Martino Bolognesi

List of Publications by Citations

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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	Refined crystal structure of ascorbate oxidase at 1.9 A resolution. *Journal of Molecular Biology*, **1992**, 224, 179-205	6.5	420
411	X-ray crystal structure of the blue oxidase ascorbate oxidase from zucchini. Analysis of the polypeptide fold and a model of the copper sites and ligands. *Journal of Molecular Biology*, **1989**, 206, 513-29	6.5	361
410	Atlas of the clinical genetics of human dilated cardiomyopathy. *European Heart Journal*, **2015**, 36, 1123-35a	9.5	334
409	Crystal structure of the trigonal form of bovine beta-lactoglobulin and of its complex with retinol at 2.5 A resolution. *Journal of Molecular Biology*, **1987**, 197, 695-706	6.5	328
408	Truncated hemoglobins: a new family of hemoglobins widely distributed in bacteria, unicellular eukaryotes, and plants. *Journal of Biological Chemistry*, **2002**, 277, 871-4	5.4	314
407	Three-dimensional structure of the tetragonal crystal form of egg-white avidin in its functional complex with biotin at 2.7 A resolution. *Journal of Molecular Biology*, **1993**, 231, 698-710	6.5	286
406	Human brain neuroglobin structure reveals a distinct mode of controlling oxygen affinity. *Structure*, **2003**, 11, 1087-95	5.2	270
405	Crystal structure of D-amino acid oxidase: a case of active site mirror-image convergent evolution with flavocytochrome b2. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 7496-501	11.5	265
404	Structure of a bacteriochlorophyll a-protein from the green photosynthetic bacterium Prosthecochloris aestuarii. *Journal of Molecular Biology*, **1979**, 131, 259-85	6.5	259
403	Neuroglobin and cytoglobin in search of their role in the vertebrate globin family. *Journal of Inorganic Biochemistry*, **2005**, 99, 110-9	4.2	249
402	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, 1884-94	5.1	247
401	Neuroglobin and cytoglobin. Fresh blood for the vertebrate globin family. *EMBO Reports*, **2002**, 3, 1146-51	6.5	245
400	Structure and functionality in flavivirus NS-proteins: perspectives for drug design. *Antiviral Research*, **2010**, 87, 125-48	10.8	227
399	CD81 extracellular domain 3D structure: insight into the tetraspanin superfamily structural motifs. *EMBO Journal*, **2001**, 20, 12-8	13	214
398	The redox state of the cell regulates the ligand binding affinity of human neuroglobin and cytoglobin. *Journal of Biological Chemistry*, **2003**, 278, 51713-21	5.4	206
397	Rapid proton-detected NMR assignment for proteins with fast magic angle spinning. *Journal of the American Chemical Society*, **2014**, 136, 12489-97	16.4	205
396	Conserved patterns in the Cu,Zn superoxide dismutase family. *Journal of Molecular Biology*, **1994**, 238, 366-86	6.5	202

395	A novel two-over-two alpha-helical sandwich fold is characteristic of the truncated hemoglobin family. *EMBO Journal*, **2000**, 19, 2424-34	13	199
394	Mycobacterium tuberculosis hemoglobin N displays a protein tunnel suited for O2 diffusion to the heme. *EMBO Journal*, **2001**, 20, 3902-9	13	180
393	Sequence-specific transcription factor NF-Y displays histone-like DNA binding and H2B-like ubiquitination. *Cell*, **2013**, 152, 132-43	56.2	178
392	Three-dimensional structure of the complex between pancreatic secretory trypsin inhibitor (Kazal type) and trypsinogen at 1.8 A resolution. Structure solution, crystallographic refinement and preliminary structural interpretation. *Journal of Molecular Biology*, **1982**, 162, 839-68	6.5	177
391	Nonvertebrate hemoglobins: structural bases for reactivity. *Progress in Biophysics and Molecular Biology*, **1997**, 68, 29-68	4.7	149
390	Crystal structure of cytoglobin: the fourth globin type discovered in man displays heme hexa-coordination. *Journal of Molecular Biology*, **2004**, 336, 917-27	6.5	147
389	Hereditary systemic amyloidosis due to Asp76Asn variant β2-microglobulin. *New England Journal of Medicine*, **2012**, 366, 2276-83	59.2	135
388	The bovine basic pancreatic trypsin inhibitor (Kunitz inhibitor): a milestone protein. *Current Protein and Peptide Science*, **2003**, 4, 231-51	2.8	133
387	Aplysia limacina myoglobin. Crystallographic analysis at 1.6 A resolution. *Journal of Molecular Biology*, **1989**, 205, 529-44	6.5	131
386	CtBP/BARS: a dual-function protein involved in transcription co-repression and Golgi membrane fission. *EMBO Journal*, **2003**, 22, 3122-30	13	126
385	Unusual structure of the oxygen-binding site in the dimeric bacterial hemoglobin from Vitreoscilla sp. *Structure*, **1997**, 5, 497-507	5.2	118
384	Crystal structure of Escherichia coli pyruvate kinase type I: molecular basis of the allosteric transition. *Structure*, **1995**, 3, 729-41	5.2	115
383	Structural bases for heme binding and diatomic ligand recognition in truncated hemoglobins. *Journal of Inorganic Biochemistry*, **2005**, 99, 97-109	4.2	113
382	Bone marrow transplantation from unrelated donors: the impact of mismatches with substitutions at position 116 of the human leukocyte antigen class I heavy chain. *Blood*, **2001**, 98, 3150-5	2.2	111
381	Crystal structure of yeast Cu,Zn superoxide dismutase. Crystallographic refinement at 2.5 A resolution. *Journal of Molecular Biology*, **1992**, 225, 791-809	6.5	110
380	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, 10278-83	11.5	107
379	Heme-ligand tunneling in group I truncated hemoglobins. *Journal of Biological Chemistry*, **2004**, 279, 21530-5	5.4	107
378	A TyrCD1/TrpG8 hydrogen bond network and a TyrB10TyrCD1 covalent link shape the heme distal site of Mycobacterium tuberculosis hemoglobin O. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 5766-71	11.5	107

377	Anthrax toxin: a tripartite lethal combination. *FEBS Letters*, **2002**, 531, 384-8	3.8	101
376	Monitoring the process of HypF fibrillization and liposome permeabilization by protofibrils. *Journal of Molecular Biology*, **2004**, 338, 943-57	6.5	96
375	The allosteric regulation of pyruvate kinase. *FEBS Letters*, **1996**, 389, 15-9	3.8	92
374	The X-ray three-dimensional structure of avidin. *New Biotechnology*, **1999**, 16, 5-12		90
373	Crystal and molecular structure of the bovine alpha-chymotrypsin-eglin c complex at 2.0 A resolution. *Journal of Molecular Biology*, **1992**, 225, 107-23	6.5	90
372	Ligand-induced dynamical regulation of NO conversion in Mycobacterium tuberculosis truncated hemoglobin-N. *Proteins: Structure, Function and Bioinformatics*, **2006**, 64, 457-64	4.2	89
371	Kinetic and crystallographic analyses support a sequential-ordered bi bi catalytic mechanism for Escherichia coli glucose-1-phosphate thymidylyltransferase. *Journal of Molecular Biology*, **2001**, 313, 831-43	6.5	89
370	Reactivity of ferric Aplysia and sperm whale myoglobins towards imidazole. X-ray and binding study. *Journal of Molecular Biology*, **1982**, 158, 305-15	6.5	89
369	Tetramerization dynamics of C-terminal domain underlies isoform-specific cAMP gating in hyperpolarization-activated cyclic nucleotide-gated channels. *Journal of Biological Chemistry*, **2011**, 286, 44811-20	5.4	88
368	The three-dimensional structure of the human NK cell receptor NKp44, a triggering partner in natural cytotoxicity. *Structure*, **2003**, 11, 725-34	5.2	84
367	The crystal structure of a sulfurtransferase from Azotobacter vinelandii highlights the evolutionary relationship between the rhodanese and phosphatase enzyme families. *Journal of Molecular Biology*, **2000**, 298, 691-704	6.5	82
366	Active site plasticity in D-amino acid oxidase: a crystallographic analysis. *Biochemistry*, **1997**, 36, 5853-60	3.2	79
365	Preliminary characterization of (nucleoside-2?-O-)-methyltransferase crystals from Meaban and Yokose flaviviruses. Corrigendum. *Acta Crystallographica Section F: Structural Biology Communications*, **2007**, 63, 252-252		78
364	Proteins: stay tuned!. *Current Opinion in Structural Biology*, **2006**, 16, 710-713	8.1	78
363	Cyanide binding to Lucina pectinata hemoglobin I and to sperm whale myoglobin: an x-ray crystallographic study. *Biophysical Journal*, **1999**, 77, 1093-9	2.9	78
362	The controlling roles of Trp60 and Trp95 in beta2-microglobulin function, folding and amyloid aggregation properties. *Journal of Molecular Biology*, **2008**, 378, 887-97	6.5	76
361	X-ray crystal structure of ferric Aplysia limacina myoglobin in different liganded states. *Journal of Molecular Biology*, **1993**, 233, 498-508	6.5	75
360	Unique structural features of the monomeric Cu,Zn superoxide dismutase from Escherichia coli, revealed by X-ray crystallography. *Journal of Molecular Biology*, **1997**, 274, 408-20	6.5	73

