

# Ekaterina Shelest

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

4,282  
citations

257450

24  
h-index

302126

39  
g-index

48  
all docs

48  
docs citations

48  
times ranked

5990  
citing authors

#	ARTICLE	IF	CITATIONS
1	antiSMASH 4.0â€”improvements in chemistry prediction and gene cluster boundary identification. <i>Nucleic Acids Research</i> , 2017, 45, W36-W41.	14.5	1,196
2	Intimate bacterialâ€”fungal interaction triggers biosynthesis of archetypal polyketides in <i>Aspergillus nidulans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14558-14563.	7.1	607
3	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	8.8	417
4	Comparative Genome Analysis of <i>Trichophyton rubrum</i> and Related Dermatophytes Reveals Candidate Genes Involved in Infection. <i>MBio</i> , 2012, 3, e00259-12.	4.1	211
5	Comparative and functional genomics provide insights into the pathogenicity of dermatophytic fungi. <i>Genome Biology</i> , 2011, 12, R7.	9.6	181
6	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	3.9	175
7	Activation of a Silent Fungal Polyketide Biosynthesis Pathway through Regulatory Cross Talk with a Cryptic Nonribosomal Peptide Synthetase Gene Cluster. <i>Applied and Environmental Microbiology</i> , 2010, 76, 8143-8149.	3.1	143
8	Transcription factors in fungi. <i>FEMS Microbiology Letters</i> , 2008, 286, 145-151.	1.8	142
9	Glucocorticoids limit acute lung inflammation in concert with inflammatory stimuli by induction of SphK1. <i>Nature Communications</i> , 2015, 6, 7796.	12.8	131
10	Novel traits of <i>Trichoderma</i> predicted through the analysis of its secretome. <i>FEMS Microbiology Letters</i> , 2012, 337, 1-9.	1.8	106
11	Terrein Biosynthesis in <i>Aspergillus terreus</i> and Its Impact on Phytotoxicity. <i>Chemistry and Biology</i> , 2014, 21, 719-731.	6.0	106
12	Transcription Factors in Fungi: TFome Dynamics, Three Major Families, and Dual-Specificity TFs. <i>Frontiers in Genetics</i> , 2017, 8, 53.	2.3	105
13	CASSIS and SMIPS: promoter-based prediction of secondary metabolite gene clusters in eukaryotic genomes. <i>Bioinformatics</i> , 2016, 32, 1138-1143.	4.1	102
14	Gene Expansion Shapes Genome Architecture in the Human Pathogen <i>Lichtheimia corymbifera</i> : An Evolutionary Genomics Analysis in the Ancient Terrestrial Mucorales (Mucoromycotina). <i>PLoS Genetics</i> , 2014, 10, e1004496.	3.5	80
15	Breaking the Silence: Protein Stabilization Uncovers Silenced Biosynthetic Gene Clusters in the Fungus <i>Aspergillus nidulans</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 8234-8244.	3.1	64
16	The fungal Î±-amino adipate pathway for lysine biosynthesis requires two enzymes of the aconitase family for the isomerization of homocitrate to homoisocitrate. <i>Molecular Microbiology</i> , 2012, 86, 1508-1530.	2.5	46
17	The <i>Aspergillus fumigatus</i> conidial melanin production is regulated by the bifunctional bHLH DevR and MADSâ€”box RlmA transcription factors. <i>Molecular Microbiology</i> , 2016, 102, 321-335.	2.5	46
18	Chromatin mapping identifies BasR, a key regulator of bacteria-triggered production of fungal secondary metabolites. <i>ELife</i> , 2018, 7, .	6.0	44

