

Martino Bolognesi

List of Publications by Year in descending order

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420
papers

18,455
citations

14614

66
h-index

21474

114
g-index

433
all docs

433
docs citations

433
times ranked

16233
citing authors

#	ARTICLE	IF	CITATIONS
1	Refined crystal structure of ascorbate oxidase at 1.9 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 224, 179-205.	2.0	479
2	Atlas of the clinical genetics of human dilated cardiomyopathy. <i>European Heart Journal</i> , 2015, 36, 1123-1135.	1.0	456
3	X-ray crystal structure of the blue oxidase ascorbate oxidase from Zucchini. <i>Journal of Molecular Biology</i> , 1989, 206, 513-529.	2.0	427
4	Truncated Hemoglobins: A New Family of Hemoglobins Widely Distributed in Bacteria, Unicellular Eukaryotes, and Plants. <i>Journal of Biological Chemistry</i> , 2002, 277, 871-874.	1.6	351
5	Crystal structure of the trigonal form of bovine beta-lactoglobulin and of its complex with retinol at 2.5 Å... resolution. <i>Journal of Molecular Biology</i> , 1987, 197, 695-706.	2.0	348
6	Ivermectin is a potent inhibitor of flavivirus replication specifically targeting NS3 helicase activity: new prospects for an old drug. <i>Journal of Antimicrobial Chemotherapy</i> , 2012, 67, 1884-1894.	1.3	329
7	Three-dimensional Structure of the Tetragonal Crystal Form of Egg-white Avidin in its functional Complex with Biotin at 2Å·7 Å... Resolution. <i>Journal of Molecular Biology</i> , 1993, 231, 698-710.	2.0	307
8	Crystal structure of D-amino acid oxidase: a case of active site mirror-image convergent evolution with flavocytochrome b2.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 7496-7501.	3.3	291
9	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. <i>Antiviral Research</i> , 2010, 87, 125-148.	1.9	289
10	Human Brain Neuroglobin Structure Reveals a Distinct Mode of Controlling Oxygen Affinity. <i>Structure</i> , 2003, 11, 1087-1095.	1.6	286
11	Neuroglobin and cytoglobin in search of their role in the vertebrate globin family. <i>Journal of Inorganic Biochemistry</i> , 2005, 99, 110-119.	1.5	286
12	Neuroglobin and cytoglobin. <i>EMBO Reports</i> , 2002, 3, 1146-1151.	2.0	273
13	Structure of a bacteriochlorophyll a-protein from the green photosynthetic bacterium <i>Prosthecochloris aestuarii</i> . <i>Journal of Molecular Biology</i> , 1979, 131, 259-285.	2.0	271
14	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	6.6	254
15	Sequence-Specific Transcription Factor NF-Y Displays Histone-like DNA Binding and H2B-like Ubiquitination. <i>Cell</i> , 2013, 152, 132-143.	13.5	249
16	CD81 extracellular domain 3D structure: insight into the tetraspanin superfamily structural motifs. <i>EMBO Journal</i> , 2001, 20, 12-18.	3.5	247
17	The Redox State of the Cell Regulates the Ligand Binding Affinity of Human Neuroglobin and Cytoglobin. <i>Journal of Biological Chemistry</i> , 2003, 278, 51713-51721.	1.6	242
18	Conserved Patterns in the Cu,Zn Superoxide Dismutase Family. <i>Journal of Molecular Biology</i> , 1994, 238, 366-386.	2.0	222

