# JÃ¶rg Stelling

## List of Publications by Year
## in descending order

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|---|---|---|---|
| 106<br>papers | 8,222<br>citations | 87888<br>38<br>h-index | 51608<br>86<br>g-index |
| 122<br>all docs | 122<br>docs citations | 122<br>times ranked | 8166<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Robustness of Cellular Functions. Cell, 2004, 118, 675-685. | 28.9 | 930 |
| 2 | Metabolic network structure determines key aspects of functionality and regulation. Nature, 2002, 420, 190-193. | 27.8 | 712 |
| 3 | A tunable synthetic mammalian oscillator. Nature, 2009, 457, 309-312. | 27.8 | 530 |
| 4 | Comparison of network-based pathway analysis methods. Trends in Biotechnology, 2004, 22, 400-405. | 9.3 | 347 |
| 5 | Large-scale computation of elementary flux modes with bit pattern trees. Bioinformatics, 2008, 24, 2229-2235. | 4.1 | 291 |
| 6 | Microbial network disturbances in relapsing refractory Crohn's disease. Nature Medicine, 2019, 25, 323-336. | 30.7 | 277 |
| 7 | Two approaches for metabolic pathway analysis?. Trends in Biotechnology, 2003, 21, 64-69. | 9.3 | 257 |
| 8 | Global Network Reorganization During Dynamic Adaptations of *Bacillus subtilis* Metabolism. Science, 2012, 335, 1099-1103. | 12.6 | 255 |
| 9 | Robustness properties of circadian clock architectures. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13210-13215. | 7.1 | 249 |
| 10 | Self-sufficient control of urate homeostasis in mice by a synthetic circuit. Nature Biotechnology, 2010, 28, 355-360. | 17.5 | 244 |
| 11 | Ensemble modeling for analysis of cell signaling dynamics. Nature Biotechnology, 2007, 25, 1001-1006. | 17.5 | 214 |
| 12 | Combinatorial complexity of pathway analysis in metabolic networks. Molecular Biology Reports, 2002, 29, 233-236. | 2.3 | 196 |
| 13 | FluxAnalyzer: exploring structure, pathways, and flux distributions in metabolic networks on interactive flux maps. Bioinformatics, 2003, 19, 261-269. | 4.1 | 187 |
| 14 | SBML Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110. | 7.2 | 178 |
| 15 | β-cell–mimetic designer cells provide closed-loop glycemic control. Science, 2016, 354, 1296-1301. | 12.6 | 173 |
| 16 | Accurate cell segmentation in microscopy images using membrane patterns. Bioinformatics, 2014, 30, 2644-2651. | 4.1 | 170 |
| 17 | Transcriptional regulation is insufficient to explain substrate-induced flux changes in *Bacillus subtilis*. Molecular Systems Biology, 2013, 9, 709. | 7.2 | 149 |
| 18 | Mathematical models in microbial systems biology. Current Opinion in Microbiology, 2004, 7, 513-518. | 5.1 | 145 |

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|---|---------|----|-----------|
| 19 | Inducible, tightly regulated and growth condition-independent transcription factor in Saccharomyces cerevisiae. Nucleic Acids Research, 2014, 42, e130-e130. | 14.5 | 140 |
| 20 | A synthetic time-delay circuit in mammalian cells and mice. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2643-2648. | 7.1 | 130 |
| 21 | MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. Bioinformatics, 2013, 29, 815-816. | 4.1 | 120 |
| 22 | Genome‐scale metabolic networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2009, 1, 285-297. | 6.6 | 115 |
| 23 | Computational design tools for synthetic biology. Current Opinion in Biotechnology, 2009, 20, 479-485. | 6.6 | 101 |
| 24 | Multistable and dynamic CRISPRi-based synthetic circuits. Nature Communications, 2020, 11, 2746. | 12.8 | 98 |
| 25 | Synthetic two-way communication between mammalian cells. Nature Biotechnology, 2012, 30, 991-996. | 17.5 | 97 |
| 26 | Subnetwork analysis reveals dynamic features of complex (bio)chemical networks. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19175-19180. | 7.1 | 96 |
