Nozomi Nagano

List of Publications by Year
in descending order

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28 papers	1,610 citations	516710 16 h-index	526287 27 g-index
29 all docs	29 docs citations	29 times ranked	2039 citing authors

#	Article	IF	Citations
1	One Fold with Many Functions: The Evolutionary Relationships between TIM Barrel Families Based on their Sequences, Structures and Functions. Journal of Molecular Biology, 2002, 321, 741-765.	4.2	568
2	Strong hydrophobic nature of cysteine residues in proteins. FEBS Letters, 1999, 458, 69-71.	2.8	135
3	Characterization of the biosynthetic gene cluster for the ribosomally synthesized cyclic peptide ustiloxin B in Aspergillus flavus. Fungal Genetics and Biology, 2014, 68, 23-30.	2.1	130
4	MIDDAS-M: Motif-Independent De Novo Detection of Secondary Metabolite Gene Clusters through the Integration of Genome Sequencing and Transcriptome Data. PLoS ONE, 2013, 8, e84028.	2.5	106
5	Motif-based searching in TOPS protein topology databases. Bioinformatics, 1999, 15, 317-326.	4.1	93
6	Class of cyclic ribosomal peptide synthetic genes in filamentous fungi. Fungal Genetics and Biology, 2016, 86, 58-70.	2.1	84
7	Unveiling the Biosynthetic Pathway of the Ribosomally Synthesized and Postâ€translationally Modified Peptide Ustiloxin B in Filamentous Fungi. Angewandte Chemie - International Edition, 2016, 55, 8072-8075.	13.8	76
8	EzCatDB: the Enzyme Catalytic-mechanism Database. Nucleic Acids Research, 2004, 33, D407-D412.	14.5	67
9	Barrel structures in proteins: Automatic identification and classification including a sequence analysis of TIM barrels. Protein Science, 1999, 8, 2072-2084.	7.6	65
10	Ustiloxins, fungal cyclic peptides, are ribosomally synthesized in <i>Ustilaginoidea virens</i>. Bioinformatics, 2015, 31, 981-985.	4.1	62
11	The (Î²Î±)8 glycosidases: sequence and structure analyses suggest distant evolutionary relationships. Protein Engineering, Design and Selection, 2001, 14, 845-855.	2.1	41
12	Prediction of Detailed Enzyme Functions and Identification of Specificity Determining Residues by Random Forests. PLoS ONE, 2014, 9, e84623.	2.5	32
13	EzCatDB: the enzyme reaction database, 2015 update. Nucleic Acids Research, 2015, 43, D453-D458.	14.5	24
14	Metric learning for enzyme active-site search. Bioinformatics, 2010, 26, 2698-2704.	4.1	22
15	Expression of ustR and the Golgi protease KexB are required for ustiloxin B biosynthesis in Aspergillus oryzae. AMB Express, 2016, 6, 9.	3.0	22
16	Systematic comparison of catalytic mechanisms of hydrolysis and transfer reactions classified in the EzCatDB database. Proteins: Structure, Function and Bioinformatics, 2006, 66, 147-159.	2.6	16
17	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	2.6	13
18	SAHG, a comprehensive database of predicted structures of all human proteins. Nucleic Acids Research, 2011, 39, D487-D493.	14.5	12

#	ARTICLE	IF	CITATIONS
19	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063.	3.0	8
20	Unveiling the Biosynthetic Pathway of the Ribosomally Synthesized and Postâ€translationally Modified Peptide Ustiloxin B in Filamentous Fungi. Angewandte Chemie, 2016, 128, 8204-8207.	2.0	7
21	Relationships between functional subclasses and information contained in activeâ€site and ligandâ€binding residues in diverse superfamilies. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2369-2384.	2.6	6
22	Transfer RNA docking pair model in the ribosomal pre- and post- translocational states. Nucleic Acids Research, 1997, 25, 1254-1264.	14.5	5
23	Such Hydrophobic Peptides as Dansylated Mastoparan Can Elevate the Fertilization Membrane of Sea Urchin Eggs. Biochemical and Biophysical Research Communications, 1995, 215, 828-834.	2.1	4
24	Discriminative structural approaches for enzyme active-site prediction. BMC Bioinformatics, 2011, 12, S49.	2.6	4
25	Using Bregmann Divergence Regularized Machine for Comparison of Molecular Local Structures. IEICE Transactions on Information and Systems, 2016, E99.D, 275-278.	0.7	3
26	Mechanism of translation based on intersubunit complementarities of ribosomal RNAs and tRNAs. Journal of Theoretical Biology, 2007, 245, 644-668.	1.7	2
27	Parametric Templates: A New Enzyme Active-Site Prediction Algorithm. , 2010, , .		1
28	2P-238 Functional classification of enzymes by clustering of subsequences consisting of active sites and ligand interaction sites(Bioinformatics:Functional genomics,The 47th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0