

The Pfam protein families database

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A Random Sequencing Approach for the Analysis of the Trypanosoma cruzi Genome: General Structure, Large Gene and Repetitive DNA Families, and Gene Discovery. Genome Research, 2000, 10, 1996-2005.	2.4	49
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4164	A Developmental Transcriptome Map for Allotetraploid <i>Arachis hypogaea</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1446.	1.7	178
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4559	In silico characterization of tandem repeats in <i>Trichophyton rubrum</i> and related dermatophytes provides new insights into their role in pathogenesis. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	4
4560	Comparative analysis of double-stranded RNA degradation and processing in insects. <i>Scientific Reports</i> , 2017, 7, 17059.	1.6	153
4561	Genetic adaptation of microbial populations present in high-intensity catfish production systems with therapeutic oxytetracycline treatment. <i>Scientific Reports</i> , 2017, 7, 17491.	1.6	20
4562	Systematic CRISPR-Cas9-Mediated Modifications of <i>Plasmodium yoelii</i> ApiAP2 Genes Reveal Functional Insights into Parasite Development. <i>MBio</i> , 2017, 8, .	1.8	66
4563	Long noncoding RNAs that respond to <i>Fusarium oxysporum</i> infection in 'Cavendish' banana (<i>Musa</i>) Tj ETQqQ 0 0 rgBT /Overlock	1.6	22
4564	Genomic assessment in <i>Lactobacillus plantarum</i> links the butyrogenic pathway with glutamine metabolism. <i>Scientific Reports</i> , 2017, 7, 15975.	1.6	25
4565	Computational design of fully overlapping coding schemes for protein pairs and triplets. <i>Scientific Reports</i> , 2017, 7, 15873.	1.6	22
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4570	Plant polysaccharide degrading enzyme system of <i>Thermobifida cellulolytica</i> TB100T revealed by de novo genome project data. <i>Acta Alimentaria</i> , 2017, 46, 323-335.	0.3	3
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4583	Comparative genome and transcriptome analysis reveals distinctive surface characteristics and unique physiological potentials of <i>Pseudomonas aeruginosa</i> ATCC 27853. <i>BMC Genomics</i> , 2017, 18, 459.	1.2	33
4584	Genome-wide analysis of UDP-glycosyltransferase super family in <i>Brassica rapa</i> and <i>Brassica oleracea</i> reveals its evolutionary history and functional characterization. <i>BMC Genomics</i> , 2017, 18, 474.	1.2	54

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4602	Genome-wide identification, characterisation and expression profiles of calcium-dependent protein kinase genes in barley (<i>Hordeum vulgare</i> L.). <i>Journal of Applied Genetics</i> , 2017, 58, 11-22.	1.0	17

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4620	Molecular Characterization and Expression Profiling of <i>Brachypodium distachyon</i> L. Cystatin Genes Reveal High Evolutionary Conservation and Functional Divergence in Response to Abiotic Stress. <i>Frontiers in Plant Science</i> , 2017, 8, 743.	1.7	15

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4641	Dynamics of genomic innovation in the unicellular ancestry of animals. <i>ELife</i> , 2017, 6, .	2.8	121
4642	The Distinct Transcriptional Response of the Midgut of <i>Amblyomma sculptum</i> and <i>Amblyomma aureolatum</i> Ticks to <i>Rickettsia rickettsii</i> Correlates to Their Differences in Susceptibility to Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 129.	1.8	23
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4653	<i>Alternaria</i> Toxins: Potential Virulence Factors and Genes Related to Pathogenesis. <i>Frontiers in Microbiology</i> , 2017, 8, 1451.	1.5	163
4654	The Lacl Family Transcription Factor, RbsR, Is a Pleiotropic Regulator of Motility, Virulence, Siderophore and Antibiotic Production, Gas Vesicle Morphogenesis and Flotation in <i>Serratia</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1678.	1.5	20
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4676	Inferring repeat-protein energetics from evolutionary information. <i>PLoS Computational Biology</i> , 2017, 13, e1005584.	1.5	11
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