Research Networking Programmes

Science Meeting – Scientific Report

Scientific report (one single document in WORD or PDF file) should be submitted online within two months of the event. It should not exceed seven A4 pages.

Proposal Title: ***Systems Biology of Infection Symposium, held at Centro Stefano Franscini, Monte Verità, Switzerland 23/06/2013 – 27/06/2013***

Application Reference N°: 4282

1) Summary (up to one page)

Infectious diseases are a major cause of morbidity and mortality worldwide. Growing resistance to current antimicrobials and lean pipelines for novel therapeutics increasingly limit treatment options. New strategies to combat infections are required. In the past two decades a vast progress has been made in basic infection biology research including molecular characterisation of a large number of pathogen virulence factors and host immune effector mechanisms. However, knowledge about a particular mechanism cannot be easily translated into new control strategies since infectious diseases are usually the consequence of a fight between two networks of hundreds to thousands of individual factors. The new field of Systems Biology of Infection aims at an integrated understanding of complex host/pathogen interactions during infectious diseases and provides a basis for rational development of novel control strategies.

The Systems Biology of Infection Symposium held in Ascona, Switzerland, on June 23-27, 2013, was initiated by the leaders of two Swiss SystemsX.ch Research, Technology, and Development (RTD) projects InfectX (www.infectx.ch) and BattleX (www.battlex.ch) in order to enlarge scientific exchange among leading experts in the emerging field of Systems Biology of Infection. The conference gathered together leading international scientists as well as students and young researchers that have entered or are interested in entering this emerging research field. It brought together 96 participants from 14 countries.

The topics discussed were: (i) pathogen and host activities during infection with a focus on key aspects such as pathogen invasion of the host, metabolism as a basis for pathogen growth and fuelling of the host immune response, (ii) current methodologies for Systems Biology of Infection including genetics and genome-scale knock-down screening to study host susceptibility, (iii) large-scale pathogen epidemiology, and (iv) opportunities to translate emerging system-level understanding into development of new strategies to combat infectious diseases.

Two keynote lectures, nineteen talks from invited speakers, 22 short talks, and two poster sessions provided a comprehensive overview of recent developments in the field of Systems Biology of Infection and adjacent disciplines and promoted fruitful discussions and the building of new collaborations. Eight bursaries were granted to allow promising young researchers to attend the conference. One best oral presentation and two best poster prizes were awarded to young researchers to acknowledge their contribution to the field and excellent presentation skills.

Overall, the conference was to the highest standard and an enthusiastic feedback from participants was collected. The scientific content, the organisation, and the location in the historical venue Centro Stefano Franscini in Monte Verità, Ascona, Switzerland, all contributed to the productive atmosphere and numerous interactions between the scientists and facilitated future progress in the systems biology of infection field. Based on the overwhelmingly positive feedback by the participants and the continuous challenges in the field of the conference the organisers will consider organising a similar event in 2015 and thus establishing a conference series on this timely topic.

2) Description of the scientific content of and discussions at the event (up to four pages)

The conference spanned over five days and included two key note lectures, 19 talks from invited speakers and 22 short talks. The sessions were dedicated to “Pathogen epidemiology”, “Metabolism”, "Endocytosis”, “Pathogen invasion", “Host susceptibility”, “Pathogen activities” and “Applications in infection control”. Two poster sessions covered all above topics and promoted further scientific discussions and establishment of new collaborations.

In the “**Pathogen Epidemiology**” session molecular evolutionary analysis and genetic diversity of pathogens were presented. High resolution phylogenetic method and comparative genomic analysis revealed genetic mechanisms which have contributed to the capacity of *Staphylococcus aureus* to infect different host species (Dr. Ross Fitzgerald, University of Edinburgh, UK). RNAseq analysis of *Mycobacterium tuberculosis* complex lineages revealed that they exhibited distinct gene expression profiles which corresponded to their phylogenomic diversity (Dr. Sebastien Gagneux, Swiss TPH, Basel, Switzerland). A novel systems immunology approach which allows to quantitatively profile humoral immune responses that develop following immunisation with the complex pathogen *Streptococcus pneumonia* was introduced (Dr. Ulrike Haessler, ETH Zurich, Germany). Finally, a dynamic model of the cytokine response to influenza infections which can elucidate specific impact points for therapeutic intervention and vaccination was demonstrated (Dr. Sebastian Binder, Helmholtz Centre for Infection Research, Braunschweig, Germany).

