beutenberg Campus.



From city centre or Westbahnhof, take **buses No. 10, 11, 12 or 13** (directions Damaschkeweg, Beutenberg Campus, Burgau or Göschwitz). **IMPORTANT:** tickets (zone 1) can be bought in the bus, but exclusively using coins or "Geldkarte". Get off at bus stop **Beutenberg Campus** and walk to

1 - Abbe Center

Hans-Knöll-Str. 1 (Beutenberg Campus Nord)

Registration Desk
WS Systems Biology of Aging

2 - Hans-Knöll-Institute (HKI) - Leibniz Institute for Natural Product Research and Infection Biology - Centre for Systems Biology of Infection

Beutenbergstr. 11a (Beutenberg Campus Süd) - rooms will be signposted on site

WS Image-based Systems Biology
WS Network Reconstruction and Analysis in Systems Biology
WS Computational Proteomics and Metabolomics
DECHEMA board meeting

3 - BioControl Jena GmbH: Technologie- und Innovationspark Jena (TIP)

Wildenbruchstr. 15 (Beutenberg Campus Nord)

WS Organ-oriented Systems Biology (3rd Floor, Conference Room 1 and 2)

Sightseeing

“Ara, caput, draco, mons, pons, vulpecula turris, Weigeliana domus, septem miracula Jenae”

Seven landmarks of Jena already amazed many visitors in the 17th century:

ara	an underpass beneath the altar of the gothic “Michaelskirche”
caput	“Snatching Hans” (“Schnapphans”) at the astronomical clock of the town hall
draco	the dragon, a prank build by students, that can be visited in the town museum
mons	a chalk rock, called Jenzig, that glows red in the rising and setting sun
pons	“Camsdorfer Brücke”, first stone arch bridge across the river Saale (replaced in 1912)
vulpecula turris	“Fuchsturm”, the keep of an ancient castle
Weigeliana domus	designed by Erhard Weigel (demolished in 1898)

Further historical attractions, among many others, are the **monument to John Frederick the Magnanimous** (founder of the University of Jena) in the market square or the numerous towers from the medieval fortifications, including the **Powder Tower** (13th-14th centuries). Several places remind of two famous German poets: **Friedrich Schiller** and **Johann Wolfgang von Goethe**. Schiller’s summer house, where he wrote “Wallenstein”, is certainly worth a visit.

Jena is home to the famous companies Carl Zeiss and SCHOTT JENAer GLAS. Carl Zeiss, Otto Schott, and Ernst Abbe provided the fundamentals of modern optics here. To learn more about this topic, visit the **Optical Museum** Jena. The **Zeiss-Planetarium** is the oldest still existing planetarium of the world. In the **Science Center Imaginata**, one can try out experiments with optical illusions and discover the laws of physics.

Ernst Haeckel formed the history of evolutionary biology in Jena. He discovered, described and named thousands of new species and was first to draw up a genealogical tree relating the various orders of animals. We recommend visiting the **Museum of Phylogeny**, founded by him.

Jena is not only surrounded by nature worth an excursion, but also the city has splendid parks to offer. Directly alongside the planetarium is the **“Botanische Garten Jena”**, founded in 1580, the second oldest botanical garden in Germany. The biggest park along the Saale is called **Jena Paradies** (paradise), with several cocktail bars to visit in the warm season.

The most striking building of Jena is the **Jen-Tower** (also called “Keksrolle”), with a restaurant and viewing platform at the 27th floor, offering a beautiful view over the town. Right beside the tower is the entrance to the **Wagnergasse**, the center of the nightlife with several pubs and cafés.

To get in touch with arts in Jena, we recommend to check the schedules of the **Theaterhaus Jena** or the **Volkshaus**, or visit the art collection in the **Neue Göhre** or the abstract sculptures of Frank Stella on the campus.



