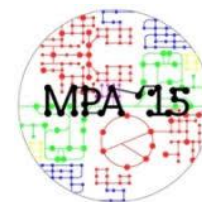# Participants list in the MPA 2015 conference poster sessions

Poster session 1: Tuesday 9th June (5 pm - 8:00pm)

Poster ID	Title	Presenting author
MPA_01	Integrated Contextualisation and Analysis of Metabolic Networks	Thomas Pfau
MPA_02	Shifts in the bacterial metatranscriptome accompanying draught in Namibian agricultural soils	Sixing Huang
MPA_03	FECorr: An algorithm to improve FBA predictions using transcriptomic data	Abdelmoneim Desouki
MPA_04	Impact of intermediate toxicity on the regulation of metabolic pathways	Jan Ewald
MPA_05	Dynamic constraint-based modeling of phototrophic metabolism	Alexandra-Mirela Reimers
MPA_06	Genome-scale and Flux modeling in the Lemnaceae (*Spirodela polyrhiza*) isoprenoid pathway for predictive metabolic engineering	Nadine Toepfer
MPA_07	Biofuel production with cyanobacteria: new strain design strategies revealed by computational modeling.	Philipp Erdrich
MPA_08	The steady-state assumption for oscillating and growing systems	Arne Reimers
MPA_09	Evaluation of methods for the reconstruction of specific models from omics data	Sara Correia
MPA_10	Investigation of physiological impacts of knockout mutants using a genome scale model of Arabidopsis.	Kailash Adhikari
MPA_11	Hub Reactions in Storage of Selected Compounds in Heterotrophic Plant Cell Network.	Marie Beurton-Aimar
MPA_12	Drug target identification in a *Salmonella* Typhimurium metabolic model	Hassan Hartman
MPA_13	A comparison between Flux Balance Analysis and cellular constrained models of simplified metabolic networks	Hugo Dourado
MPA_14	Flux variability analysis to understand *Arabidopsis* response to sulfur limitation.	Alex Calderwood
MPA_15	Interpreting systematic properties of the tomato photorespiratory metabolism by using a genome-scale metabolic model	Huili Yuan
MPA_16	Ancestral metabolic networks and phenotypic evolution in *E. coli*	Tin Yau Pang
MPA_17	Reconstruction and validation of *i*TR383, a genome-scale metabolic model for *Helicobacter pylori* 26695	Tiago Resende
MPA_18	The severity of enzyme mutations strongly influences the number of affected metabolic pathways	Deya Alzoubi
MPA_19	Dynamic modelling of cell metabolic behaviour: A work in progress	Mario Jolicoeur
MPA_20	A Model for the Expression Dynamics of the Nicotinic Acid Degradation Pathway in *Pseudomonas Putida* KT2440	Noah Mesfin
MPA_21	Imputing enzyme kinetic constants	Martin Lercher
MPA_22	Dynamic metabolic flux analysis of hybridoma cells cultivated in perfusion mode	Sofia Fernandes de Sousa

Poster ID	Title	Presenting author
MPA_23	Reconstruction of a genome-scale metabolic model for *Actinobacillus succinogenes*	Sonia Carneiro
MPA_24	Metabolic modeling of microalgae growth and lipids production during day/night cycles and nitrogen starvation	Caroline Baroukh
MPA_25	Visualizing omics data in the OptFlux workbench	Paulo Maia
MPA_26	Mathematical models of glucosinolate metabolism in plants	Suraj Sharma
MPA_27	Evaluation of carbon sources for recombinant enzymes production in *E. coli* – an *in silico* analysis of the host metabolism	Sindélia Freitas
MPA_28	In silico analysis of retinoid metabolism	Jennifer Chase
MPA_29	The evolutionary footprint in metabolic genes of *Arabidopsis thaliana*	Ahmad Mannan
MPA_30	Flux balance analysis of integrated host-virus metabolic models	Sean Aller

