

# Heiko A Schmidt

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

27,234  
citations

331259

21  
h-index

500791

28  
g-index

39  
all docs

39  
docs citations

39  
times ranked

32097  
citing authors

#	ARTICLE	IF	CITATIONS
1	Want to track pandemic variants faster? Fix the bioinformatics bottleneck. <i>Nature</i> , 2021, 591, 30-33.	13.7	92
2	Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12522-12523.	3.3	68
3	Distinguishing Felsenstein Zone from Farris Zone Using Neural Networks. <i>Molecular Biology and Evolution</i> , 2020, 37, 3632-3641.	3.5	16
4	It Takes Two to Tango: Activation of Protein Kinase D by Dimerization. <i>BioEssays</i> , 2020, 42, e1900222.	1.2	15
5	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.	3.5	5,960
6	Ammonia Oxidation by the Arctic Terrestrial Thaumarchaeote <i>Candidatus Nitrosocosmicus arcticus</i> Is Stimulated by Increasing Temperatures. <i>Frontiers in Microbiology</i> , 2019, 10, 1571.	1.5	51
7	INO80 represses osmostress induced gene expression by resetting promoter proximal nucleosomes. <i>Nucleic Acids Research</i> , 2017, 45, gkw1292.	6.5	15
8	Comparative Genomics Identifies Epidermal Proteins Associated with the Evolution of the Turtle Shell. <i>Molecular Biology and Evolution</i> , 2016, 33, 726-737.	3.5	46
9	IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. <i>Molecular Biology and Evolution</i> , 2015, 32, 268-274.	3.5	16,610
10	Nodal signalling determines biradial asymmetry in Hydra. <i>Nature</i> , 2014, 515, 112-115.	13.7	100
11	DAGwoman. , 2012, , .		2
12	Expression of secreted Wnt pathway components reveals unexpected complexity of the planarian amputation response. <i>Developmental Biology</i> , 2010, 347, 24-39.	0.9	186
13	Accuracy of phylogeny reconstruction methods combining overlapping gene data sets. <i>Algorithms for Molecular Biology</i> , 2010, 5, 37.	0.3	50
14	Testing tree topologies. , 2009, , 381-404.		18
15	Phylogenetic inference using maximum likelihood methods. , 2009, , 181-209.		24
16	First DNA sequences from Asian cave bear fossils reveal deep divergences and complex phylogeographic patterns. <i>Molecular Ecology</i> , 2009, 18, 1225-1238.	2.0	80
17	Multiple Wnts are involved in Hydra organizer formation and regeneration. <i>Developmental Biology</i> , 2009, 330, 186-199.	0.9	277
18	The phylogenetic information profile of HIV-1 and the degradation effect of recombination. <i>Infection, Genetics and Evolution</i> , 2008, 8, 139-145.	1.0	0

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19	Rooted triple consensus and anomalous gene trees. <i>BMC Evolutionary Biology</i> , 2008, 8, 118.	3.2	57
20	Maximum-Likelihood Analysis Using TREE-PUZZLE. <i>Current Protocols in Bioinformatics</i> , 2007, 17, Unit 6.6.	25.8	41
21	pIPHULA parallel inference of population parameters using a likelihood approach. <i>Bioinformatics</i> , 2007, 23, 2636-2637.	1.8	0
22	An ancient Wnt-Dickkopf antagonism in Hydra. <i>Development (Cambridge)</i> , 2006, 133, 901-911.	1.2	155
23	Phylogenetic Parameter Estimation on COWs. , 2005, , 347-368.		0
24	pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. <i>Bioinformatics</i> , 2005, 21, 3794-3796.	1.8	69
25	Unexpected complexity of the Wnt gene family in a sea anemone. <i>Nature</i> , 2005, 433, 156-160.	13.7	516
26	Molecular phylogenetics: parallelized parameter estimation and quartet puzzling. <i>Journal of Parallel and Distributed Computing</i> , 2003, 63, 719-727.	2.7	27
27	Genetic Interaction between Dobrava and Saaremaa Hantaviruses: Now or Millions of Years Ago?. <i>Journal of Virology</i> , 2003, 77, 7156-7158.	1.5	14
28	Genetic Interaction between Distinct Dobrava Hantavirus Subtypes in <i>Apodemus agrarius</i> and <i>A. flavicollis</i> in Nature. <i>Journal of Virology</i> , 2003, 77, 804-809.	1.5	74
29	Maximum-Likelihood Analysis Using TREE-PUZZLE. <i>Current Protocols in Bioinformatics</i> , 2003, 1, 6.6.1-6.6.23.	25.8	24
30	TREE-PUZZLE: maximum likelihood phylogenetic analysis using quartets and parallel computing. <i>Bioinformatics</i> , 2002, 18, 502-504.	1.8	2,389
31	Quartet Trees as a Tool to Reconstruct Large Trees from Sequences. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2002, , 379-388.	0.1	0
32	Axeldb: a <i>Xenopus laevis</i> database focusing on gene expression. <i>Nucleic Acids Research</i> , 2000, 28, 139-140.	6.5	22
33	The Phylogeny of Thermophiles and Hyperthermophiles and the Three Domains of Life. , 1999, , 291-304.		7
34	Division Glaucocystophyta. <i>Plant Systematics and Evolution Supplementum = Entwicklungsgeschichte Und Systematik Der Pflanzen Supplementum</i> , 1997, , 139-148.	1.5	22
35	Phylogeny Reconstruction. , 0, , 83-128.		1