The first keynote lecture by Dr. Gordon Dougan from the Wellcome Trust Sanger Institute, UK, was on “Pathogen populations and host genomes”. In this lecture several common features of microbial populations as well as their evolution under selection were discussed and new approaches to identifying infection-susceptibility loci in the host were presented.

The “**Metabolism**” session was focused on metabolism as a basis for pathogen growth and fuelling of the host immune response. The session was opened with a presentation on the missing link between the glycolysis and mitochondrial carboxylic acid metabolism in *Plasmodium* species and *Toxoplasma gondii* (Dr. Dominique Soldati-Favre, University of Geneva, Switzerland). Then, a comprehensive metabolic and flux analysis of human cytomegalovirus infection highlighted the key metabolic pathways during infection and helped to point to potential new sites for therapeutic intervention (Dr. Joshua D. Rabinowitz, Princeton University, USA). Metabolic and flux analysis and model predictions of mycobacteria (Paul Murima, EPF Lausanne, Switzerland), plant-pathogenic bacteria (Dr. Frank-Jörg Vorhölter, University of Bielefeld, Germany), and *Shigella flexneri* were also elucidated (Dr. Dirk Bumann, Biozentrum, University of Basel, Switzerland). Finally, a combination of various omics methods with computational analysis to study the regulation mechanisms which microbes use for coordinating metabolism was presented and discussed (Dr. Soumaya Zlitni, McMaster University, Hamilton, Canada).

The second keynote lecture by Prof. Alan Aderem from Seattle Biomed, USA, was on “A system approach to dissecting immunity”. In this lecture he highlighted the role of the innate immunity in host defence and illustrated the use of systems biology to identify and explore two novel anti-viral innate immune networks. In conclusion, he demonstrated the application of systems biology to rational vaccine design.

The “**Endocytosis**” session covered different aspects of intracellular trafficking and endocytic pathways during infection. In the first talk, three compounds causing the intracellular killing of *Mycobacteria tuberculosis* in primary human macrophages were identified, validated and their mechanism of action presented (Dr. Marino Zerial, MPI-CBG Dresden, Germany). In the second talk the mechanism of endosomal cholesterol transport and its role in disease progression was elucidated (Dr. Jean Gruenberg, University of Geneva, Switzerland). Then, a ligand-based receptor capture technology for the unbiased identification of receptors for ligands of almost every description was provided (Dr. Bernd Wollscheid, ETH Zurich, Switzerland). A targeted mass spectrometry based lipidomics approach was demonstrated to quantify the altered levels of different lipid species in influenza virus infected cells and reveal a novel and critical role of peroxisomal lipid metabolism for influenza virus replication (Dr. Lukas Tanner, National University of Singapore). Finally, a proteomic analysis of purified *Legionella pneumophila* identified more than 550 host proteins, including a number of small GTPases and other factors implicated in vesicle trafficking (Dr. Hubert Hilbi, University of Munich, Germany).