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19	A novel two-over-two alpha-helical sandwich fold is characteristic of the truncated hemoglobin family. <i>EMBO Journal</i> , 2000, 19, 2424-2434.	3.5	217
20	<i>Mycobacterium tuberculosis</i> hemoglobin N displays a protein tunnel suited for O ₂ diffusion to the heme. <i>EMBO Journal</i> , 2001, 20, 3902-3909.	3.5	198
21	Three-dimensional structure of the complex between pancreatic secretory trypsin inhibitor (Kazal) Tj ETQq1 1 0.784314 rgBT /Overloc 2.0 196	2.0	196
22	Nonvertebrate hemoglobins: Structural bases for reactivity. <i>Progress in Biophysics and Molecular Biology</i> , 1997, 68, 29-68.	1.4	177
23	Hereditary Systemic Amyloidosis Due to Asp76Asn Variant \hat{I}^2 -Microglobulin. <i>New England Journal of Medicine</i> , 2012, 366, 2276-2283.	13.9	172
24	The Bovine Basic Pancreatic Trypsin Inhibitor (Kunitz Inhibitor): A Milestone Protein. <i>Current Protein and Peptide Science</i> , 2003, 4, 231-251.	0.7	163
25	Crystal Structure of Cytoglobin: The Fourth Globin Type Discovered in Man Displays Heme Hexa-coordination. <i>Journal of Molecular Biology</i> , 2004, 336, 917-927.	2.0	157
26	CtBP/BARS: a dual-function protein involved in transcription co-repression and Golgi membrane fission. <i>EMBO Journal</i> , 2003, 22, 3122-3130.	3.5	144
27	<i>Aplysia limacina</i> myoglobin. <i>Journal of Molecular Biology</i> , 1989, 205, 529-544.	2.0	143
28	Bone marrow transplantation from unrelated donors: the impact of mismatches with substitutions at position 116 of the human leukocyte antigen class I heavy chain. <i>Blood</i> , 2001, 98, 3150-3155.	0.6	134
29	Structure-based approach to rationally design a chimeric protein for an effective vaccine against Group B <i>Streptococcus</i> infections. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10278-10283.	3.3	132
30	Crystal structure of <i>Escherichia coli</i> pyruvate kinase type I: molecular basis of the allosteric transition. <i>Structure</i> , 1995, 3, 729-741.	1.6	131
31	Unusual structure of the oxygen-binding site in the dimeric bacterial hemoglobin from <i>Vitreoscilla</i> sp. <i>Structure</i> , 1997, 5, 497-507.	1.6	127
32	Crystal structure of yeast Cu,Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 1992, 225, 791-809.	2.0	121
33	Heme-Ligand Tunneling in Group I Truncated Hemoglobins. <i>Journal of Biological Chemistry</i> , 2004, 279, 21520-21525.	1.6	117
34	Structural bases for heme binding and diatomic ligand recognition in truncated hemoglobins. <i>Journal of Inorganic Biochemistry</i> , 2005, 99, 97-109.	1.5	117
35	Anthrax toxin: a tripartite lethal combination1. <i>FEBS Letters</i> , 2002, 531, 384-388.	1.3	116
36	The X-ray three-dimensional structure of avidin. <i>New Biotechnology</i> , 1999, 16, 5-12.	2.7	114

