

Martino Bolognesi

List of Publications by Year in descending order

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421
papers

18,455
citations

14655

66
h-index

21540

114
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433
all docs

433
docs citations

433
times ranked

16233
citing authors

#	ARTICLE	IF	CITATIONS
1	Truncated (2/2) hemoglobin: Unconventional structures and functional roles in vivo and in human pathogenesis. <i>Molecular Aspects of Medicine</i> , 2022, 84, 101049.	6.4	5
2	Elucidating the 3D Structure of a Surface Membrane Antigen from <i>Trypanosoma cruzi</i> as a Serodiagnostic Biomarker of Chagas Disease. <i>Vaccines</i> , 2022, 10, 71.	4.4	0
3	Solution Structure of the BPSL1445 Protein of <i>Burkholderia pseudomallei</i> Reveals the SYLF Domain Three-Dimensional Fold. <i>ACS Chemical Biology</i> , 2022, 17, 230-239.	3.4	2
4	Virucidal Activity of the Pyridobenzothiazolone Derivative HeE1-17Y against Enveloped RNA Viruses. <i>Viruses</i> , 2022, 14, 1157.	3.3	4
5	Mycobacterial and Human Ferrous Nitrobindins: Spectroscopic and Reactivity Properties. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1674.	4.1	10
6	Structure, Immunoreactivity, and In Silico Epitope Determination of SmSPI <i>S. mansoni</i> Serpin for Immunodiagnostic Application. <i>Vaccines</i> , 2021, 9, 322.	4.4	4
7	Gating movements and ion permeation in HCN4 pacemaker channels. <i>Molecular Cell</i> , 2021, 81, 2929-2943.e6.	9.7	41
8	Structural and Functional Characterization of the Globin-Coupled Sensors of <i>Azotobacter vinelandii</i> and <i>Bordetella pertussis</i> . <i>Antioxidants and Redox Signaling</i> , 2020, 32, 378-395.	5.4	4
9	The structural bases for agonist diversity in an <i>Arabidopsis thaliana</i> glutamate receptor-like channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 752-760.	7.1	70
10	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. <i>Journal of Molecular Biology</i> , 2020, 432, 845-860.	4.2	26
11	Embelin as Lead Compound for New Neuroserpin Polymerization Inhibitors. <i>Life</i> , 2020, 10, 111.	2.4	10
12	High-Light versus Low-Light: Effects on Paired Photosystem II Supercomplex Structural Rearrangement in Pea Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8643.	4.1	13
13	Structural and functional properties of Antarctic fish cytoglobins-1: Cold-reactivity in multi-ligand reactions. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2132-2144.	4.1	10
14	Detecting the nature and solving the crystal structure of a contaminant protein from an opportunistic pathogen. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 392-397.	0.8	3
15	Basic and applied science at the time of COVID-19. <i>FEBS Letters</i> , 2020, 594, 2933-2934.	2.8	1
16	Glycosylation Tunes Neuroserpin Physiological and Pathological Properties. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3235.	4.1	11
17	Functional and structural analysis of trehalose-6-phosphate phosphatase from <i>Burkholderia pseudomallei</i> : Insights into the catalytic mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2020, 523, 979-984.	2.1	4
18	Mycobacterial and Human Nitrobindins: Structure and Function. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 229-246.	5.4	17

