

# Rainer Machne

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3005392/publications.pdf>

Version: 2024-02-01

16  
papers

828  
citations

933447

10  
h-index

1058476

14  
g-index

23  
all docs

23  
docs citations

23  
times ranked

1408  
citing authors

#	ARTICLE	IF	CITATIONS
1	Weighted Consensus Segmentations. <i>Computation</i> , 2021, 9, 17.	2.0	0
2	The Future of Origin of Life Research: Bridging Decades-Old Divisions. <i>Life</i> , 2020, 10, 20.	2.4	63
3	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178
4	Similarity-Based Segmentation of Multi-Dimensional Signals. <i>Scientific Reports</i> , 2017, 7, 12355.	3.3	15
5	The structural code of cyanobacterial genomes. <i>Nucleic Acids Research</i> , 2014, 42, 8873-8883.	14.5	11
6	Temporal Partitioning of the Yeast Cellular Network. <i>Springer Series in Biophysics</i> , 2014, , 323-349.	0.4	8
7	Time resolved DNA occupancy dynamics during the respiratory oscillation uncover a global reset point in the yeast growth program. <i>Microbial Cell</i> , 2014, 1, 279-288.	3.2	9
8	How cyanobacteria pose new problems to old methods: challenges in microarray time series analysis. <i>BMC Bioinformatics</i> , 2013, 14, 133.	2.6	21
9	Mapping the RNA-Seq trash bin. <i>RNA Biology</i> , 2013, 10, 1204-1210.	3.1	13
10	The dynamics of cellular energetics during continuous yeast culture. , 2013, 2013, 2708-11.		9
11	Modelling cyanobacteria: from metabolism to integrative models of phototrophic growth. <i>Journal of Experimental Botany</i> , 2012, 63, 2259-2274.	4.8	45
12	A new dynamic model for highly efficient mass transfer in aerated bioreactors and consequences for identification. <i>Biotechnology and Bioengineering</i> , 2012, 109, 2997-3006.	3.3	5
13	The Yin and Yang of Yeast Transcription: Elements of a Global Feedback System between Metabolism and Chromatin. <i>PLoS ONE</i> , 2012, 7, e37906.	2.5	42
14	Controlled vocabularies and semantics in systems biology. <i>Molecular Systems Biology</i> , 2011, 7, 543.	7.2	246
15	Evolutionary footprints of nucleosome positions in yeast. <i>Trends in Genetics</i> , 2008, 24, 583-587.	6.7	70
16	The SBML ODE Solver Library: a native API for symbolic and fast numerical analysis of reaction networks. <i>Bioinformatics</i> , 2006, 22, 1406-1407.	4.1	88