Christian von Mering

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.

133	49,194	64	151
papers	citations	h-index	g-index
151	66,457	14.6	7.53
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
133	STRING v10: protein-protein interaction networks, integrated over the tree of life. *Nucleic Acids Research*, **2015**, 43, D447-52	20.1	6276
132	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Research*, **2019**, 47, D607-D613	20.1	5966
131	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. *Nucleic Acids Research*, **2017**, 45, D362-D368	20.1	4068
130	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. *Nucleic Acids Research*, **2013**, 41, D808-15	20.1	3033
129	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. *Nucleic Acids Research*, **2011**, 39, D561-8	20.1	2514
128	Comparative assessment of large-scale data sets of protein-protein interactions. *Nature*, **2002**, 417, 399-403	50.4	1856
127	STRING 8--a global view on proteins and their functional interactions in 630 organisms. *Nucleic Acids Research*, **2009**, 37, D412-6	20.1	1799
126	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. *Nucleic Acids Research*, **2016**, 44, D286-93	20.1	1211
125	Comparative metagenomics of microbial communities. *Science*, **2005**, 308, 554-7	33.3	1211
124	Toward automatic reconstruction of a highly resolved tree of life. *Science*, **2006**, 311, 1283-7	33.3	1197
123	STRING: a database of predicted functional associations between proteins. *Nucleic Acids Research*, **2003**, 31, 258-61	20.1	1182
122	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. *Molecular Biology and Evolution*, **2017**, 34, 2115-2122	8.3	966
121	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. *Nucleic Acids Research*, **2005**, 33, D433-7	20.1	953
120	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. *Nucleic Acids Research*, **2019**, 47, D309-D314	20.1	850
119	Immunity-related genes and gene families in Anopheles gambiae. *Science*, **2002**, 298, 159-65	33.3	743
118	Salmonella enterica serovar typhimurium exploits inflammation to compete with the intestinal microbiota. *PLoS Biology*, **2007**, 5, 2177-89	9.7	736
117	The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. *Nucleic Acids Research*, **2021**, 49, D605-D612	20.1	661

116	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. *Nucleic Acids Research*, **2016**, 44, D380-4	20.1	641
115	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 16428-33	11.5	595
114	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	504
113	The HUPO PSIS molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83	44.5	504
112	STRING 7--recent developments in the integration and prediction of protein interactions. *Nucleic Acids Research*, **2007**, 35, D358-62	20.1	503
111	STITCH: interaction networks of chemicals and proteins. *Nucleic Acids Research*, **2008**, 36, D684-8	20.1	471
110	Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. *ISME Journal*, **2012**, 6, 1378-90	11.9	458
109	Comparative genome and proteome analysis of Anopheles gambiae and Drosophila melanogaster. *Science*, **2002**, 298, 149-59	33.3	455
108	Expression of amino-terminally truncated PrP in the mouse leading to ataxia and specific cerebellar lesions. *Cell*, **1998**, 93, 203-14	56.2	454
107	eggNOG v4.0: nested orthology inference across 3686 organisms. *Nucleic Acids Research*, **2014**, 42, D231-9	20.1	387
106	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. *Nucleic Acids Research*, **2012**, 40, D284-9	20.1	387
105	Pathogens and host immunity in the ancient human oral cavity. *Nature Genetics*, **2014**, 46, 336-44	36.3	353
104	PaxDb, a database of protein abundance averages across all three domains of life. *Molecular and Cellular Proteomics*, **2012**, 11, 492-500	7.6	351
103	eggNOG: automated construction and annotation of orthologous groups of genes. *Nucleic Acids Research*, **2008**, 36, D250-4	20.1	313
102	A global network of coexisting microbes from environmental and whole-genome sequence data. *Genome Research*, **2010**, 20, 947-59	9.7	305
101	Like will to like: abundances of closely related species can predict susceptibility to intestinal colonization by pathogenic and commensal bacteria. *PLoS Pathogens*, **2010**, 6, e1000711	7.6	304
100	STITCH 4: integration of protein-chemical interactions with user data. *Nucleic Acids Research*, **2014**, 42, D401-7	20.1	290
99	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cell-lines. *Proteomics*, **2015**, 15, 3163-8	4.8	283

