

Iddo Friedberg

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.

59
papers

6,913
citations

27
h-index

76
g-index

76
ext. papers

8,817
ext. citations

8.7
avg, IF

5.48
L-index

#	Paper	IF	Citations
59	Vertical transmission of attaching and invasive <i>E. coli</i> from the dam to neonatal mice predisposes to more severe colitis following exposure to a colitic insult later in life.. <i>PLoS ONE</i> , 2022 , 17, e0266005	3.7	0
58	Crowdsourcing biocuration: The Community Assessment of Community Annotation with Ontologies (CACAO). <i>PLoS Computational Biology</i> , 2021 , 17, e1009463	5	3
57	Deploying MMEJ using MENdel in precision gene editing applications for gene therapy and functional genomics. <i>Nucleic Acids Research</i> , 2021 , 49, 67-78	20.1	0
56	Unraveling a Tangled Skein: Evolutionary Analysis of the Bacterial Gibberellin Biosynthetic Operon. <i>MSphere</i> , 2020 , 5,	5	4
55	Finding orthologous gene blocks in bacteria: the computational hardness of the problem and novel methods to address it. <i>Bioinformatics</i> , 2020 , 36, i668-i674	7.2	
54	Novel antimicrobial peptide discovery using machine learning and biophysical selection of minimal bacteriocin domains. <i>Drug Development Research</i> , 2020 , 81, 43-51	5.1	12
53	Tracing the ancestry of operons in bacteria. <i>Bioinformatics</i> , 2019 , 35, 2998-3004	7.2	3
52	MaizeDIG: Maize Database of Images and Genomes. <i>Frontiers in Plant Science</i> , 2019 , 10, 1050	6.2	3
51	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. <i>Human Mutation</i> , 2019 , 40, 1530-1545	4.7	3
50	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. <i>Cell Systems</i> , 2019 , 9, 600-608.e4	10.6	26
49	SwiftOrtho: A fast, memory-efficient, multiple genome orthology classifier. <i>GigaScience</i> , 2019 , 8,	7.6	13
48	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019 , 20, 244	18.3	111
47	Expanding the CRISPR Toolbox with ErCas12a in Zebrafish and Human Cells. <i>CRISPR Journal</i> , 2019 , 2, 417-433	2.5	13
46	New Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 251-267	3.2	11
45	Identifying antimicrobial peptides using word embedding with deep recurrent neural networks. <i>Bioinformatics</i> , 2019 , 35, 2009-2016	7.2	43
44	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. <i>PLoS Computational Biology</i> , 2018 , 14, e1006337	5	27
43	Maize GO Annotation-Methods, Evaluation, and Review (maize-GAMER). <i>Plant Direct</i> , 2018 , 2, e00052	3.3	50

42	Community-Wide Evaluation of Computational Function Prediction. <i>Methods in Molecular Biology</i> , 2017 , 1446, 133-146	1.4	15
41	Highly Bi-Connected Subgraphs for Computational Protein Function Annotation. <i>Lecture Notes in Computer Science</i> , 2016 , 573-584	0.9	
40	Chikungunya Virus in Febrile Humans and Aedes aegypti Mosquitoes, Yucatan, Mexico. <i>Emerging Infectious Diseases</i> , 2016 , 22, 1804-7	10.2	17
39	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
38	Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. <i>ELife</i> , 2015 , 4, e06416	8.9	171
37	A large scale prediction of bacteriocin gene blocks suggests a wide functional spectrum for bacteriocins. <i>BMC Bioinformatics</i> , 2015 , 16, 381	3.6	27
36	An event-driven approach for studying gene block evolution in bacteria. <i>Bioinformatics</i> , 2015 , 31, 2075-83.2	3.2	13
35	The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective. <i>Bioinformatics</i> , 2014 , 30, i609-16	7.2	33
34	Comparative analysis of error-prone replication mononucleotide repeats across baculovirus genomes. <i>Virus Research</i> , 2013 , 178, 217-25	6.4	3
33	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587
32	The COMBREX project: design, methodology, and initial results. <i>PLoS Biology</i> , 2013 , 11, e1001638	9.7	47
31	Biases in the experimental annotations of protein function and their effect on our understanding of protein function space. <i>PLoS Computational Biology</i> , 2013 , 9, e1003063	5	79
30	Biological database of images and genomes: tools for community annotations linking image and genomic information. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat016	5	5
29	A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response. <i>Genome Biology</i> , 2012 , 13, r32	18.3	173
28	Host-microbe interactions in the neonatal intestine: role of human milk oligosaccharides. <i>Advances in Nutrition</i> , 2012 , 3, 450S-5S	10	86
27	Protist diversity in a permanently ice-covered Antarctic lake during the polar night transition. <i>ISME Journal</i> , 2011 , 5, 1559-64	11.9	61
26	A primer on metagenomics. <i>PLoS Computational Biology</i> , 2010 , 6, e1000667	5	412
25	Meeting Report: BioSharing at ISMB 2010. <i>Standards in Genomic Sciences</i> , 2010 , 3, 254-8		18

