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Citation Report

#	ARTICLE	IF	CITATIONS
1	Small-angle scattering studies of biological macromolecules in solution. Reports on Progress in Physics, 2003, 66, 1735-1782.	8.1	867
2	Evaluation of small-angle x-ray scattering data of a Raney-type Ni catalyst with computer simulation. Journal of Chemical Physics, 2004, 121, 10634-10640.	1.2	4
3	Structural Insights into the Mechanism of Formation of Cellulosomes Probed by Small Angle X-ray Scattering. Journal of Biological Chemistry, 2004, 279, 55985-55994.	1.6	48
4	Conformational Variability of Nucleo-cytoplasmic Transport Factors. Journal of Biological Chemistry, 2004, 279, 2176-2181.	1.6	74
5	The Crystal and Solution Structure of a Putative Transcriptional Antiterminator from Mycobacterium tuberculosis. Structure, 2004, 12, 1595-1605.	1.6	42
6	Structure and RNA Interactions of the N-Terminal RRM Domains of PTB. Structure, 2004, 12, 1631-1643.	1.6	87
7	Synergistic use of synchrotron radiation techniques for biological samples in solution: a case study on protein-ligand recognition by the peroxisomal import receptor Pex5p. Journal of Synchrotron Radiation, 2004, 11, 490-496.	1.0	15
8	Platinum Nanoparticles Generated in Functionality-Enhanced Reaction Media Based on Polyoctadecylsiloxane with Long-Chain Functional Modifiers. Journal of Physical Chemistry B, 2004, 108, 6175-6185.	1.2	15
9	The Solution Structure and Oligomerization Behavior of Two Bacterial Toxins: Pneumolysin and Perfringolysin O. Biophysical Journal, 2004, 87, 540-552.	0.2	48
10	Structural analysis of the stalk subunit Vma5p of the yeast V-ATPase in solution. FEBS Letters, 2004, 570, 119-125.	1.3	44
11	Structural characterization of the nonameric assembly of an Archaeal β -l-fucosidase by synchrotron small angle X-ray scattering. Biochemical and Biophysical Research Communications, 2004, 320, 176-182.	1.0	21
12	Solution Structure of the Tn3 Resolvase-Crossover Site Synaptic Complex. Molecular Cell, 2004, 16, 127-137.	4.5	44
13	Crystal Structure of the Coiled-coil Dimerization Motif of Geminin: Structural and Functional Insights on DNA Replication Regulation. Journal of Molecular Biology, 2004, 342, 275-287.	2.0	29
14	Structural Flexibility of the N-terminal β -Barrel Domain of 15-Lipoxygenase-1 Probed by Small Angle X-ray Scattering. Functional Consequences for Activity Regulation and Membrane Binding. Journal of Molecular Biology, 2004, 343, 917-929.	2.0	51
15	Low-Resolution Reconstruction of a Synthetic DNA Holliday Junction. Biophysical Journal, 2004, 86, 3060-3069.	0.2	18
16	Structural Basis of Cellulosome Efficiency Explored by Small Angle X-ray Scattering. Journal of Biological Chemistry, 2005, 280, 38562-38568.	1.6	95
17	Detection of submicron-sized raft-like domains in membranes by small-angle neutron scattering. European Physical Journal E, 2005, 18, 447-458.	0.7	91
18	Saturated phospholipids promote crystallization but slow down polymorphic transitions in triglyceride nanoparticles. Journal of Controlled Release, 2005, 107, 229-243.	4.8	122

#	ARTICLE	IF	CITATIONS
19	Small-Angle X-Ray Scattering Reveals the Solution Structure of the Full-Length DNA Gyrase A Subunit. <i>Structure</i> , 2005, 13, 287-296.	1.6	65
20	A New Type of Metalloprotein: The Mo Storage Protein from <i>Azotobacter vinelandii</i> Contains a Polynuclear Molybdenum-Oxide Cluster. <i>ChemBioChem</i> , 2005, 6, 405-413.	1.3	49
21	High Charge-Carrier Mobility in π -Deficient Discotic Mesogens: Design and Structure-Property Relationship. <i>Chemistry - A European Journal</i> , 2005, 11, 3349-3362.	1.7	168
22	Glucose isomerase from <i>Streptomyces rubiginosus</i> â€” potential molecular weight standard for small-angle X-ray scattering. <i>Journal of Applied Crystallography</i> , 2005, 38, 555-558.	1.9	47
23	The spatial structure of dendritic macromolecules. <i>Journal of Applied Crystallography</i> , 2005, 38, 996-1003.	1.9	24
24	Activation of the LicT Transcriptional Antiterminator Involves a Domain Swing/Lock Mechanism Provoking Massive Structural Changes. <i>Journal of Biological Chemistry</i> , 2005, 280, 14780-14789.	1.6	64
25	Computational docking and solution x-ray scattering predict a membrane-interacting role for the histone domain of the Ras activator son of sevenless. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16632-16637.	3.3	58
26	Solution X-ray Scattering Evidence for Agonist- and Antagonist-induced Modulation of Cleft Closure in a Glutamate Receptor Ligand-binding Domain. <i>Journal of Biological Chemistry</i> , 2005, 280, 23637-23642.	1.6	24
27	X-ray Snapshots of Peptide Processing in Mutants of Tricorn-interacting Factor F1 from <i>Thermoplasma acidophilum</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33387-33396.	1.6	23
28	<i>Triticum durum</i> Metallothionein. <i>Journal of Biological Chemistry</i> , 2005, 280, 13701-13711.	1.6	54
29	Study of Structural Transition in Low-Temperature Ferroelectric Liquid Crystal Mixture. <i>Molecular Crystals and Liquid Crystals</i> , 2005, 439, 179/[2045]-187/[2053].	0.4	0
30	Metalated Diblock and Triblock Poly(ethylene oxide)-block-poly(4-vinylpyridine) Copolymers:â€” Understanding of Micelle and Bulk Structure. <i>Journal of Physical Chemistry B</i> , 2005, 109, 18786-18798.	1.2	45
31	SAS Solution Structures of the Apo and Mg ²⁺ /BeF ₃ ⁻ -Bound Receiver Domain of DctD from <i>Sinorhizobium meliloti</i> . <i>Biochemistry</i> , 2005, 44, 13962-13969.	1.2	10
32	Sequential Generation of Two Structurally Distinct Ovine Prion Protein Soluble Oligomers Displaying Different Biochemical Reactivities. <i>Journal of Molecular Biology</i> , 2005, 347, 665-679.	2.0	92
33	Negative Regulation of AAA+ ATPase Assembly by Two Component Receiver Domains: A Transcription Activation Mechanism that is Conserved in Mesophilic and Extremely Hyperthermophilic Bacteria. <i>Journal of Molecular Biology</i> , 2005, 353, 242-255.	2.0	53
34	Crosstalk between Primase Subunits Can Act to Regulate Primer Synthesis in trans. <i>Molecular Cell</i> , 2005, 20, 391-401.	4.5	100
35	The SAXS Solution Structure of RF1 Differs from Its Crystal Structure and Is Similar to Its Ribosome Bound Cryo-EM Structure. <i>Molecular Cell</i> , 2005, 20, 929-938.	4.5	98
36	Structure of the Autoinhibited Kinase Domain of CaMKII and SAXS Analysis of the Holoenzyme. <i>Cell</i> , 2005, 123, 849-860.	13.5	293