359	The Escherichia coli Lpt transenvelope protein complex for lipopolysaccharide export is assembled via conserved structurally homologous domains. *Journal of Bacteriology*, **2013**, 195, 1100-8	3.5	72
358	Ebolavirus and Marburgvirus: insight the Filoviridae family. *Molecular Aspects of Medicine*, **2008**, 29, 151-85	15.7	72
357	Structure-based inhibition of Norovirus RNA-dependent RNA polymerases. *Journal of Molecular Biology*, **2012**, 419, 198-210	6.5	71
356	Evolutionary conservativeness of electric field in the Cu,Zn superoxide dismutase active site. Evidence for co-ordinated mutation of charged amino acid residues. *Journal of Molecular Biology*, **1992**, 223, 337-42	6.5	70
355	Cryo-EM structure of cardiac amyloid fibrils from an immunoglobulin light chain AL amyloidosis patient. *Nature Communications*, **2019**, 10, 1269	17.4	68
354	Structure of the sulfide-reactive hemoglobin from the clam Lucina pectinata. Crystallographic analysis at 1.5 A resolution. *Journal of Molecular Biology*, **1994**, 244, 86-99	6.5	67
353	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, 444-55	6.5	66
352	Structural bases for sulfide recognition in Lucina pectinata hemoglobin I. *Journal of Molecular Biology*, **1996**, 258, 1-5	6.5	66
351	Absence of water at the sixth co-ordination site in ferric Aplysia myoglobin. *Journal of Molecular Biology*, **1981**, 151, 315-9	6.5	65
350	Specific recognition of ZNF217 and other zinc finger proteins at a surface groove of C-terminal binding proteins. *Molecular and Cellular Biology*, **2006**, 26, 8159-72	4.8	64
349	Inhibition of cysteine protease activity by NO-donors. *Current Protein and Peptide Science*, **2001**, 2, 137-53	2.8	64
348	Novel SMAC-mimetics synergistically stimulate melanoma cell death in combination with TRAIL and Bortezomib. *British Journal of Cancer*, **2010**, 102, 1707-16	8.7	63
347	Recognition of RNA cap in the Wesselsbron virus NS5 methyltransferase domain: implications for RNA-capping mechanisms in Flavivirus. *Journal of Molecular Biology*, **2009**, 385, 140-52	6.5	63
346	Crystal structure and anion binding in the prokaryotic hydrogenase maturation factor HypF acylphosphatase-like domain. *Journal of Molecular Biology*, **2002**, 321, 785-96	6.5	62
345	Protein fold and structure in the truncated (2/2) globin family. *Gene*, **2007**, 398, 2-11	3.8	61
344	Interaction between serine (pro)enzymes, and Kazal and Kunitz inhibitors. *Journal of Molecular Biology*, **1983**, 165, 543-58	6.5	61
343	Re-evaluation of amino acid sequence and structural consensus rules for cysteine-nitric oxide reactivity. *Biological Chemistry*, **2000**, 381, 623-7	4.5	60
342	X-ray crystal structure of the ferric sperm whale myoglobin: imidazole complex at 2.0 A resolution. *Journal of Molecular Biology*, **1991**, 217, 409-12	6.5	60

341	Cyanide binding to truncated hemoglobins: a crystallographic and kinetic study. *Biochemistry*, **2004**, 43, 5213-21	3.2	59
340	Evolutionary constraints for dimer formation in prokaryotic Cu,Zn superoxide dismutase. *Journal of Molecular Biology*, **1999**, 285, 283-96	6.5	59
339	X-ray crystal structure of the fluoride derivative of Aplysia limacina ferric myoglobin at 2.0 A resolution. Stabilization of the fluoride ion by hydrogen bonding to Arg66 (E10). *Journal of Molecular Biology*, **1990**, 213, 621-5	6.5	59
338	Flaviviral methyltransferase/RNA interaction: structural basis for enzyme inhibition. *Antiviral Research*, **2009**, 83, 28-34	10.8	57
337	FAD-binding site and NADP reactivity in human renalase: a new enzyme involved in blood pressure regulation. *Journal of Molecular Biology*, **2011**, 411, 463-73	6.5	56
336	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. *Structure*, **1998**, 6, 1453-65	5.2	56
335	Mapping protein matrix cavities in human cytoglobin through Xe atom binding. *Biochemical and Biophysical Research Communications*, **2004**, 316, 1217-21	3.4	56
334	Exploring the molecular basis of heme coordination in human neuroglobin. *Proteins: Structure, Function and Bioinformatics*, **2008**, 71, 695-705	4.2	51
333	Structural determinants in the group III truncated hemoglobin from Campylobacter jejuni. *Journal of Biological Chemistry*, **2006**, 281, 37803-12	5.4	51
332	Reactivity of ferric Aplysia myoglobin towards anionic ligands in the acidic region. Proposal for a structural model. *Journal of Molecular Biology*, **1981**, 146, 363-74	6.5	51
331	The 109 residue nerve tissue minihemoglobin from Cerebratulus lacteus highlights striking structural plasticity of the alpha-helical globin fold. *Structure*, **2002**, 10, 725-35	5.2	50
330	Mycobacterial truncated hemoglobins: from genes to functions. *Gene*, **2007**, 398, 42-51	3.8	48
329	Structural determinants of CCR5 recognition and HIV-1 blockade in RANTES. *Nature Structural Biology*, **2001**, 8, 611-5		48
328	Structural determinants of fluoride and formate binding to hemoglobin and myoglobin: crystallographic and 1H-NMR relaxometric study. *Biophysical Journal*, **1996**, 70, 482-8	2.9	48
327	Purification, inhibitory properties and amino acid sequence of a new serine proteinase inhibitor from white mustard (Sinapis alba L.) seed. *FEBS Letters*, **1992**, 301, 10-4	3.8	48
326	Enhancement of the HIV-1 inhibitory activity of RANTES by modification of the N-terminal region: dissociation from CCR5 activation. *European Journal of Immunology*, **2000**, 30, 3190-8	6.1	47
325	Structural determinants of ligand migration in Mycobacterium tuberculosis truncated hemoglobin O. *Proteins: Structure, Function and Bioinformatics*, **2008**, 73, 372-9	4.2	46
324	Crystal structure solution and refinement of the semisynthetic cobalt-substituted bovine erythrocyte superoxide dismutase at 2.0 A resolution. *Journal of Molecular Biology*, **1992**, 226, 227-38	6.5	46

323	Designing Smac-mimetics as antagonists of XIAP, cIAP1, and cIAP2. *Biochemical and Biophysical Research Communications*, **2009**, 378, 162-7	3.4	45
322	Role of the C-terminal binding protein PXDLS motif binding cleft in protein interactions and transcriptional repression. *Molecular and Cellular Biology*, **2006**, 26, 8202-13	4.8	45
321	Modulation of the catalytic rate of Cu,Zn superoxide dismutase in single and double mutants of conserved positively and negatively charged residues. *Biochemistry*, **1995**, 34, 6043-9	3.2	45
320	Ligand interactions in the distal heme pocket of Mycobacterium tuberculosis truncated hemoglobin N: roles of TyrB10 and GlnE11 residues. *Biochemistry*, **2006**, 45, 8770-81	3.2	44
319	An active-like structure in the unphosphorylated StyR response regulator suggests a phosphorylation- dependent allosteric activation mechanism. *Structure*, **2005**, 13, 1289-97	5.2	44
318	Functional and crystallographic characterization of Salmonella typhimurium Cu,Zn superoxide dismutase coded by the sodCI virulence gene. *Journal of Molecular Biology*, **2000**, 302, 465-78	6.5	44
317	Anticooperative ligand binding properties of recombinant ferric Vitreoscilla homodimeric hemoglobin: a thermodynamic, kinetic and X-ray crystallographic study. *Journal of Molecular Biology*, **1999**, 291, 637-50	6.5	44
316	Epstein syndrome: another renal disorder with mutations in the nonmuscle myosin heavy chain 9 gene. *Human Genetics*, **2002**, 110, 182-6	6.3	43
315	Probing the catalytic mechanism of GDP-4-keto-6-deoxy-d-mannose Epimerase/Reductase by kinetic and crystallographic characterization of site-specific mutants. *Journal of Molecular Biology*, **2000**, 303, 77-91	6.5	43
314	Crystal structure of apo-avidin from hen egg-white. *Journal of Molecular Biology*, **1994**, 235, 42-6	6.5	43
313	Targeting flavivirus RNA dependent RNA polymerase through a pyridobenzothiazole inhibitor. *Antiviral Research*, **2016**, 134, 226-235	10.8	42
312	Reversible hexa- to penta-coordination of the heme Fe atom modulates ligand binding properties of neuroglobin and cytoglobin. *IUBMB Life*, **2004**, 56, 657-64	4.7	42
311	Subunit association and conformational flexibility in the head subdomain of human CD81 large extracellular loop. *Biological Chemistry*, **2002**, 383, 1447-52	4.5	42
310	Very high resolution structure of a trematode hemoglobin displaying a TyrB10-TyrE7 heme distal residue pair and high oxygen affinity. *Journal of Molecular Biology*, **2001**, 309, 1153-64	6.5	42
309	Exploiting the Burkholderia pseudomallei acute phase antigen BPSL2765 for structure-based epitope discovery/design in structural vaccinology. *Chemistry and Biology*, **2013**, 20, 1147-56		41
308	Structural bases of norovirus RNA dependent RNA polymerase inhibition by novel suramin-related compounds. *PLoS ONE*, **2014**, 9, e91765	3.7	41
307	HisE11 and HisF8 provide bis-histidyl heme hexa-coordination in the globin domain of Geobacter sulfurreducens globin-coupled sensor. *Journal of Molecular Biology*, **2009**, 386, 246-60	6.5	41
306	A novel deamido-NAD+-binding site revealed by the trapped NAD-adenylate intermediate in the NAD+ synthetase structure. *Structure*, **1998**, 6, 1129-40	5.2	41

