

Robert D Finn

List of Publications by Year in descending order

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Version: 2024-02-01

103
papers

68,239
citations

19608

61
h-index

30010

103
g-index

110
all docs

110
docs citations

110
times ranked

76123
citing authors

#	ARTICLE	IF	CITATIONS
1	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2007, 36, D281-D288.	6.5	6,372
2	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014, 42, D222-D230.	6.5	5,425
3	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016, 44, D279-D285.	6.5	5,391
4	HMMER web server: interactive sequence similarity searching. <i>Nucleic Acids Research</i> , 2011, 39, W29-W37.	6.5	4,492
5	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019, 47, D427-D432.	6.5	3,937
6	The EMBL-EBI search and sequence analysis tools APIs in 2019. <i>Nucleic Acids Research</i> , 2019, 47, W636-W641.	6.5	3,820
7	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012, 40, D290-D301.	6.5	3,306
8	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004, 32, 138D-141.	6.5	3,084
9	Pfam: The protein families database in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D412-D419.	6.5	3,068
10	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010, 38, D211-D222.	6.5	2,693
11	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006, 34, D247-D251.	6.5	2,030
12	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
13	HMMER web server: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, W200-W204.	6.5	1,432
14	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	6.5	1,385
15	InterPro in 2017—beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
16	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
17	The MEROPS database of proteolytic enzymes, their substrates and inhibitors in 2017 and a comparison with peptidases in the PANTHER database. <i>Nucleic Acids Research</i> , 2018, 46, D624-D632.	6.5	1,234
18	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013, 41, e121-e121.	6.5	1,214

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19	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	6.5	1,205
20	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	6.5	1,000
21	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
22	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019, 568, 499-504.	13.7	901
23	HMMER web server: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, W30-W38.	6.5	849
24	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. <i>Nucleic Acids Research</i> , 2018, 46, D335-D342.	6.5	819
25	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021, 39, 105-114.	9.4	628
26	The Dfam database of repetitive DNA families. <i>Nucleic Acids Research</i> , 2016, 44, D81-D89.	6.5	543
27	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	6.5	489
28	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	6.5	475
29	A human gut bacterial genome and culture collection for improved metagenomic analyses. <i>Nature Biotechnology</i> , 2019, 37, 186-192.	9.4	420
30	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145.	6.5	355
31	Massive expansion of human gut bacteriophage diversity. <i>Cell</i> , 2021, 184, 1098-1109.e9.	13.5	331
32	Non-coding RNA Analysis Using the Rfam Database. <i>Current Protocols in Bioinformatics</i> , 2018, 62, e51.	25.8	309
33	Skyline: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models. <i>BMC Bioinformatics</i> , 2014, 15, 7.	1.2	298
34	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019, 10, 1014.	5.8	298
35	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D570-D578.	6.5	296
36	iPFam: visualization of protein-protein interactions in PDB at domain and amino acid resolutions. <i>Bioinformatics</i> , 2005, 21, 410-412.	1.8	295

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37	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , 2012, 41, D70-D82.	6.5	243
38	Predicting active site residue annotations in the Pfam database. <i>BMC Bioinformatics</i> , 2007, 8, 298.	1.2	239
39	DUFs: families in search of function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1148-1152.	0.7	203
40	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. <i>Nucleic Acids Research</i> , 2018, 46, D726-D735.	6.5	175
41	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
42	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021, 27, 1885-1892.	15.2	170
43	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	6.5	160
44	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. <i>Nucleic Acids Research</i> , 2014, 42, D364-D373.	6.5	156
45	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
46	Cache Domains That are Homologous to, but Different from PAS Domains Comprise the Largest Superfamily of Extracellular Sensors in Prokaryotes. <i>PLoS Computational Biology</i> , 2016, 12, e1004862.	1.5	147
47	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2022, 50, D996-D1003.	6.5	141
48	The HMMER Web Server for Protein Sequence Similarity Search. <i>Current Protocols in Bioinformatics</i> , 2017, 60, 3.15.1-3.15.23.	25.8	119
49	Pfam 10 years on: 10 000 families and still growing. <i>Briefings in Bioinformatics</i> , 2008, 9, 210-219.	3.2	114
50	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	3.2	110
51	The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , 2016, 44, D20-D26.	6.5	108
52	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015, 43, D123-D129.	6.5	103
53	EBI metagenomics in 2016 - an expanding and evolving resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2016, 44, D595-D603.	6.5	97
54	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. <i>GigaScience</i> , 2018, 7, .	3.3	95