#	ARTICLE	IF	CITATIONS
37	Contribution of the copper ions in the dinuclear active site to the stability of <i>Carcinus aestuarii</i> hemocyanin. <i>Archives of Biochemistry and Biophysics</i> , 2005, 439, 42-52.	1.4	6
38	Behavior of Tn3 Resolvase in Solution and Its Interaction with res. <i>Biophysical Journal</i> , 2005, 89, 1920-1931.	0.2	12
39	Effects of Urea and Trimethylamine-N-Oxide (TMAO) on the Interactions of Lysozyme in Solution. <i>Biophysical Journal</i> , 2005, 89, 1978-1983.	0.2	43
40	Binding of Full-Length HIV-1 gp120 to CD4 Induces Structural Reorientation around the gp120 Core. <i>Biophysical Journal</i> , 2006, 91, L69-L71.	0.2	9
41	Hybrid Polymer Particles with a Protective Shell: Synthesis, Structure, and Templating. <i>Chemistry of Materials</i> , 2006, 18, 2418-2430.	3.2	14
42	Substrate-induced double sided H-bond network as a means of domain closure in 3-phosphoglycerate kinase. <i>FEBS Letters</i> , 2006, 580, 2698-2706.	1.3	28
43	Dimerisation and an Increase in Active Site Aromatic Groups as Adaptations to High Temperatures: X-ray Solution Scattering and Substrate-bound Crystal Structures of <i>Rhodothermus marinus</i> Endoglucanase Cel12A. <i>Journal of Molecular Biology</i> , 2006, 356, 57-71.	2.0	21
44	Dynamic Flexibility of Double-stranded RNA Activated PKR in Solution. <i>Journal of Molecular Biology</i> , 2006, 359, 610-623.	2.0	21
45	Multiple Assembly States of Lumazine Synthase: A Model Relating Catalytic Function and Molecular Assembly. <i>Journal of Molecular Biology</i> , 2006, 362, 753-770.	2.0	43
46	Mechanism of Oligomerisation of Cyclase-associated Protein from <i>Dictyostelium discoideum</i> in Solution. <i>Journal of Molecular Biology</i> , 2006, 362, 1072-1081.	2.0	8
47	Organization of the SH3-SH2 Unit in Active and Inactive Forms of the c-Abl Tyrosine Kinase. <i>Molecular Cell</i> , 2006, 21, 787-798.	4.5	192
48	Evidence for a dimeric assembly of two titin/teletonin complexes induced by the telethonin C-terminus. <i>Journal of Structural Biology</i> , 2006, 155, 239-250.	1.3	25
49	The ubiquitin-associated domain of AMPK-related kinases regulates conformation and LKB1-mediated phosphorylation and activation. <i>Biochemical Journal</i> , 2006, 394, 545-555.	1.7	95
50	Activation of a Cu/ZnO catalyst for methanol synthesis. <i>Journal of Applied Crystallography</i> , 2006, 39, 209-221.	1.9	28
51	ATSAS2.1, a program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2006, 39, 277-286.	1.9	557
52	Reverse Monte Carlo analysis of small-angle scattering data on colloids and nanoparticles. <i>Journal of Molecular Liquids</i> , 2006, 129, 108-114.	2.3	12
53	Structure of composites prepared via polypyrrole synthesis in supercritical CO ₂ on microporous polyethylene. <i>Polymer Science - Series A</i> , 2006, 48, 827-840.	0.4	6
54	The C-terminal domain of the transcriptional corepressor CtBP is intrinsically unstructured. <i>Protein Science</i> , 2006, 15, 1042-1050.	3.1	44

#	ARTICLE	IF	CITATIONS
55	Structure validation of the Josephin domain of ataxin-3: Conclusive evidence for an open conformation. <i>Journal of Biomolecular NMR</i> , 2006, 36, 267-277.	1.6	44
56	Structural and functional analysis of the coupling subunit F in solution and topological arrangement of the stalk domains of the methanogenic A1AO ATP synthase. <i>Journal of Bioenergetics and Biomembranes</i> , 2006, 38, 83-92.	1.0	33
57	Poly-Ig tandems from I-band titin share extended domain arrangements irrespective of the distinct features of their modular constituents. <i>Journal of Muscle Research and Cell Motility</i> , 2006, 26, 355-365.	0.9	42
58	Small-Angle X-Ray Scattering to Characterize Nanostructures in Inorganic and Hybrid Materials Chemistry. <i>Monatshefte für Chemie</i> , 2006, 137, 529-543.	0.9	42
59	Structural and Functional Aspects of the Sensor Histidine Kinase PrrB from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2006, 14, 275-285.	1.6	41
60	Conformation of Polypyrimidine Tract Binding Protein in Solution. <i>Structure</i> , 2006, 14, 1021-1027.	1.6	60
61	Crystal Structure of the β^2 Domains of the Protein Disulfide Isomerase ERp57. <i>Structure</i> , 2006, 14, 1331-1339.	1.6	127
62	The Ig Doublet Z1Z2: A Model System for the Hybrid Analysis of Conformational Dynamics in Ig Tandems from Titin. <i>Structure</i> , 2006, 14, 1437-1447.	1.6	42
63	Solution scattering studies of conformation stability of xylanase XYNII from <i>Trichoderma longibrachiatum</i> . <i>Biopolymers</i> , 2006, 83, 95-102.	1.2	9
64	Synchrotron radiation small angle scattering studies of thermal stability of xylanase XYNII from <i>Trichoderma longibrachiatum</i> . <i>Biopolymers</i> , 2006, 83, 668-674.	1.2	4
65	Molecular insights into the self-assembly mechanism of dystrophin myotonia kinase. <i>FASEB Journal</i> , 2006, 20, 1142-1151.	0.2	24
66	Nanostructure of fibrillin-1 reveals compact conformation of EGF arrays and mechanism for extensibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 11922-11927.	3.3	56
67	Structural basis of hepatocyte growth factor/scatter factor and MET signalling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4046-4051.	3.3	193
68	Structural and Mutational Analysis of Substrate Complexation by Anthranilate Phosphoribosyltransferase from <i>Sulfolobus solfataricus</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 21410-21421.	1.6	23
69	Effects of organomontmorillonite concentration on the structure formation of nanocomposites with 5CB liquid crystal. <i>Liquid Crystals</i> , 2006, 33, 1113-1119.	0.9	7
70	A New Level of Architectural Complexity in the Human Pyruvate Dehydrogenase Complex. <i>Journal of Biological Chemistry</i> , 2006, 281, 19772-19780.	1.6	74
71	Marfan Syndrome-causing Mutations in Fibrillin-1 Result in Gross Morphological Alterations and Highlight the Structural Importance of the Second Hybrid Domain. <i>Journal of Biological Chemistry</i> , 2006, 281, 31854-31862.	1.6	25
72	The Crystal and Solution Structures of Glyceraldehyde-3-phosphate Dehydrogenase Reveal Different Quaternary Structures. <i>Journal of Biological Chemistry</i> , 2006, 281, 33433-33440.	1.6	34

