

Janet M Thornton

List of Publications by Year in descending order

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408
papers

63,035
citations

1231

110
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942

239
g-index

541
all docs

541
docs citations

541
times ranked

58363
citing authors

#	ARTICLE	IF	CITATIONS
1	The rapid generation of mutation data matrices from protein sequences. <i>Bioinformatics</i> , 1992, 8, 275-282.	1.8	4,891
2	AQUA and PROCHECK-NMR: Programs for checking the quality of protein structures solved by NMR. <i>Journal of Biomolecular NMR</i> , 1996, 8, 477-86.	1.6	4,736
3	LIGPLOT: a program to generate schematic diagrams of protein-ligand interactions. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 127-134.	1.0	4,648
4	Satisfying Hydrogen Bonding Potential in Proteins. <i>Journal of Molecular Biology</i> , 1994, 238, 777-793.	2.0	2,001
5	Stereochemical quality of protein structure coordinates. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992, 12, 345-364.	1.5	1,436
6	Main-chain Bond Lengths and Bond Angles in Protein Structures. <i>Journal of Molecular Biology</i> , 1993, 231, 1049-1067.	2.0	1,142
7	Influence of proline residues on protein conformation. <i>Journal of Molecular Biology</i> , 1991, 218, 397-412.	2.0	1,071
8	Ribosomal Protein S6 Kinase 1 Signaling Regulates Mammalian Life Span. <i>Science</i> , 2009, 326, 140-144.	6.0	1,009
9	PROMOTIF: A program to identify and analyze structural motifs in proteins. <i>Protein Science</i> , 1996, 5, 212-220.	3.1	955
10	A revised set of potentials for β -turn formation in proteins. <i>Protein Science</i> , 1994, 3, 2207-2216.	3.1	918
11	PDBsum: Structural summaries of PDB entries. <i>Protein Science</i> , 2018, 27, 129-134.	3.1	910
12	Metal ions in biological catalysis: from enzyme databases to general principles. <i>Journal of Biological Inorganic Chemistry</i> , 2008, 13, 1205-1218.	1.1	868
13	Protein superfamilies and domain superfolds. <i>Nature</i> , 1994, 372, 631-634.	13.7	783
14	NEW EMBO MEMBER'S REVIEW: Diversity of protein-protein interactions. <i>EMBO Journal</i> , 2003, 22, 3486-3492.	3.5	739
15	Evolution of function in protein superfamilies, from a structural perspective 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 2001, 307, 1113-1143.	2.0	644
16	π - π interactions: the geometry and energetics of phenylalanine-phenylalanine interactions in proteins. <i>Journal of Molecular Biology</i> , 1991, 218, 837-846.	2.0	616
17	Analysis of protein-protein interaction sites using surface patches 1 Edited by G.Von Heijne. <i>Journal of Molecular Biology</i> , 1997, 272, 121-132.	2.0	584
18	ProFunc: a server for predicting protein function from 3D structure. <i>Nucleic Acids Research</i> , 2005, 33, W89-W93.	6.5	576

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19	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.	2.0	568
20	The Catalytic Site Atlas: a resource of catalytic sites and residues identified in enzymes using structural data. <i>Nucleic Acids Research</i> , 2004, 32, 129D-133.	6.5	541
21	Structural Characterisation and Functional Significance of Transient Protein-Protein Interactions. <i>Journal of Molecular Biology</i> , 2003, 325, 991-1018.	2.0	537
22	PDBsum: a web-based database of summaries and analyses of all PDB structures. <i>Trends in Biochemical Sciences</i> , 1997, 22, 488-490.	3.7	536
23	An overview of the structures of protein-DNA complexes. <i>Genome Biology</i> , 2000, 1, reviews001.1.	13.9	531
24	Analysis of Catalytic Residues in Enzyme Active Sites. <i>Journal of Molecular Biology</i> , 2002, 324, 105-121.	2.0	529
25	Protein-protein interactions: A review of protein dimer structures. <i>Progress in Biophysics and Molecular Biology</i> , 1995, 63, 31-65.	1.4	507
26	Conformation of β -hairpins in protein structures. <i>Journal of Molecular Biology</i> , 1989, 206, 759-777.	2.0	490
27	Evidence for lifespan extension and delayed age-related biomarkers in insulin receptor substrate 1 null mice. <i>FASEB Journal</i> , 2008, 22, 807-818.	0.2	487
28	Antibody-antigen Interactions: Contact Analysis and Binding Site Topography. <i>Journal of Molecular Biology</i> , 1996, 262, 732-745.	2.0	456
29	Protein promiscuity and its implications for biotechnology. <i>Nature Biotechnology</i> , 2009, 27, 157-167.	9.4	434
30	Prediction of protein-protein interaction sites using patch analysis 1 Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 1997, 272, 133-143.	2.0	411
31	CATH: comprehensive structural and functional annotations for genome sequences. <i>Nucleic Acids Research</i> , 2015, 43, D376-D381.	6.5	399
32	Protein-DNA interactions: a structural analysis. <i>Journal of Molecular Biology</i> , 1999, 287, 877-896.	2.0	397
33	Genome-wide Responses to Mitochondrial Dysfunction. <i>Molecular Biology of the Cell</i> , 2001, 12, 297-308.	0.9	391
34	Analysis of Main Chain Torsion Angles in Proteins: Prediction of NMR Coupling Constants for Native and Random Coil Conformations. <i>Journal of Molecular Biology</i> , 1996, 255, 494-506.	2.0	379
35	PDBsum more: new summaries and analyses of the known 3D structures of proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2004, 33, D266-D268.	6.5	373
36	Predicting Protein Ligand Binding Sites by Combining Evolutionary Sequence Conservation and 3D Structure. <i>PLoS Computational Biology</i> , 2009, 5, e1000585.	1.5	356

