

BioSysBio 2007

Systems Biology
Bioinformatics
Synthetic Biology

www.biosysbio.com

Thu 11th – Sat 13th
Jan 2007
Manchester UK

Abstracts edited by:

John Cumbers, Xu Gu, and Jong Sze Weng

Welcome message

About BioSysBio 2007

BioSysBio 2007 was held at the Manchester Conference Centre. It is aimed at students, post-docs and junior faculty working in biotechnology and all are welcome to attend.

The conference included sessions in Computational Systems Biology, Bioinformatics and Synthetic Biology.

The new session in Synthetic Biology highlighted some of the European entries in the MIT based International Genetically Engineered Machines competition (iGEM)

Organisers

Conference Chairs



John Cumbers

A graduate student at Brown University, Rhode Island, USA.
His research interests are centered around ageing. This includes the study of the molecular pathways that extend lifespan. His research uses both computational and wetlab techniques for modelling gene regulatory networks and predicting transcription factor binding sites.

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E-mail enquiries: JohnCumbers@BioSysBio.com.



Dr Jonathan Rees

UK Bioinformatics Forum

Project Manager for UK Bioinformatics Forum. Prior to that Jon spent 3 years as a post-doctoral research officer at the University of Oxford. He is also the founder of Bioinformatics.Net, one of the leading online directories of bioinformatics software.

Tel. +44(0)1865 484224



Manuel Corpas (head)

University of Manchester (UK)

Manuel's research has focused on the development of bioinformatics techniques that combine sequence and structure protein data for characterisation of evolutionarily determinant protein regions. More specifically, his research systematically discriminates functional and structural motifs based on a protein folding score. His research involved computational statistics, machine learning and visualisation techniques.

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Dr Dieter Weichart

MCISB Project Manager
Tel. UK +44(0)161 30 65197
MCISB



Frank Bruggeman

University of Manchester, UK / Free University Amsterdam, Netherlands

Research: Systems Biology: the application of combined experimental, theoretical and modelling approaches to better understand living systems, from cells to ecosystems.

Current Research: Application of Metabolomics Profiling of recombinant mammalian cells to bioprocess design. In this project we hope to optimize the production of heterologous proteins by mammalian cells using a systems-biological approach involving metabolomics, isotopomer flux balancing, machine learning, and kinetic modelling.



Julia Handl

University of Manchester

Julia Handl is a PhD student in the School of Chemistry at the University of Manchester. Her publications over the past three years (<http://dbkgroup.org/handl/publications.html>) have covered a variety of topics related to unsupervised and semi-supervised classification including cluster validation techniques, ant-based clustering and multiobjective approaches to clustering and feature selection. She chaired the special session on evolutionary clustering at the 2005 and 2006 IEEE Congress on Evolutionary Computation, and serves as a referee for a number of international conferences and journals in the field of evolutionary computation and bioinformatics.

Organising Committee



James Brown

University of Cambridge

Having graduated with an Engineering Masters degree from Cambridge earlier this year, James has spent the summer working out of MIT as an iGEM Ambassador. He has since returned to Cambridge to undertake a PhD program in the Haseloff Lab, Department of Plant Sciences to work on biological pattern formation and morphogenesis. He is looking to engineer self-organising, synthetic morphogenetic systems in both bacteria and ultimately plants.



Mackenzie Cowell

Boston University, USA



Luna De Ferrari

University of Edinburgh, UK

Luna is a Software Developer in Prof. Goryanin's Computational Systems Biology group. She is interested in web services and data mining. Right now she's trying to put together Taverna workflows and data mining with Weka to do some Bayesian learning of enzyme properties. She is a strong supporter of Open Source software and the Wiki master for the ECB and CSBE centres. She is involved in the teaching of the Computational Systems Biology Master course and collaborates with the RiboSys European project on yeast RNA. Luna has an MSc in Informatics and a BSc + MSc in Biotechnology and is now a PhD candidate.

<http://homepages.inf.ed.ac.uk/ldeferra/>



Derek Gatherer

University of Glasgow, UK

Derek Gatherer trained as a molecular developmental biologist at Imperial College and, after postdocs in Quito, Warwick and Cambridge, was Lecturer in Molecular Genetics at Liverpool John Moores University from 1996 to 1999. Since 2003 he has been at the Medical Research Council Virology Unit in Glasgow. During the intervening period he worked in the pharmaceutical industry in various bioinformatics-related capacities for Organon, EraGen, RiboTargets and Chemical Computing Group (CCG Inc). His interests are anything that can be done on a computer with application to biology, but for practical purposes over the last couple of years this has meant the comparative molecular evolution of herpesviruses. His previous work has covered the origin and evolution of periodically-structured proteins, the relationship of codon bias with genomic GC content, and, while in industry, the production of exhaustive catalogues of G-protein coupled receptors from completed genomes. He is currently writing an unreasonably long review article on the pioneering systems biology work of Walter Elsasser (1904-1991).

