

Robert D Finn

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.

105
papers

41,925
citations

56
h-index

110
g-index

110
ext. papers

56,231
ext. citations

15.2
avg, IF

7.5
L-index

#	Paper	IF	Citations
105	Unifying the known and unknown microbial coding sequence space.. <i>ELife</i> , 2022 , 11,	8.9	4
104	A catalogue of 1,167 genomes from the human gut archaeome.. <i>Nature Microbiology</i> , 2021 ,	26.6	9
103	Metagenomics approach for <i>Polymyxa betae</i> genome assembly enables comparative analysis towards deciphering the intracellular parasitic lifestyle of the plasmodiophorids. <i>Genomics</i> , 2021 , 114, 9-22	4.3	0
102	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2021 ,	20.1	12
101	Reporting guidelines for human microbiome research: the STORMS checklist. <i>Nature Medicine</i> , 2021 , 27, 1885-1892	50.5	19
100	Predicted Input of Uncultured Fungal Symbionts to a Lichen Symbiosis from Metagenome-Assembled Genomes. <i>Genome Biology and Evolution</i> , 2021 , 13,	3.9	8
99	Recovering prokaryotic genomes from host-associated, short-read shotgun metagenomic sequencing data. <i>Nature Protocols</i> , 2021 , 16, 2520-2541	18.8	2
98	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	4.9	3
97	R2DT is a framework for predicting and visualising RNA secondary structure using templates. <i>Nature Communications</i> , 2021 , 12, 3494	17.4	16
96	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	13.4	56
95	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021 , 49, D344-D354	10.1	358
94	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021 , 49, D212-D220	20.1	42
93	A unified catalog of 204,938 reference genomes from the human gut microbiome. <i>Nature Biotechnology</i> , 2021 , 39, 105-114	44.5	185
92	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021 , 49, D192-D200	20.1	108
91	Pfam: The protein families database in 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D412-D419	20.1	620
90	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
89	Massive expansion of human gut bacteriophage diversity. <i>Cell</i> , 2021 , 184, 1098-1109.e9	56.2	93

88	ELIXIR-EXCELERATE: establishing Europe-wide data infrastructure for the life science research of the future. <i>EMBO Journal</i> , 2021 , 40, e107409	13	11
87	Integrating cultivation and metagenomics for a multi-kingdom view of skin microbiome diversity and functions.. <i>Nature Microbiology</i> , 2021 ,	26.6	6
86	COVID-19 pandemic reveals the peril of ignoring metadata standards. <i>Scientific Data</i> , 2020 , 7, 188	8.2	30
85	Phylogenomics of expanding uncultured environmental Tenericutes provides insights into their pathogenicity and evolutionary relationship with Bacilli. <i>BMC Genomics</i> , 2020 , 21, 408	4.5	19
84	Microbial composition of Kombucha determined using amplicon sequencing and shotgun metagenomics. <i>Journal of Food Science</i> , 2020 , 85, 455-464	3.4	28
83	MGnify: the microbiome analysis resource in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D570-D578	20.1	127
82	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	20.1	7
81	Exploring Non-Coding RNAs in RNAcentral. <i>Current Protocols in Bioinformatics</i> , 2020 , 71, e104	24.2	3
80	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis with EukCC. <i>Genome Biology</i> , 2020 , 21, 244	18.3	19
79	Microbial community drivers of PK/NRP gene diversity in selected global soils. <i>Microbiome</i> , 2019 , 7, 78	16.6	15
78	Microbial abundance, activity and population genomic profiling with mOTUs2. <i>Nature Communications</i> , 2019 , 10, 1014	17.4	134
77	A new genomic blueprint of the human gut microbiota. <i>Nature</i> , 2019 , 568, 499-504	50.4	484
76	3DPatch: fast 3D structure visualization with residue conservation. <i>Bioinformatics</i> , 2019 , 35, 332-334	7.2	2
75	The EMBL-EBI search and sequence analysis tools APIs in 2019. <i>Nucleic Acids Research</i> , 2019 , 47, W636-W641	26.1	2132
74	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019 , 7, e6160	3.1	22
73	A human gut bacterial genome and culture collection for improved metagenomic analyses. <i>Nature Biotechnology</i> , 2019 , 37, 186-192	44.5	224
72	A vaccinology Approach to the Identification and Characterization of Candidate Protective Antigens for the Control of Poultry Red Mite Infestations. <i>Vaccines</i> , 2019 , 7,	5.3	9
71	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019 , 47, D221-D229	10.2	90

