

Martino Bolognesi

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

412
papers

16,157
citations

64
h-index

107
g-index

433
ext. papers

17,531
ext. citations

5.3
avg, IF

5.8
L-index

#	Paper	IF	Citations
412	Truncated (2/2) hemoglobin: Unconventional structures and functional roles in vivo and in human pathogenesis. <i>Molecular Aspects of Medicine</i> , 2021 , 101049	16.7	1
411	Gating movements and ion permeation in HCN4 pacemaker channels. <i>Molecular Cell</i> , 2021 , 81, 2929-2943, e6	7.6	8
410	Mycobacterial and Human Ferrous Nitrobindins: Spectroscopic and Reactivity Properties. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
409	Glycosylation Tunes Neuroserpin Physiological and Pathological Properties. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	9
408	Functional and structural analysis of trehalose-6-phosphate phosphatase from Burkholderia pseudomallei: Insights into the catalytic mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 523, 979-984	3.4	2
407	The structural bases for agonist diversity in an glutamate receptor-like channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 752-760	11.5	37
406	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. <i>Journal of Molecular Biology</i> , 2020 , 432, 845-860	6.5	10
405	Embelin as Lead Compound for New Neuroserpin Polymerization Inhibitors. <i>Life</i> , 2020 , 10,	3	3
404	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,	6.3	3
403	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	6.8	5
402	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	1.1	1
401	Structural and Functional Characterization of the Globin-Coupled Sensors of and. <i>Antioxidants and Redox Signaling</i> , 2020 , 32, 378-395	8.4	4
400	Mycobacterial and Human Nitrobindins: Structure and Function. <i>Antioxidants and Redox Signaling</i> , 2020 , 33, 229-246	8.4	9
399	Cryo-EM Structures of Azospirillum brasilense Glutamate Synthase in Its Oligomeric Assemblies. <i>Journal of Molecular Biology</i> , 2019 , 431, 4523-4526	6.5	2
398	Cryo-EM structure of cardiac amyloid fibrils from an immunoglobulin light chain AL amyloidosis patient. <i>Nature Communications</i> , 2019 , 10, 1269	17.4	68
397	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	2.7	2
396	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	2.7	2

395	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	5.7	7
394	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. <i>Nature Communications</i> , 2018 , 9, 1658	17.4	35
393	BPSL1626: Reverse and Structural Vaccinology Reveal a Novel Candidate for Vaccine Design against. <i>Antibodies</i> , 2018 , 7,	7	5
392	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	2.7	1
391	Structure and Computation in Immunoreagent Design: From Diagnostics to Vaccines. <i>Trends in Biotechnology</i> , 2017 , 35, 1208-1220	15.1	14
390	Designing Probes for Immunodiagnostics: Structural Insights into an Epitope Targeting Burkholderia Infections. <i>ACS Infectious Diseases</i> , 2017 , 3, 736-743	5.5	4
389	Structural Vaccinology for Melioidosis Vaccine Design and Immunodiagnostics. <i>Current Tropical Medicine Reports</i> , 2017 , 4, 103-110	5	1
388	Concurrent structural and biophysical traits link with immunoglobulin light chains amyloid propensity. <i>Scientific Reports</i> , 2017 , 7, 16809	4.9	31
387	Targeting flavivirus RNA dependent RNA polymerase through a pyridobenzothiazole inhibitor. <i>Antiviral Research</i> , 2016 , 134, 226-235	10.8	42
386	Immunisation with proteins expressed during chronic murine melioidosis provides enhanced protection against disease. <i>Vaccine</i> , 2016 , 34, 1665-71	4.1	19
385	Flexible vs Rigid Epitope Conformations for Diagnostic- and Vaccine-Oriented Applications: Novel Insights from the Burkholderia pseudomallei BPSL2765 Pal3 Epitope. <i>ACS Infectious Diseases</i> , 2016 , 2, 221-30	5.5	19
384	The N-terminal pre-A region of Mycobacterium tuberculosis 2/2HbN promotes NO-dioxygenase activity. <i>FEBS Journal</i> , 2016 , 283, 305-22	5.7	9
383	Embelin binds to human neuroserpin and impairs its polymerisation. <i>Scientific Reports</i> , 2016 , 6, 18769	4.9	11
382	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	4.9	41
381	TREX1 C-terminal frameshift mutations in the systemic variant of retinal vasculopathy with cerebral leukodystrophy. <i>Neurological Sciences</i> , 2015 , 36, 323-30	3.5	40
380	Backbone and side-chain (1)H, (15)N, (13)C assignment and secondary structure of BPSL1445 from Burkholderia pseudomallei. <i>Biomolecular NMR Assignments</i> , 2015 , 9, 347-50	0.7	0
379	Crystal structure of LptH, the periplasmic component of the lipopolysaccharide transport machinery from Pseudomonas aeruginosa. <i>FEBS Journal</i> , 2015 , 282, 1980-97	5.7	22
378	From crystal structure to in silico epitope discovery in the Burkholderia pseudomallei flagellar hook-associated protein FlgK. <i>FEBS Journal</i> , 2015 , 282, 1319-33	5.7	30

