Gergely J Szőllősi

List of Publications by Year
in descending order

59 papers	3,935 citations	201674 27 h-index	161849 54 g-index
80 all docs	80 docs citations	80 times ranked	4273 citing authors

#	ARTICLE	IF	CITATIONS
1	Phase transition in the collective migration of tissue cells: Experiment and model. Physical Review E, 2006, 74, 061908.	2.1	382
2	Damage and Fluctuations Induce Loops in Optimal Transport Networks. Physical Review Letters, 2010, 104, 048704.	7.8	261
3	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. Nature Communications, 2020, 11, 5125.	12.8	258
4	Integrative modeling of gene and genome evolution roots the archaeal tree of life. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4602-E4611.	7.1	232
5	The Inference of Gene Trees with Species Trees. Systematic Biology, 2015, 64, e42-e62.	5.6	226
6	Genome-scale coestimation of species and gene trees. Genome Research, 2013, 23, 323-330.	5.5	223
7	Megaphylogeny resolves global patterns of mushroom evolution. Nature Ecology and Evolution, 2019, 3, 668-678.	7.8	187
8	Efficient Exploration of the Space of Reconciled Gene Trees. Systematic Biology, 2013, 62, 901-912.	5.6	176
9	Phylogenomics provides robust support for a two-domains tree of life. Nature Ecology and Evolution, 2020, 4, 138-147.	7.8	159
10	Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17513-17518.	7.1	150
11	A rooted phylogeny resolves early bacterial evolution. Science, 2021, 372, .	12.6	128
12	Emergent Neutrality in Adaptive Asexual Evolution. Genetics, 2011, 189, 1361-1375.	2.9	109
13	Lateral Gene Transfer from the Dead. Systematic Biology, 2013, 62, 386-397.	5.6	100
14	ecceTERA: comprehensive gene tree-species tree reconciliation using parsimony. Bioinformatics, 2016, 32, 2056-2058.	4.1	98
15	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene ÂFamily Tree Inference under Gene Duplication, Transfer, and Loss. Molecular Biology and Evolution, 2020, 37, 2763-2774.	8.9	87
16	How Long Does Wolbachia Remain on Board?. Molecular Biology and Evolution, 2017, 34, 1183-1193.	8.9	82
17	Horizontal Gene Transfer and the History of Life. Cold Spring Harbor Perspectives in Biology, 2016, 8, a018036.	5.5	79
18	An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers. Lecture Notes in Computer Science, 2010, , 93-108.	1.3	78

#	Article	IF	Citations
19	Genome-scale phylogenetic analysis finds extensive gene transfer among fungi. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140335.	4.0	77
20	Gene transfers can date the tree of life. Nature Ecology and Evolution, 2018, 2, 904-909.	7.8	52
21	Congruent Evolution of Genetic and Environmental Robustness in Micro-RNA. Molecular Biology and Evolution, 2009, 26, 867-874.	8.9	45
22	Hierarchical tissue organization as a general mechanism to limit the accumulation of somatic mutations. Nature Communications, 2017, 8, 14545.	12.8	45
23	Joint amalgamation of most parsimonious reconciled gene trees. Bioinformatics, 2015, 31, 841-848.	4.1	44
24	Toward More Accurate Ancestral Protein Genotypeâ€"Phenotype Reconstructions with the Use of Species Tree-Aware Gene Trees. Molecular Biology and Evolution, 2015, 32, 13-22.	8.9	43
25	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. ELife, 2022, 11, .	6.0	43
26	How similar are nut-cracking and stone-flaking? A functional approach to percussive technology. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20140355.	4.0	40
27	Gene Acquisitions from Bacteria at the Origins of Major Archaeal Clades Are Vastly Overestimated. Molecular Biology and Evolution, 2016, 33, 305-310.	8.9	37
28	Evolution of gene neighborhoods within reconciled phylogenies. Bioinformatics, 2012, 28, i382-i388.	4.1	34
29	Scalable Empirical Mixture Models That Account for Across-Site Compositional Heterogeneity. Molecular Biology and Evolution, 2020, 37, 3616-3631.	8.9	32
30	Modeling Gene Family Evolution and Reconciling Phylogenetic Discord. Methods in Molecular Biology, 2012, 856, 29-51.	0.9	29
31	SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. Molecular Biology and Evolution, 2022, 39, .	8.9	29
32	Quantifying GC-Biased Gene Conversion in Great Ape Genomes Using Polymorphism-Aware Models. Genetics, 2019, 212, 1321-1336.	2.9	28
33	Zombi: a phylogenetic simulator of trees, genomes and sequences that accounts for dead linages. Bioinformatics, 2020, 36, 1286-1288.	4.1	25
34	The effect of recombination on the neutral evolution of genetic robustness. Mathematical Biosciences, 2008, 214, 58-62.	1.9	24
35	Genome size evolution in the Archaea. Emerging Topics in Life Sciences, 2018, 2, 595-605.	2.6	23
36	RecPhyloXML: a format for reconciled gene trees. Bioinformatics, 2018, 34, 3646-3652.	4.1	22