305	Escherichia coli GlpE is a prototype sulfurtransferase for the single-domain rhodanese homology superfamily. *Structure*, **2001**, 9, 1117-25	5.2	41
304	Rational design of mutations that change the aggregation rate of a protein while maintaining its native structure and stability. *Scientific Reports*, **2016**, 6, 25559	4.9	41
303	TREX1 C-terminal frameshift mutations in the systemic variant of retinal vasculopathy with cerebral leukodystrophy. *Neurological Sciences*, **2015**, 36, 323-30	3.5	40
302	Cyclic dinucleotides bind the C-linker of HCN4 to control channel cAMP responsiveness. *Nature Chemical Biology*, **2014**, 10, 457-62	11.7	40
301	Human neuroserpin: structure and time-dependent inhibition. *Journal of Molecular Biology*, **2009**, 388, 109-21	6.5	40
300	The "rhodanese" fold and catalytic mechanism of 3-mercaptopyruvate sulfurtransferases: crystal structure of SseA from Escherichia coli. *Journal of Molecular Biology*, **2004**, 335, 583-93	6.5	40
299	DE-loop mutations affect beta2 microglobulin stability, oligomerization, and the low-pH unfolded form. *Protein Science*, **2010**, 19, 1386-94	6.3	39
298	Archaeal protoglobin structure indicates new ligand diffusion paths and modulation of haem-reactivity. *EMBO Reports*, **2008**, 9, 157-63	6.5	39
297	The C-terminal domain of the transcriptional corepressor CtBP is intrinsically unstructured. *Protein Science*, **2006**, 15, 1042-50	6.3	39
296	Bishistidyl heme hexacoordination, a key structural property in Drosophila melanogaster hemoglobin. *Journal of Biological Chemistry*, **2005**, 280, 27222-9	5.4	39
295	The diversity of 2/2 (truncated) globins. *Advances in Microbial Physiology*, **2013**, 63, 49-78	4.4	38
294	Identification of the molecular site of ivabradine binding to HCN4 channels. *PLoS ONE*, **2013**, 8, e53132	3.7	38
293	Structure-function relationships in the growing hexa-coordinate hemoglobin sub-family. *IUBMB Life* , **2004**, 56, 643-51	4.7	38
292	The truncated hemoglobin from Mycobacterium leprae. *Biochemical and Biophysical Research Communications*, **2002**, 294, 1064-70	3.4	38
291	A structure-based strategy for epitope discovery in Burkholderia pseudomallei OppA antigen. *Structure*, **2013**, 21, 167-175	5.2	37
290	Crystal structure of the bovine alpha-chymotrypsin:Kunitz inhibitor complex. An example of multiple protein:protein recognition sites. *Journal of Molecular Recognition*, **1997**, 10, 26-35	2.6	37
289	Structure, conformational stability, and enzymatic properties of acylphosphatase from the hyperthermophile Sulfolobus solfataricus. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 64-79	4.2	37
288	Monomer-dimer equilibrium and oxygen binding properties of ferrous Vitreoscilla hemoglobin. *Biochemistry*, **2001**, 40, 9311-6	3.2	37

287	Binding of non-catalytic ATP to human hexokinase I highlights the structural components for enzyme-membrane association control. *Structure*, **1999**, 7, 1427-37	5.2	37
286	The structural bases for agonist diversity in an glutamate receptor-like channel. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 752-760	11.5	37
285	Structural basis for bivalent Smac-mimetics recognition in the IAP protein family. *Journal of Molecular Biology*, **2009**, 392, 630-44	6.5	36
284	Determining mutational fingerprints at the human p53 locus with a yeast functional assay: a new tool for molecular epidemiology. *Oncogene*, **1997**, 14, 1307-13	9.2	36
283	Targeting the X-linked inhibitor of apoptosis protein through 4-substituted azabicyclo[5.3.0]alkane smac mimetics. Structure, activity, and recognition principles. *Journal of Molecular Biology*, **2008**, 384, 673-89	6.5	36
282	Ferredoxin-NADP+ reductase from Plasmodium falciparum undergoes NADP+-dependent dimerization and inactivation: functional and crystallographic analysis. *Journal of Molecular Biology*, **2007**, 367, 501-13	6.5	36
281	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. *Biochemical Journal*, **2004**, 377, 717-24	3.8	36
280	Thr-E11 regulates O2 affinity in Cerebratulus lacteus mini-hemoglobin. *Journal of Biological Chemistry*, **2004**, 279, 33662-72	5.4	36
279	Conformational dynamics in crystals reveal the molecular bases for D76N beta-2 microglobulin aggregation propensity. *Nature Communications*, **2018**, 9, 1658	17.4	35
278	The roles of Tyr(CD1) and Trp(G8) in Mycobacterium tuberculosis truncated hemoglobin O in ligand binding and on the heme distal site architecture. *Biochemistry*, **2007**, 46, 11440-50	3.2	35
277	beta2-microglobulin H31Y variant 3D structure highlights the protein natural propensity towards intermolecular aggregation. *Journal of Molecular Biology*, **2004**, 335, 1051-64	6.5	35
276	New structures of allosteric proteins revealing remarkable conformational changes. *Current Opinion in Structural Biology*, **1996**, 6, 824-9	8.1	35
275	Solution 1H nuclear magnetic resonance determination of hydrogen bonding of the E10 (66) Arg side-chain to the bound ligand in Aplysia cyano-met myoglobin. *Journal of Molecular Biology*, **1992**, 224, 891-7	6.5	35
274	Proton nuclear magnetic resonance study of the molecular and electronic structure of the heme cavity in Aplysia cyanometmyoglobin. *Biochemistry*, **1989**, 28, 4880-7	3.2	35
273	Biochemical characterization and crystal structure of a recombinant hen avidin and its acidic mutant expressed in Escherichia coli. *FEBS Journal*, **1998**, 256, 453-60		34
272	Structural bases for substrate recognition and activity in Meaban virus nucleoside-2'-O-methyltransferase. *Protein Science*, **2007**, 16, 1133-45	6.3	34
271	Control and recognition of anionic ligands in myoglobin. *FEBS Letters*, **1991**, 282, 281-4	3.8	34
270	Nicotinic acetylcholine receptor: a structural model for alpha-subunit peptide 188-201, the putative binding site for cholinergic agents. *FEBS Letters*, **1988**, 228, 118-22	3.8	34

269	Determination of ligand pathways in globins: apolar tunnels versus polar gates. *Journal of Biological Chemistry*, **2012**, 287, 33163-78	5.4	33
268	Rational design, synthesis and characterization of potent, non-peptidic Smac mimics/XIAP inhibitors as proapoptotic agents for cancer therapy. *Bioorganic and Medicinal Chemistry*, **2009**, 17, 5834-56	3.4	33
267	DE loop mutations affect beta2-microglobulin stability and amyloid aggregation. *Biochemical and Biophysical Research Communications*, **2008**, 377, 146-50	3.4	33
266	Truncated hemoglobins and nitric oxide action. *IUBMB Life*, **2003**, 55, 623-7	4.7	33
265	Coupling of the heme and an internal disulfide bond in human neuroglobin. *Micron*, **2004**, 35, 59-62	2.3	33
264	Crystal structure of ferric Aplysia limacina myoglobin at 2 X 0 A resolution. *Journal of Molecular Biology*, **1985**, 183, 113-5	6.5	33
263	Naphthalene-sulfonate inhibitors of human norovirus RNA-dependent RNA-polymerase. *Antiviral Research*, **2014**, 102, 23-8	10.8	32
262	Nitric oxide scavenging by Mycobacterium leprae GlbO involves the formation of the ferric heme-bound peroxynitrite intermediate. *Biochemical and Biophysical Research Communications*, **2006**, 339, 450-6	3.4	32
261	Concurrent structural and biophysical traits link with immunoglobulin light chains amyloid propensity. *Scientific Reports*, **2017**, 7, 16809	4.9	31
260	Fibrillar vs crystalline full-length beta-2-microglobulin studied by high-resolution solid-state NMR spectroscopy. *Journal of the American Chemical Society*, **2010**, 132, 5556-7	16.4	31
259	The apolar channel in Cerebratulus lacteus hemoglobin is the route for O2 entry and exit. *Journal of Biological Chemistry*, **2008**, 283, 35689-702	5.4	31
258	From crystal structure to in silico epitope discovery in the Burkholderia pseudomallei flagellar hook-associated protein FlgK. *FEBS Journal*, **2015**, 282, 1319-33	5.7	30
257	Neuroglobin and cytoglobin: Two new entries in the hemoglobin superfamily*. *Biochemistry and Molecular Biology Education*, **2004**, 32, 305-13	1.3	30
256	A redox signalling globin is essential for reproduction in Caenorhabditis elegans. *Nature Communications*, **2015**, 6, 8782	17.4	29
255	Structure of the human NK cell triggering receptor NKp46 ectodomain. *Biochemical and Biophysical Research Communications*, **2003**, 309, 317-23	3.4	29
254	Crystal structure of the cyanide-inhibited Xenopus laevis Cu,Zn superoxide dismutase at 98 K. *FEBS Letters*, **1994**, 349, 93-8	3.8	29
253	Binding mode of azide to ferric Aplysia limacina myoglobin. Crystallographic analysis at 1.9 A resolution. *Journal of Molecular Recognition*, **1991**, 4, 1-6	2.6	29
252	Structural features of neutral protease from Bacillus subtilis deduced from model-building and limited proteolysis experiments. *FEBS Journal*, **1990**, 189, 221-7		29