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19	Modulating the cardiotoxic behaviour of immunoglobulin light chain dimers through point mutations. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 105-106.	3.0	4
20	The concurrency of several biophysical traits links immunoglobulin light chains with toxicity in AL amyloidosis. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2019, 26, 107-108.	3.0	2
21	Cryo-EM Structures of AzospirillumÂbrasilense Glutamate Synthase in Its Oligomeric Assemblies. <i>Journal of Molecular Biology</i> , 2019, 431, 4523-4526.	4.2	4
22	Cryo-EM structure of cardiac amyloid fibrils from an immunoglobulin light chain AL amyloidosis patient. <i>Nature Communications</i> , 2019, 10, 1269.	12.8	113
23	A stereospecific carboxyl esterase from <i>Bacillus coagulans</i> hosting nonlipase activity within a lipase-like fold. <i>FEBS Journal</i> , 2018, 285, 903-914.	4.7	10
24	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. <i>Nature Communications</i> , 2018, 9, 1658.	12.8	53
25	BPSL1626: Reverse and Structural Vaccinology Reveal a Novel Candidate for Vaccine Design Against <i>Burkholderia pseudomallei</i> . <i>Antibodies</i> , 2018, 7, 26.	2.5	11
26	An Asp to Asn mutation is a toxic trigger in beta-2 microglobulin: structure and biophysics. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2017, 24, 15-16.	3.0	2
27	Structure and Computation in Immunoreagent Design: From Diagnostics to Vaccines. <i>Trends in Biotechnology</i> , 2017, 35, 1208-1220.	9.3	22
28	Designing Probes for Immunodiagnostics: Structural Insights into an Epitope Targeting <i>Burkholderia</i> Infections. <i>ACS Infectious Diseases</i> , 2017, 3, 736-743.	3.8	8
29	Structural Vaccinology for Melioidosis Vaccine Design and Immunodiagnostics. <i>Current Tropical Medicine Reports</i> , 2017, 4, 103-110.	3.7	1
30	Concurrent structural and biophysical traits link with immunoglobulin light chains amyloid propensity. <i>Scientific Reports</i> , 2017, 7, 16809.	3.3	50
31	The N-terminal pre-A region of <i>MycobacteriumÂtuberculosis</i> 2/2HbN promotes NO-dioxygenase activity. <i>FEBS Journal</i> , 2016, 283, 305-322.	4.7	10
32	Embelin binds to human neuroserpin and impairs its polymerisation. <i>Scientific Reports</i> , 2016, 6, 18769.	3.3	13
33	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.	3.3	47
34	Targeting flavivirus RNA dependent RNA polymerase through a pyridobenzothiazole inhibitor. <i>Antiviral Research</i> , 2016, 134, 226-235.	4.1	49
35	Immunisation with proteins expressed during chronic murine melioidosis provides enhanced protection against disease. <i>Vaccine</i> , 2016, 34, 1665-1671.	3.8	27
36	Flexible vs Rigid Epitope Conformations for Diagnostic- and Vaccine-Oriented Applications: Novel Insights from the <i>Burkholderia pseudomallei</i> BPSL2765 Pal3 Epitope. <i>ACS Infectious Diseases</i> , 2016, 2, 221-230.	3.8	22

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37	Selecting soluble/foldable protein domains through single-gene or genomic ORF filtering: structure of the head domain of Burkholderia pseudomallei antigen BPSL2063. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2227-2235.	2.5	15
38	A redox signalling globin is essential for reproduction in Caenorhabditis elegans. Nature Communications, 2015, 6, 8782.	12.8	42
39	A covalent homodimer probing early oligomers along amyloid aggregation. Scientific Reports, 2015, 5, 14651.	3.3	13
40	Structural flexibility of the heme cavity in the cold-adapted truncated hemoglobin from the Antarctic marine bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. FEBS Journal, 2015, 282, 2948-2965.	4.7	24
41	Wild Type Beta-2 Microglobulin and DE Loop Mutants Display a Common Fibrillar Architecture. PLoS ONE, 2015, 10, e0122449.	2.5	14
42	Structural Bases for the Regulation of CO Binding in the Archaeal Protoglobin from Methanosarcina acetivorans. PLoS ONE, 2015, 10, e0125959.	2.5	3
43	Sequence- and Structure-Based Immunoreactive Epitope Discovery for Burkholderia pseudomallei Flagellin. PLoS Neglected Tropical Diseases, 2015, 9, e0003917.	3.0	40
44	Decoding the Structural Bases of D76N Å2-Microglobulin High Amyloidogenicity through Crystallography and Asn-Scan Mutagenesis. PLoS ONE, 2015, 10, e0144061.	2.5	22
45	Functional and dysfunctional conformers of human neuroserpin characterized by optical spectroscopies and Molecular Dynamics. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 110-117.	2.3	13
46	The Activator of Apoptosis Smac-DIABLO Acts as a Tetramer in Solution. Biophysical Journal, 2015, 108, 714-723.	0.5	12
47	NF023 binding to XIAP-BIR1: Searching drugs for regulation of the NF-κB pathway. Proteins: Structure, Function and Bioinformatics, 2015, 83, 612-620.	2.6	6
48	TREX1 C-terminal frameshift mutations in the systemic variant of retinal vasculopathy with cerebral leukodystrophy. Neurological Sciences, 2015, 36, 323-330.	1.9	45
49	Backbone and side-chain 1H, 15N, 13C assignment and secondary structure of BPSL1445 from Burkholderia pseudomallei. Biomolecular NMR Assignments, 2015, 9, 347-350.	0.8	1
50	Crystal structure of LptH, the periplasmic component of the lipopolysaccharide transport machinery from <i>Pseudomonas aeruginosa</i> . FEBS Journal, 2015, 282, 1980-1997.	4.7	31
51	From crystal structure to <i>in silico</i> epitope discovery in the Burkholderia pseudomallei flagellar hook-associated protein FlgK. FEBS Journal, 2015, 282, 1319-1333.	4.7	42
52	Atlas of the clinical genetics of human dilated cardiomyopathy. European Heart Journal, 2015, 36, 1123-1135.	2.2	456
53	Synchrotron Radiation and Bio-crystallography. , 2015, , 615-639.		0
54	Structural Bases of Norovirus RNA Dependent RNA Polymerase Inhibition by Novel Suramin-Related Compounds. PLoS ONE, 2014, 9, e91765.	2.5	53

