

Peer Bork

List of Publications by Year in descending order

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631
papers

294,087
citations

¹⁹

203
h-index

⁵

510
g-index

684
all docs

684
docs citations

684
times ranked

231296
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	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
3	A method and server for predicting damaging missense mutations. <i>Nature Methods</i> , 2010, 7, 248-249.	9.0	11,491
4	A human gut microbial gene catalogue established by metagenomic sequencing. <i>Nature</i> , 2010, 464, 59-65.	13.7	9,342
5	STRING v10: protein-protein interaction networks, integrated over the tree of life. <i>Nucleic Acids Research</i> , 2015, 43, D447-D452.	6.5	9,029
6	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
7	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
8	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	13.7	5,800
9	Interactive tree of life (iTOL) v3: an online tool for the display and annotation of phylogenetic and other trees. <i>Nucleic Acids Research</i> , 2016, 44, W242-W245.	6.5	4,967
10	Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. <i>Nucleic Acids Research</i> , 2021, 49, W293-W296.	6.5	4,856
11	Interactive Tree Of Life (iTOL) v4: recent updates and new developments. <i>Nucleic Acids Research</i> , 2019, 47, W256-W259.	6.5	4,604
12	Functional organization of the yeast proteome by systematic analysis of protein complexes. <i>Nature</i> , 2002, 415, 141-147.	13.7	4,509
13	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
14	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
15	Richness of human gut microbiome correlates with metabolic markers. <i>Nature</i> , 2013, 500, 541-546.	13.7	3,641
16	SMART, a simple modular architecture research tool: Identification of signaling domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 5857-5864.	3.3	3,370
17	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
18	Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. <i>Bioinformatics</i> , 2007, 23, 127-128.	1.8	2,609

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19	PAL2NAL: robust conversion of protein sequence alignments into the corresponding codon alignments. <i>Nucleic Acids Research</i> , 2006, 34, W609-W612.	6.5	2,575
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	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	13.7	2,421
22	Proteome survey reveals modularity of the yeast cell machinery. <i>Nature</i> , 2006, 440, 631-636.	13.7	2,347
23	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	13.7	2,222
24	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
25	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
26	Comparative assessment of large-scale data sets of protein-protein interactions. <i>Nature</i> , 2002, 417, 399-403.	13.7	2,137
27	Structure and function of the global ocean microbiome. <i>Science</i> , 2015, 348, 1261359.	6.0	2,137
28	Human non-synonymous SNPs: server and survey. <i>Nucleic Acids Research</i> , 2002, 30, 3894-3900.	6.5	1,995
29	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
30	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
31	STRING: a database of predicted functional associations between proteins. <i>Nucleic Acids Research</i> , 2003, 31, 258-261.	6.5	1,897
32	The Genome Sequence of the Malaria Mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 129-149.	6.0	1,859
33	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
34	ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 1635-1638.	3.5	1,692
35	An integrated catalog of reference genes in the human gut microbiome. <i>Nature Biotechnology</i> , 2014, 32, 834-841.	9.4	1,664
36	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	13.7	1,648

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37	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. <i>Nature</i> , 2015, 528, 262-266.	13.7	1,627
38	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	6.0	1,551
39	20 years of the SMART protein domain annotation resource. <i>Nucleic Acids Research</i> , 2018, 46, D493-D496.	6.5	1,525
40	SMART: recent updates, new developments and status in 2015. <i>Nucleic Acids Research</i> , 2015, 43, D257-D260.	6.5	1,519
41	Minimum information about a single amplified genome (MISAG) and a metagenome-assembled genome (MIMAG) of bacteria and archaea. <i>Nature Biotechnology</i> , 2017, 35, 725-731.	9.4	1,512
42	Human gut microbes impact host serum metabolome and insulin sensitivity. <i>Nature</i> , 2016, 535, 376-381.	13.7	1,506
43	SMART 7: recent updates to the protein domain annotation resource. <i>Nucleic Acids Research</i> , 2012, 40, D302-D305.	6.5	1,462
44	Toward Automatic Reconstruction of a Highly Resolved Tree of Life. <i>Science</i> , 2006, 311, 1283-1287.	6.0	1,435
45	Comparative Metagenomics of Microbial Communities. <i>Science</i> , 2005, 308, 554-557.	6.0	1,432
46	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
47	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	6.5	1,385
48	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	13.7	1,370
49	Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy. <i>Nucleic Acids Research</i> , 2011, 39, W475-W478.	6.5	1,361
50	InterPro in 2017—beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
51	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018, 555, 623-628.	13.7	1,339
52	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
53	The genome of the model beetle and pest <i>Tribolium castaneum</i> . <i>Nature</i> , 2008, 452, 949-955.	13.7	1,255
54	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205