377	Atlas of the clinical genetics of human dilated cardiomyopathy. <i>European Heart Journal</i> , 2015 , 36, 1123-35	3.9	334
376	Selecting soluble/foldable protein domains through single-gene or genomic ORF filtering: structure of the head domain of Burkholderia pseudomallei antigen BPSL2063. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 2227-35		8
375	A redox signalling globin is essential for reproduction in Caenorhabditis elegans. <i>Nature Communications</i> , 2015 , 6, 8782	17.4	29
374	A covalent homodimer probing early oligomers along amyloid aggregation. <i>Scientific Reports</i> , 2015 , 5, 14651	4.9	11
373	Structural flexibility of the heme cavity in the cold-adapted truncated hemoglobin from the Antarctic marine bacterium Pseudoalteromonas haloplanktis TAC125. <i>FEBS Journal</i> , 2015 , 282, 2948-65	5.7	21
372	Wild type beta-2 microglobulin and DE loop mutants display a common fibrillar architecture. <i>PLoS ONE</i> , 2015 , 10, e0122449	3.7	13
371	Structural Bases for the Regulation of CO Binding in the Archaeal Protoglobin from Methanosarcina acetivorans. <i>PLoS ONE</i> , 2015 , 10, e0125959	3.7	2
370	Sequence- and Structure-Based Immunoreactive Epitope Discovery for Burkholderia pseudomallei Flagellin. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003917	4.8	27
369	Decoding the Structural Bases of D76N β -Microglobulin High Amyloidogenicity through Crystallography and Asn-Scan Mutagenesis. <i>PLoS ONE</i> , 2015 , 10, e0144061	3.7	18
368	Functional and dysfunctional conformers of human neuroserpin characterized by optical spectroscopies and Molecular Dynamics. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015 , 1854, 110-7	4	13
367	The activator of apoptosis Smac-DIABLO acts as a tetramer in solution. <i>Biophysical Journal</i> , 2015 , 108, 714-23	2.9	10
366	NF023 binding to XIAP-BIR1: searching drugs for regulation of the NF- κ B pathway. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 612-20	4.2	6
365	Synchrotron Radiation and Bio-crystallography 2015 , 615-639		
364	Cyclic dinucleotides bind the C-linker of HCN4 to control channel cAMP responsiveness. <i>Nature Chemical Biology</i> , 2014 , 10, 457-62	11.7	40
363	Naphthalene-sulfonate inhibitors of human norovirus RNA-dependent RNA-polymerase. <i>Antiviral Research</i> , 2014 , 102, 23-8	10.8	32
362	Rapid proton-detected NMR assignment for proteins with fast magic angle spinning. <i>Journal of the American Chemical Society</i> , 2014 , 136, 12489-97	16.4	205
361	Edge strand engineering prevents native-like aggregation in Sulfolobus solfataricus acylphosphatase. <i>FEBS Journal</i> , 2014 , 281, 4072-84	5.7	12
360	Delivery of suramin as an antiviral agent through liposomal systems. <i>ChemMedChem</i> , 2014 , 9, 933-9	3.7	24

