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871	Combining evolutionary information and neural networks to predict protein secondary structure. 1994 , 19, 55-72		1319
870	Proteinotopic feature maps. 1994 , 6, 443-454		122
869	Expression of an olfactory receptor in Escherichia coli: purification, reconstitution, and ligand binding. 1996 , 35, 16077-84		156
868	A comparison of structural relationships among alpha-crystallin, human Hsp27, gamma-crystallins and beta B2-crystallin. <i>International Journal of Biological Macromolecules</i> , 1996 , 19, 227-33	7.9	16
867	Evaluation of the secondary structure of vaccinia-virus thymidine kinase by circular-dichroism spectroscopy of overlapping synthetic peptides. 1996 , 241, 126-32		1
866	Structural comparison of the precursor and the mature form of napin, the 2S storage protein in Brassica napus. 1996 , 242, 214-9		18
865	Determination of Protein Secondary Structure. 1996 , 69-107		160
864	Intrinsic fluorescence properties and structural analysis of p13(suc1) from Schizosaccharomyces pombe. 1996 , 271, 27249-58		10
863	Primary structure and catalytic mechanism of the epoxide hydrolase from Agrobacterium radiobacter AD1. 1997 , 272, 14650-7		134
862	Cooperativity and dimerization of recombinant human estrogen receptor hormone-binding domain. 1997 , 272, 4843-9		42
861	Modular structure of the trigger factor required for high activity in protein folding. 1997 , 271, 827-37		79
860	The N tails of histones H3 and H4 adopt a highly structured conformation in the nucleosome. 1997 , 273, 503-8		74
859	Effects of temperature and concentration on bovine lens alpha-crystallin secondary structure: a circular dichroism spectroscopic study. <i>International Journal of Biological Macromolecules</i> , 1997 , 20, 283-319		27
858	Overexpression of a glutamate receptor (GluR2) ligand binding domain in Escherichia coli: application of a novel protein folding screen. 1997 , 94, 13431-6		145
857	Subunit c from the sodium-ion-translocating F1F0-ATPase of Propionigenium modestum--production, purification and properties of the protein in dodecylsulfate solution. 1997 , 247, 820-5		22
856	Monofunctional domains of formiminotransferase-cyclodeaminase retain similar conformational stabilities outside the bifunctional octamer. 1997 , 1338, 223-32		2

855	Conformational study of the preferred conformations of the peptide sequence VP3(110-121) of HAV by circular dichroism and molecular mechanics. 1997 , 4, 13-19		1
854	Flexible glycine rich motif of Escherichia coli deoxyuridine triphosphate nucleotidohydrolase is important for functional but not for structural integrity of the enzyme. 1997 , 28, 568-579		47
853	A new approach to secondary structure evaluation: secondary structure prediction of porcine adenylate kinase and yeast guanylate kinase by CD spectroscopy of overlapping synthetic peptide segments. 1997 , 41, 213-31		11
852	Protein domains and conformational changes in the activation of RepA, a DNA replication initiator. 1998 , 17, 4511-26		56
851	Non-homology knowledge-based prediction of the papain prosegment folding pattern: a description of plausible folding and activation mechanisms. 1998 , 3, 271-84		6
850	Conformational behavior of the HAV-VP3(110-121) peptidic sequence and synthetic analogs in membrane environments studied by CD and computational methods. 1998 , 45, 479-92		19
849	Enhanced antigenicity of a four-contact-residue epitope of the measles virus hemagglutinin protein by phage display libraries: evidence of a helical structure in the putative active site. 1998 , 35, 435-43		20
848	Refinement of 3D structure of bovine lens alpha A-crystallin. <i>International Journal of Biological Macromolecules</i> , 1998 , 22, 175-85	7.9	23
847	Interaction of DNA with bovine lens alpha-crystallin: its functional implications. <i>International Journal of Biological Macromolecules</i> , 1998 , 22, 315-20	7.9	10
846	UV resonance Raman-selective amide vibrational enhancement: quantitative methodology for determining protein secondary structure. 1998 , 37, 2854-64		254
845	Stabilization of alpha-synuclein secondary structure upon binding to synthetic membranes. 1998 , 273, 9443-9		1165
844	Secondary Structure and Stability of Marsh Grapefruit Thermolabile Pectinesterase. 1998 , 46, 3480-3483		2
843	Structural studies of synthetic peptide fragments derived from the HIV-1 Vpr protein. 1998 , 244, 732-6		22
842	Isolation and physical characterization of random insertions in Staphylococcal nuclease. 1998 , 282, 751-9		11
841	Self-organizing neural networks bridge the biomolecular resolution gap. 1998 , 284, 1247-54		71
840	Structural and functional properties of two mutants of lecithin-cholesterol acyltransferase (T123I and N228K). 1998 , 273, 32561-7		23
839	pH-induced conformational transitions of the propeptide of human cathepsin L. A role for a molten globule state in zymogen activation. 1998 , 273, 11498-504		80
838	Secondary structure composition and pH-dependent conformational changes of soluble recombinant HLA-DM. 1998 , 273, 27557-64		37

837	Determination of Protein Concentration from CD Spectrum. 1998 , 31, 1825-1835	
836	Divalent cations can induce the exposure of GroEL hydrophobic surfaces and strengthen GroEL hydrophobic binding interactions. Novel effects of Zn ²⁺ GroEL interactions. 1998 , 273, 3257-63	33
835	Structural requirements for the cytotoxicity of the N-terminal region of HIV type 1 Nef. 1998 , 14, 1543-51	5
834	Sequence and structural relationships of leucocins A-, B- and C-TA33a from <i>Leuconostoc mesenteroides</i> TA33a. 1998 , 144 (Pt 5), 1343-1348	47
833	Secondary structure of bacteriorhodopsin fragments. External sequence constraints specify the conformation of transmembrane helices. 1998 , 273, 28822-30	28
832	The cation-binding domain from the alpha subunit of integrin alpha5 beta1 is a minimal domain for fibronectin recognition. 1998 , 273, 24744-53	32
831	Assembly of a ternary complex by the predicted minimal coiled-coil-forming domains of syntaxin, SNAP-25, and synaptobrevin. A circular dichroism study. 1998 , 273, 34214-21	23
830	Salt-resistant alpha-helical cationic antimicrobial peptides. 1999 , 43, 1542-8	168
829	Role of a conserved acidic cluster in bovine beta1,4 galactosyltransferase-1 probed by mutagenesis of a bacterially expressed recombinant enzyme. 1999 , 9, 815-22	23
828	Engineering and Chemical Synthesis of a Transmembrane Protein: The HCV Protease Cofactor Protein NS4A. 1999 , 121, 7698-7699	37
827	Phosphoinositide-AP-2 interactions required for targeting to plasma membrane clathrin-coated pits. 1999 , 146, 755-64	246
826	Stability and DNA binding of the phd protein of the phage P1 plasmid addiction system. 1999 , 274, 2652-7	57
825	Proteolytic dissection of Zab, the Z-DNA-binding domain of human ADAR1. 1999 , 274, 2899-906	46
824	Biophysical and functional characterization of full-length, recombinant human tissue inhibitor of metalloproteinases-2 (TIMP-2) produced in <i>Escherichia coli</i> . Comparison of wild type and amino-terminal alanine appended variant with implications for the mechanism of TIMP functions. 1999 , 274, 21362-8	85
823	The progressive development of structure and stability during the equilibrium folding of the alpha subunit of tryptophan synthase from <i>Escherichia coli</i> . <i>Protein Science</i> , 1999 , 8, 1623-35	6.3 72
822	The prolyl aminopeptidase from <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> belongs to the alpha/beta hydrolase fold family. 1999 , 1429, 501-5	16
821	The structure of human parathyroid hormone-related protein(1-34) in near-physiological solution. 1999 , 444, 239-44	23
820	Structural features and assembly of the soluble overexpressed PsaD subunit of photosystem I. 1999 , 1410, 7-18	11

819	Auto-inactivation by cleavage within the dimer interface of Kaposi's sarcoma-associated herpesvirus protease. 1999 , 289, 197-203	24
818	Bacterial expression and characterization of the ligand-binding domain of the vitamin D receptor. <i>Archives of Biochemistry and Biophysics</i> , 1999 , 364, 42-52	4.1 13
817	Carboxyl-terminal fragment of Alzheimer's APP destabilizes calcium homeostasis and renders neuronal cells vulnerable to excitotoxicity. 2000 , 14, 1508-1517	67
816	The position of the LysN epsilon H2-grafted antigens along the sequential oligopeptide carrier, Ac-(Aib-Lys-Aib-Gly) _n (SOCn-II), influences the antibody recognition: application to the Sm main autoimmune epitope. 2000 , 54, 1-10	9
815	Estimation of protein secondary structure from circular dichroism spectra: inclusion of denatured proteins with native proteins in the analysis. 2000 , 287, 243-51	480
814	Estimation of protein secondary structure from circular dichroism spectra: comparison of CONTIN, SELCON, and CDSSTR methods with an expanded reference set. 2000 , 287, 252-60	2387
813	The role of amino-acid residues in the hydrophobic patch surrounding the haem group of cytochrome f in the interaction with plastocyanin. 2000 , 267, 1732-42	15
812	The role of individual lysine residues in the basic patch on turnip cytochrome f for electrostatic interactions with plastocyanin in vitro. 2000 , 267, 3461-8	34
811	High Level Production, Characterization and Construct Optimization of the Ionotropic Glutamate Receptor Ligand Binding Core. 2000 , 56, 9409-9419	4
810	Engineering a compact non-native state of intestinal fatty acid-binding protein. 2000 , 1476, 203-18	18
809	On the domain structure and the polymerization state of the sendai virus P protein. 2000 , 266, 99-109	79
808	Analysis of the interaction between the HIV-inactivating protein cyanovirin-N and soluble forms of the envelope glycoproteins gp120 and gp41. 2000 , 58, 982-92	62
807	Conformational lability of herpesvirus protein VP22. 2000 , 275, 33213-21	33
806	Physical characterization of the procollagen module of human thrombospondin 1 expressed in insect cells. 2000 , 275, 40938-45	38
805	Copper(II)-induced conformational changes and protease resistance in recombinant and cellular PrP. Effect of protein age and deamidation. 2000 , 275, 19121-31	126
804	Imaging DNA loops induced by restriction endonuclease EcoRII. A single amino acid substitution uncouples target recognition from cooperative DNA interaction and cleavage. 2000 , 275, 30631-7	22
803	A minimized human integrin alpha(5)beta(1) that retains ligand recognition. 2000 , 275, 5888-903	41
802	Characterization of the N-terminal domain of the yeast transcriptional repressor Tup1. Proposal for an association model of the repressor complex Tup1 x Ssn6. 2000 , 275, 9011-8	32

801	Bivalent sequential binding model of a <i>Bacillus thuringiensis</i> toxin to gypsy moth aminopeptidase N receptor. 2000 , 275, 14423-31		102
800	Interfacial asparagine residues within an amide tetrad contribute to Max helix-loop-helix leucine zipper homodimer stability. 2000 , 275, 37454-61		8
799	Equilibrium and kinetic binding interactions between DNA and a group of novel, nonspecific DNA-binding proteins from spores of <i>Bacillus</i> and <i>Clostridium</i> species. 2000 , 275, 35040-50		17
798	3-Methyladenine-DNA glycosylase I from <i>Escherichia coli</i> -computer modeling and supporting experimental evidence. 2000 , 268, 724-7		1
797	Characterization of a recombinant murine 18.5-kDa myelin basic protein. <i>Protein Expression and Purification</i> , 2000 , 20, 285-99	2	66
796	Salt dependent stability and unfolding of [Fe ₂ -S ₂] ferredoxin of <i>Halobacterium salinarum</i> : spectroscopic investigations. 2000 , 79, 501-10		17
795	Inhibition of collagenase by Cr(III): its relevance to stabilization of collagen. 2000 , 1524, 228-37		12
794	Requirement of the hinge domain for dimerization of Ca ²⁺ -ATPase large cytoplasmic portion expressed in bacteria. 2000 , 1467, 73-84		7
793	Consequences of cAMP-binding site mutations on the structural stability of the type I regulatory subunit of cAMP-dependent protein kinase. 2000 , 39, 15022-31		29
792	Glutathione S-transferase P1-1 (GSTP1-1) inhibits c-Jun N-terminal kinase (JNK1) signaling through interaction with the C terminus. 2001 , 276, 20999-1003		237
791	Structural and functional stability of the mature transferrin receptor from human placenta. <i>Archives of Biochemistry and Biophysics</i> , 2001 , 386, 79-88	4.1	13
790	Structural consequences of divalent metal binding by the adenyl cyclase toxin of <i>Bordetella pertussis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2001 , 395, 169-76	4.1	25
789	Involvement of a lysine residue in the active site of a thermostable xylanase from <i>Thermomonospora</i> sp. 2001 , 282, 48-54		16
788	Novel bifunctional alkaline protease inhibitor: protease inhibitory activity as the biochemical basis of antifungal activity. 2001 , 285, 1018-24		11
787	Divide-and-conquer crystallographic approach towards an atomic structure of intermediate filaments. 2001 , 306, 773-81		111
786	Biochemical characterization of the structure-specific DNA-binding protein Cmb1 from <i>Schizosaccharomyces pombe</i> . 2001 , 309, 1101-15		5
785	Functional determinants of the Epstein-Barr virus protease. 2001 , 311, 217-28		21
784	Redox-regulated chaperone function and conformational changes of <i>Escherichia coli</i> Hsp33. 2001 , 489, 19-24		26

783	The role of a proline-induced broken-helix motif in alpha-helix 2 of <i>Bacillus thuringiensis</i> delta-endotoxins. 2001 , 490, 70-4	19
782	Alzheimer β disease amyloid-beta binds copper and zinc to generate an allosterically ordered membrane-penetrating structure containing superoxide dismutase-like subunits. 2001 , 276, 20466-73	53 ^o
781	Interactions between mastoparan B and the membrane studied by ¹ H NMR spectroscopy. 2001 , 18, 595-606	14
78 ^o	Coactosin-like protein, a human F-actin-binding protein: critical role of lysine-75. <i>Biochemical Journal</i> , 2001 , 359, 255-63	3.8 40
779	Structural and functional properties of <i>Escherichia coli</i> -derived nucleoplasmin. 2001 , 268, 1739-1748	24
778	Artificial chaperone mediated refolding of xylanase from an alkalophilic thermophilic <i>Bacillus</i> sp. Implications for in vitro protein renaturation via a folding intermediate. 2001 , 268, 5471-8	39
777	Differences in secondary structure of HAV-synthetic peptides induced by the sequential order of T- and B-cell epitopes. 2001 , 58, 117-28	7
776	SOMCD: method for evaluating protein secondary structure from UV circular dichroism spectra. 2001 , 42, 460-70	71
775	Quantitation of pulmonary surfactant protein SP-B in the absence or presence of phospholipids by enzyme-linked immunosorbent assay. 2001 , 293, 78-87	5
774	Combined results from solution studies on intact influenza virus M1 protein and from a new crystal form of its N-terminal domain show that M1 is an elongated monomer. 2001 , 279, 439-46	101
773	Membrane activity of the southern cowpea mosaic virus coat protein: the role of basic amino acids, helix-forming potential, and lipid composition. 2001 , 291, 299-310	9
772	Thermal stability and enzymatic activity of a smaller lysozyme from silk moth (<i>Bombyx mori</i>). 2001 , 20, 107-13	10
771	All-D-cecropin B: synthesis, conformation, lipopolysaccharide binding, and antibacterial activity. 2001 , 218, 105-11	31
77 ^o	N-terminal amino acid residues mediate protein-protein interactions between DNA-bound alpha /beta -type small, acid-soluble spore proteins from <i>Bacillus</i> species. 2001 , 276, 2267-75	16
769	Disulfide connectivity of recombinant C-terminal region of human thrombospondin 2. 2001 , 276, 45882-7	23
768	Specificity and mechanism of metal ion activation in UDP-galactose:beta -galactoside-alpha -1,3-galactosyltransferase. 2001 , 276, 11567-74	43
767	Interactions of a novel inhibitor from an extremophilic <i>Bacillus</i> sp. with HIV-1 protease: implications for the mechanism of inactivation. 2001 , 276, 2487-93	17
766	5-Lipoxygenase interacts with coactosin-like protein. 2001 , 276, 16520-7	76