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37	The SDR (short-chain dehydrogenase/reductase and related enzymes) nomenclature initiative. <i>Chemico-Biological Interactions</i> , 2009, 178, 94-98.	1.7	329
38	Amino/Aromatic Interactions in Proteins: Is the Evidence Stacked Against Hydrogen Bonding?. <i>Journal of Molecular Biology</i> , 1994, 239, 315-331.	2.0	319
39	Protein-protein interfaces: Analysis of amino acid conservation in homodimers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 42, 108-124.	1.5	299
40	Tess: A geometric hashing algorithm for deriving 3D coordinate templates for searching structural databases. Application to enzyme active sites. <i>Protein Science</i> , 1997, 6, 2308-2323.	3.1	297
41	PROTEIN FAMILIES AND THEIR EVOLUTION—A STRUCTURAL PERSPECTIVE. <i>Annual Review of Biochemistry</i> , 2005, 74, 867-900.	5.0	295
42	Buried waters and internal cavities in monomeric proteins. <i>Protein Science</i> , 1994, 3, 1224-1235.	3.1	293
43	Predicting protein function from sequence and structural data. <i>Current Opinion in Structural Biology</i> , 2005, 15, 275-284.	2.6	280
44	PDBsum additions. <i>Nucleic Acids Research</i> , 2014, 42, D292-D296.	6.5	279
45	The CATH domain structure database: new protocols and classification levels give a more comprehensive resource for exploring evolution. <i>Nucleic Acids Research</i> , 2007, 35, D291-D297.	6.5	274
46	Construction, Visualisation, and Clustering of Transcription Networks from Microarray Expression Data. <i>PLoS Computational Biology</i> , 2007, 3, e206.	1.5	261
47	Structural Families in Loops of Homologous Proteins: Automatic Classification, Modelling and Application to Antibodies. <i>Journal of Molecular Biology</i> , 1996, 263, 800-815.	2.0	257
48	Protein-DNA Interactions: Amino Acid Conservation and the Effects of Mutations on Binding Specificity. <i>Journal of Molecular Biology</i> , 2002, 320, 991-1009.	2.0	243
49	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	13.7	243
50	Solvent-induced distortions and the curvature of α -helices. <i>Nature</i> , 1983, 306, 281-283.	13.7	235
51	Derivation of 3D coordinate templates for searching structural databases: Application to serine catalytic triads in the serine proteinases and lipases. <i>Protein Science</i> , 1996, 5, 1001-1013.	3.1	229
52	From protein structure to function. <i>Current Opinion in Structural Biology</i> , 1999, 9, 374-382.	2.6	229
53	The CATH Domain Structure Database and related resources Gene3D and DHS provide comprehensive domain family information for genome analysis. <i>Nucleic Acids Research</i> , 2004, 33, D247-D251.	6.5	226
54	Intrinsic α -helix propensities of amino acids, derived from the coil regions of known structures. <i>Nature Structural Biology</i> , 1995, 2, 596-603.	9.7	225