98	Protein interaction networks from yeast to human. *Current Opinion in Structural Biology*, **2004**, 14, 292-9	8.1	278
97	Quantitative phylogenetic assessment of microbial communities in diverse environments. *Science*, **2007**, 315, 1126-30	33.3	259
96	Arabidopsis female gametophyte gene expression map reveals similarities between plant and animal gametes. *Current Biology*, **2010**, 20, 506-12	6.3	255
95	The microbiota mediates pathogen clearance from the gut lumen after non-typhoidal Salmonella diarrhea. *PLoS Pathogens*, **2010**, 6, e1001097	7.6	252
94	Phosphoproteomic analysis reveals interconnected system-wide responses to perturbations of kinases and phosphatases in yeast. *Science Signaling*, **2010**, 3, rs4	8.8	229
93	Prion protein devoid of the octapeptide repeat region restores susceptibility to scrapie in PrP knockout mice. *Neuron*, **2000**, 27, 399-408	13.9	221
92	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
91	STITCH 3: zooming in on protein-chemical interactions. *Nucleic Acids Research*, **2012**, 40, D876-80	20.1	219
90	Prediction of effective genome size in metagenomic samples. *Genome Biology*, **2007**, 8, R10	18.3	219
89	Environments shape the nucleotide composition of genomes. *EMBO Reports*, **2005**, 6, 1208-13	6.5	200
88	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. *Science*, **2017**, 355,	33.3	198
87	STITCH 2: an interaction network database for small molecules and proteins. *Nucleic Acids Research*, **2010**, 38, D552-6	20.1	183
86	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. *Nucleic Acids Research*, **2010**, 38, D190-5	20.1	179
85	Comparative functional analysis of the Caenorhabditis elegans and Drosophila melanogaster proteomes. *PLoS Biology*, **2009**, 7, e48	9.7	179
84	Unexplored therapeutic opportunities in the human genome. *Nature Reviews Drug Discovery*, **2018**, 17, 317-332	64.1	156
83	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. *Nature Biotechnology*, **2004**, 22, 911-7	44.5	142
82	Standardized benchmarking in the quest for orthologs. *Nature Methods*, **2016**, 13, 425-30	21.6	133
81	Genome evolution reveals biochemical networks and functional modules. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 15428-33	11.5	123

80	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. *Molecular Systems Biology*, **2008**, 4, 198	12.2	118
79	Function prediction and protein networks. *Current Opinion in Cell Biology*, **2003**, 15, 191-8	9	118
78	Microbiota-derived hydrogen fuels Salmonella typhimurium invasion of the gut ecosystem. *Cell Host and Microbe*, **2013**, 14, 641-51	23.4	105
77	MLTreeMap--accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. *BMC Genomics*, **2010**, 11, 461	4.5	93
76	Complex genomic rearrangements lead to novel primate gene function. *Genome Research*, **2005**, 15, 343-51	9.7	82
75	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. *BMC Genomics*, **2014**, 15, 82	4.5	78
74	Limits to robustness and reproducibility in the demarcation of operational taxonomic units. *Environmental Microbiology*, **2015**, 17, 1689-706	5.2	76
73	Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. *Microbiome*, **2017**, 5, 20	16.6	74
72	RNAi screen of Salmonella invasion shows role of COPI in membrane targeting of cholesterol and Cdc42. *Molecular Systems Biology*, **2011**, 7, 474	12.2	68
71	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 13913-8	11.5	66
70	Microbial rhodopsins on leaf surfaces of terrestrial plants. *Environmental Microbiology*, **2012**, 14, 140-6	5.2	64
69	Bacterial anoxygenic photosynthesis on plant leaf surfaces. *Environmental Microbiology Reports*, **2012**, 4, 209-16	3.7	63
68	Assessing systems properties of yeast mitochondria through an interaction map of the organelle. *PLoS Genetics*, **2006**, 2, e170	6	63
67	Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. *PLoS Computational Biology*, **2014**, 10, e1003594	5	58
66	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. *Viruses*, **2018**, 10,	6.2	58
65	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. *Bioinformatics*, **2016**, 32, 1085-7	7.2	56
64	Identification and analysis of evolutionarily cohesive functional modules in protein networks. *Genome Research*, **2006**, 16, 374-82	9.7	54
63	Distinct and regulated activities of human Gli proteins in Drosophila. *Current Biology*, **1999**, 9, 1319-22	6.3	54

