

Jacquelyn S Fetrow

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

1,297
citations

567281

15
h-index

610901

24
g-index

28
all docs

28
docs citations

28
times ranked

1665
citing authors

#	ARTICLE	IF	CITATIONS
1	Method for prediction of protein function from sequence using the sequence-to-structure-to-function paradigm with application to Glutaredoxins/Thioredoxins and T 1 Ribonucleases 1 1 Edited by F. Cohen. <i>Journal of Molecular Biology</i> , 1998, 281, 949-968.	4.2	207
2	Analysis of the peroxiredoxin family: Using active site structure and sequence information for global classification and residue analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 947-964.	2.6	159
3	A Kinetic Analysis of the Auxin Transcriptome Reveals Cell Wall Remodeling Proteins That Modulate Lateral Root Development in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2013, 25, 3329-3346.	6.6	147
4	Functional analysis of the <i>Escherichia coli</i> genome using the sequence-to-structure-to-function paradigm: identification of proteins exhibiting the Glutaredoxin/Thioredoxin disulfide oxidoreductase activity 1 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1998, 282, 703-711.	4.2	97
5	PREX: PeroxiRedoxin classification indEX, a database of subfamily assignments across the diverse peroxiredoxin family. <i>Nucleic Acids Research</i> , 2011, 39, D332-D337.	14.5	94
6	Structure-based functional motif identifies a potential disulfide oxidoreductase active site in the serine/threonine protein phosphatase subfamily. <i>FASEB Journal</i> , 1999, 13, 1866-1874.	0.5	81
7	Genomic-scale comparison of sequence- and structure-based methods of function prediction: Does structure provide additional insight?. <i>Protein Science</i> , 2001, 10, 1005-1014.	7.6	68
8	Mutating a Highly Conserved Residue in Diverse Cytochrome P450s Facilitates Diastereoselective Olefin Cyclopropanation. <i>ChemBioChem</i> , 2016, 17, 394-397.	2.6	64
9	Structure-based Active Site Profiles for Genome Analysis and Functional Family Subclassification. <i>Journal of Molecular Biology</i> , 2003, 334, 387-401.	4.2	56
10	Integration of gene expression data with network-based analysis to identify signaling and metabolic pathways regulated during the development of osteoarthritis. <i>Gene</i> , 2014, 542, 38-45.	2.2	47
11	Synergistic Computational and Experimental Proteomics Approaches for More Accurate Detection of Active Serine Hydrolases in Yeast. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 209-225.	3.8	46
12	Conformational and Oligomeric Effects on the Cysteine pKa of Tryparedoxin Peroxidase. <i>Journal of Biomolecular Structure and Dynamics</i> , 2010, 28, 51-70.	3.5	46
13	Identification of Transcriptional and Receptor Networks That Control Root Responses to Ethylene. <i>Plant Physiology</i> , 2018, 176, 2095-2118.	4.8	41
14	Chemical and Structural Diversity in Cyclooxygenase Protein Active Sites. <i>Chemistry and Biodiversity</i> , 2005, 2, 1533-1552.	2.1	19
15	An Atlas of Peroxiredoxins Created Using an Active Site Profile-Based Approach to Functionally Relevant Clustering of Proteins. <i>PLoS Computational Biology</i> , 2017, 13, e1005284.	3.2	19
16	Structural and Electrostatic Asymmetry at the Active Site in Typical and Atypical Peroxiredoxin Dimers. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6832-6843.	2.6	16
17	Comparison of topological clustering within protein networks using edge metrics that evaluate full sequence, full structure, and active site microenvironment similarity. <i>Protein Science</i> , 2015, 24, 1423-1439.	7.6	14
18	An approach to functionally relevant clustering of the protein universe: Active site profile-based clustering of protein structures and sequences. <i>Protein Science</i> , 2017, 26, 677-699.	7.6	13

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19	Dynamics of dendritic cell maturation are identified through a novel filtering strategy applied to biological time-course microarray replicates. <i>BMC Immunology</i> , 2010, 11, 41.	2.2	11
20	New computational approaches to understanding molecular protein function. <i>PLoS Computational Biology</i> , 2018, 14, e1005756.	3.2	11
21	SC2ATmd: a tool for integration of the figure of merit with cluster analysis for gene expression data. <i>Bioinformatics</i> , 2011, 27, 1330-1331.	4.1	10
22	Active Site Profiling to Identify Protein Functional Sites in Sequences and Structures Using the Deacon Active Site Profiler (DASP). , 2006, Chapter 8, Unit 8.10.		8
23	DASP3: identification of protein sequences belonging to functionally relevant groups. <i>BMC Bioinformatics</i> , 2016, 17, 458.	2.6	6
24	Metropolis-Hastings Algorithm and Continuous Regression for finding Next-State Models of Protein Modification using Information Scores. , 2007, , .		5
25	Isofunctional Clustering and Conformational Analysis of the Arsenate Reductase Superfamily Reveals Nine Distinct Clusters. <i>Biochemistry</i> , 2020, 59, 4262-4284.	2.5	4
26	Impact of the Type I Interferon Receptor on the Global Gene Expression Program During the Course of Dendritic Cell Maturation Induced by Polyinosinic Polycytidylic Acid. <i>Journal of Interferon and Cytokine Research</i> , 2016, 36, 382-400.	1.2	3
27	USING INFORMATION THEORY TO DISCOVER SIDE CHAIN ROTAMER CLASSES: ANALYSIS OF THE EFFECTS OF LOCAL BACKBONE STRUCTURE. , 1998, , 278-89.		3
28	Comparison of Co-temporal Modeling Algorithms on Sparse Experimental Time Series Data Sets. , 2010, 2010, 79-85.		2