CITATION REPORT List of articles citing

Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus

DOI: 10.1186/s13059-017-1151-0 Genome Biology, 2017, 18, 28.

Source: https://exaly.com/paper-pdf/66041530/citation-report.pdf

Version: 2024-04-09

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper IF	Citations
368	Cultivation of Podospora anserina on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. 2017 , 37, 162-171	19
367	Future insights in fungal metabolic engineering. 2017 , 245, 1314-1326	43
366	Incorporating comparative genomics into the design-test-learn cycle of microbial strain engineering. 2017 , 17,	6
365	Sex and the Imperfect Fungi. <i>Microbiology Spectrum</i> , 2017 , 5,	22
364	Aspergilli: Models for systems biology in filamentous fungi. 2017 , 6, 67-73	15
363	Diversity, Application, and Synthetic Biology of Industrially Important Aspergillus Fungi. 2017 , 100, 161-202	68
362	How to boost marine fungal research: A first step towards a multidisciplinary approach by combining molecular fungal ecology and natural products chemistry. 2017 , 36, 57-75	29
361	The novel Aspergillus fumigatus MAT1-2-4 mating-type gene is required for mating and cleistothecia formation. 2017 , 108, 1-12	15
360	Involvement of Penicillium digitatum PdSUT1 in fungicide sensitivity and virulence during citrus fruit infection. 2017 , 203, 57-67	15
359	Evolution of Ecological Niche Breadth. 2017 , 48, 183-206	138
358	Developmental evolution facilitates rapid adaptation. 2017 , 7, 15891	4
357	Fungal Gene Cluster Diversity and Evolution. 2017 , 100, 141-178	29
356	Sex and the Imperfect Fungi. 2017 , 193-214	6
355	Expression-based clustering of CAZyme-encoding genes of Aspergillus niger. 2017 , 18, 900	36
354	Does Osmotic Stress Affect Natural Product Expression in Fungi?. 2017 , 15,	24
353	A Comparison of Microsatellites in Phytopathogenic Species in Order to Develop Markers for the Assessment of Genetic Diversity among Its Isolates. 2017 , 8, 1774	8
352	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. 2017 , 15, e2003583	102

351	Characterization of sulfhydryl oxidase from Aspergillus tubingensis. 2017 , 18, 15	3
350	ATNT: an enhanced system for expression of polycistronic secondary metabolite gene clusters in. 2017 , 4, 13	21
349	Response to Pitt & Taylor 2016: Conservation of Aspergillus with A. niger as the conserved type is unnecessary and potentially disruptive. 2017 , 66, 1439-1446	4
348	Black yeasts in the omics era: Achievements and challenges. 2018 , 56, 32-41	20
347	Genomic diversity in ochratoxigenic and non ochratoxigenic strains of Aspergillus carbonarius. 2018 , 8, 5439	11
346	Advances in molecular and genomic research to safeguard food and feed supply from aflatoxin contamination. 2018 , 11, 47-72	20
345	Inducer-independent production of pectinases in Aspergillus niger by overexpression of the D-galacturonic acid-responsive transcription factor gaaR. 2018 , 102, 2723-2736	29
344	Production of Eketo carboxylic acid dimers in yeast by overexpression of NRPS-like genes from Aspergillus terreus. 2018 , 102, 1663-1672	8
343	Forward genetics screen coupled with whole-genome resequencing identifies novel gene targets for improving heterologous enzyme production in Aspergillus niger. 2018 , 102, 1797-1807	9
342	Efficient oligo nucleotide mediated CRISPR-Cas9 gene editing in Aspergilli. 2018 , 115, 78-89	86
341	Purification and Characterisation of a Thermostable Exylosidase from Aspergillus niger van Tieghem of Potential Application in Lignocellulosic Bioethanol Production. <i>Applied Biochemistry and Biotechnology</i> , 2018 , 186, 712-730	13
340	The fungus Aspergillus niger consumes sugars in a sequential manner that is not mediated by the carbon catabolite repressor CreA. 2018 , 8, 6655	14
339	Comparative study of genome-wide plant biomass-degrading CAZymes in white rot, brown rot and soft rot fungi. 2018 , 9, 93-105	53
338	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. 2018 , 41, 9-14	20
337	A morphological, enzymatic and metabolic approach to elucidate apoptotic-like cell death in fungi exposed to h- and Emolybdenum trioxide nanoparticles. 2018 , 10, 20702-20716	12
336	The gold-standard genome of NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. 2018 , 91, 61-78	33
335	Evolution of asexual and sexual reproduction in the aspergilli. 2018 , 91, 37-59	54
334	Duplications and losses of genes encoding known elements of the stress defence system of the Aspergilli contribute to the evolution of these filamentous fungi but do not directly influence their environmental stress tolerance. 2018 , 91, 23-36	8

333	UrdA Controls Secondary Metabolite Production and the Balance between Asexual and Sexual Development in. 2018 , 9,	1
332	Genomic and exoproteomic diversity in plant biomass degradation approaches among Aspergilli. 2018 , 91, 79-99	12
331	Fungal Stress Database (FSD)a repository of fungal stress physiological data. 2018 , 2018,	9
330	Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. 2018 , 8, 17957	22
329	Identification of the decumbenone biosynthetic gene cluster in and the importance for production of calbistrin. 2018 , 5, 18	14
328	Potential for CRISPR Genetic Engineering to Increase Xenobiotic Degradation Capacities in Model Fungi. 2018 , 61-78	19
327	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). 2018 , 9, 3058	23
326	Microbial communities in different regions of the gastrointestinal tract in East Asian finless porpoises (Neophocaena asiaeorientalis sunameri). 2018 , 8, 14142	9
325	Modulating Transcriptional Regulation of Plant Biomass Degrading Enzyme Networks for Rational Design of Industrial Fungal Strains. 2018 , 6, 133	22
324	Importance of Stress Response Mechanisms in Filamentous Fungi for Agriculture and Industry. 2018 , 189-222	1
323	Hybrid Transcription Factor Engineering Activates the Silent Secondary Metabolite Gene Cluster for (+)-Asperlin in Aspergillus nidulans. 2018 , 13, 3193-3205	22
322	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. 2018 , 50, 1688-1695	100
321	Cyclins in aspergilli: Phylogenetic and functional analyses of group I cyclins. 2018, 91, 1-22	1
320	Metabolic Gene Clusters in Eukaryotes. 2018 , 52, 159-183	81
319	The birth, evolution and death of metabolic gene clusters in fungi. 2018, 16, 731-744	94
318	Encyclopedia of Biophysics. 2018 , 1-6	2
317	Physiological background of the remarkably high Cd tolerance of the Aspergillus fumigatus Af293 strain. 2018 , 58, 957-967	6
316	Broad Genomic Sampling Reveals a Smut Pathogenic Ancestry of the Fungal Clade Ustilaginomycotina. 2018 , 35, 1840-1854	28