| 27 | A Synthetic Multifunctional Mammalian pH Sensor and $CO_2$ Transgene-Control Device. Molecular Cell, 2014, 55, 397-408. | 9.7 | 96 |
| 28 | A synthetic low-frequency mammalian oscillator. Nucleic Acids Research, 2010, 38, 2702-2711. | 14.5 | 93 |
| 29 | Automatic Design of Digital Synthetic Gene Circuits. PLoS Computational Biology, 2011, 7, e1001083. | 3.2 | 85 |
| 30 | Efficient characterization of high-dimensional parameter spaces for systems biology. BMC Systems Biology, 2011, 5, 142. | 3.0 | 78 |
| 31 | System-Level Insights into Yeast Metabolism by Thermodynamic Analysis of Elementary Flux Modes. PLoS Computational Biology, 2012, 8, e1002415. | 3.2 | 61 |
| 32 | Systems interface biology. Journal of the Royal Society Interface, 2006, 3, 603-616. | 3.4 | 53 |
| 33 | Inflammatory signals directly instruct PU.1 in HSCs via TNF. Blood, 2019, 133, 816-819. | 1.4 | 53 |
| 34 | Circadian Phase Resetting via Single and Multiple Control Targets. PLoS Computational Biology, 2008, 4, e1000104. | 3.2 | 50 |
| 35 | Inferring causal metabolic signals that regulate the dynamic <scp>TORC</scp>1‐dependent transcriptome. Molecular Systems Biology, 2015, 11, 802. | 7.2 | 49 |
| 36 | Sensitivity analysis of oscillatory (bio)chemical systems. Computers and Chemical Engineering, 2005, 29, 663-673. | 3.8 | 48 |

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|---|---------|-----|-----------|
| 37 | Automatic Generation of Predictive Dynamic Models Reveals Nuclear Phosphorylation as the Key Msn2 Control Mechanism. Science Signaling, 2013, 6, ra41. | 3.6 | 44 |
| 38 | Quantitative performance metrics for robustness in circadian rhythms. Bioinformatics, 2007, 23, 358-364. | 4.1 | 42 |
| 39 | Integrating â€"omics data into genome-scale metabolic network models: principles and challenges. Essays in Biochemistry, 2018, 62, 563-574. | 4.7 | 40 |
| 40 | Predicting ligand-dependent tumors from multi-dimensional signaling features. Npj Systems Biology and Applications, 2017, 3, 27. | 3.0 | 39 |
| 41 | Counter-Intuitive Stochastic Behavior of Simple Gene Circuits with Negative Feedback. Biophysical Journal, 2010, 98, 1742-1750. | 0.5 | 38 |
| 42 | Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734. | 2.1 | 38 |
| 43 | Near-optimal experimental design for model selection in systems biology. Bioinformatics, 2013, 29, 2625-2632. | 4.1 | 37 |
| 44 | Signaling cascades as cellular devices for spatial computations. Journal of Mathematical Biology, 2009, 58, 35-55. | 1.9 | 36 |
| 45 | Systems analysis of cellular networks under uncertainty. FEBS Letters, 2009, 583, 3923-3930. | 2.8 | 35 |
| 46 | Chemical Reaction Network Theory elucidates sources of multistability in interferon signaling. PLoS Computational Biology, 2017, 13, e1005454. | 3.2 | 34 |
| 47 | The Galactose Switch in Kluyveromyces lactis Depends on Nuclear Competition between Gal4 and Gal1 for Gal80 Binding. Journal of Biological Chemistry, 2006, 281, 29337-29348. | 3.4 | 31 |
| 48 | Design of a biological half adder. IET Synthetic Biology, 2007, 1, 53-58. | 0.2 | 30 |
| 49 | Dephosphorylation activates the purified plant plasma membrane H+-ATPase . Possible function of phosphothreonine residues in a mechanism not involving the regulatory C-terminal domain of the enzyme. FEBS Journal, 1998, 251, 496-503. | 0.2 | 29 |
| 50 | Effect of Immunosuppression on T-Helper 2 and B-Cell Responses to Influenza Vaccination. Journal of Infectious Diseases, 2015, 212, 137-146. | 4.0 | 28 |
| 51 | Modular Analysis of Biological Networks. Advances in Experimental Medicine and Biology, 2012, 736, 3-17. | 1.6 | 27 |
| 52 | Genome-scale metabolic networks in time and space. Current Opinion in Systems Biology, 2018, 8, 51-58. | 2.6 | 27 |