The “**Pathogen Invasion**” session focused on pathogen and host activities during initial stages of infection. Understanding the pathway(s) a virus and bacteria follow during infectious penetration will greatly facilitate development of useful entry inhibitors. The first talk outlined examples of how the use of contemporary tools of live-cell imaging to track the behaviour of individual virions during early stages of infection can provide quantitative descriptions of the invasion of mammalian cells by viral pathogens, including analysis of molecular mechanisms of penetration by non-enveloped viruses (Dr. Tomas Kirchausen, Harvard Medical School, Boston, USA). Next, a construction of a database of virus-host interactions which offers a global vision of how cellular functions can be manipulated and defines a unique framework from which molecules are designed or repositioned for drugging the human and viral proteomes, was presented and discussed (Dr. Vincent Lotteau, INSERM, Lyon, France). A statistical overview of siRNA screens of eight different pathogens using several commercially available siRNA libraries with its pitfalls and hints on how to improve the reproducibility of the assays and minimise false-positive results was a popular topic and triggered numerous questions and comments (Dr. Pauli Rämö, Biozentrum, University of Basel, Switzerland). Mathematical model of

Aspergillus fumigatus infection of lung epithelium identified the major contributors to fungal proliferation and to reduction of barrier integrity, and allowed quantitative understanding of the pro- and anti-curative effects of neutrophils and identifying the conditions that shift the response to infection from “clearance” to “damage” Dr. Katarina Vrcelj, Imperial College London, UK). Another approach, using high-end light microscopy, automated high through-put siRNA and drug screening as well as biochemical approaches, was presented to analyse the stepwise entry of animal viruses of different families into their host cells (Dr. Ari Helenius, ETH Zurich, Switzerland). In the next presentation, a large scale RNAi screen performed to investigate *Brucella* entry and replication in HeLa cells revealed numerous synthetic miRNAs that strongly affect infection and thus might represent interesting regulatory molecules for basic research and therapeutic intervention (Dr. Alain Casanova, Biozentrum, University of Basel). The session was closed by the presentation on the use of high-throughput genomics to elucidate the molecular mechanisms during co-infection in *Pseudomonas aeruginosa* wound infections (Dr. Marvin Whiteley, University of Texas at Austin, USA).

In the “**Host Susceptibility**” session the human genetic studies on tuberculosis and malaria were presented (Dr. Rolf D. Horstmann, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany). It was followed by a presentation on a new screening approach called “Haploid Genetic Screen” that enables the generation of compete knockouts for most human genes in cells that are haploid or nearly haploid and is used to identify host factors hijacked by different viruses to enter human cells (Dr. Thijn Brummelkamp, Netherlands Cancer Institute, Netherlands). A work on genetics of susceptibility to mycobacterial infections in zebrafish presented the identification of a gene critical in controlling the balance of pro- and anti-inflammatory responses suggesting that host-directed therapies against this gene can serve as a therapy for mycobacterial infections (Dr. David Tobin, Duke University, Durham, USA). Then, a global miRNA-mRNA transcriptomics was used to construct an miRNA-mRNA network and to study the role of miRNAs in *Mycobacterium tuberculosis*-infected macrophages (Dr. Joyoti Basu, Bose Institute, University of Calcutta, India). Finally, a mathematical model at single-cell resolution of type I interferon induction by virus and the cellular response to secreted interferon was presented (Dr. Mario Köster, Helmholtz Centre for Infection Research, Braunschweig, Germany).

In the “**Pathogen Activities**” session an RNA deep sequencing method was presented which was used to identify new small RNAs associated with the invasion and replication programmes of *Salmonella* Typhimurium (Dr. Jörg Vogel, University of Würzburg, Germany). Next, a method on measuring perturbations in host hepatocyte signalling was used to reveal susceptible host target nodes for intervention against malaria liver stage infection (Dr. Stefan Kappe, Seattle Biomedical Research Institute, USA). A work on dynamic quantification of the extracellular metabolome of non-replicating mycobacteria shed light on active metabolic pathways and demonstrated that the usage of metabolic pathways differs significantly between fast and slow growing mycobacteria (Dr. Michael Zimmermann, ETH Zurich, Switzerland). RNA-Seq to measure the transcriptome of two fungal pathogens *Aspergillus fumigatus* and *Candida albicans* during invasion of host cells was used to understand pathogenicity mechanisms and predict drug targets (Dr. Jörg Linde, Hans-Knöll-Institute, Jena, Germany). An automated time-lapse fluorescence microscopy in conjunction with custom-made microfluidic and microelectromechanical systems for real-time single-cell analysis of bacterial responses to antibiotics and other stresses was used to understand the mechanistic basis of the reversible persistent state in bacteria. The authors confirmed the theory that stochastic fluctuations in gene expression at the single-cell level can determine the fate of individual cells and cell populations in unpredictable and potentially hostile environments (Dr. John McKinney, EPF Lausanne, Switzerland). A novel approach of “dual RNA-seq”,

