

Patricia C Babbitt

List of Publications by Year in descending order

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121
papers

11,971
citations

34016

52
h-index

28224

105
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129
all docs

129
docs citations

129
times ranked

15561
citing authors

#	ARTICLE	IF	CITATIONS
1	Parallel molecular mechanisms for enzyme temperature adaptation. <i>Science</i> , 2021, 371, .	6.0	48
2	Kinetic and Structural Analysis of Two Linkers in the Tautomerase Superfamily: Analysis and Implications. <i>Biochemistry</i> , 2021, 60, 1776-1786.	1.2	3
3	A strategy for large-scale comparison of evolutionary- and reaction-based classifications of enzyme function. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	5
4	Structural Basis for the Asymmetry of a 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2020, 59, 1592-1603.	1.2	6
5	Effusion: prediction of protein function from sequence similarity networks. <i>Bioinformatics</i> , 2019, 35, 442-451.	1.8	12
6	Structural, Kinetic, and Mechanistic Analysis of an Asymmetric 4-Oxalocrotonate Tautomerase Trimer. <i>Biochemistry</i> , 2019, 58, 2617-2627.	1.2	6
7	Exploring the sequence, function, and evolutionary space of protein superfamilies using sequence similarity networks and phylogenetic reconstructions. <i>Methods in Enzymology</i> , 2019, 620, 315-347.	0.4	13
8	The CAFA challenge reports improved protein function prediction and new functional annotations for hundreds of genes through experimental screens. <i>Genome Biology</i> , 2019, 20, 244.	3.8	261
9	InterPro in 2019: improving coverage, classification and access to protein sequence annotations. <i>Nucleic Acids Research</i> , 2019, 47, D351-D360.	6.5	1,291
10	A global view of structureâ€“function relationships in the tautomerase superfamily. <i>Journal of Biological Chemistry</i> , 2018, 293, 2342-2357.	1.6	39
11	Atlas of the Radical SAM Superfamily: Divergent Evolution of Function Using a â€œPlug and Playâ€• Domain. <i>Methods in Enzymology</i> , 2018, 606, 1-71.	0.4	99
12	Revealing Unexplored Sequence-Function Space Using Sequence Similarity Networks. <i>Biochemistry</i> , 2018, 57, 4651-4662.	1.2	58
13	New computational approaches to understanding molecular protein function. <i>PLoS Computational Biology</i> , 2018, 14, e1005756.	1.5	11
14	An approach to functionally relevant clustering of the protein universe: Active site profileâ€“based clustering of protein structures and sequences. <i>Protein Science</i> , 2017, 26, 677-699.	3.1	13
15	Biocuration in the structureâ€“function linkage database: the anatomy of a superfamily. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	6
16	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	6.5	1,358
17	Evaluating Functional Annotations of Enzymes Using the Gene Ontology. <i>Methods in Molecular Biology</i> , 2017, 1446, 111-132.	0.4	14
18	Evolutionary and molecular foundations of multiple contemporary functions of the nitroreductase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9549-E9558.	3.3	111