#	ARTICLE	IF	CITATIONS
73	The structural basis for regulated assembly and function of the transcriptional activator NtrC. <i>Genes and Development</i> , 2006, 20, 1485-1495.	2.7	109
74	The Structural Basis of Signal Transduction for the Response Regulator PrrA from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2006, 281, 9659-9666.	1.6	75
75	Structural Variations in the Catalytic and Ubiquitin-associated Domains of Microtubule-associated Protein/Microtubule Affinity Regulating Kinase (MARK) 1 and MARK2. <i>Journal of Biological Chemistry</i> , 2006, 281, 27586-27599.	1.6	54
76	Monitoring intermediate filament assembly by small-angle x-ray scattering reveals the molecular architecture of assembly intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16206-16211.	3.3	89
77	Structure of PlcR: Insights into virulence regulation and evolution of quorum sensing in Gram-positive bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18490-18495.	3.3	132
78	A Helical Structural Nucleus Is the Primary Elongating Unit of Insulin Amyloid Fibrils. <i>PLoS Biology</i> , 2007, 5, e134.	2.6	229
79	Plant Transformation by <i>Agrobacterium tumefaciens</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 3458-3464.	1.6	31
80	The Structure of a Full-length Response Regulator from <i>Mycobacterium tuberculosis</i> in a Stabilized Three-dimensional Domain-swapped, Activated State. <i>Journal of Biological Chemistry</i> , 2007, 282, 37717-37729.	1.6	37
81	Global Structure Changes Associated with Ca ²⁺ Activation of Full-length Human Plasma Gelsolin. <i>Journal of Biological Chemistry</i> , 2007, 282, 25884-25892.	1.6	53
82	Structure Analysis of Macromolecular Complexes by Solution Small-Angle Scattering. , 2007, , 317-365.		2
83	Fine-tuning of intrinsic N-Oct-3 POU domain allostery by regulatory DNA targets. <i>Nucleic Acids Research</i> , 2007, 35, 4420-4432.	6.5	7
84	Structural Characterization of the Ribosomal P1A~P2B Protein Dimer by Small-Angle X-ray Scattering and NMR Spectroscopy. <i>Biochemistry</i> , 2007, 46, 1988-1998.	1.2	25
85	NMR in soft materials: A study of DMPC/DHPC bicellar system. <i>Journal of Non-Crystalline Solids</i> , 2007, 353, 4246-4251.	1.5	12
86	Structural characterization of β^2 -sheeted oligomers formed on the pathway of oxidative prion protein aggregation in vitro. <i>Journal of Structural Biology</i> , 2007, 157, 308-320.	1.3	51
87	Structural analysis of flexible proteins in solution by small angle X-ray scattering combined with crystallography. <i>Journal of Structural Biology</i> , 2007, 158, 214-223.	1.3	63
88	Structural features of the Bluetongue virus NS2 protein. <i>Journal of Structural Biology</i> , 2007, 160, 157-167.	1.3	19
89	The HC Fragment of Tetanus Toxin forms Stable, Concentration-dependent Dimers via an Intermolecular Disulphide Bond. <i>Journal of Molecular Biology</i> , 2007, 365, 123-134.	2.0	14
90	The Structure of the KinA-Sda Complex Suggests an Allosteric Mechanism of Histidine Kinase Inhibition. <i>Journal of Molecular Biology</i> , 2007, 368, 407-420.	2.0	77

#	ARTICLE	IF	CITATIONS
91	Crystal Structure of Human Filamin C Domain 23 and Small Angle Scattering Model for Filamin C 23-24 Dimer. <i>Journal of Molecular Biology</i> , 2007, 368, 1011-1023.	2.0	28
92	Crystal Structure and Activity of Kunjin Virus NS3 Helicase; Protease and Helicase Domain Assembly in the Full Length NS3 Protein. <i>Journal of Molecular Biology</i> , 2007, 372, 444-455.	2.0	78
93	The Crystal and Solution Studies of Glucosamine-6-phosphate Synthase from <i>Candida albicans</i> . <i>Journal of Molecular Biology</i> , 2007, 372, 672-688.	2.0	34
94	Molecular analysis and solution structure from small-angle X-ray scattering of the human natural killer inhibitory receptor IRp60 (CD300a). <i>International Journal of Biological Macromolecules</i> , 2007, 40, 193-200.	3.6	13
95	Two-Component Systems of <i>Mycobacterium tuberculosis</i> —Structure-Based Approaches. <i>Methods in Enzymology</i> , 2007, 423, 479-501.	0.4	15
96	Small-Angle X-ray Scattering Reveals the Solution Structure of the Peripheral Stalk Subunit H of the A1AO ATP Synthase from <i>Methanocaldococcus jannaschii</i> and Its Binding to the Catalytic A Subunit. <i>Biochemistry</i> , 2007, 46, 2070-2078.	1.2	21
97	Investigation of the Conformational States of Wzz and the Wzz-O-Antigen Complex under Near-Physiological Conditions. <i>Biochemistry</i> , 2007, 46, 11744-11752.	1.2	36
98	Structure and Properties of Iron Oxide Nanoparticles Encapsulated by Phospholipids with Poly(ethylene glycol) Tails. <i>Journal of Physical Chemistry C</i> , 2007, 111, 18078-18086.	1.5	70
99	Conformational Differences between <i>Azotobacter vinelandii</i> Nitrogenase MoFe Proteins As Studied by Small-Angle X-ray Scattering. <i>Biochemistry</i> , 2007, 46, 8066-8074.	1.2	23
100	Protein-Protein Interactions in Complex Cosolvent Solutions. <i>ChemPhysChem</i> , 2007, 8, 679-689.	1.0	53
101	Gain-of-Function Mutational Activation of Human tRNA Synthetase Procytokine. <i>Chemistry and Biology</i> , 2007, 14, 1323-1333.	6.2	33
102	The effect of selected surfactants on the structure of a bicellar system (DMPC/DHPC) studied by SAXS. <i>Journal of Molecular Structure</i> , 2007, 846, 108-111.	1.8	7
103	Accuracy of molecular mass determination of proteins in solution by small-angle X-ray scattering. <i>Journal of Applied Crystallography</i> , 2007, 40, s245-s249.	1.9	328
104	ATSAS 2.1 — towards automated and web-supported small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2007, 40, s223-s228.	1.9	404
105	Rapid shape determination of tissue transglutaminase using high-throughput computing. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2007, 63, 1022-1024.	2.5	2
106	Holoenzyme assembly and ATP-mediated conformational dynamics of topoisomerase VI. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 611-619.	3.6	86
107	Insights into the structure of plant β -type phospholipase- β . <i>FEBS Journal</i> , 2007, 274, 2630-2640.	2.2	17
108	Modular Structure of the Full-Length DNA Gyrase B Subunit Revealed by Small-Angle X-Ray Scattering. <i>Structure</i> , 2007, 15, 329-339.	1.6	35