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37	Cryo-EM structure of cardiac amyloid fibrils from an immunoglobulin light chain AL amyloidosis patient. <i>Nature Communications</i> , 2019, 10, 1269.	5.8	113
38	A TyrCD1/TrpG8 hydrogen bond network and a TyrB10-TyrCD1 covalent link shape the heme distal site of <i>Mycobacterium tuberculosis</i> hemoglobin O. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5766-5771.	3.3	111
39	Kinetic and crystallographic analyses support a sequential-ordered bi bi catalytic mechanism for <i>Escherichia coli</i> glucose-1-phosphate thymidyltransferase. <i>Journal of Molecular Biology</i> , 2001, 313, 831-843.	2.0	102
40	Monitoring the Process of HypF Fibrillization and Liposome Permeabilization by Protofibrils. <i>Journal of Molecular Biology</i> , 2004, 338, 943-957.	2.0	101
41	Tetramerization Dynamics of C-terminal Domain Underlies Isoform-specific cAMP Gating in Hyperpolarization-activated Cyclic Nucleotide-gated Channels. <i>Journal of Biological Chemistry</i> , 2011, 286, 44811-44820.	1.6	101
42	The allosteric regulation of pyruvate kinase. <i>FEBS Letters</i> , 1996, 389, 15-19.	1.3	100
43	Reactivity of ferric Aplysia and sperm whale myoglobins towards imidazole. <i>Journal of Molecular Biology</i> , 1982, 158, 305-315.	2.0	96
44	Crystal and molecular structure of the bovine β -chymotrypsin-eglin c complex at 2.0 Å... resolution. <i>Journal of Molecular Biology</i> , 1992, 225, 107-123.	2.0	95
45	Ligand-induced dynamical regulation of NO conversion in <i>Mycobacterium tuberculosis</i> truncated hemoglobin-N. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 457-464.	1.5	95
46	The <i>Escherichia coli</i> Lpt Transenvelope Protein Complex for Lipopolysaccharide Export Is Assembled via Conserved Structurally Homologous Domains. <i>Journal of Bacteriology</i> , 2013, 195, 1100-1108.	1.0	90
47	Active Site Plasticity ind-Amino Acid Oxidase: A Crystallographic Analysis. <i>Biochemistry</i> , 1997, 36, 5853-5860.	1.2	89
48	The Three-Dimensional Structure of the Human NK Cell Receptor NKp44, a Triggering Partner in Natural Cytotoxicity. <i>Structure</i> , 2003, 11, 725-734.	1.6	89
49	The crystal structure of a sulfurtransferase from <i>Azotobacter vinelandii</i> highlights the evolutionary relationship between the rhodanese and phosphatase enzyme families. <i>Journal of Molecular Biology</i> , 2000, 298, 691-704.	2.0	86
50	Structure-Based Inhibition of Norovirus RNA-Dependent RNA Polymerases. <i>Journal of Molecular Biology</i> , 2012, 419, 198-210.	2.0	86
51	Cyanide Binding to <i>Lucina pectinata</i> Hemoglobin I and to Sperm Whale Myoglobin: An X-Ray Crystallographic Study. <i>Biophysical Journal</i> , 1999, 77, 1093-1099.	0.2	85
52	Ebolavirus and Marburgvirus: Insight the Filoviridae family. <i>Molecular Aspects of Medicine</i> , 2008, 29, 151-185.	2.7	84
53	Unique structural features of the monomeric Cu,Zn superoxide dismutase from <i>Escherichia coli</i> , revealed by X-ray crystallography. <i>Journal of Molecular Biology</i> , 1997, 274, 408-420.	2.0	83
54	The Controlling Roles of Trp60 and Trp95 in β 2-Microglobulin Function, Folding and Amyloid Aggregation Properties. <i>Journal of Molecular Biology</i> , 2008, 378, 887-897.	2.0	82

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55	Evolutionary conservativeness of electric field in the Cu,Zn superoxide dismutase active site. Journal of Molecular Biology, 1992, 223, 337-342.	2.0	81
56	X-ray Crystal Structure of Ferric Aplysia limacina Myoglobin in Different Liganded States. Journal of Molecular Biology, 1993, 233, 498-508.	2.0	78
57	Crystal Structure and Activity of Kunjin Virus NS3 Helicase; Protease and Helicase Domain Assembly in the Full Length NS3 Protein. Journal of Molecular Biology, 2007, 372, 444-455.	2.0	78
58	Recognition of RNA Cap in the Wesselsbron Virus NS5 Methyltransferase Domain: Implications for RNA-Capping Mechanisms in Flavivirus. Journal of Molecular Biology, 2009, 385, 140-152.	2.0	78
59	Structural Bases for Sulfide Recognition in Lucina pectinata Hemoglobin I. Journal of Molecular Biology, 1996, 258, 1-5.	2.0	77
60	Structure of the Sulfide-reactive Hemoglobin from the Clam Lucina pectinata. Journal of Molecular Biology, 1994, 244, 86-99.	2.0	76
61	Specific Recognition of ZNF217 and Other Zinc Finger Proteins at a Surface Groove of C-Terminal Binding Proteins. Molecular and Cellular Biology, 2006, 26, 8159-8172.	1.1	74
62	Novel SMAC-mimetics synergistically stimulate melanoma cell death in combination with TRAIL and Bortezomib. British Journal of Cancer, 2010, 102, 1707-1716.	2.9	70
63	The structural bases for agonist diversity in an <i>Arabidopsis thaliana</i> glutamate receptor-like channel. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 752-760.	3.3	70
64	Absence of water at the sixth co-ordination site in ferric Aplysia myoglobin. Journal of Molecular Biology, 1981, 151, 315-319.	2.0	69
65	Re-Evaluation of Amino Acid Sequence and Structural Consensus Rules for Cysteine-Nitric Oxide Reactivity. Biological Chemistry, 2000, 381, 623-627.	1.2	68
66	Inhibition of Cysteine Protease Activity by NO-donors. Current Protein and Peptide Science, 2001, 2, 137-153.	0.7	68
67	FAD-Binding Site and NADP Reactivity in Human Renalase: A New Enzyme Involved in Blood Pressure Regulation. Journal of Molecular Biology, 2011, 411, 463-473.	2.0	67
68	The 109 Residue Nerve Tissue Minihemoglobin from Cerebratulus lacteus Highlights Striking Structural Plasticity of the Î±-Helical Globin Fold. Structure, 2002, 10, 725-735.	1.6	66
69	Protein fold and structure in the truncated (2/2) globin family. Gene, 2007, 398, 2-11.	1.0	66
70	Cyanide Binding to Truncated Hemoglobins: A Crystallographic and Kinetic Study. Biochemistry, 2004, 43, 5213-5221.	1.2	65
71	X-ray crystal structure of the ferric sperm whale myoglobin: Imidazole complex at 2.0 Å... resolution. Journal of Molecular Biology, 1991, 217, 409-412.	2.0	64
72	Flaviviral methyltransferase/RNA interaction: Structural basis for enzyme inhibition. Antiviral Research, 2009, 83, 28-34.	1.9	64

