

# Asa Ben-Hur

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1566475/publications.pdf>

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	RODAN: a fully convolutional architecture for basecalling nanopore RNA sequencing data. BMC Bioinformatics, 2022, 23, 142.	2.6	7
2	A self-attention model for inferring cooperativity between regulatory features. Nucleic Acids Research, 2021, 49, e77-e77.	14.5	24
3	Extended Archaeal Histone-Based Chromatin Structure Regulates Global Gene Expression in <i>Thermococcus kodakarensis</i> . Frontiers in Microbiology, 2021, 12, 681150.	3.5	13
4	Splicing Factor Transcript Abundance in Saliva as a Diagnostic Tool for Breast Cancer. Genes, 2020, 11, 880.	2.4	5
5	Transcriptome Analysis of Drought-Resistant and Drought-Sensitive Sorghum ( <i>Sorghum bicolor</i> ) Genotypes in Response to PEG-Induced Drought Stress. International Journal of Molecular Sciences, 2020, 21, 772.	4.1	79
6	Digital Image Analysis of Heterogeneous Tuberculosis Pulmonary Pathology in Non-Clinical Animal Models using Deep Convolutional Neural Networks. Scientific Reports, 2020, 10, 6047.	3.3	13
7	Decoding co-/post-transcriptional complexities of plant transcriptomes and epitranscriptome using next-generation sequencing technologies. Biochemical Society Transactions, 2020, 48, 2399-2414.	3.4	9
8	Comprehensive evaluation of deep learning architectures for prediction of DNA/RNA sequence binding specificities. Bioinformatics, 2019, 35, i269-i277.	4.1	118
9	Development of the Automated Primer Design Workflow Uniqprimer and Diagnostic Primers for the Broad-Host-Range Plant Pathogen <i>Dickeya dianthicola</i> . Plant Disease, 2019, 103, 2893-2902.	1.4	10
10	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. Genome Biology, 2019, 20, 244.	8.8	261
11	BLRM: A Basic Linear Ranking Model for Protein Interface Prediction. , 2018, , .		1
12	Learning protein binding affinity using privileged information. BMC Bioinformatics, 2018, 19, 425.	2.6	29
13	Abiotic Stresses Modulate Landscape of Poplar Transcriptome via Alternative Splicing, Differential Intron Retention, and Isoform Ratio Switching. Frontiers in Plant Science, 2018, 9, 5.	3.6	122
14	Exploring the relationship between intron retention and chromatin accessibility in plants. BMC Genomics, 2018, 19, 21.	2.8	61
15	Amino acid composition predicts prion activity. PLoS Computational Biology, 2017, 13, e1005465.	3.2	34
16	GOstruct 2.0. , 2017, , .		8
17	aPPRove: An HMM-Based Method for Accurate Prediction of RNA-Pentatricopeptide Repeat Protein Binding Events. PLoS ONE, 2016, 11, e0160645.	2.5	14
18	Predicting metamorphic relations for testing scientific software: a machine learning approach using graph kernels. Software Testing Verification and Reliability, 2016, 26, 245-269.	2.0	73