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55	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. PLoS ONE, 2011, 6, e18910.	1.1	94
56	Integrating biological data into the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	1.2	87
57	Defining the in Vivo Role for Cytochrome b5 in Cytochrome P450 Function through the Conditional Hepatic Deletion of Microsomal Cytochrome b5. Journal of Biological Chemistry, 2008, 283, 31385-31393.	1.6	75
58	Unsaturated fatty acid regulation of cytochrome P450 expression via a CAR-dependent pathway. Biochemical Journal, 2009, 417, 43-58.	1.7	74
59	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. Journal of Food Science, 2020, 85, 455-464.	1.5	72
60	A catalogue of 1,167 genomes from the human gut archaeome. Nature Microbiology, 2022, 7, 48-61.	5.9	72
61	Integrating sequence and structural biology with DAS. BMC Bioinformatics, 2007, 8, 333.	1.2	68
62	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. BMC Genomics, 2020, 21, 408.	1.2	65
63	Deletion of Microsomal Cytochrome b5 Profoundly Affects Hepatic and Extrahepatic Drug Metabolism. Molecular Pharmacology, 2010, 78, 269-278.	1.0	64
64	Identifying Protein Domains with the Pfam Database. Current Protocols in Bioinformatics, 2008, 23, Unit 2.5.	25.8	61
65	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. Nucleic Acids Research, 2016, 44, D604-D609.	6.5	60
66	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. Genome Biology, 2020, 21, 244.	3.8	58
67	R2DT is a framework for predicting and visualising RNA secondary structure using templates. Nature Communications, 2021, 12, 3494.	5.8	58
68	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions. Nature Microbiology, 2022, 7, 169-179.	5.9	58
69	COVID-19 pandemic reveals the peril of ignoring metadata standards. Scientific Data, 2020, 7, 188.	2.4	56
70	SCOOP: a simple method for identification of novel protein superfamily relationships. Bioinformatics, 2007, 23, 809-814.	1.8	49
71	The metagenomic data life-cycle: standards and best practices. GigaScience, 2017, 6, 1-11.	3.3	42
72	Unifying the known and unknown microbial coding sequence space. ELife, 2022, 11, .	2.8	41

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73	Conditional Deletion of Cytochrome P450 Oxidoreductase in the Liver and Gastrointestinal Tract: A New Model for Studying the Functions of the P450 System. <i>Journal of Pharmacology and Experimental Therapeutics</i> , 2007, 322, 40-47.	1.3	35
74	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019, 7, e6160.	0.9	34
75	Modifier Effects between Regulatory and Protein-Coding Variation. <i>PLoS Genetics</i> , 2008, 4, e1000244.	1.5	33
76	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. <i>Journal of Molecular Biology</i> , 2010, 396, 31-46.	2.0	32
77	Making your database available through Wikipedia: the pros and cons. <i>Nucleic Acids Research</i> , 2012, 40, D9-D12.	6.5	31
78	Microbial community drivers of PK/NRP gene diversity in selected global soils. <i>Microbiome</i> , 2019, 7, 78.	4.9	30
79	Genome properties in 2019: a new companion database to InterPro for the inference of complete functional attributes. <i>Nucleic Acids Research</i> , 2019, 47, D564-D572.	6.5	27
80	Cytochrome b 5 null mouse: a new model for studying inherited skin disorders and the role of unsaturated fatty acids in normal homeostasis. <i>Transgenic Research</i> , 2011, 20, 491-502.	1.3	25
81	Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. <i>Nature Protocols</i> , 2021, 16, 2520-2541.	5.5	25
82	Experience using web services for biological sequence analysis. <i>Briefings in Bioinformatics</i> , 2008, 9, 493-505.	3.2	24
83	The challenge of increasing Pfam coverage of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat023.	1.4	22
84	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. <i>Bioinformatics</i> , 2019, 35, 518-520.	1.8	22
85	GO annotation in InterPro: why stability does not indicate accuracy in a sea of changing annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw027.	1.4	19
86	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	19
87	Eleven quick tips to build a usable REST API for life sciences. <i>PLoS Computational Biology</i> , 2018, 14, e1006542.	1.5	18
88	ELIXIRâ€œEXCELERATE: establishing Europe's data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021, 40, e107409.	3.5	18
89	A Vaccinology Approach to the Identification and Characterization of <i>Dermanyssus gallinae</i> Candidate Protective Antigens for the Control of Poultry Red Mite Infestations. <i>Vaccines</i> , 2019, 7, 190.	2.1	17
90	An inter-laboratory study to investigate the impact of the bioinformatics component on microbiome analysis using mock communities. <i>Scientific Reports</i> , 2021, 11, 10590.	1.6	17

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91	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	1.5	13
92	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020, 48, D314-D319.	6.5	13
93	The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. <i>Protein Science</i> , 2010, 19, 2131-2140.	3.1	12
94	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770.	6.5	10
95	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	1.4	8
96	ELIXIR pilot action: Marine metagenomics – towards a domain specific set of sustainable services. <i>F1000Research</i> , 2017, 6, 70.	0.8	8
97	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015, 16, 865-872.	3.2	6
98	Exploring Non-Coding RNAs in RNACentral. <i>Current Protocols in Bioinformatics</i> , 2020, 71, e104.	25.8	6
99	Determination of Escherichia coli RNA Polymerase Structure by Single Particle Cryoelectron Microscopy. <i>Methods in Enzymology</i> , 2003, 370, 24-42.	0.4	4
100	Conformational Changes of Escherichia coli σ 54-RNA-Polymerase upon Closed Promoter Complex Formation. <i>Journal of Molecular Biology</i> , 2005, 354, 201-205.	2.0	4
101	Metagenomics approach for Polymyxa betae genome assembly enables comparative analysis towards deciphering the intracellular parasitic lifestyle of the plasmodiophorids. <i>Genomics</i> , 2022, 114, 9-22.	1.3	4
102	3DPatch: fast 3D structure visualization with residue conservation. <i>Bioinformatics</i> , 2019, 35, 332-334.	1.8	2
103	A Comprehensive Analysis of the Global Human Gut Archaeome from a Thousand Genome Catalogue. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0