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37	Lateral gene transfer, rearrangement, reconciliation. BMC Bioinformatics, 2013, 14, S4.	2.6	21
38	The Maintenance of Sex in Bacteria Is Ensured by Its Potential to Reload Genes. Genetics, 2006, 174, 2173-2180.	2.9	19
39	Inferring the Deep Past from Molecular Data. Genome Biology and Evolution, 2021, 13, .	2.5	19
40	Fungal Phylogeny in the Age of Genomics: Insights Into Phylogenetic Inference From Genome-Scale Datasets. Advances in Genetics, 2017, 100, 49-72.	1.8	16
41	Temperature dependence of internal friction in enzyme reactions. FASEB Journal, 2011, 25, 2804-2813.	0.5	13
42	Evolutionary games on minimally structured populations. Physical Review E, 2008, 78, 031919.	2.1	11
43	Resurrection of Ancestral Malate Dehydrogenases Reveals the Evolutionary History of Halobacterial Proteins: Deciphering Gene Trajectories and Changes in Biochemical Properties. Molecular Biology and Evolution, 2021, 38, 3754-3774.	8.9	10
44	Neck-Linker Docking Coordinates the Kinetics of Kinesin's Heads. Biophysical Journal, 2011, 100, 1729-1736.	0.5	9
45	A compartment size-dependent selective threshold limits mutation accumulation in hierarchical tissues. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1606-1611.	7.1	9
46	Relative Time Constraints Improve Molecular Dating. Systematic Biology, 2022, 71, 797-809.	5.6	9
47	Recoding Amino Acids to a Reduced Alphabet may Increase or Decrease Phylogenetic Accuracy. Systematic Biology, 2023, 72, 723-737.	5.6	8
48	Nucleotide Usage Biases Distort Inferences of the Species Tree. Genome Biology and Evolution, 2022, 14, .	2.5	7
49	The relevance of neck linker docking in the motility of kinesin. BioSystems, 2008, 93, 29-33.	2.0	6
50	Effective Temperature of Mutations. Physical Review Letters, 2015, 114, 058101.	7.8	6
51	Trade-off between reducing mutational accumulation and increasing commitment to differentiation determines tissue organization. Nature Communications, 2022, 13, 1666.	12.8	5
52	How Does Kinesin Walk And Coordinate Its Heads?. Biophysical Journal, 2009, 96, 136a.	0.5	1
53	The Relative Significance of External and Internal Friction in Protein Conformational Changes. Biophysical Journal, 2010, 98, 237a.	0.5	1
54	Relationship Between Internal Friction and the Roughness of the Energy Landscape of Protein Conformational Changes. Biophysical Journal, 2011, 100, 537a.	0.5	0

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55	Protein Flexibility Partitions the Effects of Energy Landscape Roughness Between Activation Energy and Internal Friction. Biophysical Journal, 2011, 100, 537a.	0.5	0
56	The Effective Temperature of Mutations: A General Mechanism for the Congruent Evolution of Robustness. Biophysical Journal, 2014, 106, 657a.	0.5	0
57	On Cancer Risk and the Hierarchical Architecture of Tissues. Biophysical Journal, 2016, 110, 479a.	0.5	0
58	Hierarchical Tissue Organization as a General Mechanism to Limit Somatic Evolution. Biophysical Journal, 2017, 112, 284a.	0.5	0
59	Distinguishing excess mutations and increased cell death based on variant allele frequencies. PLoS Computational Biology, 2022, 18, e1010048.	3.2	0