#	ARTICLE	IF	CITATIONS
109	Synaptic Arrangement of the Neuroligin/β2-Neurexin Complex Revealed by X-Ray and Neutron Scattering. <i>Structure</i> , 2007, 15, 693-705.	1.6	64
110	Insights into the Structure and Domain Flexibility of Full-Length Pro-Matrix Metalloproteinase-9/Gelatinase B. <i>Structure</i> , 2007, 15, 1227-1236.	1.6	113
111	Structure of nanocomposites based on lead sulfide and poly-p-xylylene. <i>Polymer Science - Series A</i> , 2007, 49, 809-815.	0.4	10
112	X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution. <i>Quarterly Reviews of Biophysics</i> , 2007, 40, 191-285.	2.4	1,026
113	H2A and H2B tails are essential to properly reconstitute nucleosome core particles. <i>European Biophysics Journal</i> , 2007, 36, 1083-1094.	1.2	23
114	The boxing glove shape of subunit d of the yeast V-ATPase in solution and the importance of disulfide formation for folding of this protein. <i>Journal of Bioenergetics and Biomembranes</i> , 2007, 39, 275-289.	1.0	24
115	Refined solution structure of the 82-kDa enzyme malate synthase G from joint NMR and synchrotron SAXS restraints. <i>Journal of Biomolecular NMR</i> , 2008, 40, 95-106.	1.6	103
116	Low resolution structure of subunit b (b ₂₂ ~156) of Escherichia coli F1FO ATP synthase in solution and the b ₂₂ ~156 assembly. <i>Journal of Bioenergetics and Biomembranes</i> , 2008, 40, 245-55.	1.0	9
117	Structural Relationships Among the Ribosomal Stalk Proteins from the Three Domains of Life. <i>Journal of Molecular Evolution</i> , 2008, 67, 154-167.	0.8	46
118	Interaction between the C-terminal region of human myelin basic protein and calmodulin: analysis of complex formation and solution structure. <i>BMC Structural Biology</i> , 2008, 8, 10.	2.3	43
119	A covalent S~F heterodimer of leucotoxin reveals molecular plasticity of β-barrel pore-forming toxins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 485-496.	1.5	28
120	Crystal and solution structure, stability and post-translational modifications of collapsin response mediator protein 2. <i>FEBS Journal</i> , 2008, 275, 4583-4596.	2.2	35
121	Isolation and oligomeric composition of cytochrome c nitrite reductase from the haloalkaliphilic bacterium <i>Halobacterium salinarum</i> . <i>Biochemistry (Moscow)</i> , 2008, 73, 164-170.	0.7	8
122	Molecular basis of the C-terminal tail-to-tail assembly of the sarcomeric filament protein myomesin. <i>EMBO Journal</i> , 2008, 27, 253-264.	3.5	33
123	Fold and function of polypeptide transport-associated domains responsible for delivering unfolded proteins to membranes. <i>Molecular Microbiology</i> , 2008, 68, 1216-1227.	1.2	142
124	Structural characterization of soluble E~yt2. <i>FEBS Letters</i> , 2008, 582, 3941-3947.	1.3	7
125	Structure of the Yeast tRNA m7G Methylation Complex. <i>Structure</i> , 2008, 16, 52-61.	1.6	95
126	Multiple Conformations of E. coli Hsp90 in Solution: Insights into the Conformational Dynamics of Hsp90. <i>Structure</i> , 2008, 16, 755-765.	1.6	154

#	ARTICLE	IF	CITATIONS
127	X-Ray Scattering Study of Activated Arp2/3 Complex with Bound Actin-WCA. <i>Structure</i> , 2008, 16, 695-704.	1.6	71
128	The Structure and Binding Behavior of the Bacterial Cell Surface Layer Protein SbsC. <i>Structure</i> , 2008, 16, 1226-1237.	1.6	79
129	Quaternary Structure of Flavorubredoxin as Revealed by Synchrotron Radiation Small-Angle X-Ray Scattering. <i>Structure</i> , 2008, 16, 1428-1436.	1.6	14
130	Structure and Plasticity of Endophilin and Sorting Nexin 9. <i>Structure</i> , 2008, 16, 1574-1587.	1.6	66
131	A Different Conformation for EGC Stator Subcomplex in Solution and in the Assembled Yeast V-ATPase: Possible Implications for Regulatory Disassembly. <i>Structure</i> , 2008, 16, 1789-1798.	1.6	69
132	Structural Basis for Calcium Sensing by GCaMP2. <i>Structure</i> , 2008, 16, 1817-1827.	1.6	148
133	The Acacia Gum Arabinogalactan Fraction Is a Thin Oblate Ellipsoid: A New Model Based on Small-Angle Neutron Scattering and Ab Initio Calculation. <i>Biophysical Journal</i> , 2008, 94, 629-639.	0.2	88
134	Low Resolution Structural Models of the Basic Helix-Loop-Helix Leucine Zipper Domain of Upstream Stimulatory Factor 1 and Its Complexes with DNA from Small Angle X-Ray Scattering Data. <i>Biophysical Journal</i> , 2008, 94, 193-197.	0.2	4
135	Solution Structure of Poly(ethylene) Glycol-Conjugated Hemoglobin Revealed by Small-Angle X-Ray Scattering: Implications for a New Oxygen Therapeutic. <i>Biophysical Journal</i> , 2008, 94, 173-181.	0.2	80
136	Biophysical Characterization of the Unstructured Cytoplasmic Domain of the Human Neuronal Adhesion Protein Neuroligin 3. <i>Biophysical Journal</i> , 2008, 95, 1928-1944.	0.2	45
137	Domain Conformation of Tau Protein Studied by Solution Small-Angle X-ray Scattering. <i>Biochemistry</i> , 2008, 47, 10345-10353.	1.2	187
138	The novel p53 isoform δ p53 is a misfolded protein and does not bind the p21 promoter site. <i>Protein Science</i> , 2008, 17, 1671-1678.	3.1	8
139	A simple nanostructured polymer/ZnO hybrid solar cell's preparation and operation in air. <i>Nanotechnology</i> , 2008, 19, 424013.	1.3	149
140	Hydrophilic Monodisperse Magnetic Nanoparticles Protected by an Amphiphilic Alternating Copolymer. <i>Journal of Physical Chemistry C</i> , 2008, 112, 16809-16817.	1.5	59
141	Structural features of the single-stranded DNA-binding protein of Epstein-Barr virus. <i>Journal of Structural Biology</i> , 2008, 161, 172-187.	1.3	10
142	Structural Characterization of the Active and Inactive States of Src Kinase in Solution by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2008, 376, 492-505.	2.0	49
143	Fab MOR03268 Triggers Absorption Shift of a Diagnostic Dye via Packaging in a Solvent-shielded Fab Dimer Interface. <i>Journal of Molecular Biology</i> , 2008, 377, 206-219.	2.0	9
144	X-ray and Neutron Small-Angle Scattering Analysis of the Complex Formed by the Met Receptor and the <i>Listeria monocytogenes</i> Invasion Protein InlB. <i>Journal of Molecular Biology</i> , 2008, 377, 489-500.	2.0	34