765	Design and properties of N(CCG)-gp41, a chimeric gp41 molecule with nanomolar HIV fusion inhibitory activity. 2001 , 276, 29485-9		80
764	Substrate recognition by the collagen-binding domain of Clostridium histolyticum class I collagenase. 2001 , 276, 8761-70		91
763	Truncated aspartate aminotransferase from alkalophilic Bacillus circulans with deletion of N-terminal 32 amino acids is a non-functional monomer in a partially structured state. <i>Protein Engineering, Design and Selection</i> , 2001 , 14, 279-85	1.9	8
762	Novel bifunctional inhibitor of xylanase and aspartic protease: implications for inhibition of fungal growth. 2001 , 45, 2008-17		24
761	Evaluation of a structural model of Pseudomonas aeruginosa outer membrane protein OprM, an efflux component involved in intrinsic antibiotic resistance. <i>Journal of Bacteriology</i> , 2001 , 183, 367-74	3.5	57
760	Phe71 is essential for chaperone-like function in alpha A-crystallin. 2001 , 276, 47094-9		47
759	S179D-human PRL, a pseudophosphorylated human PRL analog, is an agonist and not an antagonist. 2001 , 142, 3950-63		35
758	Structural and functional variation within the alanine-rich repetitive domain of streptococcal antigen I/II. <i>Infection and Immunity</i> , 2002 , 70, 6389-98	3.7	18
757	Partially folded structure of flavin adenine dinucleotide-depleted ferredoxin-NADP+ reductase with residual NADP+ binding domain. 2002 , 277, 17101-7		15
756	Role of tryptophan residues in interfacial binding of phosphatidylinositol-specific phospholipase C. 2002 , 277, 19867-75		44
755	Replacement of trifluoroacetic acid with HCl in the hydrophobic purification steps of pediocin PA-1: a structural effect. 2002 , 68, 4803-8		78
754	Cytotoxic potency of cardiotoxin from Naja sputatrix: development of a new cytolytic assay. <i>Biochemical Journal</i> , 2002 , 366, 35-43	3.8	30
753	Methods for preparation of recombinant cytokine proteins V. mutant analogues of human interferon-gamma with higher stability and activity. <i>Protein Expression and Purification</i> , 2002 , 24, 173-80 ²		7
752	A modular assembly strategy for improving the substrate specificity of small catalytic peptides. 2002 , 124, 3510-1		34
751	A multitechnique approach in protein/surfactant interaction study: physicochemical aspects of sodium dodecyl sulfate in the presence of trypsin in aqueous medium. 2002 , 3, 9-16		110
750	Expression, purification, and characterization of subunit E, an essential subunit of the vacuolar ATPase. 2002 , 298, 383-91		65
749	Structural Modelling of the Sm-like Protein Hfq from Escherichia coli. 2002 , 320, 705-12		50
748	Recombinant human insulin IX. Investigation of factors, influencing the folding of fusion protein-S-sulfonates, biotechnological precursors of human insulin. <i>Protein Expression and Purification</i> , 2002 , 26, 187-93	2	10

747	Characterization of antimalarial SPf66 peptide using MALDI-TOF MS, CD and SEC. 2002 , 23, 1527-35		2
746	Interaction between Btk TH and SH3 domain. 2002 , 63, 325-34		14
745	Transient vesicle leakage initiated by a synthetic apoptotic peptide derived from the death domain of neurotrophin receptor, p75NTR. 2002 , 59, 149-58		15
744	The unique sites in Sula protein preferentially cleaved by ATP-dependent Lon protease from <i>Escherichia coli</i> . 2002 , 269, 451-7		27
743	A novel localized amyloidosis associated with lactoferrin in the cornea. 2002 , 82, 757-66		29
742	Synthesis and conformational studies of a transmembrane domain from a diverged microsomal Delta(12)-desaturase. 2002 , 308, 134-40		10
741	Effect of trifluoroethanol on the structural and functional properties of alpha-crystallin. 2002 , 21, 87-95		8
740	Characterization of Ad5 E3-14.7K, an adenoviral inhibitor of apoptosis: structure, oligomeric state, and metal binding. <i>Protein Science</i> , 2002 , 11, 1117-28	6.3	11
739	Erythroid spectrin in micellar detergents. 2003 , 54, 16-28		25
738	Expression, purification and spectroscopic studies of full-length Kir3.1 channel C-terminus. 2003 , 1652, 83-90		3
737	Interaction of an anionic surfactant with a recombinant cutinase from <i>Fusarium solani pisi</i> : a spectroscopic study. 2003 , 32, 868-879		19
736	Monosaccharide composition and properties of a deglycosylated turnip peroxidase isozyme. 2003 , 62, 5-11		16
735	Role of the hinge peptide and the intersubunit interface in the swapping of N-termini in dimeric bovine seminal RNase. 2003 , 270, 4729-35		15
734	The major peanut allergen, Ara h 2, functions as a trypsin inhibitor, and roasting enhances this function. 2003 , 112, 190-5		172
733	Analyses of circular dichroism spectra of membrane proteins. <i>Protein Science</i> , 2003 , 12, 875-84	6.3	138
732	Structure, activity, and distribution of fish osteocalcin. 2003 , 278, 11843-8		41
731	The binding of maize DHN1 to lipid vesicles. Gain of structure and lipid specificity. 2003 , 131, 309-16		276
730	Effect of naturally occurring mutations in human glycine N-methyltransferase on activity and conformation. 2003 , 312, 1067-72		15

729	Folding of DsbB in mixed micelles: a kinetic analysis of the stability of a bacterial membrane protein. 2003 , 330, 641-9	96
728	Biochemical analysis of hyalin gelation: an essential step in the assembly of the sea urchin extraembryonic matrix, the hyaline layer. <i>Archives of Biochemistry and Biophysics</i> , 2003 , 414, 279-86	4-1 3
727	Water-miscible organic cosolvents enhance phosphatidylinositol-specific phospholipase C phosphotransferase as well as phosphodiesterase activity. 2003 , 1613, 15-27	16
726	Glycation induces formation of amyloid cross-beta structure in albumin. 2003 , 278, 41810-9	210
725	Apoptin induces tumor-specific apoptosis as a globular multimer. 2003 , 278, 9042-51	50
724	Inactivation and conformational changes of creatine kinase at low concentrations of hexafluoroisopropanol solutions. 2003 , 81, 327-33	3
723	dUTPase and nucleocapsid polypeptides of the Mason-Pfizer monkey virus form a fusion protein in the virion with homotrimeric organization and low catalytic efficiency. 2003 , 278, 38803-12	18
722	NMR-detected hydrogen exchange and molecular dynamics simulations provide structural insight into fibril formation of prion protein fragment 106-126. 2003 , 100, 14790-5	123
721	Catalytic and thermodynamic properties of tetrahydromethanopterin-dependent serine hydroxymethyltransferase from <i>Methanococcus jannaschii</i> . 2003 , 278, 41789-97	25
720	Binding of the anticonvulsant drug lamotrigine and the neurotoxin batrachotoxin to voltage-gated sodium channels induces conformational changes associated with block and steady-state activation. 2003 , 278, 10675-82	35
719	Optimizing the interfacial binding and activity of a bacterial phosphatidylinositol-specific phospholipase C. 2003 , 278, 24651-7	18
718	Asp274 and his346 are essential for heme binding and catalytic function of human indoleamine 2,3-dioxygenase. 2003 , 278, 29525-31	58
717	Delineation of the hydroxyapatite-nucleating domains of bone sialoprotein. 2003 , 278, 7949-55	159
716	Identification, purification, and characterization of an eukaryotic-like phosphopantetheine adenylyltransferase (coenzyme A biosynthetic pathway) in the hyperthermophilic archaeon <i>Pyrococcus abyssi</i> . 2003 , 278, 31078-87	26
715	Effects of various forms of surfactant protein C on tidal volume in ventilated immature newborn rabbits. 2003 , 94, 1519-26	1
714	Association of villin with phosphatidylinositol 4,5-bisphosphate regulates the actin cytoskeleton. 2004 , 279, 3096-110	63
713	Modulating calcitonin fibrillogenesis: an antiparallel alpha-helical dimer inhibits fibrillation of salmon calcitonin. 2004 , 279, 6364-70	18
712	Estimation of protein secondary structure from synchrotron radiation circular dichroism spectra. 2004 , 2004, 2893-6	

711	Conformation of membrane-associated proapoptotic tBid. 2004 , 279, 28954-60	47
710	Herpesvirus protease inhibition by dimer disruption. 2004 , 78, 6657-65	47
709	Saccharomyces cerevisiae Hop1 zinc finger motif is the minimal region required for its function in vitro. 2004 , 279, 28961-9	11
708	Ataxin-10, the spinocerebellar ataxia type 10 neurodegenerative disorder protein, is essential for survival of cerebellar neurons. 2004 , 279, 35542-50	48
707	A molecular handoff between bacteriophage T7 DNA primase and T7 DNA polymerase initiates DNA synthesis. 2004 , 279, 30554-62	33
706	Identification and biochemical characterization of two novel collagen binding MSCRAMMs of Bacillus anthracis. 2004 , 279, 51760-8	40
705	Probing solvent accessibility of transthyretin amyloid by solution NMR spectroscopy. 2004 , 279, 5699-707	90
704	Cns1 is an activator of the Ssa1 ATPase activity. 2004 , 279, 23267-73	42
703	Building the stator of the yeast vacuolar-ATPase: specific interaction between subunits E and G. 2004 , 279, 40670-6	42
702	Altered active site flexibility and a structural metal-binding site in eukaryotic dUTPase: kinetic characterization, folding, and crystallographic studies of the homotrimeric Drosophila enzyme. 2004 , 279, 17932-44	36
701	The optimization of protein secondary structure determination with infrared and circular dichroism spectra. 2004 , 271, 2937-48	137
700	Folding of epidermal growth factor-like repeats from human tenascin studied through a sequence frame-shift approach. 2004 , 271, 4229-40	4
699	Alpha-helical structure in the C-terminus of vasoactive intestinal peptide: functional and structural consequences. 2004 , 485, 307-16	23
698	Reductive alkylation of lipase: experimental and molecular modeling approaches. 2004 , 118, 11-20	6
697	Analysis of the secondary structure of the cys-less yeast mitochondrial citrate transport protein and four single-cys variants by circular dichroism. 2004 , 36, 429-38	2
696	Human glutaminyl cyclase and bacterial zinc aminopeptidase share a common fold and active site. 2004 , 2, 2	17
695	Bovine serum albumin conformational changes upon adsorption on titania and on hydroxyapatite and their relation with biomineralization. 2004 , 70, 420-7	55
694	Charge-transfer transitions in protein circular dichroism spectra. 2004 , 675, 53-60	24

693	CDtool-an integrated software package for circular dichroism spectroscopic data processing, analysis, and archiving. 2004 , 332, 285-9		210
692	Biophysical characterization of the catalytic domain of guanine nucleotide exchange factor BopE from <i>Burkholderia pseudomallei</i> . 2004 , 1698, 111-9		5
691	Structural analysis of <i>Salmonella enterica</i> effector protein SopD. 2004 , 1698, 219-26		5
690	DICHROWEB, an online server for protein secondary structure analyses from circular dichroism spectroscopic data. 2004 , 32, W668-73		1879
689	Computation and analysis of protein circular dichroism spectra. 2004 , 383, 318-51		380
688	Thermodynamics of ligand binding by the yeast mRNA-capping enzyme reveals different modes of binding. <i>Biochemical Journal</i> , 2004 , 384, 411-20	3.8	12
687	Analysis of circular dichroism data. 2004 , 383, 282-317		87
686	On the analysis of membrane protein circular dichroism spectra. <i>Protein Science</i> , 2004 , 13, 100-12	6.3	188
685	The N-terminal domain (IF2N) of bacterial translation initiation factor IF2 is connected to the conserved C-terminal domains by a flexible linker. <i>Protein Science</i> , 2004 , 13, 230-9	6.3	17
684	A novel 8.7 kDa protease inhibitor from chan seeds (<i>Hyptis suaveolens</i> L.) inhibits proteases from the larger grain borer <i>Prostephanus truncatus</i> (Coleoptera: Bostrichidae). 2004 , 138, 81-9		25
683	Structural analysis of the stalk subunit Vma5p of the yeast V-ATPase in solution. 2004 , 570, 119-25		38
682	The N-terminal rhodanese domain from <i>Azotobacter vinelandii</i> has a stable and folded structure independently of the C-terminal domain. 2004 , 577, 403-8		7
681	Role of hydration in the conformational transitions between unliganded and liganded forms of loop 13 of the Na ⁺ /glucose cotransporter 1. 2004 , 315, 1018-24		1
680	Intracellular domains of the delta-subunits of Torpedo and rat acetylcholine receptors--expression, purification, and characterization. <i>Protein Expression and Purification</i> , 2004 , 38, 237-47	2	10
679	Autoantigenicity of DFS70 is restricted to the conformational epitope of C-terminal alpha-helical domain. 2004 , 23, 221-31		41
678	Multiple forms of equine β -lactalbumin: evidence for N-glycosylated and deamidated forms. 2004 , 14, 207-217		21
677	Features of the plasmid pMV158-encoded MobM, a protein involved in its mobilization. 2004 , 335, 733-43		25
676	Structural determinants of PLD2 inhibition by alpha-synuclein. 2004 , 337, 1001-9		84

675	Binding of phlorizin to the C-terminal loop 13 of the Na(+)/glucose cotransporter does not depend on the [560-608] disulfide bond. <i>Archives of Biochemistry and Biophysics</i> , 2004 , 425, 58-64	4.1	4
674	Heterologous expression and biophysical characterization of soluble oligosaccharyl transferase subunits. <i>Archives of Biochemistry and Biophysics</i> , 2004 , 431, 63-70	4.1	8
673	Structural roles of the active site iron(III) ions in catechol 1,2-dioxygenases and differential secondary structure changes in isoenzymes A and B from <i>Acinetobacter radioresistens</i> S13. <i>Archives of Biochemistry and Biophysics</i> , 2004 , 431, 79-87	4.1	10
672	Raman spectroscopic characterization of secondary structure in natively unfolded proteins: alpha-synuclein. 2004 , 126, 2399-408		338
671	Conformational transitions in beta-lactoglobulin induced by cationic amphiphiles: equilibrium studies. 2004 , 86, 2392-402		120
670	Functional analysis of pyrimidine 5Pnucleotidase mutants causing nonspherocytic hemolytic anemia. 2005 , 105, 3340-5		21
669	Functional domain organization of the potato alpha-glucan, water dikinase (GWD): evidence for separate site catalysis as revealed by limited proteolysis and deletion mutants. <i>Biochemical Journal</i> , 2005 , 385, 355-61	3.8	21
668	Truncated human serum albumin retains general anaesthetic binding activity. <i>Biochemical Journal</i> , 2005 , 388, 39-45	3.8	17
667	Fluorescence probing of albumin-surfactant interaction. 2005 , 285, 562-73		153
666	Thermal denaturation of the BRCT tandem repeat region of human tumour suppressor gene product BRCA1. 2005 , 114, 1-12		8
665	Binding behaviour and conformational properties of globular proteins in the presence of immobilised non-polar ligands used in reversed-phase liquid chromatography. 2005 , 1079, 173-86		14
664	Physicochemical and conformational studies of papain/sodium dodecyl sulfate system in aqueous medium. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2005 , 264, 6-16	5.1	39
663	Conformational study of papain in the presence of sodium dodecyl sulfate in aqueous medium. <i>Colloids and Surfaces B: Biointerfaces</i> , 2005 , 41, 209-16	6	43
662	How to study proteins by circular dichroism. 2005 , 1751, 119-39		2175
661	Structure and possible function of N-glycans of an invertebrate C-type lectin from the acorn barnacle <i>megabalanus rosa</i> . 2005 , 71, 931-940		5
660	Characterization of the secreted chorismate mutase from the pathogen <i>Mycobacterium tuberculosis</i> . 2005 , 272, 375-89		57
659	Mechanism of binding of serum response factor to serum response element. 2005 , 272, 3105-19		8
658	Site-directed mutations (Asp405Ile and Glu124Ile) in cytochrome P450 _{sc} : effect on adrenodoxin binding. 2005 , 95, 720-30		0

657	Secondary structure estimation of recombinant psbH, encoding a photosynthetic membrane protein of cyanobacterium <i>Synechocystis</i> sp. PCC 6803. 2005 , 43, 421-424		1
656	Crystallization and preliminary X-ray characterization of a lectin from <i>Cicer arietinum</i> (chickpea). 2005 , 61, 141-3		12
655	Structure of purine nucleoside phosphorylase (DeoD) from <i>Bacillus anthracis</i> . 2005 , 61, 459-62		13
654	Deciphering structure and topology of conserved COG2042 orphan proteins. 2005 , 5, 3		6
653	Role of trehalose and heat in the structure of the C-terminal activation domain of the heat shock transcription factor. 2005 , 58, 826-35		16
652	A folding inhibitor of the HIV-1 protease. 2006 , 62, 928-33		23
651	Characterization of the multiple transferable resistance repressor, MtrR, from <i>Neisseria gonorrhoeae</i> . <i>Journal of Bacteriology</i> , 2005 , 187, 5008-12	3.5	38
650	Key role of cysteine residues in catalysis and subcellular localization of sulfur oxygenase-reductase of <i>Acidianus tengchongensis</i> . 2005 , 71, 621-8		43
649	Structural and functional analysis of essential pre-mRNA splicing factor Prp19p. 2005 , 25, 451-60		68
648	Characterization of four variant forms of human propionyl-CoA carboxylase expressed in <i>Escherichia coli</i> . 2005 , 280, 27719-27		32
647	The YoeB toxin is a folded protein that forms a physical complex with the unfolded YefM antitoxin. Implications for a structural-based differential stability of toxin-antitoxin systems. 2005 , 280, 30063-72		29
646	Critical assessment of important regions in the subunit association and catalytic action of the severe acute respiratory syndrome coronavirus main protease. 2005 , 280, 22741-8		85
645	Sequence specific peptidomimetic molecules inhibitors of a protein-protein interaction at the helix 1 level of c-Myc. 2005 , 19, 632-4		20
644	Functional analysis of the glycerol-manno-heptose 7-phosphate kinase domain from the bifunctional HldE protein, which is involved in ADP-L-glycerol-D-manno-heptose biosynthesis. <i>Journal of Bacteriology</i> , 2005 , 187, 5292-300	3.5	32
643	Dopamine promotes alpha-synuclein aggregation into SDS-resistant soluble oligomers via a distinct folding pathway. 2005 , 19, 1377-9		217
642	Tyrosine modification is not required for myeloperoxidase-induced loss of apolipoprotein A-I functional activities. 2005 , 280, 33775-84		63
641	NMR Structure Determination of Proteins in Bilayer Lipid Membranes: The FXYD Family Proteins. 2005 , 2, 77-93		2
640	Purification and characterization of a beta-D-mannosidase from the marine anaspidean <i>Aplysia fasciata</i> . 2005 , 119, 26-35		21