24	Meeting Report: Metagenomics, Metadata and MetaAnalysis (M3) at ISMB 2010. <i>Standards in Genomic Sciences</i> , 2010 , 3, 232-4		3
23	IPRStats: visualization of the functional potential of an InterProScan run. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 12, S13	3.6	11
22	Biopython: freely available Python tools for computational molecular biology and bioinformatics. <i>Bioinformatics</i> , 2009 , 25, 1422-3	7.2	2308
21	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Special Interest Group at ISMB 2009. <i>Standards in Genomic Sciences</i> , 2009 , 1, 278-82		4
20	Identification and characterization of DUSP27, a novel dual-specific protein phosphatase. <i>FEBS Letters</i> , 2007 , 581, 2527-33	3.8	17
19	Functional differentiation of proteins: implications for structural genomics. <i>Structure</i> , 2007 , 15, 405-15	5.2	9
18	Computational protein function prediction: are we making progress?. <i>Cellular and Molecular Life Sciences</i> , 2007 , 64, 2505-11	10.3	42
17	Using an alignment of fragment strings for comparing protein structures. <i>Bioinformatics</i> , 2007 , 23, e219-24		33
16	JAJA: a protein function annotation meta-server. <i>Nucleic Acids Research</i> , 2006 , 34, W379-81	20.1	31
15	Automated protein function prediction--the genomic challenge. <i>Briefings in Bioinformatics</i> , 2006 , 7, 225-43	4.4	259
14	Fragnostic: walking through protein structure space. <i>Nucleic Acids Research</i> , 2005 , 33, W249-51	20.1	19
13	Connecting the protein structure universe by using sparse recurring fragments. <i>Structure</i> , 2005 , 13, 1213-24		53
12	The interplay of fold recognition and experimental structure determination in structural genomics. <i>Current Opinion in Structural Biology</i> , 2004 , 14, 307-12	8.1	38
11	Protein tyrosine phosphatases in the human genome. <i>Cell</i> , 2004 , 117, 699-711	56.2	1492
10	Persistently conserved positions in structurally similar, sequence dissimilar proteins: roles in preserving protein fold and function. <i>Protein Science</i> , 2002 , 11, 350-60	6.3	46
9	PeCoP: automatic determination of persistently conserved positions in protein families. <i>Bioinformatics</i> , 2002 , 18, 1276-7	7.2	2
8	Evaluation of PSI-BLAST alignment accuracy in comparison to structural alignments. <i>Protein Science</i> , 2000 , 9, 2278-84	6.3	40
7	Submitochondrial distribution of three key steroidogenic proteins (steroidogenic acute regulatory protein and cytochrome p450scc and 3beta-hydroxysteroid dehydrogenase isomerase enzymes) upon stimulation by intracellular calcium in adrenal glomerulosa cells. <i>Journal of Biological Chemistry</i> , 1997 , 272, 7000-07	5.4	137

6	MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides	1
5	New Drosophila long-term memory genes revealed by assessing computational function prediction methods	3
4	Hierarchical Markov Random Field model captures spatial dependency in gene expression, demonstrating regulation via the 3D genome	1
3	Identifying Core Operons in Metagenomic Data	2
2	Identifying Antimicrobial Peptides using Word Embedding with Deep Recurrent Neural Networks	2
1	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens	7