Keynote Speakers

Thomas Kirkwood

Newcastle University, Newcastle, UK

Probing the deep complexity of ageing

Thursday, 20 September 2012, 09:15

Oliver Fiehn

University of California, Davis, USA

Comprehensive metabolomic databases and annotation workflows:

The U.S. West Coast Metabolomics Center

Thursday, 20 September 2012, 14:00

Erik van Nimwegen

University of Basel, Basel, Switzerland

A democracy of transcription factors: Inferring transcription regulatory interactions from high-throughput data

Friday, 21 September 2012, 09:00

Arndt von Haeseler

Max F. Perutz Laboratories, Vienna, Austria

Exploring the sampling universe of RNA-seq

Friday, 21 September 2012, 14:15

Ruth Nussinov

National Cancer Institute, Frederick, USA

Structural proteome scale prediction of protein-protein interactions using interfaces

Saturday, 22 September 2012, 09:00

Claude dePamphilis

Pennsylvania State University, University Park, USA

*The draft genome sequence of *Amborella trichopoda* sheds light on the ancestral angiosperm genome*

Saturday, 22 September 2012, 11:30

Conference Schedule

Wednesday, 19 September 2012

Satellite Workshops (Beutenberg Campus)

- 16:00 DECHEMA board meeting (Beutenberg Campus, HKI)
19:00 - **Welcome Reception**
21:00 Atrium of the University Main Building, Fürstengraben 1

Thursday, 20 September 2012

Main conference takes place at Ernst Abbe Campus, lecture hall 2.

R... Regular Paper H... Highlight Paper

- 8:00 Registration opens, poster mounting
9:00 **Welcome**
Prof. Dr. Klaus Dicke, Rector FSU Jena
9:10 **Opening**
Stefan Schuster and Sebastian Böcker, Program Chairs
9:15 **KEYNOTE**
Probing the deep complexity of ageing
Thomas Kirkwood (Newcastle University, Newcastle, UK)
10:00 *Dynamic modeling resolves complex hormonal crosstalk in infected plants (H)*
Thomas Dandekar, Muhammad Naseem and Dominik Schaack
10:25 *Two new perspectives on NAD metabolism (H)*
Toni I. Gossmann, Mathias Ziegler, Pal Puntervoll, Luis F. de Figueiredo,
Stefan Schuster and Ines Heiland

10:50 Coffee Break

11:20 *ModeScore: A method to infer changed activity of metabolic function from transcript profiles (R)*
Andreas Hoppe and Hermann-Georg Holzhütter
11:45 *Image-based systems biology: A quantitative approach to elucidate the kinetics of fungal morphologies and virulence (H)*
Franziska Mech and Marc Thilo Figge
12:10 *Comparing fragmentation trees from electron impact mass spectra with annotated fragmentation pathways (R)*
Franziska Hufsky and Sebastian Böcker



12:35 Lunch Break

14:00 **KEYNOTE**

*Comprehensive metabolomic databases and annotation workflows:
The U.S. West Coast Metabolomics Center*
Oliver Fiehn (University of California, Davis, USA)

14:45 *Identifying the unknowns by aligning fragmentation trees (H)*
Florian Rasche, Kerstin Scheubert, Franziska Hufsky, Thomas Zichner,
Marco Kai, Aleš Svatoš and Sebastian Böcker

15:10 *KeyPathwayMiner – Combining OMICS data and biological networks (H)*
Josch Pauling, Nicolas Alcaraz, Alexander Junge and Jan Baumbach

15:35 Coffee Break

16:00 *MetaboLights: Towards a new COSMOS of metabolomics data management (H)*

Kenneth Haug, Reza Salek, Pablo Conesa, Paula de Matos, Tejasvi Mahendraker, Eamonn Maguire, Philippe Rocca-Serra, Susanna-Assunta Sansone, Julian Griffin and Christoph Steinbeck

16:25 *Finding characteristic substructures for metabolite classes (R)*
Marcus Ludwig, Franziska Hufsky, Samy Elshamy and Sebastian Böcker

16:50 *A two-step soft segmentation procedure for MALDI imaging mass spectrometry data (R)*
Ilya Chernyavsky, Theodore Alexandrov, Peter Maass and Sergey Nikolenko

18:30 & **Social Event:** Guided walks through Jena's center
20:00

Friday, 21 September 2012

9:00 **KEYNOTE**

A democracy of transcription factors: Inferring transcription regulatory interactions from high-throughput data
Erik van Nimwegen (University of Basel, Basel, Switzerland)

9:45 *How little do we actually know? – On the size of gene regulatory networks (H)*
Richard Röttger and Jan Baumbach

