

# New developments in the InterPro database

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Complete Genomic Structure of the Bloom-forming Toxic Cyanobacterium <i>Microcystis aeruginosa</i> NIES-843. <i>DNA Research</i> , 2007, 14, 247-256.	1.5	253
2	Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees. <i>Nucleic Acids Research</i> , 2007, 36, D787-D792.	6.5	33
3	Gene3D: comprehensive structural and functional annotation of genomes. <i>Nucleic Acids Research</i> , 2007, 36, D414-D418.	6.5	68
4	Web Services at the European Bioinformatics Institute. <i>Nucleic Acids Research</i> , 2007, 35, W6-W11.	6.5	166
5	Scanning the Genome of <i>Mycobacterium tuberculosis</i> to Identify Potential Lectins. <i>Protein and Peptide Letters</i> , 2007, 14, 683-691.	0.4	9
6	GenoList: an integrated environment for comparative analysis of microbial genomes. <i>Nucleic Acids Research</i> , 2007, 36, D469-D474.	6.5	62
7	The Cytochrome P450 Enzyme CYP96A15 Is the Midchain Alkane Hydroxylase Responsible for Formation of Secondary Alcohols and Ketones in Stem Cuticular Wax of <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2007, 145, 653-667.	2.3	267
8	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. <i>Briefings in Bioinformatics</i> , 2007, 9, 34-45.	3.2	4
9	Current progress in network research: toward reference networks for key model organisms. <i>Briefings in Bioinformatics</i> , 2007, 8, 318-332.	3.2	46
10	ProSAS: a database for analyzing alternative splicing in the context of protein structures. <i>Nucleic Acids Research</i> , 2007, 36, D63-D68.	6.5	24
11	Selection of Genes and Single Nucleotide Polymorphisms for Fine Mapping Starting From a Broad Linkage Region. <i>Twin Research and Human Genetics</i> , 2007, 10, 871-885.	0.3	9
12	ToxoDB: an integrated <i>Toxoplasma gondii</i> database resource. <i>Nucleic Acids Research</i> , 2007, 36, D553-D556.	6.5	418
13	The Molecule Pages database. <i>Nucleic Acids Research</i> , 2007, 36, D700-D706.	6.5	19
14	SIMAP structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2007, 36, D289-D292.	6.5	24
15	DIMA 2.0 predicted and known domain interactions. <i>Nucleic Acids Research</i> , 2007, 36, D651-D655.	6.5	17
16	A novel family of transmembrane proteins interacting with $\hat{I}^2$ subunits of the Na,K-ATPase. <i>Human Molecular Genetics</i> , 2007, 16, 2394-2410.	1.4	45
17	New Type III Effectors from <i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> Trigger Plant Reactions Dependent on a Conserved N-Myristoylation Motif. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 1250-1261.	1.4	79
18	Exploiting new genome data and Internet resources for the phylogenetic analysis of proteases, substrates and inhibitors. <i>Biochemical Society Transactions</i> , 2007, 35, 599-603.	1.6	2

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19	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	6.5	57
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