315	How a fungus shapes biotechnology: 100lyears of research. 2018 , 5, 13	104
314	Molecular Insights Into Development and Virulence Determinants of : A Proteomic Perspective. 2018 , 8, 180	13
313	Heavy Metal-Induced Expression of PcaA Provides Cadmium Tolerance to and Supports Its Virulence in the Model. 2018 , 9, 744	23
312	Analysis of Putative Sugar Transporter Genes in Using Phylogeny and Comparative Transcriptomics. 2018 , 9, 1045	22
311	On the Evolution of Specificity in Members of the Yeast Amino Acid Transporter Family as Parts of Specific Metabolic Pathways. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	8
310	Analysis of the Relationship between Alternative Respiration and Sterigmatocystin Formation in. 2018 , 10,	6
309	Epigenetic and Posttranslational Modifications in Regulating the Biology of Aspergillus Species. 2018 , 105, 191-226	9
308	Whole-genome sequencing of Aspergillus tubingensis G131 and overview of its secondary metabolism potential. 2018 , 19, 200	16
307	High oxygen tension increases itaconic acid accumulation, glucose consumption, and the expression and activity of alternative oxidase in Aspergillus terreus. 2018 , 102, 8799-8808	14
306	Systematic Dissection of the Evolutionarily Conserved WetA Developmental Regulator across a Genus of Filamentous Fungi. 2018 , 9,	39
305	Inducible promoters and functional genomic approaches for the genetic engineering of filamentous fungi. 2018 , 102, 6357-6372	32
304	Reconstruction of 24 Penicillium genome-scale metabolic models shows diversity based on their secondary metabolism. 2018 , 115, 2604-2612	7
303	Introduction: Overview of Fungal Genomics. 2018 , 1775, 1-7	
302	Banksialactones and Banksiamarins: Isochromanones and Isocoumarins from an Australian Fungus, Aspergillus banksianus. 2018 , 81, 1517-1526	16
301	Fungal Genomes and Genotyping. 2018 , 102, 37-81	6
300	Zombie Cells, Composite Cells of Fungal-Human Keratinocytes of Plantar Hyperkeratosis-Like Lesions. 2019 , 184, 597-605	1
299	MycopathologiaGENOMES: The New @ome@or the Publication of Fungal Genomes. 2019 , 184, 551-554	16
298	Oxidative Stress Response of Induced by Hydrogen Peroxide and Menadione Sodium Bisulfite. 2019 , 7,	9

297	Marine Fungal Diversity: Present Status and Future Perspectives. 2019 , 267-291	2
296	Effects of Different G-Protein	10
295	Enzymes of early-diverging, zoosporic fungi. 2019 , 103, 6885-6902	14
294	A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera and. 2019 , 10,	56
293	Rewiring of transcriptional networks as a major event leading to the diversity of asexual multicellularity in fungi. 2019 , 45, 548-563	12
292	Cinnamic Acid and Sorbic acid Conversion Are Mediated by the Same Transcriptional Regulator in. 2019 , 7, 249	13
291	Practical guidance for the implementation of the CRISPR genome editing tool in filamentous fungi. 2019 , 6, 15	23
2 90	Unconventional Cell Division Cycles from Marine-Derived Yeasts. 2019 , 29, 3439-3456.e5	21
289	The velvet repressed vidA gene plays a key role in governing development in Aspergillus nidulans. 2019 , 57, 893-899	9
288	Citric Acid. 2019 , 158-165	6
288	Citric Acid. 2019, 158-165 Metabolic and regulatory insights from the experimental horizontal gene transfer of the aurofusarin and bikaverin gene clusters to Aspergillus nidulans. 2019, 112, 1684-1700	6
	Metabolic and regulatory insights from the experimental horizontal gene transfer of the	
287	Metabolic and regulatory insights from the experimental horizontal gene transfer of the aurofusarin and bikaverin gene clusters to Aspergillus nidulans. 2019 , 112, 1684-1700	6
287 286	Metabolic and regulatory insights from the experimental horizontal gene transfer of the aurofusarin and bikaverin gene clusters to Aspergillus nidulans. 2019 , 112, 1684-1700 Xyr1 is predominantly involved in xylan degradation and xylose catabolism. 2019 , 12, 220 Structure revision of cryptosporioptides and determination of the genetic basis for dimeric	5
287 286 285	Metabolic and regulatory insights from the experimental horizontal gene transfer of the aurofusarin and bikaverin gene clusters to Aspergillus nidulans. 2019, 112, 1684-1700 Xyr1 is predominantly involved in xylan degradation and xylose catabolism. 2019, 12, 220 Structure revision of cryptosporioptides and determination of the genetic basis for dimeric xanthone biosynthesis in fungi. 2019, 10, 2930-2939 Whole-Genome Sequence Data Uncover Widespread Heterothallism in the Largest Group of	5
287 286 285 284	Metabolic and regulatory insights from the experimental horizontal gene transfer of the aurofusarin and bikaverin gene clusters to Aspergillus nidulans. 2019, 112, 1684-1700 Xyr1 is predominantly involved in xylan degradation and xylose catabolism. 2019, 12, 220 Structure revision of cryptosporioptides and determination of the genetic basis for dimeric xanthone biosynthesis in fungi. 2019, 10, 2930-2939 Whole-Genome Sequence Data Uncover Widespread Heterothallism in the Largest Group of Lichen-Forming Fungi. 2019, 11, 721-730 Integration of Fungus-Specific CandA-C1 into a Trimeric CandA Complex Allowed Splitting of the Gene for the Conserved Receptor Exchange Factor of CullinA E3 Ubiquitin Ligases in Aspergilli.	6 5 22 10
287 286 285 284 283	Metabolic and regulatory insights from the experimental horizontal gene transfer of the aurofusarin and bikaverin gene clusters to Aspergillus nidulans. 2019, 112, 1684-1700 Xyr1 is predominantly involved in xylan degradation and xylose catabolism. 2019, 12, 220 Structure revision of cryptosporioptides and determination of the genetic basis for dimeric xanthone biosynthesis in fungi. 2019, 10, 2930-2939 Whole-Genome Sequence Data Uncover Widespread Heterothallism in the Largest Group of Lichen-Forming Fungi. 2019, 11, 721-730 Integration of Fungus-Specific CandA-C1 into a Trimeric CandA Complex Allowed Splitting of the Gene for the Conserved Receptor Exchange Factor of CullinA E3 Ubiquitin Ligases in Aspergilli. 2019, 10, The polyubiquitin gene is required for conidiation, conidial germination, and stress tolerance in the	6 5 22 10 4

