

Michael Kuhn

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

26,645
citations

29
h-index

49
g-index

49
ext. papers

33,794
ext. citations

17.9
avg, IF

6.81
L-index

#	Paper	IF	Citations
44	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015 , 43, D447-52	20.1	6276
43	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017 , 45, D362-D368	20.1	4068
42	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2013 , 41, D808-15	20.1	3033
41	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. <i>Nucleic Acids Research</i> , 2011 , 39, D561-8	20.1	2514
40	STRING 8—a global view on proteins and their functional interactions in 630 organisms. <i>Nucleic Acids Research</i> , 2009 , 37, D412-6	20.1	1799
39	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. <i>Nucleic Acids Research</i> , 2016 , 44, D286-93	20.1	1211
38	Drug target identification using side-effect similarity. <i>Science</i> , 2008 , 321, 263-6	33.3	937
37	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018 , 555, 623-628	50.4	834
36	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. <i>Nucleic Acids Research</i> , 2016 , 44, D380-4	20.1	641
35	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010 , 6, 343	12.2	608
34	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016 , 44, D1075-9	20.1	516
33	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007 , 35, D358-62	20.1	503
32	STITCH: interaction networks of chemicals and proteins. <i>Nucleic Acids Research</i> , 2008 , 36, D684-8	20.1	471
31	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2008 , 36, D919-22	20.1	416
30	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014 , 42, D23120-1	20.1	387
29	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012 , 40, D284-9	20.1	387
28	eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2008 , 36, D250-4	20.1	313

27	STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014 , 42, D401-7	20.1	290
26	STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012 , 40, D876-80	20.1	219
25	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010 , 38, D552-6	20.1	183
24	Prediction of drug combinations by integrating molecular and pharmacological data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002323	5	145
23	A systematic screen for protein-lipid interactions in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2010 , 6, 430	12.2	132
22	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018 , 3, 514-522	26.6	119
21	Drug-induced regulation of target expression. <i>PLoS Computational Biology</i> , 2010 , 6, e1000925	5	100
20	Systematic identification of proteins that elicit drug side effects. <i>Molecular Systems Biology</i> , 2013 , 9, 663	12.2	91
19	Characterization of drug-induced transcriptional modules: towards drug repositioning and functional understanding. <i>Molecular Systems Biology</i> , 2013 , 9, 662	12.2	86
18	Reflect: augmented browsing for the life scientist. <i>Nature Biotechnology</i> , 2009 , 27, 508-10	44.5	78
17	Large-scale prediction of drug-target relationships. <i>FEBS Letters</i> , 2008 , 582, 1283-90	3.8	75
16	Strand-loop-strand motifs: prediction of hairpins and diverging turns in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 54, 282-8	4.2	39
15	Disentangling Genetic and Environmental Effects on the Proteotypes of Individuals. <i>Cell</i> , 2019 , 177, 1308-1318.e10	96.2	18
14	The DBCLS BioHackathon: standardization and interoperability for bioinformatics web services and workflows. The DBCLS BioHackathon Consortium*. <i>Journal of Biomedical Semantics</i> , 2010 , 1, 8	2.2	24
13	Coiled-coil proteins facilitated the functional expansion of the centrosome. <i>PLoS Computational Biology</i> , 2014 , 10, e1003657	5	23
12	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021 , 599, 120-124	50.4	21
11	Dispersal strategies shape persistence and evolution of human gut bacteria. <i>Cell Host and Microbe</i> , 2021 , 29, 1167-1176.e9	23.4	15
10	Reflect: A practical approach to web semantics. <i>Web Semantics</i> , 2010 , 8, 182-189	2.9	12

9	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021 ,	50.4	11
8	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features. <i>Bioinformatics</i> , 2020 , 36, 1213-1218	7.2	10
7	Microblogging the ISMB: a new approach to conference reporting. <i>PLoS Computational Biology</i> , 2009 , 5, e1000263	5	10
6	Live coverage of scientific conferences using web technologies. <i>PLoS Computational Biology</i> , 2010 , 6, e1000563	5	7
5	Live Coverage of Intelligent Systems for Molecular Biology/European Conference on computational biology (ISMB/ECCB) 2009. <i>PLoS Computational Biology</i> , 2010 , 6, e1000640	5	4
4	Dissecting the collateral damage of antibiotics on gut microbes		4
3	Coupling proteomics and metabolomics for the unsupervised identification of protein-metabolite interactions in <i>Chaetomium thermophilum</i> . <i>PLoS ONE</i> , 2021 , 16, e0254429	3.7	3
2	Development of a Kinetic Assay for Late Endosome Movement. <i>Journal of Biomolecular Screening</i> , 2014 , 19, 1070-8		2
1	Identification of metabolites from tandem mass spectra with a machine learning approach utilizing structural features		1