#	ARTICLE	IF	CITATIONS
145	Engineering the NK1 Fragment of Hepatocyte Growth Factor/Scatter Factor as a MET Receptor Antagonist. <i>Journal of Molecular Biology</i> , 2008, 377, 616-622.	2.0	38
146	Small-Angle X-ray Scattering Reveals the N-Terminal Domain Organization of Cardiac Myosin Binding Protein C. <i>Journal of Molecular Biology</i> , 2008, 377, 1186-1199.	2.0	56
147	Structural Basis for Autoinhibition of ESCRT-III CHMP3. <i>Journal of Molecular Biology</i> , 2008, 378, 818-827.	2.0	125
148	Structural Basis of Guanine Nucleotide Exchange Mediated by the T-Cell Essential Vav1. <i>Journal of Molecular Biology</i> , 2008, 380, 828-843.	2.0	51
149	Dissecting NGF Interactions with TrkA and p75 Receptors by Structural and Functional Studies of an Anti-NGF Neutralizing Antibody. <i>Journal of Molecular Biology</i> , 2008, 381, 881-896.	2.0	43
150	Integration of Small-Angle X-Ray Scattering Data into Structural Modeling of Proteins and Their Assemblies. <i>Journal of Molecular Biology</i> , 2008, 382, 1089-1106.	2.0	139
151	Structural Basis of Dcp2 Recognition and Activation by Dcp1. <i>Molecular Cell</i> , 2008, 29, 337-349.	4.5	130
152	Encapsulation of Semiconducting Polymers in Vault Protein Cages. <i>Nano Letters</i> , 2008, 8, 3503-3509.	4.5	31
153	A Novel View on Crystallization and Melting of Semirigid Chain Polymers: The Case of Poly(trimethylene terephthalate). <i>Macromolecules</i> , 2008, 41, 9224-9233.	2.2	66
154	High-Throughput Small Angle X-ray Scattering from Proteins in Solution Using a Microfluidic Front-End. <i>Analytical Chemistry</i> , 2008, 80, 3648-3654.	3.2	88
155	Evidence of Reciprocal Reorientation of the Catalytic and Hemopexin-Like Domains of Full-Length MMP-12. <i>Journal of the American Chemical Society</i> , 2008, 130, 7011-7021.	6.6	84
156	Native and Methylated Cyclodextrins with Positive and Negative Solubility Coefficients in Water Studied by SAXS and SANS. <i>Journal of Physical Chemistry B</i> , 2008, 112, 12888-12898.	1.2	19
157	Dynamics in a Pure Encounter Complex of Two Proteins Studied by Solution Scattering and Paramagnetic NMR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2008, 130, 6395-6403.	6.6	96
158	A Covalent Linker Allows for Membrane Targeting of an Oxylin Biosynthetic Complex. <i>Biochemistry</i> , 2008, 47, 10665-10676.	1.2	13
159	Mixed Co/Fe Oxide Nanoparticles in Block Copolymer Micelles. <i>Langmuir</i> , 2008, 24, 12618-12626.	1.6	17
160	The BARD1 C-Terminal Domain Structure and Interactions with Polyadenylation Factor CstF-50. <i>Biochemistry</i> , 2008, 47, 11446-11456.	1.2	27
161	Structural and Thermodynamic Characterization of T4 Lysozyme Mutants and the Contribution of Internal Cavities to Pressure Denaturation. <i>Biochemistry</i> , 2008, 47, 11097-11109.	1.2	55
162	Solution Conformation and Thermodynamic Characteristics of RNA Binding by the Splicing Factor U2AF65. <i>Journal of Biological Chemistry</i> , 2008, 283, 33641-33649.	1.6	30

#	ARTICLE	IF	CITATIONS
163	Intra- and Intermonomer Interactions Are Required to Synergistically Facilitate ATP Hydrolysis in Hsp90. <i>Journal of Biological Chemistry</i> , 2008, 283, 21170-21178.	1.6	92
164	Evidence for an Elongated Dimeric Structure of Heparin-Binding Hemagglutinin from <i>Mycobacterium tuberculosis</i> . <i>Journal of Bacteriology</i> , 2008, 190, 4749-4753.	1.0	28
165	Structure of tumor suppressor p53 and its intrinsically disordered N-terminal transactivation domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5762-5767.	3.3	359
166	The Subnanometer Resolution Structure of the Glutamate Synthase 1.2-MDa Hexamer by Cryoelectron Microscopy and Its Oligomerization Behavior in Solution. <i>Journal of Biological Chemistry</i> , 2008, 283, 8237-8249.	1.6	30
167	Conformational Rearrangement within the Soluble Domains of the CD4 Receptor Is Ligand-specific. <i>Journal of Biological Chemistry</i> , 2008, 283, 2761-2772.	1.6	30
168	S1 Ribosomal Protein Functions in Translation Initiation and Ribonuclease RegB Activation Are Mediated by Similar RNA-Protein Interactions. <i>Journal of Biological Chemistry</i> , 2008, 283, 13289-13301.	1.6	45
169	Evidence for a Coiled-coil Interaction Mode of Disordered Proteins from Bacterial Type III Secretion Systems. <i>Journal of Biological Chemistry</i> , 2008, 283, 34062-34068.	1.6	38
170	Structural Properties of AMP-activated Protein Kinase. <i>Journal of Biological Chemistry</i> , 2008, 283, 18331-18343.	1.6	82
171	Structural Analysis of a Periplasmic Binding Protein in the Tripartite ATP-independent Transporter Family Reveals a Tetrameric Assembly That May Have a Role in Ligand Transport. <i>Journal of Biological Chemistry</i> , 2008, 283, 32812-32820.	1.6	27
172	Absence of equilibrium cluster phase in concentrated lysozyme solutions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5075-5080.	3.3	163
173	Small Angle X-ray Studies Reveal That <i>Aspergillus niger</i> Glucoamylase Has a Defined Extended Conformation and Can Form Dimers in Solution. <i>Journal of Biological Chemistry</i> , 2008, 283, 14772-14780.	1.6	19
174	The MutS±-Proliferating Cell Nuclear Antigen Interaction in Human DNA Mismatch Repair. <i>Journal of Biological Chemistry</i> , 2008, 283, 13310-13319.	1.6	40
175	Solution structures of 2 : 1 and 1 : 1 DNA polymerase±DNA complexes probed by ultracentrifugation and small-angle X-ray scattering. <i>Nucleic Acids Research</i> , 2008, 36, 849-860.	6.5	20
176	Interaction of Human Complement with Sbi, a Staphylococcal Immunoglobulin-binding Protein. <i>Journal of Biological Chemistry</i> , 2008, 283, 17579-17593.	1.6	139
177	A regular pattern of Ig super-motifs defines segmental flexibility as the elastic mechanism of the titin chain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1186-1191.	3.3	80
178	A Molecular Ruler for Measuring Quantitative Distance Distributions. <i>PLoS ONE</i> , 2008, 3, e3229.	1.1	57
179	Covalently bound substrate at the regulatory site triggers allosteric enzyme activation. <i>Nature Precedings</i> , 2008, , .	0.1	0
180	Domain Swapping and Different Oligomeric States for the Complex Between Calmodulin and the Calmodulin-Binding Domain of Calcineurin A. <i>PLoS ONE</i> , 2009, 4, e5402.	1.1	37

