

Gemma L Holliday

List of Publications by Year in descending order

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37
papers

4,312
citations

218662

26
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330122

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docs citations

39
times ranked

7567
citing authors

#	ARTICLE	IF	CITATIONS
1	A global analysis of function and conservation of catalytic residues in enzymes. <i>Journal of Biological Chemistry</i> , 2020, 295, 314-324.	3.4	68
2	A global view of structure–function relationships in the tautomerase superfamily. <i>Journal of Biological Chemistry</i> , 2018, 293, 2342-2357.	3.4	39
3	Mechanism and Catalytic Site Atlas (M-CSA): a database of enzyme reaction mechanisms and active sites. <i>Nucleic Acids Research</i> , 2018, 46, D618-D623.	14.5	151
4	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a “Plug and Play” Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	1.0	99
5	Biocuration in the structure–function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	6
6	InterPro in 2017—beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	14.5	1,358
7	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 111-132.	0.9	14
8	Biocuration in the structure–function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	2
9	Reaction Decoder Tool (RDT): extracting features from chemical reactions. <i>Bioinformatics</i> , 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.. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	3.0	8
11	The Confidence Information Ontology: a step towards a standard for asserting confidence in annotations. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav043-bav043.	3.0	37
12	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
13	[FeFe]-Hydrogenase Maturation: Insights into the Role HydE Plays in Dithiomethylamine Biosynthesis. <i>Biochemistry</i> , 2015, 54, 1807-1818.	2.5	57
14	The Structure–Function Linkage Database. <i>Nucleic Acids Research</i> , 2014, 42, D521-D530.	14.5	210
15	The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. <i>Nucleic Acids Research</i> , 2014, 42, D485-D489.	14.5	168
16	Predicting the Functions and Specificity of Triterpenoid Synthases: A Mechanism-Based Multi-intermediate Docking Approach. <i>PLoS Computational Biology</i> , 2014, 10, e1003874.	3.2	23
17	EC-BLAST: a tool to automatically search and compare enzyme reactions. <i>Nature Methods</i> , 2014, 11, 171-174.	19.0	112
18	Exploring the Biological and Chemical Complexity of the Ligases. <i>Journal of Molecular Biology</i> , 2014, 426, 2098-2111.	4.2	11

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

#	ARTICLE	IF	CITATIONS
37	First examples of Mâ€“Seâ€“Pâ€“Nâ€“N heterocycles. <i>Inorganic Chemistry Communication</i> , 2001, 4, 115-118.	3.9	4