Christian von Mering

List of Publications by Year
in descending order

132 papers	76,828 citations	11608 70 h-index	12910 131 g-index
151 all docs	151 docs citations	151 times ranked	97192 citing authors

#	Article	IF	Citations
1	STRING v11: protein–protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. Nucleic Acids Research, 2019, 47, D607-D613.	6.5	12,237
2	STRING v10: protein–protein interaction networks, integrated over the tree of life. Nucleic Acids Research, 2015, 43, D447-D452.	6.5	9,029
3	The STRING database in 2017: quality-controlled protein–protein association networks, made broadly accessible. Nucleic Acids Research, 2017, 45, D362-D368.	6.5	6,303
4	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.	6.5	4,274
5	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. Nucleic Acids Research, 2012, 41, D808-D815.	6.5	3,816
6	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. Nucleic Acids Research, 2011, 39, D561-D568.	6.5	3,014
7	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.	6.5	2,575
8	STRING 8--a global view on proteins and their functional interactions in 630 organisms. Nucleic Acids Research, 2009, 37, D412-D416.	6.5	2,195
9	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	3.5	2,156
10	Comparative assessment of large-scale data sets of protein–protein interactions. Nature, 2002, 417, 399-403.	13.7	2,137
11	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	6.5	1,937
12	STRING: a database of predicted functional associations between proteins. Nucleic Acids Research, 2003, 31, 258-261.	6.5	1,897
13	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. Science, 2006, 311, 1283-1287.	6.0	1,435
14	Comparative Metagenomics of Microbial Communities. Science, 2005, 308, 554-557.	6.0	1,432
15	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. Nucleic Acids Research, 2004, 33, D433-D437.	6.5	1,418
16	STITCH 5: augmenting protein–chemical interaction networks with tissue and affinity data. Nucleic Acids Research, 2016, 44, D380-D384.	6.5	1,112
17	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, baw100.	1.4	1,085
18	Salmonella enterica Serovar Typhimurium Exploits Inflammation to Compete with the Intestinal Microbiota. PLoS Biology, 2007, 5, e244.	2.6	905

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19	Immunity-Related Genes and Gene Families inAnopheles gambiae. Science, 2002, 298, 159-165.	6.0	845
20	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, 16428-16433.	3.3	774
21	STITCH: interaction networks of chemicals and proteins. Nucleic Acids Research, 2007, 36, D684-D688.	6.5	669
22	Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. ISME Journal, 2012, 6, 1378-1390.	4.4	635
23	The HUPO PSI's Molecular Interaction formatâ€"a community standard for the representation of protein interaction data. Nature Biotechnology, 2004, 22, 177-183.	9.4	581
24	STRING 7--recent developments in the integration and prediction of protein interactions. Nucleic Acids Research, 2007, 35, D358-D362.	6.5	568
25	Comparative Genome and Proteome Analysis ofAnopheles gambiaeandDrosophila melanogaster. Science, 2002, 298, 149-159.	6.0	531
26	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
27	Expression of Amino-Terminally Truncated PrP in the Mouse Leading to Ataxia and Specific Cerebellar Lesions. Cell, 1998, 93, 203-214.	13.5	506
28	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cellâ€lines. Proteomics, 2015, 15, 3163-3168.	1.3	493
29	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. Nucleic Acids Research, 2012, 40, D284-D289.	6.5	490
30	Pathogens and host immunity in the ancient human oral cavity. Nature Genetics, 2014, 46, 336-344.	9.4	482
31	eggNOG: automated construction and annotation of orthologous groups of genes. Nucleic Acids Research, 2007, 36, D250-D254.	6.5	428
32	A global network of coexisting microbes from environmental and whole-genome sequence data. Genome Research, 2010, 20, 947-959.	2.4	425
33	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
34	PaxDb, a Database of Protein Abundance Averages Across All Three Domains of Life. Molecular and Cellular Proteomics, 2012, 11, 492-500.	2.5	413
35	STITCH 4: integration of proteinâ€"chemical interactions with user data. Nucleic Acids Research, 2014, 42, D401-D407.	6.5	388
36	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.	2.1	367

