

# Ina Koch

## List of Publications by Year in descending order

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48  
papers

1,539  
citations

430874

18  
h-index

330143

37  
g-index

55  
all docs

55  
docs citations

55  
times ranked

2357  
citing authors

#	ARTICLE	IF	CITATIONS
1	The canonical and non-canonical NF- $\kappa$ B pathways and their crosstalk: A comparative study based on Petri nets. <i>BioSystems</i> , 2022, 211, 104564.	2.0	7
2	PTGL: extension to graph-based topologies of cryo-EM data for large protein structures. <i>Bioinformatics</i> , 2021, 37, 1032-1034.	4.1	3
3	Bioinformatics in theory and application highlights of the 36th German Conference on Bioinformatics. <i>Biological Chemistry</i> , 2021, 402, 869-870.	2.5	1
4	Impact of rescanning and repositioning on radiomic features employing a multi-object phantom in magnetic resonance imaging. <i>Scientific Reports</i> , 2021, 11, 14248.	3.3	21
5	3D connectomes of reactive and neoplastic CD30 positive lymphoid cells and surrounding cell types. <i>Acta Histochemica</i> , 2021, 123, 151750.	1.8	3
6	Potential of high dimensional radiomic features to assess blood components in intraaortic vessels in non-contrast CT scans. <i>BMC Medical Imaging</i> , 2021, 21, 123.	2.7	5
7	Prediction and analysis of redox-sensitive cysteines using machine learning and statistical methods. <i>Biological Chemistry</i> , 2021, 402, 925-935.	2.5	5
8	Detection of follicular regions in actin-stained whole slide images of the human lymph node by $\hat{A}$ shock filter. <i>Biological Chemistry</i> , 2021, 402, 991-999.	2.5	3
9	Comparison of machine learning algorithms to predict clinically significant prostate cancer of the peripheral zone with multiparametric MRI using clinical assessment categories and radiomic features. <i>European Radiology</i> , 2020, 30, 6757-6769.	4.5	33
10	Quantitative genome-wide association study of six phenotypic subdomains identifies novel genome-wide significant variants in autism spectrum disorder. <i>Translational Psychiatry</i> , 2020, 10, 215.	4.8	13
11	Bioinformatics analysis of whole slide images reveals significant neighborhood preferences of tumor cells in Hodgkin lymphoma. <i>PLoS Computational Biology</i> , 2020, 16, e1007516.	3.2	10
12	Reconstruction of Protein-Protein Interaction Networks Using Homology-Based Search: Application to the Autophagy Pathway of Aging in <i>Podospora anserina</i> . <i>Methods in Molecular Biology</i> , 2020, 2074, 45-55.	0.9	0
13	isiKnock: <i>in silico</i> knockouts in signaling pathways. <i>Bioinformatics</i> , 2019, 35, 892-894.	4.1	7
14	Optimizing the dynamics of protein expression. <i>Scientific Reports</i> , 2019, 9, 7511.	3.3	24
15	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	7.7	49
16	Protein super-secondary structure and quaternary structure topology: theoretical description and application. <i>Current Opinion in Structural Biology</i> , 2018, 50, 134-143.	5.7	7
17	Common functional variants of the glutamatergic system in Autism spectrum disorder with high and low intellectual abilities. <i>Journal of Neural Transmission</i> , 2018, 125, 259-271.	2.8	6
18	The autophagy interaction network of the aging model <i>Podospora anserina</i> . <i>BMC Bioinformatics</i> , 2017, 18, 196.	2.6	6