279	Biaryl-Forming Enzymes from Aspergilli Exhibit Substrate-Dependent Stereoselectivity. 2019 , 58, 2589-2593	16
278	Comparative Transcriptome Analysis Shows Conserved Metabolic Regulation during Production of Secondary Metabolites in Filamentous Fungi. <i>MSystems</i> , 2019 , 4,	7
277	Resistance Gene-Directed Genome Mining of 50 Species. <i>MSystems</i> , 2019 , 4, 7.6	12
276	Aspergillus: A Multifaceted Genus. 2019 ,	
275	Cpf1 enables fast and efficient genome editing in Aspergilli. 2019 , 6, 6	30
274	MrArk1, an actin-regulating kinase gene, is required for endocytosis and involved in sustaining conidiation capacity and virulence in Metarhizium robertsii. 2019 , 103, 4859-4868	8
273	Genomic analysis of ant domatia-associated melanized fungi (Chaetothyriales, Ascomycota). 2019 , 18, 541-552	10
272	Proteome analysis of biofilm produced by a Fusarium falciforme keratitis infectious agent. 2019 , 130, 232-241	7
271	Unraveling the Contribution of High Temperature Stage to Jiang-Flavor Daqu, a Liquor Starter for Production of Chinese Jiang-Flavor Baijiu, With Special Reference to Metatranscriptomics. 2019 , 10, 472	26
270	A novel transcriptional regulator RXE1 modulates the essential transactivator XYR1 and cellulase gene expression in Trichoderma reesei. 2019 , 103, 4511-4523	19
269	Mutations in AraR leading to constitutive expression of arabinolytic genes in Aspergillus niger under derepressing conditions [corrected]. 2019 , 103, 4125-4136	3
268	Heterologous Expression and Characterization of a New Clade of Aspergillus &L-Rhamnosidase Suitable for Citrus Juice Processing. 2019 , 67, 2926-2935	8
267	The presence of trace components significantly broadens the molecular response of Aspergillus niger to guar gum. 2019 , 51, 57-66	6
266	Decrease of citric acid produced by through disruption of the gene encoding a putative mitochondrial citrate-oxoglutarate shuttle protein. 2019 , 83, 1538-1546	7
265	Itaconic acid degradation in : the role of unexpected bioconversion pathways. 2019, 6, 1	11
264	Updating genome annotation for the microbial cell factory Aspergillus niger using gene co-expression networks. 2019 , 47, 559-569	36
263	On top of biosynthetic gene clusters: How epigenetic machinery influences secondary metabolism in fungi. 2019 , 37, 107345	57
262	Developments and opportunities in fungal strain engineering for the production of novel enzymes and enzyme cocktails for plant biomass degradation. 2019 , 37, 107361	26

261	Significance of Aspergillus niger aggregate species as contaminants of food products in Spain regarding their occurrence and their ability to produce mycotoxins. 2019 , 82, 240-248	20
260	Contribution of proteases and cellulases produced by solid-state fermentation to the improvement of corn ethanol production. 2019 , 6,	5
259	Species-Specific Differences in the Susceptibility of Fungi to the Antifungal Protein AFP Depend on C-3 Saturation of Glycosylceramides. 2019 , 4,	7
258	Supporting supervised learning in fungal Biosynthetic Gene Cluster discovery: new benchmark datasets. 2019 ,	1
257	Wild toxicity, cultivated safety: aflatoxin and kji classification as knowledge infrastructure. 2019 , 35, 405-424	1
256	Identification and Characterization of Mutants Impaired in Asexual Development under Phosphate Stress. 2019 , 8,	4
255	Genomes and secretomes of Ascomycota fungi reveal diverse functions in plant biomass decomposition and pathogenesis. 2019 , 20, 976	26
254	Biodegradable Drug-Delivery Peptide Nanocapsules. 2019 , 4, 20059-20063	5
253	Can interaction specificity in the fungus-farming termite symbiosis be explained by nutritional requirements of the fungal crop?. 2019 , 38, 54-61	10
252	RNA polymerase II ChIP-seq-a powerful and highly affordable method for studying fungal genomics and physiology. 2019 , 11, 79-82	10
251	Genetic Diversity Among Candida albicans Isolated from Humans and Cattle with Respiratory Distress in Egypt. 2019 , 19, 199-206	1
250	Aspergillus nidulans in the post-genomic era: a top-model filamentous fungus for the study of signaling and homeostasis mechanisms. 2020 , 23, 5-22	10
249	Recombinant production and characterization of six novel GH27 and GH36 lgalactosidases from Penicillium subrubescens and their synergism with a commercial mannanase during the hydrolysis of lignocellulosic biomass. 2020 , 295, 122258	12
248	Characterization of gfdB, putatively encoding a glycerol 3-phosphate dehydrogenase in Aspergillus nidulans. <i>Fungal Biology</i> , 2020 , 124, 352-360	1
247	Identification of a novel anthocyanin synthesis pathway in the fungus Aspergillus sydowii H-1. 2020 , 21, 29	16
246	Limitation of nitrogen source facilitated the production of nonmeiotic recombinants in Aspergillus nidulans. 2020 , 60, 380-385	O
245	Analysis of polysaccharide hydrolases secreted by FP-500 on corn cobs and wheat bran as complex carbon sources. 2020 , 50, 390-400	3
244	Combined Comparative Genomics and Gene Expression Analyses Provide Insights into the Terpene Synthases Inventory in. 2020 , 8,	16

(2020-2020)