639	Chemoenzymatic synthesis of HIV-1 V3 glycopeptides carrying two N-glycans and effects of glycosylation on the peptide domain. 2005 , 70, 9990-6		79
638	Structure and inter-domain interactions of domain II from the blood-stage malarial protein, apical membrane antigen 1. 2005 , 350, 641-56		29
637	The effects of metal ions on the structure and stability of the DNA gyrase B protein. 2005 , 353, 1152-60		23
636	Structural characterization of the fusion core in syncytin, envelope protein of human endogenous retrovirus family W. 2005 , 331, 1193-200		40
635	Expression, purification, and characterization of rat protein tyrosine phosphatase eta catalytic domain. <i>Protein Expression and Purification</i> , 2005 , 41, 113-20	2	6
634	Spectroscopic characterization of the EF-hand domain of phospholipase C delta1: identification of a lipid interacting domain. <i>Archives of Biochemistry and Biophysics</i> , 2005 , 440, 191-203	4.1	11
633	Structural variation in human apolipoprotein E3 and E4: secondary structure, tertiary structure, and size distribution. 2005 , 88, 455-66		47
632	Spectral magnitude effects on the analyses of secondary structure from circular dichroism spectroscopic data. <i>Protein Science</i> , 2005 , 14, 368-74	6.3	48
631	The conformational stability and thermodynamics of Fur A (ferric uptake regulator) from <i>Anabaena</i> sp. PCC 7119. 2005 , 89, 4188-200		10
630	TraA and its N-terminal relaxase domain of the Gram-positive plasmid pIP501 show specific oriT binding and behave as dimers in solution. <i>Biochemical Journal</i> , 2005 , 387, 401-9	3.8	33
629	De novo generation of cationic antimicrobial peptides: influence of length and tryptophan substitution on antimicrobial activity. 2005 , 49, 316-22		192
628	Structural aspects of the <i>Mucor bacilliformis</i> proteinase, a new member of the aspartyl-proteinase family. 2006 , 123, 443-52		11
627	Synchrotron radiation circular dichroism spectroscopy of proteins and applications in structural and functional genomics. 2006 , 35, 39-51		183
626	Peptide Controls on Calcite Mineralization: Polyaspartate Chain Length Affects Growth Kinetics and Acts as a Stereochemical Switch on Morphology. 2006 , 6, 197-201		138
625	Synthesis of a highly pure lipid core peptide based self-adjuvanting triepitopic group A streptococcal vaccine, and subsequent immunological evaluation. 2006 , 49, 6364-70		38
624	Energetics of RNA binding by the West Nile virus RNA triphosphatase. 2006 , 580, 867-77		10
623	Characterization of <i>Saccharomyces cerevisiae</i> Atm1p: functional studies of an ABC7 type transporter. 2006 , 1760, 1857-65		6
622	Apolipoprotein A-I lysine modification: effects on helical content, lipid binding and cholesterol acceptor activity. 2006 , 1761, 64-72		28

621	Solvent-dependent structure of two tryptophan-rich antimicrobial peptides and their analogs studied by FTIR and CD spectroscopy. 2006 , 1758, 1596-608		53
620	Engineering functional artificial hybrid proteins between poplar peroxiredoxin II and glutaredoxin or thioredoxin. 2006 , 341, 1300-8		12
619	Functional insights from the molecular modelling of a novel two-component system. 2006 , 344, 1327-33		14
618	The oxidation state of DJ-1 regulates its chaperone activity toward alpha-synuclein. 2006 , 356, 1036-48		303
617	Mechanism by which the amyloid-like fibrils of a beta 2-microglobulin fragment are induced by fluorine-substituted alcohols. 2006 , 363, 279-88		98
616	Albumin binds self-assembling dyes as specific polymolecular ligands. <i>International Journal of Biological Macromolecules</i> , 2006 , 40, 1-8	7.9	22
615	Evidence for independent mechanisms and a multiple-hit model of tau assembly. 2006 , 339, 858-64		9
614	Expression in <i>Escherichia coli</i> and in vitro refolding of the human protein pLG72. <i>Protein Expression and Purification</i> , 2006 , 46, 150-5	2	35
613	Definition, expression, and characterization of a protein domain in the N-terminus of pregnancy-associated plasma protein-A distantly related to the family of laminin G-like modules. <i>Protein Expression and Purification</i> , 2006 , 48, 261-73	2	13
612	Cloning, expression, purification, and characterization of <i>Vibrio cholerae</i> transcriptional activator, HlyU. <i>Protein Expression and Purification</i> , 2006 , 48, 118-25	2	10
611	Expression in <i>E. coli</i> and purification of the nucleoside diphosphate kinase b from <i>Leishmania major</i> . <i>Protein Expression and Purification</i> , 2006 , 49, 244-50	2	9
610	A conserved tyrosine residue of <i>Saccharomyces cerevisiae</i> leukotriene A4 hydrolase stabilizes the transition state of the peptidase activity. 2006 , 27, 1701-9		10
609	Circular Dichroism in Protein Analysis. 2006 ,		2
608	Functional characterization of the dimerization domain of the ferric uptake regulator (Fur) of <i>Pseudomonas aeruginosa</i> . <i>Biochemical Journal</i> , 2006 , 400, 385-92	3.8	4
607	Circular Dichroism in Analysis of Biomolecules. 2006 ,		1
606	Native-specific stabilization of flavodoxin by the FMN cofactor: structural and thermodynamical explanation. 2006 , 63, 581-94		21
605	Equilibrium heat-induced denaturation of chitinase 40 from <i>Streptomyces thermoviolaceus</i> . 2006 , 64, 513-23		6
604	Biochemical analysis of a Ca ²⁺ -dependent membrane-membrane interaction mediated by the sea urchin yolk granule protein, toposome. 2006 , 48, 401-9		19

603	Using circular dichroism spectra to estimate protein secondary structure. 2006 , 1, 2876-90		2235
602	Expression and physicochemical characterization of an extracellular segment of the receptor protein tyrosine phosphatase IA-2. 2006 , 1764, 174-81		5
601	Circular dichroism studies of subtilisin Carlsberg immobilised on micron sized silica particles. 2006 , 1764, 1119-25		34
600	Hofmeister effects in protein unfolding kinetics: estimation of changes in surface area upon formation of the transition state. 2006 , 1764, 1260-7		11
599	Electronic circular dichroism for chiral analysis. 2006 , 397-459		6
598	Thermal unfolding of eosinophil cationic protein/ribonuclease 3: a nonreversible process. <i>Protein Science</i> , 2006 , 15, 2816-27	6.3	15
597	Engineering human cytochrome P450 enzymes into catalytically self-sufficient chimeras using molecular Lego. 2006 , 11, 903-16		66
596	Exploring the protease mediated conformational stability in a trypsin inhibitor from <i>Archidendron ellipticum</i> seeds. 2006 , 44, 637-44		7
595	Molecular dynamics and circular dichroism studies of human and rat C-peptides. 2006 , 25, 532-42		9
594	A fluorimetric and circular dichroism study of hemoglobin--effect of pH and anionic amphiphiles. 2006 , 296, 324-31		73
593	Cell mimetic lateral stabilization of outer cell mimetic bilayer on polymer surfaces by peptide bonding and their blood compatibility. 2006 , 79, 23-35		16
592	Reovirus mu1 structural rearrangements that mediate membrane penetration. 2006 , 80, 12367-76		45
591	N- and C-terminal cooperation in rotavirus enterotoxin: novel mechanism of modulation of the properties of a multifunctional protein by a structurally and functionally overlapping conformational domain. 2006 , 80, 412-25		26
590	N-acetylanthranilate amidase from <i>Arthrobacter nitroguajacolicus</i> R β 1a, an alpha/beta-hydrolase-fold protein active towards aryl-acylamides and -esters, and properties of its cysteine-deficient variant. <i>Journal of Bacteriology</i> , 2006 , 188, 8430-40	3.5	15
589	Characterization of the DNA binding and structural properties of the BRCT region of human replication factor C p140 subunit. 2006 , 281, 4308-17		23
588	The Ile128Thr polymorphism influences stability and ligand binding properties of the microsomal triglyceride transfer protein. 2006 , 47, 1378-85		18
587	Direct protein interaction underlies gene-for-gene specificity and coevolution of the flax resistance genes and flax rust avirulence genes. 2006 , 103, 8888-93		592
586	NMR and alanine scan studies of glucose-dependent insulinotropic polypeptide in water. 2006 , 281, 16370-6		32

585	Hemicentin assembly in the extracellular matrix is mediated by distinct structural modules. 2006 , 281, 23606-10		20
584	Structure of the calmodulin alphaII-spectrin complex provides insight into the regulation of cell plasticity. 2006 , 281, 34333-40		37
583	Intrinsic inhibition of the Hsp90 ATPase activity. 2006 , 281, 11301-11		61
582	A novel regulatory metal binding domain is present in the C terminus of Arabidopsis Zn ²⁺ -ATPase HMA2. 2006 , 281, 33881-91		54
581	Regulation of FNR dimerization by subunit charge repulsion. 2006 , 281, 33268-75		35
580	Structural determinants of salmon calcitonin bioactivity: the role of the Leu-based amphipathic alpha-helix. 2006 , 281, 24193-203		44
579	Engineered sarafotoxins as tissue inhibitor of metalloproteinases-like matrix metalloproteinase inhibitors. 2007 , 282, 26948-26955		13
578	Neutralization of acidic residues in helix II stabilizes the folded conformation of acyl carrier protein and variably alters its function with different enzymes. 2007 , 282, 4494-4503		31
577	Novel n-3 fatty acid oxidation products activate Nrf2 by destabilizing the association between Keap1 and Cullin3. 2007 , 282, 2529-37		216
576	The domain structure of Helicobacter pylori DnaB helicase: the N-terminal domain can be dispensable for helicase activity whereas the extreme C-terminal region is essential for its function. 2007 , 35, 2861-74		18
575	Effect of Solvent and Temperature on Secondary and Tertiary Structure of Zein by Circular Dichroism. 2007 , 84, 265-270		73
574	An iron-sulfur cluster in the C-terminal domain of the p58 subunit of human DNA primase. 2007 , 282, 33444-33451		95
573	Probing the antiprotease activity of lambdaCIII, an inhibitor of the Escherichia coli metalloprotease HflB (FtsH). <i>Journal of Bacteriology</i> , 2007 , 189, 8130-8	3-5	13
572	Identification of the protein receptor binding site of botulinum neurotoxins B and G proves the double-receptor concept. 2007 , 104, 359-64		154
571	Characterization of Mycobacterium tuberculosis WhiB1/Rv3219 as a protein disulfide reductase. <i>Protein Expression and Purification</i> , 2007 , 52, 422-32	2	27
570	Expression, purification and characterization of recombinant severe acute respiratory syndrome coronavirus non-structural protein 1. <i>Protein Expression and Purification</i> , 2007 , 52, 249-57	2	1
569	Characterization of two soluble inorganic pyrophosphatases from Arabidopsis thaliana. 2007 , 172, 796-807		16
568	Astaxanthin binding and structural stability of the apple snail carotenoprotein ovorubin. <i>Archives of Biochemistry and Biophysics</i> , 2007 , 460, 107-12	4-1	22

567	Investigation of the ligand spectrum of human sterol carrier protein 2 using a direct mass spectrometry assay. <i>Archives of Biochemistry and Biophysics</i> , 2007 , 461, 50-8	4.1	8
566	Structural properties of caleosin: a MS and CD study. <i>Archives of Biochemistry and Biophysics</i> , 2007 , 464, 335-43	4.1	21
565	Refolding of HLA-B27 heavy chains in the absence of beta2m yields stable high molecular weight (HMW) protein forms displaying native-like as well as non-native-like conformational features: implications for autoimmune disease. 2007 , 1772, 1258-69		9
564	Four disulfide-bridged scorpion beta neurotoxin Cssl: heterologous expression and proper folding in vitro. 2007 , 1770, 1161-8		48
563	Nogo-B receptor possesses an intrinsically unstructured ectodomain and a partially folded cytoplasmic domain. 2007 , 360, 128-34		14
562	HHP: a novel class of hexameric, tyrosine-coordinated heme proteins. 2007 , 368, 1122-31		22
561	Role of green tea polyphenols in the inhibition of collagenolytic activity by collagenase. <i>International Journal of Biological Macromolecules</i> , 2007 , 41, 16-22	7.9	105
560	Circular and linear dichroism of proteins. 2007 , 9, 2020-35		125
559	The extracellular region of the receptor for advanced glycation end products is composed of two independent structural units. 2007 , 46, 6957-70		134
558	Probing the role of the conserved beta-II turn Pro-76/Gly-77 of mitochondrial cytochrome c. 2007 , 85, 366-74		6
557	The yefM-yoeB toxin-antitoxin systems of Escherichia coli and Streptococcus pneumoniae: functional and structural correlation. <i>Journal of Bacteriology</i> , 2007 , 189, 1266-78	3.5	53
556	Broccoli processing wastes as a source of peroxidase. 2007 , 55, 10396-404		24
555	Effect of high-pressure processing on activity and structure of alkaline phosphatase and lactate dehydrogenase in buffer and milk. 2007 , 55, 9520-9		13
554	Conformational changes upon calcium binding and phosphorylation in a synthetic fragment of calmodulin. 2007 , 88, 373-85		21
553	Compensatory secondary structure alterations in protein glycation. 2007 , 1774, 233-42		62
552	Spectroscopic probing of bile salt-albumin interaction. <i>Colloids and Surfaces B: Biointerfaces</i> , 2007 , 54, 74-81	6	20
551	Structural studies on Vibrio cholerae ToxR periplasmic and cytoplasmic domains. 2007 , 1774, 1331-8		4
550	Characterization of the RNA binding energetics of the Candida albicans poly(A) polymerase. 2007 , 24, 431-46		4

549	The bioactive conformation of glucose-dependent insulinotropic polypeptide by NMR and CD spectroscopy. 2007 , 68, 92-9	31	
548	Investigating the structural stability of the Tup1-interaction domain of Ssn6: evidence for a conformational change on the complex. 2008 , 70, 72-82	13	
547	Optimization of the hydrochloric acid concentration used for trifluoroacetate removal from synthetic peptides. 2007 , 13, 37-43	84	
546	Human p16gamma, a novel transcriptional variant of p16(INK4A), coexpresses with p16(INK4A) in cancer cells and inhibits cell-cycle progression. 2007 , 26, 7017-27	26	
545	The redox-switch domain of Hsp33 functions as dual stress sensor. 2007 , 14, 556-63	143	
544	Molecular function of WhiB4/Rv3681c of Mycobacterium tuberculosis H37Rv: a [4Fe-4S] cluster co-ordinating protein disulphide reductase. 2007 , 63, 1414-31	62	
543	The solution structure of the periplasmic domain of the TonB system ExbD protein reveals an unexpected structural homology with siderophore-binding proteins. 2007 , 66, 872-89	37	
542	Biochemical characterization of the recombinant human Nogo-A ectodomain. 2007 , 274, 2603-13	12	
541	Insights into the structure of plant alpha-type phospholipase D. 2007 , 274, 2630-40	15	
540	A new sulfurtransferase from the hyperthermophilic bacterium Aquifex aeolicus. Being single is not so simple when temperature gets high. 2007 , 274, 4572-87	19	
539	Expression, purification and characterization of critical domains of Munc13-1. 2007 , 39, 617-23	1	
538	The temperature activated HtrA protease from pathogen Chlamydia trachomatis acts as both a chaperone and protease at 37 degrees C. 2007 , 581, 3382-6	40	
537	Orphan nuclear receptor NGFI-B forms dimers with nonclassical interface. <i>Protein Science</i> , 2007 , 16, 1762-72	5	
536	Modification of chicken avian beta-defensin-8 at positively selected amino acid sites enhances specific antimicrobial activity. 2007 , 59, 573-80	31	
535	Cloning and characterization of dihydrofolate reductase from a facultative alkaliphilic and halotolerant bacillus strain. 2007 , 11, 75-83	4	
534	Conformational stability and integrity of alpha-amylase from mung beans: evidence of kinetic intermediate in GdmCl-induced unfolding. 2008 , 137, 95-9	20	
533	Infrared and circular dichroism spectroscopic characterisation of secondary structure components of a water treatment coagulant protein extracted from Moringa oleifera seeds. <i>Colloids and Surfaces B: Biointerfaces</i> , 2008 , 64, 118-25	6	65
532	Two-level Clustering of Web Sites Using Self-Organizing Maps. 2008 , 27, 85-95	8	