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55	Class I Major Histocompatibility Complex, the Trojan Horse for Secretion of Amyloidogenic β 2-Microglobulin. <i>Journal of Biological Chemistry</i> , 2014, 289, 3318-3327.	3.4	22
56	Novel neurofibromatosis type 2 mutation presenting with status epilepticus. <i>Epileptic Disorders</i> , 2014, 16, 132-137.	1.3	7
57	Cyclic dinucleotides bind the C-linker of HCN4 to control channel cAMP responsiveness. <i>Nature Chemical Biology</i> , 2014, 10, 457-462.	8.0	50
58	Naphthalene-sulfonate inhibitors of human norovirus RNA-dependent RNA-polymerase. <i>Antiviral Research</i> , 2014, 102, 23-28.	4.1	39
59	Rapid Proton-Detected NMR Assignment for Proteins with Fast Magic Angle Spinning. <i>Journal of the American Chemical Society</i> , 2014, 136, 12489-12497.	13.7	254
60	Edge strand engineering prevents native-like aggregation in <i>Sulfolobus solfataricus</i> acylphosphatase. <i>FEBS Journal</i> , 2014, 281, 4072-4084.	4.7	13
61	Delivery of Suramin as an Antiviral Agent through Liposomal Systems. <i>ChemMedChem</i> , 2014, 9, 933-939.	3.2	28
62	PPNDS inhibits murine Norovirus RNA-dependent RNA-polymerase mimicking two RNA stacking bases. <i>FEBS Letters</i> , 2014, 588, 1720-1725.	2.8	21
63	Discovery and Characterization of a Distinct Cyclic Nucleotide Binding Pocket in HCN Channels. <i>Biophysical Journal</i> , 2014, 106, 627a.	0.5	0
64	Redefining the PF06864 Pfam Family Based on Burkholderia pseudomallei PilO2Bp S-SAD Crystal Structure. <i>PLoS ONE</i> , 2014, 9, e94981.	2.5	4
65	Nitrite-Reductase and Peroxynitrite Isomerization Activities of Methanosarcina acetivorans Protoglobin. <i>PLoS ONE</i> , 2014, 9, e95391.	2.5	13
66	Exploiting the Burkholderia pseudomallei Acute Phase Antigen BPSL2765 for Structure-Based Epitope Discovery/Design in Structural Vaccinology. <i>Chemistry and Biology</i> , 2013, 20, 1147-1156.	6.0	50
67	Functional and structural roles of the N-terminal extension in Methanosarcina acetivorans protoglobin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1813-1823.	2.3	11
68	The Diversity of 2/2 (Truncated) Globins. <i>Advances in Microbial Physiology</i> , 2013, 63, 49-78.	2.4	38
69	Protoglobin. <i>Advances in Microbial Physiology</i> , 2013, 63, 79-96.	2.4	25
70	Non-covalent and covalent modifications modulate the reactivity of monomeric mammalian globins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1750-1756.	2.3	27
71	Reductive nitrosylation of Methanosarcina acetivorans protoglobin: A comparative study. <i>Biochemical and Biophysical Research Communications</i> , 2013, 430, 1301-1305.	2.1	16
72	A Structure-Based Strategy for Epitope Discovery in Burkholderia pseudomallei OppA Antigen. <i>Structure</i> , 2013, 21, 167-175.	3.3	49

