

Christian von Mering

List of Publications by Year in descending order

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Version: 2024-02-01

132
papers

76,828
citations

13332

70
h-index

14779

131
g-index

151
all docs

151
docs citations

151
times ranked

106473
citing authors

#	ARTICLE	IF	CITATIONS
1	The Evolution of Ecological Diversity in Acidobacteria. <i>Frontiers in Microbiology</i> , 2022, 13, 715637.	1.5	15
2	Reproducible Propagation of Species-Rich Soil Bacterial Communities Suggests Robust Underlying Deterministic Principles of Community Formation. <i>MSystems</i> , 2022, 7, e0016022.	1.7	10
3	Sequence-Specific Features of Short Double-Strand, Blunt-End RNAs Have RIG-I- and Type 1 Interferon-Dependent or -Independent Anti-Viral Effects. <i>Viruses</i> , 2022, 14, 1407.	1.5	1
4	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.	6.5	4,274
5	Strain-Resolved Dynamics of the Lung Microbiome in Patients with Cystic Fibrosis. <i>MBio</i> , 2021, 12, .	1.8	13
6	treeclimbR pinpoints the data-dependent resolution of hierarchical hypotheses. <i>Genome Biology</i> , 2021, 22, 157.	3.8	7
7	Probing Isoform Switching Events in Various Cancer Types: Lessons From Pan-Cancer Studies. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 726902.	1.6	4
8	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.	1.6	27
9	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020, 36, 2636-2642.	1.8	47
10	ChromID identifies the protein interactome at chromatin marks. <i>Nature Biotechnology</i> , 2020, 38, 728-736.	9.4	90
11	Disentangling the impact of environmental and phylogenetic constraints on prokaryotic within-species diversity. <i>ISME Journal</i> , 2020, 14, 1247-1259.	4.4	74
12	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	5.8	73
13	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
14	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.	1.4	10
15	Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data. <i>Cell Systems</i> , 2019, 9, 286-296.e8.	2.9	96
16	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.	4.5	32
17	Tree reconciliation combined with subsampling improves large scale inference of orthologous group hierarchies. <i>BMC Bioinformatics</i> , 2019, 20, 228.	1.2	1
18	Cross-Regulation between TDP-43 and Paraspeckles Promotes Pluripotency-Differentiation Transition. <i>Molecular Cell</i> , 2019, 74, 951-965.e13.	4.5	85

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19	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.	6.5	12,237
20	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.	6.5	2,575
21	Protein tyrosine phosphatase non-receptor type 22 modulates colitis in a microbiota-dependent manner. <i>Journal of Clinical Investigation</i> , 2019, 129, 2527-2541.	3.9	15
22	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	21.5	263
23	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.	6.5	7
24	Viruses.STRING: A Virus-Host Protein-Protein Interaction Database. <i>Viruses</i> , 2018, 10, 519.	1.5	100
25	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.	4.9	25
26	A family of interaction-adjusted indices of community similarity. <i>ISME Journal</i> , 2017, 11, 791-807.	4.4	39
27	Cell-wide analysis of protein thermal unfolding reveals determinants of thermostability. <i>Science</i> , 2017, 355, .	6.0	313
28	Sputum DNA sequencing in cystic fibrosis: non-invasive access to the lung microbiome and to pathogen details. <i>Microbiome</i> , 2017, 5, 20.	4.9	100
29	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. <i>Molecular Biology and Evolution</i> , 2017, 34, 2115-2122.	3.5	2,156
30	High-Resolution RNA Maps Suggest Common Principles of Splicing and Polyadenylation Regulation by TDP-43. <i>Cell Reports</i> , 2017, 19, 1056-1067.	2.9	83
31	The STRING database in 2017: quality-controlled protein-protein association networks, made broadly accessible. <i>Nucleic Acids Research</i> , 2017, 45, D362-D368.	6.5	6,303
32	RAIN: RNA-protein Association and Interaction Networks. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, baw167.	1.4	53
33	MAPseq: highly efficient k-mer search with confidence estimates, for rRNA sequence analysis. <i>Bioinformatics</i> , 2017, 33, 3808-3810.	1.8	98
34	Effects of oral antibiotics and isotretinoin on the murine gut microbiota. <i>International Journal of Antimicrobial Agents</i> , 2017, 50, 342-351.	1.1	27
35	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.	1.6	17
36	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.	1.1	18

