Michael Kuhn

List of Publications by Year
in descending order

45 papers	37,174 citations	126907 33 h-index	265206 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. Nucleic Acids Research, 2015, 43, D447-D452.	14.5	9,029
2	The STRING database in 2017: quality-controlled protein–protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	14.5	6,303
3	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. Nucleic Acids Research, 2012, 41, D808-D815.	14.5	3,816
4	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Research, 2011, 39, D561-D568.	14.5	3,014
5	STRING 8--a global view on proteins and their functional interactions in 630 organisms. Nucleic Acids Research, 2009, 37, D412-D416.	14.5	2,195
6	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	14.5	1,937
7	Extensive impact of non-antibiotic drugs on human gut bacteria. Nature, 2018, 555, 623-628.	27.8	1,339
8	STITCH 5: augmenting protein–chemical interaction networks with tissue and affinity data. Nucleic Acids Research, 2016, 44, D380-D384.	14.5	1,112
9	Drug Target Identification Using Side-Effect Similarity. Science, 2008, 321, 263-266.	12.6	1,097
10	The SIDER database of drugs and side effects. Nucleic Acids Research, 2016, 44, D1075-D1079.	14.5	914
11	A side effect resource to capture phenotypic effects of drugs. Molecular Systems Biology, 2010, 6, 343.	7.2	757
12	STITCH: interaction networks of chemicals and proteins. Nucleic Acids Research, 2007, 36, D684-D688.	14.5	669
13	STRING 7--recent developments in the integration and prediction of protein interactions. Nucleic Acids Research, 2007, 35, D358-D362.	14.5	568
14	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	14.5	526
15	SuperTarget and Matador: resources for exploring drug-target relationships. Nucleic Acids Research, 2007, 36, D919-D922.	14.5	518
16	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. Nucleic Acids Research, 2012, 40, D284-D289.	14.5	490
17	eggNOG: automated construction and annotation of orthologous groups of genes. Nucleic Acids Research, 2007, 36, D250-D254.	14.5	428
18	STITCH 4: integration of protein–chemical interactions with user data. Nucleic Acids Research, 2014, 42, D401-D407.	14.5	388

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19	STITCH 3: zooming in on protein-chemical interactions. Nucleic Acids Research, 2012, 40, D876-D880.	14.5	254
20	STITCH 2: an interaction network database for small molecules and proteins. Nucleic Acids Research, 2010, 38, D552-D556.	14.5	215
21	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. Nature Microbiology, 2018, 3, 514-522.	13.3	196
22	Prediction of Drug Combinations by Integrating Molecular and Pharmacological Data. PLoS Computational Biology, 2011, 7, e1002323.	3.2	173
23	Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124.	27.8	159
24	A systematic screen for protein–lipid interactions in *Saccharomyces cerevisiae*. Molecular Systems Biology, 2010, 6, 430.	7.2	146
25	Drug-Induced Regulation of Target Expression. PLoS Computational Biology, 2010, 6, e1000925.	3.2	120
26	Characterization of drug–induced transcriptional modules: towards drug repositioning and functional understanding. Molecular Systems Biology, 2013, 9, 662.	7.2	110
27	Systematic identification of proteins that elicit drug side effects. Molecular Systems Biology, 2013, 9, 663.	7.2	110
28	Combinatorial, additive and dose-dependent drug–microbiome associations. Nature, 2021, 600, 500-505.	27.8	102
29	Reflect: augmented browsing for the life scientist. Nature Biotechnology, 2009, 27, 508-510.	17.5	91
30	Large–scale prediction of drug–target relationships. FEBS Letters, 2008, 582, 1283-1290.	2.8	84
31	Dispersal strategies shape persistence and evolution of human gut bacteria. Cell Host and Microbe, 2021, 29, 1167-1176.e9.	11.0	66
32	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. Cell, 2019, 177, 1308-1318.e10.	28.9	48
33	Strand-loop-strand motifs: Prediction of hairpins and diverging turns in proteins. Proteins: Structure, Function and Bioinformatics, 2003, 54, 282-288.	2.6	45
34	Coiled-Coil Proteins Facilitated the Functional Expansion of the Centrosome. PLoS Computational Biology, 2014, 10, e1003657.	3.2	32
35	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. Journal of Biomedical Semantics, 2010, 1, 8.	1.6	31
36	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features. Bioinformatics, 2020, 36, 1213-1218.	4.1	31

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37	Microblogging the ISMB: A New Approach to Conference Reporting. PLoS Computational Biology, 2009, 5, e1000263.	3.2	14
38	Reflect: A practical approach to web semantics. Web Semantics, 2010, 8, 182-189.	2.9	14
39	Live Coverage of Scientific Conferences Using Web Technologies. PLoS Computational Biology, 2010, 6, e1000563.	3.2	8
40	Coupling proteomics and metabolomics for the unsupervised identification of protein–metabolite interactions in Chaetomium thermophilum. PLoS ONE, 2021, 16, e0254429.	2.5	5
41	Live Coverage of Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2009. PLoS Computational Biology, 2010, 6, e1000640.	3.2	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