243	: Genome Analysis and Characterization of Two Heterologous Expressed, Non-redundant Xylanases. 2020 , 11, 2154		2
242	Dynamics in Secondary Metabolite Gene Clusters in Otherwise Highly Syntenic and Stable Genomes in the Fungal Genus Botrytis. 2020 , 12, 2491-2507		8
241	Transcriptomic analysis of polyaromatic hydrocarbon degradation by the halophilic fungus Aspergillus sydowii at hypersaline conditions. <i>Environmental Microbiology</i> , 2021 , 23, 3435-3459	5.2	13
240	A brief introduction to microbiology and biotechnology. 2020 , 1-30		1
239	Genome sequence of Acremonium strictum AAJ6 strain isolated from the Cerrado biome in Brazil and CAZymes expression in thermotolerant industrial yeast for ethanol production. 2020 , 98, 139-150		2
238	The Intermediates in Branched-Chain Amino Acid Biosynthesis Are Indispensable for Conidial Germination of the Insect-Pathogenic Fungus Metarhizium. 2020 , 86,		6
237	Combinatorial Action of Different Stress Factors on the Composition of Membrane Lipids and Osmolytes of Aspergillus niger. 2020 , 89, 405-412		0
236	Comprehensive chemotaxonomic and genomic profiling of a biosynthetically talented Australian fungus, Aspergillus burnettii sp. nov. 2020 , 143, 103435		11
235	Peculiar genomic traits in the stress-adapted cryptoendolithic Antarctic fungus Friedmanniomyces endolithicus. <i>Fungal Biology</i> , 2020 , 124, 458-467	2.8	16
234	Draft Genome Sequences of Four Section Clinical Strains. 2020 , 9,		3
234	Draft Genome Sequences of Four Section Clinical Strains. 2020, 9, Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid concentration and parasitizing its sclerotia. <i>Environmental Microbiology</i> , 2020, 22, 5265-5279	5.2	6
	Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid	5.2	
233	Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid concentration and parasitizing its sclerotia. <i>Environmental Microbiology</i> , 2020 , 22, 5265-5279 Genome Wide Analysis Reveals the Role of VadA in Stress Response, Germination, and	5.2	6
233	Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid concentration and parasitizing its sclerotia. <i>Environmental Microbiology</i> , 2020 , 22, 5265-5279 Genome Wide Analysis Reveals the Role of VadA in Stress Response, Germination, and Sterigmatocystin Production in Conidia. 2020 , 8,	5.2	6
233 232 231	Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid concentration and parasitizing its sclerotia. <i>Environmental Microbiology</i> , 2020 , 22, 5265-5279 Genome Wide Analysis Reveals the Role of VadA in Stress Response, Germination, and Sterigmatocystin Production in Conidia. 2020 , 8, LBM 134 isolated from rotten wood and its potential cellulolytic ability. 2021 , 12, 160-173 Comparative Characterization of Pectin Lyases by Discriminative Substrate Degradation Profiling.	6.3	6 1 2
233 232 231 230	Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid concentration and parasitizing its sclerotia. <i>Environmental Microbiology</i> , 2020 , 22, 5265-5279 Genome Wide Analysis Reveals the Role of VadA in Stress Response, Germination, and Sterigmatocystin Production in Conidia. 2020 , 8, LBM 134 isolated from rotten wood and its potential cellulolytic ability. 2021 , 12, 160-173 Comparative Characterization of Pectin Lyases by Discriminative Substrate Degradation Profiling. 2020 , 8, 873 The Gene Deletion Reveals That Patulin Biosynthesis Is Not Related to Conidiation in. <i>International</i>		6 1 2
233 232 231 230 229	Aspergillus spp. eliminate Sclerotinia sclerotiorum by imbalancing the ambient oxalic acid concentration and parasitizing its sclerotia. <i>Environmental Microbiology</i> , 2020 , 22, 5265-5279 Genome Wide Analysis Reveals the Role of VadA in Stress Response, Germination, and Sterigmatocystin Production in Conidia. 2020 , 8, LBM 134 isolated from rotten wood and its potential cellulolytic ability. 2021 , 12, 160-173 Comparative Characterization of Pectin Lyases by Discriminative Substrate Degradation Profiling. 2020 , 8, 873 The Gene Deletion Reveals That Patulin Biosynthesis Is Not Related to Conidiation in. <i>International Journal of Molecular Sciences</i> , 2020 , 21, Velvet activated McrA plays a key role in cellular and metabolic development in Aspergillus		6 1 2 4 3

225	Unconventional Secretion of Nigerolysins A from Species. 2020 , 8,	О
224	Shed Light in the DaRk LineagES of the Fungal Tree of Life-STRES. 2020 , 10,	4
223	Identification and Expression Analysis of Sugar Transporter Gene Family in. 2020 , 2020, 7146701	2
222	Heterotrimeric G-protein signalers and RGSs in. 2020 , 9,	5
221	Genomic and Phenotypic Heterogeneity of Clinical Isolates of the Human Pathogens , , and. 2020 , 11, 459	21
220	Recurrent Loss of abaA, a Master Regulator of Asexual Development in Filamentous Fungi, Correlates with Changes in Genomic and Morphological Traits. 2020 , 12, 1119-1130	4
219	Supplementation of Aspergillus glaucus with gfdB gene encoding a glycerol 3-phosphate dehydrogenase in Aspergillus nidulans. 2020 , 60, 691-698	O
218	Rare earth element sequestration by biomass. 2021 , 42, 3725-3735	3
217	Improvement of homologous GH10 xylanase production by deletion of genes with predicted function in the Aspergillus nidulans secretion pathway. 2020 , 13, 1245-1253	7
216	Evolving moldy murderers: Aspergillus section Fumigati as a model for studying the repeated evolution of fungal pathogenicity. 2020 , 16, e1008315	17
215	Classification of , , and related genera (): An overview of families, genera, subgenera, sections, series and species. 2020 , 95, 5-169	135
214	Sugar transporters from industrial fungi: Key to improving second-generation ethanol production. 2020 , 131, 109991	15
213	Pathogenic Allodiploid Hybrids of Aspergillus Fungi. 2020 , 30, 2495-2507.e7	15
212	Evolutionary compromises in fungal fitness: hydrophobins can hinder the adverse dispersal of conidiospores and challenge their survival. 2020 , 14, 2610-2624	17
211	Nitric oxide homeostasis is required for light-dependent regulation of conidiation in Aspergillus. 2020 , 137, 103337	8
210	Identification and Characterization of a Cellodextrin Transporter in. 2020 , 11, 145	2
209	Identification of Secondary Metabolites from by Untargeted UPLC-ESI-HRMS/MS and Genome Mining. 2020 , 25,	2
208	A comparative genomics study of 23 Aspergillus species from section Flavi. 2020 , 11, 1106	54