| 53 | Use of YouScope to Implement Systematic Microscopy Protocols. Current Protocols in Molecular Biology, 2012, 98, Unit 14.21.1-23. | 2.9 | 25 |
| 54 | Model-based integration of genomics and metabolomics reveals SNP functionality in *Mycobacterium tuberculosis*. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 8494-8502. | 7.1 | 24 |

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|---|---------|-----|-----------|
| 55 | Mathematical Modeling of Complex Regulatory Networks. IEEE Transactions on Nanobioscience, 2004, 3, 172-179. | 3.3 | 23 |
| 56 | Remote control of microtubule plus-end dynamics and function from the minus-end. ELife, 2019, 8, . | 6.0 | 23 |
| 57 | Modular, rule-based modeling for the design of eukaryotic synthetic gene circuits. BMC Systems Biology, 2013, 7, 42. | 3.0 | 21 |
| 58 | Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011. | 3.0 | 21 |
| 59 | Efficient Reconstruction of Predictive Consensus Metabolic Network Models. PLoS Computational Biology, 2016, 12, e1005085. | 3.2 | 19 |
| 60 | Computational design of biological circuits: putting parts into context. Molecular Systems Design and Engineering, 2017, 2, 410-421. | 3.4 | 19 |
| 61 | A Simple and Flexible Computational Framework for Inferring Sources of Heterogeneity from Single-Cell Dynamics. Cell Systems, 2019, 8, 15-26.e11. | 6.2 | 19 |
| 62 | Efficient Characterization of Parametric Uncertainty of Complex (Bio)chemical Networks. PLoS Computational Biology, 2015, 11, e1004457. | 3.2 | 18 |
| 63 | Automated Planning Enables Complex Protocols on Liquid-Handling Robots. ACS Synthetic Biology, 2018, 7, 922-932. | 3.8 | 18 |
| 64 | Stoichiometric and Constraint-based Modeling. , 2006, , 73-96. | | 18 |
| 65 | Modeling the <i>Drosophila melanogaster</i> Circadian Oscillator via Phase Optimization. Journal of Biological Rhythms, 2008, 23, 525-537. | 2.6 | 17 |
| 66 | Using CellX to Quantify Intracellular Events. , 2013, Chapter 14, Unit 14.22.. | | 17 |
| 67 | An Orthogonal Permeaseâ€"Inducerâ€"Repressor Feedback Loop Shows Bistability. ACS Synthetic Biology, 2016, 5, 1098-1107. | 3.8 | 17 |
| 68 | Probabilistic thermodynamic analysis of metabolic networks. Bioinformatics, 2021, 37, 2938-2945. | 4.1 | 16 |
| 69 | A specialized ODE integrator for the efficient computation of parameter sensitivities. BMC Systems Biology, 2012, 6, 46. | 3.0 | 15 |
| 70 | Accelerating the Computation of Elementary Modes Using Pattern Trees. Lecture Notes in Computer Science, 2006, , 333-343. | 1.3 | 13 |
| 71 | Precise Regulation of Gene Expression Dynamics Favors Complex Promoter Architectures. PLoS Computational Biology, 2009, 5, e1000279. | 3.2 | 12 |
| 72 | Topological augmentation to infer hidden processes in biological systems. Bioinformatics, 2014, 30, 221-227. | 4.1 | 12 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 73 | Model Extension and Model Selection. Studies in Mechanobiology, Tissue Engineering and Biomaterials, 2016, , 213-241. | 1.0 | 12 |
| 74 | Predicting network functions with nested patterns. Nature Communications, 2014, 5, 3006. | 12.8 | 11 |
| 75 | A rationally engineered decoder of transient intracellular signals. Nature Communications, 2021, 12, 1886. | 12.8 | 11 |
| 76 | BioSwitch: a tool for the detection of bistability and multi-steady state behaviour in signalling and gene regulatory networks. Bioinformatics, 2020, 36, 1640-1641. | 4.1 | 10 |
| 77 | Challenges in synthetically designing mammalian circadian clocks. Current Opinion in Biotechnology, 2010, 21, 556-565. | 6.6 | 8 |
| 78 | A method for inverse bifurcation of biochemical switches: inferring parameters from dose response curves. BMC Systems Biology, 2014, 8, 114. | 3.0 | 8 |
| 79 | Changing Face of Vaccination in Immunocompromised Hosts. Current Infectious Disease Reports, 2014, 16, 420. | 3.0 | 8 |