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55	eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. <i>Molecular Biology and Evolution</i> , 2021, 38, 5825-5829.	3.5	1,174
56	SMART: a web-based tool for the study of genetically mobile domains. <i>Nucleic Acids Research</i> , 2000, 28, 231-234.	6.5	1,159
57	Protein Disorder Prediction. <i>Structure</i> , 2003, 11, 1453-1459.	1.6	1,119
58	STITCH 5: augmenting protein-chemical interaction networks with tissue and affinity data. <i>Nucleic Acids Research</i> , 2016, 44, D380-D384.	6.5	1,112
59	Drug Target Identification Using Side-Effect Similarity. <i>Science</i> , 2008, 321, 263-266.	6.0	1,097
60	The Ecoresponsive Genome of <i>Daphnia pulex</i> . <i>Science</i> , 2011, 331, 555-561.	6.0	1,086
61	The genome of the choanoflagellate <i>Monosiga brevicollis</i> and the origin of metazoans. <i>Nature</i> , 2008, 451, 783-788.	13.7	1,006
62	Conservation of gene order: a fingerprint of proteins that physically interact. <i>Trends in Biochemical Sciences</i> , 1998, 23, 324-328.	3.7	991
63	Potential of fecal microbiota for early-stage detection of colorectal cancer. <i>Molecular Systems Biology</i> , 2014, 10, 766.	3.2	991
64	STRING: a web-server to retrieve and display the repeatedly occurring neighbourhood of a gene. <i>Nucleic Acids Research</i> , 2000, 28, 3442-3444.	6.5	976
65	Prediction of deleterious human alleles. <i>Human Molecular Genetics</i> , 2001, 10, 591-597.	1.4	955
66	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
67	The SIDER database of drugs and side effects. <i>Nucleic Acids Research</i> , 2016, 44, D1075-D1079.	6.5	914
68	Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. <i>Nature Biotechnology</i> , 2014, 32, 822-828.	9.4	909
69	SMART: recent updates, new developments and status in 2020. <i>Nucleic Acids Research</i> , 2021, 49, D458-D460.	6.5	899
70	Salt-responsive gut commensal modulates TH17 axis and disease. <i>Nature</i> , 2017, 551, 585-589.	13.7	896
71	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004, 32, 142D-144.	6.5	892
72	SMART 5: domains in the context of genomes and networks. <i>Nucleic Acids Research</i> , 2006, 34, D257-D260.	6.5	884