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55	Mitochondria-to-Nuclear Signaling Is Regulated by the Subcellular Localization of the Transcription Factors Rtg1p and Rtg3p. <i>Molecular Biology of the Cell</i> , 2000, 11, 2103-2115.	0.9	223
56	Discriminating between homodimeric and monomeric proteins in the crystalline state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 47-57.	1.5	217
57	Protein folds and functions. <i>Structure</i> , 1998, 6, 875-884.	1.6	207
58	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	3.3	206
59	Amino and carboxy-terminal regions in globular proteins. <i>Journal of Molecular Biology</i> , 1983, 167, 443-460.	2.0	198
60	The European dimension for the mouse genome mutagenesis program. <i>Nature Genetics</i> , 2004, 36, 925-927.	9.4	195
61	Protein Function Prediction Using Local 3D Templates. <i>Journal of Molecular Biology</i> , 2005, 351, 614-626.	2.0	195
62	BLEEP?potential of mean force describing protein-ligand interactions: I. Generating potential. <i>Journal of Computational Chemistry</i> , 1999, 20, 1165-1176.	1.5	194
63	From structure to function: approaches and limitations. <i>Nature Structural Biology</i> , 2000, 7, 991-994.	9.7	193
64	Identification, classification, and analysis of betaâ€bulges in proteins. <i>Protein Science</i> , 1993, 2, 1574-1590.	3.1	191
65	An algorithm for constraint-based structural template matching: application to 3D templates with statistical analysis. <i>Bioinformatics</i> , 2003, 19, 1644-1649.	1.8	191
66	Shape Variation in Protein Binding Pockets and their Ligands. <i>Journal of Molecular Biology</i> , 2007, 368, 283-301.	2.0	188
67	New functional families (FunFams) in CATH to improve the mapping of conserved functional sites to 3D structures. <i>Nucleic Acids Research</i> , 2012, 41, D490-D498.	6.5	188
68	Structural and Chemical Profiling of the Human Cytosolic Sulfotransferases. <i>PLoS Biology</i> , 2007, 5, e97.	2.6	187
69	The structural basis of allosteric regulation in proteins. <i>FEBS Letters</i> , 2009, 583, 1692-1698.	1.3	187
70	SIRIUS. <i>Journal of Molecular Biology</i> , 1990, 211, 595-615.	2.0	186
71	Using electrostatic potentials to predict DNA-binding sites on DNA-binding proteins. <i>Nucleic Acids Research</i> , 2003, 31, 7189-7198.	6.5	186
72	Determinants of strand register in antiparallel Î²â€sheets of proteins. <i>Protein Science</i> , 1998, 7, 2287-2300.	3.1	182

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73	Protein function annotation by homology-based inference. <i>Genome Biology</i> , 2009, 10, 207.	13.9	182
74	A method for localizing ligand binding pockets in protein structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 479-488.	1.5	181
75	Understanding nature's catalytic toolkit. <i>Trends in Biochemical Sciences</i> , 2005, 30, 622-629.	3.7	177
76	The CATH classification revisited--architectures reviewed and new ways to characterize structural divergence in superfamilies. <i>Nucleic Acids Research</i> , 2009, 37, D310-D314.	6.5	174
77	Evolutionary conservation of regulated longevity assurance mechanisms. <i>Genome Biology</i> , 2007, 8, R132.	13.9	173
78	Validation of protein models derived from experiment. <i>Current Opinion in Structural Biology</i> , 1998, 8, 631-639.	2.6	172
79	Real spherical harmonic expansion coefficients as 3D shape descriptors for protein binding pocket and ligand comparisons. <i>Bioinformatics</i> , 2005, 21, 2347-2355.	1.8	170
80	The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. <i>Nucleic Acids Research</i> , 2014, 42, D485-D489.	6.5	168
81	Using A Neural Network and Spatial Clustering to Predict the Location of Active Sites in Enzymes. <i>Journal of Molecular Biology</i> , 2003, 330, 719-734.	2.0	167
82	Deviations from Planarity of the Peptide Bond in Peptides and Proteins. <i>Journal of Molecular Biology</i> , 1996, 264, 1180-1195.	2.0	163
83	Protein folds, functions and evolution. <i>Journal of Molecular Biology</i> , 1999, 293, 333-342.	2.0	163
84	Lithium Promotes Longevity through GSK3/NRF2-Dependent Hormesis. <i>Cell Reports</i> , 2016, 15, 638-650.	2.9	163
85	Plasticity of enzyme active sites. <i>Trends in Biochemical Sciences</i> , 2002, 27, 419-426.	3.7	162
86	Conservation helps to identify biologically relevant crystal contacts. <i>Journal of Molecular Biology</i> , 2001, 313, 399-416.	2.0	159
87	Alpha plus beta folds revisited: some favoured motifs. <i>Structure</i> , 1993, 1, 105-120.	1.6	156
88	Conformational Changes Observed in Enzyme Crystal Structures upon Substrate Binding. <i>Journal of Molecular Biology</i> , 2005, 346, 21-28.	2.0	153
89	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.	6.5	151
90	Domain assignment for protein structures using a consensus approach: Characterization and analysis. <i>Protein Science</i> , 1998, 7, 233-242.	3.1	147

