Gemma L Holliday

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5617239/publications.pdf

Version: 2024-02-01

37 papers	4,312 citations	218677 26 h-index	330143 37 g-index
39 all docs	39 docs citations	39 times ranked	7567 citing authors

#	Article	IF	Citations
1	A global analysis of function and conservation of catalytic residues in enzymes. Journal of Biological Chemistry, 2020, 295, 314-324.	3.4	68
2	A global view of structureâ€“function relationships in the tautomerase superfamily. Journal of Biological Chemistry, 2018, 293, 2342-2357.	3.4	39
3	Mechanism and Catalytic Site Atlas (M-CSA): a database of enzyme reaction mechanisms and active sites. Nucleic Acids Research, 2018, 46, D618-D623.	14.5	151
4	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a â€œPlug and Playâ€• Domain. Methods in Enzymology, 2018, 606, 1-71.	1.0	99
5	Biocuration in the structureâ€“function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	6
6	InterPro in 2017â€”beyond protein family and domain annotations. Nucleic Acids Research, 2017, 45, D190-D199.	14.5	1,358
7	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. Methods in Molecular Biology, 2017, 1446, 111-132.	0.9	14
8	Biocuration in the structureâ€“function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	2
9	Reaction Decoder Tool (RDT): extracting features from chemical reactions. Bioinformatics, 2016, 32, 2065-2066.	4.1	73
10	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
11	The Confidence Information Ontology: a step towards a standard for asserting confidence in annotations. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav043-bav043.	3.0	37
12	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	2.6	13
13	[FeFe]-Hydrogenase Maturation: Insights into the Role HydE Plays in Dithiomethylamine Biosynthesis. Biochemistry, 2015, 54, 1807-1818.	2.5	57
14	The Structureâ€“Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	14.5	210
15	The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. Nucleic Acids Research, 2014, 42, D485-D489.	14.5	168
16	Predicting the Functions and Specificity of Triterpenoid Synthases: A Mechanism-Based Multi-intermediate Docking Approach. PLoS Computational Biology, 2014, 10, e1003874.	3.2	23
17	EC-BLAST: a tool to automatically search and compare enzyme reactions. Nature Methods, 2014, 11, 171-174.	19.0	112
18	Exploring the Biological and Chemical Complexity of the Ligases. Journal of Molecular Biology, 2014, 426, 2098-2111.	4.2	11

#	Article	IF	Citations
19	The EBI enzyme portal. Nucleic Acids Research, 2013, 41, D773-D780.	14.5	19
20	Exploring the Evolution of Novel Enzyme Functions within Structurally Defined Protein Superfamilies. PLoS Computational Biology, 2012, 8, e1002403.	3.2	80
21	MACiE: exploring the diversity of biochemical reactions. Nucleic Acids Research, 2012, 40, D783-D789.	14.5	73
22	FunTree: a resource for exploring the functional evolution of structurally defined enzyme superfamilies. Nucleic Acids Research, 2012, 40, D776-D782.	14.5	44
23	Characterizing the complexity of enzymes on the basis of their mechanisms and structures with a bioâ€computational analysis. FEBS Journal, 2011, 278, 3835-3845.	4.7	30
24	The CoFactor database: organic cofactors in enzyme catalysis. Bioinformatics, 2010, 26, 2496-2497.	4.1	57
25	The Structures and Physicochemical Properties of Organic Cofactors in Biocatalysis. Journal of Molecular Biology, 2010, 403, 803-824.	4.2	63
26	Metal-MACiE: a database of metals involved in biological catalysis. Bioinformatics, 2009, 25, 2088-2089.	4.1	73
27	Small Molecule Subgraph Detector (SMSD) toolkit. Journal of Cheminformatics, 2009, 1, 12.	6.1	117
28	Understanding the Functional Roles of Amino Acid Residues in Enzyme Catalysis. Journal of Molecular Biology, 2009, 390, 560-577.	4.2	117
29	Metal ions in biological catalysis: from enzyme databases to general principles. Journal of Biological Inorganic Chemistry, 2008, 13, 1205-1218.	2.6	868
30	MACiE (Mechanism, Annotation and Classification in Enzymes): novel tools for searching catalytic mechanisms. Nucleic Acids Research, 2007, 35, D515-D520.	14.5	64
31	Using Reaction Mechanism to Measure Enzyme Similarity. Journal of Molecular Biology, 2007, 368, 1484-1499.	4.2	39
32	The Geometry of Interactions between Catalytic Residues and their Substrates. Journal of Molecular Biology, 2007, 369, 1140-1152.	4.2	12
33	The Chemistry of Protein Catalysis. Journal of Molecular Biology, 2007, 372, 1261-1277.	4.2	43
34	Evolution of enzymes and pathways for the biosynthesis of cofactors. Natural Product Reports, 2007, 24, 972.	10.3	62
35	Chemical Markup, XML, and the World Wide Web. 6. CMLReact, an XML Vocabulary for Chemical Reactions. Journal of Chemical Information and Modeling, 2006, 46, 145-157.	5.4	51
36	MACiE: a database of enzyme reaction mechanisms. Bioinformatics, 2005, 21, 4315-4316.	4.1	47

#	Article	IF	Citations
37	First examples of Mâ€“Seâ€“Pâ€“Nâ€“N heterocycles. Inorganic Chemistry Communication, 2001, 4, 115-118.	3.9	4