

Christian von Mering

List of Publications by Year in Descending Order

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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
papers

49,194
citations

64
h-index

151
g-index

151
ext. papers

66,457
ext. citations

14.6
avg, IF

7.53
L-index

#	Paper	IF	Citations
133	The Evolution of Ecological Diversity in .. <i>Frontiers in Microbiology</i> , 2022 , 13, 715637	5.7	4
132	Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation.. <i>MSystems</i> , 2022 , e0016022	7.6	1
131	Probing Isoform Switching Events in Various Cancer Types: Lessons From Pan-Cancer Studies. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 726902	5.6	
130	Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. <i>MBio</i> , 2021 , 12,	7.8	6
129	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. <i>Genome Biology</i> , 2021 , 22, 157	18.3	2
128	The STRING database in 2021: customizable protein-protein networks, and functional characterization of user-uploaded gene/measurement sets. <i>Nucleic Acids Research</i> , 2021 , 49, D605-D612	20.1	661
127	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020 , 36, 2636-2642	7.2	29
126	ChromID identifies the protein interactome at chromatin marks. <i>Nature Biotechnology</i> , 2020 , 38, 728-736	14.5	31
125	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020 , 14, 1247-1259	11.9	23
124	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020 , 11, 729	17.4	38
123	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
122	Fermentation Ability of Gut Microbiota of Wild Japanese Macaques in the Highland and Lowland Yakushima: In Vitro Fermentation Assay and Genetic Analyses. <i>Microbial Ecology</i> , 2020 , 80, 459-474	4.4	2
121	Pathogenic impact of transcript isoform switching in 1,209 cancer samples covering 27 cancer types using an isoform-specific interaction network. <i>Scientific Reports</i> , 2020 , 10, 14453	4.9	6
120	Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data. <i>Cell Systems</i> , 2019 , 9, 286-296.e8	10.6	33
119	Analysis of the Human Kinome and Phosphatome by Mass Cytometry Reveals Overexpression-Induced Effects on Cancer-Related Signaling. <i>Molecular Cell</i> , 2019 , 74, 1086-1102.e5	17.6	18
118	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. <i>BMC Bioinformatics</i> , 2019 , 20, 228	3.6	0
117	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. <i>Molecular Cell</i> , 2019 , 74, 951-965.e13	17.6	45

116	Protein tyrosine phosphatase non-receptor type 22 modulates colitis in a microbiota-dependent manner. <i>Journal of Clinical Investigation</i> , 2019 , 129, 2527-2541	15.9	8
115	STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. <i>Nucleic Acids Research</i> , 2019 , 47, D607-D613	20.1	5966
114	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. <i>Nucleic Acids Research</i> , 2019 , 47, D309-D314	20.1	850
113	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018 , 17, 317-332	64.1	156
112	Growth-restricting effects of siRNA transfections: a largely deterministic combination of off-target binding and hybridization-independent competition. <i>Nucleic Acids Research</i> , 2018 , 46, 9309-9320	20.1	6
111	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018 , 10,	6.2	58
110	Ecologically informed microbial biomarkers and accurate classification of mixed and unmixed samples in an extensive cross-study of human body sites. <i>Microbiome</i> , 2018 , 6, 192	16.6	15
109	A family of interaction-adjusted indices of community similarity. <i>ISME Journal</i> , 2017 , 11, 791-807	11.9	24
108	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. <i>Science</i> , 2017 , 355,	33.3	198
107	Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. <i>Microbiome</i> , 2017 , 5, 20	16.6	74
106	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2115-2122	8.3	966
105	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. <i>Cell Reports</i> , 2017 , 19, 1056-1067	10.6	49
104	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
103	RAIN: RNA-protein Association and Interaction Networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	42
102	MAPseq: highly efficient k-mer search with confidence estimates, for rRNA sequence analysis. <i>Bioinformatics</i> , 2017 , 33, 3808-3810	7.2	44
101	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. <i>International Journal of Antimicrobial Agents</i> , 2017 , 50, 342-351	14.3	19
100	Preventive <i>Trichuris suis ova</i> (TSO) treatment protects immunocompetent rabbits from DSS colitis but may be detrimental under conditions of immunosuppression. <i>Scientific Reports</i> , 2017 , 7, 16500	4.9	10
99	Suppression of the <i>Escherichia coli</i> dnaA46 mutation by changes in the activities of the pyruvate-acetate node links DNA replication regulation to central carbon metabolism. <i>PLoS ONE</i> , 2017 , 12, e0176050	3.7	10