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91	Heme proteinsâ€™ Diversity in structural characteristics, function, and folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2349-2368.	1.5	147
92	PoreWalker: A Novel Tool for the Identification and Characterization of Channels in Transmembrane Proteins from Their Three-Dimensional Structure. <i>PLoS Computational Biology</i> , 2009, 5, e1000440.	1.5	146
93	Elucidating Human Phosphatase-Substrate Networks. <i>Science Signaling</i> , 2013, 6, rs10.	1.6	145
94	Potential energy functions for threading. <i>Current Opinion in Structural Biology</i> , 1996, 6, 210-216.	2.6	144
95	Searching for functional sites in protein structures. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 3-7.	2.8	138
96	Progress of Structural Genomics Initiatives: An Analysis of Solved Target Structures. <i>Journal of Molecular Biology</i> , 2005, 348, 1235-1260.	2.0	136
97	Quantifying the Similarities within Fold Space. <i>Journal of Molecular Biology</i> , 2002, 323, 909-926.	2.0	133
98	CATH: expanding the horizons of structure-based functional annotations for genome sequences. <i>Nucleic Acids Research</i> , 2019, 47, D280-D284.	6.5	131
99	Recognition of super-secondary structure in proteins. <i>Journal of Molecular Biology</i> , 1984, 173, 487-514.	2.0	128
100	Sequence and Structural Differences between Enzyme and Nonenzyme Homologs. <i>Structure</i> , 2002, 10, 1435-1451.	1.6	127
101	Extending CATH: increasing coverage of the protein structure universe and linking structure with function. <i>Nucleic Acids Research</i> , 2011, 39, D420-D426.	6.5	126
102	Protein Recognition of Adenylate: An Example of a Fuzzy Recognition Template. <i>Journal of Molecular Biology</i> , 1996, 263, 486-500.	2.0	125
103	Integrating mutation data and structural analysis of the TP53 tumor-suppressor protein. <i>Human Mutation</i> , 2002, 19, 149-164.	1.1	122
104	Retrograde Signaling Is Regulated by the Dynamic Interaction between Rtg2p and Mks1p. <i>Molecular Cell</i> , 2003, 12, 401-411.	4.5	122
105	Using a Library of Structural Templates to Recognise Catalytic Sites and Explore their Evolution in Homologous Families. <i>Journal of Molecular Biology</i> , 2005, 347, 565-581.	2.0	122
106	DamID in <i>C. elegans</i> reveals longevity-associated targets of DAF-16/FoxO. <i>Molecular Systems Biology</i> , 2010, 6, 399.	3.2	122
107	Small Molecule Subgraph Detector (SMSD) toolkit. <i>Journal of Cheminformatics</i> , 2009, 1, 12.	2.8	117
108	Understanding the Functional Roles of Amino Acid Residues in Enzyme Catalysis. <i>Journal of Molecular Biology</i> , 2009, 390, 560-577.	2.0	117

