

Stefan Wuchty

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1876662/publications.pdf>

Version: 2024-02-01

72
papers

6,866
citations

159525

30
h-index

95218

68
g-index

75
all docs

75
docs citations

75
times ranked

7591
citing authors

#	ARTICLE	IF	CITATIONS
1	The Increasing Dominance of Teams in Production of Knowledge. <i>Science</i> , 2007, 316, 1036-1039.	6.0	2,397
2	Multi-University Research Teams: Shifting Impact, Geography, and Stratification in Science. <i>Science</i> , 2008, 322, 1259-1262.	6.0	575
3	The online competition between pro- and anti-vaccination views. <i>Nature</i> , 2020, 582, 230-233.	13.7	417
4	Centers of complex networks. <i>Journal of Theoretical Biology</i> , 2003, 223, 45-53.	0.8	317
5	Scale-Free Behavior in Protein Domain Networks. <i>Molecular Biology and Evolution</i> , 2001, 18, 1694-1702.	3.5	242
6	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	9.4	218
7	Peeling the yeast protein network. <i>Proteomics</i> , 2005, 5, 444-449.	1.3	204
8	Controllability in protein interaction networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7156-7160.	3.3	183
9	Identifying Causal Genes and Dysregulated Pathways in Complex Diseases. <i>PLoS Computational Biology</i> , 2011, 7, e1001095.	1.5	163
10	Evolution and Topology in the Yeast Protein Interaction Network. <i>Genome Research</i> , 2004, 14, 1310-1314.	2.4	129
11	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	9.4	110
12	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. <i>PLoS ONE</i> , 2013, 8, e66273.	1.1	102
13	Human Communication Dynamics in Digital Footsteps: A Study of the Agreement between Self-Reported Ties and Email Networks. <i>PLoS ONE</i> , 2011, 6, e26972.	1.1	99
14	Prediction of human-virus protein-protein interactions through a sequence embedding-based machine learning method. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 153-161.	1.9	98
15	Actionable Cytopathogenic Host Responses of Human Alveolar Type 2 Cells to SARS-CoV-2. <i>Molecular Cell</i> , 2020, 80, 1104-1122.e9.	4.5	94
16	Interaction and domain networks of yeast. <i>Proteomics</i> , 2002, 2, 1715-1723.	1.3	84
17	New online ecology of adversarial aggregates: ISIS and beyond. <i>Science</i> , 2016, 352, 1459-1463.	6.0	83
18	The Relationship Between Social Media Use and Beliefs in Conspiracy Theories and Misinformation. <i>Political Behavior</i> , 2023, 45, 781-804.	1.7	76

#	ARTICLE	IF	CITATIONS
19	Prediction of Associations between microRNAs and Gene Expression in Glioma Biology. PLoS ONE, 2011, 6, e14681.	1.1	73
20	Computational Prediction of Host-Parasite Protein Interactions between P. falciparum and H. sapiens. PLoS ONE, 2011, 6, e26960.	1.1	72
21	Epigenomic signatures underpin the axonal regenerative ability of dorsal root ganglia sensory neurons. Nature Neuroscience, 2019, 22, 1913-1924.	7.1	71
22	Regulatory Hotspots in the Malaria Parasite Genome Dictate Transcriptional Variation. PLoS Biology, 2008, 6, e238.	2.6	64
23	The Team Science Toolkit. American Journal of Preventive Medicine, 2013, 45, 787-789.	1.6	64
24	Predicting Protein-Protein Interactions from Protein Domains Using a Set Cover Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 78-87.	1.9	56
25	A Second-generation Protein-Protein Interaction Network of Helicobacter pylori. Molecular and Cellular Proteomics, 2014, 13, 1318-1329.	2.5	55
26	HVIDB: a comprehensive database for human-virus protein-protein interactions. Briefings in Bioinformatics, 2021, 22, 832-844.	3.2	48
27	Large-scale mapping of human protein interactome using structural complexes. EMBO Reports, 2012, 13, 266-271.	2.0	43
28	The EHEC-host interactome reveals novel targets for the translocated intimin receptor. Scientific Reports, 2014, 4, 7531.	1.6	35
29	Essentiality and centrality in protein interaction networks revisited. BMC Bioinformatics, 2015, 16, 109.	1.2	35
30	Do conspiracy beliefs form a belief system? Examining the structure and organization of conspiracy beliefs. Journal of Social and Political Psychology, 2021, 9, 255-271.	0.6	35
31	Protein-protein interactions of human viruses. Seminars in Cell and Developmental Biology, 2020, 99, 31-39.	2.3	34
32	Transfer learning via multi-scale convolutional neural layers for human-virus protein-protein interaction prediction. Bioinformatics, 2021, 37, 4771-4778.	1.8	33
33	What is a social tie?. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15099-15100.	3.3	32
34	Viral Organization of Human Proteins. PLoS ONE, 2010, 5, e11796.	1.1	32
35	The Protein Interaction Network of Bacteriophage Lambda with Its Host, Escherichia coli. Journal of Virology, 2013, 87, 12745-12755.	1.5	30
36	Structure-based prediction of host-pathogen protein interactions. Current Opinion in Structural Biology, 2017, 44, 119-124.	2.6	28

