Iddo Friedberg

List of Publications by Citations

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	Biopython: freely available Python tools for computational molecular biology and bioinformatics. *Bioinformatics*, **2009**, 25, 1422-3	7.2	2308
58	Protein tyrosine phosphatases in the human genome. *Cell*, **2004**, 117, 699-711	56.2	1492
57	A large-scale evaluation of computational protein function prediction. *Nature Methods*, **2013**, 10, 221-7	21.6	587
56	A primer on metagenomics. *PLoS Computational Biology*, **2010**, 6, e1000667	5	412
55	Automated protein function prediction--the genomic challenge. *Briefings in Bioinformatics*, **2006**, 7, 225-42	13.4	259
54	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
53	A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response. *Genome Biology*, **2012**, 13, r32	18.3	173
52	Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. *ELife*, **2015**, 4, e06416	8.9	171
51	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. *Journal of Biological Chemistry*, **1997**, 272, 7899-907	5.4	137
50	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. *Genome Biology*, **2019**, 20, 244	18.3	111
49	Host-microbe interactions in the neonatal intestine: role of human milk oligosaccharides. *Advances in Nutrition*, **2012**, 3, 450S-5S	10	86
48	Biases in the experimental annotations of protein function and their effect on our understanding of protein function space. *PLoS Computational Biology*, **2013**, 9, e1003063	5	79
47	Protist diversity in a permanently ice-covered Antarctic lake during the polar night transition. *ISME Journal*, **2011**, 5, 1559-64	11.9	61
46	Connecting the protein structure universe by using sparse recurring fragments. *Structure*, **2005**, 13, 1213-24	5.2	53
45	Maize GO Annotation-Methods, Evaluation, and Review (maize-GAMER). *Plant Direct*, **2018**, 2, e00052	3.3	50
44	The COMBREX project: design, methodology, and initial results. *PLoS Biology*, **2013**, 11, e1001638	9.7	47
43	Persistently conserved positions in structurally similar, sequence dissimilar proteins: roles in preserving protein fold and function. *Protein Science*, **2002**, 11, 350-60	6.3	46

42	Identifying antimicrobial peptides using word embedding with deep recurrent neural networks. *Bioinformatics*, **2019**, 35, 2009-2016	7.2	43
41	Computational protein function prediction: are we making progress?. *Cellular and Molecular Life Sciences*, **2007**, 64, 2505-11	10.3	42
40	Evaluation of PSI-BLAST alignment accuracy in comparison to structural alignments. *Protein Science*, **2000**, 9, 2278-84	6.3	40
39	The interplay of fold recognition and experimental structure determination in structural genomics. *Current Opinion in Structural Biology*, **2004**, 14, 307-12	8.1	38
38	The impact of incomplete knowledge on the evaluation of protein function prediction: a structured-output learning perspective. *Bioinformatics*, **2014**, 30, i609-16	7.2	33
37	Using an alignment of fragment strings for comparing protein structures. *Bioinformatics*, **2007**, 23, e219-24	7.4	33
36	JAFA: a protein function annotation meta-server. *Nucleic Acids Research*, **2006**, 34, W379-81	20.1	31
35	A large scale prediction of bacteriocin gene blocks suggests a wide functional spectrum for bacteriocins. *BMC Bioinformatics*, **2015**, 16, 381	3.6	27
34	Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. *PLoS Computational Biology*, **2018**, 14, e1006337	5	27
33	MetaMiner: A Scalable Peptidogenomics Approach for Discovery of Ribosomal Peptide Natural Products with Blind Modifications from Microbial Communities. *Cell Systems*, **2019**, 9, 600-608.e4	10.6	26
32	Fragnostic: walking through protein structure space. *Nucleic Acids Research*, **2005**, 33, W249-51	20.1	19
31	Meeting Report: BioSharing at ISMB 2010. *Standards in Genomic Sciences*, **2010**, 3, 254-8		18
30	Identification and characterization of DUSP27, a novel dual-specific protein phosphatase. *FEBS Letters*, **2007**, 581, 2527-33	3.8	17
29	Chikungunya Virus in Febrile Humans and Aedes aegypti Mosquitoes, Yucatan, Mexico. *Emerging Infectious Diseases*, **2016**, 22, 1804-7	10.2	17
28	Community-Wide Evaluation of Computational Function Prediction. *Methods in Molecular Biology*, **2017**, 1446, 133-146	1.4	15
27	SwiftOrtho: A fast, memory-efficient, multiple genome orthology classifier. *GigaScience*, **2019**, 8,	7.6	13
26	An event-driven approach for studying gene block evolution in bacteria. *Bioinformatics*, **2015**, 31, 2075-83	7.2	13
25	Expanding the CRISPR Toolbox with ErCas12a in Zebrafish and Human Cells. *CRISPR Journal*, **2019**, 2, 417-433	2.5	13