531	Low resolution structure of subunit b (b (22-156)) of Escherichia coli F(1)F(O) ATP synthase in solution and the b-delta assembly. 2008 , 40, 245-55		9
530	Formation of a molten globule like state in bovine serum albumin at alkaline pH. 2008 , 37, 1303-8		51
529	Expression of thymosin alpha1-thymopentin fusion peptide in Pichia pastoris and its characterization. 2008 , 31, 1471-6		13
528	Biological and structural analysis of truncated analogs of PACAP27. 2008 , 36, 260-9		24
527	First characterisation of the active oligomer form of sulfur oxygenase reductase from the bacterium Aquifex aeolicus. 2008 , 12, 205-15		25
526	Interaction between the C-terminal region of human myelin basic protein and calmodulin: analysis of complex formation and solution structure. 2008 , 8, 10		42
525	K2D2: estimation of protein secondary structure from circular dichroism spectra. 2008 , 8, 25		306
524	Improved sequence-based prediction of protein secondary structures by combining vacuum-ultraviolet circular dichroism spectroscopy with neural network. 2008 , 73, 104-12		25
523	Identification of the critical regions in hepatitis B virus preS required for its stability. 2008 , 14, 307-12		7
522	T-20 and T-1249 HIV fusion inhibitorsPstructure and conformation in solution: a molecular dynamics study. 2008 , 14, 442-7		16
521	Protein secondary structure analyses from circular dichroism spectroscopy: methods and reference databases. 2008 , 89, 392-400		1709
520	Stabilization of collagen by the plant polyphenolics Acacia mollissima and Terminalia chebula. 2008 , 108, 199-205		15
519	A chemical lipid modification of recombinant preS antigen to study the mechanism of HBV attachment to the host cell. 2008 , 137, 8-13		
518	Nisin antimicrobial activity and structural characteristics at hydrophobic surfaces coated with the PEO-PPO-PEO triblock surfactant Pluronic F108. 2008 , 322, 104-11		36
517	Copper-induced structural changes in the ovine prion protein are influenced by a polymorphism at codon 112. 2008 , 1784, 683-92		12
516	Protein structure and oligomerization are important for the formation of export-competent HIV-1 Rev-RRE complexes. <i>Protein Science</i> , 2008 , 17, 420-30	6.3	28
515	Miranda cargo-binding domain forms an elongated coiled-coil homodimer in solution: implications for asymmetric cell division in Drosophila. <i>Protein Science</i> , 2008 , 17, 908-17	6.3	9
514	Cloning, expression, purification, and preliminary characterization of a putative hemoglobin from the cyanobacterium Synechocystis sp. PCC 6803. <i>Protein Science</i> , 2000 , 9, 587-97	6.3	39

513	Identification of critical residues of subunit H in its interaction with subunit E of the A-ATP synthase from <i>Methanocaldococcus jannaschii</i> . 2008 , 275, 1803-12		10
512	Global shape and pH stability of ovorubin, an oligomeric protein from the eggs of <i>Pomacea canaliculata</i> . 2008 , 275, 4522-30		15
511	Functional analysis of the aglycone-binding site of the maize beta-glucosidase Zm-p60.1. 2008 , 275, 6123-35		14
510	Genome segment 6 of <i>Antheraea mylitta</i> cytovirus encodes a structural protein with ATPase activity. 2008 , 377, 7-18		12
509	Circular dichroism and its application to the study of biomolecules. 2008 , 84, 263-93		104
508	Solid-phase synthesis of europium-labeled human INSL3 as a novel probe for the study of ligand-receptor interactions. 2008 , 19, 1456-63		52
507	Chemical modification of turnip peroxidase with methoxypolyethylene glycol enhances activity and stability for phenol removal using the immobilized enzyme. 2008 , 56, 8058-65		23
506	The stator complex of the A1A0-ATP synthase--structural characterization of the E and H subunits. 2008 , 375, 673-85		18
505	Crystal structure of human epidermal kallikrein 7 (hK7) synthesized directly in its native state in <i>E. coli</i> : insights into the atomic basis of its inhibition by LEKTI domain 6 (LD6). 2008 , 377, 1488-97		14
504	The Orf18 gene product from conjugative transposon Tn916 is an ArdA antirestriction protein that inhibits type I DNA restriction-modification systems. 2008 , 383, 970-81		36
503	Putative outer membrane proteins of <i>Leptospira interrogans</i> stimulate human umbilical vein endothelial cells (HUVECS) and express during infection. 2008 , 45, 315-22		34
502	Expression, purification and crystallization of cysteine-rich human protein muskelin in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2008 , 60, 82-8	2	11
501	Matrix-assisted refolding and redox properties of WhiB3/Rv3416 of <i>Mycobacterium tuberculosis</i> H37Rv. <i>Protein Expression and Purification</i> , 2008 , 61, 83-91	2	10
500	Interactions of the C-terminus of lung surfactant protein B with lipid bilayers are modulated by acyl chain saturation. 2008 , 1778, 2544-54		13
499	Mechanism of copper induced fluorescence quenching of red fluorescent protein, DsRed. 2008 , 370, 57-61		57
498	DNA gyrase requires DNA for effective two-site coordination of divalent metal ions: further insight into the mechanism of enzyme action. 2008 , 47, 8538-45		13
497	The helical structure of surfactant peptide KL4 when bound to POPC: POPG lipid vesicles. 2008 , 47, 8292-300		20
496	Quercetinase QueD of <i>Streptomyces</i> sp. FLA, a monocupin dioxygenase with a preference for nickel and cobalt. 2008 , 47, 12185-96		62

495	Characterization of a lysine-specific histone demethylase from <i>Arabidopsis thaliana</i> . 2008 , 47, 4936-47	21
494	Structural impact of three Parkinsonism-associated missense mutations on human DJ-1. 2008 , 47, 1381-92	40
493	Biochemical characterization of a novel thermostable beta-1,3-1,4-glucanase (lichenase) from <i>Paecilomyces thermophila</i> . 2008 , 56, 5345-51	54
492	<i>Brucella abortus</i> MFP: a trimeric coiled-coil protein with membrane fusogenic activity. 2008 , 47, 8165-75	6
491	Analysis of PrP conformation using circular dichroism. <i>Methods in Molecular Biology</i> , 2008 , 459, 145-59	1.4 6
490	Detergent-associated solution conformations of helical and beta-barrel membrane proteins. 2008 , 112, 13349-54	13
489	Role of helix B residues in interfacial activation of a bacterial phosphatidylinositol-specific phospholipase C. 2008 , 47, 4201-10	17
488	Sequence-specific binding of a chloroplast pentatricopeptide repeat protein to its native group II intron ligand. 2008 , 14, 1930-41	94
487	Ethylene controls autophosphorylation of the histidine kinase domain in ethylene receptor ETR1. 2008 , 1, 380-7	55
486	The flexible C terminus of the rotavirus non-structural protein NSP4 is an important determinant of its biological properties. 2008 , 89, 1485-1496	17
485	Structural mechanism of signal transduction between the RNA-binding domain and the phosphotransferase system regulation domain of the LicT antiterminator. 2008 , 283, 30838-49	15
484	Structural and mutational characterization of the catalytic A-module of the mannuronan C-5-epimerase AlgE4 from <i>Azotobacter vinelandii</i> . 2008 , 283, 23819-28	38
483	ATP/ADP binding to a novel nucleotide binding domain of the reticulocyte-binding protein Py235 of <i>Plasmodium yoelii</i> . 2008 , 283, 36386-96	12
482	Structural and functional characterization of transmembrane segment IX of the NHE1 isoform of the Na ⁺ /H ⁺ exchanger. 2008 , 283, 22018-30	32
481	Microsecond acquisition of heterogeneous structure in the folding of a TIM barrel protein. 2008 , 105, 13367-72	57
480	Probing the interaction between the coiled coil leucine zipper of cGMP-dependent protein kinase alpha and the C terminus of the myosin binding subunit of the myosin light chain phosphatase. 2008 , 283, 32860-9	52
479	Design and characterization of a soluble fragment of the extracellular ligand-binding domain of the peptide hormone receptor guanylyl cyclase-C. <i>Protein Engineering, Design and Selection</i> , 2009 , 22, 1-7	1.9 5
478	Evaluation of leptospiral recombinant antigens MPL17 and MPL21 for serological diagnosis of leptospirosis by enzyme-linked immunosorbent assays. 2008 , 15, 1715-22	32

477	Interaction of Porphyromonas gingivalis with oral streptococci requires a motif that resembles the eukaryotic nuclear receptor box protein-protein interaction domain. <i>Infection and Immunity</i> , 2008 , 76, 3273-80	3-7	58
476	Severe acute respiratory syndrome coronavirus nsp9 dimerization is essential for efficient viral growth. 2009 , 83, 3007-18		73
475	Large-scale production and study of a synthetic G protein-coupled receptor: human olfactory receptor 17-4. 2009 , 106, 11925-30		83
474	Domain architecture of the stator complex of the A1A0-ATP synthase from Thermoplasma acidophilum. 2009 , 284, 12031-40		13
473	Intramolecular interactions between the SRC homology 3 and guanylate kinase domains of discs large regulate its function in asymmetric cell division. 2009 , 284, 12924-32		20
472	Modulation of Bacillus thuringiensis phosphatidylinositol-specific phospholipase C activity by mutations in the putative dimerization interface. 2009 , 284, 15607-18		15
471	Properties of HflX, an enigmatic protein from Escherichia coli. <i>Journal of Bacteriology</i> , 2009 , 191, 2307-14	5	26
470	Double superhelix model of high density lipoprotein. 2009 , 284, 36605-36619		78
469	Stable docking of neutralizing human immunodeficiency virus type 1 gp41 membrane-proximal external region monoclonal antibodies 2F5 and 4E10 is dependent on the membrane immersion depth of their epitope regions. 2009 , 83, 10211-23		55
468	Expression and characterization of Kunitz domain 3 and C-terminal of human tissue factor pathway inhibitor-2. 2009 , 41, 948-54		6
467	Conformational stability of cytochrome C probed by optical spectroscopy. 2009 , 466, 109-53		11
466	Trypanosoma cruzi calmodulin: cloning, expression and characterization. 2009 , 123, 326-33		6
465	Superoxide radical protects liposome-contained cytochrome c against oxidative damage promoted by peroxynitrite and free radicals. 2009 , 47, 841-9		11
464	Structural modification of proteins by direct electric current from low voltage. 2009 , 23, 309-17		7
463	Conformational analysis of a peptide approximating the HCCH motif in HIV-1 Vif. 2009 , 92, 417-25		15
462	Manganese-induced changes of the biochemical characteristics of the recombinant wild-type and mutant PrPs. 2009 , 198, 239-45		11
461	Properties of a purified thermostable glucoamylase from Aspergillus niveus. 2009 , 36, 1439-46		23
460	Iron binding effects on the kinetic stability and unfolding energetics of a thermophilic phenylalanine hydroxylase from Chloroflexus aurantiacus. 2009 , 14, 521-31		15

459	Purification and biochemical characterization of a novel alpha-glucosidase from <i>Aspergillus niveus</i> . 2009 , 96, 569-78		18
458	Dynamics of apomyoglobin in the alpha-to-beta transition and of partially unfolded aggregated protein. 2009 , 38, 237-44		17
457	Molecular dynamics simulation of the acidic compact state of apomyoglobin from yellowfin tuna. 2009 , 74, 273-90		6
456	Zn ²⁺ -linked dimerization of UreG from <i>Helicobacter pylori</i> , a chaperone involved in nickel trafficking and urease activation. 2009 , 74, 222-39		68
455	The inherent flexibility of peptides and protein fragments quantitized by CD in conjunction with CCA+. 2009 , 15, 738-52		9
454	Atomic structures of IAPP (amylin) fusions suggest a mechanism for fibrillation and the role of insulin in the process. <i>Protein Science</i> , 2009 , 18, 1521-30	6.3	172
453	Integrity of N- and C-termini is important for <i>E. coli</i> Hsp31 chaperone activity. <i>Protein Science</i> , 2009 , 18, 1439-47	6.3	13
452	Solubilization and characterization of the anthrax toxin pore in detergent micelles. <i>Protein Science</i> , 2009 , 18, 1882-95	6.3	16
451	The acidic domains of the Toc159 chloroplast preprotein receptor family are intrinsically disordered protein domains. 2009 , 10, 35		31
450	The targeting of the oxysterol-binding protein ORP3a to the endoplasmic reticulum relies on the plant VAP33 homolog PVA12. 2009 , 58, 817-30		52
449	Production of native and modified recombinant Der p 1 molecules in tobacco plants. 2009 , 39, 760-70		18
448	Molecular analysis of restriction endonuclease EcoRII from <i>Escherichia coli</i> reveals precise regulation of its enzymatic activity by autoinhibition. 2009 , 72, 1011-21		3
447	Spectroscopic characterization of <i>Cicer arietinum</i> metallothionein 1. 2009 , 362, 714-724		34
446	Oxindole-Schiff base copper(II) complexes interactions with human serum albumin: spectroscopic, oxidative damage, and computational studies. 2009 , 103, 1331-41		21
445	Purification and biochemical characterization of a serine proteinase inhibitor from <i>Derris trifoliata</i> Lour. seeds: insight into structural and antimalarial features. 2009 , 70, 703-12		52
444	Spectroscopic studies on the interaction of cationic surfactants with bovine serum albumin. <i>Colloids and Surfaces B: Biointerfaces</i> , 2009 , 69, 122-8	6	64
443	Interactions of the <i>M. tuberculosis</i> UsfX with the cognate sigma factor SigF and the anti-anti sigma factor RsfA. 2009 , 1794, 541-53		10
442	Heterologous expressed toxic and non-toxic peptide variants of toxin CstII are capable to produce neutralizing antibodies against the venom of the scorpion <i>Centruroides suffusus suffusus</i> . 2009 , 125, 93-9		18

441	An alternative assay to discover potential calmodulin inhibitors using a human fluorophore-labeled CaM protein. 2009 , 387, 64-70		19
440	Resistance of bromelain to SDS binding. 2009 , 1794, 698-708		21
439	Role of conserved residues in structure and stability: tryptophans of human serum retinol-binding protein, a model for the lipocalin superfamily. <i>Protein Science</i> , 2001 , 10, 2301-16	6.3	61
438	Mechanism of lysophosphatidic acid-induced amyloid fibril formation of beta(2)-microglobulin in vitro under physiological conditions. 2009 , 48, 5689-99		27
437	Characterization of [4Fe-4S]-containing and cluster-free forms of Streptomyces WhiD. 2009 , 48, 12252-64		58
436	Comparisons of the conformational stability of cyclin-dependent kinase (CDK) 4-interacting ankyrin repeat (AR) proteins. 2009 , 48, 4050-62		8
435	A molecular mimic of phosphorylated prolactin (S179D PRL) secreted by eukaryotic cells has a conformation with an increased positive surface charge compared to that of unmodified prolactin. 2009 , 48, 6887-97		5
434	Molecular structure and biochemical properties of the HCCH-Zn ²⁺ site in HIV-1 Vif. 2009 , 48, 7969-78		16
433	Nucleic acid binding of the RTN1-C C-terminal region: toward the functional role of a reticulon protein. 2009 , 48, 242-53		23
432	Physicochemical and pharmacological characterization of novel vasoactive intestinal peptide derivatives with improved stability. 2009 , 73, 95-101		14
431	Overexpression and purification of rat peroxisomal membrane protein 22, PMP22, in <i>Pichia pastoris</i> . <i>Protein Expression and Purification</i> , 2009 , 64, 47-54	2	2
430	Refolding and purification of the human secreted group IID phospholipase A2 expressed as inclusion bodies in <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2009 , 67, 82-7	2	5
429	Biochemical characterization of Arabidopsis developmentally regulated G-proteins (DRGs). <i>Protein Expression and Purification</i> , 2009 , 67, 88-95	2	13
428	How methyl cyanide induces aggregation in all-alpha proteins: a case study in four albumins. <i>International Journal of Biological Macromolecules</i> , 2009 , 44, 163-9	7.9	15
427	Pathways and mechanisms for product release in the engineered haloalkane dehalogenases explored using classical and random acceleration molecular dynamics simulations. 2009 , 392, 1339-56		75
426	Crystal structure of the antitoxin-toxin protein complex RelB-RelE from <i>Methanococcus jannaschii</i> . 2009 , 393, 898-908		36
425	Structural, functional and unfolding characteristics of glutathione S-transferase of <i>Plasmodium vivax</i> . <i>Archives of Biochemistry and Biophysics</i> , 2009 , 487, 115-22	4.1	14
424	Effect of divalent ions on the minimal relaxase domain of MobA. <i>Archives of Biochemistry and Biophysics</i> , 2009 , 488, 42-7	4.1	5