98	IFN- β Hinders Recovery from Mucosal Inflammation during Antibiotic Therapy for Salmonella Gut Infection. <i>Cell Host and Microbe</i> , 2016 , 20, 238-49	23.4	26
97	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	504
96	The SIB Swiss Institute of Bioinformatics Resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
95	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1670-80	7.6	15
94	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. <i>Nucleic Acids Research</i> , 2016 , 44, D380-4	20.1	641
93	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. <i>Bioinformatics</i> , 2016 , 32, 1085-7	7.2	56
92	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
91	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016 , 13, 425-30	21.6	133
90	Bacterial diversity and composition in the fluid of pitcher plants of the genus <i>Nepenthes</i> . <i>Systematic and Applied Microbiology</i> , 2015 , 38, 330-9	4.2	22
89	Limits to robustness and reproducibility in the demarcation of operational taxonomic units. <i>Environmental Microbiology</i> , 2015 , 17, 1689-706	5.2	76
88	gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens. <i>Genome Biology</i> , 2015 , 16, 220	18.3	25
87	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cell-lines. <i>Proteomics</i> , 2015 , 15, 3163-8	4.8	283
86	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015 , 43, D447-52	20.1	6276
85	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014 , 46, 336-44	36.3	353
84	Chromothripsis-like patterns are recurring but heterogeneously distributed features in a survey of 22,347 cancer genome screens. <i>BMC Genomics</i> , 2014 , 15, 82	4.5	78
83	Genome-wide small interfering RNA screens reveal VAMP3 as a novel host factor required for Uukuniemi virus late penetration. <i>Journal of Virology</i> , 2014 , 88, 8565-78	6.6	39
82	A sentinel protein assay for simultaneously quantifying cellular processes. <i>Nature Methods</i> , 2014 , 11, 1045-8	21.6	52
81	A phylogeny-based benchmarking test for orthology inference reveals the limitations of function-based validation. <i>PLoS ONE</i> , 2014 , 9, e111122	3.7	12

80	STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014 , 42, D401-7	20.1	290
79	Ecological consistency of SSU rRNA-based operational taxonomic units at a global scale. <i>PLoS Computational Biology</i> , 2014 , 10, e1003594	5	58
78	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014 , 42, W436-41	20.1	12
77	Simultaneous analysis of large-scale RNAi screens for pathogen entry. <i>BMC Genomics</i> , 2014 , 15, 1162	4.5	28
76	HPC-CLUST: distributed hierarchical clustering for large sets of nucleotide sequences. <i>Bioinformatics</i> , 2014 , 30, 287-8	7.2	35
75	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. <i>Science Signaling</i> , 2014 , 7, rs6	8.8	26
74	Specific inhibition of diverse pathogens in human cells by synthetic microRNA-like oligonucleotides inferred from RNAi screens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 4548-53	11.5	52
73	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014 , 42, D2312-1	20.1	387
72	Microbiota-derived hydrogen fuels <i>Salmonella typhimurium</i> invasion of the gut ecosystem. <i>Cell Host and Microbe</i> , 2013 , 14, 641-51	23.4	105
71	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2013 , 41, D808-15	20.1	3033
70	Bacterial anoxygenic photosynthesis on plant leaf surfaces. <i>Environmental Microbiology Reports</i> , 2012 , 4, 209-16	3.7	63
69	STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012 , 40, D876-80	20.1	219
68	Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. <i>ISME Journal</i> , 2012 , 6, 1378-90	11.9	458
67	High confidence prediction of essential genes in <i>Burkholderia cenocepacia</i> . <i>PLoS ONE</i> , 2012 , 7, e40064	3.7	48
66	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012 , 12, 340-5	4.8	8
65	Microbial rhodopsins on leaf surfaces of terrestrial plants. <i>Environmental Microbiology</i> , 2012 , 14, 140-6	5.2	64
64	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
63	PaxDb, a database of protein abundance averages across all three domains of life. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 492-500	7.6	351