when RNA-seq is used to analyse gene expression changes in both pathogen and host simultaneously, was presented and discussed (Dr. Alexander Westermann, University of Würzburg, Germany). At the end, an in-silico prediction of the combinatorial stress responses of *Candida albicans* was shown (Dr. Komalapriya Chandrasekaran, University of Aberdeen, UK).

In the "**Application in Infection Control**" session a development of the first vaccine against meningococcal B disease using a "Reverse Vaccinology" approach was described. There an "*in silico*" analysis of the bacterial genome was first performed to identify the antigens based on their potential to be surface-exposed and therefore available for antibody binding; these antigens were later found to be important virulence factors necessary for the bacterial survival in the human blood and for bacterial adhesion to human epithelial cells (Dr. Mariagrazia Pizza, Novartis Vaccines, Sciena, Italy). Another study using a repertoire of novel bioactive compounds and characterising these compounds with genomic methods in the model bacterium *Escherichia coli* was presented to understand bacterial physiology and facilitate antibacterial drug discovery (Eric Brown, McMaster University, Hamilton, Canada). A work on target overexpression and its effects on antibiotic resistance were then discussed (Dr. Adam Palmer, Harvard University, Boston, USA). The effect of antibiotic treatment on metabolic response in *Escherichia coli* and identification of potential genes capable of mediating the interplay between the drug perturbation and internal metabolic changes were then highlighted (Dr. Mattia Zampieri, ETH Zurich, Switzerland). A single-molecule real-time sequencing technology to establish genome wide DNA modification profiles of two closely related *Neisseria meningitidis* strains was presented and discussed (Dr. Mohamad R. Abdul Sater, University of Basel, Switzerland. In conclusion, a talk describing the use of amoebae as model hosts to study mechanisms of mycobacteria infection to identify novel antitubercular compounds was presented (Dr. Thierry Soldati, University of Geneva, Switzerland).

The best oral presentation among short talks and two best posters were selected by a jury consisting of the session chairs. The best oral presentation was by Soumaya Zlitni, McMaster University, Canada, on "Metabolic suppression profiling identifies new antibacterial inhibitors under nutrient limitation". The first poster prize was awarded to Roger Meier, ETH Zurich, Switzerland, for the poster on "Regulation of virus endocytosis by miRNAs". The second poster prize was awarded to Paul Murima, EPF Lausanne, Switzerland, for the poster on "Molecular flux sensors regulating the metabolic branch-point between the TCA cycle & the glyoxylate shunt in mycobacateria".

3) Assessment of the results and impact of the event on the future directions of the field (up to two pages)

Infectious agents, including bacteria, viruses and parasites, represent major threats to human health. Emergence of drug-resistance, immune suppression and changes in human life-style promote the pathogen transmission and disease severity which has an increasing impact in the medical and public health sectors. Over the past 25 years, multi-disciplinary but, typically, reductionist research approaches have led to a detailed understanding of some central molecular pathways that enable pathogen entry and replication, as well as host immune responses to control infection. However, only current systems-level approaches that integrate holistic experimental and computational modelling approaches will deliver a comprehensive understanding of the complex interplay of pathogen and host that causes disease and pathogen transmission.

The “Systems Biology of Infection” Symposium focused on recent progress and the prospects in the new field of Systems Biology of Infection. This emerging field already has a broad foundation in Switzerland due to the Swiss research consortia InfectX and BattleX coordinated by the main organizer and co-organizer, respectively, that comprise 16 research groups at 5 different universities. We were delighted to see that the “Systems Biology of Infection” Symposium brought together widely recognised researchers from 14 different countries.