359	PPNDS inhibits murine Norovirus RNA-dependent RNA-polymerase mimicking two RNA stacking bases. <i>FEBS Letters</i> , 2014 , 588, 1720-5	3.8	19
358	Structural bases of norovirus RNA dependent RNA polymerase inhibition by novel suramin-related compounds. <i>PLoS ONE</i> , 2014 , 9, e91765	3.7	41
357	Class I major histocompatibility complex, the trojan horse for secretion of amyloidogenic β -microglobulin. <i>Journal of Biological Chemistry</i> , 2014 , 289, 3318-27	5.4	20
356	Novel neurofibromatosis type 2 mutation presenting with status epilepticus. <i>Epileptic Disorders</i> , 2014 , 16, 132-7	1.9	7
355	Redefining the PF06864 Pfam family based on Burkholderia pseudomallei PilO2(Bp) S-SAD crystal structure. <i>PLoS ONE</i> , 2014 , 9, e94981	3.7	4
354	Nitrite-reductase and peroxynitrite isomerization activities of Methanosarcina acetivorans protoglobin. <i>PLoS ONE</i> , 2014 , 9, e95391	3.7	12
353	Exploiting the Burkholderia pseudomallei acute phase antigen BPSL2765 for structure-based epitope discovery/design in structural vaccinology. <i>Chemistry and Biology</i> , 2013 , 20, 1147-56		41
352	Functional and structural roles of the N-terminal extension in Methanosarcina acetivorans protoglobin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 1813-23	4	6
351	The diversity of 2/2 (truncated) globins. <i>Advances in Microbial Physiology</i> , 2013 , 63, 49-78	4.4	38
350	Protoglobin: structure and ligand-binding properties. <i>Advances in Microbial Physiology</i> , 2013 , 63, 79-96	4.4	18
349	Non-covalent and covalent modifications modulate the reactivity of monomeric mammalian globins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013 , 1834, 1750-6	4	26
348	Reductive nitrosylation of Methanosarcina acetivorans protoglobin: a comparative study. <i>Biochemical and Biophysical Research Communications</i> , 2013 , 430, 1301-5	3.4	13
347	A structure-based strategy for epitope discovery in Burkholderia pseudomallei OppA antigen. <i>Structure</i> , 2013 , 21, 167-175	5.2	37
346	Sequence-specific transcription factor NF-Y displays histone-like DNA binding and H2B-like ubiquitination. <i>Cell</i> , 2013 , 152, 132-43	56.2	178
345	One hundred years of X-ray diffraction, 50 years of structural biology. <i>Rendiconti Lincei</i> , 2013 , 24, 93-99	1.7	1
344	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, 9794-9	11.5	24
343	The Escherichia coli Lpt transenvelope protein complex for lipopolysaccharide export is assembled via conserved structurally homologous domains. <i>Journal of Bacteriology</i> , 2013 , 195, 1100-8	3.5	72
342	CO rebinding kinetics and molecular dynamics simulations highlight dynamic regulation of internal cavities in human cytoglobin. <i>PLoS ONE</i> , 2013 , 8, e49770	3.7	24