62	The hedgehog signaling pathway: where did it come from?. *PLoS Biology*, **2009**, 7, e1000146	9.7	53
61	A sentinel protein assay for simultaneously quantifying cellular processes. *Nature Methods*, **2014**, 11, 1045-8	21.6	52
60	Specific inhibition of diverse pathogens in human cells by synthetic microRNA-like oligonucleotides inferred from RNAi screens. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 4548-53	11.5	52
59	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. *Proteomics*, **2010**, 10, 1297-306	4.8	51
58	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. *Cell Reports*, **2017**, 19, 1056-1067	10.6	49
57	Functional clues for hypothetical proteins based on genomic context analysis in prokaryotes. *Nucleic Acids Research*, **2004**, 32, 6321-6	20.1	49
56	High confidence prediction of essential genes in Burkholderia cenocepacia. *PLoS ONE*, **2012**, 7, e40064	3.7	48
55	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. *Molecular Cell*, **2019**, 74, 951-965.e13	17.6	45
54	MAPseq: highly efficient k-mer search with confidence estimates, for rRNA sequence analysis. *Bioinformatics*, **2017**, 33, 3808-3810	7.2	44
53	RAIN: RNA-protein Association and Interaction Networks. *Database: the Journal of Biological Databases and Curation*, **2017**, 2017,	5	42
52	The SIB Swiss Institute of BioinformaticsSresources: focus on curated databases. *Nucleic Acids Research*, **2016**, 44, D27-37	20.1	41
51	Genome-wide small interfering RNA screens reveal VAMP3 as a novel host factor required for Uukuniemi virus late penetration. *Journal of Virology*, **2014**, 88, 8565-78	6.6	39
50	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
49	Shared components of protein complexes--versatile building blocks or biochemical artefacts?. *BioEssays*, **2004**, 26, 1333-43	4.1	38
48	HPC-CLUST: distributed hierarchical clustering for large sets of nucleotide sequences. *Bioinformatics*, **2014**, 30, 287-8	7.2	35
47	A comprehensive set of protein complexes in yeast: mining large scale protein-protein interaction screens. *Bioinformatics*, **2003**, 19, 1901-8	7.2	34
46	Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data. *Cell Systems*, **2019**, 9, 286-296.e8	10.6	33
45	ChromID identifies the protein interactome at chromatin marks. *Nature Biotechnology*, **2020**, 38, 728-736	44.5	31

44	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. *Bioinformatics*, **2020**, 36, 2636-2642	7.2	29
43	Simultaneous analysis of large-scale RNAi screens for pathogen entry. *BMC Genomics*, **2014**, 15, 1162	4.5	28
42	IFN-□Hinders Recovery from Mucosal Inflammation during Antibiotic Therapy for Salmonella Gut Infection. *Cell Host and Microbe*, **2016**, 20, 238-49	23.4	26
41	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. *Science Signaling*, **2014**, 7, rs6	8.8	26
40	Sequence-based factors influencing the expression of heterologous genes in the yeast Pichia pastoris--A comparative view on 79 human genes. *Journal of Biotechnology*, **2007**, 130, 1-10	3.7	26
39	In situ enzyme activity in the dissolved and particulate fraction of the fluid from four pitcher plant species of the genus Nepenthes. *PLoS ONE*, **2011**, 6, e25144	3.7	26
38	gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens. *Genome Biology*, **2015**, 16, 220	18.3	25
37	Cell-sorting at the A/P boundary in the Drosophila wing primordium: a computational model to consolidate observed non-local effects of Hh signaling. *PLoS Computational Biology*, **2011**, 7, e1002025	5	25
36	A family of interaction-adjusted indices of community similarity. *ISME Journal*, **2017**, 11, 791-807	11.9	24
35	ArrayProspector: a web resource of functional associations inferred from microarray expression data. *Nucleic Acids Research*, **2004**, 32, W445-8	20.1	24
34	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. *ISME Journal*, **2020**, 14, 1247-1259	11.9	23
33	Bacterial diversity and composition in the fluid of pitcher plants of the genus Nepenthes. *Systematic and Applied Microbiology*, **2015**, 38, 330-9	4.2	22
32	Comparative analysis of environmental sequences: potential and challenges. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2006**, 361, 519-23	5.8	22
31	Consistency of genome-based methods in measuring Metazoan evolution. *FEBS Letters*, **2005**, 579, 3355-61	3.8	22
30	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. *International Journal of Antimicrobial Agents*, **2017**, 50, 342-351	14.3	19
29	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. *Molecular Cell*, **2019**, 74, 1086-1102.e5	17.6	18
28	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in Caenorhabditis elegans. *Molecular and Cellular Proteomics*, **2016**, 15, 1670-80	7.6	15
27	Ecologically informed microbial biomarkers and accurate classification of mixed and unmixed samples in an extensive cross-study of human body sites. *Microbiome*, **2018**, 6, 192	16.6	15