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73	Sequence-Specific Transcription Factor NF-Y Displays Histone-like DNA Binding and H2B-like Ubiquitination. <i>Cell</i> , 2013, 152, 132-143.	28.9	249
74	One hundred years of X-ray diffraction, 50 years of structural biology. <i>Rendiconti Lincei</i> , 2013, 24, 93-99.	2.2	1
75	Molecular mechanism and functional role of brefeldin A-mediated ADP-ribosylation of CtBP1/BARS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9794-9799.	7.1	37
76	The Escherichia coli Lpt Transenvelope Protein Complex for Lipopolysaccharide Export Is Assembled via Conserved Structurally Homologous Domains. <i>Journal of Bacteriology</i> , 2013, 195, 1100-1108.	2.2	90
77	CO Rebinding Kinetics and Molecular Dynamics Simulations Highlight Dynamic Regulation of Internal Cavities in Human Cytochrome. <i>PLoS ONE</i> , 2013, 8, e49770.	2.5	28
78	Identification of the Molecular Site of Ivabradine Binding to HCN4 Channels. <i>PLoS ONE</i> , 2013, 8, e53132.	2.5	51
79	Kinetic and Structural Evidences on Human Prolidase Pathological Mutants Suggest Strategies for Enzyme Functional Rescue. <i>PLoS ONE</i> , 2013, 8, e58792.	2.5	21
80	Structure and Haem-Distal Site Plasticity in Methanosarcina acetivorans Protoglobin. <i>PLoS ONE</i> , 2013, 8, e66144.	2.5	19
81	High Resolution Crystal Structures of the Cerebratulus lacteus Mini-Hb in the Unligated and Carbomonoxy States. <i>International Journal of Molecular Sciences</i> , 2012, 13, 8025-8037.	4.1	4
82	Hereditary Systemic Amyloidosis Due to Asp76Asn Variant β_2 -Microglobulin. <i>New England Journal of Medicine</i> , 2012, 366, 2276-2283.	27.0	172
83	Determination of Ligand Pathways in Globins. <i>Journal of Biological Chemistry</i> , 2012, 287, 33163-33178.	3.4	34
84	Structure-Based Inhibition of Norovirus RNA-Dependent RNA Polymerases. <i>Journal of Molecular Biology</i> , 2012, 419, 198-210.	4.2	86
85	Flaviviral helicase: Insights into the mechanism of action of a motor protein. <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 84-87.	2.1	19
86	Structures of the lamin A/C R335W and E347K mutants: Implications for dilated cardiomyopathies. <i>Biochemical and Biophysical Research Communications</i> , 2012, 418, 217-221.	2.1	21
87	Dimeric Smac mimetics/IAP inhibitors as in vivo-active pro-apoptotic agents. Part II: Structural and biological characterization. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 6709-6723.	3.0	29
88	Structure, Stability, and Aggregation of β_2 -Microglobulin Mutants: Insights from a Fourier Transform Infrared Study in Solution and in the Crystalline State. <i>Biophysical Journal</i> , 2012, 102, 1676-1684.	0.5	31
89	Structure Based Inhibition of the Calicivirus RNA-Dependent RNA-Polymerase. <i>Biophysical Journal</i> , 2012, 102, 462a.	0.5	0
90	Quantitative Expression of the Mutated Lamin A/C Gene in Patients With Cardiomyopathy. <i>Journal of the American College of Cardiology</i> , 2012, 60, 1916-1920.	2.8	34