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Nils Gehlenborg

Institute for Systems Biology, Seattle, USA

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Indrani Halder

Pennsylvania State University, USA

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Sarath Chandra Janga

UNAM, México City

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Ramazan Saeed
Oxford University, UK

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Venkata P. Satagopam
EMBL Heidelberg, Germany

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Dominic Tolle
European Bioinformatics Institute, UK



Ole Schulz-Trieglaff
Free University of Berlin, Germany
I studied in Informatics in Berlin and Edinburgh. During my studies. I specialized in Applied Mathematics and Machine Learning applied to biological data. Currently I am PhD candidate at the Max Planck graduate school for Computational Biology and Scientific Computing in Berlin, Germany. My Phd research involves the identification of peptides from mass spectrometry that are associated with allograft rejection after renal transplantations.

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Naji Valeyev
University of Oxford, UK

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James Wasmuth
Hospital for Sick Children, Toronto, Canada

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Joanna Young
University of Edinburgh, UK

Scientific Advisory Board

Douglas Armstrong	<i>University of Edinburgh, UK</i>
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Sven Panke	<i>ETH Zurich, Switzerland</i>
Bonnie Webber	<i>University of Edinburgh, UK</i>
Hans V. Westerhoff	<i>University of Manchester, UK</i>

Plenary Speakers:



Hans V. Westerhoff

University of Manchester

Hans Westerhoff is Professor of Systems Biology at Manchester University and also Professor of Microbial Physiology (Free University Amsterdam, VUA) and Professor of Mathematical Biochemistry (University of Amsterdam, UvA) at the BioCentrum Amsterdam. He heads a transnational research group on Systems Biology which spans the Manchester Centre for Integrative Systems Biology (MCISB) in the Manchester Interdisciplinary BioCentre (MIB) and the BioCentrum Amsterdam (see also <http://www.bio.vu.nl/hwconf>). His research interest focuses on how the interactions of macromolecules can lead to biological functioning, and integrates quantitative experimentation with mathematical analyses



Alfonso Valencia

Universidad Autonoma Madrid

Alfonso Valencia is a biologist by training. He has a Ph.D. in molecular biology by the U. Autonoma (Madrid). Since 1986 he has been working in the field of Bioinformatics (initially combined with experimental approaches). From 1988 to 1994 he worked at the EMBL-Heidelberg in the group of Chris Sander, studying the evolution of protein function with a combination of sequence and structure based approaches. In 1994 he started his own group in Madrid, the Protein Design Group (PDG). The PDG is currently composed of more than 28 scientists, engineers and technicians. Alfonso Valencia is the coordinator of the Spanish network of bioinformatics, former VP and founder member of the International Society of Computational Biology, and Executive Editor of the journal Bioinformatics.

Ron Weiss

Princeton University



Developments in Synthetic Biology Ron Weiss is an Assistant Professor of Electrical Engineering at Princeton University, and also holds a faculty appointment in the Department of Molecular Biology. He received his PhD from the Massachusetts Institute of Technology in Computer Science and Electrical Engineering (2001). His research focuses primarily on Synthetic Biology, where he programs cell behavior by constructing and modeling biochemical and cellular computing systems.

Session speakers



Roland Eils - DKFZ (German Cancer Research Centre)
Gene regulation and profiling
Roland Eils is the head of the Department of Bioinformatics and Functional Genetics at the Institute of Molecular Biotechnology at the University of Heidelberg as well as head of the Department of Theoretical Bioinformatics at the DKFZ (German Cancer Research Centre). He specializes in gene regulation and expression profiles from microarrays.