207	The Third International Symposium on Fungal Stress - ISFUS. <i>Fungal Biology</i> , 2020 , 124, 235-252 2.8	4
206	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. 2020 , 28, 487-499	12
205	Genomic diversity in flavobacterial pathogens of aquatic origin. 2020 , 142, 104053	7
204	The role of the VosA-repressed dnjA gene in development and metabolism in Aspergillus species. 2020 , 66, 621-633	7
203	Comparative genomics of the aconidial Aspergillus niger strain LDM3 predicts genes associated with its high protein secretion capacity. 2020 , 104, 2623-2637	5
202	The Regulator VosA Governs Survival and Secondary Metabolism of Sexual Spores in. 2020 , 11,	8
201	Identification of SclB, a Zn(II)Cys transcription factor involved in sclerotium formation in Aspergillus niger. 2020 , 139, 103377	10
200	Molecular Mechanisms of Conidial Germination in spp. 2020 , 84,	27
199	Exploring the Brazilian diversity of Aspergillus sp. strains for lovastatin and itaconic acid production. 2020 , 138, 103367	1
198	Fungal evolution: cellular, genomic and metabolic complexity. 2020 , 95, 1198-1232	27
197	Homeobox proteins are essential for fungal differentiation and secondary metabolism in Aspergillus nidulans. 2020 , 10, 6094	5
196	Succession of physiological stages hallmarks the transcriptomic response of thelfungus to lignocellulose. 2020 , 13, 69	2
195	Applications of Fungal Pectinases. 2021 , 316-325	1
194	Identification and characterization of Aspergillus species of fruit rot fungi using microscopy, FT-IR, Raman and UV-Vis spectroscopy. 2021 , 246, 119010	12
193	Genetic Manipulation and Transformation Methods for Aspergillus spp 2021 , 49, 95-104	3
192	Penicilliumdigitatum MFS transporters can display different roles during pathogen-fruit interaction. 2021 , 337, 108918	2
191	High Quality Genomes and Transcriptomes: A Platform for Cellulase Activity Optimization Toward Industrial Applications. 2020 , 8, 607176	3
190	Clinker & clustermap.js: Automatic generation of gene cluster comparison figures. <i>Bioinformatics</i> , 7.2	89

189 Bioinformatics Approaches for Fungal Biotechnology. **2021**, 536-554

188	Fungi endophytes for biofactory of secondary metabolites: Genomics and metabolism. 2021 , 1-21		1
187	Distribution of methionine sulfoxide reductases in fungi and conservation of the free-methionine-R-sulfoxide reductase in multicellular eukaryotes.		
186	Protein expression and secretion by filamentous fungi. 2021 , 46, 1		2
185	Development of a CRISPR/Cpf1 system for targeted gene disruption in Aspergillus aculeatus TBRC 277. 2021 , 21, 15		2
184	The Functional Order (FunOrder) tool Identification of essential biosynthetic genes through computational molecular co-evolution.		1
183	Transcriptomic, Protein-DNA Interaction, and Metabolomic Studies of VosA, VelB, and WetA in Aspergillus nidulans Asexual Spores. 2021 , 12,		7
182	$H\Pi$ e-cell-mediated protection of fungal reproductive and overwintering structures against fungivorous animals.		
181	DIVERSIFY: A Fungal Multispecies Gene Expression Platform. 2021 , 10, 579-588		3
180	Cutaneous Aspergillosis in Children and Adolescents. 2021 , 15, 41-48		1
179	Transcription factors in the fungus Aspergillus nidulans: Markers of genetic innovation, network rewiring and conflict between genomics and transcriptomics.		1
178	Revisiting a @imple@fungal metabolic pathway reveals redundancy, complexity and diversity. 2021 , 14, 2525-2537		5
177	Optimization of Inulin Hydrolysis by Inulinases and Efficient Conversion Into Polyhydroxyalkanoates. 2021 , 9, 616908		5
176	Loss of function of the carbon catabolite repressor CreA leads to low but inducer-independent expression from the feruloyl esterase B promoter in Aspergillus niger. 2021 , 43, 1323-1336		O
175	The glucoamylase from Aspergillus wentii: Purification and characterization. 2021 , 61, 443-458		3
174	Heterologous Biosynthesis of Tetrahydroxanthone Dimers: Determination of Key Factors for Selective or Divergent Synthesis. 2021 , 84, 1544-1549		3
173	Identifying Conserved Generic spp. Co-Expressed Gene Modules Associated with Germination Using Cross-Platform and Cross-Species Transcriptomics. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	1
172	Distinctive role of fluG in the adaptation of Beauveria bassiana to insect-pathogenic lifecycle and environmental stresses. <i>Environmental Microbiology</i> , 2021 , 23, 5184-5199	5.2	4

(2021-2021)