251	Ligand migration in Methanosarcina acetivorans protoglobin: effects of ligand binding and dimeric assembly. *Journal of Physical Chemistry B*, **2011**, 115, 13771-80	3.4	28
250	Group B streptococcus pullulanase crystal structures in the context of a novel strategy for vaccine development. *Journal of Bacteriology*, **2009**, 191, 3544-52	3.5	28
249	Human beta-2 microglobulin W60V mutant structure: Implications for stability and amyloid aggregation. *Biochemical and Biophysical Research Communications*, **2009**, 380, 543-7	3.4	28
248	Ligand binding to truncated hemoglobin N from Mycobacterium tuberculosis is strongly modulated by the interplay between the distal heme pocket residues and internal water. *Journal of Biological Chemistry*, **2008**, 283, 27270-8	5.4	28
247	Proteinase inhibitors from the European medicinal leech Hirudo medicinalis: structural, functional and biomedical aspects. *Molecular Aspects of Medicine*, **1995**, 16, 215-313	16.7	28
246	Inhibition of bovine beta-trypsin, human alpha-thrombin and porcine pancreatic beta-kallikrein-B by 4',6-diamidino-2-phenylindole, 6-amidinoindole and benzamidine: a comparative thermodynamic and X-ray structural study. *Biophysical Chemistry*, **1995**, 54, 75-81	3.5	28
245	Sequence- and Structure-Based Immunoreactive Epitope Discovery for Burkholderia pseudomallei Flagellin. *PLoS Neglected Tropical Diseases*, **2015**, 9, e0003917	4.8	27
244	Reductive nitrosylation and peroxynitrite-mediated oxidation of heme-hemopexin. *FEBS Journal*, **2007**, 274, 551-62	5.7	27
243	The human brain hexacoordinated neuroglobin three-dimensional structure. *Micron*, **2004**, 35, 63-5	2.3	27
242	Crystallographic study of azide-inhibited bovine Cu,Zn superoxide dismutase. *Journal of Molecular Biology*, **1994**, 240, 179-83	6.5	27
241	Non-covalent and covalent modifications modulate the reactivity of monomeric mammalian globins. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2013**, 1834, 1750-6	4	26
240	Dimeric Smac mimetics/IAP inhibitors as in vivo-active pro-apoptotic agents. Part II: Structural and biological characterization. *Bioorganic and Medicinal Chemistry*, **2012**, 20, 6709-23	3.4	26
239	On the coordination and oxidation states of the active-site copper ion in prokaryotic Cu,Zn superoxide dismutases. *Biochemical and Biophysical Research Communications*, **1998**, 249, 579-82	3.4	26
238	Reptile heme protein structure: X-ray crystallographic study of the aquo-met and cyano-met derivatives of the loggerhead sea turtle (Caretta caretta) myoglobin at 2.0 A resolution. *Journal of Molecular Biology*, **1995**, 247, 459-65	6.5	26
237	Binding of the bovine basic pancreatic trypsin inhibitor (Kunitz) to human alpha-, beta- and gamma-thrombin; a kinetic and thermodynamic study. *BBA - Proteins and Proteomics*, **1988**, 956, 156-61		26
236	Structure, stability, and aggregation of β2 microglobulin mutants: insights from a Fourier transform infrared study in solution and in the crystalline state. *Biophysical Journal*, **2012**, 102, 1676-84	2.9	25
235	Nitric oxide and Mycobacterium leprae pathogenicity. *IUBMB Life*, **2002**, 54, 95-9	4.7	25
234	Patterns in ionizable side chain interactions in protein structures. *Proteins: Structure, Function and Bioinformatics*, **1996**, 24, 439-49	4.2	25

233	The tempered polymerization of human neuroserpin. *PLoS ONE*, **2012**, 7, e32444	3.7	25
232	Delivery of suramin as an antiviral agent through liposomal systems. *ChemMedChem*, **2014**, 9, 933-9	3.7	24
231	Molecular mechanism and functional role of brefeldin A-mediated ADP-ribosylation of CtBP1/BARS. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 9794-9	11.5	24
230	CO rebinding kinetics and molecular dynamics simulations highlight dynamic regulation of internal cavities in human cytoglobin. *PLoS ONE*, **2013**, 8, e49770	3.7	24
229	Structural determinants of trypsin affinity and specificity for cationic inhibitors. *Protein Science*, **1999**, 8, 2621-9	6.3	24
228	Ferrous Campylobacter jejuni truncated hemoglobin P displays an extremely high reactivity for cyanide - a comparative study. *FEBS Journal*, **2008**, 275, 633-45	5.7	24
227	Substrate channeling: Molecular bases. *Biochemistry and Molecular Biology Education*, **2003**, 31, 228-233	1.3	24
226	A persulfurated cysteine promotes active site reactivity in Azotobacter vinelandii Rhodanese. *Biological Chemistry*, **2001**, 382, 1245-52	4.5	24
225	Quantitative expression of the mutated lamin A/C gene in patients with cardiolaminopathy. *Journal of the American College of Cardiology*, **2012**, 60, 1916-20	15.1	23
224	Recognition of Smac-mimetic compounds by the BIR domain of cIAP1. *Protein Science*, **2010**, 19, 2418-29	6.3	23
223	Expression, purification, and crystallization of neuro- and cytoglobin. *Methods in Enzymology*, **2008**, 436, 341-57	1.7	23
222	Crystal structure of LptH, the periplasmic component of the lipopolysaccharide transport machinery from Pseudomonas aeruginosa. *FEBS Journal*, **2015**, 282, 1980-97	5.7	22
221	Gabexate mesylate inhibition of serine proteases: thermodynamic and computer-graphics analysis. *Journal of Pharmaceutical Sciences*, **1986**, 75, 1171-4	3.9	22
220	Structural flexibility of the heme cavity in the cold-adapted truncated hemoglobin from the Antarctic marine bacterium Pseudoalteromonas haloplanktis TAC125. *FEBS Journal*, **2015**, 282, 2948-65	5.7	21
219	Binding of hirudin to human alpha, beta and gamma-thrombin. A comparative kinetic and thermodynamic study. *Journal of Molecular Biology*, **1992**, 225, 177-84	6.5	21
218	Binding of the recombinant proteinase inhibitor eglin c from leech Hirudo medicinalis to human leukocyte elastase, bovine alpha-chymotrypsin and subtilisin Carlsberg: thermodynamic study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1988**, 2, 167-72		21
217	Binding of the bovine basic pancreatic trypsin inhibitor (Kunitz) to human urinary kallikrein and to porcine pancreatic beta-kallikreins A and B. *Journal of Molecular Biology*, **1984**, 176, 425-30	6.5	21
216	Class I major histocompatibility complex, the trojan horse for secretion of amyloidogenic β-microglobulin. *Journal of Biological Chemistry*, **2014**, 289, 3318-27	5.4	20

215	Two latent and two hyperstable polymeric forms of human neuroserpin. *Biophysical Journal*, **2010**, 99, 3402-11	2.9	20
214	Ligand migration in the apolar tunnel of Cerebratulus lacteus mini-hemoglobin. *Journal of Biological Chemistry*, **2011**, 286, 5347-58	5.4	20
213	Structural characterization of the nonameric assembly of an Archaeal alpha-L-fucosidase by synchrotron small angle X-ray scattering. *Biochemical and Biophysical Research Communications*, **2004**, 320, 176-82	3.4	20
212	Two distinct heme distal site states define Cerebratulus lacteus mini-hemoglobin oxygen affinity. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 641-8	4.2	20
211	Structure solution and molecular dynamics refinement of the yeast Cu,Zn enzyme superoxide dismutase. *Acta Crystallographica Section B: Structural Science*, **1991**, 47 (Pt 6), 918-27		20
210	Kinetic control of ligand binding processes in hemoproteins. *Journal of Molecular Liquids*, **1989**, 42, 175-193	6	20
209	Immunisation with proteins expressed during chronic murine melioidosis provides enhanced protection against disease. *Vaccine*, **2016**, 34, 1665-71	4.1	19
208	Flexible vs Rigid Epitope Conformations for Diagnostic- and Vaccine-Oriented Applications: Novel Insights from the Burkholderia pseudomallei BPSL2765 Pal3 Epitope. *ACS Infectious Diseases*, **2016**, 2, 221-30	5.5	19
207	PPNDS inhibits murine Norovirus RNA-dependent RNA-polymerase mimicking two RNA stacking bases. *FEBS Letters*, **2014**, 588, 1720-5	3.8	19
206	The VIZIER project: preparedness against pathogenic RNA viruses. *Antiviral Research*, **2008**, 78, 37-46	10.8	19
205	Single mutations at the subunit interface modulate copper reactivity in Photobacterium leiognathi Cu,Zn superoxide dismutase. *Journal of Molecular Biology*, **2001**, 308, 555-63	6.5	19
204	Biotin and biotin analogues specifically modify the fluorescence decay of avidin. *Journal of Molecular Biology*, **1994**, 242, 559-65	6.5	19
203	Tetra-p-amidinophenoxy-propane as a probe of the specificity site of serine proteases. *FEBS Letters* , **1982**, 141, 33-6	3.8	19
202	Protoglobin: structure and ligand-binding properties. *Advances in Microbial Physiology*, **2013**, 63, 79-96	4.4	18
201	Decoding the Structural Bases of D76N -Microglobulin High Amyloidogenicity through Crystallography and Asn-Scan Mutagenesis. *PLoS ONE*, **2015**, 10, e0144061	3.7	18
200	Structures of the lamin A/C R335W and E347K mutants: implications for dilated cardiolaminopathies. *Biochemical and Biophysical Research Communications*, **2012**, 418, 217-21	3.4	18
199	Evidence of his61 imidazolate bridge rupture in reduced crystalline Cu,Zn superoxide dismutase. *Biochemical and Biophysical Research Communications*, **1997**, 241, 119-21	3.4	18
198	Crystal structures of HIV-1 reverse transcriptase complexes with thiocarbamate non-nucleoside inhibitors. *Biochemical and Biophysical Research Communications*, **2008**, 365, 764-70	3.4	18