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109	Integrating Structure, Bioinformatics, and Enzymology to Discover Function. <i>Journal of Biological Chemistry</i> , 2003, 278, 26039-26045.	1.6	115
110	Evolution of protein function, from a structural perspective. <i>Current Opinion in Chemical Biology</i> , 1999, 3, 548-556.	2.8	114
111	Prediction of protein structure from amino acid sequence. <i>Nature</i> , 1978, 271, 15-20.	13.7	112
112	Prediction of the location and type of turns in proteins using neural networks. <i>Protein Science</i> , 1999, 8, 1045-1055.	3.1	112
113	BLEEP?potential of mean force describing protein-ligand interactions: II. Calculation of binding energies and comparison with experimental data. <i>Journal of Computational Chemistry</i> , 1999, 20, 1177-1185.	1.5	112
114	Genome-wide dFOXO targets and topology of the transcriptomic response to stress and insulin signalling. <i>Molecular Systems Biology</i> , 2011, 7, 502.	3.2	112
115	EC-BLAST: a tool to automatically search and compare enzyme reactions. <i>Nature Methods</i> , 2014, 11, 171-174.	9.0	112
116	Coordinated multitissue transcriptional and plasma metabolomic profiles following acute caloric restriction in mice. <i>Physiological Genomics</i> , 2006, 27, 187-200.	1.0	109
117	AlphaFold heralds a data-driven revolution in biology and medicine. <i>Nature Medicine</i> , 2021, 27, 1666-1669.	15.2	108
118	The impact of AlphaFold2 one year on. <i>Nature Methods</i> , 2022, 19, 15-20.	9.0	107
119	Protein Superfamily Evolution and the Last Universal Common Ancestor (LUCA). <i>Journal of Molecular Evolution</i> , 2006, 63, 513-525.	0.8	105
120	Longevity GWAS Using the <i>Drosophila</i> Genetic Reference Panel. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 1470-1478.	1.7	105
121	HERA?A program to draw schematic diagrams of protein secondary structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 203-212.	1.5	104
122	Structures of N-termini of helices in proteins. <i>Protein Science</i> , 1997, 6, 147-155.	3.1	104
123	Towards an understanding of the arginine-aspartate interaction. <i>Journal of Molecular Biology</i> , 1992, 226, 251-262.	2.0	103
124	A Structure-based Anatomy of the E.coli Metabolome. <i>Journal of Molecular Biology</i> , 2003, 334, 697-719.	2.0	103
125	Conformational Diversity of Ligands Bound to Proteins. <i>Journal of Molecular Biology</i> , 2006, 356, 928-944.	2.0	103
126	Direct Keap1-Nrf2 disruption as a potential therapeutic target for Alzheimer's disease. <i>PLoS Genetics</i> , 2017, 13, e1006593.	1.5	102

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127	The evolution and structural anatomy of the small molecule metabolic pathways in Escherichia coli. <i>Journal of Molecular Biology</i> , 2001, 311, 693-708.	2.0	101
128	Protein structural topology: Automated analysis and diagrammatic representation. <i>Protein Science</i> , 1999, 8, 897-904.	3.1	101
129	Knowledge-based validation of protein structure coordinates derived by X-ray crystallography and NMR spectroscopy. <i>Current Opinion in Structural Biology</i> , 1994, 4, 731-737.	2.6	100
130	Analysis and prediction of carbohydrate binding sites. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 89-98.	1.0	100
131	Identifying DNA-binding proteins using structural motifs and the electrostatic potential. <i>Nucleic Acids Research</i> , 2004, 32, 4732-4741.	6.5	100
132	Diapause-associated metabolic traits reiterated in long-lived daf-2 mutants in the nematode <i>Caenorhabditis elegans</i> . <i>Mechanisms of Ageing and Development</i> , 2006, 127, 458-472.	2.2	99
133	Small binding proteins selected from a combinatorial repertoire of knottins displayed on phage. <i>Journal of Molecular Biology</i> , 1998, 277, 317-332.	2.0	98
134	Successful protein fold recognition by optimal sequence threading validated by rigorous blind testing. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 387-397.	1.5	97
135	Catalysing New Reactions during Evolution: Economy of Residues and Mechanism. <i>Journal of Molecular Biology</i> , 2003, 331, 829-860.	2.0	96
136	Evolution of Protein Superfamilies and Bacterial Genome Size. <i>Journal of Molecular Biology</i> , 2004, 336, 871-887.	2.0	95
137	The Classification and Evolution of Enzyme Function. <i>Biophysical Journal</i> , 2015, 109, 1082-1086.	0.2	95
138	Molecular basis of inherited diseases: a structural perspective. <i>Trends in Genetics</i> , 2003, 19, 505-513.	2.9	92
139	Wavelet transforms for the characterization and detection of repeating motifs. <i>Journal of Molecular Biology</i> , 2002, 316, 341-363.	2.0	91
140	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2010, 38, D17-D25.	6.5	90
141	X-SITE: Use of Empirically Derived Atomic Packing Preferences to Identify Favourable Interaction Regions in the Binding Sites of Proteins. <i>Journal of Molecular Biology</i> , 1996, 259, 175-201.	2.0	89
142	Detection of 3D atomic similarities and their use in the discrimination of small molecule protein-binding sites. <i>Bioinformatics</i> , 2008, 24, i105-i111.	1.8	89
143	Rebuilding flavodoxin from C α coordinates: A test study. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 5, 170-182.	1.5	88
144	Three-dimensional structure analysis of PROSITE patterns 1 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1999, 286, 1673-1691.	2.0	88