26	Termites in the woodwork. *Genome Biology*, **2007**, 8, 229	18.3	13
25	Fast genome-wide functional annotation through orthology assignment by eggNOG-mapper		13
24	A phylogeny-based benchmarking test for orthology inference reveals the limitations of function-based validation. *PLoS ONE*, **2014**, 9, e111122	3.7	12
23	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. *Nucleic Acids Research*, **2014**, 42, W436-41	20.1	12
22	Global analysis of bacterial transcription factors to predict cellular target processes. *Trends in Genetics*, **2004**, 20, 126-31	8.5	12
21	Preventive Trichuris suis ova (TSO) treatment protects immunocompetent rabbits from DSS colitis but may be detrimental under conditions of immunosuppression. *Scientific Reports*, **2017**, 7, 16500	4.9	10
20	Suppression of the Escherichia coli dnaA46 mutation by changes in the activities of the pyruvate-acetate node links DNA replication regulation to central carbon metabolism. *PLoS ONE*, **2017**, 12, e0176050	3.7	10
19	Open Community Challenge Reveals Molecular Network Modules with Key Roles in Diseases		10
18	The HUPO initiative on Model Organism Proteomes, iMOP. *Proteomics*, **2012**, 12, 340-5	4.8	8
17	Protein tyrosine phosphatase non-receptor type 22 modulates colitis in a microbiota-dependent manner. *Journal of Clinical Investigation*, **2019**, 129, 2527-2541	15.9	8
16	Rapid inference of direct interactions in large-scale ecological networks from heterogeneous microbial sequencing data		7
15	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses		6
14	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. *Scientific Reports*, **2020**, 10, 14453	4.9	6
13	Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. *MBio*, **2021**, 12,	7.8	6
12	Growth-restricting effects of siRNA transfections: a largely deterministic combination of off-target binding and hybridization-independent competition. *Nucleic Acids Research*, **2018**, 46, 9309-9320	20.1	6
11	The Evolution of Ecological Diversity in .. *Frontiers in Microbiology*, **2022**, 13, 715637	5.7	4
10	Pathway and network analysis of more than 2,500 whole cancer genomes		4
9	Specific genomic regions are differentially affected by copy number alterations across distinct cancer types, in aggregated cytogenetic data. *PLoS ONE*, **2012**, 7, e43689	3.7	3

8	Fermentation Ability of Gut Microbiota of Wild Japanese Macaques in the Highland and Lowland Yakushima: In Vitro Fermentation Assay and Genetic Analyses. *Microbial Ecology*, **2020**, 80, 459-474	4.4	2
7	Pathogenic impact of transcript isoform switching in 1209 cancer samples covering 27 cancer types using an isoform-specific interaction network		2
6	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. *Genome Biology*, **2021**, 22, 157	18.3	2
5	Inferring Protein Function from Genomic Context1179-1210		1
4	CanIsoNet: A Database to Study the Functional Impact of Isoform Switching Events in Cancer		1
3	Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation.. *MSystems*, **2022**, e0016022	7.6	1
2	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. *BMC Bioinformatics*, **2019**, 20, 228	3.6	0
1	Probing Isoform Switching Events in Various Cancer Types: Lessons From Pan-Cancer Studies. *Frontiers in Molecular Biosciences*, **2021**, 8, 726902	5.6	