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73	Evolutionary constraints for dimer formation in prokaryotic Cu,Zn superoxide dismutase 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 285, 283-296.	2.0	63
74	Crystal Structure and Anion Binding in the Prokaryotic Hydrogenase Maturation Factor HypF Acylphosphatase-like Domain. <i>Journal of Molecular Biology</i> , 2002, 321, 785-796.	2.0	63
75	Interaction between serine (pro)enzymes, and kazal and kunitz inhibitors. <i>Journal of Molecular Biology</i> , 1983, 165, 543-558.	2.0	62
76	X-ray crystal structure of the fluoride derivative of Aplysia limacina ferric myoglobin at 2.0 Å resolution. <i>Journal of Molecular Biology</i> , 1990, 213, 621-625.	2.0	62
77	GDP-4-keto-6-deoxy-D-mannose epimerase/reductase from Escherichia coli, a key enzyme in the biosynthesis of GDP-L-fucose, displays the structural characteristics of the RED protein homology superfamily. <i>Structure</i> , 1998, 6, 1453-1465.	1.6	59
78	Mapping protein matrix cavities in human cytoglobin through Xe atom binding. <i>Biochemical and Biophysical Research Communications</i> , 2004, 316, 1217-1221.	1.0	58
79	Purification, inhibitory properties and amino acid sequence of a new serine proteinase inhibitor from white mustard (<i>Sinapis alba</i> L.) seed. <i>FEBS Letters</i> , 1992, 301, 10-14.	1.3	56
80	Structural Determinants in the Group III Truncated Hemoglobin from <i>Campylobacter jejuni</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 37803-37812.	1.6	54
81	Exploring the molecular basis of heme coordination in human neuroglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 695-705.	1.5	54
82	Reactivity of ferric Aplysia myoglobin towards anionic ligands in the acidic region. <i>Journal of Molecular Biology</i> , 1981, 146, 363-374.	2.0	53
83	Crystal structure solution and refinement of the semisynthetic cobalt-substituted bovine erythrocyte superoxide dismutase at 2.0 Å resolution. <i>Journal of Molecular Biology</i> , 1992, 226, 227-238.	2.0	53
84	Role of the C-Terminal Binding Protein PxDLS Motif Binding Cleft in Protein Interactions and Transcriptional Repression. <i>Molecular and Cellular Biology</i> , 2006, 26, 8202-8213.	1.1	53
85	Structural Bases of Norovirus RNA Dependent RNA Polymerase Inhibition by Novel Suramin-Related Compounds. <i>PLoS ONE</i> , 2014, 9, e91765.	1.1	53
86	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. <i>Nature Communications</i> , 2018, 9, 1658.	5.8	53
87	Enhancement of the HIV-1 inhibitory activity of RANTES by modification of the N-terminal region: dissociation from CCR5 activation. <i>European Journal of Immunology</i> , 2000, 30, 3190-3198.	1.6	52
88	Probing the catalytic mechanism of GDP-4-keto-6-deoxy-d-mannose epimerase/reductase by kinetic and crystallographic characterization of site-specific mutants. <i>Journal of Molecular Biology</i> , 2000, 303, 77-91.	2.0	52
89	Mycobacterial truncated hemoglobins: From genes to functions. <i>Gene</i> , 2007, 398, 42-51.	1.0	51
90	Identification of the Molecular Site of Ivabradine Binding to HCN4 Channels. <i>PLoS ONE</i> , 2013, 8, e53132.	1.1	51