341	Identification of the molecular site of ivabradine binding to HCN4 channels. <i>PLoS ONE</i> , 2013 , 8, e53132	3.7	38
340	Kinetic and structural evidences on human prolidase pathological mutants suggest strategies for enzyme functional rescue. <i>PLoS ONE</i> , 2013 , 8, e58792	3.7	17
339	Structure and haem-distal site plasticity in Methanosarcina acetivorans protoglobin. <i>PLoS ONE</i> , 2013 , 8, e66144	3.7	12
338	A recurrent D-strand association interface is observed in β_2 microglobulin oligomers. <i>FEBS Journal</i> , 2012 , 279, 1131-43	5.7	17
337	Determination of ligand pathways in globins: apolar tunnels versus polar gates. <i>Journal of Biological Chemistry</i> , 2012 , 287, 33163-78	5.4	33
336	Structure-based inhibition of Norovirus RNA-dependent RNA polymerases. <i>Journal of Molecular Biology</i> , 2012 , 419, 198-210	6.5	71
335	Flaviviral helicase: insights into the mechanism of action of a motor protein. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 417, 84-7	3.4	15
334	Structures of the lamin A/C R335W and E347K mutants: implications for dilated cardiomyopathies. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 418, 217-21	3.4	18
333	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, 6709-23	3.4	26
332	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, 1676-84	2.9	25
331	Quantitative expression of the mutated lamin A/C gene in patients with cardiomyopathy. <i>Journal of the American College of Cardiology</i> , 2012 , 60, 1916-20	15.1	23
330	Structural insight into inhibitor of apoptosis proteins recognition by a potent divalent smac-mimetic. <i>PLoS ONE</i> , 2012 , 7, e49527	3.7	10
329	On the molecular structure of human neuroserpin polymers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 8-13	4.2	11
328	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, 1884-94	5.1	247
327	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, 8025-37	6.3	4
326	Hereditary systemic amyloidosis due to Asp76Asn variant β_2 -microglobulin. <i>New England Journal of Medicine</i> , 2012 , 366, 2276-83	59.2	135
325	The tempered polymerization of human neuroserpin. <i>PLoS ONE</i> , 2012 , 7, e32444	3.7	25
324	Ligation tunes protein reactivity in an ancient haemoglobin: kinetic evidence for an allosteric mechanism in Methanosarcina acetivorans protoglobin. <i>PLoS ONE</i> , 2012 , 7, e33614	3.7	10

323	FAD-binding site and NADP reactivity in human renalase: a new enzyme involved in blood pressure regulation. <i>Journal of Molecular Biology</i> , 2011 , 411, 463-73	6.5	56
322	D-strand perturbation and amyloid propensity in beta-2 microglobulin. <i>FEBS Journal</i> , 2011 , 278, 2349-58	5.7	13
321	The two tryptophans of β -microglobulin have distinct roles in function and folding and might represent two independent responses to evolutionary pressure. <i>BMC Evolutionary Biology</i> , 2011 , 11, 159	3	13
320	Characterization of β -microglobulin conformational intermediates associated to different fibrillation conditions. <i>Journal of Mass Spectrometry</i> , 2011 , 46, 734-41	2.2	12
319	Structural heterogeneity and ligand gating in ferric <i>Methanosarcina acetivorans</i> protoglobin mutants. <i>IUBMB Life</i> , 2011 , 63, 287-94	4.7	12
318	Ligand migration in <i>Methanosarcina acetivorans</i> protoglobin: effects of ligand binding and dimeric assembly. <i>Journal of Physical Chemistry B</i> , 2011 , 115, 13771-80	3.4	28
317	Structural characterization of a group II 2/2 hemoglobin from the plant pathogen <i>Agrobacterium tumefaciens</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2011 , 1814, 810-6	4	12
316	Ligand migration in the apolar tunnel of <i>Cerebratulus lacteus</i> mini-hemoglobin. <i>Journal of Biological Chemistry</i> , 2011 , 286, 5347-58	5.4	20
315	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, 44811-20	5.4	88
314	The effects of an ideal beta-turn on beta-2 microglobulin fold stability. <i>Journal of Biochemistry</i> , 2011 , 150, 39-47	3.1	9
313	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, 10278-83	11.5	107
312	Molecular bases of neuroserpin function and pathology. <i>Biomolecular Concepts</i> , 2010 , 1, 117-30	3.7	9
311	Two latent and two hyperstable polymeric forms of human neuroserpin. <i>Biophysical Journal</i> , 2010 , 99, 3402-11	2.9	20
310	Novel SMAC-mimetics synergistically stimulate melanoma cell death in combination with TRAIL and Bortezomib. <i>British Journal of Cancer</i> , 2010 , 102, 1707-16	8.7	63
309	Fibrillar vs crystalline full-length beta-2-microglobulin studied by high-resolution solid-state NMR spectroscopy. <i>Journal of the American Chemical Society</i> , 2010 , 132, 5556-7	16.4	31
308	Structure and functionality in flavivirus NS-proteins: perspectives for drug design. <i>Antiviral Research</i> , 2010 , 87, 125-48	10.8	227
307	Globin-like proteins in <i>Caenorhabditis elegans</i> : in vivo localization, ligand binding and structural properties. <i>BMC Biochemistry</i> , 2010 , 11, 17	4.8	17
306	DE-loop mutations affect beta2 microglobulin stability, oligomerization, and the low-pH unfolded form. <i>Protein Science</i> , 2010 , 19, 1386-94	6.3	39