Douglas Kell - University of Manchester, UK
Metabolomics and machine learning:
quantitative bioanalysis for systems biology
Douglas Kell is the Director of the Manchester Centre for Integrative Systems Biology (MCISB) based in the Manchester Interdisciplinary Biocentre (MIB) His research covers a broad range of topics from analytical chemistry to systems biology, usually coupled to biochemical and data modeling. University of Manchester, UK



Nicolas Le Novere - European Bioinformatics Institute, UK
Modeling and databases in systems Biology
After graduate in Paris and postdoctoral work in Paris and Cambridge (UK), Nicolas Le Novere now runs a research group at the EBI (European Bioinformatics Institute) near to Cambridge, UK. His previous work in Systems Biology includes the development of SBML (the Systems Biology Markup Language), the modeling of signaling systems and BioModels Database.



Randy Rettberg - MIT (Massachusetts Institute of Technology), USA
Synthetic Biology and iGEM
Randy organizes iGEM and runs MIT's Registry of Standard Biological Parts. More information to follow.



Herbert Sauro - University of Washington, USA
Modeling and modularity, tools for systems biology
Herbert Sauro is one of the authors of the Systems Biology Workbench, a collection of tools that allows the sharing and cross compatibility of models using the Systems Biology Markup Language, which he also pioneered the development of. He also has also written other tools for Systems Biology including drag and drop modeling tool Jdesigner and the simulation tool Jarnac. His current research focuses on functional modularity in Cellular Networks.



Sarah Teichmann - Laboratory of Molecular Biology, Cambridge, UK
Gene regulatory networks, Structural and Computational Genomics

Sarah Teichmann works on the evolution of protein-protein and protein-nucleic acid interaction at the level of both protein structure and comparative genomics. Over the past few years, she has been focusing on the functional annotation of DNA-binding transcription factors, and their evolution and dynamic expression. Recently, this computational research has been complemented by experimental molecular biology in her group at Cambridge.



Chris Voigt - UCSF (University of California, San Diego) USA
Synthetic Biology

As a pioneer in Synthetic Biology, Chris Voigt is producing standard biological parts that function like electrical devices in cells. His joint iGEM team last year produced "E. coli that could see light" and his recent research includes bacteria capable of spinning silk and invasion of cancer cells by engineered bacteria.

Program

Thursday 11th Jan

Workshops

A

9.00am - 10.15am

1. **Modeling with the Systems Biology Workbench**, Herbert Sauro, University of Washington, USA.
2. **Flux Balance Analysis and its applications**, Evangelos Simeonidis and Balázs Papp University of Manchester
3. **Edinburgh Pathway Editor part I**, Stuart Moodie, Anatoly Sorokin, Edinburgh University.
4. **Statistics for Microarrays**, Ernst Wit, Lancaster University
5. **Probabilistic models and Bayesian inference**, Magnus Rattray, University of Manchester
6. **Protein Annotation** Jennifer McDowell, EBI

10.15 - 10.45 Refreshments break

B

10.45am - 12.15am

1. **Prediction and evolution of transcription factors and their evolutionary families in prokaryotes**, Sarath Chandra Janga
2. **Development and analysis of kinetic models of intracellular networks**, Frank Bruggeman, MIB
3. **Edinburgh Pathway Editor part II**, Stuart Moodie, Anatoly Sorokin, Edinburgh University.
4. **Statistics for Microarrays**, Ernst Wit, Lancaster University
5. **Bioconductor tools for graphs**, Wolfgang Huber, EBI
6. To be confirmed

Apologies, there is no longer a workshop on BioPerl/Bioruby

Thursday 11th Jan

Conference

12.00 – 13.00 Registration
13.00 – 13.15 Opening and welcome

Opening plenary speakers:

13.15 – 14.00 Steve Oliver - University of Manchester
14.00– 14.45 Alfonso Valencia - Universidad Autonoma Madrid

14.45 – 15.15 Refreshments

Session 1: Gene regulation and profiling

15.15 - 15.55 Roland Eils - DKFZ (German Cancer Research Centre)

15.55 - 16.20 Martino Barenco - Institute of Child Health UCL (University College London)

"rHVDM – A fast and user-friendly R package to predict transcription factor targets from microarray time series data."

16.20 - 16.45 Alok Mishra - Imperial College London

"Effect of microarray data heterogeneity on gene regulatory module discovery"

18.00 – 21.00 Industry Partnership Fair and Welcome party sponsored by the Doctoral Training Centre

Friday 12th Jan

08.00 - 8.45: Breakfast

Session 2: Metabolomics and machine learning: quantitative bioanalysis for systems biology

08.45– 09.25 Douglas Kell - University of Manchester, UK

09.25 - 09.50 Raul Munoz Hernandez - University of Manchester, UK
Metabolic flux analysis to study the production of a non-ribosomal lipopeptide, cda, by streptomyces coelicolor

09.50 - 10.15 Daniel Mateus - CEA/List Saclay, France
Modeling Genetic Regulatory Networks from specified behaviours

10.15– 11.45 Break & poster session 1

Session 3: Synthetic Biology and iGEM

11.45– 12.15 Randy Rettberg - MIT (Massachusetts Institute of Technology), USA

12.15– 12.35 University of Edinburgh iGEM team, UK
Modeling Arsenic Biosensor System

12.35– 12.55 Imperial College London iGEM team
Engineering a synthetic molecular oscillator based on the Lotka-Volterra dynamic.

