

Michael Kuhn

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

37,174
citations

126708

33
h-index

264894

42
g-index

49
all docs

49
docs citations

49
times ranked

58128
citing authors

#	ARTICLE	IF	CITATIONS
1	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
2	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017, 45, D362-D368.	6.5	6,303
3	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2012, 41, D808-D815.	6.5	3,816
4	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. <i>Nucleic Acids Research</i> , 2011, 39, D561-D568.	6.5	3,014
5	STRING 8—a global view on proteins and their functional interactions in 630 organisms. <i>Nucleic Acids Research</i> , 2009, 37, D412-D416.	6.5	2,195
6	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016, 44, D286-D293.	6.5	1,937
7	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018, 555, 623-628.	13.7	1,339
8	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. <i>Nucleic Acids Research</i> , 2016, 44, D380-D384.	6.5	1,112
9	Drug Target Identification Using Side-Effect Similarity. <i>Science</i> , 2008, 321, 263-266.	6.0	1,097
10	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016, 44, D1075-D1079.	6.5	914
11	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010, 6, 343.	3.2	757
12	STITCH: interaction networks of chemicals and proteins. <i>Nucleic Acids Research</i> , 2007, 36, D684-D688.	6.5	669
13	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007, 35, D358-D362.	6.5	568
14	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
15	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2007, 36, D919-D922.	6.5	518
16	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	6.5	490
17	eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2007, 36, D250-D254.	6.5	428
18	STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014, 42, D401-D407.	6.5	388

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19	STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012, 40, D876-D880.	6.5	254
20	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010, 38, D552-D556.	6.5	215
21	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018, 3, 514-522.	5.9	196
22	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002323.	1.5	173
23	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021, 599, 120-124.	13.7	159
24	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010, 6, 430.	3.2	146
25	Drug-Induced Regulation of Target Expression. <i>PLoS Computational Biology</i> , 2010, 6, e1000925.	1.5	120
26	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013, 9, 662.	3.2	110
27	Systematic identification of proteins that elicit drug side effects. <i>Molecular Systems Biology</i> , 2013, 9, 663.	3.2	110
28	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	13.7	102
29	Reflect: augmented browsing for the life scientist. <i>Nature Biotechnology</i> , 2009, 27, 508-510.	9.4	91
30	Large-scale prediction of drug-target relationships. <i>FEBS Letters</i> , 2008, 582, 1283-1290.	1.3	84
31	Dispersal strategies shape persistence and evolution of human gut bacteria. <i>Cell Host and Microbe</i> , 2021, 29, 1167-1176.e9.	5.1	66
32	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. <i>Cell</i> , 2019, 177, 1308-1318.e10.	13.5	48
33	Strand-loop-strand motifs: Prediction of hairpins and diverging turns in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 282-288.	1.5	45
34	Coiled-Coil Proteins Facilitated the Functional Expansion of the Centrosome. <i>PLoS Computational Biology</i> , 2014, 10, e1003657.	1.5	32
35	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. <i>Journal of Biomedical Semantics</i> , 2010, 1, 8.	0.9	31
36	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features. <i>Bioinformatics</i> , 2020, 36, 1213-1218.	1.8	31

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37	Microblogging the ISMB: A New Approach to Conference Reporting. PLoS Computational Biology, 2009, 5, e1000263.	1.5	14
38	Reflect: A practical approach to web semantics. Web Semantics, 2010, 8, 182-189.	2.2	14
39	Live Coverage of Scientific Conferences Using Web Technologies. PLoS Computational Biology, 2010, 6, e1000563.	1.5	8
40	Coupling proteomics and metabolomics for the unsupervised identification of proteinâ€“metabolite interactions in Chaetomium thermophilum. PLoS ONE, 2021, 16, e0254429.	1.1	5
41	Live Coverage of Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2009. PLoS Computational Biology, 2010, 6, e1000640.	1.5	4
42	Development of a Kinetic Assay for Late Endosome Movement. Journal of Biomolecular Screening, 2014, 19, 1070-1078.	2.6	2
43	STRING and STITCH: known and predicted interactions between proteins and chemicals. Nature Precedings, 0, , .	0.1	1
44	Reflect: Augmented Browsing for the Life Scientist. Nature Precedings, 0, , .	0.1	1
45	Reflect: A Practical Approach to Web Semantics. SSRN Electronic Journal, 0, , .	0.4	1