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91	Crystal structure of apo-avidin from hen egg-white. <i>Journal of Molecular Biology</i> , 1994, 235, 42-46.	2.0	50
92	<i>Escherichia coli</i> GlpE Is a Prototype Sulfurtransferase for the Single-Domain Rhodanese Homology Superfamily. <i>Structure</i> , 2001, 9, 1117-1125.	1.6	50
93	Subunit Association and Conformational Flexibility in the Head Subdomain of Human CD81 Large Extracellular Loop. <i>Biological Chemistry</i> , 2002, 383, 1447-52.	1.2	50
94	Designing Smac-mimetics as antagonists of XIAP, cIAP1, and cIAP2. <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 162-167.	1.0	50
95	Exploiting the <i>Burkholderia pseudomallei</i> Acute Phase Antigen BPSL2765 for Structure-Based Epitope Discovery/Design in Structural Vaccinology. <i>Chemistry and Biology</i> , 2013, 20, 1147-1156.	6.2	50
96	Cyclic dinucleotides bind the C-linker of HCN4 to control channel cAMP responsiveness. <i>Nature Chemical Biology</i> , 2014, 10, 457-462.	3.9	50
97	Concurrent structural and biophysical traits link with immunoglobulin light chains amyloid propensity. <i>Scientific Reports</i> , 2017, 7, 16809.	1.6	50
98	Structural determinants of fluoride and formate binding to hemoglobin and myoglobin: crystallographic and 1H-NMR relaxometric study. <i>Biophysical Journal</i> , 1996, 70, 482-488.	0.2	49
99	Structural determinants of CCR5 recognition and HIV-1 blockade in RANTES. <i>Nature Structural Biology</i> , 2001, 8, 611-615.	9.7	49
100	A Structure-Based Strategy for Epitope Discovery in <i>Burkholderia pseudomallei</i> OppA Antigen. <i>Structure</i> , 2013, 21, 167-175.	1.6	49
101	Targeting flavivirus RNA dependent RNA polymerase through a pyridobenzothiazole inhibitor. <i>Antiviral Research</i> , 2016, 134, 226-235.	1.9	49
102	Modulation of the Catalytic Rate of Cu,Zn Superoxide Dismutase in Single and Double Mutants of Conserved Positively and Negatively Charged Residues. <i>Biochemistry</i> , 1995, 34, 6043-6049.	1.2	48
103	Bishistidyl Heme Hexacoordination, a Key Structural Property in <i>Drosophila melanogaster</i> Hemoglobin. <i>Journal of Biological Chemistry</i> , 2005, 280, 27222-27229.	1.6	48
104	Binding of non-catalytic ATP to human hexokinase I highlights the structural components for enzyme-membrane association control. <i>Structure</i> , 1999, 7, 1427-1437.	1.6	47
105	Functional and crystallographic characterization of <i>Salmonella typhimurium</i> Cu,Zn superoxide dismutase coded by the sodCI virulence gene 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 302, 465-478.	2.0	47
106	Reversible hexa- to penta- coordination of the heme Fe atom modulates ligand binding properties of neuroglobin and cytoglobin. <i>IUBMB Life</i> , 2004, 56, 657-664.	1.5	47
107	The α -Rhodanese-Fold and Catalytic Mechanism of 3-Mercaptopyruvate Sulfurtransferases: Crystal Structure of SseA from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 2004, 335, 583-593.	2.0	47
108	Structural determinants of ligand migration in <i>Mycobacterium tuberculosis</i> truncated hemoglobin O. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 372-379.	1.5	47

