

# Asaf Salamov

## List of Publications by Year in descending order

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Version: 2024-02-01

27  
papers

10,657  
citations

361413

20  
h-index

552781

26  
g-index

33  
all docs

33  
docs citations

33  
times ranked

12785  
citing authors

#	ARTICLE	IF	CITATIONS
1	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
2	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	27.8	1,458
3	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
4	MycoCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014, 42, D699-D704.	14.5	1,187
5	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	21.4	870
6	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
7	Pan genome of the phytoplankton <i>Emiliania</i> underpins its global distribution. <i>Nature</i> , 2013, 499, 209-213.	27.8	448
8	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377
9	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	27.8	332
10	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017, 49, 964-968.	21.4	292
11	Niche of harmful alga <i>Aureococcus anophagefferens</i> revealed through ecogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4352-4357.	7.1	256
12	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
13	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	3.9	175
14	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018, 50, 1688-1695.	21.4	160
15	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. <i>Nature Microbiology</i> , 2021, 6, 499-511.	13.3	116
16	Leveraging single-cell genomics to expand the fungal tree of life. <i>Nature Microbiology</i> , 2018, 3, 1417-1428.	13.3	101
17	PhycoCosm, a comparative algal genomics resource. <i>Nucleic Acids Research</i> , 2021, 49, D1004-D1011.	14.5	98
18	Anaerobic gut fungi are an untapped reservoir of natural products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35

#	ARTICLE	IF	CITATIONS
19	Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 2020, 110, 1180-1188.	2.2	34
20	Phylogenomic Analyses of Non-Dikarya Fungi Supports Horizontal Gene Transfer Driving Diversification of Secondary Metabolism in the Amphibian Gastrointestinal Symbiont, <i>Basidiobolus</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3417-3433.	1.8	27
21	Genome-scale phylogenetic analyses confirm <i>Olpidium</i> as the closest living zoosporic fungus to the non-flagellated, terrestrial fungi. <i>Scientific Reports</i> , 2021, 11, 3217.	3.3	24
22	Persistence and plasticity in bacterial gene regulation. <i>Nature Methods</i> , 2021, 18, 1499-1505.	19.0	23
23	Co-cultivation of the anaerobic fungus <i>Caecomyces churrovis</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. <i>Biotechnology for Biofuels</i> , 2021, 14, 234.	6.2	21
24	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. <i>Microbiome</i> , 2022, 10, 67.	11.1	17
25	Kingdom-Wide Analysis of Fungal Protein-Coding and tRNA Genes Reveals Conserved Patterns of Adaptive Evolution. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	12
26	A single-cell genomics pipeline for environmental microbial eukaryotes. <i>IScience</i> , 2021, 24, 102290.	4.1	7
27	Near-Complete Genome Sequence of <i>Zygosaccharomyces rouxii</i> NRRL Y-64007, a Yeast Capable of Growing on Lignocellulosic Hydrolysates. <i>Microbiology Resource Announcements</i> , 2022, , e0005022.	0.6	0