#	ARTICLE	IF	CITATIONS
37	Modeling information flow in biological networks. <i>Physical Biology</i> , 2011, 8, 035012.	0.8	26
38	microRNA regulation in an ancient obligate endosymbiosis. <i>Molecular Ecology</i> , 2018, 27, 1777-1793.	2.0	25
39	Women's connectivity in extreme networks. <i>Science Advances</i> , 2016, 2, e1501742.	4.7	24
40	A Draft of Protein Interactions in the Malaria Parasite <i>P. falciparum</i> . <i>Journal of Proteome Research</i> , 2007, 6, 1461-1470.	1.8	22
41	eQTL Epistasis – Challenges and Computational Approaches. <i>Frontiers in Genetics</i> , 2013, 4, 51.	1.1	22
42	Small worlds in RNA structures. <i>Nucleic Acids Research</i> , 2003, 31, 1108-1117.	6.5	21
43	Links between critical proteins drive the controllability of protein interaction networks. <i>Proteomics</i> , 2017, 17, e1700056.	1.3	20
44	The 2020 presidential election and beliefs about fraud: Continuity or change?. <i>Electoral Studies</i> , 2021, 72, 102366.	1.0	20
45	Bacterial protein meta-interactomes predict cross-species interactions and protein function. <i>BMC Bioinformatics</i> , 2017, 18, 171.	1.2	19
46	A comprehensive <i>Plasmodium falciparum</i> protein interaction map reveals a distinct architecture of a core interactome. <i>Proteomics</i> , 2009, 9, 1841-1849.	1.3	18
47	Involvement of microRNA families in cancer. <i>Nucleic Acids Research</i> , 2012, 40, 8219-8226.	6.5	18
48	A network biology approach to unraveling inherited axonopathies. <i>Scientific Reports</i> , 2019, 9, 1692.	1.6	18
49	Identifying Novel Cell Cycle Proteins in Apicomplexa Parasites through Co-Expression Decision Analysis. <i>PLoS ONE</i> , 2014, 9, e97625.	1.1	16
50	Integration of peripheral transcriptomics, genomics, and interactomics following trauma identifies causal genes for symptoms of post-traumatic stress and major depression. <i>Molecular Psychiatry</i> , 2021, 26, 3077-3092.	4.1	15
51	Transcriptome-wide association study of post-trauma symptom trajectories identified GRIN3B as a potential biomarker for PTSD development. <i>Neuropsychopharmacology</i> , 2021, 46, 1811-1820.	2.8	15
52	Rich-Club Phenomenon in the Interactome of <i>P. falciparum</i> – Artifact or Signature of a Parasitic Life Style?. <i>PLoS ONE</i> , 2007, 2, e335.	1.1	15
53	MODULE COVER – A NEW APPROACH TO GENOTYPE-PHENOTYPE STUDIES. , 2012, , .		12
54	The interactome of <i>Streptococcus pneumoniae</i> and its bacteriophages show highly specific patterns of interactions among bacteria and their phages. <i>Scientific Reports</i> , 2016, 6, 24597.	1.6	10

#	ARTICLE	IF	CITATIONS
55	Beyond degree and betweenness centrality: Alternative topological measures to predict viral targets. PLoS ONE, 2018, 13, e0197595.	1.1	10
56	Promoter conservation in HDACs points to functional implications. BMC Genomics, 2019, 20, 613.	1.2	9
57	Local Action with Global Impact: Highly Similar Infection Patterns of Human Viruses and Bacteriophages. MSystems, 2016, 1, .	1.7	8
58	Proteome Data Improves Protein Function Prediction in the Interactome of Helicobacter pylori. Molecular and Cellular Proteomics, 2018, 17, 961-973.	2.5	8
59	Shared Molecular Strategies of the Malaria Parasite P. falciparum and the Human Virus HIV-1. Molecular and Cellular Proteomics, 2011, 10, M111.009035.	2.5	7
60	Collective influencers in protein interaction networks. Scientific Reports, 2019, 9, 3948.	1.6	7
61	The green peach aphid gut contains host plant microRNAs identified by comprehensive annotation of Brassica oleracea small RNA data. Scientific Reports, 2019, 9, 18904.	1.6	7
62	Controllability analysis of molecular pathways points to proteins that control the entire interaction network. Scientific Reports, 2020, 10, 2943.	1.6	7
63	Genome-wide associations of signaling pathways in glioblastoma multiforme. BMC Medical Genomics, 2013, 6, 11.	0.7	3
64	MicroRNA miR-1002 Enhances NMNAT-Mediated Stress Response by Modulating Alternative Splicing. IScience, 2019, 19, 1048-1064.	1.9	3
65	Computational Large-scale Mapping of Protein-Protein Interactions Using Structural Complexes. Current Protocols in Protein Science, 2013, 73, 3.9.1-3.9.9.	2.8	2
66	Important miRs of Pathways in Different Tumor Types. PLoS Computational Biology, 2013, 9, e1002883.	1.5	2
67	Computational Identification of Kinases That Control Axon Growth in Mouse. SLAS Discovery, 2020, 25, 792-800.	1.4	2
68	Promoter/enhancer-based controllability of regulatory networks. Scientific Reports, 2022, 12, 3528.	1.6	2
69	Symmetric Epistasis Estimation (SEE) and its application to dissecting interaction map of Plasmodium falciparum. Molecular BioSystems, 2012, 8, 1544.	2.9	1
70	Deep Learning-Powered Prediction of Human-Virus Protein-Protein Interactions. Frontiers in Microbiology, 2022, 13, 842976.	1.5	1
71	Cell-free Determination of Binary Complexes That Comprise Extended Protein-Protein Interaction Networks of Yersinia pestis. Molecular and Cellular Proteomics, 2016, 15, 3220-3232.	2.5	0
72	CombAlign: a protein sequence comparison algorithm considering recombinations. In Silico Biology, 2004, 4, 243-54.	0.4	0