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19	Biocuration in the structure–function linkage database: the anatomy of a superfamily. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	2
20	Kinetic and structural characterization of a cis -3-Chloroacrylic acid dehalogenase homologue in Pseudomonas sp. UW4: A potential step between subgroups in the tautomerase superfamily. Archives of Biochemistry and Biophysics, 2017, 636, 50-56.	1.4	9
21	3D Motifs. , 2017, , 361-392.		7
22	An Atlas of Peroxiredoxins Created Using an Active Site Profile-Based Approach to Functionally Relevant Clustering of Proteins. PLoS Computational Biology, 2017, 13, e1005284.	1.5	19
23	DASP3: identification of protein sequences belonging to functionally relevant groups. BMC Bioinformatics, 2016, 17, 458.	1.2	6
24	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
25	Molecular Diversity of Terpene Synthases in the Liverwort Marchantia polymorpha. Plant Cell, 2016, 28, tpc.00062.2016.	3.1	48
26	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.	1.4	8
27	Comparison of topological clustering within protein networks using edge metrics that evaluate full sequence, full structure, and active site microenvironment similarity. Protein Science, 2015, 24, 1423-1439.	3.1	14
28	Determinants of the CmoB carboxymethyl transferase utilized for selective tRNA wobble modification. Nucleic Acids Research, 2015, 43, 4602-4613.	6.5	23
29	Covalent Docking Predicts Substrates for Haloalkanoate Dehalogenase Superfamily Phosphatases. Biochemistry, 2015, 54, 528-537.	1.2	26
30	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	1.5	13
31	[FeFe]-Hydrogenase Maturation: Insights into the Role HydE Plays in Dithiomethylamine Biosynthesis. Biochemistry, 2015, 54, 1807-1818.	1.2	57
32	Evolutionary Reprogramming of Protein-Protein Interaction Specificity. Cell, 2015, 163, 535-537.	13.5	1
33	Large-Scale Determination of Sequence, Structure, and Function Relationships in Cytosolic Glutathione Transferases across the Biosphere. PLoS Biology, 2014, 12, e1001843.	2.6	79
34	The Structure–Function Linkage Database. Nucleic Acids Research, 2014, 42, D521-D530.	6.5	210
35	Using the Structure–Function Linkage Database to Characterize Functional Domains in Enzymes. Current Protocols in Bioinformatics, 2014, 48, 2.10.1-16.	25.8	5
36	Predicting the Functions and Specificity of Triterpenoid Synthases: A Mechanism-Based Multi-intermediate Docking Approach. PLoS Computational Biology, 2014, 10, e1003874.	1.5	23

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37	New Insights about Enzyme Evolution from Large Scale Studies of Sequence and Structure Relationships. <i>Journal of Biological Chemistry</i> , 2014, 289, 30221-30228.	1.6	57
38	Mechanistic and Bioinformatic Investigation of a Conserved Active Site Helix in β -Isopropylmalate Synthase from <i>Mycobacterium tuberculosis</i> , a Member of the DRE-TIM Metallolyase Superfamily. <i>Biochemistry</i> , 2014, 53, 2915-2925.	1.2	14
39	Prediction and characterization of enzymatic activities guided by sequence similarity and genome neighborhood networks. <i>ELife</i> , 2014, 3, .	2.8	81
40	Discovery of new enzymes and metabolic pathways by using structure and genome context. <i>Nature</i> , 2013, 502, 698-702.	13.7	124
41	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
42	Structure-guided discovery of the metabolite carboxy-SAM that modulates tRNA function. <i>Nature</i> , 2013, 498, 123-126.	13.7	84
43	Biases in the Experimental Annotations of Protein Function and Their Effect on Our Understanding of Protein Function Space. <i>PLoS Computational Biology</i> , 2013, 9, e1003063.	1.5	103
44	Prediction of function for the polyprenyl transferase subgroup in the isoprenoid synthase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1196-202.	3.3	75
45	Consequences of domain insertion on sequence-structure divergence in a superfold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3381-7.	3.3	25
46	The nature of sequence and structure divergence in the Haloalkanoate Dehalogenase SuperFamily (HADSF). <i>FASEB Journal</i> , 2013, 27, 797.2.	0.2	0
47	Pythoscape: a framework for generation of large protein similarity networks. <i>Bioinformatics</i> , 2012, 28, 2845-2846.	1.8	42
48	A Global Comparison of the Human and <i>T. brucei</i> Degradomes Gives Insights about Possible Parasite Drug Targets. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1942.	1.3	3
49	Inference of Functional Properties from Large-scale Analysis of Enzyme Superfamilies. <i>Journal of Biological Chemistry</i> , 2012, 287, 35-42.	1.6	45
50	Divergent Evolution in Enolase Superfamily: Strategies for Assigning Functions. <i>Journal of Biological Chemistry</i> , 2012, 287, 29-34.	1.6	118
51	Homology models guide discovery of diverse enzyme specificities among dipeptide epimerases in the enolase superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4122-4127.	3.3	56
52	The Enzyme Function Initiative. <i>Biochemistry</i> , 2011, 50, 9950-9962.	1.2	169
53	Topological variation in the evolution of new reactions in functionally diverse enzyme superfamilies. <i>Current Opinion in Structural Biology</i> , 2011, 21, 391-397.	2.6	22
54	The evolution of function in strictosidine synthase-like proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3082-3098.	1.5	43