#	ARTICLE	IF	CITATIONS
181	The TCL1A Oncoprotein Interacts Directly with the NF- κ B Inhibitor I κ B. PLoS ONE, 2009, 4, e6567.	1.1	10
182	Rigidity, conformation, and solvation of native and oxidized tannin macromolecules in water-ethanol solution. Journal of Chemical Physics, 2009, 130, 245103.	1.2	34
183	A Molecular Insight into Complement Evasion by the Staphylococcal Complement Inhibitor Protein Family. Journal of Immunology, 2009, 183, 2565-2574.	0.4	63
184	Structural Insights of the Nucleotide-Dependent Conformational Changes of Thermotoga maritima MutL Using Small-Angle X-ray Scattering Analysis. Journal of Biochemistry, 2009, 145, 199-206.	0.9	8
185	Portrait of an Enzyme, a Complete Structural Analysis of a Multimodular β -N-Acetylglucosaminidase from Clostridium perfringens. Journal of Biological Chemistry, 2009, 284, 9876-9884.	1.6	40
186	Ca ²⁺ regulation in the Na ⁺ /Ca ²⁺ exchanger features a dual electrostatic switch mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14333-14338.	3.3	73
187	DC-SIGN Neck Domain Is a pH-sensor Controlling Oligomerization. Journal of Biological Chemistry, 2009, 284, 21229-21240.	1.6	105
188	Golgi protein FAPP2 tubulates membranes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21121-21125.	3.3	52
189	Sensing Domain Dynamics in Protein Kinase A-I κ B Complexes by Solution X-ray Scattering. Journal of Biological Chemistry, 2009, 284, 35916-35925.	1.6	21
190	Interdomain Flexibility in Full-length Matrix Metalloproteinase-1 (MMP-1). Journal of Biological Chemistry, 2009, 284, 12821-12828.	1.6	73
191	The Family X DNA Polymerase from Deinococcus radiodurans Adopts a Non-standard Extended Conformation. Journal of Biological Chemistry, 2009, 284, 11992-11999.	1.6	27
192	Solution Structure of Human Pex5 Δ Pex14 Δ PTS1 Protein Complexes Obtained by Small Angle X-ray Scattering. Journal of Biological Chemistry, 2009, 284, 25334-25342.	1.6	41
193	Central Domain of DivIB Caps the C-terminal Regions of the FtsL/DivIC Coiled-coil Rod. Journal of Biological Chemistry, 2009, 284, 27687-27700.	1.6	37
194	Double Superhelix Model of High Density Lipoprotein. Journal of Biological Chemistry, 2009, 284, 36605-36619.	1.6	85
195	Covalently Bound Substrate at the Regulatory Site of Yeast Pyruvate Decarboxylases Triggers Allosteric Enzyme Activation. Journal of Biological Chemistry, 2009, 284, 12136-12144.	1.6	40
196	Structural Characterization of the Bradyzoite Surface Antigen (BSR4) from Toxoplasma gondii, a Unique Addition to the Surface Antigen Glycoprotein 1-related Superfamily. Journal of Biological Chemistry, 2009, 284, 9192-9198.	1.6	31
197	Structure of the Noncatalytic Domains and Global Fold of the Protein Disulfide Isomerase ERp72. Structure, 2009, 17, 651-659.	1.6	44
198	Crystal and Solution Structures of a Prokaryotic M16B Peptidase: an Open and Shut Case. Structure, 2009, 17, 1465-1475.	1.6	29

#	ARTICLE	IF	CITATIONS
199	Molecular shape and prominent role of β -strand swapping in organization of dUTPase oligomers. <i>FEBS Letters</i> , 2009, 583, 865-871.	1.3	23
200	Large-scale movement of functional domains facilitates aminoacylation by human mitochondrial phenylalanyl-tRNA synthetase. <i>FEBS Letters</i> , 2009, 583, 3204-3208.	1.3	22
201	Metal-Mediated Self-Assembly of a β -Sandwich Protein. <i>Chemistry - A European Journal</i> , 2009, 15, 12672-12680.	1.7	7
202	Synchrotron radiation small angle scattering studies of d(TTAGGG) ₄ oligomer in solution. <i>Radiation Physics and Chemistry</i> , 2009, 78, S134-S136.	1.4	2
203	The three-dimensional structure of diaminopimelate decarboxylase from <i>Mycobacterium tuberculosis</i> reveals a tetrameric enzyme organisation. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 209-217.	1.2	14
204	Structural basis for sugar recognition, including the Tn carcinoma antigen, by the lectin SNA-II from <i>Sambucus nigra</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 89-103.	1.5	33
205	Intrinsic structural disorder of mouse proNGF. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 990-1009.	1.5	54
206	Insight into the substrate length restriction of M32 carboxypeptidases: Characterization of two distinct subfamilies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 647-657.	1.5	16
207	Grp94, the endoplasmic reticulum Hsp90, has a similar solution conformation to cytosolic Hsp90 in the absence of nucleotide. <i>Protein Science</i> , 2009, 18, 1815-1827.	3.1	52
208	The solution structure and dynamics of the DH-PH module of PDZRhoGEF in isolation and in complex with nucleotide-free RhoA. <i>Protein Science</i> , 2009, 18, 2067-2079.	3.1	18
209	Structural characterization of unphosphorylated STAT5a oligomerization equilibrium in solution by small-angle X-ray scattering. <i>Protein Science</i> , 2009, 18, 716-726.	3.1	26
210	Structure of the sporulation histidine kinase inhibitor Sda from <i>Bacillus subtilis</i> and insights into its solution state. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 574-581.	2.5	11
211	Techniques and tactics used in determining the structure of the trimeric ebolavirus glycoprotein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1162-1180.	2.5	26
212	High-pressure small-angle neutron scattering studies of glucose isomerase conformation in solution. <i>Journal of Applied Crystallography</i> , 2009, 42, 461-468.	1.9	9
213	BioXTAS RAW, a software program for high-throughput automated small-angle X-ray scattering data reduction and preliminary analysis. <i>Journal of Applied Crystallography</i> , 2009, 42, 959-964.	1.9	203
214	Combined sampler robot and high-performance liquid chromatography: a fully automated system for biological small-angle X-ray scattering experiments at the Synchrotron SOLEIL SWING beamline. <i>Journal of Applied Crystallography</i> , 2009, 42, 892-900.	1.9	306
215	SoftWAXS: a computational tool for modeling wide-angle X-ray solution scattering from biomolecules. <i>Journal of Applied Crystallography</i> , 2009, 42, 932-943.	1.9	60
216	The structural and biochemical characterizations of a novel TET peptidase complex from <i>Pyrococcus horikoshii</i> reveal an integrated peptide degradation system in hyperthermophilic Archaea. <i>Molecular Microbiology</i> , 2009, 72, 26-40.	1.2	32