12.55– 13.15 University of Cambridge iGEM team, UK
Autonomous pattern formation between bacterial populations

13.15– 14.15 Lunch + iGEM workshop - What do I need to do to take part in iGEM 2007?

Session 4: Modeling and databases in systems Biology

14.15– 14.55 Nicolas Le Novere - European Bioinformatics Institute, UK

14.55– 15.20 Michael Lees - University of Nottingham
BacGrid: Simulations of Bacteria using the GRID

15.20– 15.45 Isabel Rojas - EML Research gGmbH, Heidelberg, Germany
SABIO-RK: a database of biochemical reactions and their kinetics

15.45– 17.15 Break & poster session 2

Session 5: Modeling and modularity, tools for systems biology

17.15– 17.55 Herbert Sauro - University of Washington, USA

17.55– 18.20 Martin Hemberg - Imperial College London
A study of the properties of stochastic genetic oscillators

18.20– 18.45 talk to be confirmed

*19.30– onwards, Conference meal –
sponsored by Chemical Computing Group.*

Saturday 13th Jan

08.00 - 8.45: Breakfast

Session 6: Gene regulatory networks, Structural and Computational Genomics

08.45– 09.25 Sarah Teichmann - Laboratory of Molecular Biology, Cambridge, UK

09.25– 09.50 Sanne Abeln - University of Oxford
Linking evolution of protein structures through fragments

09.50– 10.15 Emily Jefferson - University of Dundee
The relationship between domain-domain interaction orientation and sequence similarity

10.15– 10.45 Refreshments break

Session 7: Synthetic Biology

10.45– 11.25 Chris Voigt - UCSD (University of California, San Diego) USA

11.25– 11.50 James Brown - University of Cambridge
Navigational Control of Bacteria

11.50– 12.15 Alfonso Jaramillo - Ecole Polytechnique, France
Computational Design of Proteins With New Functions

12.15– 13.00 Closing Plenary: Ron Weiss - Princeton University
Developments in Synthetic Biology

13.00– 13.15 Prize giving and conference close

Registered Delegates

Khairiah Abd Karim - The University of Manchester
Mohd Basyaruddin Abdul Rahman - University of Edinburgh
Sanne Abeln - University of Oxford
Oyeniya Abioye - Olabisi Onabanjo University
Ibrahim Alabdulkareem - KAMC
Mohammed Albalwi - KAMC
Hosam Aleem - University of Manchester
Jamie Allen - Newcastle University
Ricardo Almeida - Wellcome Trust Centre for Cell Biology University of Edinburgh
Enkhbayar Altantsetseg - Mongols Life Science Institute
Martyn Amos - Manchester Metropolitan University
Simon Andrews - The Babraham Institute
Camargo Anyela - University of Ulster
Mohammed Atee - Alnahrain university, Biotechnology department, Iraq
DAWIT AYALEW - self
Gowri Shankar Bagavananthen Andavan - University of Sydney
David Bakewell - Liverpool University
ABHIJIT G. BANERJEE - University of Manitoba, Winnipeg, Canada
AMAL BANIK - Notre Dame College, Dhaka
Martino Barenco - Institute of Child Health UCL
Michael Barton - University of Manchester
Kaj Bernhardt - University of Cambridge
David Blinco - University of Manchester
Costas Bouyioukos - University off East Anglia
Soren Brage - MRC Epidemiology Unit
Chris Bridson - John Innes Centre
James Brown - University of Cambridge
Martin Brown - University of Manchester
Frank Bruggeman - MIB Manchester
Jan Christian Bryne - CBU Bergen Center for Computational Science
Yizhi Cai - Univ. of Edinburgh
Dr Kathleen Carroll - MCISB University of Manchester
Nikhilesh Chand - University of Cambridge
Sarath Chandra Janga - UNAM, Mexico
Lukas Chavez – Max Planck Institute for Molecular Genomics
ChihChun Chen - UCL
Claudia Choi - Technische Universität Braunschweig, Germany
John Coadwell - The Babraham Institute
Ornella Cominetti - University of Chile, CMM, LBMG
Manuel Corpas - University of Manchester
John Cumbers - Brown University
Alberto de la Fuente - Virginia Bioinformatics Institute, USA
Kim de Mora - University of Edinburgh
Vinayak Doraiswamy - Postdoc - National University of Singapore
Warwick Dunn - University of Manchester
Witold Dyrka - Kingston University
Roland Eils - DKFZ (German Cancer Research Centre)
Alistair Elfick - University of Edinburgh