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55	Toward mechanistic classification of enzyme functions. <i>Current Opinion in Chemical Biology</i> , 2011, 15, 435-442.	2.8	40
56	Mutations in PNKD causing paroxysmal dyskinesia alters protein cleavage and stability. <i>Human Molecular Genetics</i> , 2011, 20, 2322-2332.	1.4	52
57	Improving the quality of protein similarity network clustering algorithms using the network edge weight distribution. <i>Bioinformatics</i> , 2011, 27, 326-333.	1.8	36
58	Quantitative Comparison of Catalytic Mechanisms and Overall Reactions in Convergenly Evolved Enzymes: Implications for Classification of Enzyme Function. <i>PLoS Computational Biology</i> , 2010, 6, e1000700.	1.5	33
59	Mechanisms of Protein Evolution and their Application to Protein Engineering. <i>Advances in Enzymology and Related Areas of Molecular Biology</i> , 2010, 75, 193-239.	1.3	25
60	Annotation Error in Public Databases: Misannotation of Molecular Function in Enzyme Superfamilies. <i>PLoS Computational Biology</i> , 2009, 5, e1000605.	1.5	587
61	A Mapping of Drug Space from the Viewpoint of Small Molecule Metabolism. <i>PLoS Computational Biology</i> , 2009, 5, e1000474.	1.5	34
62	The global cysteine peptidase landscape in parasites. <i>Trends in Parasitology</i> , 2009, 25, 573-581.	1.5	88
63	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 107-125.	1.2	25
64	Biophysical studies support a predicted superhelical structure with armadillo repeats for Ricin. <i>Protein Science</i> , 2009, 18, 1139-1145.	3.1	16
65	Evolutionary constraints on structural similarity in orthologs and paralogs. <i>Protein Science</i> , 2009, 18, 1306-1315.	3.1	58
66	Enzyme (re)design: lessons from natural evolution and computation. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 10-18.	2.8	126
67	Annotating Enzymes of Uncertain Function: The Deacylation of <i>d</i> -Amino Acids by Members of the Amidohydrolase Superfamily. <i>Biochemistry</i> , 2009, 48, 6469-6481.	1.2	15
68	Glutathione Transferases Are Structural and Functional Outliers in the Thioredoxin Fold. <i>Biochemistry</i> , 2009, 48, 11108-11116.	1.2	125
69	An Atlas of the Thioredoxin Fold Class Reveals the Complexity of Function-Enabling Adaptations. <i>PLoS Computational Biology</i> , 2009, 5, e1000541.	1.5	114
70	Evolution of Enzymatic Activities in the Enolase Superfamily: Stereochemically Distinct Mechanisms in Two Families of <i>cis</i> -Muconate Lactonizing Enzymes. <i>Biochemistry</i> , 2009, 48, 1445-1453.	1.2	36
71	3D Motifs. , 2009, , 187-216.		3
72	SmCL3, a Gastrodermal Cysteine Protease of the Human Blood Fluke <i>Schistosoma mansoni</i> . <i>PLoS Neglected Tropical Diseases</i> , 2009, 3, e449.	1.3	45