#	ARTICLE	IF	CITATIONS
217	Structural insights into the molecular organization of the S-layer from <i>Clostridium difficile</i> . <i>Molecular Microbiology</i> , 2009, 71, 1308-1322.	1.2	115
218	Insights into complement convertase formation based on the structure of the factor B-cobra venom factor complex. <i>EMBO Journal</i> , 2009, 28, 2469-2478.	3.5	61
219	The origin of the electrostatic perturbation in acetoacetate decarboxylase. <i>Nature</i> , 2009, 459, 393-397.	13.7	86
220	The abscisic acid receptor PYR1 in complex with abscisic acid. <i>Nature</i> , 2009, 462, 665-668.	13.7	457
221	Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). <i>Nature Methods</i> , 2009, 6, 606-612.	9.0	610
222	Resistance of λ -crystallin quaternary structure to UV irradiation. <i>Biochemistry (Moscow)</i> , 2009, 74, 633-642.	0.7	14
223	E2 interaction and dimerization in the crystal structure of TRAF6. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 658-666.	3.6	301
224	The molecular basis for the regulation of the cap-binding complex by the importins. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 930-937.	3.6	83
225	Kinetic and mechanistic characterization of <i>Mycobacterium tuberculosis</i> glutamyl-tRNA synthetase and determination of its oligomeric structure in solution. <i>FEBS Journal</i> , 2009, 276, 1398-1417.	2.2	23
226	Distinct oligomeric forms of the <i>Pseudomonas aeruginosa</i> RetS sensor domain modulate accessibility to the ligand binding site. <i>Environmental Microbiology</i> , 2010, 12, 1775-1786.	1.8	39
227	SAXS/WAXS studies of the low-resolution structure in solution of xylose/glucose isomerase from <i>Streptomyces rubiginosus</i> . <i>Radiation Physics and Chemistry</i> , 2009, 78, S125-S128.	1.4	5
228	The FTIR and SAXS studies of influence of a morpholine derivatives on the DMPC-based biological membrane systems. <i>Radiation Physics and Chemistry</i> , 2009, 78, S129-S133.	1.4	8
229	Assessment of long-term molecular dynamics calculations with experimental information on protein shape from X-ray scattering – SOD1 as a case study. <i>Chemical Physics Letters</i> , 2009, 481, 112-117.	1.2	5
230	Characterization of a fluorophore binding RNA aptamer by fluorescence correlation spectroscopy and small angle X-ray scattering. <i>Analytical Biochemistry</i> , 2009, 389, 52-62.	1.1	21
231	Urea-Induced Denaturation Process on Defatted Human Serum Albumin and in the Presence of Palmitic Acid. <i>Journal of Physical Chemistry B</i> , 2009, 113, 12590-12602.	1.2	46
232	Formation of silver nanoparticles in PVP matrix in supercritical CO ₂ : Small-angle X-ray scattering and modeling. <i>Nanotechnologies in Russia</i> , 2009, 4, 700-710.	0.7	7
233	Determination of the size and phase composition of silver nanoparticles in a gel film of bacterial cellulose by small-angle X-ray scattering, electron diffraction, and electron microscopy. <i>Crystallography Reports</i> , 2009, 54, 169-173.	0.1	18
234	Low-Resolution Structures of Transient Protein-Protein Complexes Using Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2009, 131, 4378-4386.	6.6	59

#	ARTICLE	IF	CITATIONS
235	Montmorilloniteâ€“polycation multilayers incorporated in polyacrylamide. <i>Applied Clay Science</i> , 2009, 46, 88-94.	2.6	4
236	Structural and functional characterization of soluble endoglin receptor. <i>Biochemical and Biophysical Research Communications</i> , 2009, 383, 386-391.	1.0	15
237	On the quaternary association of the type III secretion system HrcQB-C protein: Experimental evidence differentiates among the various oligomerization models. <i>Journal of Structural Biology</i> , 2009, 166, 214-225.	1.3	10
238	A picornaviral loop-to-loop replication complex. <i>Journal of Structural Biology</i> , 2009, 166, 251-262.	1.3	21
239	Small-angle X-ray scattering from phase-separating amorphous metallic alloys undergoing nanocrystallization. <i>Journal of Alloys and Compounds</i> , 2009, 483, 116-119.	2.8	16
240	Nanocrystalline semiconductor materials for solar water-splitting. <i>Journal of Alloys and Compounds</i> , 2009, 483, 445-449.	2.8	8
241	Superoxide Dismutase from the Eukaryotic Thermophile <i>Alvinella pompejana</i> : Structures, Stability, Mechanism, and Insights into Amyotrophic Lateral Sclerosis. <i>Journal of Molecular Biology</i> , 2009, 385, 1534-1555.	2.0	126
242	Structural Insights into the Association between BCAR3 and Cas Family Members, an Atypical Complex Implicated in Anti-Oestrogen Resistance. <i>Journal of Molecular Biology</i> , 2009, 386, 190-203.	2.0	31
243	Domain Organization of the Monomeric Form of the Tom70 Mitochondrial Import Receptor. <i>Journal of Molecular Biology</i> , 2009, 388, 1043-1058.	2.0	38
244	Structural Basis for Bivalent Smac-Mimetics Recognition in the IAP Protein Family. <i>Journal of Molecular Biology</i> , 2009, 392, 630-644.	2.0	40
245	pH-Dependent Conformational Changes in Bacterial Hsp90 Reveal a Grp94-Like Conformation at pH 6 That Is Highly Active in Suppression of Citrate Synthase Aggregation. <i>Journal of Molecular Biology</i> , 2009, 390, 278-291.	2.0	52
246	A Common Structural Basis for pH- and Calmodulin-mediated Regulation in Plant Glutamate Decarboxylase. <i>Journal of Molecular Biology</i> , 2009, 392, 334-351.	2.0	71
247	The Structure and Conformation of Lys63-Linked Tetraubiquitin. <i>Journal of Molecular Biology</i> , 2009, 392, 1117-1124.	2.0	106
248	A Mechanism for Histone Chaperoning Activity of Nucleoplasmin: Thermodynamic and Structural Models. <i>Journal of Molecular Biology</i> , 2009, 393, 448-463.	2.0	44
249	Binding of Rabies Virus Polymerase Cofactor to Recombinant Circular Nucleoproteinâ€“RNA Complexes. <i>Journal of Molecular Biology</i> , 2009, 394, 558-575.	2.0	46
250	The Quaternary Structure of Amalgam, a <i>Drosophila</i> Neuronal Adhesion Protein, Explains Its Dual Adhesion Properties. <i>Biophysical Journal</i> , 2009, 97, 2316-2326.	0.2	11
251	A Self-Consistent Description of the Conformational Behavior of Chemically Denatured Proteins from NMR and Small Angle Scattering. <i>Biophysical Journal</i> , 2009, 97, 2839-2845.	0.2	120
252	The Effect of Glycosylation on Interparticle Interactions and Dimensions of Native and Denatured Phytase. <i>Biophysical Journal</i> , 2009, 96, 153-161.	0.2	15