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109	HisE11 and HisF8 Provide Bis-histidyl Heme Hexa-coordination in the Globin Domain of <i>Geobacter sulfurreducens</i> Globin-coupled Sensor. <i>Journal of Molecular Biology</i> , 2009, 386, 246-260.	2.0	47
110	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. <i>Scientific Reports</i> , 2016, 6, 25559.	1.6	47
111	A novel deamido-NAD ⁺ -binding site revealed by the trapped NAD-adenylate intermediate in the NAD ⁺ synthetase structure. <i>Structure</i> , 1998, 6, 1129-1140.	1.6	46
112	An Active-like Structure in the Unphosphorylated StyR Response Regulator Suggests a Phosphorylation- Dependent Allosteric Activation Mechanism. <i>Structure</i> , 2005, 13, 1289-1297.	1.6	46
113	Anticooperative ligand binding properties of recombinant ferric <i>Vitreoscilla</i> homodimeric hemoglobin: A thermodynamic, kinetic and X-ray crystallographic study 1 Edited by K. Nagei 2 This paper is dedicated to Professor Ciampaolo Bolognesi on the occasion of his 75th birthday.. <i>Journal of Molecular Biology</i> , 1999, 291, 637-650.	2.0	45
114	Epstein syndrome: another renal disorder with mutations in the nonmuscle myosin heavy chain ⁹ gene. <i>Human Genetics</i> , 2002, 110, 182-186.	1.8	45
115	Ligand Interactions in the Distal Heme Pocket of <i>Mycobacterium tuberculosis</i> Truncated Hemoglobin N: Roles of TyrB10 and GlnE11 Residues. <i>Biochemistry</i> , 2006, 45, 8770-8781.	1.2	45
116	TREX1 C-terminal frameshift mutations in the systemic variant of retinal vasculopathy with cerebral leukodystrophy. <i>Neurological Sciences</i> , 2015, 36, 323-330.	0.9	45
117	Very high resolution structure of a trematode hemoglobin displaying a TyrB10-TyrE7 heme distal residue pair and high oxygen affinity. <i>Journal of Molecular Biology</i> , 2001, 309, 1153-1164.	2.0	44
118	The C-terminal domain of the transcriptional corepressor CtBP is intrinsically unstructured. <i>Protein Science</i> , 2006, 15, 1042-1050.	3.1	44
119	Monomer [~] Dimer Equilibrium and Oxygen Binding Properties of Ferrous <i>Vitreoscilla</i> Hemoglobin. <i>Biochemistry</i> , 2001, 40, 9311-9316.	1.2	43
120	Structure, conformational stability, and enzymatic properties of acylphosphatase from the hyperthermophile <i>Sulfolobus solfataricus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 64-79.	1.5	43
121	Archaeal protoglobin structure indicates new ligand diffusion paths and modulation of haem reactivity. <i>EMBO Reports</i> , 2008, 9, 157-163.	2.0	43
122	DE loop mutations affect ² microglobulin stability, oligomerization, and the low pH unfolded form. <i>Protein Science</i> , 2010, 19, 1386-1394.	3.1	43
123	A redox signalling globin is essential for reproduction in <i>Caenorhabditis elegans</i> . <i>Nature Communications</i> , 2015, 6, 8782.	5.8	42
124	From crystal structure to <i>in silico</i> epitope discovery in the <i>Burkholderia pseudomallei</i> flagellar hook-associated protein FlgK. <i>FEBS Journal</i> , 2015, 282, 1319-1333.	2.2	42
125	Structure-Function Relationships in the Growing Hexa-coordinate Hemoglobin Subfamily. <i>IUBMB Life</i> , 2004, 56, 643-651.	1.5	41
126	Human Neuroserpin: Structure and Time-Dependent Inhibition. <i>Journal of Molecular Biology</i> , 2009, 388, 109-121.	2.0	41