10:10 *Out of (transcriptional) control? Design principles of the regulatory network controlling metabolic pathways in Escherichia coli (H)*
Frank Wessely, Martin Bartl, Reinhard Guthke, Pu Li and Christoph Kaleta

10:35 *Building and documenting workflows with Python-based snakemake (R)*
Johannes Köster and Sven Rahmann

11:00	Coffee Break					
11:30	<i>Online transitivity clustering of biological data with missing values (R)</i> Richard Röttger, Christoph Kreutzer, Thuy Duong Vu, Tobias Wittkop and Jan Baumbach					
11:55	<i>ConReg: Analysis and visualization of conserved regulatory networks in eukaryotes (R)</i> Robert Pesch, Matthias Böck, and Ralf Zimmer					
12:20	<i>Designing q-unique DNA sequences with integer linear programs and Euler tours in de Bruijn graphs (R)</i> Marianna D'Addario, Nils Kriege and Sven Rahmann					
12:45	Lunch Break					
14:15	KEYNOTE <i>Exploring the sampling universe of RNA-seq</i> Arndt von Haeseler (Max F. Perutz Laboratories, Vienna, Austria)					
15:00	<i>Polyglutamine and polyalanine tracts are enriched in transcription factors of plants (R)</i> Nina Kottenhagen, Lydia Gramzow, Fabian Horn, Martin Pohl and Günter Theißen					
15:25	<i>Readjoiner: a fast and memory efficient string graph-based sequence assembler (H)</i> Giorgio Gonnella and Stefan Kurtz					
15:50	Sponsor Presentation <i>Better computing for better bioinformatics</i> Ernst M. Mutke (HMK-Supercomputing, Convey Computer)	<table border="1"> <tr> <td>16:00</td> <td>GI meeting R 222 (second floor)</td> </tr> <tr> <td>17:00</td> <td>GBM meeting R 222 (second floor)</td> </tr> </table>	16:00	GI meeting R 222 (second floor)	17:00	GBM meeting R 222 (second floor)
16:00	GI meeting R 222 (second floor)					
17:00	GBM meeting R 222 (second floor)					
18:00 - 21:00	Poster Session with "Poster Party"					
18:00	Even numbers					
19:00	Odd numbers					

Saturday, 22 September 2012

- 9:00 **KEYNOTE**
Structural proteome scale prediction of protein-protein interactions using interfaces
Ruth Nussinov (National Cancer Institute, Frederick, USA)
- 9:45 *Computation and visualization of protein topology graphs including ligand information (R)*
Tim Schäfer, Patrick May and Ina Koch
- 10:10 *Unbiased protein interface prediction based on ligand diversity quantification (R)*
Reyhaneh Esmailbeiki and Jean-Christophe Nebel
- 10:35 *Footprints of modular evolution in a dense taxonomic clade (H)*
Andrew Moore and Erich Bornberg-Bauer

11:00 Coffee Break


- 11:30 **KEYNOTE**
*The draft genome sequence of *Amborella trichopoda* sheds light on the ancestral angiosperm genome*
Claude dePamphilis (Pennsylvania State University, University Park, USA)
- 12:15 Closing Remarks, Award of Best Poster Prize

