

# Asa Ben-Hur

## List of Publications by Year in descending order

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Version: 2024-02-01

65  
papers

6,602  
citations

136950

32  
h-index

149698

56  
g-index

68  
all docs

68  
docs citations

68  
times ranked

8254  
citing authors

#	ARTICLE	IF	CITATIONS
1	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	19.0	789
2	Support Vector Machines and Kernels for Computational Biology. <i>PLoS Computational Biology</i> , 2008, 4, e1000173.	3.2	515
3	A User's Guide to Support Vector Machines. <i>Methods in Molecular Biology</i> , 2010, 609, 223-239.	0.9	507
4	A survey of the sorghum transcriptome using single-molecule long reads. <i>Nature Communications</i> , 2016, 7, 11706.	12.8	496
5	Kernel methods for predicting protein-protein interactions. <i>Bioinformatics</i> , 2005, 21, i38-i46.	4.1	447
6	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016, 17, 184.	8.8	308
7	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.	8.8	261
8	Large-scale identification of yeast integral membrane protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12123-12128.	7.1	260
9	Genotypic predictors of human immunodeficiency virus type 1 drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17355-17360.	7.1	211
10	Choosing negative examples for the prediction of protein-protein interactions. <i>BMC Bioinformatics</i> , 2006, 7, S2.	2.6	189
11	A stability based method for discovering structure in clustered data. , 2001, , .		159
12	Remote homology detection: a motif based approach. <i>Bioinformatics</i> , 2003, 19, i26-i33.	4.1	146
13	De novo design of synthetic prion domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6519-6524.	7.1	144
14	SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. <i>Genome Biology</i> , 2012, 13, R4.	9.6	140
15	Detecting Stable Clusters Using Principal Component Analysis. , 2003, 224, 159-182.		125
16	Abiotic Stresses Modulate Landscape of Poplar Transcriptome via Alternative Splicing, Differential Intron Retention, and Isoform Ratio Switching. <i>Frontiers in Plant Science</i> , 2018, 9, 5.	3.6	122
17	PAIRpred: Partner-specific prediction of interacting residues from sequence and structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1142-1155.	2.6	119
18	Comprehensive evaluation of deep learning architectures for prediction of DNA/RNA sequence binding specificities. <i>Bioinformatics</i> , 2019, 35, i269-i277.	4.1	118

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19	Universality in sandpile models. <i>Physical Review E</i> , 1996, 53, R1317-R1320.	2.1	112
20	Transcriptome-Wide Identification of RNA Targets of Arabidopsis SERINE/ARGININE-RICH45 Uncovers the Unexpected Roles of This RNA Binding Protein in RNA Processing. <i>Plant Cell</i> , 2015, 27, 3294-3308.	6.6	107
21	Transcriptome Analysis of Drought-Resistant and Drought-Sensitive Sorghum ( <i>Sorghum bicolor</i> ) Genotypes in Response to PEG-Induced Drought Stress. <i>International Journal of Molecular Sciences</i> , 2020, 21, 772.	4.1	79
22	Deciphering the Plant Splicing Code: Experimental and Computational Approaches for Predicting Alternative Splicing and Splicing Regulatory Elements. <i>Frontiers in Plant Science</i> , 2012, 3, 18.	3.6	78
23	Predicting metamorphic relations for testing scientific software: a machine learning approach using graph kernels. <i>Software Testing Verification and Reliability</i> , 2016, 26, 245-269.	2.0	73
24	Identification of an intronic splicing regulatory element involved in auto-regulation of alternative splicing of <i>SCL33</i> pre-mRNA. <i>Plant Journal</i> , 2012, 72, 935-946.	5.7	71
25	Genome-wide analysis of alternative splicing in <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2010, 11, 114.	2.8	69
26	Comparative Analysis of Serine/Arginine-Rich Proteins across 27 Eukaryotes: Insights into Sub-Family Classification and Extent of Alternative Splicing. <i>PLoS ONE</i> , 2011, 6, e24542.	2.5	69
27	HIERARCHICAL CLASSIFICATION OF GENE ONTOLOGY TERMS USING THE GOstruct METHOD. <i>Journal of Bioinformatics and Computational Biology</i> , 2010, 08, 357-376.	0.8	62
28	Exploring the relationship between intron retention and chromatin accessibility in plants. <i>BMC Genomics</i> , 2018, 19, 21.	2.8	61
29	InSite: a computational method for identifying protein-protein interaction binding sites on a proteome-wide scale. <i>Genome Biology</i> , 2007, 8, R192.	9.6	53
30	Support vector clustering. <i>Scholarpedia Journal</i> , 2008, 3, 5187.	0.3	49
31	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. <i>Nucleic Acids Research</i> , 2012, 41, D142-D151.	14.5	47
32	Experimental and computational approaches for the study of calmodulin interactions. <i>Phytochemistry</i> , 2011, 72, 1007-1019.	2.9	45
33	The use of gene ontology evidence codes in preventing classifier assessment bias. <i>Bioinformatics</i> , 2009, 25, 1173-1177.	4.1	44
34	Combining heterogeneous data sources for accurate functional annotation of proteins. <i>BMC Bioinformatics</i> , 2013, 14, S10.	2.6	41
35	Amino acid composition predicts prion activity. <i>PLoS Computational Biology</i> , 2017, 13, e1005465.	3.2	34
36	A Theory of Complexity for Continuous Time Systems. <i>Journal of Complexity</i> , 2002, 18, 51-86.	1.3	33