197	A recurrent D-strand association interface is observed in □2 microglobulin oligomers. *FEBS Journal*, **2012**, 279, 1131-43	5.7	17
196	Kinetic and structural evidences on human prolidase pathological mutants suggest strategies for enzyme functional rescue. *PLoS ONE*, **2013**, 8, e58792	3.7	17
195	Globin-like proteins in Caenorhabditis elegans: in vivo localization, ligand binding and structural properties. *BMC Biochemistry*, **2010**, 11, 17	4.8	17
194	Mapping heme-ligand tunnels in group I truncated(2/2) hemoglobins. *Methods in Enzymology*, **2008**, 436, 303-15	1.7	17
193	Cyanide binding and heme cavity conformational transitions in Drosophila melanogaster hexacoordinate hemoglobin. *Biochemistry*, **2006**, 45, 10054-61	3.2	17
192	Viscosity-dependent relaxation significantly modulates the kinetics of CO recombination in the truncated hemoglobin TrHbN from Mycobacterium tuberculosis. *Journal of Biological Chemistry*, **2004**, 279, 38844-53	5.4	17
191	Single mutation at the intersubunit interface confers extra efficiency to Cu,Zn superoxide dismutase. *FEBS Letters*, **2000**, 483, 17-20	3.8	17
190	Expression, purification, crystallization, and preliminary X-ray diffraction analysis of the homodimeric bacterial hemoglobin from Vitreoscilla stercoraria. *Proteins: Structure, Function and Bioinformatics*, **1997**, 27, 154-6	4.2	16
189	Three-dimensional structural characterization of a novel Drosophila melanogaster acylphosphatase. *Acta Crystallographica Section D: Biological Crystallography*, **2004**, 60, 1177-9		16
188	Crystallization and preliminary crystallographic studies on the large extracellular domain of human CD81, a tetraspanin receptor for hepatitis C virus. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 156-8		16
187	Flaviviral helicase: insights into the mechanism of action of a motor protein. *Biochemical and Biophysical Research Communications*, **2012**, 417, 84-7	3.4	15
186	Probing the active site of the sugar isomerase domain from E. coli arabinose-5-phosphate isomerase via X-ray crystallography. *Protein Science*, **2010**, 19, 2430-9	6.3	15
185	CO sniffing through heme-based sensor proteins. *IUBMB Life*, **2004**, 56, 309-15	4.7	15
184	Static and dynamic water molecules in Cu,Zn superoxide dismutase. *Proteins: Structure, Function and Bioinformatics*, **2003**, 51, 607-15	4.2	15
183	Active-site copper and zinc ions modulate the quaternary structure of prokaryotic Cu,Zn superoxide dismutase. *Journal of Molecular Biology*, **2003**, 326, 1351-60	6.5	15
182	Ultrastructural organization of ex vivo amyloid fibrils formed by the apolipoprotein A-I Leu174Ser variant: an atomic force microscopy study. *Biochimica Et Biophysica Acta - Molecular Basis of Disease*, **2004**, 1690, 33-41	6.9	15
181	Binding of the recombinant proteinase inhibitor eglin c from leech Hirudo medicinalis to serine (pro)enzymes: a comparative thermodynamic study. *Journal of Molecular Recognition*, **1991**, 4, 113-9	2.6	15
180	Structure and Computation in Immunoreagent Design: From Diagnostics to Vaccines. *Trends in Biotechnology*, **2017**, 35, 1208-1220	15.1	14

179	Human alpha-thrombin inhibition by the highly selective compounds N-ethoxycarbonyl-D-Phe-Pro-alpha-azaLys p-nitrophenyl ester and N-carbobenzoxy-Pro-alpha-azaLys p-nitrophenyl ester: a kinetic, thermodynamic and X-ray crystallographic study. *Journal of Molecular Biology*, **1997**, 269, 558-69	6.5	14
178	Protein structure in the truncated (2/2) hemoglobin family. *IUBMB Life*, **2007**, 59, 535-41	4.7	14
177	*NO dissociation represents the rate limiting step for O2-mediated oxidation of ferrous nitrosylated Mycobacterium leprae truncated hemoglobin O. *Biochemical and Biophysical Research Communications*, **2007**, 357, 809-14	3.4	14
176	The crystal structure of FdxA, a 7Fe ferredoxin from Mycobacterium smegmatis. *Biochemical and Biophysical Research Communications*, **2007**, 360, 97-102	3.4	14
175	Modulation of oxygen binding to insect hemoglobins: the structure of hemoglobin from the botfly Gasterophilus intestinalis. *Protein Science*, **2005**, 14, 3057-63	6.3	14
174	Human alpha-thrombin inhibition by the active site titrant N alpha-(N,N-dimethylcarbamoyl)-alpha-azalysine p-nitrophenyl ester: a comparative kinetic and X-ray crystallographic study. *Journal of Molecular Biology*, **1996**, 258, 851-9	6.5	14
173	Reductive nitrosylation of Methanosarcina acetivorans protoglobin: a comparative study. *Biochemical and Biophysical Research Communications*, **2013**, 430, 1301-5	3.4	13
172	Wild type beta-2 microglobulin and DE loop mutants display a common fibrillar architecture. *PLoS ONE*, **2015**, 10, e0122449	3.7	13
171	Functional and dysfunctional conformers of human neuroserpin characterized by optical spectroscopies and Molecular Dynamics. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2015**, 1854, 110-7	4	13
170	D-strand perturbation and amyloid propensity in beta-2 microglobulin. *FEBS Journal*, **2011**, 278, 2349-58	5.7	13
169	The two tryptophans of □-microglobulin have distinct roles in function and folding and might represent two independent responses to evolutionary pressure. *BMC Evolutionary Biology*, **2011**, 11, 159	3	13
168	Human neuroglobin: crystals and preliminary X-ray diffraction analysis. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1848-50		13
167	Crystal structure of the glutaredoxin-like protein SH3BGRL3 at 1.6 Angstrom resolution. *Biochemical and Biophysical Research Communications*, **2004**, 318, 470-6	3.4	13
166	Binding of the bovine basic pancreatic trypsin inhibitor (Kunitz inhibitor) to human and bovine factor Xa. A thermodynamic study. *Biological Chemistry Hoppe-Seyler*, **1990**, 371, 389-93		13
165	Different primary specificity of porcine pancreatic beta-kallikrein-B and bovine beta-trypsin. A comparative steady-state and pre-steady-state study. *BBA - Proteins and Proteomics*, **1984**, 789, 99-103		13
164	Catalytic and ligand binding properties of bovine trypsinogen and its complex with the effector dipeptide Ile-Val. A comparative study. *Molecular and Cellular Biochemistry*, **1984**, 60, 163-81	4.2	13
163	Edge strand engineering prevents native-like aggregation in Sulfolobus solfataricus acylphosphatase. *FEBS Journal*, **2014**, 281, 4072-84	5.7	12
162	Characterization of □-microglobulin conformational intermediates associated to different fibrillation conditions. *Journal of Mass Spectrometry*, **2011**, 46, 734-41	2.2	12