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37	Protein interaction networks from yeast to human. Current Opinion in Structural Biology, 2004, 14, 292-299.	2.6	323
38	The Microbiota Mediates Pathogen Clearance from the Gut Lumen after Non-Typhoidal Salmonella Diarrhea. PLoS Pathogens, 2010, 6, e1001097.	2.1	314
39	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. Science, 2017, 355, .	6.0	313
40	Arabidopsis Female Gametophyte Gene Expression Map Reveals Similarities between Plant and Animal Gametes. Current Biology, 2010, 20, 506-512.	1.8	302
41	Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. Science, 2007, 315, 1126-1130.	6.0	300
42	Prediction of effective genome size in metagenomic samples. Genome Biology, 2007, 8, R10.	13.9	281
43	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. Science Signaling, 2010, 3, rs4.	1.6	277
44	Unexplored therapeutic opportunities in the human genome. Nature Reviews Drug Discovery, 2018, 17, 317-332.	21.5	263
45	Environments shape the nucleotide composition of genomes. EMBO Reports, 2005, 6, 1208-1213.	2.0	258
46	STITCH 3: zooming in on protein-chemical interactions. Nucleic Acids Research, 2012, 40, D876-D880.	6.5	254
47	Prion Protein Devoid of the Octapeptide Repeat Region Restores Susceptibility to Scrapie in PrP Knockout Mice. Neuron, 2000, 27, 399-408.	3.8	252
48	STITCH 2: an interaction network database for small molecules and proteins. Nucleic Acids Research, 2010, 38, D552-D556.	6.5	215
49	Comparative Functional Analysis of the Caenorhabditis elegans and Drosophila melanogaster Proteomes. PLoS Biology, 2009, 7, e1000048.	2.6	208
50	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-D195.	6.5	202
51	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
52	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. Nature Biotechnology, 2004, 22, 911-917.	9.4	166
53	Microbiota-Derived Hydrogen Fuels Salmonella Typhimurium Invasion of the Gut Ecosystem. Cell Host and Microbe, 2013, 14, 641-651.	5.1	145
54	Genome evolution reveals biochemical networks and functional modules. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15428-15433.	3.3	140

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55	Millimeter‐scale genetic gradients and community‐level molecular convergence in a hypersaline microbial mat. Molecular Systems Biology, 2008, 4, 198.	3.2	139
56	Function prediction and protein networks. Current Opinion in Cell Biology, 2003, 15, 191-198.	2.6	133
57	Complex genomic rearrangements lead to novel primate gene function. Genome Research, 2005, 15, 343-351.	2.4	104
58	MLTreeMap - accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. BMC Genomics, 2010, 11, 461.	1.2	100
59	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. BMC Genomics, 2014, 15, 82.	1.2	100
60	Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. Microbiome, 2017, 5, 20.	4.9	100
61	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. Viruses, 2018, 10, 519.	1.5	100
62	MAPseq: highly efficient k-mer search with confidence estimates, for rRNA sequence analysis. Bioinformatics, 2017, 33, 3808-3810.	1.8	98
63	Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data. Cell Systems, 2019, 9, 286-296.e8.	2.9	96
64	Limits to robustness and reproducibility in the demarcation of operational taxonomic units. Environmental Microbiology, 2015, 17, 1689-1706.	1.8	95
65	Bacterial anoxygenic photosynthesis on plant leaf surfaces. Environmental Microbiology Reports, 2012, 4, 209-216.	1.0	94
66	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. Bioinformatics, 2016, 32, 1085-1087.	1.8	91
67	ChromID identifies the protein interactome at chromatin marks. Nature Biotechnology, 2020, 38, 728-736.	9.4	90
68	RNAi screen of <i>Salmonella</i> invasion shows role of COPI in membrane targeting of cholesterol and Cdc42. Molecular Systems Biology, 2011, 7, 474.	3.2	89
69	Ecological Consistency of SSU rRNA-Based Operational Taxonomic Units at a Global Scale. PLoS Computational Biology, 2014, 10, e1003594.	1.5	85
70	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. Molecular Cell, 2019, 74, 951-965.e13.	4.5	85
71	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. Cell Reports, 2017, 19, 1056-1067.	2.9	83
72	Microbial rhodopsins on leaf surfaces of terrestrial plants. Environmental Microbiology, 2012, 14, 140-146.	1.8	78

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73	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. ISME Journal, 2020, 14, 1247-1259.	4.4	74
74	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
75	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, 13913-13918.	3.3	72
76	A sentinel protein assay for simultaneously quantifying cellular processes. Nature Methods, 2014, 11, 1045-1048.	9.0	70
77	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. PLoS Genetics, 2006, 2, e170.	1.5	67
78	The Hedgehog Signaling Pathway: Where Did It Come From?. PLoS Biology, 2009, 7, e1000146.	2.6	65
79	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
80	Identification and analysis of evolutionarily cohesive functional modules in protein networks. Genome Research, 2006, 16, 374-382.	2.4	60
81	High Confidence Prediction of Essential Genes in Burkholderia Cenocepacia. PLoS ONE, 2012, 7, e40064.	1.1	60
82	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, 4548-4553.	3.3	60
83	Distinct and regulated activities of human Gli proteins in Drosophila. Current Biology, 1999, 9, 1319-1322.	1.8	58
84	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. Proteomics, 2010, 10, 1297-1306.	1.3	58
85	Functional clues for hypothetical proteins based on genomic context analysis in prokaryotes. Nucleic Acids Research, 2004, 32, 6321-6326.	6.5	57
86	RAIN: RNAâ€"protein Association and Interaction Networks. Database: the Journal of Biological Databases and Curation, 2017, 2017, baw167.	1.4	53
87	HPC-CLUST: distributed hierarchical clustering for large sets of nucleotide sequences. Bioinformatics, 2014, 30, 287-288.	1.8	49
88	Genome-Wide Small Interfering RNA Screens Reveal VAMP3 as a Novel Host Factor Required for Uukuniemi Virus Late Penetration. Journal of Virology, 2014, 88, 8565-8578.	1.5	48
89	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	1.8	47
90	Shared components of protein complexes?versatile building blocks or biochemical artefacts?. BioEssays, 2004, 26, 1333-1343.	1.2	40