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37	Standardized benchmarking in the quest for orthologs. <i>Nature Methods</i> , 2016, 13, 425-430.	9.0	198
38	Sa1872 EB12 Plays a Role in the Development of Intestinal Lymphoid Structures. <i>Gastroenterology</i> , 2016, 150, S386.	0.6	0
39	IFN- γ Hinders Recovery from Mucosal Inflammation during Antibiotic Therapy for Salmonella Gut Infection. <i>Cell Host and Microbe</i> , 2016, 20, 238-249.	5.1	33
40	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, baw100.	1.4	1,085
41	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
42	Natural Genetic Variation Differentially Affects the Proteome and Transcriptome in <i>Caenorhabditis elegans</i> . <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1670-1680.	2.5	23
43	STITCH 5: augmenting protein's chemical interaction networks with tissue and affinity data. <i>Nucleic Acids Research</i> , 2016, 44, D380-D384.	6.5	1,112
44	SVD-phy: improved prediction of protein functional associations through singular value decomposition of phylogenetic profiles. <i>Bioinformatics</i> , 2016, 32, 1085-1087.	1.8	91
45	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-D293.	6.5	1,937
46	gespeR: a statistical model for deconvoluting off-target-confounded RNA interference screens. <i>Genome Biology</i> , 2015, 16, 220.	3.8	35
47	Version 4.0 of PaxDb: Protein abundance data, integrated across model organisms, tissues, and cell lines. <i>Proteomics</i> , 2015, 15, 3163-3168.	1.3	493
48	STRING v10: protein's protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
49	Bacterial diversity and composition in the fluid of pitcher plants of the genus <i>Nepenthes</i> . <i>Systematic and Applied Microbiology</i> , 2015, 38, 330-339.	1.2	27
50	Limits to robustness and reproducibility in the demarcation of operational taxonomic units. <i>Environmental Microbiology</i> , 2015, 17, 1689-1706.	1.8	95
51	A Phylogeny-Based Benchmarking Test for Orthology Inference Reveals the Limitations of Function-Based Validation. <i>PLoS ONE</i> , 2014, 9, e111122.	1.1	14
52	STITCH 4: integration of protein's chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014, 42, D401-D407.	6.5	388
53	Ecological Consistency of SSU rRNA-Based Operational Taxonomic Units at a Global Scale. <i>PLoS Computational Biology</i> , 2014, 10, e1003594.	1.5	85
54	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	6.5	13

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55	Simultaneous analysis of large-scale RNAi screens for pathogen entry. <i>BMC Genomics</i> , 2014, 15, 1162.	1.2	38
56	HPC-CLUST: distributed hierarchical clustering for large sets of nucleotide sequences. <i>Bioinformatics</i> , 2014, 30, 287-288.	1.8	49
57	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. <i>Science Signaling</i> , 2014, 7, rs6.	1.6	32
58	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, 4548-4553.	3.3	60
59	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
60	Pathogens and host immunity in the ancient human oral cavity. <i>Nature Genetics</i> , 2014, 46, 336-344.	9.4	482
61	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.	1.2	100
62	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, 8565-8578.	1.5	48
63	A sentinel protein assay for simultaneously quantifying cellular processes. <i>Nature Methods</i> , 2014, 11, 1045-1048.	9.0	70
64	Microbiota-Derived Hydrogen Fuels Salmonella Typhimurium Invasion of the Gut Ecosystem. <i>Cell Host and Microbe</i> , 2013, 14, 641-651.	5.1	145
65	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	6.5	490
66	STRING v9.1: protein-protein interaction networks, with increased coverage and integration. <i>Nucleic Acids Research</i> , 2012, 41, D808-D815.	6.5	3,816
67	PaxDb, a Database of Protein Abundance Averages Across All Three Domains of Life. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 492-500.	2.5	413
68	STITCH 3: zooming in on protein-chemical interactions. <i>Nucleic Acids Research</i> , 2012, 40, D876-D880.	6.5	254
69	Metaproteogenomic analysis of microbial communities in the phyllosphere and rhizosphere of rice. <i>ISME Journal</i> , 2012, 6, 1378-1390.	4.4	635
70	High Confidence Prediction of Essential Genes in Burkholderia Cenocepacia. <i>PLoS ONE</i> , 2012, 7, e40064.	1.1	60
71	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	1.3	9
72	Microbial rhodopsins on leaf surfaces of terrestrial plants. <i>Environmental Microbiology</i> , 2012, 14, 140-146.	1.8	78