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127	Gating movements and ion permeation in HCN4 pacemaker channels. <i>Molecular Cell</i> , 2021, 81, 2929-2943.e6.	4.5	41
128	Crystal structure of the bovine $\hat{\pm}$ -chymotrypsin:kunitz inhibitor complex. An example of multiple protein:protein recognition sites. , 1997, 10, 26-35.		40
129	The truncated hemoglobin from <i>Mycobacterium leprae</i> . <i>Biochemical and Biophysical Research Communications</i> , 2002, 294, 1064-1070.	1.0	40
130	Ferredoxin-NADP+ Reductase from <i>Plasmodium falciparum</i> Undergoes NADP+-dependent Dimerization and Inactivation: Functional and Crystallographic Analysis. <i>Journal of Molecular Biology</i> , 2007, 367, 501-513.	2.0	40
131	Targeting the X-Linked Inhibitor of Apoptosis Protein through 4-Substituted Azabicyclo[5.3.0]alkane Smac Mimetics. Structure, Activity, and Recognition Principles. <i>Journal of Molecular Biology</i> , 2008, 384, 673-689.	2.0	40
132	Structural Basis for Bivalent Smac-Mimetics Recognition in the IAP Protein Family. <i>Journal of Molecular Biology</i> , 2009, 392, 630-644.	2.0	40
133	Sequence- and Structure-Based Immunoreactive Epitope Discovery for <i>Burkholderia pseudomallei</i> Flagellin. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003917.	1.3	40
134	Solution 1H nuclear magnetic resonance determination of hydrogen bonding of the E10 (66) Arg side-chain to the bound ligand in <i>Aplysia cyano-met</i> myoglobin. <i>Journal of Molecular Biology</i> , 1992, 224, 891-897.	2.0	39
135	Determining mutational fingerprints at the human p53 locus with a yeast functional assay: a new tool for molecular epidemiology. <i>Oncogene</i> , 1997, 14, 1307-1313.	2.6	39
136	Structural bases for substrate recognition and activity in Meaban virus nucleoside-2 $\hat{\epsilon}$ -O-methyltransferase. <i>Protein Science</i> , 2007, 16, 1133-1145.	3.1	39
137	Naphthalene-sulfonate inhibitors of human norovirus RNA-dependent RNA-polymerase. <i>Antiviral Research</i> , 2014, 102, 23-28.	1.9	39
138	Control and recognition of anionic ligands in myoglobin. <i>FEBS Letters</i> , 1991, 282, 281-284.	1.3	38
139	Engineering peroxidase activity in myoglobin: the haem cavity structure and peroxide activation in the T67R/S92D mutant and its derivative reconstituted with protohaemin-l-histidine. <i>Biochemical Journal</i> , 2004, 377, 717-724.	1.7	38
140	Thr-E11 Regulates O ₂ Affinity in <i>Cerebratulus lacteus</i> Mini-hemoglobin. <i>Journal of Biological Chemistry</i> , 2004, 279, 33662-33672.	1.6	38
141	Truncated Hemoglobins and Nitric Oxide Action. <i>IUBMB Life</i> , 2004, 55, 623-627.	1.5	38
142	$\hat{\pm}$ 2-Microglobulin H31Y Variant 3D Structure Highlights the Protein Natural Propensity Towards Intermolecular Aggregation. <i>Journal of Molecular Biology</i> , 2004, 335, 1051-1064.	2.0	38
143	The Roles of Tyr(CD1) and Trp(G8) in <i>Mycobacterium tuberculosis</i> Truncated Hemoglobin O in Ligand Binding and on the Heme Distal Site Architecture., <i>Biochemistry</i> , 2007, 46, 11440-11450.	1.2	38
144	The Diversity of 2/2 (Truncated) Globins. <i>Advances in Microbial Physiology</i> , 2013, 63, 49-78.	1.0	38

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145	Coupling of the heme and an internal disulfide bond in human neuroglobin. <i>Micron</i> , 2004, 35, 59-62.	1.1	37
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