Posters

- P01 Large-Scale Evolutionary Patterns of Protein Domain Distributions in Eukaryotes
Arli A Parikesit, Peter F Stadler and Sonja J Prohaska
- P02 e!DAL: A Framework for Storing, Sharing and Citing Primary Life Science Data
Daniel Arend, Matthias Lange, Christian Colmsee, Steffen Flemming, Jinbo Chen and Uwe Scholz
- P03 Involvement of mTor-pathway in aging during cultivation of primary mouse hepatocytes
Wolfgang Schmidt-Heck, Uwe Menzel and Reinhard Guthke
- P04 Analysis of the relation of replication mechanism and nucleotide composition in metazoan mitogenomes
Abdullah Sahyoun, Matthias Bernt, Peter Stadler and Kifah Tout
- P05 An Automaton-Based View on Error-Tolerant Pattern Matching with Backward Search
Dominik Kopczynski and Sven Rahmann
- P06 Modelling of Influenza Virus Infection in Mice
Himanshu Manchanda, Nora Seidel, Michaela Schmidtke and Reinhard Guthke
- P07 A novel approach for genome-wide prediction of secondary metabolite gene clusters
Thomas Wolf, Vladimir Shelest, Reinhard Guthke and Ekaterina Shelest
- P08 Analysis of the transcriptome of rat liver in response to PPAR antagonists
Martin Bens, Sebastian Vlaic, Reinhard Guthke and Jürgen Borlak
- P09 MicroRNA-Seq data analysis for age-related comparison of mouse and short-lived fish *Nothobranchius furzeri*
Andreas Dix, Steffen Priebe, Reinhard Guthke, Mario Baumgart and Alessandro Cellerino
- P10 Structural Features of Protein-Protein Interfaces analyzed with Concepts of Information Theory
Christophe Jardin, Arno Stefani, Olaf Othersen, Johannes Huber and Heinrich Sticht
- P11 MetaCrop: A Database for Plant Metabolism and Plant Metabolic Modelling
Stephan Weise, Christian Colmsee, Tobias Czauderna, Eva Grafahrend-Belau, Anja Hartmann, Astrid Junker, Björn Junker, Matthias Klapperstück, Uwe Scholz and Falk Schreiber
- P12 The mutually exclusive spliced exome of *Drosophila melanogaster*
Klas Hatje and Martin Kollmar
- P13 Trans-species transcriptome analysis to identify novel lifespan-affecting genes
Consortium Jenage
- P14 Comparison of high-throughput technologies of *Aspergillus fumigatus* using RNA-Seq
Sebastian Müller, Marco Groth, Konrad Grützmann, Reinhard Guthke, Olaf Kniemeyer, Axel Brakhage and Vito Valiante
- P15 Visualization of Protein Ligand Graphs
Tim Schäfer and Ina Koch

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- P16 **Comparative Genomics in the Social Amoebae**
Andrew Heidel, Hajara Lawal, Marius Felder, Christina Schilde, Nicholas Helps, Budi Tunggal, Francisco Rivero, Uwe John, Michael Schleicher, Ludwig Eichinger, Matthias Platzer, Angelika Noegel, Pauline Schaap and Gernot Glöckner
- P17 **Eukaryotic Gene Prediction Maximizing Posterior Accuracy**
Lizzy Gerischer and Mario Stanke
- P18 **The transcript catalogue of the short-lived fish *Nothobranchius furzeri* provides insights into age-dependent changes of mRNA levels.**
Andreas Petzold, Kathrin Reichwald, Marco Groth, Stefan Taudien, Nils Hartmann, Steffen Priebe, Dmitry Shagin, Christoph Englert and Matthias Platzer
- P19 **Quantitative Model of Cell Cycle Arrest and Cellular Senescence in Human Fibroblasts**
Sascha Schäuble, Karolin Klement, Shiva Marthandan, Sandra Münch, Ines Heiland, Stefan Schuster, Peter Hemmerich and Stephan Diekmann
- P20 **An Effective Framework for Reconstructing Gene Regulatory Networks From Genetical Genomics Data**
Robert J Flassig, Sandra Heise, Kai Sundmacher and Steffen Klant
- P21 **Analysis of evolutionary constraints on transcription factor binding sites in *Arabidopsis thaliana***
Paula Korkuc and Dirk Walther
- P22 **Predicting protein interfaces by modeling spatial structures**
Torsten Wierschin and Mario Stanke
- P23 **Theoretical design and experimental verification of amino acid overproducing strains of *Escherichia coli* using CASOP GS**
Silvio Waschina, Christoph Kaleta and Christian Kost
- P24 **Supervised Penalized Canonical Correlation Analysis**
Andrea Thum, Lore Westphal, Tilo Lübken, Sabine Rosahl, Steffen Neumann and Stefan Posch
- P25 **An Efficient Data Structure for Pangenomes**
Corinna Ernst and Sven Rahmann
- P26 **ISOQuant - an integrated bioinformatics pipeline for evaluation and reporting of data independent (LC-MSE) label-free quantitative proteomics data**
Jörg Kuharev, Hansjörg Schild and Stefan Tenzer
- P27 **On the evolutionary significance of the size and planarity of the proline ring**
Jörn Behre, Roland Voigt, Ingo Althöfer and Stefan Schuster
- P28 **rBiopaxParser: A new package to parse, modify and merge BioPAX-Ontologies within R**
Frank Kramer, Michaela Bayerlova, Annalen Bleckmann and Tim Beissbarth
- P29 **Visualizing Peptide Spectrum Matches in Genome Browsers**
Mathias Kuhring and Bernhard Renard
- P30 **Detecting and investigating substrate cycles in a genome-scale human metabolic network**
Juliane Gebauer, Stefan Schuster, Luis F de Figueiredo and Christoph Kaleta

