Itay Mayrose

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/6444011/itay-mayrose-publications-by-year.pdf
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67	papers
9,884	citations
33	h-index
75	g-index
75	ext. papers
13,072	ext. citations
8.4	avg, IF
6.27	L-index

#	Paper	IF	Citations
67	Panoramic: A package for constructing eukaryotic pan-genomes. *Molecular Ecology Resources*, **2021**, 21, 1393-1403	8.4	1
66	Harnessing machine learning to guide phylogenetic-tree search algorithms. *Nature Communications* , **2021**, 12, 1983	17.4	5
65	Mechanisms Underlying Host Range Variation in Flavivirus: From Empirical Knowledge to Predictive Models. *Journal of Molecular Evolution*, **2021**, 89, 329-340	3.1	0
64	The Evolution of Chromosome Numbers: Mechanistic Models and Experimental Approaches. *Genome Biology and Evolution*, **2021**, 13,	3.9	8
63	Model adequacy tests for probabilistic models of chromosome-number evolution. *New Phytologist*, **2021**, 229, 3602-3613	9.8	4
62	A Codon Model for Associating Phenotypic Traits with Altered Selective Patterns of Sequence Evolution. *Systematic Biology*, **2021**, 70, 608-622	8.4	2
61	Bee flowers drive macroevolutionary diversification in long-horned bees. *Proceedings of the Royal Society B: Biological Sciences*, **2021**, 288, 20210533	4.4	1
60	A Probabilistic Model for Indel Evolution: Differentiating Insertions from Deletions. *Molecular Biology and Evolution*, **2021**, 38, 5769-5781	8.3	4
59	COVID-19 pandemic-related lockdown: response time is more important than its strictness. *EMBO Molecular Medicine*, **2020**, 12, e13171	12	14
58	Heterogeneity in the rate of molecular sequence evolution substantially impacts the accuracy of detecting shifts in diversification rates. *Evolution; International Journal of Organic Evolution*, **2020**, 74, 1620-1639	3.8	8
57	ModelTeller: Model Selection for Optimal Phylogenetic Reconstruction Using Machine Learning. *Molecular Biology and Evolution*, **2020**, 37, 3338-3352	8.3	8
56	TRY plant trait database - enhanced coverage and open access. *Global Change Biology*, **2020**, 26, 119-188	11.4	399
55	Phenology and polyploidy in annual Brachypodium species (Poaceae) along the aridity gradient in Israel. *Journal of Systematics and Evolution*, **2020**, 58, 189-199	2.9	3
54	The global biogeography of polyploid plants. *Nature Ecology and Evolution*, **2019**, 3, 265-273	12.3	86
53	Meiotic drive shapes rates of karyotype evolution in mammals. *Evolution; International Journal of Organic Evolution*, **2019**, 73, 511-523	3.8	17
52	Interaction among ploidy, breeding system and lineage diversification. *New Phytologist*, **2019**, 224, 1252-1265	9.8	25
51	Model selection may not be a mandatory step for phylogeny reconstruction. *Nature Communications*, **2019**, 10, 934	17.4	136

(2015-2018)

50	Macroevolutionary Patterns of Flowering Plant Speciation and Extinction. *Annual Review of Plant Biology*, **2018**, 69, 685-706	30.7	40
49	CRISPys: Optimal sgRNA Design for Editing Multiple Members of a Gene Family Using the CRISPR System. *Journal of Molecular Biology*, **2018**, 430, 2184-2195	6.5	10
48	OneTwoTree: An online tool for phylogeny reconstruction. *Molecular Ecology Resources*, **2018**, 18, 1492-1499	8.4	13
47	Broad phylogenetic analysis of cation/proton antiporters reveals transport determinants. *Nature Communications*, **2018**, 9, 4205	17.4	30
46	Macroevolutionary synthesis of flowering plant sexual systems. *Evolution; International Journal of Organic Evolution*, **2017**, 71, 898-912	3.8	42
45	TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites. *Nucleic Acids Research*, **2017**, 45, W260-W264	20.1	6
44	Multispeed genome diploidization and diversification after an ancient allopolyploidization. *Molecular Ecology*, **2017**, 26, 6445-6462	5.7	26
43	An Integrated Model of Phenotypic Trait Changes and Site-Specific Sequence Evolution. *Systematic Biology*, **2017**, 66, 917-933	8.4	22
42	A machine learning approach for predicting CRISPR-Cas9 cleavage efficiencies and patterns underlying its mechanism of action. *PLoS Computational Biology*, **2017**, 13, e1005807	5	73
41	Whole-genome duplication as a key factor in crop domestication. *Nature Plants*, **2016**, 2, 16115	11.5	119
40	ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. *Nucleic Acids Research*, **2016**, 44, W344-50	20.1	1295
39	Polyploidy and sexual system in angiosperms: Is there an association?. *American Journal of Botany*, **2016**, 103, 1223-35	2.7	29
38	Body sizes and diversification rates of lizards, snakes, amphisbaenians and the tuatara. *Global Ecology and Biogeography*, **2016**, 25, 187-197	6.1	92
37	Dioecy does not consistently accelerate or slow lineage diversification across multiple genera of angiosperms. *New Phytologist*, **2016**, 209, 1290-300	9.8	27
36	Sex determination, longevity, and the birth and death of reptilian species. *Ecology and Evolution*, **2016**, 6, 5207-20	2.8	29
35	Phylogenetic evidence for cladogenetic polyploidization in land plants. *American Journal of Botany*, **2016**, 103, 1252-8	2.7	22
34	Methods for studying polyploid diversification and the dead end hypothesis: a reply to Soltis et al. (2014). *New Phytologist*, **2015**, 206, 27-35	9.8	55
33	Clumpak: a program for identifying clustering modes and packaging population structure inferences across K. *Molecular Ecology Resources*, **2015**, 15, 1179-91	8.4	1526