70	The Pfam protein families database in 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D427-D432	20.1	2298
69	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	20.1	15
68	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019 , 47, D351-D360	20.1	835
67	TreeGrafter: phylogenetic tree-based annotation of proteins with Gene Ontology terms and other annotations. <i>Bioinformatics</i> , 2019 , 35, 518-520	7.2	12
66	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018 , 46, D802-D808	20.1	330
65	Rfam 13.0: shifting to a genome-centric resource for non-coding RNA families. <i>Nucleic Acids Research</i> , 2018 , 46, D335-D342	20.1	533
64	EBI Metagenomics in 2017: enriching the analysis of microbial communities, from sequence reads to assemblies. <i>Nucleic Acids Research</i> , 2018 , 46, D726-D735	20.1	130
63	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	20.1	643
62	Non-Coding RNA Analysis Using the Rfam Database. <i>Current Protocols in Bioinformatics</i> , 2018 , 62, e51	24.2	152
61	HMMER web server: 2018 update. <i>Nucleic Acids Research</i> , 2018 , 46, W200-W204	20.1	596
60	Eleven quick tips to build a usable REST API for life sciences. <i>PLoS Computational Biology</i> , 2018 , 14, e1006542		7
59	Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. <i>GigaScience</i> , 2018 , 7,	7.6	61
58	InterPro in 2017-beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017 , 45, D190-D199	20.1	970
57	The HMMER Web Server for Protein Sequence Similarity Search. <i>Current Protocols in Bioinformatics</i> , 2017 , 60, 3.15.1-3.15.23	24.2	49
56	The metagenomic data life-cycle: standards and best practices. <i>GigaScience</i> , 2017 , 6, 1-11	7.6	29
55	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017 , 45, D128-D134	20.1	119
54	ELIXIR pilot action: Marine metagenomics - towards a domain specific set of sustainable services. <i>F1000Research</i> , 2017 , 6,	3.6	6
53	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,	5	16

52	The Dfam database of repetitive DNA families. <i>Nucleic Acids Research</i> , 2016 , 44, D81-9	20.1	295
51	The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , 2016 , 44, D20-6	20.1	91
50	The Pfam protein families database: towards a more sustainable future. <i>Nucleic Acids Research</i> , 2016 , 44, D279-85	20.1	3678
49	HPMCD: the database of human microbial communities from metagenomic datasets and microbial reference genomes. <i>Nucleic Acids Research</i> , 2016 , 44, D604-9	20.1	50
48	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	5	95
47	EBI metagenomics in 2016--an expanding and evolving resource for the analysis and archiving of metagenomic data. <i>Nucleic Acids Research</i> , 2016 , 44, D595-603	20.1	81
46	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015 , 43, D213-21	20.1	954
45	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015 , 16, 865-72	13.4	5
44	RNAcentral: an international database of ncRNA sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D123-9	20.1	89
43	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015 , 43, D130-7	20.1	723
42	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav063	5	5
41	HMMER web server: 2015 update. <i>Nucleic Acids Research</i> , 2015 , 43, W30-8	20.1	590
40	iPfam: a database of protein family and domain interactions found in the Protein Data Bank. <i>Nucleic Acids Research</i> , 2014 , 42, D364-73	20.1	120
39	Pfam: the protein families database. <i>Nucleic Acids Research</i> , 2014 , 42, D222-30	20.1	3975
38	Skyglin: a tool for creating informative, interactive logos representing sequence alignments and profile hidden Markov models. <i>BMC Bioinformatics</i> , 2014 , 15, 7	3.6	196
37	Dfam: a database of repetitive DNA based on profile hidden Markov models. <i>Nucleic Acids Research</i> , 2013 , 41, D70-82	20.1	147
36	The challenge of increasing Pfam coverage of the human proteome. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat023	5	16
35	Challenges in homology search: HMMER3 and convergent evolution of coiled-coil regions. <i>Nucleic Acids Research</i> , 2013 , 41, e121	20.1	629