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145	Automatic inference of protein quaternary structure from crystals. <i>Journal of Applied Crystallography</i> , 2003, 36, 1116-1122.	1.9	88
146	The CATH protein family database: A resource for structural and functional annotation of genomes. <i>Proteomics</i> , 2002, 2, 11-21.	1.3	87
147	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	6.5	87
148	Conformational change in substrate binding, catalysis and product release: an open and shut case?. <i>FEBS Letters</i> , 2004, 567, 67-73.	1.3	86
149	Assessment of comparative modeling in CASP2. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 29, 14-28.	1.5	85
150	The European Bioinformatics Institute's data resources: towards systems biology. <i>Nucleic Acids Research</i> , 2004, 33, D46-D53.	6.5	85
151	Protein fold recognition. <i>Journal of Computer-Aided Molecular Design</i> , 1993, 7, 439-456.	1.3	83
152	Accommodating Sequence Changes in β^2 -Hairpins in Proteins. <i>Journal of Molecular Biology</i> , 1993, 229, 428-447.	2.0	82
153	[5] Conformation of β^2 hairpins in protein structures: Classification and diversity in homologous structures. <i>Methods in Enzymology</i> , 1991, 202, 59-82.	0.4	81
154	RTG-dependent Mitochondria-to-Nucleus Signaling Is Regulated by MKS1 and Is Linked to Formation of Yeast Prion [URE3]. <i>Molecular Biology of the Cell</i> , 2002, 13, 795-804.	0.9	80
155	Ligand selectivity and competition between enzymes in silico. <i>Nature Biotechnology</i> , 2004, 22, 1039-1045.	9.4	80
156	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669.	21.5	80
157	Exploring the Evolution of Novel Enzyme Functions within Structurally Defined Protein Superfamilies. <i>PLoS Computational Biology</i> , 2012, 8, e1002403.	1.5	80
158	Emerging concepts in pseudoenzyme classification, evolution, and signaling. <i>Science Signaling</i> , 2019, 12, .	1.6	80
159	Recognizing the fold of a protein structure. <i>Bioinformatics</i> , 2003, 19, 1748-1759.	1.8	79
160	Towards Fully Automated Structure-based Function Prediction in Structural Genomics: A Case Study. <i>Journal of Molecular Biology</i> , 2007, 367, 1511-1522.	2.0	79
161	Correlation of observed fold frequency with the occurrence of local structural motifs. <i>Journal of Molecular Biology</i> , 1999, 287, 969-981.	2.0	78
162	Retrograde Response to Mitochondrial Dysfunction Is Separable from TOR1/2 Regulation of Retrograde Gene Expression. <i>Journal of Biological Chemistry</i> , 2005, 280, 42528-42535.	1.6	78

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163	ELIXIR: a distributed infrastructure for European biological data. <i>Trends in Biotechnology</i> , 2012, 30, 241-242.	4.9	78
164	Prediction of progress at last. <i>Nature</i> , 1991, 354, 105-106.	13.7	77
165	A study into the effects of protein binding on nucleotide conformation. <i>Nucleic Acids Research</i> , 1993, 21, 1369-1380.	6.5	77
166	VarSite: Disease variants and protein structure. <i>Protein Science</i> , 2020, 29, 111-119.	3.1	77
167	A bioinformatician's view of the metabolome. <i>BioEssays</i> , 2006, 28, 534-545.	1.2	76
168	The Greek key motif: extraction, classification and analysis. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 233-245.	1.0	75
169	Regulation of Lifespan, Metabolism, and Stress Responses by the Drosophila SH2B Protein, Lnk. <i>PLoS Genetics</i> , 2010, 6, e1000881.	1.5	75
170	Chopping and Changing: the Evolution of the Flavin-dependent Monooxygenases. <i>Journal of Molecular Biology</i> , 2016, 428, 3131-3146.	2.0	75
171	Pathway evolution, structurally speaking. <i>Current Opinion in Structural Biology</i> , 2002, 12, 374-382.	2.6	73
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