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73	Using Sequence Similarity Networks for Visualization of Relationships Across Diverse Protein Superfamilies. PLoS ONE, 2009, 4, e4345.	1.1	385
74	Redesigning Enzymes Based on Adaptive Evolution for Optimal Function in Synthetic Metabolic Pathways. Chemistry and Biology, 2008, 15, 607-618.	6.2	53
75	Discovery of a Dipeptide Epimerase Enzymatic Function Guided by Homology Modeling and Virtual Screening. Structure, 2008, 16, 1668-1677.	1.6	52
76	Differential use of protease families for invasion by schistosome cercariae. Biochimie, 2008, 90, 345-358.	1.3	100
77	At the Periphery of the Amidohydrolase Superfamily: Bh0493 from <i>Bacillus halodurans</i> Catalyzes the Isomerization of <i>N</i> -Galacturonate to <i>N</i> -Tagaturonate. Biochemistry, 2008, 47, 1194-1206.	1.2	25
78	Evolutionarily Conserved Substrate Substructures for Automated Annotation of Enzyme Superfamilies. PLoS Computational Biology, 2008, 4, e1000142.	1.5	21
79	Evolution of Function in the Two Dinucleotide Binding Domains of Flavoproteins. PLoS Computational Biology, 2007, 3, e121.	1.5	58
80	structureViz: linking Cytoscape and UCSF Chimera. Bioinformatics, 2007, 23, 2345-2347.	1.8	71
81	Structural Diversity within the Mononuclear and Binuclear Active Sites of <i>N</i> -Acetyl- <i>D</i> -glucosamine-6-phosphate Deacetylase. Biochemistry, 2007, 46, 7953-7962.	1.2	23
82	Prediction and assignment of function for a divergent <i>N</i> -succinyl amino acid racemase. Nature Chemical Biology, 2007, 3, 486-491.	3.9	98
83	A gold standard set of mechanistically diverse enzyme superfamilies. Genome Biology, 2006, 7, R8.	13.9	62
84	Leveraging Enzyme Structure-Function Relationships for Functional Inference and Experimental Design: The Structure-Function Linkage Database. Biochemistry, 2006, 45, 2545-2555.	1.2	157
85	Evolution of Structure and Function in the <i>o</i> -Succinylbenzoate Synthase/ <i>N</i> -Acylamino Acid Racemase Family of the Enolase Superfamily. Journal of Molecular Biology, 2006, 360, 228-250.	2.0	65
86	Evolution of enzyme superfamilies. Current Opinion in Chemical Biology, 2006, 10, 492-497.	2.8	209
87	Automated discovery of 3D motifs for protein function annotation. Bioinformatics, 2006, 22, 723-730.	1.8	73
88	Divergent evolution in the enolase superfamily: the interplay of mechanism and specificity. Archives of Biochemistry and Biophysics, 2005, 433, 59-70.	1.4	194
89	Introduction to informatics approaches in structural genomics: modeling and representation of function from macromolecular structure. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 319-21.	0.7	0
90	Representing structure-function relationships in mechanistically diverse enzyme superfamilies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 358-69.	0.7	14

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91	Superfamily active site templates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 962-976.	1.5	49
92	Divergence of Function in the Thioredoxin Fold Suprafamily: Evidence for Evolution of Peroxiredoxins from a Thioredoxin-like Ancestor. <i>Biochemistry</i> , 2004, 43, 13981-13995.	1.2	141
93	REPRESENTING STRUCTURE-FUNCTION RELATIONSHIPS IN MECHANISTICALLY DIVERSE ENZYME SUPERFAMILIES. , 2004, , .		10
94	Session Introduction. , 2004, , .		0
95	A semiautomated approach to gene discovery through expressed sequence tag data mining: Discovery of new human transporter genes. <i>AAPS PharmSci</i> , 2003, 5, 1-18.	1.3	15
96	Definitions of enzyme function for the structural genomics era. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 230-237.	2.8	71
97	Evolutionary Potential of (Î²/Î±)-Barrels: Functional Promiscuity Produced by Single Substitutions in the Enolase Superfamily. <i>Biochemistry</i> , 2003, 42, 8387-8393.	1.2	171
98	BayGenomics: a resource of insertional mutations in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2003, 31, 278-281.	6.5	220
99	Intersect: identification and visualization of overlaps in database search results. <i>Bioinformatics</i> , 2003, 19, 1997-1999.	1.8	0
100	New functions from old scaffolds: How nature reengineers enzymes for new functions. <i>Advances in Protein Chemistry</i> , 2001, 55, 1-28.	4.4	36
101	Divergent Evolution of Enzymatic Function: Mechanistically Diverse Superfamilies and Functionally Distinct Suprafamilies. <i>Annual Review of Biochemistry</i> , 2001, 70, 209-246.	5.0	502
102	Barrels in pieces?. , 2001, 8, 5-7.		29
103	Functional Assignment of the 20 S Proteasome from <i>Trypanosoma brucei</i> Using Mass Spectrometry and New Bioinformatics Approaches. <i>Journal of Biological Chemistry</i> , 2001, 276, 28327-28339.	1.6	64
104	A comparative study of human muscle and brain creatine kinases expressed in <i>Escherichia coli</i> . <i>The Protein Journal</i> , 2000, 19, 59-66.	1.1	22
105	Reengineering the glutathione S-transferase scaffold: A rational design strategy pays off. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10298-10300.	3.3	27
106	Can sequence determine function?. <i>Genome Biology</i> , 2000, 1, reviews0005.1.	13.9	132
107	Evidence That <i>pcpA</i> Encodes 2,6-Dichlorohydroquinone Dioxygenase, the Ring Cleavage Enzyme Required for Pentachlorophenol Degradation in <i>Sphingomonas chlorophenolica</i> Strain ATCC 39723. <i>Biochemistry</i> , 1999, 38, 7659-7669.	1.2	81
108	Unexpected Divergence of Enzyme Function and Sequence: N-Acylamino Acid Racemase vs. Iso-Succinylbenzoate Synthase. <i>Biochemistry</i> , 1999, 38, 4252-4258.	1.2	118

