

# Gergely J Szűcs

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6490204/publications.pdf>

Version: 2024-02-01

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	Recoding Amino Acids to a Reduced Alphabet may Increase or Decrease Phylogenetic Accuracy. <i>Systematic Biology</i> , 2023, 72, 723-737.	5.6	8
2	Relative Time Constraints Improve Molecular Dating. <i>Systematic Biology</i> , 2022, 71, 797-809.	5.6	9
3	Nucleotide Usage Biases Distort Inferences of the Species Tree. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	7
4	SpeciesRax: A Tool for Maximum Likelihood Species Tree Inference from Gene Family Trees under Duplication, Transfer, and Loss. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	29
5	An estimate of the deepest branches of the tree of life from ancient vertically evolving genes. <i>ELife</i> , 2022, 11, .	6.0	43
6	Trade-off between reducing mutational accumulation and increasing commitment to differentiation determines tissue organization. <i>Nature Communications</i> , 2022, 13, 1666.	12.8	5
7	Distinguishing excess mutations and increased cell death based on variant allele frequencies. <i>PLoS Computational Biology</i> , 2022, 18, e1010048.	3.2	0
8	Inferring the Deep Past from Molecular Data. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	19
9	A rooted phylogeny resolves early bacterial evolution. <i>Science</i> , 2021, 372, .	12.6	128
10	Resurrection of Ancestral Malate Dehydrogenases Reveals the Evolutionary History of Halobacterial Proteins: Deciphering Gene Trajectories and Changes in Biochemical Properties. <i>Molecular Biology and Evolution</i> , 2021, 38, 3754-3774.	8.9	10
11	Zombi: a phylogenetic simulator of trees, genomes and sequences that accounts for dead lineages. <i>Bioinformatics</i> , 2020, 36, 1286-1288.	4.1	25
12	Phylogenomics provides robust support for a two-domains tree of life. <i>Nature Ecology and Evolution</i> , 2020, 4, 138-147.	7.8	159
13	Scalable Empirical Mixture Models That Account for Across-Site Compositional Heterogeneity. <i>Molecular Biology and Evolution</i> , 2020, 37, 3616-3631.	8.9	32
14	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	12.8	258
15	GeneRax: A Tool for Species-Tree-Aware Maximum Likelihood-Based Gene Family Tree Inference under Gene Duplication, Transfer, and Loss. <i>Molecular Biology and Evolution</i> , 2020, 37, 2763-2774.	8.9	87
16	A compartment size-dependent selective threshold limits mutation accumulation in hierarchical tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1606-1611.	7.1	9
17	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	7.8	187
18	Quantifying GC-Biased Gene Conversion in Great Ape Genomes Using Polymorphism-Aware Models. <i>Genetics</i> , 2019, 212, 1321-1336.	2.9	28

#	ARTICLE	IF	CITATIONS
19	Gene transfers can date the tree of life. <i>Nature Ecology and Evolution</i> , 2018, 2, 904-909.	7.8	52
20	Genome size evolution in the Archaea. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 595-605.	2.6	23
21	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
22	Hierarchical tissue organization as a general mechanism to limit the accumulation of somatic mutations. <i>Nature Communications</i> , 2017, 8, 14545.	12.8	45
23	How Long Does Wolbachia Remain on Board?. <i>Molecular Biology and Evolution</i> , 2017, 34, 1183-1193.	8.9	82
24	Integrative modeling of gene and genome evolution roots the archaeal tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4602-E4611.	7.1	232
25	Hierarchical Tissue Organization as a General Mechanism to Limit Somatic Evolution. <i>Biophysical Journal</i> , 2017, 112, 284a.	0.5	0
26	Fungal Phylogeny in the Age of Genomics: Insights Into Phylogenetic Inference From Genome-Scale Datasets. <i>Advances in Genetics</i> , 2017, 100, 49-72.	1.8	16
27	On Cancer Risk and the Hierarchical Architecture of Tissues. <i>Biophysical Journal</i> , 2016, 110, 479a.	0.5	0
28	ecceTERA: comprehensive gene tree-species tree reconciliation using parsimony. <i>Bioinformatics</i> , 2016, 32, 2056-2058.	4.1	98
29	Horizontal Gene Transfer and the History of Life. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018036.	5.5	79
30	Gene Acquisitions from Bacteria at the Origins of Major Archaeal Clades Are Vastly Overestimated. <i>Molecular Biology and Evolution</i> , 2016, 33, 305-310.	8.9	37
31	How similar are nut-cracking and stone-flaking? A functional approach to percussive technology. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140355.	4.0	40
32	The Inference of Gene Trees with Species Trees. <i>Systematic Biology</i> , 2015, 64, e42-e62.	5.6	226
33	Genome-scale phylogenetic analysis finds extensive gene transfer among fungi. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140335.	4.0	77
34	Effective Temperature of Mutations. <i>Physical Review Letters</i> , 2015, 114, 058101.	7.8	6
35	Joint amalgamation of most parsimonious reconciled gene trees. <i>Bioinformatics</i> , 2015, 31, 841-848.	4.1	44
36	Toward More Accurate Ancestral Protein Genotypeâ€“Phenotype Reconstructions with the Use of Species Tree-Aware Gene Trees. <i>Molecular Biology and Evolution</i> , 2015, 32, 13-22.	8.9	43