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19	Modeling the Metabolism of <i>Arabidopsis thaliana</i> : Application of Network Decomposition and Network Reduction in the Context of Petri Nets. <i>Frontiers in Genetics</i> , 2017, 8, 85.	2.3	10
20	Manatee invariants reveal functional pathways in signaling networks. <i>BMC Systems Biology</i> , 2017, 11, 72.	3.0	9
21	CD30 cell graphs of Hodgkin lymphoma are not scale-free—an image analysis approach. <i>Bioinformatics</i> , 2016, 32, 122-129.	4.1	15
22	In Silico Knockout Studies of Xenophagic Capturing of Salmonella. <i>PLoS Computational Biology</i> , 2016, 12, e1005200.	3.2	24
23	Path2PPI: an R package to predict protein–protein interaction networks for a set of proteins. <i>Bioinformatics</i> , 2016, 32, 1427-1429.	4.1	12
24	The new protein topology graph library web server. <i>Bioinformatics</i> , 2016, 32, 474-476.	4.1	7
25	Unsupervised image segmentation for microarray spots with irregular contours and inner holes. <i>BMC Bioinformatics</i> , 2015, 16, 412.	2.6	11
26	Quasi-Steady-State Analysis based on Structural Modules and Timed Petri Net Predict System’s Dynamics: The Life Cycle of the Insulin Receptor. <i>Metabolites</i> , 2015, 5, 766-793.	2.9	12
27	Petri nets in systems biology. <i>Software and Systems Modeling</i> , 2015, 14, 703-710.	2.7	31
28	Next-generation sequencing reveals novel differentially regulated mRNAs, lncRNAs, miRNAs, sdrRNAs and a piRNA in pancreatic cancer. <i>Molecular Cancer</i> , 2015, 14, 94.	19.2	210
29	MONALISA for stochastic simulations of Petri net models of biochemical systems. <i>BMC Bioinformatics</i> , 2015, 16, 215.	2.6	21
30	NOVA: a software to analyze complexome profiling data. <i>Bioinformatics</i> , 2015, 31, 440-441.	4.1	70
31	Petri Nets in the Biosciences. <i>IT - Information Technology</i> , 2014, 56, 43-45.	0.9	1
32	APADB: a database for alternative polyadenylation and microRNA regulation events. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau076-bau076.	3.0	90
33	Image database analysis of Hodgkin lymphoma. <i>Computational Biology and Chemistry</i> , 2013, 46, 1-7.	2.3	14
34	MonaLisa—visualization and analysis of functional modules in biochemical networks. <i>Bioinformatics</i> , 2013, 29, 1469-1470.	4.1	28
35	On Functional Module Detection in Metabolic Networks. <i>Metabolites</i> , 2013, 3, 673-700.	2.9	13
36	A Genome-Wide Longitudinal Transcriptome Analysis of the Aging Model <i>Podospora anserine</i> . <i>PLoS ONE</i> , 2013, 8, e83109.	2.5	30

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37	Reduction techniques for network validation in systems biology. <i>Journal of Theoretical Biology</i> , 2012, 315, 71-80.	1.7	15
38	Hierarchical Representation of Supersecondary Structures Using a Graph-Theoretical Approach. <i>Methods in Molecular Biology</i> , 2012, 932, 7-33.	0.9	0
39	Petri Nets – A Mathematical Formalism to Analyze Chemical Reaction Networks. <i>Molecular Informatics</i> , 2010, 29, 838-843.	2.5	27
40	Exhaustive Analysis of the Modular Structure of the Spliceosomal Assembly Network: A Petri Net Approach. <i>In Silico Biology</i> , 2010, 10, 89-123.	0.9	11
41	Petri Nets and GRN Models. , 2010, , 604-637.		5
42	Petri net modelling of gene regulation of the Duchenne muscular dystrophy. <i>BioSystems</i> , 2008, 92, 189-205.	2.0	76
43	Modularization of biochemical networks based on classification of Petri net t-invariants. <i>BMC Bioinformatics</i> , 2008, 9, 90.	2.6	63
44	An analysis of the Petri net based model of the human body iron homeostasis process. <i>Computational Biology and Chemistry</i> , 2007, 31, 1-10.	2.3	60
45	Application of Petri net based analysis techniques to signal transduction pathways. <i>BMC Bioinformatics</i> , 2006, 7, 482.	2.6	153
46	Application of Petri net theory for modelling and validation of the sucrose breakdown pathway in the potato tuber. <i>Bioinformatics</i> , 2005, 21, 1219-1226.	4.1	117
47	Steady state analysis of metabolic pathways using Petri nets. <i>In Silico Biology</i> , 2003, 3, 367-87.	0.9	46
48	Petri Nets. , 0, , 139-179.		32