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73	SMART 6: recent updates and new developments. <i>Nucleic Acids Research</i> , 2009, 37, D229-D232.	6.5	882
74	The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14422-14427.	3.3	874
75	Functional genomic analysis of cell division in <i>C. elegans</i> using RNAi of genes on chromosome III. <i>Nature</i> , 2000, 408, 331-336.	13.7	854
76	Immunity-Related Genes and Gene Families in <i>Anopheles gambiae</i> . <i>Science</i> , 2002, 298, 159-165.	6.0	845
77	Determinants of community structure in the global plankton interactome. <i>Science</i> , 2015, 348, 1262073.	6.0	842
78	mRNA degradation by miRNAs and GW182 requires both CCR4:NOT deadenylase and DCP1:DCP2 decapping complexes. <i>Genes and Development</i> , 2006, 20, 1885-1898.	2.7	824
79	Mother-to-Infant Microbial Transmission from Different Body Sites Shapes the Developing Infant Gut Microbiome. <i>Cell Host and Microbe</i> , 2018, 24, 133-145.e5.	5.1	822
80	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. <i>Science</i> , 2010, 327, 343-348.	6.0	808
81	An ATPase domain common to prokaryotic cell cycle proteins, sugar kinases, actin, and hsp70 heat shock proteins.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 7290-7294.	3.3	795
82	Genomic variation landscape of the human gut microbiome. <i>Nature</i> , 2013, 493, 45-50.	13.7	783
83	A side effect resource to capture phenotypic effects of drugs. <i>Molecular Systems Biology</i> , 2010, 6, 343.	3.2	757
84	Meta-analysis of fecal metagenomes reveals global microbial signatures that are specific for colorectal cancer. <i>Nature Medicine</i> , 2019, 25, 679-689.	15.2	734
85	Enterotypes in the landscape of gut microbial community composition. <i>Nature Microbiology</i> , 2018, 3, 8-16.	5.9	717
86	Systematic Discovery of In Vivo Phosphorylation Networks. <i>Cell</i> , 2007, 129, 1415-1426.	13.5	702
87	Identification of attenuation and antitermination regulation in prokaryotes. <i>Genome Biology</i> , 2002, 3, 1.	3.8	698
88	A superfamily of conserved domains in DNA damage-responsive cell cycle checkpoint proteins. <i>FASEB Journal</i> , 1997, 11, 68-76.	0.2	684
89	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
90	STITCH: interaction networks of chemicals and proteins. <i>Nucleic Acids Research</i> , 2007, 36, D684-D688.	6.5	669

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91	Genome phylogeny based on gene content. <i>Nature Genetics</i> , 1999, 21, 108-110.	9.4	658
92	The Immunoglobulin Fold Structural Classification, Sequence Patterns and Common Core. <i>Journal of Molecular Biology</i> , 1994, 242, 309-320.	2.0	652
93	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	6.5	640
94	Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. <i>Nature</i> , 2016, 537, 689-693.	13.7	629
95	Patterns and ecological drivers of ocean viral communities. <i>Science</i> , 2015, 348, 1261-1268.	6.0	617
96	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002, 30, 242-244.	6.5	613
97	Minimum information about a marker gene sequence (MIMARKS) and minimum information about any (x) sequence (MlxS) specifications. <i>Nature Biotechnology</i> , 2011, 29, 415-420.	9.4	608
98	Metagenomic analysis of colorectal cancer datasets identifies cross-cohort microbial diagnostic signatures and a link with choline degradation. <i>Nature Medicine</i> , 2019, 25, 667-678.	15.2	602
99	Metabolic dependencies drive species co-occurrence in diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6449-6454.	3.3	588
100	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
101	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
102	The modular architecture of a new family of growth regulators related to connective tissue growth factor. <i>FEBS Letters</i> , 1993, 327, 125-130.	1.3	570
103	Charting the Proteomes of Organisms with Unsequenced Genomes by MALDI-Quadrupole Time-of-Flight Mass Spectrometry and BLAST Homology Searching. <i>Analytical Chemistry</i> , 2001, 73, 1917-1926.	3.2	569
104	STRING 7—recent developments in the integration and prediction of protein interactions. <i>Nucleic Acids Research</i> , 2007, 35, D358-D362.	6.5	568
105	Literature mining for the biologist: from information retrieval to biological discovery. <i>Nature Reviews Genetics</i> , 2006, 7, 119-129.	7.7	565
106	The Human Gut Microbiome: From Association to Modulation. <i>Cell</i> , 2018, 172, 1198-1215.	13.5	558
107	Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. <i>Nature Communications</i> , 2016, 7, 10410.	5.8	557
108	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	6.5	555

