Robert D. Finn

List of Publications by Year
in descending order

198 **papers**	110,975 **citations**	6840 81 **h-index**	2823 197 **g-index**
226 **all docs**	226 **docs citations**	226 **times ranked**	116735 **citing authors**

#	Article	IF	Citations
1	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. Nucleic Acids Research, 2022, 50, D765-D770.	6.5	10
2	Metagenomics approach for Polymyxa betae genome assembly enables comparative analysis towards deciphering the intracellular parasitic lifestyle of the plasmodiophorids. Genomics, 2022, 114, 9-22.	1.3	4
3	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	6.5	141
4	The European Bioinformatics Institute (EMBL-EBI) in 2021. Nucleic Acids Research, 2022, 50, D11-D19.	6.5	34
5	A catalogue of 1,167 genomes from the human gut archaeome. Nature Microbiology, 2022, 7, 48-61.	5.9	72
6	Using deep learning to annotate the protein universe. Nature Biotechnology, 2022, 40, 932-937.	9.4	133
7	Unifying the known and unknown microbial coding sequence space. ELife, 2022, 11, .	2.8	41
8	A mouse model of occult intestinal colonization demonstrating antibiotic-induced outgrowth of carbapenem-resistant Enterobacteriaceae. Microbiome, 2022, 10, 43.	4.9	8
9	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions. Nature Microbiology, 2022, 7, 169-179.	5.9	58
10	Large-Scale Discovery of Microbial Fibrillar Adhesins and Identification of Novel Members of Adhesive Domain Families. Journal of Bacteriology, 2022, 204, .	1.0	6
11	Priorities for ocean microbiome research. Nature Microbiology, 2022, 7, 937-947.	5.9	27
12	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. Briefings in Bioinformatics, 2021, 22, 642-663.	3.2	110
13	The InterPro protein families and domains database: 20 years on. Nucleic Acids Research, 2021, 49, D344-D354.	6.5	1,385
14	A unified catalog of 204,938 reference genomes from the human gut microbiome. Nature Biotechnology, 2021, 39, 105-114.	9.4	628
15	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. Nucleic Acids Research, 2021, 49, D192-D200.	6.5	475
16	UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research, 2021, 49, D480-D489.	6.5	4,709
17	Pfam: The protein families database in 2021. Nucleic Acids Research, 2021, 49, D412-D419.	6.5	3,068
18	How to use the <scp><i>MEROPS</i></scp> database and website to help understand peptidase specificity. Protein Science, 2021, 30, 83-92.	3.1	44

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19	Navigating bacterial taxonomy in a world of unchartered microbial organisms.. , 2021, , 179-197.		0
20	Massive expansion of human gut bacteriophage diversity. Cell, 2021, 184, 1098-1109.e9.	13.5	331
21	Cryo-EM structures of human RNA polymerase III in its unbound and transcribing states. Nature Structural and Molecular Biology, 2021, 28, 210-219.	3.6	59
22	ELIXIRâ€EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	3.5	18
23	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. Genome Biology and Evolution, 2021, 13, .	1.1	19
24	Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. Nature Protocols, 2021, 16, 2520-2541.	5.5	25
25	Sequence analysis of tyrosine recombinases allows annotation of mobile genetic elements in prokaryotic genomes. Molecular Systems Biology, 2021, 17, e9880.	3.2	33
26	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. Scientific Reports, 2021, 11, 10590.	1.6	17
27	R2DT is a framework for predicting and visualising RNA secondary structure using templates. Nature Communications, 2021, 12, 3494.	5.8	58
28	Periscope Proteins are variable-length regulators of bacterial cell surface interactions. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
29	Highly accurate protein structure prediction for the human proteome. Nature, 2021, 596, 590-596.	13.7	1,773
30	Discovery of fibrillar adhesins across bacterial species. BMC Genomics, 2021, 22, 550.	1.2	7
31	Ten simple rules to make your computing more environmentally sustainable. PLoS Computational Biology, 2021, 17, e1009324.	1.5	27
32	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
33	MGnify: the microbiome analysis resource in 2020. Nucleic Acids Research, 2020, 48, D570-D578.	6.5	296
34	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	6.5	13
35	*Caenorhabditis elegans* AF4/FMR2 Family Homolog *affl-2* Regulates Heat-Shock-Induced Gene Expression. Genetics, 2020, 215, 1039-1054.	1.2	5
36	Acetylation of Surface Carbohydrates in Bacterial Pathogens Requires Coordinated Action of a Two-Domain Membrane-Bound Acyltransferase. MBio, 2020, 11, .	1.8	22