305	Recognition of Smac-mimetic compounds by the BIR domain of cIAP1. <i>Protein Science</i> , 2010 , 19, 2418-296.3		23
304	Probing the active site of the sugar isomerase domain from E. coli arabinose-5-phosphate isomerase via X-ray crystallography. <i>Protein Science</i> , 2010 , 19, 2430-9	6.3	15
303	Why is a protective antigen protective?. <i>Hum Vaccin</i> , 2009 , 5, 872-5		4
302	Group B streptococcus pullulanase crystal structures in the context of a novel strategy for vaccine development. <i>Journal of Bacteriology</i> , 2009 , 191, 3544-52	3.5	28
301	Flaviviral methyltransferase/RNA interaction: structural basis for enzyme inhibition. <i>Antiviral Research</i> , 2009 , 83, 28-34	10.8	57
300	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, 5834-34	3.4	33
299	Plasmodium falciparum ferredoxin-NADP+ reductase His286 plays a dual role in NADP(H) binding and catalysis. <i>Biochemistry</i> , 2009 , 48, 9525-33	3.2	10
298	Designing Smac-mimetics as antagonists of XIAP, cIAP1, and cIAP2. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 378, 162-7	3.4	45
297	Human beta-2 microglobulin W60V mutant structure: Implications for stability and amyloid aggregation. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 380, 543-7	3.4	28
296	Crystal structure of a methyltransferase from a no-known-vector Flavivirus. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 382, 200-4	3.4	9
295	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, 140-52	6.5	63
294	HisE11 and HisF8 provide bis-histidyl heme hexa-coordination in the globin domain of Geobacter sulfurreducens globin-coupled sensor. <i>Journal of Molecular Biology</i> , 2009 , 386, 246-60	6.5	41
293	Human neuroserpin: structure and time-dependent inhibition. <i>Journal of Molecular Biology</i> , 2009 , 388, 109-21	6.5	40
292	Structural basis for bivalent Smac-mimetics recognition in the IAP protein family. <i>Journal of Molecular Biology</i> , 2009 , 392, 630-44	6.5	36
291	CtBP1/BARS Gly172-->Glu mutant structure: impairing NAD(H)-binding and dimerization. <i>Biochemical and Biophysical Research Communications</i> , 2009 , 381, 70-4	3.4	12
290	Archaeal protoglobin structure indicates new ligand diffusion paths and modulation of haem-reactivity. <i>EMBO Reports</i> , 2008 , 9, 157-63	6.5	39
289	The VIZIER project: preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008 , 78, 37-46	10.8	19
288	Mapping heme-ligand tunnels in group I truncated(2/2) hemoglobins. <i>Methods in Enzymology</i> , 2008 , 436, 303-15	1.7	17