423	Penetration depth of surfactant peptide KL4 into membranes is determined by fatty acid saturation. 2009 , 96, 4085-98		20
422	Domain features of the peripheral stalk subunit H of the methanogenic A1AO ATP synthase and the NMR solution structure of H(1-47). 2009 , 97, 286-94		6
421	Cloning, overexpression, and characterization of a bacterial Ca ²⁺ -dependent phospholipase D. <i>Protein Science</i> , 2002 , 11, 2958-68	6.3	40
420	Protein characterisation by synchrotron radiation circular dichroism spectroscopy. 2009 , 42, 317-70		81
419	p25alpha is flexible but natively folded and binds tubulin with oligomeric stoichiometry. <i>Protein Science</i> , 2005 , 14, 1396-409	6.3	40
418	Interaction of bovine (BSA), rabbit (RSA), and porcine (PSA) serum albumins with cationic single-chain/gemini surfactants: a comparative study. 2009 , 25, 11686-91		108
417	Allergenicity of main birch allergen rBet v1 and high-pressure treatment. 2009 , 29, 680-685		3
416	Mutational, inhibitory and microcalorimetric analyses of Plasmodium falciparum TMP kinase. Implications for drug discovery. 2009 , 136, 11-25		35
415	The structure of the ankyrin-binding site of beta-spectrin reveals how tandem spectrin-repeats generate unique ligand-binding properties. 2009 , 113, 5377-84		56
414	New insight in ethylene signaling: autokinase activity of ETR1 modulates the interaction of receptors and EIN2. 2010 , 3, 882-9		90
413	Expression and structural characterization of peripherin/RDS, a membrane protein implicated in photoreceptor outer segment morphology. 2010 , 39, 679-88		11
412	Effect of helix-promoting strategies on the biological activity of novel analogues of the B-chain of INSL3. 2010 , 38, 121-31		10
411	Acid-induced unfolding of didecameric keyhole limpet hemocyanin: detection and characterizations of decameric and tetrameric intermediate states. 2010 , 39, 899-910		36
410	Non-enzymatic glycation induces structural modifications of myoglobin. 2010 , 338, 105-14		30
409	Influence of production process design on inclusion bodies protein: the case of an Antarctic flavohemoglobin. 2010 , 9, 19		12
408	Expression, purification and structural analysis of the Pyrococcus abyssi RNA binding protein PAB1135. 2010 , 3, 97		
407	Disulfide linkage in the coiled-coil domain of subunit H of A1AO ATP synthase from Methanocaldococcus jannaschii and the NMR structure of the C-terminal segment H(85-104). 2010 , 584, 713-8		2
406	Unfolding of rabbit serum albumin by cationic surfactants: surface tensiometry, small-angle neutron scattering, intrinsic fluorescence, resonance Rayleigh scattering and circular dichroism studies. 2010 , 352, 436-43		30

405	Purification, characterisation, and quantification of the soy allergen profilin (Gly m 3) in soy products. 2010 , 119, 1671-1680		37
404	Structure and conformation of HIV fusion inhibitor peptide T-1249 in presence of model membranes: A molecular dynamics study. 2010 , 946, 119-124		8
403	Structure and stability of the neurotoxin PV2 from the eggs of the apple snail <i>Pomacea canaliculata</i> . 2010 , 1804, 1492-9		20
402	Aquifex aeolicus FlgM protein exhibits a temperature-dependent disordered nature. 2010 , 1804, 1457-66		7
401	Biophysical characterization of highly active recombinant Gaussia luciferase expressed in <i>Escherichia coli</i> . 2010 , 1804, 1902-7		23
400	An A β monomer with altered aggregation propensities. 2010 , 1804, 2025-35		1
399	Crystallographic studies of the coupling segment NBD94(674-781) of the nucleotide-binding domain of the <i>Plasmodium yoelii</i> reticulocyte-binding protein Py235. 2010 , 66, 1631-4		
398	N-terminal domain of the V-ATPase α 2-subunit displays integral membrane protein properties. <i>Protein Science</i> , 2010 , 19, 1850-62	6.3	9
397	UV and X-ray structural studies of a 101-residue long Tat protein from a HIV-1 primary isolate and of its mutated, detoxified, vaccine candidate. 2010 , 78, 1441-56		25
396	A weak DD-carboxypeptidase activity explains the inability of PBP 6 to substitute for PBP 5 in maintaining normal cell shape in <i>Escherichia coli</i> . 2010 , 303, 76-83		27
395	Physiological truncation and domain organization of a novel uracil-DNA-degrading factor. 2010 , 277, 1245-59		5
394	The effect of zinc oxide nanoparticles on the structure of the periplasmic domain of the <i>Vibrio cholerae</i> ToxR protein. 2010 , 277, 4184-94		62
393	Methyl cyanide induces alpha to beta transition and aggregation at high concentrations in E-state of human serum albumin. 2010 , 75, 367-74		5
392	Structural determination of functional units of the nucleotide binding domain (NBD94) of the reticulocyte binding protein Py235 of <i>Plasmodium yoelii</i> . <i>PLoS ONE</i> , 2010 , 5, e9146	3.7	8
391	ABCG2 transports and transfers heme to albumin through its large extracellular loop. 2010 , 285, 33123-33133		67
390	Interaction of extracellular domain 2 of the human retina-specific ATP-binding cassette transporter (ABCA4) with all-trans-retinal. 2010 , 285, 19372-83		14
389	Gentisic acid, a compound associated with plant defense and a metabolite of aspirin, heads a new class of in vivo fibroblast growth factor inhibitors. 2010 , 285, 11714-29		70
388	Site-specific phosphorylation induces functionally active conformation in the intrinsically disordered N-terminal activation function (AF1) domain of the glucocorticoid receptor. 2010 , 30, 220-30		74

387	A contribution to identification of novel regulators of plant response to sulfur deficiency: characteristics of a tobacco gene UP9C, its protein product and the effects of UP9C silencing. 2010 , 3, 347-60		35
386	Phytolacca americana lectin (Pa-2; pokeweed mitogen): an intrinsically unordered protein and its conversion into partial order at low pH. 2009 , 30, 125-34		11
385	Crystal structure and trimer-monomer transition of N-terminal domain of EhCaBP1 from Entamoeba histolytica. 2010 , 98, 2933-42		7
384	Lipid polymorphism induced by surfactant peptide SP-B(1-25). 2010 , 99, 1773-82		16
383	Molecular basis of differential B-pentamer stability of Shiga toxins 1 and 2. <i>PLoS ONE</i> , 2010 , 5, e15153	3.7	24
382	Two-photon and time-resolved fluorescence conformational studies of aggregation in amyloid peptides. 2010 , 114, 7112-20		14
381	Identification of a functionally important loop in Salmonella typhimurium ArnT. 2010 , 49, 29-35		8
380	Modulating the pH-activity profile of cellulase by substitution: replacing the general base catalyst aspartate with cysteinesulfinate in cellulase A from Cellulomonas fimi. 2010 , 49, 2042-50		13
379	Purification and characterization of a peroxidase isozyme from Indian turnip roots. 2010 , 58, 5545-52		9
378	The catalytic and other residues essential for the activity of the midgut trehalase from Spodoptera frugiperda. 2010 , 40, 733-41		24
377	2,2,2-Trifluoroethanol induces simultaneous increase in alpha-helicity and aggregation in alkaline unfolded state of bovine serum albumin. <i>International Journal of Biological Macromolecules</i> , 2010 , 46, 250-4	7.9	33
376	Identifying assembly-inhibiting and assembly-tolerant sites in the SbsB S-layer protein from Geobacillus stearothermophilus. 2010 , 395, 742-53		14
375	SDS-induced fibrillation of alpha-synuclein: an alternative fibrillation pathway. 2010 , 401, 115-33		154
374	Isolation and characterization of the core single-stranded DNA-binding domain of purine-rich element binding protein B (PurB) 2010 , 400, 340-5		8
373	Kinetic and structural characterization of human mortalin. <i>Protein Expression and Purification</i> , 2010 , 72, 75-81	2	22
372	Metabolic and structural properties of human obestatin {1-23} and two fragment peptides. 2010 , 31, 1697-705		13
371	Characterization of leptospiral proteins that afford partial protection in hamsters against lethal challenge with Leptospira interrogans. 2010 , 59, 1005-1015		15
370	Effects of high hydrostatic pressure on the structure of bovine alpha-lactalbumin. 2010 , 93, 1420-8		23

369	Advanced statistical and numerical methods for spectroscopic characterization of protein structural evolution. 2010 , 110, 5692-713		52
368	The second RNA chaperone, Hfq2, is also required for survival under stress and full virulence of <i>Burkholderia cenocepacia</i> J2315. <i>Journal of Bacteriology</i> , 2011 , 193, 1515-26	3.5	28
367	Effect of tin oxide nanoparticle binding on the structure and activity of α -amylase from <i>Bacillus amyloliquefaciens</i> . 2011 , 22, 455708		26
366	Conferment of folding ability to a naturally unfolded apocytochrome c through introduction of hydrophobic amino acid residues. 2011 , 50, 2313-20		15
365	Manipulating cofactor binding thermodynamics in an artificial oxygen transport protein. 2011 , 50, 10254-61		17
364	Explaining the structural plasticity of β -synuclein. 2011 , 133, 19536-46		86
363	Adjustment of codon usage frequencies by codon harmonization improves protein expression and folding. <i>Methods in Molecular Biology</i> , 2011 , 705, 1-13	1.4	35
362	Thiol-targeted introduction of selenocysteine to polypeptides for synthesis of glutathione peroxidase mimics. 2011 , 3, 702-9		5
361	A reference dataset for the analyses of membrane protein secondary structures and transmembrane residues using circular dichroism spectroscopy. 2011 , 27, 1630-6		106
360	Accessory cholera enterotoxin, Ace, from <i>Vibrio cholerae</i> : structure, unfolding, and virstatin binding. 2011 , 50, 2962-72		20
359	The Min oscillator uses MinD-dependent conformational changes in MinE to spatially regulate cytokinesis. 2011 , 146, 396-407		117
358	Solution structure of subunit F (Vma7p) of the eukaryotic V(1)V(O) ATPase from <i>Saccharomyces cerevisiae</i> derived from SAXS and NMR spectroscopy. 2011 , 1808, 360-8		7
357	Mode of action of parasporin-4, a cytotoxic protein from <i>Bacillus thuringiensis</i> . 2011 , 1808, 1476-82		24
356	Solubilization and folding of a fully active recombinant <i>Gaussia luciferase</i> with native disulfide bonds by using a SEP-Tag. 2011 , 1814, 1775-8		22
355	Expression and characterization of recombinant kurtoxin, an inhibitor of T-type voltage-gated calcium channels. 2011 , 416, 277-82		6
354	Fructose-induced modifications of myoglobin: Change of structure from met (Fe ³⁺) to oxy (Fe ²⁺) form. <i>International Journal of Biological Macromolecules</i> , 2011 , 48, 202-9	7.9	25
353	Biochemical studies and crystal structure determination of dihydrodipicolinate synthase from <i>Pseudomonas aeruginosa</i> . <i>International Journal of Biological Macromolecules</i> , 2011 , 48, 779-87	7.9	27
352	Structural insight into the glycosylphosphatidylinositol transamidase subunits PIG-K and PIG-S from yeast. 2011 , 173, 271-81		11

351	The anti-Parkinsonian drug selegiline delays the nucleation phase of β -synuclein aggregation leading to the formation of nontoxic species. 2011 , 405, 254-73		68
350	Simultaneous formation of right- and left-handed anti-parallel coiled-coil interfaces by a coil2 fragment of human lamin A. 2011 , 408, 135-46		25
349	The evidence of large-scale DNA-induced compaction in the mycobacterial chromosomal ParB. 2011 , 413, 901-7		12
348	Expression, purification, detergent screening and solution NMR backbone assignment of the human potassium channel accessory subunit MiRP1. <i>Protein Expression and Purification</i> , 2011 , 76, 205-10 ²		5
347	Expression, purification and characterisation of GIGANTEA: a circadian clock-controlled regulator of photoperiodic flowering in plants. <i>Protein Expression and Purification</i> , 2011 , 76, 197-204	2	11
346	Addition of positive charges at the C-terminal peptide region of Cssl, a mammalian scorpion peptide toxin, improves its affinity for sodium channels Nav1.6. 2011 , 32, 75-9		20
345	Investigation of physicochemical changes to L-asparaginase during freeze-thaw cycling. 1997 , 49, 472-7		17
344	Plasmodium vivax tryptophan-rich antigen PvTRAg33.5 contains alpha helical structure and multidomain architecture. <i>PLoS ONE</i> , 2011 , 6, e16294	3-7	9
343	Carboxylate and aromatic active-site residues are determinants of high-affinity binding of β -aminoaldehydes to plant aminoaldehyde dehydrogenases. 2011 , 278, 3130-9		20
342	NMR solution structure of NBD94(483-502) of the nucleotide-binding domain of the Plasmodium yoelii reticulocyte-binding protein Py235. 2011 , 318, 152-8		2
341	Stability of haloalkaliphilic Geomicrobium sp. protease modulated by salt. 2011 , 76, 686-93		27
340	Molecular dynamics simulations of T-20 HIV fusion inhibitor interacting with model membranes. 2011 , 159, 275-86		10
339	Modeling of the structure and interactions of the B. anthracis antitoxin, MoxX: deletion mutant studies highlight its modular structure and repressor function. 2011 , 25, 275-91		27
338	Metastability of papain and the molecular mechanism for its sequential acid-denaturation. 2011 , 30, 184-93		4
337	Identification of the copper-binding ligands of lysyl oxidase. 2011 , 118, 1101-9		29
336	Evidences of a natively unfolded state for the human topoisomerase IB N-terminal domain. 2011 , 41, 945-53		7
335	Biophysical characterization of Entamoeba histolytica phosphoserine aminotransferase (EhPSAT): role of cofactor and domains in stability and subunit assembly. 2011 , 40, 599-610		8
334	Structural stability and unfolding transition of β -glucosidases: a comparative investigation on isozymes from a thermo-tolerant yeast. 2011 , 40, 877-89		10

333	Equilibrium unfolding of <i>A. niger</i> RNase: pH dependence of chemical and thermal denaturation. 2011 , 40, 923-35		7
332	An improved procedure for the purification of catalytically active alkane hydroxylase from <i>Pseudomonas putida</i> GPo1. 2011 , 165, 823-31		10
331	Human Nek6 is a monomeric mostly globular kinase with an unfolded short N-terminal domain. 2011 , 11, 12		17
330	Engineering of an <i>E. coli</i> outer membrane protein FhuA with increased channel diameter. 2011 , 9, 33		21
329	Purification and crystallization of yeast glycosylphosphatidylinositol transamidase subunit PIG-S (PIG-S(71-467)). 2011 , 67, 896-9		3
328	YqiC of <i>Salmonella enterica</i> serovar Typhimurium is a membrane fusogenic protein required for mice colonization. 2011 , 11, 95		6
327	Apparent structural differences at the tetramerization region of erythroid and nonerythroid beta spectrin as discriminated by phage displayed scFvs. <i>Protein Science</i> , 2011 , 20, 867-79	6.3	3
326	Spectroscopic approach of the interaction study of amphiphilic drugs with the serum albumins. <i>Colloids and Surfaces B: Biointerfaces</i> , 2011 , 87, 447-53	6	36
325	Surface plasmon resonance study on functional significance of clustered organization of lectin-like oxidized LDL receptor (LOX-1). 2011 , 1814, 345-54		14
324	Extracellular poly (A) specific ribonuclease from <i>Aspergillus niger</i> ATCC 26550: Purification, biochemical, and spectroscopic studies. 2011 , 46, 135-141		11
323	Human phenotypically distinct TGFBI corneal dystrophies are linked to the stability of the fourth FAS1 domain of TGFBIp. 2011 , 286, 4951-8		49
322	Functional Study of AcoX, an Unknown Protein Involved in Acetoin Catabolism. 2011 , 393-395, 776-779		1
321	The N-terminal domain of the Flo1 flocculation protein from <i>Saccharomyces cerevisiae</i> binds specifically to mannose carbohydrates. 2011 , 10, 110-7		26
320	Functional identification of toxin-antitoxin molecules from <i>Helicobacter pylori</i> 26695 and structural elucidation of the molecular interactions. 2011 , 286, 4842-53		24
319	A novel chimeric protein-based HIV-1 fusion inhibitor targeting gp41 glycoprotein with high potency and stability. 2011 , 286, 28425-34		13
318	Structural dissection and in vivo effectiveness of a peptide inhibitor of <i>Porphyromonas gingivalis</i> adherence to <i>Streptococcus gordonii</i> . <i>Infection and Immunity</i> , 2011 , 79, 67-74	3-7	91
317	Converting the highly amyloidogenic human calcitonin into a powerful fibril inhibitor by three-dimensional structure homology with a non-amyloidogenic analogue. 2011 , 286, 2707-18		23
316	Light chain-dependent self-association of dynein intermediate chain. 2011 , 286, 1556-66		37