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91	A comprehensive set of protein complexes in yeast: mining large scale protein-protein interaction screens. Bioinformatics, 2003, 19, 1901-1908.	1.8	39
92	A family of interaction-adjusted indices of community similarity. ISME Journal, 2017, 11, 791-807.	4.4	39
93	Simultaneous analysis of large-scale RNAi screens for pathogen entry. BMC Genomics, 2014, 15, 1162.	1.2	38
94	gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens. Genome Biology, 2015, 16, 220.	3.8	35
95	Teamed up for transcription. Nature, 2002, 417, 797-798.	13.7	33
96	IFN-γ Hinders Recovery from Mucosal Inflammation during Antibiotic Therapy for Salmonella Gut Infection. Cell Host and Microbe, 2016, 20, 238-249.	5.1	33
97	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. Science Signaling, 2014, 7, rs6.	1.6	32
98	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.	4.5	32
99	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.	1.9	30
100	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.	1.1	30
101	ArrayProspector: a web resource of functional associations inferred from microarray expression data. Nucleic Acids Research, 2004, 32, W445-W448.	6.5	28
102	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.	1.5	28
103	Bacterial diversity and composition in the fluid of pitcher plants of the genus Nepenthes. Systematic and Applied Microbiology, 2015, 38, 330-339.	1.2	27
104	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. International Journal of Antimicrobial Agents, 2017, 50, 342-351.	1.1	27
105	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.	1.6	27
106	Consistency of genome-based methods in measuring Metazoan evolution. FEBS Letters, 2005, 579, 3355-3361.	1.3	26
107	Comparative analysis of environmental sequences: potential and challenges. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 519-523.	1.8	26
108	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.	4.9	25

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109	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in Caenorhabditis elegans. Molecular and Cellular Proteomics, 2016, 15, 1670-1680.	2.5	23
110	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.	1.1	18
111	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.	1.6	17
112	Protein tyrosine phosphatase non-receptor type 22 modulates colitis in a microbiota-dependent manner. Journal of Clinical Investigation, 2019, 129, 2527-2541.	3.9	15
113	The Evolution of Ecological Diversity in Acidobacteria. Frontiers in Microbiology, 2022, 13, 715637.	1.5	15
114	Termites in the woodwork. Genome Biology, 2007, 8, 229.	13.9	14
115	A Phylogeny-Based Benchmarking Test for Orthology Inference Reveals the Limitations of Function-Based Validation. PLoS ONE, 2014, 9, e111122.	1.1	14
116	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	6.5	13
117	Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. MBio, 2021, 12, .	1.8	13
118	Global analysis of bacterial transcription factors to predict cellular target processes. Trends in Genetics, 2004, 20, 126-131.	2.9	12
119	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.	1.4	10
120	Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation. MSystems, 2022, 7, e0016022.	1.7	10
121	The HUPO initiative on Model Organism Proteomes, iMOP. Proteomics, 2012, 12, 340-345.	1.3	9
122	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.	6.5	7
123	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. Genome Biology, 2021, 22, 157.	3.8	7
124	Specific Genomic Regions Are Differentially Affected by Copy Number Alterations across Distinct Cancer Types, in Aggregated Cytogenetic Data. PLoS ONE, 2012, 7, e43689.	1.1	5
125	Probing Isoform Switching Events in Various Cancer Types: Lessons From Pan-Cancer Studies. Frontiers in Molecular Biosciences, 2021, 8, 726902.	1.6	4
126	Inferring Protein Function from Genomic Context. , 0, , 1179-1210.		1

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127	STRING and STITCH: known and predicted interactions between proteins and chemicals. Nature Precedings, 0, , .	0.1	1
128	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. BMC Bioinformatics, 2019, 20, 228.	1.2	1
129	Sequence-Specific Features of Short Double-Strand, Blunt-End RNAs Have RIG-I- and Type 1 Interferon-Dependent or -Independent Anti-Viral Effects. Viruses, 2022, 14, 1407.	1.5	1
130	Sa1872 EBI2 Plays a Role in the Development of Intestinal Lymphoid Structures. Gastroenterology, 2016, 150, S386.	0.6	0
131	Protein–Protein Interaction Networks: Assembly and Analysis. , 2009, , 197-217.		0
132	Analysis of the Human Kinome and Phosphatome Reveals Diseased Signaling Networks Induced by Overexpression. SSRN Electronic Journal, 0, , .	0.4	0