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73	Bacterial anoxygenic photosynthesis on plant leaf surfaces. <i>Environmental Microbiology Reports</i> , 2012, 4, 209-216.	1.0	94
74	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.	1.1	5
75	The STRING database in 2011: functional interaction networks of proteins, globally integrated and scored. <i>Nucleic Acids Research</i> , 2011, 39, D561-D568.	6.5	3,014
76	RNAi screen of <i>Salmonella</i> invasion shows role of COPI in membrane targeting of cholesterol and Cdc42. <i>Molecular Systems Biology</i> , 2011, 7, 474.	3.2	89
77	Cell-Sorting at the A/P Boundary in the <i>Drosophila</i> Wing Primordium: A Computational Model to Consolidate Observed Non-Local Effects of Hh Signaling. <i>PLoS Computational Biology</i> , 2011, 7, e1002025.	1.5	28
78	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.	1.1	30
79	MLTreeMap - accurate Maximum Likelihood placement of environmental DNA sequences into taxonomic and functional reference phylogenies. <i>BMC Genomics</i> , 2010, 11, 461.	1.2	100
80	<i>Arabidopsis</i> Female Gametophyte Gene Expression Map Reveals Similarities between Plant and Animal Gametes. <i>Current Biology</i> , 2010, 20, 506-512.	1.8	302
81	Shotgun proteomics data from multiple organisms reveals remarkable quantitative conservation of the eukaryotic core proteome. <i>Proteomics</i> , 2010, 10, 1297-1306.	1.3	58
82	Phosphoproteomic Analysis Reveals Interconnected System-Wide Responses to Perturbations of Kinases and Phosphatases in Yeast. <i>Science Signaling</i> , 2010, 3, rs4.	1.6	277
83	STITCH 2: an interaction network database for small molecules and proteins. <i>Nucleic Acids Research</i> , 2010, 38, D552-D556.	6.5	215
84	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-D195.	6.5	202
85	The Microbiota Mediates Pathogen Clearance from the Gut Lumen after Non-Typhoidal <i>Salmonella</i> Diarrhea. <i>PLoS Pathogens</i> , 2010, 6, e1001097.	2.1	314
86	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.	2.1	367
87	A global network of coexisting microbes from environmental and whole-genome sequence data. <i>Genome Research</i> , 2010, 20, 947-959.	2.4	425
88	STRING 8—a global view on proteins and their functional interactions in 630 organisms. <i>Nucleic Acids Research</i> , 2009, 37, D412-D416.	6.5	2,195
89	The Hedgehog Signaling Pathway: Where Did It Come From?. <i>PLoS Biology</i> , 2009, 7, e1000146.	2.6	65
90	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, 16428-16433.	3.3	774

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91	Comparative Functional Analysis of the <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> Proteomes. <i>PLoS Biology</i> , 2009, 7, e1000048.	2.6	208
92	Protein-Protein Interaction Networks: Assembly and Analysis. , 2009, , 197-217.		0
93	Millimeter-scale genetic gradients and community-level molecular convergence in a hypersaline microbial mat. <i>Molecular Systems Biology</i> , 2008, 4, 198.	3.2	139
94	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, 13913-13918.	3.3	72
95	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007, 35, D358-D362.	6.5	568
96	eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2007, 36, D250-D254.	6.5	428
97	STITCH: interaction networks of chemicals and proteins. <i>Nucleic Acids Research</i> , 2007, 36, D684-D688.	6.5	669
98	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.	1.9	30
99	Termites in the woodwork. <i>Genome Biology</i> , 2007, 8, 229.	13.9	14
100	Prediction of effective genome size in metagenomic samples. <i>Genome Biology</i> , 2007, 8, R10.	13.9	281
101	<i>Salmonella enterica</i> Serovar Typhimurium Exploits Inflammation to Compete with the Intestinal Microbiota. <i>PLoS Biology</i> , 2007, 5, e244.	2.6	905
102	Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. <i>Science</i> , 2007, 315, 1126-1130.	6.0	300
103	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. <i>Science</i> , 2006, 311, 1283-1287.	6.0	1,435
104	Assessing Systems Properties of Yeast Mitochondria through an Interaction Map of the Organelle. <i>PLoS Genetics</i> , 2006, 2, e170.	1.5	67
105	Comparative analysis of environmental sequences: potential and challenges. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 519-523.	1.8	26
106	Identification and analysis of evolutionarily cohesive functional modules in protein networks. <i>Genome Research</i> , 2006, 16, 374-382.	2.4	60
107	Environments shape the nucleotide composition of genomes. <i>EMBO Reports</i> , 2005, 6, 1208-1213.	2.0	258
108	Complex genomic rearrangements lead to novel primate gene function. <i>Genome Research</i> , 2005, 15, 343-351.	2.4	104