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109	The human small intestinal microbiota is driven by rapid uptake and conversion of simple carbohydrates. <i>ISME Journal</i> , 2012, 6, 1415-1426.	4.4	544
110	Marine DNA Viral Macro- and Microdiversity from Pole to Pole. <i>Cell</i> , 2019, 177, 1109-1123.e14.	13.5	541
111	The CUB Domain. <i>Journal of Molecular Biology</i> , 1993, 231, 539-545.	2.0	532
112	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
113	Systematic Identification of Novel Protein Domain Families Associated with Nuclear Functions. <i>Genome Research</i> , 2002, 12, 47-56.	2.4	527
114	eggNOG v4.0: nested orthology inference across 3686 organisms. <i>Nucleic Acids Research</i> , 2014, 42, D231-D239.	6.5	526
115	SuperTarget and Matador: resources for exploring drug-target relationships. <i>Nucleic Acids Research</i> , 2007, 36, D919-D922.	6.5	518
116	HEAT repeats in the Huntington's disease protein. <i>Nature Genetics</i> , 1995, 11, 115-116.	9.4	517
117	Alternative splicing and genome complexity. <i>Nature Genetics</i> , 2002, 30, 29-30.	9.4	490
118	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
119	Identification and mutation analysis of the complete gene for Chediak-Higashi syndrome. <i>Nature Genetics</i> , 1996, 14, 307-311.	9.4	485
120	Recovery of gut microbiota of healthy adults following antibiotic exposure. <i>Nature Microbiology</i> , 2018, 3, 1255-1265.	5.9	483
121	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	6.5	478
122	Hundreds of ankyrin-like repeats in functionally diverse proteins: Mobile modules that cross phyla horizontally?. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 363-374.	1.5	468
123	Comparison of ARM and HEAT protein repeats. <i>Journal of Molecular Biology</i> , 2001, 309, 1-18.	2.0	464
124	Durable coexistence of donor and recipient strains after fecal microbiota transplantation. <i>Science</i> , 2016, 352, 586-589.	6.0	461
125	Predicting Protein Function by Genomic Context: Quantitative Evaluation and Qualitative Inferences. <i>Genome Research</i> , 2000, 10, 1204-1210.	2.4	453
126	KEGG Atlas mapping for global analysis of metabolic pathways. <i>Nucleic Acids Research</i> , 2008, 36, W423-W426.	6.5	445

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127	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	6.5	444
128	Metagenomic species profiling using universal phylogenetic marker genes. <i>Nature Methods</i> , 2013, 10, 1196-1199.	9.0	442
129	Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.	6.0	440
130	Predicting function: from genes to genomes and back 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1998, 283, 707-725.	2.0	433
131	eggNOG: automated construction and annotation of orthologous groups of genes. <i>Nucleic Acids Research</i> , 2007, 36, D250-D254.	6.5	428
132	Measuring genome evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 5849-5856.	3.3	424
133	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	1.6	418
134	Prediction of Potential GPI-modification Sites in Proprotein Sequences. <i>Journal of Molecular Biology</i> , 1999, 292, 741-758.	2.0	417
135	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
136	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycKeys</i> , 0, 10, 1-43.	0.8	409
137	A Novel Class of RanGTP Binding Proteins. <i>Journal of Cell Biology</i> , 1997, 138, 65-80.	2.3	398
138	Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.	6.0	394
139	STITCH 4: integration of protein-chemical interactions with user data. <i>Nucleic Acids Research</i> , 2014, 42, D401-D407.	6.5	388
140	Genome-Wide Experimental Determination of Barriers to Horizontal Gene Transfer. <i>Science</i> , 2007, 318, 1449-1452.	6.0	383
141	Dynamic Complex Formation During the Yeast Cell Cycle. <i>Science</i> , 2005, 307, 724-727.	6.0	382
142	The WW domain: a signalling site in dystrophin?. <i>Trends in Biochemical Sciences</i> , 1994, 19, 531-533.	3.7	373
143	Structure-Based Assembly of Protein Complexes in Yeast. <i>Science</i> , 2004, 303, 2026-2029.	6.0	367
144	â€¦Functional motifsâ€¦. <i>Nature Genetics</i> , 1996, 13, 266-268.	9.4	362