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19	Identification of the novel penicillin biosynthesis gene <i>aatB</i> of <i>Aspergillus nidulans</i> and its putative evolutionary relationship to this fungal secondary metabolism gene cluster. <i>Molecular Microbiology</i> , 2008, 70, 445-461.	2.5	40
20	Evolutionary Imprint of Catalytic Domains in Fungal PKS–NRPS Hybrids. <i>ChemBioChem</i> , 2012, 13, 2363-2373.	2.6	34
21	Multimodular type I polyketide synthases in algae evolve by module duplications and displacement of AT domains in trans. <i>BMC Genomics</i> , 2015, 16, 1015.	2.8	33
22	Comparative genomics to explore phylogenetic relationship, cryptic sexual potential and host specificity of <i>Rhynchosporium</i> species on grasses. <i>BMC Genomics</i> , 2016, 17, 953.	2.8	33
23	Bacteria induce pigment formation in the basidiomycete <i>Serpula lacrymans</i> . <i>Environmental Microbiology</i> , 2016, 18, 5218-5227.	3.8	29
24	Evaluating phylogenetic footprinting for human-rodent comparisons. <i>Bioinformatics</i> , 2006, 22, 430-437.	4.1	28
25	The hypoxia-induced dehydrogenase <i>HorA</i> is required for coenzyme Q10 biosynthesis, azole sensitivity and virulence of <i>Aspergillus fumigatus</i> . <i>Molecular Microbiology</i> , 2016, 101, 92-108.	2.5	24
26	Dissimilar pigment regulation in <i>Serpula lacrymans</i> and <i>Paxillus involutus</i> during inter-kingdom interactions. <i>Microbiology (United Kingdom)</i> , 2018, 164, 65-77.	1.8	23
27	15 Genetic and Metabolic Aspects of Primary and Secondary Metabolism of the Zygomycetes. , 2016, , 361-385.		22
28	Shed Light in the DaRk LineagES of the Fungal Tree of Life—STRES. <i>Life</i> , 2020, 10, 362.	2.4	16
29	SiTaR: a novel tool for transcription factor binding site prediction. <i>Bioinformatics</i> , 2011, 27, 2806-2811.	4.1	13
30	HapX Mediates Iron Homeostasis in the Pathogenic Dermatophyte <i>Arthroderma benhamiae</i> but Is Dispensable for Virulence. <i>PLoS ONE</i> , 2016, 11, e0150701.	2.5	13
31	Data-based Reconstruction of Gene Regulatory Networks of Fungal Pathogens. <i>Frontiers in Microbiology</i> , 2016, 7, 570.	3.5	11
32	Construction of predictive promoter models on the example of antibacterial response of human epithelial cells. <i>Theoretical Biology and Medical Modelling</i> , 2005, 2, 2.	2.1	8
33	Draft Genome Sequences of Six <i>Pseudoalteromonas</i> Strains, P1-7a, P1-9, P1-13-1a, P1-16-1b, P1-25, and P1-26, Which Induce Larval Settlement and Metamorphosis in <i>Hydractinia echinata</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	8
34	Positive Selection in Gene Regulatory Factors Suggests Adaptive Pleiotropic Changes During Human Evolution. <i>Frontiers in Genetics</i> , 2021, 12, 662239.	2.3	8
35	DistanceScan: a tool for promoter modeling. <i>Bioinformatics</i> , 2010, 26, 1460-1462.	4.1	7
36	2 Genomics to Study Basal Lineage Fungal Biology: Phylogenomics Suggests a Common Origin. , 2014, , 31-60.		7

#	ARTICLE	IF	CITATIONS
37	The first draft genome of feather grasses using SMRT sequencing and its implications in molecular studies of <i>Stipa</i> . <i>Scientific Reports</i> , 2021, 11, 15345.	3.3	6
38	Comments on the distribution and phylogeny of type I polyketide synthases and nonribosomal peptide synthetases in eukaryotes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3946-E3946.	7.1	4
39	Genome Sequences of Three <i>Pseudoalteromonas</i> Strains (P1-8, P1-11, and P1-30), Isolated from the Marine Hydroid <i>Hydractinia echinata</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	4
40	Draft Genome Sequence of <i>Shewanella</i> sp. Strain P1-14-1, a Bacterial Inducer of Settlement and Morphogenesis in Larvae of the Marine Hydroid <i>Hydractinia echinata</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	4
41	Editorial: Systems Biology of Transcription Regulation. <i>Frontiers in Genetics</i> , 2016, 7, 124.	2.3	0
42	Annotation survey and life-cycle transcriptomics of transcription factors in rust fungi (Pucciniales) identify a possible role for cold shock proteins in dormancy exit. <i>Fungal Genetics and Biology</i> , 2022, , 103698.	2.1	0