Conference Information

Sebastian Fallert - Cambridge University
Gang FANG - Institut Pasteur, Paris
sondes fayeche - ISG TUNIS
Katie Finch - EPSRC
Ronan Fleming - National University of Ireland, Galway
SiewChinn Fong - University of Dundee
Derek Gatherer - MRC Virology Unit
Nils Gehlenborg - European Bioinformatics Institute
David Gilbert - University of Glasgow
Peter Giles - Cardiff University
Alexandre Gmez - University Pompeu Fabra
Eduardo Gonzalez Couto - Siena Biotech S.p.A.
Catherine Hack - University of Ulster
Luke Hakes - The University of Manchester
Katrina Halliday - Cambridge University Press
Hyesun Han - Yonsei University
Julia Handl - University of Manchester
Martin Hemberg - Imperial College London
Karl Heuer - TU Hamburg Harburg
Brendan Hickey - Brown University iGEM
MUHAMMAD HOSSAIN - NORTH SOUTH UNIVERSITY
Michael Hubank - Institute for Child Health, UCL
Wolfgang Huber - EBI
Eun ju Im - Yonsei University (Korea)
iGEM2006 Imperial College - iGEM Imperial College London
Sergii Ivakhno - School of Informatics, The University of Edinburgh
Alfonso Jaramillo - Laboratoire de BIOCHIMIE, Ecole Polytechnique, France
Emily Jefferson - University of Dundee
Dafyd Jenkins - University of Birmingham
Tieming Ji - New Mexico State University, USA
Caroline Johnston - University of Essex
Philip Jones - EMBLEuropean Bioinformatics Institute
Gabriela Kalna - University of Strathclyde
Gokhan Karakulah - Dokuz Eylul University, Health Sciences Institute,
Department of Medical Informatics
Ana Katherine de Carvalho Lima Lobato - University of Manchester
Koray Dogan Kaya - Bilkent University, Department of Molecular Biology and
Genetics
Douglas Kell - The University of Manchester
Imtiaz Khan - Cardiff University
Hyunji Kim - University of Oxford
Tom Kirkwood - Newcastle University
Christian Knuepfer - Institut fuer Informatik, Jena, Germany
Alexey Kolodkin - Vrije University
Alper Kucukural - Sabanci University
Jan Kuentzer - Center for Bioinformatics Saarland University
Judit Kumuthini - Cranfield University
Andrey Kuznetsov - Freiburg University
Nuno Lages - Faculty of Sciences of the University of Lisbon
Okoror Lawrence - Lecturer - Ambrose Alli University Ekpoma, Nigeria
Nicolas Le Novere - EBI
Michael Lees - University of Nottingham
Thorsten Lenser - FSU Jena
Hui Sun Leong - Cardiff University