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37	Exploring Nonâ€Coding RNAs in RNAcentral. Current Protocols in Bioinformatics, 2020, 71, e104.	25.8	6
38	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. Genome Biology, 2020, 21, 244.	3.8	58
39	COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific Data, 2020, 7, 188.	2.4	56
40	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. BMC Genomics, 2020, 21, 408.	1.2	65
41	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	1.8	47
42	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. Journal of Food Science, 2020, 85, 455-464.	1.5	72
43	Microbiota Characterization of Agricultural Green Waste-Based Suppressive Composts Using Omics and Classic Approaches. Agriculture (Switzerland), 2020, 10, 61.	1.4	21
44	The thrombospondin module 1 domain of the matricellular protein CCN3 shows an atypical disulfide pattern and incomplete CWR layers. Acta Crystallographica Section D: Structural Biology, 2020, 76, 124-134.	1.1	5
45	3DPatch: fast 3D structure visualization with residue conservation. Bioinformatics, 2019, 35, 332-334.	1.8	2
46	Origins of peptidases. Biochimie, 2019, 166, 4-18.	1.3	30
47	The EMBL-EBI search and sequence analysis tools APIs in 2019. Nucleic Acids Research, 2019, 47, W636-W641.	6.5	3,820
48	Tandem domain swapping: determinants of multidomain protein misfolding. Current Opinion in Structural Biology, 2019, 58, 97-104.	2.6	28
49	Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. Nucleic Acids Research, 2019, 47, 10994-11006.	6.5	236
50	Toward unrestricted use of public genomic data. Science, 2019, 363, 350-352.	6.0	45
51	Microbial community drivers of PK/NRP gene diversity in selected global soils. Microbiome, 2019, 7, 78.	4.9	30
52	Microbial abundance, activity and population genomic profiling with mOTUs2. Nature Communications, 2019, 10, 1014.	5.8	298
53	A new genomic blueprint of the human gut microbiota. Nature, 2019, 568, 499-504.	13.7	901
54	Defining the remarkable structural malleability of a bacterial surface protein Rib domain implicated in infection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26540-26548.	3.3	15

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55	Solution structure of human myeloid-derived growth factor suggests a conserved function in the endoplasmic reticulum. Nature Communications, 2019, 10, 5612.	5.8	15
56	TADOSS: computational estimation of tandem domain swap stability. Bioinformatics, 2019, 35, 2507-2508.	1.8	6
57	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	6.5	153
58	The Pfam protein families database in 2019. Nucleic Acids Research, 2019, 47, D427-D432.	6.5	3,937
59	Genome properties in 2019: a new companion database to InterPro for the inference of complete functional attributes. Nucleic Acids Research, 2019, 47, D564-D572.	6.5	27
60	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. Nucleic Acids Research, 2019, 47, D351-D360.	6.5	1,291
61	The Human RNA-Binding Proteome and Its Dynamics during Translational Arrest. Cell, 2019, 176, 391-403.e19.	13.5	289
62	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. Bioinformatics, 2019, 35, 518-520.	1.8	22
63	A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature Biotechnology, 2019, 37, 186-192.	9.4	420
64	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. PeerJ, 2019, 7, e6160.	0.9	34
65	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	6.5	489
66	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. Nucleic Acids Research, 2018, 46, D335-D342.	6.5	819
67	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. Nucleic Acids Research, 2018, 46, D726-D735.	6.5	175
68	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. Nucleic Acids Research, 2018, 46, D624-D632.	6.5	1,234
69	Eleven quick tips to build a usable REST API for life sciences. PLoS Computational Biology, 2018, 14, e1006542.	1.5	18
70	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. GigaScience, 2018, 7, .	3.3	95
71	Nonâ€Coding RNA Analysis Using the Rfam Database. Current Protocols in Bioinformatics, 2018, 62, e51.	25.8	309
72	HMMER web server: 2018 update. Nucleic Acids Research, 2018, 46, W200-W204.	6.5	1,432