161	Structural heterogeneity and ligand gating in ferric Methanosarcina acetivorans protoglobin mutants. *IUBMB Life*, **2011**, 63, 287-94	4.7	12
160	Structural characterization of a group II 2/2 hemoglobin from the plant pathogen Agrobacterium tumefaciens. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2011**, 1814, 810-6	4	12
159	CtBP1/BARS Gly172-->Glu mutant structure: impairing NAD(H)-binding and dimerization. *Biochemical and Biophysical Research Communications*, **2009**, 381, 70-4	3.4	12
158	Double-stranded deoxyribonucleic acid binds to HLA class II molecules and inhibits HLA class II-mediated antigen presentation. *European Journal of Immunology*, **1998**, 28, 3968-79	6.1	12
157	Hirunorms are true hirudin mimetics. The crystal structure of human alpha-thrombin-hirunorm V complex. *Protein Science*, **1998**, 7, 243-53	6.3	12
156	Oxygen binding by alpha(Fe2+)2beta(Ni2+)2 hemoglobin crystals. *Protein Science*, **2000**, 9, 683-92	6.3	12
155	Nitrophorins: Lipocalin-based heme proteins transporting nitric oxide. *Biochemistry and Molecular Biology Education*, **2002**, 30, 68-71	1.3	12
154	Measurement of the Surface Free Energy of Streptavidin Crystals by Atomic Force Microscopy. *Langmuir*, **2003**, 19, 2908-2912	4	12
153	The three-dimensional structure of beta2 microglobulin: results from X-ray crystallography. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2005**, 1753, 85-91	4	12
152	Reassessment of copper stoichiometry in ascorbate oxidase. *Biochemical and Biophysical Research Communications*, **1988**, 152, 623-8	3.4	12
151	The pH dependence of pre-steady-state and steady-state kinetics for the porcine pancreatic beta-kallikrein-B-catalyzed hydrolysis of N-alpha-carbobenzoxy-L-arginine p-nitrophenyl ester. *BBA - Proteins and Proteomics*, **1984**, 785, 75-80		12
150	Activating effect of the Ile-Val dipeptide on the catalytic properties of bovine trypsinogen. *BBA - Proteins and Proteomics*, **1985**, 832, 1-6		12
149	Binding of the bovine basic pancreatic trypsin inhibitor (Kunitz) to human Lys77-plasmin. *Journal of Molecular Biology*, **1986**, 191, 295-7	6.5	12
148	Selective crystallization of horse isoferritins. *BBA - Proteins and Proteomics*, **1983**, 744, 230-2		12
147	Structure and haem-distal site plasticity in Methanosarcina acetivorans protoglobin. *PLoS ONE*, **2013**, 8, e66144	3.7	12
146	Nitrite-reductase and peroxynitrite isomerization activities of Methanosarcina acetivorans protoglobin. *PLoS ONE*, **2014**, 9, e95391	3.7	12
145	A covalent homodimer probing early oligomers along amyloid aggregation. *Scientific Reports*, **2015**, 5, 14651	4.9	11
144	On the molecular structure of human neuroserpin polymers. *Proteins: Structure, Function and Bioinformatics*, **2012**, 80, 8-13	4.2	11

143	Cross-enzyme inhibition by gabexate mesylate: formulation and reactivity study. *Journal of Pharmaceutical Sciences*, **1998**, 87, 1335-40	3.9	11
142	The hemoglobins of the trematodes Fasciola hepatica and Paramphistomum epiclitum: a molecular biological, physico-chemical, kinetic, and vaccination study. *Protein Science*, **2008**, 17, 1653-62	6.3	11
141	Modulation of the catalytic activity of cruzipain, the major cysteine proteinase from Trypanosoma cruzi, by temperature and pH. *FEBS Journal*, **2001**, 268, 3253-8		11
140	Evidence for breaking of the active site dimetal cluster in Cu,Co superoxide dismutase upon copper reduction: a polarized absorption spectra study. *Biochemical and Biophysical Research Communications*, **1995**, 210, 1040-4	3.4	11
139	Spectroscopic properties of the nitric oxide derivative of ferrous man, horse, and ruminant hemoglobins: a comparative study. *Journal of Inorganic Biochemistry*, **1992**, 45, 31-7	4.2	11
138	Bovine trypsinogen activation. A thermodynamic study. *Biophysical Chemistry*, **1990**, 37, 355-62	3.5	11
137	Binding of the bovine pancreatic secretory trypsin inhibitor (Kazal) to bovine serine (pro)enzymes. *Journal of Molecular Biology*, **1987**, 198, 129-32	6.5	11
136	Crystallization of hen egg-white avidin in a tetragonal form. *Journal of Molecular Biology*, **1984**, 178, 787-9	6.5	11
135	Embelin binds to human neuroserpin and impairs its polymerisation. *Scientific Reports*, **2016**, 6, 18769	4.9	11
134	The activator of apoptosis Smac-DIABLO acts as a tetramer in solution. *Biophysical Journal*, **2015**, 108, 714-23	2.9	10
133	Structural insight into inhibitor of apoptosis proteins recognition by a potent divalent smac-mimetic. *PLoS ONE*, **2012**, 7, e49527	3.7	10
132	Plasmodium falciparum ferredoxin-NADP+ reductase His286 plays a dual role in NADP(H) binding and catalysis. *Biochemistry*, **2009**, 48, 9525-33	3.2	10
131	Nerve globins in invertebrates. *IUBMB Life*, **2004**, 56, 653-6	4.7	10
130	Crystallization and preliminary X-ray analysis of the monomeric Cu,Zn superoxide dismutase from Escherichia coli. *Protein Science*, **1996**, 5, 2125-7	6.3	10
129	Binding of the Kunitz-type trypsin inhibitor DE-3 from Erythrina caffra seeds to serine proteinases: a comparative study. *Journal of Molecular Recognition*, **1992**, 5, 105-14	2.6	10
128	X-ray crystal structure of the bovine alpha-chymotrypsin/eglin c complex at 2.6 A resolution. *Journal of Molecular Recognition*, **1990**, 3, 163-8	2.6	10
127	Crystallization of an odorant-binding protein from cow nasal mucosa. *Journal of Molecular Biology*, **1985**, 186, 211-2	6.5	10
126	Ligation tunes protein reactivity in an ancient haemoglobin: kinetic evidence for an allosteric mechanism in Methanosarcina acetivorans protoglobin. *PLoS ONE*, **2012**, 7, e33614	3.7	10

125	Inherent Biophysical Properties Modulate the Toxicity of Soluble Amyloidogenic Light Chains. *Journal of Molecular Biology*, **2020**, 432, 845-860	6.5	10
124	Glycosylation Tunes Neuroserpin Physiological and Pathological Properties. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	9
123	Molecular bases of neuroserpin function and pathology. *Biomolecular Concepts*, **2010**, 1, 117-30	3.7	9
122	Crystal structure of a methyltransferase from a no-known-vector Flavivirus. *Biochemical and Biophysical Research Communications*, **2009**, 382, 200-4	3.4	9
121	The effects of an ideal beta-turn on beta-2 microglobulin fold stability. *Journal of Biochemistry*, **2011**, 150, 39-47	3.1	9
120	Quaternary assembly and crystal structure of GDP-D-mannose 4,6 dehydratase from Paramecium bursaria Chlorella virus. *Biochemical and Biophysical Research Communications*, **2006**, 339, 191-5	3.4	9
119	Crystallization and preliminary X-ray diffraction analysis of brefeldin A-ADP ribosylated substrate (BARS). *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1068-70		9
118	The 1.6 A resolution crystal structure of a mutant plastocyanin bearing a 21-25 engineered disulfide bridge. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1735-8		9
117	Crystallographic characterization and three-dimensional model of yeast Cu,Zn superoxide dismutase. *Biochemical and Biophysical Research Communications*, **1989**, 160, 677-81	3.4	9
116	Modeling by homology of RNA binding domain in A1 hnRNP protein. *FEBS Letters*, **1990**, 277, 272-6	3.8	9
115	Binding of porcine pancreatic secretory trypsin inhibitor to bovine beta-trypsin: a kinetic study. *Biopolymers*, **1986**, 25, 2325-33	2.2	9
114	Binding of the Ile-Val and Val-Val effector dipeptides to the binary adducts of bovine trypsinogen with Kunitz and Kazal inhibitors as well as the acylating agent p-nitrophenyl p-guanidinobenzoate. A thermodynamic and kinetic study. *Journal of Molecular Biology*, **1987**, 194, 751-4	6.5	9
113	Structural alignment and analysis of two distantly related proteins: Aplysia limacina myoglobin and sea lamprey globin. *Proteins: Structure, Function and Bioinformatics*, **1988**, 4, 240-50	4.2	9
112	A new crystalline modification of the copper enzyme ascorbate oxidase. *Journal of Molecular Biology*, **1983**, 169, 351-2	6.5	9
111	Crystallization and preliminary x-ray diffraction studies on met-myoglobin from Aplysia limacina. *Journal of Molecular Biology*, **1975**, 97, 665-6	6.5	9
110	Letter: A ready synthesis of 17alpha steroids-1,2. *Journal of Organic Chemistry*, **1975**, 40, 2006-7	4.2	9
109	The N-terminal pre-A region of Mycobacterium tuberculosis 2/2HbN promotes NO-dioxygenase activity. *FEBS Journal*, **2016**, 283, 305-22	5.7	9
108	Mycobacterial and Human Nitrobindins: Structure and Function. *Antioxidants and Redox Signaling*, **2020**, 33, 229-246	8.4	9

