

# Haim Ashkenazy

## 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.

35  
papers

4,881  
citations

17  
h-index

39  
g-index

39  
ext. papers

6,436  
ext. citations

11.2  
avg, IF

5.56  
L-index

#	Paper	IF	Citations
35	Commensal <i>Pseudomonas</i> strains facilitate protective response against pathogens in the host plant.. <i>Nature Ecology and Evolution</i> , <b>2022</b> ,	12.3	3
34	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W535-W540	20.1	31
33	Genetic variation, environment and demography intersect to shape <i>Arabidopsis</i> defense metabolite variation across Europe. <i>ELife</i> , <b>2021</b> , 10,	8.9	10
32	Motifier: An IgOme Profiler Based on Peptide Motifs Using Machine Learning. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 167071	6.5	3
31	A Truncated Singleton NLR Causes Hybrid Necrosis in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 557-574	8.3	12
30	ConSurf-DB: An accessible repository for the evolutionary conservation patterns of the majority of PDB proteins. <i>Protein Science</i> , <b>2020</b> , 29, 258-267	6.3	25
29	Domain-Scan: Combinatorial Sero-Diagnosis of Infectious Diseases Using Machine Learning. <i>Frontiers in Immunology</i> , <b>2020</b> , 11, 619896	8.4	1
28	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. <i>Systematic Biology</i> , <b>2019</b> , 68, 117-130	8.4	14
27	A Simulation-Based Approach to Statistical Alignment. <i>Systematic Biology</i> , <b>2019</b> , 68, 252-266	8.4	4
26	Phage display peptide libraries: deviations from randomness and correctives. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e52	20.1	21
25	ASAP - A Webserver for Immunoglobulin-Sequencing Analysis Pipeline. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 1686	8.4	11
24	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. <i>Nature Communications</i> , <b>2018</b> , 9, 4205	17.4	30
23	TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W260-W264	20.1	6
22	Inferring Rates and Length-Distributions of Indels Using Approximate Bayesian Computation. <i>Genome Biology and Evolution</i> , <b>2017</b> , 9, 1280-1294	3.9	4
21	SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W453-W457	20.1	4
20	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W344-50	20.1	1295
19	ConTemplate Suggests Possible Alternative Conformations for a Query Protein of Known Structure. <i>Structure</i> , <b>2015</b> , 23, 2162-70	5.2	10

18	GUIDANCE2: accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W7-14	20.1	451
17	Inferring Indel Parameters using a Simulation-based Approach. <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 3226-38	3.9	4
16	PredictProtein--an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W337-43	20.1	433
15	Indel reliability in indel-based phylogenetic inference. <i>Genome Biology and Evolution</i> , <b>2014</b> , 6, 3199-209	3.9	21
14	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. <i>Israel Journal of Chemistry</i> , <b>2013</b> , 53, 199-206	3.4	325
13	CoPAP: Coevolution of presence-absence patterns. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W232-7	20.1	15
12	Uncovering the co-evolutionary network among prokaryotic genes. <i>Bioinformatics</i> , <b>2012</b> , 28, i389-i394	7.2	23
11	Deep Panning: steps towards probing the IgOme. <i>PLoS ONE</i> , <b>2012</b> , 7, e41469	3.7	41
10	FastML: a web server for probabilistic reconstruction of ancestral sequences. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W580-4	20.1	212
9	Hidden conformations in protein structures. <i>Bioinformatics</i> , <b>2011</b> , 27, 1941-7	7.2	7
8	Reducing phylogenetic bias in correlated mutation analysis. <i>Protein Engineering, Design and Selection</i> , <b>2010</b> , 23, 321-6	1.9	22
7	GUIDANCE: a web server for assessing alignment confidence scores. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W23-8	20.1	469
6	ConSurf 2010: calculating evolutionary conservation in sequence and structure of proteins and nucleic acids. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W529-33	20.1	1316
5	Peptides modulating conformational changes in secreted chaperones: from in silico design to preclinical proof of concept. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 13797-801	11.5	32
4	Optimal data collection for correlated mutation analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 74, 545-55	4.2	22
3	A singleton NLR of recent origin causes hybrid necrosis in <i>Arabidopsis thaliana</i>		1
2	Protective host-dependent antagonism among <i>Pseudomonas</i> in the <i>Arabidopsis</i> phyllosphere		1
1	PredictProtein IPredicting Protein Structure and Function for 29 Years		2