315	The catalytic architecture of leukotriene C4 synthase with two arginine residues. 2011 , 286, 16392-401	27	
314	Biochemical, mutational and in silico structural evidence for a functional dimeric form of the ornithine decarboxylase from <i>Entamoeba histolytica</i> . 2012 , 6, e1559	7	
313	Structural and functional studies of the mitochondrial cysteine desulfurase from <i>Arabidopsis thaliana</i> . 2012 , 5, 1001-10	32	
312	Polymorphic fibrillation of the destabilized fourth fasciclin-1 domain mutant A546T of the Transforming growth factor- β -induced protein (TGFB1p) occurs through multiple pathways with different oligomeric intermediates. 2012 , 287, 34730-42	19	
311	Structural features and domain organization of huntingtin fibrils. 2012 , 287, 31739-46	68	
310	EMILIN-3, peculiar member of elastin microfibril interface-located protein (EMILIN) family, has distinct expression pattern, forms oligomeric assemblies, and serves as transforming growth factor β antagonist. 2012 , 287, 11498-515	28	
309	Binding of the N-terminal region of coactivator TIF2 to the intrinsically disordered AF1 domain of the glucocorticoid receptor is accompanied by conformational reorganizations. 2012 , 287, 44546-60	38	
308	Structural Elements Regulating Interactions in the Early Stages of Fibrillogenesis: A Human Calcitonin Model System. 2012 , 351-388	1	
307	Inhibition of xyloglucanase from an alkalothermophilic <i>Thermomonospora</i> sp. by a peptidic aspartic protease inhibitor from <i>Penicillium</i> sp. VM24. 2012 , 123, 390-9		
306	A new site-specific monoPEGylated filgrastim derivative prepared by enzymatic conjugation: Production and physicochemical characterization. 2012 , 164, 355-63	29	
305	Proteolytic activation of proteose peptone component 3 by release of a C-terminal peptide with antibacterial properties. 2012 , 95, 2819-29	8	
304	Truncation of a β -barrel scaffold dissociates intrinsic stability from its propensity to aggregation. 2012 , 103, 1929-39	11	
303	Serine/threonine phosphatase (SP-STP), secreted from <i>Streptococcus pyogenes</i> , is a pro-apoptotic protein. 2012 , 287, 9147-67	23	
302	Polymeric Display of Proteins through High Affinity Leucine Zipper Peptide Adaptors. 2012 , 13, 1112-21	14	
301	A region at the C-terminus of the <i>Escherichia coli</i> global transcription factor FNR negatively mediates its degradation by the ClpXP protease. 2012 , 51, 5061-71	3	
300	Interaction of amphiphilic drugs with human and bovine serum albumins. 2012 , 97, 119-24	59	
299	The structural characteristics of human preprotein translocase of the inner mitochondrial membrane Tim23: implications for its physiological activities. <i>Protein Expression and Purification</i> , 2012 , 82, 255-62	2	5
298	Expression and purification of recombinant protein related to DAN and cerberus (PRDC). <i>Protein Expression and Purification</i> , 2012 , 82, 389-95	2	8

297	A low-molecular-mass aspartic protease inhibitor from a novel <i>Penicillium</i> sp.: implications in combating fungal infections. 2012 , 158, 1897-1907		7
296	Experimental identification and theoretical analysis of a thermally stabilized green fluorescent protein variant. 2012 , 51, 7974-82		8
295	Mutations in <i>Drosophila</i> myosin rod cause defects in myofibril assembly. 2012 , 419, 22-40		3
294	Spectral characteristics of fluorescence and circular dichroism of aflatoxin B1 reaction with its anti-idiotypic antibody. 2012 , 1028, 73-78		4
293	Slow-tight binding inhibition of pepsin by an aspartic protease inhibitor from <i>Streptomyces</i> sp. MBR04. <i>International Journal of Biological Macromolecules</i> , 2012 , 51, 165-74	7.9	6
292	Formation of low-dimensional crystalline nucleus region during insulin amyloidogenesis process. 2012 , 419, 232-7		18
291	Novel protein-protein interactions between <i>Entamoeba histolytica</i> -phosphoglycerate dehydrogenase and phosphoserine aminotransferase. 2012 , 94, 1676-86		5
290	Inhibition of caspase-9 by stabilized peptides targeting the dimerization interface. 2012 , 98, 451-65		11
289	Ara h 1 structure is retained after roasting and is important for enhanced binding to IgE. 2012 , 56, 1739-47		27
288	Moderate deacylation efficiency of DacD explains its ability to partially restore beta-lactam resistance in <i>Escherichia coli</i> PBP5 mutant. 2012 , 337, 73-80		10
287	Featuring amyloids with Fourier transform infrared and circular dichroism spectroscopies. <i>Methods in Molecular Biology</i> , 2012 , 849, 53-68	1.4	13
286	The stem region of premembrane protein plays an important role in the virus surface protein rearrangement during dengue maturation. 2012 , 287, 40525-34		38
285	Circular dichroism in protein folding studies. 2012 , Chapter 28, Unit28.3		10
284	Protein encapsulation in polymeric microneedles by photolithography. 2012 , 7, 3143-54		24
283	Electronic Circular Dichroism of Proteins. 2012 , 473-497		4
282	Electronic Circular Dichroism in Drug Discovery. 2012 , 819-842		1
281	Physicochemical and immunological studies on 4-hydroxynonenal modified HSA: implications of protein damage by lipid peroxidation products in the etiopathogenesis of SLE. 2012 , 73, 1132-9		21
280	Molecular characterization of the interaction of crotamine-derived nucleolar targeting peptides with lipid membranes. 2012 , 1818, 2707-17		25

279	A desolvation model for trifluoroethanol-induced aggregation of enhanced green fluorescent protein. 2012 , 102, 897-906		28
278	A rod domain sequence in segment 1B triggers dimerisation of the two small Branchiostoma IF proteins B2 and A3. 2012 , 91, 800-8		3
277	Interactions of sulfur oxidation repressor with its promoters involve different binding geometries. 2012 , 194, 737-47		3
276	Common and distant structural characteristics of feruloyl esterase families from <i>Aspergillus oryzae</i> . <i>PLoS ONE</i> , 2012 , 7, e39473	3-7	9
275	Abnormal SDS-PAGE migration of cytosolic proteins can identify domains and mechanisms that control surfactant binding. <i>Protein Science</i> , 2012 , 21, 1197-209	6-3	93
274	Engineering the interface between glucose oxidase and nanoparticles. 2012 , 28, 5190-200		38
273	Regulation of catalytic behaviour of hydrolases through interactions with functionalized carbon-based nanomaterials. 2012 , 14, 1		59
272	Effects of the N-terminal and C-terminal domains of <i>Meiothermus ruber</i> CBS-01 trehalose synthase on thermostability and activity. 2012 , 16, 377-85		3
271	The N-terminal domain of the Flo11 protein from <i>Saccharomyces cerevisiae</i> is an adhesin without mannose-binding activity. 2012 , 12, 78-87		22
270	PP3 forms stable tetrameric structures through hydrophobic interactions via the C-terminal amphipathic helix and undergoes reversible thermal dissociation and denaturation. 2012 , 279, 336-47		12
269	Smart polymer mediated purification and recovery of active proteins from inclusion bodies. 2012 , 1235, 10-25		19
268	Effect of tannic acid on properties of soybean (<i>Glycine max</i>) seed ferritin: a model for interaction between naturally-occurring components in foodstuffs. 2012 , 133, 410-5		29
267	The influence of maltose modified poly(propylene imine) dendrimers on hen egg white lysozyme structure and thermal stability. <i>Colloids and Surfaces B: Biointerfaces</i> , 2012 , 95, 103-8	6	34
266	Platinum-encapsulated zeolitically microcapsular catalyst for one-pot dynamic kinetic resolution of phenylethylamine. 2012 , 291, 87-94		33
265	Glu-108 is essential for subunit assembly and dimer stability of D-phosphoglycerate dehydrogenase from <i>Entamoeba histolytica</i> . 2012 , 181, 117-24		11
264	Human serum albumin interactions with C60 fullerene studied by spectroscopy, small-angle neutron scattering, and molecular dynamics simulations. 2013 , 15, 1		11
263	Amino acid transport in thermophiles: characterization of an arginine-binding protein from <i>Thermotoga maritima</i> . 3. Conformational dynamics and stability. 2013 , 118, 66-73		17
262	Purification, spectroscopic characterization and o-diphenoloxidase activity of hemocyanin from a freshwater gastropod: <i>Pila globosa</i> . 2013 , 32, 327-36		9

261	One single method to produce native and Tat-fused recombinant human β -synuclein in <i>Escherichia coli</i> . 2013 , 13, 32	17
260	Solution structure of subunit ϵ (1-204) of the <i>Mycobacterium tuberculosis</i> F-ATP synthase and the unique loop of ϵ (165-178), representing a novel TB drug target. 2013 , 45, 121-9	14
259	Recombinant S-adenosylhomocysteine hydrolase from <i>Thermotoga maritima</i> : cloning, overexpression, characterization, and thermal purification studies. 2013 , 170, 639-53	6
258	Biochemical and immunological characterization of a recombinantly-produced antifungal cysteine proteinase inhibitor from green kiwifruit (<i>Actinidia deliciosa</i>). 2013 , 94, 53-9	16
257	Identification of key residues involved in adrenomedullin binding to the AM1 receptor. 2013 , 169, 143-55	27
256	Glucoamylase from a newly isolated <i>Aspergillus niger</i> FME: Detergent-Mediated production, purification, and characterization. 2013 , 56, 427-433	9
255	Understanding the roles of strictly conserved tryptophan residues in O ₂ producing chlorite dismutases. 2013 , 42, 3156-69	17
254	Modulation of environmental dynamics at the active site and activity of an enzyme under nanoscopic confinement: Subtilisin Carlsberg in anionic AOT reverse micelle. 2013 , 117, 11565-74	12
253	The N termini of α -subunit isoforms are involved in signaling between vacuolar H ⁺ -ATPase (V-ATPase) and cytohesin-2. 2013 , 288, 5896-913	35
252	Leukemia fusion target AF9 is an intrinsically disordered transcriptional regulator that recruits multiple partners via coupled folding and binding. 2013 , 21, 176-183	69
251	Influenza A virus protein PB1-F2 from different strains shows distinct structural signatures. 2013 , 1834, 568-82	12
250	Halogenol- versus alkanol-induced structural transitions of acid-denatured glucoamylase: Characterization of alcohol-induced states. 2013 , 48, 853-862	3
249	Multiple catalytic activities of <i>Escherichia coli</i> lysyl-tRNA synthetase (LysU) are dissected by site-directed mutagenesis. 2013 , 280, 102-14	10
248	Protein l-isoaspartyl-O-methyltransferase of <i>Vibrio cholerae</i> : interaction with cofactors and effect of osmolytes on unfolding. 2013 , 95, 912-21	6
247	Chemical synthesis and formulation design of a PEGylated vasoactive intestinal peptide derivative with improved metabolic stability. 2013 , 49, 382-9	5
246	The tropomyosin binding region of cardiac troponin T modulates crossbridge recruitment dynamics in rat cardiac muscle fibers. 2013 , 425, 1565-81	20
245	Structural alterations of Lamin A protein in dilated cardiomyopathy. 2013 , 52, 4229-41	19
244	The human ITPA polymorphic variant P32T is destabilized by the unpacking of the hydrophobic core. 2013 , 182, 197-208	12

243	Overestimated accuracy of circular dichroism in determining protein secondary structure. 2013 , 42, 455-61	8
242	A facile and green ultrasonic-assisted synthesis of BSA conjugated silver nanoparticles. <i>Colloids and Surfaces B: Biointerfaces</i> , 2013 , 102, 879-83	6 19
241	Elastin binding protein and FKBP65 modulate in vitro self-assembly of human tropoelastin. 2013 , 52, 7731-41	20
240	Improved protease stability of the antimicrobial peptide Pin2 substituted with D-amino acids. 2013 , 32, 456-66	46
239	CAPITO--a web server-based analysis and plotting tool for circular dichroism data. 2013 , 29, 1750-7	163
238	Design, purification and characterization of a soluble variant of the integral membrane protein MotB for structural studies. 2013 , 10, 20120717	2
237	Recruitment of TLR adapter TRIF to TLR4 signaling complex is mediated by the second helical region of TRIF TIR domain. 2013 , 110, 19036-41	40
236	Intrinsically unstructured proteins by design-electrostatic interactions can control binding, folding, and function of a helix-loop-helix heterodimer. 2013 , 19, 461-9	4
235	Identification of key amino acid residues in the catalytic mechanism of diaminopropionate ammonialyase from <i>Salmonella typhimurium</i> . 2013 , 280, 5039-51	2
234	Elucidating protein secondary structure with circular dichroism and a neural network. 2013 , 34, 2774-86	13
233	Effect of High Pressure Microfluidization on Secondary Structure of Wheat Gluten in Different Solvents. 2013 , 781-784, 770-773	
232	Properties and mutation studies of a bacteriophage-derived chimeric recombinant staphylolytic protein P128: Comparison to recombinant lysostaphin. 2013 , 3, e26564	12
231	Expression and purification of functional human mu opioid receptor from E.coli. <i>PLoS ONE</i> , 2013 , 8, e56509	7
230	Characterization of the <i>Arabidopsis thaliana</i> E3 ubiquitin-ligase AtSINAL7 and identification of the ubiquitination sites. <i>PLoS ONE</i> , 2013 , 8, e73104	3-7 7
229	BtcA, A class IA type III chaperone, interacts with the BteA N-terminal domain through a globular/non-globular mechanism. <i>PLoS ONE</i> , 2013 , 8, e81557	3-7 6
228	N-acylated peptides derived from human lactoferricin perturb organization of cardiolipin and phosphatidylethanolamine in cell membranes and induce defects in <i>Escherichia coli</i> cell division. <i>PLoS ONE</i> , 2014 , 9, e90228	3-7 27
227	Targeting of the MYCN protein with small molecule c-MYC inhibitors. <i>PLoS ONE</i> , 2014 , 9, e97285	3-7 52
226	In silico and in vitro studies on the protein-protein interactions between <i>Brugia malayi</i> immunomodulatory protein calreticulin and human C1q. <i>PLoS ONE</i> , 2014 , 9, e106413	3-7 28

225	Purification of Recombinant Peanut Allergen Ara h 1 and Comparison of IgE Binding to the Natural Protein. 2014 , 3, 642-657		8
224	Purification and characterization of guanylate kinase, a nucleoside monophosphate kinase of <i>Brugia malayi</i> . 2014 , 141, 1341-52		3
223	Protein expression, characterization and activity comparisons of wild type and mutant DUSP5 proteins. 2014 , 15, 27		9
222	Polymorphisms at amino acid residues 141 and 154 influence conformational variation in ovine PrP. 2014 , 2014, 372491		4
221	Biophysical and structural characterization of the thioredoxin-binding domain of protein kinase ASK1 and its interaction with reduced thioredoxin. 2014 , 289, 24463-74		29
220	Characterization of RNA binding and chaperoning activities of HIV-1 Vif protein. Importance of the C-terminal unstructured tail. 2014 , 11, 906-20		11
219	Completing the structural family portrait of the human EphB tyrosine kinase domains. <i>Protein Science</i> , 2014 , 23, 627-38	6.3	12
218	HIV-1 Vif N-terminal motif is required for recruitment of Cul5 to suppress APOBEC3. 2014 , 11, 4		15
217	Perturbation of apoptosis upon binding of tRNA to the heme domain of cytochrome c. 2014 , 19, 259-68		15
216	Human heat shock protein 70 (Hsp70) as a peripheral membrane protein. 2014 , 1838, 1344-61		32
215	Facile purification of Escherichia coli expressed tag-free recombinant human tumor necrosis factor alpha from supernatant. <i>Protein Expression and Purification</i> , 2014 , 95, 195-203	2	9
214	Thermal and pH Stability of the B-Phycoerythrin from the Red Algae <i>Porphyridium cruentum</i> . 2014 , 9, 184-192		27
213	Structural insights into recognition of acetylated histone ligands by the BRPF1 bromodomain. 2014 , 588, 3844-54		22
212	Structure and functional investigation of ligand binding by a family 35 carbohydrate binding module (CtCBM35) of α -mannanase of family 26 glycoside hydrolase from <i>Clostridium thermocellum</i> . 2014 , 79, 672-86		4
211	SSNN, a method for neural network protein secondary structure fitting using circular dichroism data. 2014 , 6, 6721-6726		10
210	Ligand-binding pocket bridges DNA-binding and dimerization domains of the urate-responsive MarR homologue MftR from <i>Burkholderia thailandensis</i> . 2014 , 53, 4368-80		26
209	Transition of transferrin from native to fibrillar state: An implication for amyloid-linked diseases. 2014 , 91, 120-128		9
208	Inhibition of amyloid fibril formation of hen egg white lysozyme by trimethylamine N-oxide at low pH. <i>International Journal of Biological Macromolecules</i> , 2014 , 70, 214-21	7.9	35

