

$$S_{c8} = \sum_n V_n ([p55]_n + [DISCp55]_n + [p43]_n + [p18]_n + [p18i]_n)$$

Monday, May 27, 2019

In alphabetical order

ID	NAME	ABSTRACTTITLE
1	Noemi Andor	Modeling the evolution of ploidy in a resource restricted environment
2	Ms Rosario Astaburuaga	A mathematical model of lysosomal ion homeostasis points to differential effects of Cl ⁻ transport in Ca ²⁺ dynamics
3	Matthias Bieg	Enhancer hijacking activates oncogenic transcription factor NR4A3 in acinic cell carcinomas of the salivary gland
4	Chiara Di Ponzio	CYP3A5 expression in PDAC cells results in tumor niches protected from cytotoxic drugs
5	Dr. Elisa Dominguez-Huttlinger	A hybrid mathematical model of the interplay between keratinocyte differentiation and skin barrier function to understand epidermal homeostasis
6	Felix Dreher	CanPathPro – Development of a platform for predictive cancer pathway modelling using genetically engineered mouse models
7	Janine Egert	Realistic simulation of biological models
8	Prof. Fabian V. Filipp	Cancer systems biology identifies epigenetic and metabolic crosstalk in malignant melanoma
9	Dr. Marcel Grunert	Induced pluripotent stem cell modelling of Tetralogy of Fallot reveals alterations in cardiomyocyte differentiation
10	Dr. Anne-Christin Hauschild	Systems Biology Evaluation of Genetic Influences on Antipsychotic Induced Weight Gain in Patients with Schizophrenia
11	Dr. Tim Heinemann	Rational cancer drug-response profiling with artificial neural networks
12	Guillem Hurault	A Bayesian hidden Markov model to predict dynamic evolution of disease severity in eczema
13	Prof. Dr. Marc Hütt	A generative network model of transcriptome patterns in disease cohorts with tuneable signal strength
14	Svenja Kemmer	Model-based analysis of drug responses in breast cancer
15	Dr. Ki-jo Kim	Network-based interaction between disease-genes and drug targets in rheumatoid arthritis
16	Verena Körber	Evolutionary trajectories of glioblastomas reveal a common path of tumorigenesis instigated years ahead of diagnosis
17	Pamela Kreeger	Multivariate analysis to identify mechanisms by which macrophages promote ovarian cancer progression
18	Nan Li	Application of stepwise Elastic Net regression (sENR) with pairwise interactions to improve interpretation of drug response prediction
19	Deepa Maheshvare	Computational Modelling and Analysis of Altered Metabolism and its Relationship with Diseases
20	Dr. Anna Matveeva	Fractional cell death by death receptor activation is explained by stochastic assembly of Caspase-8 activation platform

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22	Stefan Neumann	A computational model of EGFR receptor trafficking
23	Dr. Benedikt Obermayer	Tracing tumorigenesis in a solid tumor model by single-cell transcriptomics
24	Martin Pirkl	Estimating perturbation profiles from patients mutation and gene expression data with a causal network approach.
25	Lukas Refisch	A multiscale model to improve treatment of anaemia in cancer and CKD patients
26	Dr. Manuela Salvucci	Integrated analysis of multi-omic traits from multi-tissue samples predicts drivers of disease outcome and treatment response in colorectal cancer
27	Prof. Dr. Reinhold Schäfer	Systems biology of RAS oncogene-driven malignancy
28	Ina Schmitt	Characterization of molecular alterations in chronic liver diseases using proteomics and mathematical modeling
29	Maren Sitte	Identification of target genes and signaling networks of Wnt1 1 in human breast cancer progression
30	Magdalena Szczygiel	Proteomic characterisation of the dynamics of tumor-stroma interactions in lung cancer
31	Dr. med. Rudolf Tauber	Serum glycome alterations in malignancy: a novel class of biomarkers
32	Florian Uhlitz	Multiplexed single-cell profiling of signalling and gene expression in patient-derived colorectal cancer organoids
33	Ph.D Pierre-Olivier Vidalain	Lipogenesis taught by viruses: learning from viruses how to control lipid accumulation in the liver
34	Thanutra Zhang	Chromosomal Position Effects on Epigenetic Drug Sensitivity
35	Roman Zug	Developmental disorders caused by haploinsufficiency: towards a unified explanation