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73	Gene Unprediction with Spurio: A tool to identify spurious protein sequences. F1000Research, 2018, 7, 261.	0.8	11
74	Rapid identification of novel protein families using similarity searches. F1000Research, 2018, 7, 1975.	0.8	1
75	Structure of the *Escherichia coli* ProQ RNA-binding protein. Rna, 2017, 23, 696-711.	1.6	50
76	InterPro in 2017—beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	6.5	1,358
77	Eros is a novel transmembrane protein that controls the phagocyte respiratory burst and is essential for innate immunity. Journal of Experimental Medicine, 2017, 214, 1111-1128.	4.2	50
78	The yeast noncoding RNA interaction network. Rna, 2017, 23, 1479-1492.	1.6	25
79	The HMMER Web Server for Protein Sequence Similarity Search. Current Protocols in Bioinformatics, 2017, 60, 3.15.1-3.15.23.	25.8	119
80	The metagenomic data life-cycle: standards and best practices. GigaScience, 2017, 6, 1-11.	3.3	42
81	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	6.5	174
82	On expert curation and scalability: UniProtKB/Swiss-Prot as a case study. Bioinformatics, 2017, 33, 3454-3460.	1.8	91
83	ELIXIR pilot action: Marine metagenomics — towards a domain specific set of sustainable services. F1000Research, 2017, 6, 70.	0.8	8
84	Patterns of database citation in articles and patents indicate long-term scientific and industry value of biological data resources. F1000Research, 2016, 5, 160.	0.8	16
85	EBI metagenomics in 2016 - an expanding and evolving resource for the analysis and archiving of metagenomic data. Nucleic Acids Research, 2016, 44, D595-D603.	6.5	97
86	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw027.	1.4	19
87	The Dfam database of repetitive DNA families. Nucleic Acids Research, 2016, 44, D81-D89.	6.5	543
88	UniProt-DAAC: domain architecture alignment and classification, a new method for automatic functional annotation in UniProtKB. Bioinformatics, 2016, 32, 2264-2271.	1.8	37
89	Twenty years of the *MEROPS* database of proteolytic enzymes, their substrates and inhibitors. Nucleic Acids Research, 2016, 44, D343-D350.	6.5	648
90	The European Bioinformatics Institute in 2016: Data growth and integration. Nucleic Acids Research, 2016, 44, D20-D26.	6.5	108