207	Phosphoketolases from <i>Lactococcus lactis</i> , <i>Leuconostoc mesenteroides</i> and <i>Pseudomonas aeruginosa</i> : dissimilar sequences, similar substrates but distinct enzymatic characteristics. 2014 , 98, 7855-67		7
206	Studies on the structure of the bioregulator purified from the rat brain. 2014 , 50, 398-403		3
205	Distinct circular dichroism spectroscopic signatures of polyproline II and unordered secondary structures: applications in secondary structure analyses. <i>Protein Science</i> , 2014 , 23, 1765-72	6.3	111
204	Molecular cloning and characterization of <i>Brugia malayi</i> thymidylate kinase. 2014 , 133, 83-92		8
203	Protein secondary structure prediction from circular dichroism spectra using a self-organizing map with concentration correction. 2014 , 26, 471-82		14
202	Purification and characterisation of recombinant DNA encoding the alternative oxidase from <i>Sauromatum guttatum</i> . 2014 , 19 Pt B, 261-8		10
201	Structural insights into the intertwined dimer of fyn SH2. <i>Protein Science</i> , 2015 , 24, 1964-78	6.3	6
200	Effects of Small Molecule Calcium-Activated Chloride Channel Inhibitors on Structure and Function of Accessory Cholera Enterotoxin (Ace) of <i>Vibrio cholerae</i> . <i>PLoS ONE</i> , 2015 , 10, e0141283	3.7	5
199	The changes and relationship of structure and functional properties of rabbit myosin during heat-induced gelation. 2015 , 13, 63-68		8
198	Enzymatic attributes of an l-isoaspartyl methyltransferase from and its role in cell survival. 2015 , 4, 59-75		1
197	Additivity of the Specific Effects of Additives on Protein Phase Behavior. 2015 , 119, 14986-93		8
196	Pacific oyster polyamine oxidase: a protein missing link in invertebrate evolution. 2015 , 47, 949-61		2
195	Structural basis of clade-specific HIV-1 neutralization by humanized anti-V3 monoclonal antibody KD-247. 2015 , 29, 70-80		1
194	An efficient method for the purification of proteins from four distinct toxin-antitoxin modules. <i>Protein Expression and Purification</i> , 2015 , 108, 30-40	2	11
193	Host ICAMs play a role in cell invasion by <i>Mycobacterium tuberculosis</i> and <i>Plasmodium falciparum</i> . 2015 , 6, 6049		30
192	Modulating glyoxalase I metal selectivity by deletional mutagenesis: underlying structural factors contributing to nickel activation profiles. 2015 , 7, 605-12		13
191	Identification of three important amino acid residues of xylanase AfxynA from <i>Aspergillus fumigatus</i> for enzyme activity and formation of xylobiose as the major product. 2015 , 50, 571-581		23
190	Nano-anisotropic surface coating based on drug immobilized pendant polymer to suppress macrophage adhesion response. <i>Colloids and Surfaces B: Biointerfaces</i> , 2015 , 128, 8-16	6	2

189	The surfactant-induced conformational and activity alterations in <i>Rhizopus niveus</i> lipase. 2015 , 71, 1199-206	85
188	Spectroscopic studies on interactions of the tetrakis(acetato)chloridodiruthenium(II,III) complex and the Ru ₂ (II,III)-NSAID-derived metallodrugs of ibuprofen and ketoprofen with human serum albumin. 2015 , 68, 3209-3228	12
187	Structural mechanism of complex assemblies: characterisation of beta-lactoglobulin and pectin interactions. 2015 , 11, 6790-9	49
186	Purification, characterization and kinetics of protease inhibitor from fruits of <i>Solanum aculeatissimum</i> Jacq. 2015 , 4, 97-107	18
185	Circular Dichroism. 2015 , 383-416	
184	Lipid-free antigen B subunits from <i>echinococcus granulosus</i> : oligomerization, ligand binding, and membrane interaction properties. 2015 , 9, e0003552	7
183	Multiple nucleophilic elbows leading to multiple active sites in a single module esterase from <i>Sorangium cellulosum</i> . 2015 , 190, 314-27	5
182	Isolation, purification, and characterization of avian antimicrobial glycopeptide from the posterior salivary gland of <i>Sepia pharaonis</i> . 2015 , 175, 1507-18	6
181	New potential eukaryotic substrates of the mycobacterial protein tyrosine phosphatase PtpA: hints of a bacterial modulation of macrophage bioenergetics state. <i>Scientific Reports</i> , 2015 , 5, 8819	4-9 15
180	Structural characterization of a novel peptide with antimicrobial activity from the venom gland of the scorpion <i>Tityus stigmurus</i> : Stigmurin. 2015 , 68, 3-10	30
179	Heat-induced conformational changes of TET peptidase from crenarchaeon <i>Desulfurococcus kamchatkensis</i> . 2015 , 44, 667-75	1
178	A <i>Neurospora crassa</i> β -glucosidase with potential for lignocellulose hydrolysis shows strong glucose tolerance and stimulation by glucose and xylose. 2015 , 122, 131-140	21
177	Biochemical Characterization and Substrate Specificity of Autophagin-2 from the Parasite <i>Trypanosoma cruzi</i> . 2015 , 290, 28231-28244	6
176	Circular Dichroism Spectroscopy for Protein Characterization: Biopharmaceutical Applications. 2015 , 109-137	2
175	Secondary structural changes in guanidinium hydrochloride denatured mammalian serum albumins and protective effect of small amounts of cationic gemini surfactant pentanediyldibis(cetyldimethylammonium bromide) and methyl- β -cyclodextrin: A spectroscopic study. 2015 , 439, 170-6	19
174	Deep learning in neural networks: an overview. 2015 , 61, 85-117	8538
173	Inhibition of Kallikrein-Related Peptidases 7 and 5 by Grafting Serpin Reactive-Center Loop Sequences onto Sunflower Trypsin Inhibitor-1 (SFTI-1). 2016 , 17, 719-26	26
172	Heavy-Atom Labeled Transmembrane β -Peptides: Synthesis, CD-Spectroscopy, and X-ray Diffraction Studies in Model Lipid Multilayer. 2016 , 17, 2525-34	8

171	Structural Properties of Potexvirus Coat Proteins Detected by Optical Methods. 2016 , 81, 1522-1530		3
170	Identification of a novel family of carbohydrate-binding modules with broad ligand specificity. <i>Scientific Reports</i> , 2016 , 6, 19392	4.9	21
169	Physical Characterization and Innate Immunogenicity of Aggregated Intravenous Immunoglobulin (IGIV) in an In Vitro Cell-Based Model. 2016 , 33, 1736-51		17
168	Suppression of protein inactivation during freezing by minimizing pH changes using ionic cryoprotectants. 2016 , 509, 41-49		33
167	Synthesis and self-assembly behaviour of poly(NεBoc-L-tryptophan)-block-poly(ethylene glycol)-block-poly(NεBoc-L-tryptophan). 2016 , 6, 24142-24153		
166	Interaction between Albumin and Pluronic F127 Block Copolymer Revealed by Global and Local Physicochemical Profiling. 2016 , 120, 4258-67		18
165	Circular Dichroism Spectroscopy for Structural Characterization of Proteins. 2016 , 223-251		4
164	Loss of second and sixth conserved cysteine residues from trypsin inhibitor-like cysteine-rich domain-type protease inhibitors in <i>Bombyx mori</i> may induce activity against microbial proteases. 2016 , 86, 13-23		7
163	Small-angle X-ray scattering of calpain-5 reveals a highly open conformation among calpains. 2016 , 196, 309-318		10
162	The Interaction of Melittin with Dimyristoyl Phosphatidylcholine-Dimyristoyl Phosphatidylserine Lipid Bilayer Membranes. 2016 , 1858, 2788-2794		14
161	Trans-membrane Signaling in Photosynthetic State Transitions: REDOX- AND STRUCTURE-DEPENDENT INTERACTION IN VITRO BETWEEN STT7 KINASE AND THE CYTOCHROME b6f COMPLEX. 2016 , 291, 21740-21750		14
160	Biochemical and biophysical characterization of a peroxidase isolated from <i>Euphorbia tirucalli</i> with antifungal activity. 2016 , 34, 236-248		3
159	Theranostic Nanocages for Imaging and Photothermal Therapy of Prostate Cancer Cells by Active Targeting of Neuropeptide-Y Receptor. 2016 , 27, 2911-2922		19
158	Antibiotic binding of STY3178, a yfdX protein from <i>Salmonella Typhi</i> . <i>Scientific Reports</i> , 2016 , 6, 21305	4.9	11
157	Secondary Structure of Decorin-Derived Peptides in Solution. 2016 , 1, 1965-1970		
156	Glutamine-mediated self-association of transmembrane peptides within lipid bilayers. 2016 , 7, 5900-5907		7
155	Detergent Isolation Stabilizes and Activates the <i>Shigella</i> Type III Secretion System Translocator Protein IpaC. 2016 , 105, 2240-8		6
154	Characterisation of molten globule-like state of sheep serum albumin at physiological pH. <i>International Journal of Biological Macromolecules</i> , 2016 , 89, 605-13	7.9	18

153	Adsorption and Unfolding of a Single Protein Triggers Nanoparticle Aggregation. 2016 , 10, 2103-12		135
152	Neo-epitopes on methylglyoxal modified human serum albumin lead to aggressive autoimmune response in diabetes. <i>International Journal of Biological Macromolecules</i> , 2016 , 86, 799-809	7.9	13
151	Immunochemical studies on HNE-modified HSA: Anti-HNE-HSA antibodies as a probe for HNE damaged albumin in SLE. <i>International Journal of Biological Macromolecules</i> , 2016 , 86, 145-54	7.9	16
150	Purification and characterization of oligonucleotide binding (OB)-fold protein from medicinal plant <i>Tinospora cordifolia</i> . 2016 , 1008, 38-44		5
149	The E3 ubiquitin-ligase SEVEN IN ABSENTIA like 7 mono-ubiquitinates glyceraldehyde-3-phosphate dehydrogenase 1 isoform in vitro and is required for its nuclear localization in <i>Arabidopsis thaliana</i> . 2016 , 70, 48-56		18
148	Fabrication of nanofibrous electrospun scaffolds from a heterogeneous library of co- and self-assembling peptides. 2017 , 51, 268-278		24
147	Structure and function of <i>Vibrio cholerae</i> accessory cholera enterotoxin in presence of gold nanoparticles: Dependence on morphology. 2017 , 1861, 977-986		16
146	A novel β -conotoxin from worm-hunting <i>Conus tessulatus</i> that selectively inhibit rat TTX-resistant sodium currents. 2017 , 130, 11-18		9
145	Urea-Driven Epigallocatechin Gallate (EGCG) Permeation into the Ferritin Cage, an Innovative Method for Fabrication of Protein-Polyphenol Co-assemblies. 2017 , 65, 1410-1419		33
144	Effect of chemical denaturants on the conformational stability of GyrB subunit of DNA gyrase from <i>Salmonella enterica</i> serovar Typhi. <i>International Journal of Biological Macromolecules</i> , 2017 , 103, 165-174	7.9	2
143	Caesalpinia bonduc serine proteinase inhibitor CbTI-2: Exploring the conformational features and antimalarial activity. <i>International Journal of Biological Macromolecules</i> , 2017 , 103, 294-306	7.9	2
142	DJ-1, a Parkinson's disease related protein, aggregates under denaturing conditions and co-aggregates with β -synuclein through hydrophobic interaction. 2017 , 1861, 1759-1769		10
141	Functional consequences of B-repeat sequence variation in the staphylococcal biofilm protein Aap: deciphering the assembly code. <i>Biochemical Journal</i> , 2017 , 474, 427-443	3.8	5
140	Rice Cellulose SynthaseA8 Plant-Conserved Region Is a Coiled-Coil at the Catalytic Core Entrance. 2017 , 173, 482-494		18
139	Conformational heterogeneity in tails of DNA-binding proteins is augmented by proline containing repeats. 2017 , 13, 2531-2544		1
138	Membrane binding of the insertion sequence of <i>Proteus vulgaris</i> L-amino acid deaminase stabilizes protein structure and increases catalytic activity. <i>Scientific Reports</i> , 2017 , 7, 13719	4.9	4
137	Structural features of human DJ-1 in distinct Cys106 oxidative states and their relevance to its loss of function in disease. 2017 , 1861, 2619-2629		21
136	Toxicity, teratogenicity and antibacterial activity of posterior salivary gland (PSG) toxin from the cuttlefish <i>Sepia pharaonis</i> (Ehrenberg, 1831). 2017 , 1064, 28-35		7

135	Serum amyloid A forms stable oligomers that disrupt vesicles at lysosomal pH and contribute to the pathogenesis of reactive amyloidosis. 2017 , 114, E6507-E6515		35
134	Molecular Characterization of Viral Responsive Protein 15 and Its Possible Role in Nuclear Export of Virus in Black Tiger Shrimp <i>Penaeus monodon</i> . <i>Scientific Reports</i> , 2017 , 7, 6523	4.9	6
133	Deoxycholate-Enhanced Shigella Virulence Is Regulated by a Rare β -Helix in the Type Three Secretion System Tip Protein IpaD. 2017 , 56, 6503-6514		8
132	Characterization of folding intermediates during urea-induced denaturation of human carbonic anhydrase II. <i>International Journal of Biological Macromolecules</i> , 2017 , 95, 881-887	7.9	19
131	Phosphorylation regulates the secondary structure and function of dentin phosphoprotein peptides. 2017 , 95, 65-75		8
130	Recombinant human Tat-Hsp70-2: A tool for neuroprotection. <i>Protein Expression and Purification</i> , 2017 , 138, 18-24	2	6
129	Trehalose induces functionally active conformation in the intrinsically disordered N-terminal domain of glucocorticoid receptor. 2017 , 35, 2248-2256		5
128	Discovery of Phylloseptins that Defense against Gram-Positive Bacteria and Inhibit the Proliferation of the Non-Small Cell Lung Cancer Cell Line, from the Skin Secretions of Phyllomedusa Frogs. <i>Molecules</i> , 2017 , 22,	4.8	11
127	Promiscuous DNA-binding of a mutant zinc finger protein corrupts the transcriptome and diminishes cell viability. 2017 , 45, 1130-1143		23
126	One-step fabrication of phytoferritin-chitosan-epigallocatechin shell-core nanoparticles by thermal treatment. 2018 , 80, 24-32		11
125	Hydroxynitrile lyases from cyanogenic millipedes: molecular cloning, heterologous expression, and whole-cell biocatalysis for the production of (R)-mandelonitrile. <i>Scientific Reports</i> , 2018 , 8, 3051	4.9	9
124	Alcalase Enzymolysis of Red Bean (adzuki) Ferritin Achieves Nanoencapsulation of Food Nutrients in a Mild Condition. 2018 , 66, 1999-2007		5
123	Estimation of structure and stability of MurE ligase from <i>Salmonella enterica</i> serovar Typhi. <i>International Journal of Biological Macromolecules</i> , 2018 , 109, 375-382	7.9	2
122	Tchebichef image moment approach to the prediction of protein secondary structures based on circular dichroism. 2018 , 86, 751-758		6
121	MxiN Differentially Regulates Monomeric and Oligomeric Species of the Shigella Type Three Secretion System ATPase Spa47. 2018 , 57, 2266-2277		16
120	Circular dichroism in functional quality evaluation of medicines. 2018 , 147, 50-64		25
119	Biochemical characterization of INTS3 and C9ORF80, two subunits of hNABP1/2 heterotrimeric complex in nucleic acid binding. <i>Biochemical Journal</i> , 2018 , 475, 45-60	3.8	11
118	An engineered arginine-rich β helical antimicrobial peptide exhibits broad-spectrum bactericidal activity against pathogenic bacteria and reduces bacterial infections in mice. <i>Scientific Reports</i> , 2018 , 8, 14602	4.9	21

117	The yeast GRASP Grh1 displays a high polypeptide backbone mobility along with an amyloidogenic behavior. <i>Scientific Reports</i> , 2018 , 8, 15690	4.9	11
116	Pulsed Electric Fields-Modified Ferritin Realizes Loading of Rutin by a Moderate pH Transition. 2018 , 66, 12404-12411		11
115	Control of Hexamerization, Assembly, and Excluded Strand Specificity for the Sulfolobus solfataricus MCM Helicase. 2018 , 57, 5672-5682		3
114	Mapping an Equilibrium Folding Intermediate of the Cytolytic Pore Toxin ClyA with Single-Molecule FRET. 2018 , 122, 11251-11261		9
113	Effect of atmospheric cold plasma on structure, activity, and reversible assembly of the phytoferritin. 2018 , 264, 41-48		23
112	Quantification of Intrinsically Disordered Proteins: A Problem Not Fully Appreciated. <i>Frontiers in Molecular Biosciences</i> , 2018 , 5, 83	5.6	14
111	The Kinetics of Amyloid Fibrillar Aggregation of Uperin 3.5 Is Directed by the Peptide β Secondary Structure. 2019 , 58, 3656-3668		9
110	Materials & Methods. 2019 , 31-47		
109	Effect of Substitution Pro32Thr on the Interaction between Dimer Subunits of Human Phosphatase ITPA. 2019 , 15, 46-54		
108	Breaking the Backbone: Central Arginine Residues Induce Membrane Exit and Helix Distortions within a Dynamic Membrane Peptide. 2019 , 123, 8034-8047		7
107	Formation and Stabilization of Gold Nanoparticles in Bovine Serum Albumin Solution. <i>Molecules</i> , 2019 , 24,	4.8	21
106	Assessment of the denaturation of collagen protein concentrates using different techniques. 2019 , 400, 1583-1591		7
105	Optimized production and quantification of the tryptophan-deficient sweet-tasting protein brazzein in. 2019 , 49, 790-799		4
104	Structural and immunological characterization of a new nucleotidyltransferase-like antigen from <i>Paracoccidioides brasiliensis</i> . 2019 , 112, 151-162		4
103	Influence of Manothermosonication on the Physicochemical and Functional Properties of Ferritin as a Nanocarrier of Iron or Bioactive Compounds. 2019 , 67, 6633-6641		11
102	Effect of temperature on the actomyosin-paramyosin structure from giant squid mantle (<i>Dosidicus gigas</i>). 2019 , 99, 5377-5383		2
101	Insights into the effect of imidazolium-based ionic liquids on chemical structure and hydrolytic activity of microbial lipase. 2019 , 42, 1235-1246		6
100	Expression, Purification, and Characterization of Human Diacylglycerol Kinase α 2019 , 4, 5540-5546		5