The researchers attended the conference were coming from the field of Systems Biology of Infection as well as complementary disciplines that are essential for an integrated system-level understanding of infectious diseases. This included researchers working on diverse classes of important human pathogens; researchers working on various cell culture models, animal models, and human patients; researchers employing experimental high-throughput approaches and computer modelling. All speakers made a great effort to introduce their specific approaches to this diverse audience. As a result, a large number of participants expressed their gratitude to learn about current developments in fields that are outside their own specific focus but have many connections to their work.

The conference deepened knowledge and interactions among diverse disciplines and promoted mutual inspiration and exchange of fresh ideas, which fostered collaborative research projects which is necessary to develop more effective infection control strategies. Importantly, researchers up to Master’s level attended the conference which allowed the transmission of the expertise to the younger generation of scientists.

Among specific achievements we would like to highlight:

1) Sanger stem cells facility and academics from three different countries studying endocytosis set up collaborations to create knock in mice to study endocytosis *in vivo*.

2) A fruitful discussion was initiated on limitations and opportunities to improve siRNA screening with implications for many research projects.

In conclusion, the organizers were encouraged by a large number of participants to organize a similar meeting in 2015.

4) Annexes 4a) and 4b): Programme of the meeting and full list of speakers and participants

Annex 4a: Programme of the meeting

	SUNDAY	MONDAY	TUESDAY	WEDNESDAY	THURSDAY
Morning		*Chair: Dirk Bumann* **Keynote** 8:30 - 9:15 **Gordon Dougan**, Sanger Institute **Metabolism** 09:15 – 09:45 **Dominique Soldati-Favre**, University of Geneva 09:45 – 10:15 **Joshua D. Rabinowitz**, Princeton University *10:15 - 10:45 Coffee* 11:45 – 11:00 Murima 11:00 - 11:15 Hatzimanikatis 11:15 - 11:30 Vorhölter 11:30 - 11:45 Zlitni	*Chair: Jean Gruenberg* 08:45 - 09:00 - **Presentation, CSF/ Monte Veritá** **Pathogen Invasion** 09:00 – 09:30 **Tomas Kirchausen**, Children's Hospital, Boston 09:30 – 10: 00 **Vincent Lotteau**, INSERM 10:00 – 10:15 Rämö 10:15 - 10:30 Vrcelj *10:30 - 11:00 Coffee* 11:00 - 11:30 **Ari Helenius** ETH, Zurich 11:30 - 11:45 Casanova 11:45 - 12:00 Whiteley	*Chair: Jörg Vogel* **Host susceptibility** 09:00 - 09:30 **Rolf D. Horstmann** Bernhard Nocht Instituite for Tropical Medicine, Hamburg 09:30 – 10:00 **Thijn Brummelkamp**, Netherlands Cancer Institute 10:00 - 10:30 **David Tobin**, Duke University *10:30 - 11:00 Coffee* 11:00 - 11:15 Basu 11:15 - 11:30 Köster 11.30 – 12.00 **Uwe Sauer** ETH Zurich	*Chair: Dominique Soldati-Favre* **Application in infection control** 09:00 – 09:30 **Mariagrazia Pizza**, Novartis 09:30 – 10:00 **Eric Brown**, McMaster University, Canada 10:00 – 10:30 **Adam Palmer** Harvard *10:30 – 11:00 Coffee* 11:00 – 11:15 Zampieri 11:15 - 11:30 Sater 11:30 - 11:45 Soldati 11:45 – 12:00 CSF Award and Closing Remarks
Lunch		12:00 – 14:00 Lunch	12:00 – 14:00 Lunch	12:00 – 14:00 Lunch	12:00 Lunch and departure
Afternoon	From 14:00 Arrival, Registration etc 17:00 - 17:15 Welcome Address by the organisers *Chair: Ari Helenius* **Pathogen Epidemiology** 17:15 – 17:45 **Ross Fitzgerald,** University of Edinburgh 17:45 – 18:15 **Sebastien Gagneux**, Swiss TPH 18:15 – 18:30 Haessler 18:30 - 18:45 Binder	*Chair: Christoph Dehio* **Keynote** 14:00 - 14:45 **Alan Aderem**, Seattle Biomed 14:45 - 16:45 Poster session *including coffee* **Endocytosis** 16:45 - 17:15 **Marino Zerial**, MPI-CBG Dresden 17:15 - 17:45 **Jean Gruenberg**, University of Geneva 17:45 – 18:00 Wollscheid 18:00 – 18:15 Tanner 18:15 - 18:30 Hilbi	From 14:30 Excursion followed by conference dinner	14:00 - 15:30 Poster session *Chair: Sebastien Gagneux* **Pathogen activities** 15:30 - 16:00 **Jörg Vogel** University of Würzburg 16:00 - 16:30 **Stefan Kappe**, Seattle BioMed *16:30 - 17:00 Coffee* 17:00 - 17:15 Zimmermann 17:15 - 17:30 Linde 17:30 - 18:00 **John McKinney**, EPFL 18:00 - 18:15 Westermann 18:15 - 18:30 Chandrasekaran	
Evening	*18:45 Welcome drink* *19.30 Dinner*	*19:00 Dinner*		*19:00 Dinner*	