Poster session 2: Thursday 11th June (5 pm - 8:00pm)

Poster ID	Title	Presenting author
MPA_31	An adaptive scenario for the origins of complex innovations	Claus Jonathan Fritzemeier
MPA_32	TDPS - Turnover dependent phenotypic simulation: a quantitative constraint-based simulation method that accommodates all main strain design strategies	Rui Pereira
MPA_33	The effect of light on the evolution of C_4 plants	Esther Sundermann
MPA_34	Context-specific metabolic model extraction based on regularized least squares optimization	Semidan Robaina
MPA_35	Analysis of pathways involved in glycerol fermentation by two novel anaerobic bacteria	Alfons Stams
MPA_36	*Escherichia coli* redox metabolism for the production of polyhydroxybutyrate using different substrates	Mariana Velasco Alvarez
MPA_37	Markov-Chain Monte-Carlo sampling of metabolite concentrations to identify thermodynamically feasible reaction directionalities for flux balance analysis	Ulrich Wittelsburger
MPA_38	Enhancing the production of mannosylglycerate in *S. cerevisiae* through *in silico* driven metabolic engineering	Cristiana Faria
MPA_39	Metabolic analysis of EBPR phosphate/glycogen accumulating organisms	Leonor Guedes da Silva
MPA_40	SAT-based Metabolics Pathways Analysis without Compilation	Sabine Peres
MPA_41	Exploring the Consequences of Species Heterogeneity in ^{13}C-Flux Analysis: A Case Study	Salah Azzouzi
MPA_42	Analysis of 140 published GSMs and identification of the most common representation problems	Paulo Vilaça
MPA_43	Serine and glutamine metabolism in cancer cells.	Anna Zhukova
MPA_44	Including cofactor concentrations into dynamic Flux Balance Analysis	Antonella Succurro

MPA_45	Stochastic modelling of fatty acid synthesis	Elahe Radmaneshfar
MPA_46	Integrated analysis of metabolomics and transcriptomics data in tobacco cultivars grown in various regions of China	Lifeng Jin
MPA_47	*GlobalFit*: Automatically refining metabolic network models by simultaneously matching sets of experimental growth and non-growth data	Daniel Hartleb
MPA_48	Modeling nutrient assimilation in a species of Chloroidium isolated from the United Arab Emirates	David Nelson
MPA_49	Computer simulation of mitochondrial metabolism in cardiomyocytes during hypoxia	Filmon Eyassu
MPA_50	Phylogenomic signature fluidity in metabolic network of a key species with plant and animal affinities	Bushra Dohai
MPA_51	Integration of biomass functions of genome-scale metabolic models with experimental data reveals universally essential cofactors in prokaryotes	Joana Xavier
MPA_52	VIRTUAL MITOCHONDRION :A Modular and Multi Level Whole-Mitochondrion Model	Jean-Pierre MAZAT
MPA_53	Systems level metabolic pathway analysis for understanding antibiotic resistance in *Chromobacterium violaceum*	Deepanwita Banerjee
MPA_54	*merlin* latest developments for pathways analysis	Oscar Dias
MPA_55	Metabolic flux prediction in cancer cells with altered substrate uptake	Jean-Marc Schwartz
MPA_56	Elementary flux mode analysis of irradiance-induced stress acclimation strategies in the thermophilic cyanobacterium *Thermosynechococcus elongatus* BP-1	Ashley Beck
MPA_57	Uncovering the metabolic capacities of *H. pylori* 26695 using ^{13}C labeling experiments	Daniela Marques Correia
MPA_58	Compensatory mechanisms in mitochondrial diseases revealed by computer modelling	Alan Robinson
MPA_59	Analysis of *Salmonella typhimurium* pathways and metabolic model improvement	Teresa Zangirolami
MPA_60	Elucidate robust redox metabolism of *Clostridium thermocellum*	Cong Trinh