

Haim Ashkenazy

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

7,397
citations

361045

20
h-index

395343

33
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39
all docs

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docs citations

39
times ranked

13369
citing authors

#	ARTICLE	IF	CITATIONS
1	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. <i>Nucleic Acids Research</i> , 2016, 44, W344-W350.	6.5	2,395
2	ConSurf 2010: calculating evolutionary conservation in sequence and structure of proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2010, 38, W529-W533.	6.5	1,592
3	GUIDANCE2: accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. <i>Nucleic Acids Research</i> , 2015, 43, W7-W14.	6.5	707
4	PredictProteinâ€”an open resource for online prediction of protein structural and functional features. <i>Nucleic Acids Research</i> , 2014, 42, W337-W343.	6.5	589
5	GUIDANCE: a web server for assessing alignment confidence scores. <i>Nucleic Acids Research</i> , 2010, 38, W23-W28.	6.5	560
6	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. <i>Israel Journal of Chemistry</i> , 2013, 53, 199-206.	1.0	459
7	FastML: a web server for probabilistic reconstruction of ancestral sequences. <i>Nucleic Acids Research</i> , 2012, 40, W580-W584.	6.5	295
8	PredictProtein - Predicting Protein Structure and Function for 29 Years. <i>Nucleic Acids Research</i> , 2021, 49, W535-W540.	6.5	135
9	ConSurfâ€™DB: An accessible repository for the evolutionary conservation patterns of the majority of PDB proteins. <i>Protein Science</i> , 2020, 29, 258-267.	3.1	98
10	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. <i>Nature Communications</i> , 2018, 9, 4205.	5.8	74
11	Deep Panning: Steps towards Probing the IgOme. <i>PLoS ONE</i> , 2012, 7, e41469.	1.1	46
12	Commensal <i>Pseudomonas</i> strains facilitate protective response against pathogens in the host plant. <i>Nature Ecology and Evolution</i> , 2022, 6, 383-396.	3.4	44
13	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> , 2009, 106, 13797-13801.	3.3	38
14	Uncovering the co-evolutionary network among prokaryotic genes. <i>Bioinformatics</i> , 2012, 28, i389-i394.	1.8	36
15	Genetic variation, environment and demography intersect to shape <i>Arabidopsis</i> defense metabolite variation across Europe. <i>ELife</i> , 2021, 10, .	2.8	33
16	CoPAP: Coevolution of Presenceâ€™Absence Patterns. <i>Nucleic Acids Research</i> , 2013, 41, W232-W237.	6.5	30
17	Phage display peptide libraries: deviations from randomness and correctives. <i>Nucleic Acids Research</i> , 2018, 46, e52-e52.	6.5	30
18	Indel Reliability in Indel-Based Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2014, 6, 3199-3209.	1.1	26

#	ARTICLE	IF	CITATIONS
19	A Truncated Singleton NLR Causes Hybrid Necrosis in <i>Arabidopsis thaliana</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 557-574.	3.5	26
20	Optimal data collection for correlated mutation analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 545-555.	1.5	24
21	Multiple Sequence Alignment Averaging Improves Phylogeny Reconstruction. <i>Systematic Biology</i> , 2019, 68, 117-130.	2.7	24
22	Reducing phylogenetic bias in correlated mutation analysis. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 321-326.	1.0	22
23	ASAP - A Webserver for Immunoglobulin-Sequencing Analysis Pipeline. <i>Frontiers in Immunology</i> , 2018, 9, 1686.	2.2	17
24	ConTemplate Suggests Possible Alternative Conformations for a Query Protein of Known Structure. <i>Structure</i> , 2015, 23, 2162-2170.	1.6	13
25	Commensal <i>Pseudomonas</i> protect <i>Arabidopsis thaliana</i> from a coexisting pathogen via multiple lineage-dependent mechanisms. <i>ISME Journal</i> , 2022, 16, 1235-1244.	4.4	13
26	Hidden conformations in protein structures. <i>Bioinformatics</i> , 2011, 27, 1941-1947.	1.8	9
27	TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites. <i>Nucleic Acids Research</i> , 2017, 45, W260-W264.	6.5	8
28	Inferring Rates and Length-Distributions of Indels Using Approximate Bayesian Computation. <i>Genome Biology and Evolution</i> , 2017, 9, 1280-1294.	1.1	7
29	A Simulation-Based Approach to Statistical Alignment. <i>Systematic Biology</i> , 2019, 68, 252-266.	2.7	7
30	Motifier: An IgOme Profiler Based on Peptide Motifs Using Machine Learning. <i>Journal of Molecular Biology</i> , 2021, 433, 167071.	2.0	7
31	Inferring Indel Parameters using a Simulation-based Approach. <i>Genome Biology and Evolution</i> , 2015, 7, 3226-3238.	1.1	6
32	SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. <i>Nucleic Acids Research</i> , 2017, 45, W453-W457.	6.5	5
33	Domain-Scan: Combinatorial Sero-Diagnosis of Infectious Diseases Using Machine Learning. <i>Frontiers in Immunology</i> , 2020, 11, 619896.	2.2	3