171	Multi-omics analysis provides insights into lignocellulosic biomass degradation by Laetiporus sulphureus ATCC 52600. 2021 , 14, 96		5
170	The DUG Pathway Governs Degradation of Intracellular Glutathione in Aspergillus nidulans. 2021 , 87,		2
169	Worldwide aflatoxin contamination of agricultural products and foods: From occurrence to control. 2021 , 20, 2332-2381		21
168	Identification of a Conserved Transcriptional Activator-Repressor Module Controlling the Expression of Genes Involved in Tannic Acid Degradation and Gallic Acid Utilization in Aspergillus niger. <i>Frontiers in Fungal Biology</i> , 2021 , 2,	0.3	1
167	Microevolution in the pansecondary metabolome of and its potential macroevolutionary implications for filamentous fungi. 2021 , 118,		8
166	Functions of PUF Family RNA-Binding Proteins in. 2021 , 31, 676-685		1
165	Transcriptional Analysis of Mycelia and Spherules by RNA Sequencing. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021 , 7,	5.6	3
164	Duplication and Functional Divergence of Branched-Chain Amino Acid Biosynthesis Genes in Aspergillus nidulans. 2021 , 12, e0076821		2
163	Distribution of methionine sulfoxide reductases in fungi and conservation of the free-methionine-R-sulfoxide reductase in multicellular eukaryotes. 2021 , 169, 187-215		2
162	Aspergillus terreus Species Complex. 2021 , e0031120		6
162 161	Aspergillus terreus Species Complex. 2021, e0031120 Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021, 151, 103564		3
	Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021 ,		
161	Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021 , 151, 103564		3
161 160	Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021, 151, 103564 Metabolic Engineering of Filamentous Fungi. 2021, 765-801 Blocking utilization of major plant biomass polysaccharides leads Aspergillus niger towards		3
161 160 159	Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021, 151, 103564 Metabolic Engineering of Filamentous Fungi. 2021, 765-801 Blocking utilization of major plant biomass polysaccharides leads Aspergillus niger towards utilization of minor components. 2021, 14, 1683-1698 Genomic and transcriptomic analysis of the thermophilic lignocellulose-degrading fungus Thielavia	5.6	3 4
161 160 159 158	Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021, 151, 103564 Metabolic Engineering of Filamentous Fungi. 2021, 765-801 Blocking utilization of major plant biomass polysaccharides leads Aspergillus niger towards utilization of minor components. 2021, 14, 1683-1698 Genomic and transcriptomic analysis of the thermophilic lignocellulose-degrading fungus Thielavia terrestris LPH172. 2021, 14, 131 Transcription Factors in the Fungus: Markers of Genetic Innovation, Network Rewiring and Conflict	5.6	347
161 160 159 158	Characterization of the asexual developmental genes brlA and wetA in Monascus ruber M7. 2021, 151, 103564 Metabolic Engineering of Filamentous Fungi. 2021, 765-801 Blocking utilization of major plant biomass polysaccharides leads Aspergillus niger towards utilization of minor components. 2021, 14, 1683-1698 Genomic and transcriptomic analysis of the thermophilic lignocellulose-degrading fungus Thielavia terrestris LPH172. 2021, 14, 131 Transcription Factors in the Fungus: Markers of Genetic Innovation, Network Rewiring and Conflict between Genomics and Transcriptomics. <i>Journal of Fungi (Basel, Switzerland)</i> , 2021, 7, The G-protein coupled receptor GPRK contributes to fungal development and full virulence in	5.6	3 3 4 7

153	Aspergillus sp. A31 and Curvularia geniculata P1 mitigate mercury toxicity to Oryza sativa L. 2021 , 203, 5345-5361		3
152	Biosynthetic gene cluster profiling predicts the positive association between antagonism and phylogeny in Bacillus.		O
151	Action of Extracellular Proteases of and Micromycetes on Plasma Hemostasis Proteins. 2021, 11,		O
150	Fungal tolerance to Congo red, a cell wall integrity stress, as a promising indicator of ecological niche. <i>Fungal Biology</i> , 2021 , 125, 646-657	2.8	1
149	Identification of Genes Involved in the Synthesis of the Fungal Cell Wall Component Nigeran and Regulation of Its Polymerization in Aspergillus. 2021 , 87, e0114421		3
148	Evidence for an arginine-dependent route for the synthesis of NO in the model filamentous fungus Aspergillus nidulans. <i>Environmental Microbiology</i> , 2021 , 23, 6924-6939	5.2	1
147	Examining Signatures of Natural Selection in Antifungal Resistance Genes Across Aspergillus Fungi. <i>Frontiers in Fungal Biology</i> , 2021 , 2,	0.3	О
146	FunOrder: A robust and semi-automated method for the identification of essential biosynthetic genes through computational molecular co-evolution. 2021 , 17, e1009372		1
145	Biotechnological valorization of cashew apple juice for the production of citric acid by a local strain of Aspergillus niger LCFS 5. 2021 , 19, 137		1
144	Insights into the Lignocellulose-Degrading Enzyme System of var. Based on Genome and Transcriptome Analysis. <i>Microbiology Spectrum</i> , 2021 , 9, e0108821	8.9	4
143	Beyond the Biosynthetic Gene Cluster Paradigm: Genome-Wide Coexpression Networks Connect Clustered and Unclustered Transcription Factors to Secondary Metabolic Pathways. <i>Microbiology Spectrum</i> , 2021 , 9, e0089821	8.9	2
142	Mr-AbaA Regulates Conidiation by Interacting with the Promoter Regions of Both and in Metarhizium robertsii. <i>Microbiology Spectrum</i> , 2021 , 9, e0082321	8.9	2
141	versus Genus : Conservation, Adaptive Evolution and Specific Virulence Genes. 2021 , 9,		О
140	Analysis of genomic characteristics and their influence on metabolism in Aspergillus luchuensis albino mutants using genome sequencing. 2021 , 155, 103601		1
139	MrGcn5 is required for the mycotoxin production, sexual and asexual development in Monascus ruber. 2021 , 43, 101304		1
138	Carbon utilization and growth-inhibition of citrus-colonizing Phyllosticta species. <i>Fungal Biology</i> , 2021 , 125, 815-825	2.8	О
137	Lytic polysaccharide monooxygenases (LPMOs) producing microbes: A novel approach for rapid recycling of agricultural wastes. 2022 , 806, 150451		2
136	Complete genome sequence of lovastatin producer Aspergillus terreus ATCC 20542 and evaluation of genomic diversity among A. terreus strains. 2021 , 105, 1615-1627		O