| 80 | Modular Parameter Identification of Biomolecular Networks. SIAM Journal of Scientific Computing, 2016, 38, B988-B1008. | 2.8 | 8 |
| 81 | Steady-State Differential Dose Response in Biological Systems. Biophysical Journal, 2018, 114, 723-736. | 0.5 | 8 |
| 82 | PolyRound: polytope rounding for random sampling in metabolic networks. Bioinformatics, 2022, 38, 566-567. | 4.1 | 8 |
| 83 | Structural Sensitivity Analysis of Metabolic Networks. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2008, 41, 15879-15884. | 0.4 | 7 |
| 84 | Autonomous Synchronization of Chemically Coupled Synthetic Oscillators. Bulletin of Mathematical Biology, 2011, 73, 2678-2706. | 1.9 | 7 |
| 85 | Multi-objective design of synthetic biological circuits. IFAC-PapersOnLine, 2017, 50, 9871-9876. | 0.9 | 7 |
| 86 | Bridging intracellular scales by mechanistic computational models. Current Opinion in Biotechnology, 2018, 52, 17-24. | 6.6 | 7 |
| 87 | Cutting the Wires: Modularization of Cellular Networks for Experimental Design. Biophysical Journal, 2014, 106, 321-331. | 0.5 | 6 |
| 88 | A Coupled Stochastic Model Explains Differences in Cry Knockout Behavior. IEEE Life Sciences Letters, 2015, 1, 3-6. | 1.2 | 6 |
| 89 | Synthetic gene network computational design. , 2009, , . | | 5 |
| 90 | Efficient manipulation and generation of Kirchhoff polynomials for the analysis of non-equilibrium biochemical reaction networks. Journal of the Royal Society Interface, 2020, 17, 20190828. | 3.4 | 5 |

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|---|---------|----|-----------|
| 91 | Association of Host Factors With Antibody Response to Seasonal Influenza Vaccination in Allogeneic Hematopoietic Stem Cell Transplant Patients. Journal of Infectious Diseases, 2022, 225, 1482-1493. | 4.0 | 5 |
| 92 | Controlling cell-to-cell variability with synthetic gene circuits. Biochemical Society Transactions, 2019, 47, 1795-1804. | 3.4 | 5 |
| 93 | Metabolic Networks, Microbial Consortia, and Analogies to Smart Grids. Proceedings of the IEEE, 2022, 110, 541-556. | 21.3 | 5 |
| 94 | ROBUST PERFORMANCE IN BIOPHYSICAL NETWORKS. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 31-36. | 0.4 | 4 |
| 95 | Elementary flux modes â€" state-of-the-art implementation and scope of application. BMC Systems Biology, 2007, 1, . | 3.0 | 4 |
| 96 | Experimental analysis and modeling of single-cell time-course data. Current Opinion in Systems Biology, 2021, 28, 100359. | 2.6 | 4 |
| 97 | Population Design for Synthetic Gene Circuits. Lecture Notes in Computer Science, 2021, , 181-197. | 1.3 | 3 |
| 98 | Model-based inference of neutralizing antibody avidities against influenza virus. PLoS Pathogens, 2022, 18, e1010243. | 4.7 | 3 |
| 99 | TopoFilter: a MATLAB package for mechanistic model identification in systems biology. BMC Bioinformatics, 2020, 21, 34. | 2.6 | 2 |
| 100 | Automatic Control in Systems Biology. , 2009, , 1335-1360. | | 2 |
| 101 | Microbial Community Decision Making Models in Batch and Chemostat Cultures. Lecture Notes in Computer Science, 2021, , 141-158. | 1.3 | 1 |
| 102 | Simplified Computational Design of Digital Synthetic Gene Circuits. , 2014, , 257-271. | | 1 |
| 103 | Analysis of Degenerate Chemical Reaction Networks. Lecture Notes in Control and Information Sciences, 2009, , 163-171. | 1.0 | 1 |
| 104 | Robustness of minimal biochemical oscillators. , 2008, , . | | 0 |
| 105 | Advances in Chemical Reaction Network Theory for the Identification of Kinetic Models. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 1713-1718. | 0.4 | 0 |
| 106 | Designing genetic perturbation experiments for model selection under uncertainty. IFAC-PapersOnLine, 2020, 53, 15864-15869. | 0.9 | 0 |