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109	Consistency of genome-based methods in measuring Metazoan evolution. <i>FEBS Letters</i> , 2005, 579, 3355-3361.	1.3	26
110	Comparative Metagenomics of Microbial Communities. <i>Science</i> , 2005, 308, 554-557.	6.0	1,432
111	Functional clues for hypothetical proteins based on genomic context analysis in prokaryotes. <i>Nucleic Acids Research</i> , 2004, 32, 6321-6326.	6.5	57
112	STRING: known and predicted protein-protein associations, integrated and transferred across organisms. <i>Nucleic Acids Research</i> , 2004, 33, D433-D437.	6.5	1,418
113	The HUPO PSI's Molecular Interaction format—a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	9.4	581
114	Analysis of genomic context: prediction of functional associations from conserved bidirectionally transcribed gene pairs. <i>Nature Biotechnology</i> , 2004, 22, 911-917.	9.4	166
115	Global analysis of bacterial transcription factors to predict cellular target processes. <i>Trends in Genetics</i> , 2004, 20, 126-131.	2.9	12
116	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004, 14, 292-299.	2.6	323
117	Shared components of protein complexes? versatile building blocks or biochemical artefacts?. <i>BioEssays</i> , 2004, 26, 1333-1343.	1.2	40
118	ArrayProspector: a web resource of functional associations inferred from microarray expression data. <i>Nucleic Acids Research</i> , 2004, 32, W445-W448.	6.5	28
119	Function prediction and protein networks. <i>Current Opinion in Cell Biology</i> , 2003, 15, 191-198.	2.6	133
120	STRING: a database of predicted functional associations between proteins. <i>Nucleic Acids Research</i> , 2003, 31, 258-261.	6.5	1,897
121	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, 15428-15433.	3.3	140
122	A comprehensive set of protein complexes in yeast: mining large scale protein-protein interaction screens. <i>Bioinformatics</i> , 2003, 19, 1901-1908.	1.8	39
123	Comparative Genome and Proteome Analysis of <i>Anopheles gambiae</i> and <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 298, 149-159.	6.0	531
124	Immunity-Related Genes and Gene Families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 159-165.	6.0	845
125	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002, 417, 399-403.	13.7	2,137
126	Teamed up for transcription. <i>Nature</i> , 2002, 417, 797-798.	13.7	33

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127	Prion Protein Devoid of the Octapeptide Repeat Region Restores Susceptibility to Scrapie in PrP Knockout Mice. <i>Neuron</i> , 2000, 27, 399-408.	3.8	252
128	Distinct and regulated activities of human Gli proteins in <i>Drosophila</i> . <i>Current Biology</i> , 1999, 9, 1319-1322.	1.8	58
129	Expression of Amino-Terminally Truncated PrP in the Mouse Leading to Ataxia and Specific Cerebellar Lesions. <i>Cell</i> , 1998, 93, 203-214.	13.5	506
130	Inferring Protein Function from Genomic Context. , 0, , 1179-1210.		1
131	STRING and STITCH: known and predicted interactions between proteins and chemicals. <i>Nature Precedings</i> , 0, , .	0.1	1
132	Analysis of the Human Kinome and Phosphatome Reveals Diseased Signaling Networks Induced by Overexpression. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0