62	Specific genomic regions are differentially affected by copy number alterations across distinct cancer types, in aggregated cytogenetic data. <i>PLoS ONE</i> , 2012 , 7, e43689	3.7	3
61	RNAi screen of Salmonella invasion shows role of COPI in membrane targeting of cholesterol and Cdc42. <i>Molecular Systems Biology</i> , 2011 , 7, 474	12.2	68
60	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
59	Cell-sorting at the A/P boundary in the Drosophila wing primordium: a computational model to consolidate observed non-local effects of Hh signaling. <i>PLoS Computational Biology</i> , 2011 , 7, e1002025	5	25
58	In situ enzyme activity in the dissolved and particulate fraction of the fluid from four pitcher plant species of the genus <i>Nepenthes</i> . <i>PLoS ONE</i> , 2011 , 6, e25144	3.7	26
57	Phosphoproteomic analysis reveals interconnected system-wide responses to perturbations of kinases and phosphatases in yeast. <i>Science Signaling</i> , 2010 , 3, rs4	8.8	229
56	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010 , 38, D552-6	20.1	183
55	eggNOG v2.0: extending the evolutionary genealogy of genes with enhanced non-supervised orthologous groups, species and functional annotations. <i>Nucleic Acids Research</i> , 2010 , 38, D190-5	20.1	179
54	The microbiota mediates pathogen clearance from the gut lumen after non-typhoidal Salmonella diarrhea. <i>PLoS Pathogens</i> , 2010 , 6, e1001097	7.6	252
53	Like will to like: abundances of closely related species can predict susceptibility to intestinal colonization by pathogenic and commensal bacteria. <i>PLoS Pathogens</i> , 2010 , 6, e1000711	7.6	304
52	A global network of coexisting microbes from environmental and whole-genome sequence data. <i>Genome Research</i> , 2010 , 20, 947-59	9.7	305
51	MLTreeMap--accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. <i>BMC Genomics</i> , 2010 , 11, 461	4.5	93
50	Arabidopsis female gametophyte gene expression map reveals similarities between plant and animal gametes. <i>Current Biology</i> , 2010 , 20, 506-12	6.3	255
49	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. <i>Proteomics</i> , 2010 , 10, 1297-306	4.8	51
48	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
47	The hedgehog signaling pathway: where did it come from?. <i>PLoS Biology</i> , 2009 , 7, e1000146	9.7	53
46	Community proteogenomics reveals insights into the physiology of phyllosphere bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 16428-33	11.5	595
45	Comparative functional analysis of the <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> proteomes. <i>PLoS Biology</i> , 2009 , 7, e48	9.7	179

44	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , 2008 , 4, 198	12.2	118
43	eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2008 , 36, D250-4	20.1	313
42	STITCH: interaction networks of chemicals and proteins. <i>Nucleic Acids Research</i> , 2008 , 36, D684-8	20.1	471
41	Salmonella enterica serovar typhimurium exploits inflammation to compete with the intestinal microbiota. <i>PLoS Biology</i> , 2007 , 5, 2177-89	9.7	736
40	Quantitative phylogenetic assessment of microbial communities in diverse environments. <i>Science</i> , 2007 , 315, 1126-30	33.3	259
39	Quantitative assessment of protein function prediction from metagenomics shotgun sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 13913-8	11.5	66
38	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007 , 35, D358-62	20.1	503
37	Sequence-based factors influencing the expression of heterologous genes in the yeast <i>Pichia pastoris</i> —A comparative view on 79 human genes. <i>Journal of Biotechnology</i> , 2007 , 130, 1-10	3.7	26
36	Termites in the woodwork. <i>Genome Biology</i> , 2007 , 8, 229	18.3	13
35	Prediction of effective genome size in metagenomic samples. <i>Genome Biology</i> , 2007 , 8, R10	18.3	219
34	Assessing systems properties of yeast mitochondria through an interaction map of the organelle. <i>PLoS Genetics</i> , 2006 , 2, e170	6	63
33	Comparative analysis of environmental sequences: potential and challenges. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 519-23	5.8	22
32	Identification and analysis of evolutionarily cohesive functional modules in protein networks. <i>Genome Research</i> , 2006 , 16, 374-82	9.7	54
31	Toward automatic reconstruction of a highly resolved tree of life. <i>Science</i> , 2006 , 311, 1283-7	33.3	1197
30	Consistency of genome-based methods in measuring Metazoan evolution. <i>FEBS Letters</i> , 2005 , 579, 3355-58	3.8	22
29	Comparative metagenomics of microbial communities. <i>Science</i> , 2005 , 308, 554-7	33.3	1211
28	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. <i>Nucleic Acids Research</i> , 2005 , 33, D433-7	20.1	953
27	Environments shape the nucleotide composition of genomes. <i>EMBO Reports</i> , 2005 , 6, 1208-13	6.5	200