- P31 Google goes cancer: Improving outcome prediction for cancer patients by network-based ranking of marker genes
Janine Roy
- P32 Give it AGO! - Insights into microRNA Argonaute sorting in plants
Christoph J Thieme and Dirk Walther
- P33 Modeling the Seasonal Adaptation of Circadian Clocks by Changes in the Network Structure of the Suprachiasmatic Nucleus
Christian Bodenstein, Marko Gosak, Stefan Schuster, Marko Marhl and Matjaz Perc
- P34 Genome sequence analysis of three marine fungal isolates using different next generation DNA sequencing methods
Abhishek Kumar and Frank Kempken
- P35 Sequence, structure, function and evolution of BEM46 proteins
Abhishek Kumar, Krisztina Kollath-Leiß and Frank Kempken
- P36 Establishment and analysis of fungal kinomes
Yousef Shbat, Abhishek Kumar and Frank Kempken
- P37 Classification by descent: Toward genetics-based taxonomy of RNA viruses
Chris Lauber, Igor A Sidorov, Alexander A Kravchenko, Dmitry V Samborskiy, Andrey M Leontovich and Alexander E Gorbalenya
- P38 Mathematical modelling of oxygen diffusion: Does cellular oxygen consumption cause gradients that influence intracellular oxygen sensors?
Samantha Nolan, Oliver Sawodny and Michael Ederer
- P39 Modelling the switch from type I to type II apoptosis during crosstalk of interleukin-1 β and Fas ligand signalling in cultivated hepatocytes
Julia Sanwald, Anna Lutz, Mathias Könczöl, Oliver Sawodny, Irmgard Merfort and Michael Ederer
- P40 Discovery of emphysema/COPD-relevant molecular networks from an A/J mouse COPD inhalation study by means of Reverse Engineering and Forward Simulation (REFS™)
Yang Xiang, Ulrike Kogel, Stephan Gebel, Michael Peck, Manuel Peitsch, Viatcheslav Akmaev, Boris Hayete, Jignesh Parikh, John Caprice, Julia Hoeng and Iya Khalil
- P41 BiSQUiD: Bisulfite Sequencing Quantification and Identification
Cassandra Falckenhayn, Guenter Raddatz and Frank Lyko
- P42 Large-scale organization of metabolic network models
Jens Einloft, Jörg Ackermann, Joachim Nöthen and Ina Koch
- P43 Atlas of gene-specific transcription factors and their epistatic relationships in yeast
Katrín Sameith, Marian Groot Koerkamp, Dik van Leenen, Mariel Brok, Tineke Lenstra, Joris Benschop, Sander van Hooff, Berend Snel, Patrick Kemmeren and Frank Holstege
- P44 GC content dependency of Open Reading Frame prediction
Martin Pohl, Guenter Theissen and Stefan Schuster
- P45 MetaProteomeAnalyzer: A software tool specifically developed for the functional and taxonomic characterization of metaproteome data
Thilo Muth, Robert Heyer, Alexander Behne, Fabian Kohrs, Dirk Benndorf, Erdmann Rapp and Udo Reichl