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91	The Pfam protein families database: towards a more sustainable future. Nucleic Acids Research, 2016, 44, D279-D285.	6.5	5,391
92	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. Nucleic Acids Research, 2016, 44, D604-D609.	6.5	60
93	Cache Domains That are Homologous to, but Different from PAS Domains Comprise the Largest Superfamily of Extracellular Sensors in Prokaryotes. PLoS Computational Biology, 2016, 12, e1004862.	1.5	147
94	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063.	1.4	8
95	HMMER web server: 2015 update. Nucleic Acids Research, 2015, 43, W30-W38.	6.5	849
96	The InterPro protein families database: the classification resource after 15 years. Nucleic Acids Research, 2015, 43, D213-D221.	6.5	1,205
97	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. Briefings in Bioinformatics, 2015, 16, 865-872.	3.2	6
98	Domain atrophy creates rare cases of functional partial protein domains. Genome Biology, 2015, 16, 88.	3.8	23
99	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	1.5	13
100	RNAcentral: an international database of ncRNA sequences. Nucleic Acids Research, 2015, 43, D123-D129.	6.5	103
101	Rfam 12.0: updates to the RNA families database. Nucleic Acids Research, 2015, 43, D130-D137.	6.5	1,000
102	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. Nucleic Acids Research, 2014, 42, D364-D373.	6.5	156
103	Using the MEROPS Database for Proteolytic Enzymes and Their Inhibitors and Substrates. Current Protocols in Bioinformatics, 2014, 48, 1.25.1-33.	25.8	39
104	TreeFam v9: a new website, more species and orthology-on-the-fly. Nucleic Acids Research, 2014, 42, D922-D925.	6.5	125
105	Pfam: the protein families database. Nucleic Acids Research, 2014, 42, D222-D230.	6.5	5,425
106	Skylign: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models. BMC Bioinformatics, 2014, 15, 7.	1.2	298
107	Structure and computational analysis of a novel protein with metallopeptidase-like and circularly permuted winged-helix-turn-helix domains reveals a possible role in modified polysaccharide biosynthesis. BMC Bioinformatics, 2014, 15, 75.	1.2	1
108	<i>MEROPS</i>: the database of proteolytic enzymes, their substrates and inhibitors. Nucleic Acids Research, 2014, 42, D503-D509.	6.5	782

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109	Two Pfam protein families characterized by a crystal structure of protein lpg2210 from Legionella pneumophila. BMC Bioinformatics, 2013, 14, 265.	1.2	3
110	Alternative splicing of intrinsically disordered regions and rewiring of protein interactions. Current Opinion in Structural Biology, 2013, 23, 443-450.	2.6	166
111	Filling out the structural map of the NTF2-like superfamily. BMC Bioinformatics, 2013, 14, 327.	1.2	74
112	LUD, a new protein domain associated with lactate utilization. BMC Bioinformatics, 2013, 14, 341.	1.2	8
113	ISCB Computational Biology Wikipedia Competition. PLoS Computational Biology, 2013, 9, e1003242.	1.5	8
114	Rfam 11.0: 10 years of RNA families. Nucleic Acids Research, 2013, 41, D226-D232.	6.5	745
115	A comparison of dense transposon insertion libraries in the Salmonella serovars Typhi and Typhimurium. Nucleic Acids Research, 2013, 41, 4549-4564.	6.5	108
116	The challenge of increasing Pfam coverage of the human proteome. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat023.	1.4	22
117	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. Nucleic Acids Research, 2013, 41, e121-e121.	6.5	1,214
118	The first structure in a family of peptidase inhibitors reveals an unusual Ig-like fold. F1000Research, 2013, 2, 154.	0.8	2
119	The SHOCT Domain: A Widespread Domain Under-Represented in Model Organisms. PLoS ONE, 2013, 8, e57848.	1.1	6
120	Biocurators and Biocuration: surveying the 21st century challenges. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar059-bar059.	1.4	59
121	AntiFam: a tool to help identify spurious ORFs in protein annotation. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas003-bas003.	1.4	38
122	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	6.5	3,306
123	Making your database available through Wikipedia: the pros and cons. Nucleic Acids Research, 2012, 40, D9-D12.	6.5	31
124	InterPro in 2011: new developments in the family and domain prediction database. Nucleic Acids Research, 2012, 40, D306-D312.	6.5	921
125	Dfam: a database of repetitive DNA based on profile hidden Markov models. Nucleic Acids Research, 2012, 41, D70-D82.	6.5	243
126	The YARHG Domain: An Extracellular Domain in Search of a Function. PLoS ONE, 2012, 7, e35575.	1.1	3