107	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, 2227-35		8
106	New insight into the haemoglobin superfamily: preliminary crystallographic characterization of human cytoglobin. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 1285-7		8
105	An atomic force microscopy investigation of protein crystal surface topography. *European Biophysics Journal*, **2001**, 30, 313-8	1.9	8
104	Crystallisation and preliminary crystallographic analysis of recombinant Xenopus laevis Cu,Zn superoxide dismutase b. *Biochemical and Biophysical Research Communications*, **1993**, 194, 1008-11	3.4	8
103	Binding of bovine basic pancreatic trypsin inhibitor (Kunitz) as well as bovine and porcine pancreatic secretory trypsin inhibitor (Kazal) to human cathepsin G: a kinetic and thermodynamic study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1993**, 7, 57-64		8
102	Crystal structure of a distal site double mutant of sperm whale myoglobin at 1.6 A resolution. *FEBS Letters*, **1993**, 320, 13-6	3.8	8
101	Zymogen activation: effect of peptides sequentially related to the bovine beta-trypsin N-terminus on Kazal inhibitor and benzamidine binding to bovine trypsinogen. *Journal of Molecular Recognition*, **1988**, 1, 130-7	2.6	8
100	Single crystal absorption spectra of ascorbate oxidase from green zucchini squash. *FEBS Letters*, **1988**, 231, 89-94	3.8	8
99	Trypsin activation. Effect of the Ile-Val dipeptide concentration on Kazal inhibitor binding to bovine trypsinogen. *BBA - Proteins and Proteomics*, **1985**, 832, 378-82		8
98	Gating movements and ion permeation in HCN4 pacemaker channels. *Molecular Cell*, **2021**, 81, 2929-2943.e6	17.6	8
97	A stereospecific carboxyl esterase from Bacillus coagulans hosting nonlipase activity within a lipase-like fold. *FEBS Journal*, **2018**, 285, 903-914	5.7	7
96	Novel neurofibromatosis type 2 mutation presenting with status epilepticus. *Epileptic Disorders*, **2014**, 16, 132-7	1.9	7
95	Preliminary crystallographic investigations of recombinant GDP-4-keto-6-deoxy-D-mannose epimerase/reductase from E. coli. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 684-6		7
94	The T-knot motif revisited. *Biological Chemistry*, **1999**, 380, 1247-50	4.5	7
93	Inhibition of bovine beta-trypsin by the active site titrant N alpha-(N,N-dimethylcarbamoyl)-alpha-azaornithine p-nitrophenyl ester: a kinetic and X-ray crystallographic study. *Biochemical and Biophysical Research Communications*, **1995**, 217, 437-44	3.4	7
92	Formate binding to ferric wild type and mutant myoglobins thermodynamic and X-ray crystallographic study. *FEBS Letters*, **1995**, 357, 227-9	3.8	7
91	Inhibition of serine proteinases belonging to the chymotrypsin superfamily by the cyclic thiolic compound YS3025: a comparative crystallographic study. *Biochemical and Biophysical Research Communications*, **1993**, 193, 32-9	3.4	7
90	Protein folding and chain collapse. *Biopolymers*, **1990**, 29, 1823-1833	2.2	7

89	Primary specificity of ancrod, the coagulating serine proteinase from the Malayan pit viper (Agkistrodon rhodostoma) venom. *BBA - Proteins and Proteomics*, **1986**, 871, 225-8		7
88	Inhibition of serine proteinases by tetra-p-amidinophenoxy-neo-pentane: thermodynamic and molecular modeling study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1987**, 2, 23-30		7
87	Interaction between Serine (Pro)Enzymes and Macromolecular Inhibitors. Thermodynamic and Kinetic Aspects **1987**, 117-130		7
86	Functional and structural roles of the N-terminal extension in Methanosarcina acetivorans protoglobin. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2013**, 1834, 1813-23	4	6
85	NF023 binding to XIAP-BIR1: searching drugs for regulation of the NF-B pathway. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 612-20	4.2	6
84	Hemoprotein time-resolved X-ray crystallography. *IUBMB Life*, **2008**, 60, 154-8	4.7	6
83	The crystal structure of alpha-thrombin-hirunorm IV complex reveals a novel specificity site recognition mode. *Protein Science*, **1999**, 8, 91-5	6.3	6
82	Hemopexin: The primary specific carrier of plasma heme*. *Biochemistry and Molecular Biology Education*, **2002**, 30, 332-335	1.3	6
81	Crystallization and preliminary crystallographic characterization of the extracellular Ig-like domain of human natural killer cell activating receptor NKp44. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1843-5		6
80	Expression and crystallographic characterization of the extracellular domain of human natural killer cell triggering receptor NKp46. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 2259-61		6
79	Inhibition of Azotobacter vinelandii rhodanese by NO-donors. *Biochemical and Biophysical Research Communications*, **2003**, 306, 1002-7	3.4	6
78	Crystallization and preliminary X-ray analysis of neural haemoglobin from the nemertean worm Cerebratulus lacteus. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 1897-9		6
77	Selective oxidation of Met-192 in bovine alpha-chymotrypsin. Effect on catalytic and inhibitor binding properties. *BBA - Proteins and Proteomics*, **1993**, 1161, 201-8		6
76	Binding of the bovine basic pancreatic trypsin inhibitor (Kunitz) to human Glu1-, Lys77-, Val442-, and Val561-plasmin: a comparative study. *BBA - Proteins and Proteomics*, **1990**, 1040, 134-6		6
75	Catalytic properties of bovine alpha-thrombin: a comparative steady-state and pre-steady-state study. *BBA - Proteins and Proteomics*, **1986**, 871, 319-23		6
74	Binding of kunitz and eglin c inhibitors to serine proteinases: thermodynamic, kinetic and molecular aspects. *Journal of Molecular Catalysis*, **1988**, 47, 297-306		6
73	Effect of inositol hexakisphosphate on the spectroscopic properties of the nitric oxide derivative of ferrous naturally glycated human hemoglobin HbA1c. *Journal of Inorganic Biochemistry*, **1988**, 34, 19-24	4.2	6
72	Catalytic properties of Ancrod, the thrombin-like proteinase from the Malayan pit viper (Agkistrodon rhodostoma) venom. *BBA - Proteins and Proteomics*, **1985**, 829, 415-23		6

71	Preliminary crystallographic data on buffalo beta-lactoglobulin. *Journal of Molecular Biology*, **1979**, 131, 411-3	6.5	6
70	BPSL1626: Reverse and Structural Vaccinology Reveal a Novel Candidate for Vaccine Design against. *Antibodies*, **2018**, 7,	7	5
69	Preliminary characterization of (nucleoside-2'-O-)-methyltransferase crystals from Meaban and Yokose flaviviruses. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 768-70		5
68	Preliminary crystallographic characterization of an RNA helicase from Kunjin virus. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 876-9		5
67	Crystallization and preliminary X-ray characterization of the acylphosphatase-like domain from the Escherichia coli hydrogenase maturation factor HypF. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 524-5		5
66	Does inhibition of Trypanosoma cruzi key enzymes affect parasite life cycle and geographic distribution?. *IUBMB Life*, **2002**, 53, 45-7	4.7	5
65	Preliminary crystallographic characterization of the human beta2 microglobulin His31Tyr mutant in a tetrameric assembly. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 1270-2		5
64	N-ethoxycarbonyl-D-phenylalanyl-L-prolyl-alpha-azalysine p-nitrophenyl ester: a novel, high selective and optimal chromogenic active site titrant for human and bovine alpha-, beta- and gamma-thrombin. *Biochemical and Biophysical Research Communications*, **1996**, 225, 557-61	3.4	5
63	Inhibition of human alpha-, beta- and gamma-thrombin by mono-, bis-, tris- and tetra-benzamidine structures: thermodynamic study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1992**, 6, 131-9		5
62	Molecular bases for heme:ligand recognition in sperm whale (Physeter Catodon) andAplysia limacine myoglobin. *Rendiconti Lincei*, **1993**, 4, 65-73	1.7	5
61	Preliminary crystallographic data on the complex of bovine alpha-chymotrypsin with the recombinant proteinase inhibitor eglin c from Hirudo medicinalis. *Journal of Molecular Biology*, **1989**, 208, 511-3	6.5	5
60	Crystallographic data for horse heart ferritin. *FEBS Letters*, **1984**, 165, 63-66	3.8	5
59	Structural and functional properties of Antarctic fish cytoglobins-1: Cold-reactivity in multi-ligand reactions. *Computational and Structural Biotechnology Journal*, **2020**, 18, 2132-2144	6.8	5
58	Structural Bases for the Recognition of Inhibitors by Serine Proteinases and their Zymogens **1987**, 81-100		5
57	Designing Probes for Immunodiagnostics: Structural Insights into an Epitope Targeting Burkholderia Infections. *ACS Infectious Diseases*, **2017**, 3, 736-743	5.5	4
56	Why is a protective antigen protective?. *Hum Vaccin*, **2009**, 5, 872-5		4
55	High resolution crystal structures of the Cerebratulus lacteus mini-Hb in the unligated and carbomonoxy states. *International Journal of Molecular Sciences*, **2012**, 13, 8025-37	6.3	4
54	pH dependence of bovine mast cell tryptase catalytic activity and of its inhibition by 4',6-diamidino-2-phenylindole. *FEBS Letters*, **1997**, 408, 85-8	3.8	4