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91	Structural Insight into Inhibitor of Apoptosis Proteins Recognition by a Potent Divalent Smac-Mimetic. PLoS ONE, 2012, 7, e49527.	2.5	13
92	On the molecular structure of human neuroserpin polymers. Proteins: Structure, Function and Bioinformatics, 2012, 80, 8-13.	2.6	21
93	Ivermectin is a potent inhibitor of flavivirus replication specifically targeting NS3 helicase activity: new prospects for an old drug. Journal of Antimicrobial Chemotherapy, 2012, 67, 1884-1894.	3.0	329
94	A recurrent Dâ€strand association interface is observed in Î²â€2 microglobulin oligomers. FEBS Journal, 2012, 279, 1131-1143.	4.7	18
95	The Tempered Polymerization of Human Neuroserpin. PLoS ONE, 2012, 7, e32444.	2.5	28
96	Ligation Tunes Protein Reactivity in an Ancient Haemoglobin: Kinetic Evidence for an Allosteric Mechanism in Methanosarcina acetivorans Protoglobin. PLoS ONE, 2012, 7, e33614.	2.5	13
97	Ligand Migration in Methanosarcina acetivorans Protoglobin: Effects of Ligand Binding and Dimeric Assembly. Journal of Physical Chemistry B, 2011, 115, 13771-13780.	2.6	31
98	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.	4.2	67
99	Dâ€strand perturbation and amyloid propensity in betaâ€2 microglobulin. FEBS Journal, 2011, 278, 2349-2358.	4.7	13
100	The two tryptophans of Î²2-microglobulin have distinct roles in function and folding and might represent two independent responses to evolutionary pressure. BMC Evolutionary Biology, 2011, 11, 159.	3.2	16
101	Characterization of Î²2â€microglobulin conformational intermediates associated to different fibrillation conditions. Journal of Mass Spectrometry, 2011, 46, 734-741.	1.6	13
102	Structural heterogeneity and ligand gating in ferric methanosarcina acetivorans protoglobin mutants. IUBMB Life, 2011, 63, 287-294.	3.4	15
103	Structural characterization of a group II 2/2 hemoglobin from the plant pathogen Agrobacterium tumefaciens. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2011, 1814, 810-816.	2.3	13
104	Ligand Migration in the Apolar Tunnel of Cerebratulus lacteus Mini-Hemoglobin. Journal of Biological Chemistry, 2011, 286, 5347-5358.	3.4	23
105	Tetramerization Dynamics of C-terminal Domain Underlies Isoform-specific cAMP Gating in Hyperpolarization-activated Cyclic Nucleotide-gated Channels. Journal of Biological Chemistry, 2011, 286, 44811-44820.	3.4	101
106	The effects of an ideal Î²-turn on Î²-2 microglobulin fold stability. Journal of Biochemistry, 2011, 150, 39-47.	1.7	9
107	Structure-based approach to rationally design a chimeric protein for an effective vaccine against Group B Streptococcus infections. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 10278-10283.	7.1	132
108	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. Antiviral Research, 2010, 87, 125-148.	4.1	289

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109	Globin-like proteins in <i>Caenorhabditis elegans</i> : in vivo localization, ligand binding and structural properties. <i>BMC Biochemistry</i> , 2010, 11, 17.	4.4	21
110	DE-loop mutations affect β 2 microglobulin stability, oligomerization, and the low-pH unfolded form. <i>Protein Science</i> , 2010, 19, 1386-1394.	7.6	43
111	Recognition of Smac-mimetic compounds by the BIR domain of cIAP1. <i>Protein Science</i> , 2010, 19, 2418-2429.	7.6	25
112	Probing the active site of the sugar isomerase domain from <i>E. coli</i> arabinose-5-phosphate isomerase via X-ray crystallography. <i>Protein Science</i> , 2010, 19, 2430-2439.	7.6	19
113	Molecular bases of neuroserpin function and pathology. <i>Biomolecular Concepts</i> , 2010, 1, 117-130.	2.2	9
114	Two Latent and Two Hyperstable Polymeric Forms of Human Neuroserpin. <i>Biophysical Journal</i> , 2010, 99, 3402-3411.	0.5	20
115	Novel SMAC-mimetics synergistically stimulate melanoma cell death in combination with TRAIL and Bortezomib. <i>British Journal of Cancer</i> , 2010, 102, 1707-1716.	6.4	70
116	Fibrillar vs Crystalline Full-Length β 2-Microglobulin Studied by High-Resolution Solid-State NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2010, 132, 5556-5557.	13.7	32
117	Why is a protective antigen protective?. <i>Hum Vaccin</i> , 2009, 5, 872-875.	2.4	5
118	Group B <i>Streptococcus</i> Pullulanase Crystal Structures in the Context of a Novel Strategy for Vaccine Development. <i>Journal of Bacteriology</i> , 2009, 191, 3544-3552.	2.2	30
119	Flaviviral methyltransferase/RNA interaction: Structural basis for enzyme inhibition. <i>Antiviral Research</i> , 2009, 83, 28-34.	4.1	64
120	Rational design, synthesis and characterization of potent, non-peptidic Smac mimics/XIAP inhibitors as proapoptotic agents for cancer therapy. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 5834-5856.	3.0	36
121	<i>Plasmodium falciparum</i> Ferredoxin-NADP+ Reductase His286 Plays a Dual Role in NADP(H) Binding and Catalysis. <i>Biochemistry</i> , 2009, 48, 9525-9533.	2.5	11
122	Designing Smac-mimetics as antagonists of XIAP, cIAP1, and cIAP2. <i>Biochemical and Biophysical Research Communications</i> , 2009, 378, 162-167.	2.1	50
123	Human beta-2 microglobulin W60V mutant structure: Implications for stability and amyloid aggregation. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 543-547.	2.1	29
124	Crystal structure of a methyltransferase from a no-known-vector Flavivirus. <i>Biochemical and Biophysical Research Communications</i> , 2009, 382, 200-204.	2.1	14
125	Recognition of RNA Cap in the Wesselsbron Virus NS5 Methyltransferase Domain: Implications for RNA-Capping Mechanisms in Flavivirus. <i>Journal of Molecular Biology</i> , 2009, 385, 140-152.	4.2	78
126	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.	4.2	47