- 
- P46 Structural Insights into the Inhibition of GSK-3 β by 1-amino-2,4,5-trihydroxy-7-methyl-anthracene-9,10-diones
Katja Steffi Lerche, Doris Mahn, Robert Günther, Hans-Jörg Hofmann and Rolf Gebhardt
- P47 Theoretical study of two minus mating type specific dehydrogenases of the zygomycete *Mucor mucedo*
Sabrina Ellenberger, Stefan Schuster and Johannes Wöstemeyer
- P48 Root-Games between Plants: Predicting Tendency for Cooperation along environmental Gradients
Sebastian Germerodt, Jana Schleicher, Katrin Meyer, David Ward, Stefan Schuster and Kerstin Wiegand
- P49 A Spatio-Temporal Modeling Framework to Simulate Host-Pathogen Interactions
Johannes Pollmächer and Marc Thilo Figge
- P50 Single cell track analysis of two-photon microscopy on Th 17 cells in the gut
Zeinab Mokhtariasl and Marc Thilo Figge
- P51 PAA - A New R Package for Autoimmune Biomarker Discovery with Protein Microarrays
Michael Turewicz, Maike Ahrens, Caroline May, Helmut E Meyer and Martin Eisenacher
- P52 The role of alpha-ketoglutarate dehydrogenase in stabilizing the flux through the citric acid cycle
Dorothee Girbig and Joachim Selbig
- P53 Incorporating Proteome Similarities for Improved Species Abundance Estimation in Metaproteomics
Anke Penzlin, Martin S Lindner and Bernhard Y Renard
- P54 Parameter Estimation by Simulated Annealing for Models of Whole-Blood Infection Assays with *Candida Albicans*
Teresa Lehnert and Marc Thilo Figge
- P55 Semi-Automated Evaluation of Microbial Observables from High-Throughput Time-Lapse Microscopy
Stefan Helfrich, Alexander Grünberger, Dietrich Kohlheyer, Wolfgang Wiechert and Katharina Nöh
- P56 Analysis of RNA-Seq data after knockdown of *amer* gene family members in zebrafish
Stefan Pietsch, Birgit Perner and Christoph Englert
- P57 Transcriptomic analysis of the adult life stage of the invasive Colorado potato beetle (*Leptinotarsa decemlineata*) using Roche 454
Abhishek Kumar and Alessandro Grapputo
- P58 Deep roots and stepwise evolutionary history of the vertebrate head sensory systems
Martin Sebastijan Šestak, Vedran Božičević, Robert Bakarić, Vedran Dunjko and Tomislav Domazet-Lošo
- P59 Coupled Mutation Finder: A new entropy-based method quantifying phylogenetic noise for the detection of compensatory mutations
Mehmet Gültas and Stephan Waack

- P60 Automated Image Analysis of Hodgkin lymphoma
Alexander Schmitz, Hendrik Schäfer, Tim Schäfer, Norbert Dichter, Claudia Döring, Sylvia Hartmann, Martin-Leo Hansmann and Ina Koch
- P61 DDIS - A new algorithm for comparing gene interaction graphs
Vindi Jurinovic and Ulrich Mansmann
- P62 Unraveling stress resistance from metagenomic sequence of Socompa stromatolites
Daniel Kurth, Virginia H Albarracín, Santiago Revale, Nicolas Rascovan, Bernd Timmermann, Martin Vazquez and María Eugenia Farias
- P63 Theoretical study of lipid accumulation in the liver - Implications for nonalcoholic fatty liver disease
Jana Schleicher, Reinhard Guthke, Hermann-Georg Holzhütter and Stefan Schuster
- P64 Topology separation of discriminative sequence motifs located in membrane proteins with domains of unknown functions
Steffen Grunert, Florian Heinke and Dirk Labudde
- P65 Automated Encoding of Gene Regulatory Networks from Inference Tools in SBML
Bianca Hoffmann, Sebastian Vlaic and Andreas Dräger
- P66 Introducing Tree Topology Profiling for Meta-Analysis of Whole-Genome Phylogenies
Thomas Meinel and Antje Krause
- P67 Comparative transcriptomics of *Arabidopsis thaliana* and *Arabidopsis lyrata*
Yvonne Pöschl, Carolin Delker, Jana Gentkow, Marcel Quint and Ivo Grosse
- P68 Alignment of flowgrams to strings
Marcel Martin
- P69 RNA structure: Does secondary structure define a fold?
Nikolai Hecker and Andrew E Torda
- P70 eProS - A Database and Toolbox for large-scale Analyses of energetic Properties that determine Protein Structure and Function
Florian Heinke, Daniel Stockmann, Stefan Schildbach and Dirk Labudde
- P71 Network-based Prioritization and Functional Characterization of Disease Genes
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