53	SseA, a 3-mercaptopyruvate sulfurtransferase from Escherichia coli: crystallization and preliminary crystallographic data. *Acta Crystallographica Section D: Biological Crystallography*, **2003**, 59, 168-70		4
52	Active site titration of bovine beta-trypsin by N alpha-(N,N-dimethylcarbamoyl)-alpha-aza-lysine p-nitrophenyl ester: kinetic and crystallographic analysis. *FEBS Letters*, **1995**, 358, 53-6	3.8	4
51	Crystallization of NAD+ synthetase from Bacillus subtilis. *Proteins: Structure, Function and Bioinformatics*, **1996**, 26, 236-8	4.2	4
50	Crystal structure and NMR investigation of the serine proteinase inhibitor MR889, a cyclic thiolic compound. *Journal of the Chemical Society Perkin Transactions II*, **1993**, 2253		4
49	Binding of the recombinant proteinase inhibitor eglin c, of the soybean Bowman-Birk proteinase inhibitor and of its chymotrypsin and trypsin inhibiting fragments to Leu-proteinase, the leucine specific serine proteinase from spinach (Spinacia oleracea L.) leaves: thermodynamic study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1991**, 4, 283-8		4
48	Modelling by homology of RNA binding domain. *Molecular Biology Reports*, **1990**, 14, 87-8	2.8	4
47	Binding of the soybean Bowman-Birk proteinase inhibitor and of its chymotrypsin and trypsin inhibiting fragments to bovine alpha-chymotrypsin and bovine beta-trypsin. A thermodynamic study. *Journal of Molecular Recognition*, **1990**, 3, 192-6	2.6	4
46	Crystallization and preliminary data for the ferric form of Lucina pectinata hemoglobin I. *Journal of Molecular Biology*, **1991**, 222, 447-9	6.5	4
45	Benzamidine as a spectroscopic probe for the primary specificity subsite of trypsin-like serine proteinases. A case for BPTI binding to bovine beta-trypsin. *Molecular and Cellular Biochemistry*, **1984**, 64, 139-44	4.2	4
44	Preliminary crystallographic data for the structure of the complex between Kazal trypsin inhibitor and trypsinogen. *Journal of Molecular Biology*, **1981**, 145, 603-5	6.5	4
43	Redefining the PF06864 Pfam family based on Burkholderia pseudomallei PilO2(Bp) S-SAD crystal structure. *PLoS ONE*, **2014**, 9, e94981	3.7	4
42	Structural and Functional Characterization of the Globin-Coupled Sensors of and. *Antioxidants and Redox Signaling*, **2020**, 32, 378-395	8.4	4
41	Mycobacterial and Human Ferrous Nitrobindins: Spectroscopic and Reactivity Properties. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	4
40	Preliminary characterization of two different crystal forms of acylphosphatase from the hyperthermophile archaeon Sulfolobus solfataricus. *Acta Crystallographica Section F: Structural Biology Communications*, **2005**, 61, 144-6		3
39	Serine proteinase inhibition by the active site titrant N alpha-(N, N-dimethylcarbamoyl)-alpha-azaornithine p-nitrophenyl ester. A comparative study. *FEBS Journal*, **2000**, 267, 1239-46		3
38	Selective oxidation of methionyl residues in the human recombinant secretory leukocyte proteinase inhibitor. Effect on the inhibitor binding properties. *Journal of Molecular Recognition*, **1994**, 7, 31-7	2.6	3
37	Structural study and preliminary crystallographic data for the hemoglobin from reindeer (Rangifer tarandus tarandus). *Biochemical and Biophysical Research Communications*, **1992**, 187, 1063-70	3.4	3
36	Inhibition of serine proteinases by p-carbethoxyphenyl esters of epsilon-guanidino- and epsilon-amino caproic acid: thermodynamic and molecular modeling study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1989**, 2, 249-59		3

35	Binding of the bovine and porcine pancreatic secretory trypsin inhibitor (Kazal) to human leukocyte elastase: a thermodynamic study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1991**, 5, 207-13		3
34	Embelin as Lead Compound for New Neuroserpin Polymerization Inhibitors. *Life*, **2020**, 10,	3	3
33	High-Light versus Low-Light: Effects on Paired Photosystem II Supercomplex Structural Rearrangement in Pea Plants. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	3
32	Cryo-EM Structures of Azospirillum brasilense Glutamate Synthase in Its Oligomeric Assemblies. *Journal of Molecular Biology*, **2019**, 431, 4523-4526	6.5	2
31	Functional and structural analysis of trehalose-6-phosphate phosphatase from Burkholderia pseudomallei: Insights into the catalytic mechanism. *Biochemical and Biophysical Research Communications*, **2020**, 523, 979-984	3.4	2
30	Modulating the cardiotoxic behaviour of immunoglobulin light chain dimers through point mutations. *Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis*, **2019**, 26, 105-106	2.7	2
29	The concurrency of several biophysical traits links immunoglobulin light chains with toxicity in AL amyloidosis. *Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis*, **2019**, 26, 107-108	2.7	2
28	Structural Bases for the Regulation of CO Binding in the Archaeal Protoglobin from Methanosarcina acetivorans. *PLoS ONE*, **2015**, 10, e0125959	3.7	2
27	Structural plasticity in the eight-helix fold of a trematode haemoglobin. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 719-22		2
26	Time-resolved X-ray crystallography: uncovering reaction intermediates in biochemical processes. *Biochemistry and Molecular Biology Education*, **2001**, 29, 31-32	1.3	2
25	Human rhinovirus 3C protease: a cysteine protease showing the trypsin(ogen)-like fold. *Biochemistry and Molecular Biology Education*, **2001**, 29, 169-172	1.3	2
24	Crystallization and preliminary crystallographic investigations of rhodanese from Azotobacter vinelandii. *Acta Crystallographica Section D: Biological Crystallography*, **1999**, 55, 1471-3		2
23	Effect of aromatic isothiocyanates on the functional properties of human hemoglobin. Role of the stereochemistry of the charged group. *Biophysical Chemistry*, **1990**, 37, 293-302	3.5	2
22	Thermodynamic modeling of internal equilibria involved in the activation of trypsinogen. *Journal of Biomolecular Structure and Dynamics*, **1990**, 7, 959-72	3.6	2
21	Binding of the bovine basic pancreatic trypsin inhibitor (Kunitz) to the 33,000 Mr and 54,000 Mr species of human urokinase: thermodynamic study. *Journal of Enzyme Inhibition and Medicinal Chemistry*, **1990**, 4, 51-5		2
20	Structural Consensus Rules for Cysteine Protease Inhibition by NO(-Donors). *Current Enzyme Inhibition*, **2005**, 1, 231-238	0.5	2
19	Cryo-EM structure of cardiac amyloid fibrils from an immunoglobulin light chain (AL) amyloidosis patient		2
18	Role of the Primary Specificity Subsite on the Interaction between Serine Proteinases and Low Molecular Weight Substrates and Inhibitors **1987**, 101-115		2

17	An Asp to Asn mutation is a toxic trigger in beta-2 microglobulin: structure and biophysics. *Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis*, **2017**, 24, 15-16	2.7	1
16	Structural Vaccinology for Melioidosis Vaccine Design and Immunodiagnostics. *Current Tropical Medicine Reports*, **2017**, 4, 103-110	5	1
15	One hundred years of X-ray diffraction, 50 years of structural biology. *Rendiconti Lincei*, **2013**, 24, 93-99	1.7	1
14	Time-resolved X-ray crystallography: uncovering reaction intermediates in biochemical processes. *Biochemistry and Molecular Biology Education*, **2001**, 29, 31-32	1.3	1
13	Truncated hemoglobins: trimming the classical ’three-over-three’ globin fold to a minimal size. *Biochemistry and Molecular Biology Education*, **2001**, 29, 123-125	1.3	1
12	Crystals of GlpE, a 12 kDa sulfurtransferase from escherichia coli, display 1.06 A resolution diffraction: a preliminary report. *Acta Crystallographica Section D: Biological Crystallography*, **2000**, 56, 1691-3		1
11	Binding of native and [homoserine lactone-52]-52,53-seco-bovine basic pancreatic trypsin inhibitor (Kunitz inhibitor) to porcine pancreatic beta-kallikrein-B and bovine alpha-chymotrypsin: thermodynamic study. *Journal of Molecular Recognition*, **1994**, 7, 39-46	2.6	1
10	Crystallization and preliminary X-ray analysis of pyruvate kinase type I from Escherichia coli. *Acta Crystallographica Section D: Biological Crystallography*, **1995**, 51, 1089-91		1
9	Truncated (2/2) hemoglobin: Unconventional structures and functional roles in vivo and in human pathogenesis. *Molecular Aspects of Medicine*, **2021**, 101049	16.7	1
8	Detecting the nature and solving the crystal structure of a contaminant protein from an opportunistic pathogen. *Acta Crystallographica Section F, Structural Biology Communications*, **2020**, 76, 392-397	1.1	1
7	Aplysia limacina Myoglobin: Molecular Bases for Ligand Binding **1991**, 161-170		1
6	Backbone and side-chain (1)H, (15)N, (13)C assignment and secondary structure of BPSL1445 from Burkholderia pseudomallei. *Biomolecular NMR Assignments*, **2015**, 9, 347-50	0.7	0
5	Thrombin inhibition by the highly selective ’reversible suicide substrate’ N-ethoxycarbonyl-D-phenylalanyl-L-prolyl-alpha-azalysine p-nitrophenyl ester. *Protein and Peptide Letters*, **2005**, 12, 433-8	1.9	
4	Human rhinovirus 3C protease: a cysteine protease showing the trypsin(ogen)-like fold. *Biochemistry and Molecular Biology Education*, **2001**, 29, 169-172	1.3	
3	Intramolecular interactions in macromolecules with functionally-linked heterotropic sites. *Biochemical Education*, **1990**, 18, 14-15		
2	A Crystallographer’s Perspective on the 2/2Hb Family **2008**, 17-30		
1	Synchrotron Radiation and Bio-crystallography **2015**, 615-639		