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109	Integrated Tools for Structural and Sequence Alignment and Analysis. , 1999, , 230-41.		9
110	Mechanistically diverse enzyme superfamilies: the importance of chemistry in the evolution of catalysis. <i>Current Opinion in Chemical Biology</i> , 1998, 2, 607-612.	2.8	107
111	Insights into the Mechanism of Catalysis by the P ^α C Bond-Cleaving Enzyme Phosphonoacetaldehyde Hydrolase Derived from Gene Sequence Analysis and Mutagenesis. <i>Biochemistry</i> , 1998, 37, 9305-9315.	1.2	71
112	Evolution of Enzymatic Activities in the Enolase Superfamily: A Crystal Structure of (D)-Glucarate Dehydratase from <i>Pseudomonas putida</i> . <i>Biochemistry</i> , 1998, 37, 14358-14368.	1.2	35
113	Cloning and Functional Characterization of a Rat Renal Organic Cation Transporter Isoform (rOCT1A). <i>Journal of Biological Chemistry</i> , 1997, 272, 16548-16554.	1.6	58
114	Understanding Enzyme Superfamilies. <i>Journal of Biological Chemistry</i> , 1997, 272, 30591-30594.	1.6	253
115	The Enolase Superfamily: A General Strategy for Enzyme-Catalyzed Abstraction of the α -Protons of Carboxylic Acids. <i>Biochemistry</i> , 1996, 35, 16489-16501.	1.2	331
116	On the origins and functions of the enzymes of the 4-chlorobenzoate to 4-hydroxybenzoate converting pathway. <i>Biodegradation</i> , 1994, 5, 259-276.	1.5	68
117	3-Carboxy-cis,cis-muconate lactonizing enzyme from <i>Pseudomonas putida</i> is homologous to the class II fumarase family: a new reaction in the evolution of a mechanistic motif. <i>Biochemistry</i> , 1992, 31, 9768-9776.	1.2	68
118	The principal islet of the coho salmon (<i>Oncorhynchus kisutch</i>) contains the BB isoenzyme of creatine kinase. <i>The Protein Journal</i> , 1992, 11, 489-494.	1.1	14
119	Active Creatine Kinase Refolded from Inclusion Bodies in <i>Escherichia coli</i> . <i>ACS Symposium Series</i> , 1991, , 153-168.	0.5	3
120	Removal of a Proteolytic Activity Associated with Aggregates Formed from Expression of Creatine Kinase in <i>Escherichia coli</i> Leads to Improved Recovery of Active Enzyme. <i>Nature Biotechnology</i> , 1990, 8, 945-949.	9.4	40
121	Comparisons of creatine kinase primary structures. <i>The Protein Journal</i> , 1986, 5, 1-14.	1.1	45