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145	Gene Families: The Taxonomy of Protein Paralogs and Chimeras. <i>Science</i> , 1997, 278, 609-614.	6.0	362
146	In situ structural analysis of the human nuclear pore complex. <i>Nature</i> , 2015, 526, 140-143.	13.7	361
147	Country-specific antibiotic use practices impact the human gut resistome. <i>Genome Research</i> , 2013, 23, 1163-1169.	2.4	356
148	Convergent evolution of similar enzymatic function on different protein folds: The hexokinase, ribokinase, and galactokinase families of sugar kinases. <i>Protein Science</i> , 1993, 2, 31-40.	3.1	353
149	A Holistic Approach to Marine Eco-Systems Biology. <i>PLoS Biology</i> , 2011, 9, e1001177.	2.6	353
150	Epidermal growth factor-like modules. <i>Current Opinion in Structural Biology</i> , 1993, 3, 385-392.	2.6	352
151	Molecular eco-systems biology: towards an understanding of community function. <i>Nature Reviews Microbiology</i> , 2008, 6, 693-699.	13.6	339
152	Towards a structural basis of human non-synonymous single nucleotide polymorphisms. <i>Trends in Genetics</i> , 2000, 16, 198-200.	2.9	333
153	REF, an evolutionarily conserved family of hnRNP-like proteins, interacts with TAP/Mex67p and participates in mRNA nuclear export. <i>Rna</i> , 2000, 6, 638-650.	1.6	331
154	Association of genes to genetically inherited diseases using data mining. <i>Nature Genetics</i> , 2002, 31, 316-319.	9.4	330
155	Gut Microbiota Linked to Sexual Preference and HIV Infection. <i>EBioMedicine</i> , 2016, 5, 135-146.	2.7	328
156	Characterization of a novel protein-binding module - the WW domain. <i>FEBS Letters</i> , 1995, 369, 67-71.	1.3	326
157	Protein interaction networks from yeast to human. <i>Current Opinion in Structural Biology</i> , 2004, 14, 292-299.	2.6	323
158	iPath2.0: interactive pathway explorer. <i>Nucleic Acids Research</i> , 2011, 39, W412-W415.	6.5	322
159	Eukaryotic Signalling Domain Homologues in Archaea and Bacteria. <i>Ancient Ancestry and Horizontal Gene Transfer. Journal of Molecular Biology</i> , 1999, 289, 729-745.	2.0	318
160	Extensive transmission of microbes along the gastrointestinal tract. <i>ELife</i> , 2019, 8, .	2.8	313
161	Accurate and universal delineation of prokaryotic species. <i>Nature Methods</i> , 2013, 10, 881-884.	9.0	311
162	Structure and distribution of modules in extracellular proteins. <i>Quarterly Reviews of Biophysics</i> , 1996, 29, 119-167.	2.4	307

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163	Metabolism and evolution of <i>Haemophilus influenzae</i> deduced from a whole-genome comparison with <i>Escherichia coli</i> . <i>Current Biology</i> , 1996, 6, 279-291.	1.8	307
164	Predicting functions from protein sequences—where are the bottlenecks?. <i>Nature Genetics</i> , 1998, 18, 313-318.	9.4	306
165	Dietary Modulation of Gut Microbiota Contributes to Alleviation of Both Genetic and Simple Obesity in Children. <i>EBioMedicine</i> , 2015, 2, 968-984.	2.7	306
166	Genomes in Flux: The Evolution of Archaeal and Proteobacterial Gene Content. <i>Genome Research</i> , 2002, 12, 17-25.	2.4	305
167	Quantitative Phylogenetic Assessment of Microbial Communities in Diverse Environments. <i>Science</i> , 2007, 315, 1126-1130.	6.0	300
168	A large domain common to sperm receptors (Zp2 and Zp3) and TGF- β type III receptor. <i>FEBS Letters</i> , 1992, 300, 237-240.	1.3	298
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170	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
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