26	Complex genomic rearrangements lead to novel primate gene function. <i>Genome Research</i> , 2005 , 15, 343-51	9.7	82
25	Functional clues for hypothetical proteins based on genomic context analysis in prokaryotes. <i>Nucleic Acids Research</i> , 2004 , 32, 6321-6	20.1	49
24	The HUPO PSI's molecular interaction format--a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004 , 22, 177-83	44.5	504
23	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. <i>Nature Biotechnology</i> , 2004 , 22, 911-7	44.5	142
22	Global analysis of bacterial transcription factors to predict cellular target processes. <i>Trends in Genetics</i> , 2004 , 20, 126-31	8.5	12
21	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 292-98.1	27.1	278
20	Shared components of protein complexes--versatile building blocks or biochemical artefacts?. <i>BioEssays</i> , 2004 , 26, 1333-43	4.1	38
19	ArrayProspector: a web resource of functional associations inferred from microarray expression data. <i>Nucleic Acids Research</i> , 2004 , 32, W445-8	20.1	24
18	A comprehensive set of protein complexes in yeast: mining large scale protein-protein interaction screens. <i>Bioinformatics</i> , 2003 , 19, 1901-8	7.2	34
17	Function prediction and protein networks. <i>Current Opinion in Cell Biology</i> , 2003 , 15, 191-8	9	118
16	STRING: a database of predicted functional associations between proteins. <i>Nucleic Acids Research</i> , 2003 , 31, 258-61	20.1	1182
15	Genome evolution reveals biochemical networks and functional modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 15428-33	11.5	123
14	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002 , 417, 399-403	50.1	1856
13	Comparative genome and proteome analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002 , 298, 149-59	33.3	455
12	Immunity-related genes and gene families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 159-65	33.3	743
11	Prion protein devoid of the octapeptide repeat region restores susceptibility to scrapie in PrP knockout mice. <i>Neuron</i> , 2000 , 27, 399-408	13.9	221
10	Distinct and regulated activities of human Gli proteins in <i>Drosophila</i> . <i>Current Biology</i> , 1999 , 9, 1319-22	6.3	54
9	Expression of amino-terminally truncated PrP in the mouse leading to ataxia and specific cerebellar lesions. <i>Cell</i> , 1998 , 93, 203-14	56.2	454

8	Inferring Protein Function from Genomic Context	1179-1210	1
7	Fast genome-wide functional annotation through orthology assignment by eggNOG-mapper		13
6	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses		6
5	Open Community Challenge Reveals Molecular Network Modules with Key Roles in Diseases		10
4	Pathway and network analysis of more than 2,500 whole cancer genomes		4
3	Rapid inference of direct interactions in large-scale ecological networks from heterogeneous microbial sequencing data		7
2	Pathogenic impact of transcript isoform switching in 1209 cancer samples covering 27 cancer types using an isoform-specific interaction network		2
1	CanIsoNet: A Database to Study the Functional Impact of Isoform Switching Events in Cancer		1