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38	Dr. Katharina Baum	Differential gene expression analysis at the interface of single-cell dynamics and population growth
39	Sophie Bekisz	IN SILICO LYMPHANGIOGENESIS : Development of new tools to generate novel insights in the fundamental mechanisms regulating lymphangiogenesis
40	Philipp Burt	Response-time modeling of T-helper cell differentiation
41	Heiko Enderling	Mathematical oncology approaches to identify optimal dose, time and target of radiation therapy for robust immune activation
42	James Fairbanks	Semantic Program Analysis for Epidemiological Model Augmentation
43	Christos Fotis	Platform for compound prioritization based on transcription factor activity
44	Shrey Gandhi	Evolutionary aspects of circular RNAs in the heart
45	Adrian Hauber	Estimating Time Delays in Dynamical Systems Using Profile Likelihood
46	Dr. med. Dr. rer. nat. Stefan Kallenberger	A quantitative characterization of cellular stress signaling dynamics in response to HCV infection and its role on cell death
47	Dr. Anna Klimovskaia	Hyperbolic geometry as a tool for analysis of complex hierarchies from single-cell data
48	Maria Krantz	Bipartite Boolean Modelling of the Ras/Raf/Mek/Erk pathway to explain differences between mutations
49	Dr Claire Lastrucci	Distinct metabolic and signaling networks in circulating monocytes are associated to specific Age-related Macular Degeneration features
50	PhD student Raphaëlle Lesage	An In silico approach to study Osteoarthritis development and identify potential intervention targets.
51	Carolin Loos	A hierarchical, data-driven modeling approach for single-cell populations predicts latent causes of cell-to-cell variability
69	Viktor Makarenko	Dynamic pathway modeling of TGFbeta signaling in hepatic stellate cells
52	Dr. Michael Neidlin	Weighted gene co-expression network analysis identifies preserved modules in osteoarthritis and suggests drugs for treatment of cartilage degradation
53	Dr. Michal Or-Guil	How to exploit immunological data for medical use?

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56	Prof. Dr. Rosario Piro	Identification of active mutational processes in individual tumors with the R package decompTumor2Sig
57	Veronica R. de Melo Costa	SPLICE-q: a Python tool for Genome-Wide Quantification of Splicing Efficiency
58	PD Dr. Olga Ramich (Pivovarova)	Using shotgun lipidomics for analysis of dietary effects on lipid metabolism
59	Jens Rößler	Dissecting embryonic development of hematopoietic stem cells by in vivo barcoding
60	Ahmed Sadik	Natural language processing enhances the evaluation of AHR target genes
61	Darius Schweinoch	Predicting treatment outcome against hepatitis C virus using a multi-level replication model
62	Katherine Sheu	Stimulus-specific de novo enhancer formation through epigenetic decoding of NFkB signaling dynamics
63	Mareike Simon	Computational analysis of the impact of MYCN on the metabolism of neuroblastoma cells
64	Sabine Stübler	Systems biology model of the mucosal immune system in the context of inflammatory bowel disease
65	Kirsten Thobe	Logical modeling of the crosstalk between canonical & non-canonical NF-κB signaling pathways
66	Christian Tönsing	Optimal paths between parameter estimates in nonlinear ODE systems
67	Julius Upmeier zu Belzen	Leveraging Implicit Knowledge in Neural Networks for Functional Dissection and Engineering of Proteins
68	Dr. Uwe Warnken	Two-Step Co-Immunoprecipitation (TIP) provides Highly Selective Isolation of Native Protein Complexes for MS Quantification