135	Identification of an Acidic Amino Acid Permease Involved in d-Aspartate Uptake in the Yeast. 2021 , 9,	1
134	Modification of Plant Carbohydrates Using Fungal Enzymes. 2021 , 370-384	1
133	Increased Cd biosorption capability of Aspergillus nidulans elicited by crpA deletion. 2020 , 60, 574-584	3
132	The Current Biotechnological Status and Potential of Plant and Algal Biomass Degrading/Modifying Enzymes from Ascomycete Fungi. 2020 , 81-120	9
131	Fungal Laccases and Their Potential in Bioremediation Applications. 2020 , 1-25	5
130	Coordination of Fungal Secondary Metabolism and Development. 2020 , 173-205	2
129	Encyclopedia of Biophysics. 2018 , 1-6	1
128	Production and Application of Novel Bio-active Compounds by Endophytic Microbes. 2019 , 1-40	1
127	TOUCAN: a framework for fungal biosynthetic gene cluster discovery. 2020 , 2, lqaa098	4
126	clinker & clustermap.js: Automatic generation of gene cluster comparison figures.	11
126	Clinker & clustermap.js: Automatic generation of gene cluster comparison figures. A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera Aspergillus and Penicillium.	3
	A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera	
125	A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera Aspergillus and Penicillium. The fungal sexual revolution continues: discovery of sexual development in members of the genus	3
125	A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera Aspergillus and Penicillium. The fungal sexual revolution continues: discovery of sexual development in members of the genus Aspergillus and its consequences. 2020, 7, 17	3
125 124 123	A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera Aspergillus and Penicillium. The fungal sexual revolution continues: discovery of sexual development in members of the genus Aspergillus and its consequences. 2020, 7, 17 The role of VosA/VelB-activated developmental gene vadA in Aspergillus nidulans. 2017, 12, e0177099 Secondary metabolites of HIle cells mediate protection of fungal reproductive and overwintering	3 1 15
125 124 123	A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera Aspergillus and Penicillium. The fungal sexual revolution continues: discovery of sexual development in members of the genus Aspergillus and its consequences. 2020, 7, 17 The role of VosA/VelB-activated developmental gene vadA in Aspergillus nidulans. 2017, 12, e0177099 Secondary metabolites of HIle cells mediate protection of fungal reproductive and overwintering structures against fungivorous animals. 2021, 10,	3 1 15
125 124 123 122	A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera Aspergillus and Penicillium. The fungal sexual revolution continues: discovery of sexual development in members of the genus Aspergillus and its consequences. 2020, 7, 17 The role of VosA/VelB-activated developmental gene vadA in Aspergillus nidulans. 2017, 12, e0177099 Secondary metabolites of HIle cells mediate protection of fungal reproductive and overwintering structures against fungivorous animals. 2021, 10, Sex and self defense. 2021, 10, Conservation and Divergence in the Asexual Sporulation Gene Regulatory Network Across a Genus	3 1 15

117	Rewiring of transcriptional networks as a major event leading to the diversity of asexual multicellularity in fungi.		O
116	Unconventional cell division cycles from marine-derived yeasts.		
115	Species-specific differences in the susceptibility of fungi towards the antifungal protein AFP depend on C3 saturation of glycosylceramides.		
114	Succession of physiological stages hallmarks the transcriptomic response of fungusAspergillus nigerto lignocellulose.		
113	Recurrent loss ofabaA, a master regulator of asexual development in filamentous fungi, correlates with changes in genomic and morphological traits.		
112	Network analysis reveals different strategies of Trichoderma spp. associated with XYR1 and CRE1 during cellulose degradation.		2
111	Extensive sequence divergence of non-coding regions between Aspergillus fumigatus, a major fungal pathogen of humans, and its relatives.		
110	Aspergillus fumigatus versus Genus Aspergillus: Conservation, adaptive evolution and specific virulence genes.		
109	Effect of different carbon sources on the growth and enzyme production of a toxigenic and a non-toxigenic strain of. 2021 , 51, 769-779		1
108	New Avenues Toward Drug Discovery in Fungi. 2020 , 267-295		
107	Meeting a Challenge: A View on Studying Transcriptional Control of Genes Involved in Plant Biomass Degradation in Aspergillus niger. 2020 , 211-235		O
106	G-protein-coupled Receptors in Fungi. Fungal Biology, 2020 , 37-126	2.3	O
105	Genomic and phenotypic heterogeneity of clinical isolates of the human pathogens Aspergillus fumigatus, Aspergillus lentulus and Aspergillus fumigatiaffinis.		O
104	Genome sequencing of @CHAQprovides insights into salt-stress adaptation. 2020 , 8, e8609		1
103	Fungal xylanolytic enzymes: Diversity and applications. 2022 , 344, 126290		3
102	Diversity of Lactococcus garvieae by Genomic Approaches.		
101	Transcriptomic, protein-DNA interaction, and metabolomic studies of VosA, VelB, and WetA in Aspergillus nidulans asexual spores.		
100	Identification of toxic mold species through Raman spectroscopy of fungal conidia. 2020 , 15, e0242361		4

99	Promoter exchange of the cryptic nonribosomal peptide synthetase gene for oligopeptide production in Aspergillus oryzae. 2021 , 1		1
98	Synthaser: a CD-Search enabled Python toolkit for analysing domain architecture of fungal secondary metabolite megasynth(et)ases. 2021 , 8, 13		1
97	Safety assessment of purine nucleosidase from Aspergillus luchuensis. 2021 , 5, 239784732110614		
96	Comparative characterization of nine novel GH51, GH54 and GH62 fl-arabinofuranosidases from Penicillium subrubescens 2022 ,		1
95	Novel pentose-regulated promoter of with application in controlling heterologous gene expression 2022 , 33, e00695		O
94	Role and genetic basis of specialised secondary metabolites in Trichoderma ecophysiology. 2022 , 39, 83-99		3
93	A large transposable element mediates metal resistance in the fungus Paecilomyces variotii 2022,		3
92	Acquiring novel chemicals by overexpression of a transcription factor DibT in the dibenzodioxocinone biosynthetic cluster in Pestalotiopsis microspora 2022 , 257, 126977		
91	Dermatophytes and Dermatophytosis. 2022,		
90	Whole-Genome Sequencing and Comparative Genomic Analysis of Potential Biotechnological Strains from Trichoderma harzianum, Trichoderma atroviride, and Trichoderma reesei.		
89	Biosynthetic gene cluster profiling predicts the positive association between antagonism and phylogeny in Bacillus 2022 , 13, 1023		2
88	Network Analysis Reveals Different Cellulose Degradation Strategies Across Strains Associated With XYR1 and CRE1 2022 , 13, 807243		1
87	Xylo-Oligosaccharide Utilization by Engineered to Produce Ethanol 2022, 10, 825981		O
86	Differential Roles of Five Fluffy Genes (-) in the Lifecycle In Vitro and In Vivo of the Insect-Pathogenic Fungus <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8,	5.6	1
85	Robust Profiling of Cytochrome P450s (P450ome) in Notable spp 2022 , 12,		3
84	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus 2022 , 25, 104065		1
83	Analysis of carbohydrate-active enzymes and sugar transporters in Penicillium echinulatum: A genome-wide comparative study of the fungal lignocellulolytic system 2022 , 822, 146345		1
82	High molecular weight DNA extraction methods lead to high quality filamentous ascomycete fungal genome assemblies using Oxford Nanopore sequencing 2022 , 8,		О



(-2019)