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127	Human Neuroserpin: Structure and Time-Dependent Inhibition. <i>Journal of Molecular Biology</i> , 2009, 388, 109-121.	4.2	41
128	Structural Basis for Bivalent Smac-Mimetics Recognition in the IAP Protein Family. <i>Journal of Molecular Biology</i> , 2009, 392, 630-644.	4.2	40
129	CtBP1/BARS Gly172 $\hat{\alpha}$ ' Glu mutant structure: Impairing NAD(H)-binding and dimerization. <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 70-74.	2.1	21
130	Archaeal Protoglobin Structures: Novel Ligand Diffusion Paths And Heme Reactivity Modulation. <i>Biophysical Journal</i> , 2009, 96, 558a.	0.5	0
131	Exploring the molecular basis of heme coordination in human neuroglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 695-705.	2.6	54
132	Structural determinants of ligand migration in <i>Mycobacterium tuberculosis</i> truncated hemoglobin O. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 372-379.	2.6	47
133	Hemoprotein time-resolved X-ray crystallography. <i>IUBMB Life</i> , 2008, 60, 154-158.	3.4	7
134	Ferrous <i>Campylobacter jejuni</i> truncated hemoglobin ϵ P displays an extremely high reactivity for cyanide $\hat{\alpha}$ " a comparative study. <i>FEBS Journal</i> , 2008, 275, 633-645.	4.7	24
135	Archaeal protoglobin structure indicates new ligand diffusion paths and modulation of haem $\hat{\alpha}$ reactivity. <i>EMBO Reports</i> , 2008, 9, 157-163.	4.5	43
136	The VIZIER project: Preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008, 78, 37-46.	4.1	26
137	Proteins: ever larger, stranger and more dynamic. <i>Current Opinion in Structural Biology</i> , 2008, 18, 690-692.	5.7	0
138	Mapping Heme $\hat{\alpha}$ Ligand Tunnels in Group I Truncated(2/2) Hemoglobins. <i>Methods in Enzymology</i> , 2008, 436, 303-315.	1.0	17
139	The hemoglobins of the trematodes <i>Fasciola hepatica</i> and <i>Paramphistomum epiclitum</i> : A molecular biological, physico $\hat{\alpha}$ chemical, kinetic, and vaccination study. <i>Protein Science</i> , 2008, 17, 1653-1662.	7.6	11
140	Ebolavirus and Marburgvirus: Insight the Filoviridae family. <i>Molecular Aspects of Medicine</i> , 2008, 29, 151-185.	6.4	84
141	The Controlling Roles of Trp60 and Trp95 in $\hat{\alpha}$ 2-Microglobulin Function, Folding and Amyloid Aggregation Properties. <i>Journal of Molecular Biology</i> , 2008, 378, 887-897.	4.2	82
142	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.	4.2	40
143	Crystal structures of HIV-1 reverse transcriptase complexes with thiocarbamate non-nucleoside inhibitors. <i>Biochemical and Biophysical Research Communications</i> , 2008, 365, 764-770.	2.1	19
144	DE loop mutations affect $\hat{\alpha}$ 2-microglobulin stability and amyloid aggregation. <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 146-150.	2.1	36

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145	Expression, Purification, and Crystallization of Neuro- and Cytoglobin. <i>Methods in Enzymology</i> , 2008, 436, 341-357.	1.0	28
146	The Apolar Channel in <i>Cerebratulus lacteus</i> Hemoglobin Is the Route for O ₂ Entry and Exit. <i>Journal of Biological Chemistry</i> , 2008, 283, 35689-35702.	3.4	31
147	Ligand Binding to Truncated Hemoglobin N from <i>Mycobacterium tuberculosis</i> Is Strongly Modulated by the Interplay between the Distal Heme Pocket Residues and Internal Water. <i>Journal of Biological Chemistry</i> , 2008, 283, 27270-27278.	3.4	29
148	A Crystallographer's Perspective on the 2/2Hb Family. , 2008, , 17-30.		0
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