24	Novel antimicrobial peptide discovery using machine learning and biophysical selection of minimal bacteriocin domains. *Drug Development Research*, **2020**, 81, 43-51	5.1	12
23	IPRStats: visualization of the functional potential of an InterProScan run. *BMC Bioinformatics*, **2010**, 11 Suppl 12, S13	3.6	11
22	New Long-Term Memory Genes Revealed by Assessing Computational Function Prediction Methods. *G3: Genes, Genomes, Genetics*, **2019**, 9, 251-267	3.2	11
21	Functional differentiation of proteins: implications for structural genomics. *Structure*, **2007**, 15, 405-15	5.2	9
20	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens		7
19	Biological database of images and genomes: tools for community annotations linking image and genomic information. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat016	5	5
18	Unraveling a Tangled Skein: Evolutionary Analysis of the Bacterial Gibberellin Biosynthetic Operon. *MSphere*, **2020**, 5,	5	4
17	Meeting Report: "Metagenomics, Metadata and Meta-analysis" (M3) Special Interest Group at ISMB 2009. *Standards in Genomic Sciences*, **2009**, 1, 278-82		4
16	Tracing the ancestry of operons in bacteria. *Bioinformatics*, **2019**, 35, 2998-3004	7.2	3
15	MaizeDIG: Maize Database of Images and Genomes. *Frontiers in Plant Science*, **2019**, 10, 1050	6.2	3
14	Assessing computational predictions of the phenotypic effect of cystathionine-beta-synthase variants. *Human Mutation*, **2019**, 40, 1530-1545	4.7	3
13	Comparative analysis of error-prone replication mononucleotide repeats across baculovirus genomes. *Virus Research*, **2013**, 178, 217-25	6.4	3
12	Meeting Report: Metagenomics, Metadata and MetaAnalysis (M3) at ISMB 2010. *Standards in Genomic Sciences*, **2010**, 3, 232-4		3
11	New Drosophila long-term memory genes revealed by assessing computational function prediction methods		3
10	Crowdsourcing biocuration: The Community Assessment of Community Annotation with Ontologies (CACAO). *PLoS Computational Biology*, **2021**, 17, e1009463	5	3
9	PeCoP: automatic determination of persistently conserved positions in protein families. *Bioinformatics*, **2002**, 18, 1276-7	7.2	2
8	Identifying Core Operons in Metagenomic Data		2
7	Identifying Antimicrobial Peptides using Word Embedding with Deep Recurrent Neural Networks		2

List of Publications

6	MetaRiPPquest: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides		1
5	Hierarchical Markov Random Field model captures spatial dependency in gene expression, demonstrating regulation via the 3D genome		1
4	Deploying MMEJ using MENdel in precision gene editing applications for gene therapy and functional genomics. *Nucleic Acids Research*, **2021**, 49, 67-78	20.1	0
3	Vertical transmission of attaching and invasive E. coli from the dam to neonatal mice predisposes to more severe colitis following exposure to a colitic insult later in life.. *PLoS ONE*, **2022**, 17, e0266005	3.7	0
2	Finding orthologous gene blocks in bacteria: the computational hardness of the problem and novel methods to address it. *Bioinformatics*, **2020**, 36, i668-i674	7.2	
1	Highly Bi-Connected Subgraphs for Computational Protein Function Annotation. *Lecture Notes in Computer Science*, **2016**, 573-584	0.9	