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127	HMMER web server: interactive sequence similarity searching. Nucleic Acids Research, 2011, 39, W29-W37.	6.5	4,492
128	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	1.4	30
129	RNIE: genome-wide prediction of bacterial intrinsic terminators. Nucleic Acids Research, 2011, 39, 5845-5852.	6.5	71
130	Rfam: Wikipedia, clans and the "decimal" release. Nucleic Acids Research, 2011, 39, D141-D145.	6.5	355
131	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	6.5	32
132	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
133	Asparagine Peptide Lyases. Journal of Biological Chemistry, 2011, 286, 38321-38328.	1.6	89
134	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. PLoS ONE, 2011, 6, e18910.	1.1	94
135	Clustered Coding Variants in the Glutamate Receptor Complexes of Individuals with Schizophrenia and Bipolar Disorder. PLoS ONE, 2011, 6, e19011.	1.1	54
136	The structure of Jann_2411 (DUF1470) from<i>Jannaschia</i>sp. at 1.45â€¦Ã… resolution reveals a new fold (the ABATE domain) and suggests its possible role as a transcription regulator. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1198-1204.	0.7	9
137	The structure of BVU2987 fromBacteroides vulgatusreveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1265-1273.	0.7	8
138	DUFs: families in search of function. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1148-1152.	0.7	203
139	The crystal structure of a bacterial Sufuâ€‹like protein defines a novel group of bacterial proteins that are similar to the Nâ€‹terminal domain of human Sufu. Protein Science, 2010, 19, 2131-2140.	3.1	12
140	MEROPS: the peptidase database. Nucleic Acids Research, 2010, 38, D227-D233.	6.5	786
141	Ten Simple Rules for Editing Wikipedia. PLoS Computational Biology, 2010, 6, e1000941.	1.5	36
142	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. Journal of Molecular Biology, 2010, 396, 31-46.	2.0	32
143	The Systematic Functional Analysis of Plasmodium Protein Kinases Identifies Essential Regulators of Mosquito Transmission. Cell Host and Microbe, 2010, 8, 377-387.	5.1	267
144	Quantifying the mechanisms of domain gain in animal proteins. Genome Biology, 2010, 11, R74.	13.9	93

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145	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	6.5	2,693
146	DASMI: exchanging, annotating and assessing molecular interaction data. Bioinformatics, 2009, 25, 1321-1328.	1.8	15
147	Phospholipid scramblases and Tubby-like proteins belong to a new superfamily of membrane tethered transcription factors. Bioinformatics, 2009, 25, 159-162.	1.8	59
148	InterPro: the integrative protein signature database. Nucleic Acids Research, 2009, 37, D211-D215.	6.5	1,712
149	Rfam: updates to the RNA families database. Nucleic Acids Research, 2009, 37, D136-D140.	6.5	820
150	The structure of pyogenecin immunity protein, a novel bacteriocin-like immunity protein from Streptococcus pyogenes. BMC Structural Biology, 2009, 9, 75.	2.3	6
151	The evolution of protein domain families. Biochemical Society Transactions, 2009, 37, 751-755.	1.6	106
152	Integrating biological data â€" the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	1.2	87
153	Protein interactions in human genetic diseases. Genome Biology, 2008, 9, R9.	13.9	110
154	Modifier Effects between Regulatory and Protein-Coding Variation. PLoS Genetics, 2008, 4, e1000244.	1.5	33
155	Experience using web services for biological sequence analysis. Briefings in Bioinformatics, 2008, 9, 493-505.	3.2	24
156	Pfam 10 years on: 10 000 families and still growing. Briefings in Bioinformatics, 2008, 9, 210-219.	3.2	114
157	The RNA WikiProject: Community annotation of RNA families. Rna, 2008, 14, 2462-2464.	1.6	66
158	Identifying Protein Domains with the Pfam Database. Current Protocols in Bioinformatics, 2008, 23, Unit 2.5.	25.8	61
159	New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228.	6.5	444
160	ProServer: a simple, extensible Perl DAS server. Bioinformatics, 2007, 23, 1568-1570.	1.8	34
161	SCOOP: a simple method for identification of novel protein superfamily relationships. Bioinformatics, 2007, 23, 809-814.	1.8	49
162	The Pfam protein families database. Nucleic Acids Research, 2007, 36, D281-D288.	6.5	6,372