45	pH-dependent effect of Congo Red on the growth of Aspergillus nidulans and Aspergillus niger. <i>Fungal Biology</i> , 2022 ,	2.8	
44	Genes Involved in the Secondary Metabolism of Trichoderma and the Biochemistry of These Compounds. <i>Fungal Biology</i> , 2022 , 113-135	2.3	
43	The Potential for Cellulose Deconstruction in Fungal Genomes. <i>Encyclopedia</i> , 2022 , 2, 990-1003		1
42	Polyphasic Characterization of Four Aspergillus Species as Potential Biocontrol Agents for White Mold Disease of Bean. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8, 626	5.6	1
41	Biologia futura: combinatorial stress responses in fungi. Biologia Futura,	1	0
40	Deletion of AA9 Lytic Polysaccharide Monooxygenases Impacts A. nidulans Secretome and Growth on Lignocellulose. <i>Microbiology Spectrum</i> ,	8.9	
39	Comparative Genomics of Three Aspergillus Strains Reveals Insights into Endophytic Lifestyle and Endophyte-Induced Plant Growth Promotion. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022 , 8, 690	5.6	
38	Improving candidate Biosynthetic Gene Clusters in fungi through reinforcement learning. Bioinformatics,	7.2	Ο
37	Effect of the combinatorial iron-chelation and oxidative stress on the growth of Aspergillus species. <i>Research in Microbiology</i> , 2022 , 103969	4	1
36	FluG and FluG-like FlrA Coregulate Manifold Gene Sets Vital for Fungal Insect-Pathogenic Lifestyle but Not Involved in Asexual Development. <i>MSystems</i> ,	7.6	1
35	The Exploring Functional Role of Ammonium Transporters of Aspergillus oryzae in Nitrogen Metabolism: Challenges towards Cell Biomass Production. <i>International Journal of Molecular Sciences</i> , 2022 , 23, 7567	6.3	
34	The importance of complete and high-quality genome sequences in Aspergillus niger research. <i>Frontiers in Fungal Biology</i> , 3,	0.3	
33	Extensive Non-Coding Sequence Divergence Between the Major Human Pathogen Aspergillus fumigatus and its Relatives. <i>Frontiers in Fungal Biology</i> , 3,	0.3	
32	Molecular advances in microbial Egalactosidases: challenges and prospects. <i>World Journal of Microbiology and Biotechnology</i> , 2022 , 38,	4.4	
31	Inactivation of MrSir2 in Monascus ruber Influenced the Developmental Process and the Production of Monascus Azaphilone Pigments. <i>Applied Biochemistry and Biotechnology</i> ,	3.2	0
30	Characterization of BbKlf1 as a novel transcription factor vital for asexual and infection cycles of Beauveria bassiana. <i>Environmental Microbiology Reports</i> ,	3.7	
29	Phylogeny of Regulators of G-Protein Signaling Genes in Leptographium qinlingensis and Expression Levels of Three RGSs in Response to Different Terpenoids. 2022 , 10, 1698		O
28	Starships are active eukaryotic transposable elements mobilized by a new family of tyrosine recombinases.		1

27 Evolution and codon usage bias of mitochondrial and nuclear genomes in Aspergillus section Flavi.

,		
26	Application of Aspergillus niger in Practical Biotechnology of Industrial Recovery of Potato Starch By-Products and Its Flocculation Characteristics. 2022 , 10, 1847	O
25	????????. 2022,	O
24	Monitoring of sterigmatocystin biosynthesis using RT-qPCR in airborne Aspergillus species of the series Versicolores. 2022 , 106580	O
23	Enforcement of Postzygotic Species Boundaries in the Fungal Kingdom.	0
22	Regulation of Conidiogenesis in Aspergillus flavus. 2022 , 11, 2796	O
21	Assessing the intracellular primary metabolic profile of Trichoderma reesei and Aspergillus niger grown on different carbon sources. 3,	O
20	Towards Understanding the Function of Aegerolysins. 2022 , 14, 629	O
19	Manipulation of the Global Regulator mcrA Upregulates Secondary Metabolite Production in Aspergillus wentii Using CRISPR-Cas9 with In Vitro Assembled Ribonucleoproteins.	1
18	Evolution and codon usage bias of mitochondrial and nuclear genomes in Aspergillus section Flavi.	O
17	Roles of BrlA and AbaA in Mediating Asexual and Insect Pathogenic Lifecycles of Metarhizium Probertsii. 2022 , 8, 1110	1
16	Four New Species of Aspergillus Subgenus Nidulantes from China. 2022 , 8, 1205	O
15	Purging genomes of contamination eliminates systematic bias from evolutionary analyses of ancestral genomes.	0
14	Reducing the number of accepted species in Aspergillus series Nigri. 2022,	1
13	Comparative genomic analysis of five Coprinus species.	O
12	Phylogenomics reveals extensive misidentification of fungal strains from the genusAspergillus.	O
11	Stress Responses Elicited by Glucose Withdrawal in Aspergillus fumigatus. 2022 , 8, 1226	О
10	Co-Cultivation of Aspergillus niger and Trichoderma reesei Enables Efficient Production of Enzymes for the Hydrolysis of Wheat Bran.	O

9	Whole genome sequence characterization of Aspergillus terreus ATCC 20541 and genome comparison of the fungi A. terreus. 2023 , 13,	0
8	Comparative analysis of Penicillium genomes reveals the absence of a specific genetic basis for biocontrol in Penicillium rubens strain 212. 13,	O
7	Depsipeptides Targeting Tumor Cells: Milestones from In Vitro to Clinical Trials. 2023, 28, 670	0
6	C-terminus of serine grotein kinase-like protein, SrpkF, is involved in conidiophore formation and hyphal growth under salt stress in Aspergillus aculeatus.	O
5	Genome-Wide Gene Expression Analyses of the AtfA/AtfB-Mediated Menadione Stress Response in Aspergillus nidulans. 2023 , 12, 463	0
4	Genome sequencing of Cladophialophora exuberans, a novel candidate for bioremediation of hydrocarbon and heavy metal polluted habitats. 2023 , 127, 1032-1042	O
3	Species-specific effects of the introduction of Aspergillus nidulans gfdB in osmophilic aspergilli. 2023 , 107, 2423-2436	О
2	The natural product co-evolved pyrroloquinoline quinone gene enhances their production when heterologously expressed in a variety of Streptomycetes.	O
1	Whole-genome sequencing and comparative genomic analysis of potential biotechnological strains of Trichoderma harzianum, Trichoderma atroviride, and Trichoderma reesei.	0