99	Transglutaminase induced oligochitosan glycosylation of ferritin as a novel nanocarrier for food bioactive molecules. 2019 , 94, 500-509		18
98	Tau aggregation and seeding analyses of two novel MAPT variants found in patients with motor neuron disease and progressive parkinsonism. 2019 , 84, 240.e13-240.e22		5
97	Thermodynamic Stability of the Transcription Regulator PaaR2 from Escherichia coli O157:H7. 2019 , 116, 1420-1431		3
96	Biochemical Characterization of a Novel β -Hydrolase/FSH from the White Shrimp. 2019 , 9,		1
95	X-ray structure and characterization of a thermostable lipase from Geobacillus thermoleovorans. 2019 , 508, 145-151		11
94	Structural characterization, teratogenicity and in vitro avian antimicrobial activity of posterior salivary gland (PSG) toxin from cuttlefish, Sepia prashadi. <i>International Journal of Biological Macromolecules</i> , 2019 , 124, 1145-1155	7.9	4
93	Small-angle X-ray scattering based structure, modeling and molecular dynamics analyses of a family 5 glycoside hydrolase first endo-mannanase named as GH5_7 from. 2020 , 38, 4371-4384		1
92	Optimization of recombinant maize CDKA;1 and CycD6;1 production in Escherichia coli by response surface methodology. <i>Protein Expression and Purification</i> , 2020 , 165, 105483	2	8
91	Biopharmaceutical applications of protein characterisation by circular dichroism spectroscopy. 2020 , 123-152		0
90	Structural role of essential light chains in the apicomplexan glideosome. 2020 , 3, 568		6
89	MIRRAGGE - Minimum Information Required for Reproducible AGGregation Experiments. 2020 , 13, 582488		4
88	Polyunsaturated fatty acid-containing phosphatidic acids selectively interact with L-lactate dehydrogenase A and induce its secondary structural change and inactivation. 2020 , 1865, 158768		5
87	Conformational dynamics of a G protein-coupled receptor helix 8 in lipid membranes. 2020 , 6, eaav8207		10
86	Selenoprotein N is an endoplasmic reticulum calcium sensor that links luminal calcium levels to a redox activity. 2020 , 117, 21288-21298		16
85	Hybrid Antimicrobial Peptide Targeting s and Displaying Anti-infective Activity in a Murine Model. 2020 , 11, 1767		4
84	Finding Value in Wastewaters from the Cork Industry: Carbon Dots Synthesis and Fluorescence for Hemeprotein Detection. <i>Molecules</i> , 2020 , 25,	4.8	1
83	Effects of molecular weight and structural conformation of multivalent-based elastin-like polypeptides on tumor accumulation and tissue biodistribution. 2020 , 4, 57-70		1
82	The BRPF1 bromodomain is a molecular reader of di-acetyllysine. 2020 , 2, 104-115		5

81	Combined SAXS and computational approaches for structure determination and binding characteristics of Chimera (CtGH1-L1-CtGH5-F194A) generated by assembling Eglucosidase (CtGH1) and a mutant endoglucanase (CtGH5-F194A) from <i>Clostridium thermocellum</i> . <i>International Journal of Biological Macromolecules</i> , 2020 , 148, 364-377	7.9	11
80	Identification of the Repressive Domain of the Negative Circadian Clock Component CHRONO. 2020 , 21,		8
79	Protein binding and antioxidant studies of diimine based emissive surfactant-ruthenium(II) complexes. 2021 , 39, 1535-1546		0
78	Insights into the interaction of Bovine Serum Albumin with Surface-Active Ionic Liquids in aqueous solution. 2021 , 322, 114537		19
77	CD-NuSS: A Web Server for the Automated Secondary Structural Characterization of the Nucleic Acids from Circular Dichroism Spectra Using Extreme Gradient Boosting Decision-Tree, Neural Network and Kohonen Algorithms. 2021 , 433, 166629		5
76	Enzymatic and structural properties of human glutamine:fructose-6-phosphate amidotransferase 2 (hGFAT2). 2021 , 296, 100180		0
75	Bayesian inference assessment of protein secondary structure analysis using circular dichroism data - how much structural information is contained in protein circular dichroism spectra?. 2021 , 13, 359-368		4
74	S. mansoni SmKI-1 Kunitz-domain: Leucine point mutation at P1 site generates enhanced neutrophil elastase inhibitory activity. 2021 , 15, e0009007		2
73	Molecular model of a sensor of two-component signaling system. <i>Scientific Reports</i> , 2021 , 11, 10774	4.9	2
72	Effect of gold nanoparticles on the structure and neuroprotective function of protein L-isoaspartyl methyltransferase (PIMT). <i>Scientific Reports</i> , 2021 , 11, 14296	4.9	2
71	DichroWeb, a website for calculating protein secondary structure from circular dichroism spectroscopic data. <i>Protein Science</i> , 2021 ,	6.3	31
70	Cholesterol Is a Dose-Dependent Positive Allosteric Modulator of CCR3 Ligand Affinity and G Protein Coupling. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 724603	5.6	6
69	Gallic acid anti-myotoxic activity and mechanism of action, a snake venom phospholipase A toxin inhibitor, isolated from the medicinal plant <i>Anacardium humile</i> . <i>International Journal of Biological Macromolecules</i> , 2021 , 185, 494-512	7.9	2
68	The gold nanoparticle reduces <i>Vibrio cholerae</i> pathogenesis by inhibition of biofilm formation and disruption of the production and structure of cholera toxin. <i>Colloids and Surfaces B: Biointerfaces</i> , 2021 , 204, 111811	6	3
67	Preparation of novel cinnamaldehyde derivative BSA nanoparticles with high stability, good cell penetrating ability, and promising anticancer activity. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2021 , 624, 126765	5.1	3
66	7 Circular dichroism (CD) parameters and secondary structure estimates of proteins. 7001-7018		3
65	Circular dichroism (CD) analyses of protein-protein interactions. <i>Methods in Molecular Biology</i> , 2015 , 1278, 239-65	1.4	14
64	An Overview of SOM Literature. <i>Springer Series in Information Sciences</i> , 2001 , 347-371		5

63	An Overview of SOM Literature. <i>Springer Series in Information Sciences</i> , 1995 , 231-252		1
62	Structural insight into the interaction of amyloid- β peptide with biological membranes by solid state NMR. <i>Focus on Structural Biology</i> , 2001 , 203-214		5
61	The carboxy-terminal region of the TBC1D4 (AS160) RabGAP mediates protein homodimerization. <i>International Journal of Biological Macromolecules</i> , 2017 , 103, 965-971	7.9	4
60	Interaction of silver nanoparticles with Lysozyme: Functional and structural investigations. <i>Surfaces and Interfaces</i> , 2018 , 10, 216-221	4.1	18
59	5:Metallothioneins in Plants. <i>Metal Ions in Life Sciences</i> , 2009 , 107-153		24
58	Structural role of essential light chains in the apicomplexan glideosome.		2
57	Contribution of individual disulfide bonds to biological action of Escherichia coli heat-stable enterotoxin B. <i>Infection and Immunity</i> , 1995 , 63, 4715-20	3.7	26
56	Renaturation of recombinant Treponema pallidum rare outer membrane protein 1 into a trimeric, hydrophobic, and porin-active conformation. <i>Journal of Bacteriology</i> , 1999 , 181, 7168-75	3.5	10
55	PLUNC is a novel airway surfactant protein with anti-biofilm activity. <i>PLoS ONE</i> , 2010 , 5, e9098	3.7	93
54	The regulatory subunit of PKA-I remains partially structured and undergoes β aggregation upon thermal denaturation. <i>PLoS ONE</i> , 2011 , 6, e17602	3.7	10
53	Notch ankyrin repeat domain variation influences leukemogenesis and Myc transactivation. <i>PLoS ONE</i> , 2011 , 6, e25645	3.7	7
52	Binding-folding induced regulation of AF1 transactivation domain of the glucocorticoid receptor by a cofactor that binds to its DNA binding domain. <i>PLoS ONE</i> , 2011 , 6, e25875	3.7	21
51	Pollutant-induced modulation in conformation and β actamase activity of human serum albumin. <i>PLoS ONE</i> , 2012 , 7, e38372	3.7	65
50	Hsp70 oligomerization is mediated by an interaction between the interdomain linker and the substrate-binding domain. <i>PLoS ONE</i> , 2013 , 8, e67961	3.7	60
49	Structural and biophysical characterization of the cytoplasmic domains of human BAP29 and BAP31. <i>PLoS ONE</i> , 2013 , 8, e71111	3.7	15
48	Role of the N-terminal seven residues of surfactant protein B (SP-B). <i>PLoS ONE</i> , 2013 , 8, e72821	3.7	8
47	A strategy for synthesis of pathogenic human immunoglobulin free light chains in E. coli. <i>PLoS ONE</i> , 2013 , 8, e76022	3.7	17
46	Conformational analysis of isolated domains of Helicobacter pylori CagA. <i>PLoS ONE</i> , 2013 , 8, e79367	3.7	13

45	Expression and properties of the highly alkalophilic phenylalanine ammonia-lyase of thermophilic <i>Rubrobacter xylanophilus</i> . <i>PLoS ONE</i> , 2014 , 9, e85943	3.7	16
44	C-terminal engineering of CXCL12 and CCL5 chemokines: functional characterization by electrophysiological recordings. <i>PLoS ONE</i> , 2014 , 9, e87394	3.7	5
43	Molecular characterization and expression of a novel alcohol oxidase from <i>Aspergillus terreus</i> MTCC6324. <i>PLoS ONE</i> , 2014 , 9, e95368	3.7	5
42	Characterization of antibacterial and hemolytic activity of synthetic pandinin 2 variants and their inhibition against <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2014 , 9, e101742	3.7	38
41	The Eukaryotic-Specific ISD11 Is a Complex-Orphan Protein with Ability to Bind the Prokaryotic IscS. <i>PLoS ONE</i> , 2016 , 11, e0157895	3.7	6
40	Ssn6-Tup1 global transcriptional co-repressor: Role of the N-terminal glutamine-rich region of Ssn6. <i>PLoS ONE</i> , 2017 , 12, e0186363	3.7	3
39	Conformational Differences Unfold a Wide Range of Enterotoxigenic Abilities Exhibited by rNSP4 Peptides from Different Rotavirus Strains. <i>The Open Virology Journal</i> , 2011 , 5, 124-35	1.9	4
38	Biophysical characterization and modeling of human Ecdysoless (ECD) protein supports a scaffolding function. <i>AIMS Biophysics</i> , 2016 , 3, 195-208	0.8	2
37	C9orf72, a protein associated with amyotrophic lateral sclerosis (ALS) is a guanine nucleotide exchange factor. <i>PeerJ</i> , 2018 , 6, e5815	3.1	31
36	Characterization of Conjugates between β -lactalbumin and Benzyl Isothiocyanate-Effects on Molecular Structure and Proteolytic Stability. <i>Molecules</i> , 2021 , 26,	4.8	1
35	Recombinant expression and molecular characterization of buffalo sperm lysozyme-like protein 1. <i>Protein Expression and Purification</i> , 2022 , 190, 105993	2	
34	Rapid preparation of nanodiscs for biophysical studies. <i>Archives of Biochemistry and Biophysics</i> , 2021 , 712, 109051	4.1	1
33	An Unsupervised Learning Method that Produces Organized Representations from Real Information. <i>Perspectives in Neural Computing</i> , 2000 , 45-53		0
32	Optical Spectroscopic Methods for the Analysis of Biological Macromolecules. 2013 , 33-90		
31	Biophysical characterization. <i>Advances in Experimental Medicine and Biology</i> , 2014 , 794, 41-67	3.6	
30	Spectroscopic Evidence for the Flexibility of PsaD in Solution. 1995 , 1719-1722		
29	The yeast GRASP Grh1 displays a high polypeptide backbone mobility along with an amyloidogenic behavior.		
28	Biophysical Techniques to Analyze Elastic Tissue Extracellular Matrix Proteins Interacting with ADAMTS Proteins. <i>Methods in Molecular Biology</i> , 2020 , 2043, 213-235	1.4	

27	Elucidating the Role of Val-Asn 95 and Arg-Gly 52 Mutations on Structure and Stability of Fibroblast Growth Factor Homologous Factor 2. <i>Protein and Peptide Letters</i> , 2019 , 26, 848-859	1.9	
26	Crystal structure of the membrane anchoring domain of mycobacterial Wag31: a dimer-of-dimer suggests how a Wag31 filament might self-assemble.		
25	Structural basis of self-assembly in the lipid-binding domain of mycobacterial polar growth factor Wag31. <i>IUCrJ</i> , 2020 , 7, 767-776	4.7	1
24	Updates on enzymatic and structural properties of human glutamine: fructose-6-phosphate amidotransferase 2 (hGFAT2).		
23	Zinc-Dependent Oligomerization of Trigger Factor Chaperone. <i>Biology</i> , 2021 , 10,	4.9	0
22	The BRPF1 bromodomain is a molecular reader of di-acetyllysine.		
21	Secondary structural characterization of the nucleic acids from circular dichroism spectra using extreme gradient boosting decision-tree algorithm.		1
20	References for 7. 7198-7232		
19	Cloning, post-translational modifications, heterologous expression and ligand-binding of boar salivary lipocalin. <i>Biochemical Journal</i> , 2000 , 350 Pt 2, 369-79	3.8	14
18	Surface nanotopography mediated albumin adsorption, unfolding and modulation of early innate immune responses. <i>Materials Today Advances</i> , 2021 , 12, 100187	7.4	0
17	Application of circular dichroism spectroscopy in studying protein folding, stability, and interaction. 2022 , 213-224		0
16	Effect of Graphite Oxide on the Catalytic Behavior of (S)-Selective Amine Transaminases. <i>Frontiers in Catalysis</i> , 2022 , 1,		0
15	Anti-hyperglycemic activity of HPLC-fractionated Momordica charantia seed extract enriched in a novel napin-like protein in experimental diabetic rats and its validation with recombinant napin-like protein. <i>Current Research in Biotechnology</i> , 2022 , 4, 179-189	4.8	0
14	Phosphorylated and Phosphomimicking Variants May Differ-A Case Study of 14-3-3 Protein.. <i>Frontiers in Chemistry</i> , 2022 , 10, 835733	5	0
13	Impact of Fluorinated Ionic Liquids on Human Phenylalanine Hydroxylase-A Potential Drug Delivery System.. <i>Nanomaterials</i> , 2022 , 12,	5.4	2
12	Data_Sheet_1.PDF. 2020 ,		
11	Table_1.pdf. 2018 ,		
10	Table_1.XLSX. 2020 ,		

- 9 Surface chemistry mediated albumin adsorption, conformational changes and influence on innate immune responses. *Applied Surface Science*, **2022**, 596, 153518 6.7 ○
- 8 Experimental and In Silico interaction studies of Alpha Amylase-Silver nanoparticle: a nano-bio-conjugate. 1
- 7 Recombinant Human ACE2-Fc : A promising therapy for SARS-CoV2 infection.
- 6 De Novo Self-Assembling Peptides Mediate the Conversion of Temozolomide and Delivery of a Model Drug into Glioblastoma Multiforme Cells. **2022**, 10, 2164 ○
- 5 Computationally Guided Redesign of a Heme-free Cytochrome with Native-like Structure and Stability. **2022**, 61, 2063-2072 ○
- 4 The Molecular and Evolutionary Principles of Histone Folding in Eukarya and Archaea. ○
- 3 Biochemical characterization, substrate and stereoselectivity of an outer surface putative β hydrolase from the pathogenic *Leptospira*. **2023**, 229, 803-813 ○
- 2 Cytochrome C with Peroxidase-like Activity Supported on Plasmonic AuNPs: Improved Stability and Enhanced Nanobioplasmonic Catalytic Conversion. ○
- 1 Circular Dichroism. **2023**, 445-481 ○