

# Jan Schellenberger

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11978027/publications.pdf>

Version: 2024-02-01

11  
papers

3,290  
citations

840776

11  
h-index

1281871

11  
g-index

11  
all docs

11  
docs citations

11  
times ranked

3501  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Minimal metabolic pathway structure is consistent with associated biomolecular interactions. <i>Molecular Systems Biology</i> , 2014, 10, 737.  | 7.2  | 41        |
| 2  | Predicting outcomes of steady-state <sup>13</sup> C isotope tracing experiments using Monte Carlo sampling. <i>BMC Systems Biology</i> , 2012, 6, 9.                                    | 3.0  | 30        |
| 3  | Elimination of Thermodynamically Infeasible Loops in Steady-State Metabolic Models. <i>Biophysical Journal</i> , 2011, 100, 544-553.  | 0.5  | 203       |
| 4  | Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. <i>Nature Protocols</i> , 2011, 6, 1290-1307.                                      | 12.0 | 1,408     |
| 5  | Insight into human alveolar macrophage and <i>M. tuberculosis</i> interactions via metabolic reconstructions. <i>Molecular Systems Biology</i> , 2010, 6, 422.                          | 7.2  | 246       |
| 6  | BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions. <i>BMC Bioinformatics</i> , 2010, 11, 213.  | 2.6  | 486       |
| 7  | Model-driven evaluation of the production potential for growth-coupled products of <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2010, 12, 173-186.                          | 7.0  | 221       |
| 8  | Large-scale in silico modeling of metabolic interactions between cell types in the human brain. <i>Nature Biotechnology</i> , 2010, 28, 1279-1285.                                      | 17.5 | 246       |
| 9  | Functional Characterization of Alternate Optimal Solutions of <i>Escherichia coli</i> 's Transcriptional and Translational Machinery. <i>Biophysical Journal</i> , 2010, 98, 2072-2081. | 0.5  | 58        |
| 10 | Use of Randomized Sampling for Analysis of Metabolic Networks. <i>Journal of Biological Chemistry</i> , 2009, 284, 5457-5461.   | 3.4  | 221       |
| 11 | Uniform Sampling of Steady-State Flux Spaces: Means to Design Experiments and to Interpret Enzymopathies. <i>Biophysical Journal</i> , 2004, 87, 2172-2186.                             | 0.5  | 130       |