Annex 4b: Full list of speakers and participants

№	Title	Firstname	Surname	Institute
1	Prof.	Alan	Aderem	Seattle Biomedical Research Institute
2	Dr.	Christian	Ahrens	University of Zurich
3		Arno	Andeweg	Erasmus Medical Center
4		Daniel	Andritschke	ETH Zurich
5	Prof.	Cecile	Arrieumerlou	Biozentrum, University of Basel
6	Dr.	Joyoti	Basu	Bose Institute
7	Dr.	Houchaima	Ben Tekaya	Biozentrum, University of Basel
8		Sebastian	Binder	Helmholtz Centre for Infection Research
9		Maj	Brodmann	Biozentrum, University of Basel
10	Prof.	Eric	Brown	McMaster University
11		Thijn	Brummelkamp	Netherlands Cancer Institute
12	Prof.	Dirk	Bumann	Biozentrum, University of Basel
13		Alain	Casanova	Biozentrum, University of Basel
14	Dr.	Anirikh	Chakrabarti	EPF Lausanne
15	Dr.	Komalapriya	Chandrasekaran	University of Aberdeen
16		Teresa	Cortes	MRC NIMR
17		Wanessa	de Lima	University of Geneva
18	Prof.	Christoph	Dehio	Biozentrum, University of Basel
19	Dr.	Maria Rosa	Domingo Sananes	University of Edinburgh
20	Prof.	Gordon	Dougan	Wellcome Trust Sanger Institute
21	Dr.	Amie	Eisfeld-Fenney	University of Wisconsin - Madison
22		Mario	Emmenlauer	Biozentrum, University of Basel
23		Shannon	Falconer	McMaster University
24	Prof.	Richard	Ferrero	Monash Institute of Medical Research
25		Astrid	Fieselmann	University of Würzburg
26	Prof.	Ross	Fitzgerald	University of Edinburgh
27		Claudia	Fortes	Functional Genomics Center Zurich
28		Sebastien	Gagneux	Swiss Tropical and Public Health Institute,University of Basel
29	Prof.	Qian	Gao	Fudan Unversity
30		Anna	Geffken	Research Center Borstel
31		Stan	Gorski	University of Würzburg
32	Prof.	Urs	Greber	University of Zurich
33	Prof.	Jean	Gruenberg	University of Geneva
34	Dr.	Xueli	Guan	Swiss Tropical and Public Health Institute,University of Basel
35		Aurélie	Gueho	University of Geneva
36	Dr.	Juan B.	Gutierrez	University of Georgia
37	Dr.	Ulrike	Haessler	ETH Zurich
38	Dr.	Christine	Hale	Wellcome Trust Sanger Institute
39	Prof.	Wolf-Dietrich	Hardt	ETH Zurich
40		Ari	Helenius	ETH Zurich
41		Dagmar	Heuer	Robert Koch Institute
42	Prof.	Hubert	Hilbi	Ludwig-Maximilians Universität München
43		Rolf	Horstmann	Bernhard Nocht Institutefor Tropical Medicine
44		Simon	Ittig	Biozentrum, University of Basel
45		Stefan	Kappe	Seattle Biomedical Research Institute
46		David	Kentner	Biozentrum, University of Basel
47	Prof.	Tomas	Kirchhausen	Harvard Medical School
48	Dr.	Mario	Köster	Helmholtz Centre for Infection Research
49		Saskia	Kreibich	ETH Zurich
50	Dr.	Julien	Limenitakis	Biozentrum, University of Basel
51	Dr.	Jörg	Linde	Leibniz Institute for Natural ProductResearch and Infection Biology
52	Dr.	Vincent	Lotteau	INSERM
53		Shyan Huey	Low	Biozentrum, University of Basel
54		Giuseppe	Martano	ETH Zurich
55	Prof.	John	McKinney	EPF Lausanne
56		Alaeddine	Meghraoui	Université Libre de Bruxelles
57		Roger	Meier	ETH Zurich
58	Dr.	Daria	Mudrak	University of Zurich
59		Paul	Murima	EPF Lausanne
60	Dr.	Aleksandra	Nita-Lazar	National Institutes of Health