#	ARTICLE	IF	CITATIONS
37	The Effective Temperature of Mutations: A General Mechanism for the Congruent Evolution of Robustness. <i>Biophysical Journal</i> , 2014, 106, 657a.	0.5	0
38	Lateral gene transfer, rearrangement, reconciliation. <i>BMC Bioinformatics</i> , 2013, 14, S4.	2.6	21
39	Lateral Gene Transfer from the Dead. <i>Systematic Biology</i> , 2013, 62, 386-397.	5.6	100
40	Efficient Exploration of the Space of Reconciled Gene Trees. <i>Systematic Biology</i> , 2013, 62, 901-912.	5.6	176
41	Genome-scale coestimation of species and gene trees. <i>Genome Research</i> , 2013, 23, 323-330.	5.5	223
42	Evolution of gene neighborhoods within reconciled phylogenies. <i>Bioinformatics</i> , 2012, 28, i382-i388.	4.1	34
43	Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17513-17518.	7.1	150
44	Modeling Gene Family Evolution and Reconciling Phylogenetic Discord. <i>Methods in Molecular Biology</i> , 2012, 856, 29-51.	0.9	29
45	Relationship Between Internal Friction and the Roughness of the Energy Landscape of Protein Conformational Changes. <i>Biophysical Journal</i> , 2011, 100, 537a.	0.5	0
46	Protein Flexibility Partitions the Effects of Energy Landscape Roughness Between Activation Energy and Internal Friction. <i>Biophysical Journal</i> , 2011, 100, 537a.	0.5	0
47	Neck-Linker Docking Coordinates the Kinetics of Kinesin's Heads. <i>Biophysical Journal</i> , 2011, 100, 1729-1736.	0.5	9
48	Temperature dependence of internal friction in enzyme reactions. <i>FASEB Journal</i> , 2011, 25, 2804-2813.	0.5	13
49	Emergent Neutrality in Adaptive Asexual Evolution. <i>Genetics</i> , 2011, 189, 1361-1375.	2.9	109
50	Damage and Fluctuations Induce Loops in Optimal Transport Networks. <i>Physical Review Letters</i> , 2010, 104, 048704.	7.8	261
51	The Relative Significance of External and Internal Friction in Protein Conformational Changes. <i>Biophysical Journal</i> , 2010, 98, 237a.	0.5	1
52	An Efficient Algorithm for Gene/Species Trees Parsimonious Reconciliation with Losses, Duplications and Transfers. <i>Lecture Notes in Computer Science</i> , 2010, , 93-108.	1.3	78
53	Congruent Evolution of Genetic and Environmental Robustness in Micro-RNA. <i>Molecular Biology and Evolution</i> , 2009, 26, 867-874.	8.9	45
54	How Does Kinesin Walk And Coordinate Its Heads?. <i>Biophysical Journal</i> , 2009, 96, 136a.	0.5	1

#	ARTICLE	IF	CITATIONS
55	The relevance of neck linker docking in the motility of kinesin. <i>BioSystems</i> , 2008, 93, 29-33.	2.0	6
56	The effect of recombination on the neutral evolution of genetic robustness. <i>Mathematical Biosciences</i> , 2008, 214, 58-62.	1.9	24
57	Evolutionary games on minimally structured populations. <i>Physical Review E</i> , 2008, 78, 031919.	2.1	11
58	Phase transition in the collective migration of tissue cells: Experiment and model. <i>Physical Review E</i> , 2006, 74, 061908.	2.1	382
59	The Maintenance of Sex in Bacteria Is Ensured by Its Potential to Reload Genes. <i>Genetics</i> , 2006, 174, 2173-2180.	2.9	19