32	The Chromosome Counts Database (CCDB) - a community resource of plant chromosome numbers. *New Phytologist*, **2015**, 206, 19-26	9.8	326
31	Regulation of alternative splicing at the single-cell level. *Molecular Systems Biology*, **2015**, 11, 845	12.2	15
30	The Interplay between Scientific Overlap and Cooperation and the Resulting Gain in Co-Authorship Interactions. *PLoS ONE*, **2015**, 10, e0137856	3.7	6
29	Comparative analysis reveals that polyploidy does not decelerate diversification in fish. *Journal of Evolutionary Biology*, **2014**, 27, 391-403	2.3	25
28	ChromEvol: assessing the pattern of chromosome number evolution and the inference of polyploidy along a phylogeny. *Molecular Biology and Evolution*, **2014**, 31, 1914-22	8.3	94
27	Karyotypic changes through dysploidy persist longer over evolutionary time than polyploid changes. *PLoS ONE*, **2014**, 9, e85266	3.7	51
26	Sex determination: why so many ways of doing it?. *PLoS Biology*, **2014**, 12, e1001899	9.7	606
25	ConSurf: Using Evolutionary Data to Raise Testable Hypotheses about Protein Function. *Israel Journal of Chemistry*, **2013**, 53, 199-206	3.4	325
24	Synonymous site conservation in the HIV-1 genome. *BMC Evolutionary Biology*, **2013**, 13, 164	3	21
23	Recently formed polyploid plants diversify at lower rates. *Science*, **2011**, 333, 1257	33.3	308
22	Increased growth in sunflower correlates with reduced defences and altered gene expression in response to biotic and abiotic stress. *Molecular Ecology*, **2011**, 20, 4683-94	5.7	56
21	A likelihood method for detecting trait-dependent shifts in the rate of molecular evolution. *Molecular Biology and Evolution*, **2011**, 28, 759-70	8.3	28
20	Evolutionary models accounting for layers of selection in protein-coding genes and their impact on the inference of positive selection. *Molecular Biology and Evolution*, **2011**, 28, 3297-308	8.3	32
19	Probabilistic Methods and Rate Heterogeneity **2010**, 257-280		3
18	An evolutionary analysis of lateral gene transfer in thymidylate synthase enzymes. *Systematic Biology*, **2010**, 59, 212-25	8.4	24
17	Probabilistic models of chromosome number evolution and the inference of polyploidy. *Systematic Biology*, **2010**, 59, 132-44	8.4	148
16	The frequency of polyploid speciation in vascular plants. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 13875-9	11.5	847
15	Epitopia: a web-server for predicting B-cell epitopes. *BMC Bioinformatics*, **2009**, 10, 287	3.6	138

14	A machine-learning approach for predicting B-cell epitopes. *Molecular Immunology*, **2009**, 46, 840-7	4.3	89
13	Computational characterization of B-cell epitopes. *Molecular Immunology*, **2008**, 45, 3477-89	4.3	156
12	Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. *Proteins: Structure, Function and Bioinformatics*, **2007**, 68, 294-304	4.2	69
11	Pepitope: epitope mapping from affinity-selected peptides. *Bioinformatics*, **2007**, 23, 3244-6	7.2	115
10	Epitope mapping using combinatorial phage-display libraries: a graph-based algorithm. *Nucleic Acids Research*, **2007**, 35, 69-78	20.1	88
9	Towards realistic codon models: among site variability and dependency of synonymous and non-synonymous rates. *Bioinformatics*, **2007**, 23, i319-27	7.2	46
8	Site-specific evolutionary rate inference: taking phylogenetic uncertainty into account. *Journal of Molecular Evolution*, **2005**, 60, 345-53	3.1	30
7	Selecton: a server for detecting evolutionary forces at a single amino-acid site. *Bioinformatics*, **2005**, 21, 2101-3	7.2	114
6	ConSurf 2005: the projection of evolutionary conservation scores of residues on protein structures. *Nucleic Acids Research*, **2005**, 33, W299-302	20.1	1043
5	A gamma mixture model better accounts for among site rate heterogeneity. *Bioinformatics*, **2005**, 21 Suppl 2, ii151-8	7.2	80
4	Comparison of site-specific rate-inference methods for protein sequences: empirical Bayesian methods are superior. *Molecular Biology and Evolution*, **2004**, 21, 1781-91	8.3	336
3	The DFNA15 deafness mutation affects POU4F3 protein stability, localization, and transcriptional activity. *Molecular and Cellular Biology*, **2003**, 23, 7957-64	4.8	50
2	Rate4Site: an algorithmic tool for the identification of functional regions in proteins by surface mapping of evolutionary determinants within their homologues. *Bioinformatics*, **2002**, 18 Suppl 1, S71-7	7.2	436
1	Interaction Between Ploidy, Breeding System, and Lineage Diversification		1