

Nozomi Nagano

List of Publications by Year in descending order

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Version: 2024-02-01

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	Class of cyclic ribosomal peptide synthetic genes in filamentous fungi. <i>Fungal Genetics and Biology</i> , 2016, 86, 58-70.	2.1	84
2	Unveiling the Biosynthetic Pathway of the Ribosomally Synthesized and Post-translationally Modified Peptide Ustiloxin B in Filamentous Fungi. <i>Angewandte Chemie</i> , 2016, 128, 8204-8207.	2.0	7
3	Unveiling the Biosynthetic Pathway of the Ribosomally Synthesized and Post-translationally Modified Peptide Ustiloxin B in Filamentous Fungi. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 8072-8075.	13.8	76
4	Expression of <i>ustR</i> and the Golgi protease <i>KexB</i> are required for ustiloxin B biosynthesis in <i>Aspergillus oryzae</i> . <i>AMB Express</i> , 2016, 6, 9.	3.0	22
5	Using Bregmann Divergence Regularized Machine for Comparison of Molecular Local Structures. <i>IEICE Transactions on Information and Systems</i> , 2016, E99.D, 275-278.	0.7	3
6	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
7	EzCatDB: the enzyme reaction database, 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D453-D458.	14.5	24
8	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	2.6	13
9	Ustiloxins, fungal cyclic peptides, are ribosomally synthesized in <i>Ustilaginoidea virens</i> . <i>Bioinformatics</i> , 2015, 31, 981-985.	4.1	62
10	Prediction of Detailed Enzyme Functions and Identification of Specificity Determining Residues by Random Forests. <i>PLoS ONE</i> , 2014, 9, e84623.	2.5	32
11	Characterization of the biosynthetic gene cluster for the ribosomally synthesized cyclic peptide ustiloxin B in <i>Aspergillus flavus</i> . <i>Fungal Genetics and Biology</i> , 2014, 68, 23-30.	2.1	130
12	MIDDAS-M: Motif-Independent De Novo Detection of Secondary Metabolite Gene Clusters through the Integration of Genome Sequencing and Transcriptome Data. <i>PLoS ONE</i> , 2013, 8, e84028.	2.5	106
13	Discriminative structural approaches for enzyme active-site prediction. <i>BMC Bioinformatics</i> , 2011, 12, S49.	2.6	4
14	SAHG, a comprehensive database of predicted structures of all human proteins. <i>Nucleic Acids Research</i> , 2011, 39, D487-D493.	14.5	12
15	Relationships between functional subclasses and information contained in active-site and ligand-binding residues in diverse superfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2369-2384.	2.6	6
16	Metric learning for enzyme active-site search. <i>Bioinformatics</i> , 2010, 26, 2698-2704.	4.1	22
17	Parametric Templates: A New Enzyme Active-Site Prediction Algorithm. , 2010, , .		1
18	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 rgB0/Dverlock 10 Tf 50 :		

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19	Mechanism of translation based on intersubunit complementarities of ribosomal RNAs and tRNAs. <i>Journal of Theoretical Biology</i> , 2007, 245, 644-668.	1.7	2
20	Systematic comparison of catalytic mechanisms of hydrolysis and transfer reactions classified in the EzCatDB database. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 66, 147-159.	2.6	16
21	EzCatDB: the Enzyme Catalytic-mechanism Database. <i>Nucleic Acids Research</i> , 2004, 33, D407-D412.	14.5	67
22	One Fold with Many Functions: The Evolutionary Relationships between TIM Barrel Families Based on their Sequences, Structures and Functions. <i>Journal of Molecular Biology</i> , 2002, 321, 741-765.	4.2	568
23	The (β -D-GlcNAc)8 glycosidases: sequence and structure analyses suggest distant evolutionary relationships. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 845-855.	2.1	41
24	Motif-based searching in TOPS protein topology databases. <i>Bioinformatics</i> , 1999, 15, 317-326.	4.1	93
25	Barrel structures in proteins: Automatic identification and classification including a sequence analysis of TIM barrels. <i>Protein Science</i> , 1999, 8, 2072-2084.	7.6	65
26	Strong hydrophobic nature of cysteine residues in proteins. <i>FEBS Letters</i> , 1999, 458, 69-71.	2.8	135
27	Transfer RNA docking pair model in the ribosomal pre- and post- translocational states. <i>Nucleic Acids Research</i> , 1997, 25, 1254-1264.	14.5	5
28	Such Hydrophobic Peptides as Dansylated Mastoparan Can Elevate the Fertilization Membrane of Sea Urchin Eggs. <i>Biochemical and Biophysical Research Communications</i> , 1995, 215, 828-834.	2.1	4