34	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2012 , 40, D290-301	20.1	2844
33	Making your database available through Wikipedia: the pros and cons. <i>Nucleic Acids Research</i> , 2012 , 40, D9-12	20.1	23
32	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012 , 40, D306-12	20.1	844
31	Cytochrome b5 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	3.3	24
30	HMMER web server: interactive sequence similarity searching. <i>Nucleic Acids Research</i> , 2011 , 39, W29-37	20.1	2917
29	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011 , 39, D141-5	20.1	321
28	Representative proteomes: a stable, scalable and unbiased proteome set for sequence analysis and functional annotation. <i>PLoS ONE</i> , 2011 , 6, e18910	3.7	67
27	Deletion of microsomal cytochrome b5 profoundly affects hepatic and extrahepatic drug metabolism. <i>Molecular Pharmacology</i> , 2010 , 78, 269-78	4.3	60
26	Bacterial pleckstrin homology domains: a prokaryotic origin for the PH domain. <i>Journal of Molecular Biology</i> , 2010 , 396, 31-46	6.5	25
25	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2010 , 38, D211-22	20.1	2467
24	DUFs: families in search of function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 1148-52		145
23	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, 2131-40	6.3	12
22	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009 , 37, D211-5	20.1	1379
21	Unsaturated fatty acid regulation of cytochrome P450 expression via a CAR-dependent pathway. <i>Biochemical Journal</i> , 2009 , 417, 43-54	3.8	61
20	Integrating biological data--the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 8, S3	3.6	77
19	Modifier effects between regulatory and protein-coding variation. <i>PLoS Genetics</i> , 2008 , 4, e1000244	6	30
18	Defining the in Vivo Role for cytochrome b5 in cytochrome P450 function through the conditional hepatic deletion of microsomal cytochrome b5. <i>Journal of Biological Chemistry</i> , 2008 , 283, 31385-93	5.4	69
17	Experience using web services for biological sequence analysis. <i>Briefings in Bioinformatics</i> , 2008 , 9, 493-505	3.4	22

16	Pfam 10 years on: 10,000 families and still growing. <i>Briefings in Bioinformatics</i> , 2008 , 9, 210-9	13.4	101
15	Identifying protein domains with the Pfam database. <i>Current Protocols in Bioinformatics</i> , 2008 , Chapter 2, Unit 2.5	24.2	43
14	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2008 , 36, D281-8	20.1	1806
13	Predicting active site residue annotations in the Pfam database. <i>BMC Bioinformatics</i> , 2007 , 8, 298	3.6	124
12	Integrating sequence and structural biology with DAS. <i>BMC Bioinformatics</i> , 2007 , 8, 333	3.6	57
11	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, 40-7	4.7	33
10	SCOOP: a simple method for identification of novel protein superfamily relationships. <i>Bioinformatics</i> , 2007 , 23, 809-14	7.2	36
9	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
8	Conformational changes of Escherichia coli sigma54-RNA-polymerase upon closed-promoter complex formation. <i>Journal of Molecular Biology</i> , 2005 , 354, 201-5	6.5	4
7	iPfam: visualization of protein-protein interactions in PDB at domain and amino acid resolutions. <i>Bioinformatics</i> , 2005 , 21, 410-2	7.2	263
6	The Pfam protein families database. <i>Nucleic Acids Research</i> , 2004 , 32, D138-41	20.1	2720
5	Determination of Escherichia coli RNA polymerase structure by single particle cryoelectron microscopy. <i>Methods in Enzymology</i> , 2003 , 370, 24-42	1.7	4
4	Estimating the quality of eukaryotic genomes recovered from metagenomic analysis		3
3	Unifying the known and unknown microbial coding sequence space		9
2	R2DT: computational framework for template-based RNA secondary structure visualisation across non-coding RNA types		3
1	A unified sequence catalogue of over 280,000 genomes obtained from the human gut microbiome		14