61		Kolade	Oluwagbemigun	German Institute of Human NutritionPotsdam-Rehbrücke
62		Adam	Palmer	Harvard Medical School
63	Prof.	Nito	Panganiban	Tulane National Primate Research Center
64	Dr.	Frank	Pessler	TWINCORE Center
65	Dr.	Rèmi	Peyraud	INRA-CNRS
66	Dr.	Mariagrazia	Pizza	Novartis Vaccines
67		Joshua	Rabinowitz	Princeton University
68	Dr.	Pauli	Rämö	Biozentrum, University of Basel
69	Prof.	Ute	Römling	Karolinska Institutet
70		Mohamad	Rustom Abdul Sater	Swiss Tropical and Public Health Institute,University of Basel
71	Prof.	Uwe	Sauer	ETH Zurich
72		Sarah	Schatschneider	University of Bielefeld
73	Dr.	Birgit	Schoeberl	Merrimack Pharmaceuticals
74		Elsa	Seixas	Fundação Calouste Gulbenkian
75	Prof.	Thierry	Soldati	University of Geneva
76	Prof.	Dominique	Soldati-Favre	University of Geneva
77	Dr.	Reiko	Tanaka	Imperial College London
78	Dr.	Lukas	Tanner	National University of Singapore
79		Caroline	Taouk	University of Würzburg
80		Petra	Tienz	Biozentrum, University of Basel
81	Dr.	Olga	Burton	Biozentrum, University of Basel
82	Dr.	David	Tobin	Duke University
83	Dr.	Henk-Jan	van den Ham	Erasmus Medical Center
84	Prof.	Jose	Vazquez-Boland	University of Edinburgh
85		Jörg	Vogel	University of Würzburg
86	Dr.	Frank-Joerg	Vorhoelter	University of Bielefeld
87		Katarina	Vrcelj	Imperial College London
88	Dr.	Asa	Wahlander	Functional Genomics Center Zurich
89		Alexander	Westermann	University of Würzburg
90	Dr.	Marvin	Whitley	The University of Texas at Austin
91	Dr.	Kelly	Williams	Sandia National Laboratories
92	Dr.	Bernd	Wollscheid	ETH Zurich
93	Dr.	Mattia	Zampieri	ETH Zurich
94	Prof.	Marino	Zerial	Max Planck Institute of MolecularCell Biology and Genetics
95		Michael	Zimmermann	ETH Zurich
96		Soumaya	Zlitni	McMaster University