Conference Information

Melissa Li - Georgia Institute of Technology
Peter Li - University of Manchester
Allyson Lister - Newcastle University
Lin Liu - Institute of Psychiatry, Kings College London
KoYun Lo - University of Oxford
Jason Lohmueller - Brown University
Royer Loic - TU Dresden
Adrin Lpez - UPF
Hongwu Ma - University of Edinburgh
Greg Machray - University Of Dundee
Steve Maginn - Chemical Computing Group
Jonathan Manning - University of Dundee
Olga Markova - Bogomoletz Institute of Physiology
alex marshall - Multidisciplinary Centre for Integrative Biology
Agustino MartinezAntonio - INSERM
Daniel Mateus - CEALIST Saclay, France
Patrick May - Zuse Institute Berlin
Emmet McIntyre - University of Kent
anamika mehta - na
sherif meligy - aast
Filippo Menolascina - National Cancer Institute "Giovanni Paolo II". Italy
Suraj Menon - Cardiff University
Nina Mian - AstraZeneca
Andrew Millar - University of Edinburgh
David Milroy - ITI Life Sciences
Alok Mishra - Imperial College, London
Latifa Mohamed - King Faisal Hospital
Duarte Molha - University of Ulster
Stuart Moodie - Edinburgh University
Pablo Moreno - Bioinformatics Genome Mathematics Lab, University of Chile
Elisa Mori - Universita degli studi di Siena
Mark Muldoon - University of Manchester
Jonas Nart - ETH Zurich
ADAK NASIRIPOURDORI - TMU university (tehran,iran)
Chris Neugebauer - Cambridge University
Judith Nicholson - Edinburgh iGEM team
Nadtanet Nunthaboot - Chulalongkorn University
Steve Oliver - University of Manchester
Allan Orozco - University of Costa Rica
Fernando Ortega - The University of Birmingham
Balázs Papp - Manchester University
HOSIL PARK - The University of Manchester
Helen Parsons - University of Birmingham
Ricardo Paxson - Mathworks
John Pinney - University of Manchester
Matthew Pocock - Newcastle University
abhishek pratap - Vellore Institute of Technology
Mal Primet - NS Ulm
Leighton Pritchard - Scottish Crop Research Institute
Vilda Purutcuoglu - Lancaster University
Mahbubur Rahman - AIUB
Vijayan Ramachandran - Jawaharlal Nehru University
Mattias Rantalainen - Imperial College London
Magnus Rattray - Manchester University

Conference Information

Jonathan Rees - UK Bioinformatics Forum
Randy Rettberg - MIT
Ida Retter - Technische Universität Braunschweig, Germany
CHRISTELLE ROBERT - BioSS SCRI
Guillermo Rodrigo - Universidad Politecnica Valencia, Spain
Isabel Rojas - EML Research gGmbH
DAurizio Romina - Universita di Siena (Italy)
Vincent Rouilly - Imperial College London
Alexander Rurainski - Center for Bioinformatics, Saarland University, Germany
jyoti rusia - U.I.E.T,C.S.J.M University Kanpur
Ramazan Saeed - University of Oxford
Kurt Saetzler - University of Ulster
Natasha Sahgal - Cranfield University
Padchanee Sangthong - University of Manchester
Rhodri Saunders - University of Oxford, Department of Statistics
Herbert Sauro - University of Washington
Ole SchulzTrieglaff - Free University Berlin
Michelle Scott - University of Dundee
Anne Segonds-Pichon - Babraham Institute
Huseyin Seker - De Montfort University
Shachi Sharma - Amity University
Joanna Sharman - University of Edinburgh
Evangelos Simeonidis - University of Manchester
safiyeh soofian
safyeh soofian - Tarbiat Modares University
Anatoly Sorokin - Edinburgh University
Melanie Stefan - EMBLEBI
lanzeni stefano - University of Milan Bicocca
Nadine Stein - Forschungszentrum Juelich GmbH
Dov Stekel - Birmingham University
Xiaoliang Sun - Max Planck Institute for Molecular Biology
Vaidy Sunderam - Emory University
Neil Swainston - University of Manchester
Iman Tavassoly - Mazandaran University of Medical Sciences
Sarah Teichmann - MRC Laboratory of Molecular Biology
Manoj Thapa - College For professional Studies
Nancy Thomas - bioinformatics
Dominic Tolle - EBI
Alfonso Valencia - Universidad Autonoma Madrid
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Olga Vasieva - University of Dundee, BRC
Keith Vass - The Beatson Institute for Cancer Research
Quy Vo Cam - Vietnam National University HCM City
Christopher Voigt - UCSF
Ines Wagner - MPICBG TUDresden
Katja Wegner - STRI, University of Hertfordshire
Stefan Weinges - Geneart
Ron Weiss - Princeton University
Patricia Welham - University of Birmingham
Thomas Williamson - University of Manchester
claire wilson - Epistem
Ernst Wit - Lancaster University
Kitiyaporn Wittayanarakul - Chulalongkorn University

Conference Information

ChihHsien Yang - Institute of Bioinformatics, National Yang Ming University

Abubakar Yaro - JMU

Le Yu - University of Strathclyde

mahboobeh zarrabi - university

Evgeny Zatulovskiy - SaintPetersburg State Polytechnical University, Research

Institute for Experimental Medicine of Russian Academy of Medical Sciences

Shanfeng ZHU - Bioinformatics center, Institute for Chemical Research, Kyoto

University, Japan

Xueni Zhu - Cambridge University