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37	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. <i>F1000Research</i> , 2015, 4, 259.	1.6	31
38	Learning protein binding affinity using privileged information. <i>BMC Bioinformatics</i> , 2018, 19, 425.	2.6	29
39	Computational Complexity for Continuous Time Dynamics. <i>Physical Review Letters</i> , 1999, 83, 1463-1466.	7.8	27
40	Multiple instance learning of Calmodulin binding sites. <i>Bioinformatics</i> , 2012, 28, i416-i422.	4.1	27
41	A Bioinformatics Method for Identifying Q/N-Rich Prion-Like Domains in Proteins. <i>Methods in Molecular Biology</i> , 2013, 1017, 219-228.	0.9	27
42	Computation in gene networks. <i>Chaos</i> , 2004, 14, 145-151.	2.5	25
43	A self-attention model for inferring cooperativity between regulatory features. <i>Nucleic Acids Research</i> , 2021, 49, e77-e77.	14.5	24
44	Sequence Motifs: Highly Predictive Features of Protein Function. <i>Studies in Fuzziness and Soft Computing</i> , 2006, , 625-645.	0.8	24
45	Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. <i>Journal of Biomedical Semantics</i> , 2015, 6, 9.	1.6	20
46	A close look at protein function prediction evaluation protocols. <i>GigaScience</i> , 2015, 4, 41.	6.4	18
47	A Promiscuous Prion: Efficient Induction of [URE3] Prion Formation by Heterologous Prion Domains. <i>Genetics</i> , 2009, 183, 929-940.	2.9	17
48	aPPRove: An HMM-Based Method for Accurate Prediction of RNA-Pentatricopeptide Repeat Protein Binding Events. <i>PLoS ONE</i> , 2016, 11, e0160645.	2.5	14
49	Digital Image Analysis of Heterogeneous Tuberculosis Pulmonary Pathology in Non-Clinical Animal Models using Deep Convolutional Neural Networks. <i>Scientific Reports</i> , 2020, 10, 6047.	3.3	13
50	Extended Archaeal Histone-Based Chromatin Structure Regulates Global Gene Expression in <i>Thermococcus kodakarensis</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 681150.	3.5	13
51	Probabilistic analysis of a differential equation for linear programming. <i>Journal of Complexity</i> , 2003, 19, 474-510.	1.3	11
52	On probabilistic analog automata. <i>Theoretical Computer Science</i> , 2004, 320, 449-464.	0.9	10
53	Development of the Automated Primer Design Workflow Uniqprimer and Diagnostic Primers for the Broad-Host-Range Plant Pathogen <i>Dickeya dianthicola</i> . <i>Plant Disease</i> , 2019, 103, 2893-2902.	1.4	10
54	Decoding co-/post-transcriptional complexities of plant transcriptomes and epitranscriptome using next-generation sequencing technologies. <i>Biochemical Society Transactions</i> , 2020, 48, 2399-2414.	3.4	9

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55	Random matrix theory for the analysis of the performance of an analog computer: a scaling theory. Physics Letters, Section A: General, Atomic and Solid State Physics, 2004, 323, 204-209.	2.1	8
56	GOstruct 2.0. , 2017, , .		8
57	RODAN: a fully convolutional architecture for basecalling nanopore RNA sequencing data. BMC Bioinformatics, 2022, 23, 142.	2.6	7
58	Multi-view prediction of protein function. , 2011, , .		5
59	Splicing Factor Transcript Abundance in Saliva as a Diagnostic Tool for Breast Cancer. Genes, 2020, 11, 880.	2.4	5
60	Kernel methods for Calmodulin binding and binding site prediction. , 2011, , .		2
61	SpliceGrapherXT. , 2013, , .		1
62	Mendel: A Distributed Storage Framework for Similarity Searching over Sequencing Data. , 2016, , .		1
63	BLRM: A Basic Linear Ranking Model for Protein Interface Prediction. , 2018, , .		1
64	Computation in Gene Networks. Lecture Notes in Computer Science, 2001, , 11-24.	1.3	1
65	Macroscopic Molecular Computation with Gene Networks. , 2001, , 119-120.		0