#	ARTICLE	IF	CITATIONS
19	Mendel: A Distributed Storage Framework for Similarity Searching over Sequencing Data. , 2016, , .		1
20	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	8.8	308
21	A survey of the sorghum transcriptome using single-molecule long reads. Nature Communications, 2016, 7, 11706.	12.8	496
22	A close look at protein function prediction evaluation protocols. GigaScience, 2015, 4, 41.	6.4	18
23	Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. Journal of Biomedical Semantics, 2015, 6, 9.	1.6	20
24	Transcriptome-Wide Identification of RNA Targets of Arabidopsis SERINE/ARGININE-RICH45 Uncovers the Unexpected Roles of This RNA Binding Protein in RNA Processing. Plant Cell, 2015, 27, 3294-3308.	6.6	107
25	PHENOstruct: Prediction of human phenotype ontology terms using heterogeneous data sources. F1000Research, 2015, 4, 259.	1.6	31
26	PAIRpred: Partner-specific prediction of interacting residues from sequence and structure. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1142-1155.	2.6	119
27	Combining heterogeneous data sources for accurate functional annotation of proteins. BMC Bioinformatics, 2013, 14, S10.	2.6	41
28	SpliceGrapherXT. , 2013, , .		1
29	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
30	A Bioinformatics Method for Identifying Q/N-Rich Prion-Like Domains in Proteins. Methods in Molecular Biology, 2013, 1017, 219-228.	0.9	27
31	ChiTaRS: a database of human, mouse and fruit fly chimeric transcripts and RNA-sequencing data. Nucleic Acids Research, 2012, 41, D142-D151.	14.5	47
32	Multiple instance learning of Calmodulin binding sites. Bioinformatics, 2012, 28, i416-i422.	4.1	27
33	SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. Genome Biology, 2012, 13, R4.	9.6	140
34	Identification of an intronic splicing regulatory element involved in auto-regulation of alternative splicing of <i>SCL33</i> pre-mRNA. Plant Journal, 2012, 72, 935-946.	5.7	71
35	Deciphering the Plant Splicing Code: Experimental and Computational Approaches for Predicting Alternative Splicing and Splicing Regulatory Elements. Frontiers in Plant Science, 2012, 3, 18.	3.6	78
36	De novo design of synthetic prion domains. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6519-6524.	7.1	144

#	ARTICLE	IF	CITATIONS
37	Experimental and computational approaches for the study of calmodulin interactions. <i>Phytochemistry</i> , 2011, 72, 1007-1019.	2.9	45
38	Multi-view prediction of protein function. , 2011, , .		5
39	Kernel methods for Calmodulin binding and binding site prediction. , 2011, , .		2
40	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
41	Genome-wide analysis of alternative splicing in <i>Chlamydomonas reinhardtii</i> . <i>BMC Genomics</i> , 2010, 11, 114.	2.8	69
42	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
43	A User's Guide to Support Vector Machines. <i>Methods in Molecular Biology</i> , 2010, 609, 223-239.	0.9	507
44	The use of gene ontology evidence codes in preventing classifier assessment bias. <i>Bioinformatics</i> , 2009, 25, 1173-1177.	4.1	44
45	A Promiscuous Prion: Efficient Induction of [URE3] Prion Formation by Heterologous Prion Domains. <i>Genetics</i> , 2009, 183, 929-940.	2.9	17
46	Support Vector Machines and Kernels for Computational Biology. <i>PLoS Computational Biology</i> , 2008, 4, e1000173.	3.2	515
47	Support vector clustering. <i>Scholarpedia Journal</i> , 2008, 3, 5187.	0.3	49
48	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
49	Choosing negative examples for the prediction of protein-protein interactions. <i>BMC Bioinformatics</i> , 2006, 7, S2.	2.6	189
50	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
51	Sequence Motifs: Highly Predictive Features of Protein Function. <i>Studies in Fuzziness and Soft Computing</i> , 2006, , 625-645.	0.8	24
52	Kernel methods for predicting protein-protein interactions. <i>Bioinformatics</i> , 2005, 21, i38-i46.	4.1	447
53	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
54	Computation in gene networks. <i>Chaos</i> , 2004, 14, 145-151.	2.5	25

#	ARTICLE	IF	CITATIONS
55	On probabilistic analog automata. Theoretical Computer Science, 2004, 320, 449-464.	0.9	10
56	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
57	Detecting Stable Clusters Using Principal Component Analysis. , 2003, 224, 159-182.		125
58	Probabilistic analysis of a differential equation for linear programming. Journal of Complexity, 2003, 19, 474-510.	1.3	11
59	Remote homology detection: a motif based approach. Bioinformatics, 2003, 19, i26-i33.	4.1	146
60	A Theory of Complexity for Continuous Time Systems. Journal of Complexity, 2002, 18, 51-86.	1.3	33
61	A stability based method for discovering structure in clustered data. , 2001, , .		159
62	Computation in Gene Networks. Lecture Notes in Computer Science, 2001, , 11-24.	1.3	1
63	Macroscopic Molecular Computation with Gene Networks. , 2001, , 119-120.		0
64	Computational Complexity for Continuous Time Dynamics. Physical Review Letters, 1999, 83, 1463-1466.	7.8	27
65	Universality in sandpile models. Physical Review E, 1996, 53, R1317-R1320.	2.1	112