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163	Reuse of structural domain–domain interactions in protein networks. BMC Bioinformatics, 2007, 8, 259.	1.2	44
164	Predicting active site residue annotations in the Pfam database. BMC Bioinformatics, 2007, 8, 298.	1.2	239
165	Integrating sequence and structural biology with DAS. BMC Bioinformatics, 2007, 8, 333.	1.2	68
166	Pfam. Methods in Molecular Biology, 2007, 396, 43-58.	0.4	38
167	Pfam: clans, web tools and services. Nucleic Acids Research, 2006, 34, D247-D251.	6.5	2,030
168	Pfam: the protein families database. , 2005, , .		12
169	Visualizing profile-profile alignment: pairwise HMM logos. Bioinformatics, 2005, 21, 2912-2913.	1.8	35
170	iPfam: visualization of protein-protein interactions in PDB at domain and amino acid resolutions. Bioinformatics, 2005, 21, 410-412.	1.8	295
171	The G5 domain: a potential N-acetylglucosamine recognition domain involved in biofilm formation. Bioinformatics, 2005, 21, 1301-1303.	1.8	78
172	Conformational Changes of Escherichia coli σ54-RNA-Polymerase upon Closed–Promoter Complex Formation. Journal of Molecular Biology, 2005, 354, 201-205.	2.0	4
173	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	6.5	478
174	Novel protein domains and motifs in the marine planctomycete Rhodopirellula baltica. FEMS Microbiology Letters, 2004, 236, 333-340.	0.7	25
175	The PepSY domain: a regulator of peptidase activity in the microbial environment?. Trends in Biochemical Sciences, 2004, 29, 169-172.	3.7	68
176	The Hotdog fold: wrapping up a superfamily of thioesterases and dehydratases. BMC Bioinformatics, 2004, 5, 109.	1.2	158
177	Enhanced protein domain discovery using taxonomy. BMC Bioinformatics, 2004, 5, 56.	1.2	18
178	Rfam: annotating non-coding RNAs in complete genomes. Nucleic Acids Research, 2004, 33, D121-D124.	6.5	1,255
179	The Pfam protein families database. Nucleic Acids Research, 2004, 32, 138D-141.	6.5	3,084
180	New knowledge from old: in silico discovery of novel protein domains in Streptomyces coelicolor. BMC Microbiology, 2003, 3, 3.	1.3	98

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181	Identifying Protein Domains with the Pfam Database. Current Protocols in Bioinformatics, 2003, 1, 2.5.1-2.5.19.	25.8	20
182	Rfam: an RNA family database. Nucleic Acids Research, 2003, 31, 439-441.	6.5	1,296
183	Enhanced protein domain discovery by using language modeling techniques from speech recognition. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4516-4520.	3.3	47
184	Determination of Escherichia coli RNA Polymerase Structure by Single Particle Cryoelectron Microscopy. Methods in Enzymology, 2003, 370, 24-42.	0.4	4
185	QuickTree: building huge Neighbour-Joining trees of protein sequences. Bioinformatics, 2002, 18, 1546-1547.	1.8	249
186	The Pfam Protein Families Database. Nucleic Acids Research, 2002, 30, 276-280.	6.5	2,067
187	The PASTA domain: a Î²-lactam-binding domain. Trends in Biochemical Sciences, 2002, 27, 438-440.	3.7	204
188	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
189	Single-particle electron cryo-microscopy: towards atomic resolution. Quarterly Reviews of Biophysics, 2000, 33, 307-369.	2.4	535
190	Escherichia coli RNA polymerase core and holoenzyme structures. EMBO Journal, 2000, 19, 6833-6844.	3.5	35
191	The Pfam Protein Families Database. Nucleic Acids Research, 2000, 28, 263-266.	6.5	1,173
192	The C-Terminal 12 Amino Acids of Ï„N Are Required for Structure and Function. Archives of Biochemistry and Biophysics, 1999, 371, 234-240.	1.4	3
193	Structure and distribution of pentapeptide repeats in bacteria. Protein Science, 1998, 7, 1477-1480.	3.1	87
194	A member of the immunoglobulin superfamily in bacteriophage T4. Virus Genes, 1997, 14, 163-165.	0.7	28
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