287	The hemoglobins of the trematodes <i>Fasciola hepatica</i> and <i>Paramphistomum epiclitum</i> : a molecular biological, physico-chemical, kinetic, and vaccination study. <i>Protein Science</i> , 2008 , 17, 1653-62	6.3	11
286	Ebolavirus and Marburgvirus: insight the Filoviridae family. <i>Molecular Aspects of Medicine</i> , 2008 , 29, 151-85.7		72
285	The controlling roles of Trp60 and Trp95 in beta2-microglobulin function, folding and amyloid aggregation properties. <i>Journal of Molecular Biology</i> , 2008 , 378, 887-97	6.5	76
284	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, 673-89	6.5	36
283	Crystal structures of HIV-1 reverse transcriptase complexes with thiocarbamate non-nucleoside inhibitors. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 365, 764-70	3.4	18
282	DE loop mutations affect beta2-microglobulin stability and amyloid aggregation. <i>Biochemical and Biophysical Research Communications</i> , 2008 , 377, 146-50	3.4	33
281	Expression, purification, and crystallization of neuro- and cytoglobin. <i>Methods in Enzymology</i> , 2008 , 436, 341-57	1.7	23
280	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, 35689-702	5.4	31
279	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, 27270-8	5.4	28
278	Exploring the molecular basis of heme coordination in human neuroglobin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 695-705	4.2	51
277	Structural determinants of ligand migration in <i>Mycobacterium tuberculosis</i> truncated hemoglobin O. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 73, 372-9	4.2	46
276	Hemoprotein time-resolved X-ray crystallography. <i>IUBMB Life</i> , 2008 , 60, 154-8	4.7	6
275	Ferrous <i>Campylobacter jejuni</i> truncated hemoglobin P displays an extremely high reactivity for cyanide - a comparative study. <i>FEBS Journal</i> , 2008 , 275, 633-45	5.7	24
274	A Crystallographer's Perspective on the 2/2Hb Family 2008 , 17-30		
273	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, 11440-50	3.2	35
272	Preliminary characterization of (nucleoside-2'-O-)-methyltransferase crystals from Meaban and Yokose flaviviruses. Corrigendum. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007 , 63, 252-252		78
271	Reductive nitrosylation and peroxynitrite-mediated oxidation of heme-hemopexin. <i>FEBS Journal</i> , 2007 , 274, 551-62	5.7	27
270	Structural bases for substrate recognition and activity in Meaban virus nucleoside-2'-O-methyltransferase. <i>Protein Science</i> , 2007 , 16, 1133-45	6.3	34

269	Protein structure in the truncated (2/2) hemoglobin family. <i>IUBMB Life</i> , 2007 , 59, 535-41	4.7	14
268	*NO dissociation represents the rate limiting step for O ₂ -mediated oxidation of ferrous nitrosylated Mycobacterium leprae truncated hemoglobin O. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 357, 809-14	3.4	14
267	The crystal structure of FdxA, a 7Fe ferredoxin from Mycobacterium smegmatis. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 360, 97-102	3.4	14
266	Mycobacterial truncated hemoglobins: from genes to functions. <i>Gene</i> , 2007 , 398, 42-51	3.8	48
265	Protein fold and structure in the truncated (2/2) globin family. <i>Gene</i> , 2007 , 398, 2-11	3.8	61
264	Ferredoxin-NADP ⁺ reductase from Plasmodium falciparum undergoes NADP ⁺ -dependent dimerization and inactivation: functional and crystallographic analysis. <i>Journal of Molecular Biology</i> , 2007 , 367, 501-13	6.5	36
263	Crystal structure and activity of Kunjin virus NS3 helicase; protease and helicase domain assembly in the full length NS3 protein. <i>Journal of Molecular Biology</i> , 2007 , 372, 444-55	6.5	66
262	Proteins: stay tuned!. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 710-713	8.1	78
261	Structural determinants in the group III truncated hemoglobin from Campylobacter jejuni. <i>Journal of Biological Chemistry</i> , 2006 , 281, 37803-12	5.4	51
260	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, 8202-13	4.8	45
259	Specific recognition of ZNF217 and other zinc finger proteins at a surface groove of C-terminal binding proteins. <i>Molecular and Cellular Biology</i> , 2006 , 26, 8159-72	4.8	64
258	Cyanide binding and heme cavity conformational transitions in Drosophila melanogaster hexacoordinate hemoglobin. <i>Biochemistry</i> , 2006 , 45, 10054-61	3.2	17
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