#	ARTICLE	IF	CITATIONS
253	Structural and Biophysical Characterization of the Proteins Interacting with the Herpes Simplex Virus 1 Origin of Replication. <i>Journal of Biological Chemistry</i> , 2009, 284, 16343-16353.	1.6	12
254	Study of the gel films of <i>Acetobacter Xylinum</i> cellulose and its modified samples by ¹ H NMR cryoporometry and small-angle X-ray scattering. <i>Crystallography Reports</i> , 2010, 55, 312-317.	0.1	5
255	Recognition of Nucleoplasmin by Its Nuclear Transport Receptor Importin β : Insights into a Complete Import Complex. <i>Biochemistry</i> , 2010, 49, 9756-9769.	1.2	25
256	Solution structure of the major (Spy0128) and minor (Spy0125 and Spy0130) pili subunits from <i>Streptococcus pyogenes</i> . <i>European Biophysics Journal</i> , 2010, 39, 469-480.	1.2	9
257	Effect of interdomain dynamics on the structure determination of modular proteins by small-angle scattering. <i>European Biophysics Journal</i> , 2010, 39, 769-780.	1.2	102
258	SAXS-data-based structural modeling of DNA-gadolinium complexes fixed in particles of cholesteric liquid-crystalline dispersions. <i>European Biophysics Journal</i> , 2010, 39, 1313-1322.	1.2	15
259	The structure of dopamine induced α -synuclein oligomers. <i>European Biophysics Journal</i> , 2010, 39, 1407-1419.	1.2	87
260	Human serum albumin binding ibuprofen: A 3D description of the unfolding pathway in urea. <i>Biophysical Chemistry</i> , 2010, 147, 111-122.	1.5	40
261	The Structure of PknB Extracellular PASTA Domain from <i>Mycobacterium tuberculosis</i> Suggests a Ligand-Dependent Kinase Activation. <i>Structure</i> , 2010, 18, 606-615.	1.6	89
262	Free State Conformational Sampling of the SAM-I Riboswitch Aptamer Domain. <i>Structure</i> , 2010, 18, 787-797.	1.6	167
263	Structural Diversity in Free and Bound States of Intrinsically Disordered Protein Phosphatase 1 Regulators. <i>Structure</i> , 2010, 18, 1094-1103.	1.6	110
264	Quantitative Structural Analysis of Importin- β Flexibility: Paradigm for Solenoid Protein Structures. <i>Structure</i> , 2010, 18, 1171-1183.	1.6	89
265	Structure and Flexibility of the Complete Periplasmic Domain of BamA: The Protein Insertion Machine of the Outer Membrane. <i>Structure</i> , 2010, 18, 1492-1501.	1.6	114
266	Crystal Structure of HIV-1 Primary Receptor CD4 in Complex with a Potent Antiviral Antibody. <i>Structure</i> , 2010, 18, 1632-1641.	1.6	62
267	Comb-like poly(4-vinylpyridinium) salts with dodecylsulfate, sodium bis(2-ethylhexyl) sulfosuccinate and bromide counter ions. Small-angle X-ray scattering and dynamic light scattering study. <i>Polymer</i> , 2010, 51, 122-128.	1.8	5
268	Effect of the swelling degree on the formation of magnetite nanoparticles in hydrogels. <i>European Polymer Journal</i> , 2010, 46, 2105-2111.	2.6	6
269	COMB: a comprehensive computationally accelerated structure analysis tool for solution X-ray scattering from supramolecular self-assemblies. <i>Journal of Applied Crystallography</i> , 2010, 43, 1522-1531.	1.9	66
270	Time-resolved SAXS measurements facilitated by online HPLC buffer exchange. <i>Journal of Synchrotron Radiation</i> , 2010, 17, 769-773.	1.0	18

#	ARTICLE	IF	CITATIONS
271	Crystallization and preliminary structural characterization of the two actin-depolymerization factors of the malaria parasite. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 583-587.	0.7	3
272	Structure of Rv1848 (UreA), the <i>Mycobacterium tuberculosis</i> urease β subunit. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 781-786.	0.7	10
273	Small-angle scattering for structural biology—Expanding the frontier while avoiding the pitfalls. <i>Protein Science</i> , 2010, 19, 642-657.	3.1	341
274	Structures of the autoproteolytic domain from the <i>Saccharomyces cerevisiae</i> nuclear pore complex component, Nup145. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 1992-1998.	1.5	13
275	The repeat domain of the type III effector protein PthA shows a TPR-like structure and undergoes conformational changes upon DNA interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3386-3395.	1.5	39
276	New insights into structure–function relationships of oxalyl-CoA decarboxylase from <i>Escherichia coli</i> . <i>FEBS Journal</i> , 2010, 277, 2628-2640.	2.2	20
277	Dynamin GTPase regulation is altered by PH domain mutations found in centronuclear myopathy patients. <i>EMBO Journal</i> , 2010, 29, 3054-3067.	3.5	116
278	The structure of (CENP-A α -H4) $_2$ reveals physical features that mark centromeres. <i>Nature</i> , 2010, 467, 347-351.	13.7	187
279	Structural Insights into Serine-rich Fimbriae from Gram-positive Bacteria. <i>Journal of Biological Chemistry</i> , 2010, 285, 32446-32457.	1.6	48
280	Full-length extracellular region of the var2CSA variant of PfEMP1 is required for specific, high-affinity binding to CSA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4884-4889.	3.3	137
281	Improving small-angle X-ray scattering data for structural analyses of the RNA world. <i>Rna</i> , 2010, 16, 638-646.	1.6	83
282	Order and Disorder in the Domain Organization of the Plasmid Partition Protein KorB. <i>Journal of Biological Chemistry</i> , 2010, 285, 15440-15449.	1.6	11
283	Quantitative analysis of processive RNA degradation by the archaeal RNA exosome. <i>Nucleic Acids Research</i> , 2010, 38, 5166-5176.	6.5	23
284	Physical basis of the inducer-dependent cooperativity of the Central glycolytic genes Repressor/DNA complex. <i>Nucleic Acids Research</i> , 2010, 38, 5944-5957.	6.5	15
285	Structural and mechanistic insights into <i>Helicobacter pylori</i> NikR activation. <i>Nucleic Acids Research</i> , 2010, 38, 3106-3118.	6.5	38
286	Ultra-Small-Angle X-ray Scattering of Polymers. <i>Polymer Reviews</i> , 2010, 50, 59-90.	5.3	37
287	Two distinct regions in <i>Staphylococcus aureus</i> GatCAB guarantee accurate tRNA recognition. <i>Nucleic Acids Research</i> , 2010, 38, 672-682.	6.5	26
288	Crystal Structure of Hexokinase K1Hxk1 of <i>Kluyveromyces lactis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 41019-41033.	1.6	26

#	ARTICLE	IF	CITATIONS
289	Further Insights into the Roles of GTP and the C Terminus of the Hepatitis C Virus Polymerase in the Initiation of RNA Synthesis. <i>Journal of Biological Chemistry</i> , 2010, 285, 32906-32918.	1.6	71
290	Der p 5 Crystal Structure Provides Insight into the Group 5 Dust Mite Allergens. <i>Journal of Biological Chemistry</i> , 2010, 285, 25394-25401.	1.6	52
291	Oxidation state of the XRCC1 N-terminal domain regulates DNA polymerase β binding affinity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6805-6810.	3.3	67
292	Structure of the K-turn U4 RNA: a combined NMR and SANS study. <i>Nucleic Acids Research</i> , 2010, 38, 6274-6285.	6.5	49
293	Small angle neutron scattering of native and reconstituted silk fibroin. <i>Soft Matter</i> , 2010, 6, 4389.	1.2	51
294	Structural Analysis of the Smad2 β ~MAN1 Interaction That Regulates Transforming Growth Factor- β Signaling at the Inner Nuclear Membrane. <i>Biochemistry</i> , 2010, 49, 8020-8032.	1.2	29
295	Balanced Electrostatic and Structural Forces Guide the Large Conformational Change Associated with Maturation of T = 4 Virus. <i>Biophysical Journal</i> , 2010, 98, 1337-1343.	0.2	26
296	Hydrophilization of Magnetic Nanoparticles with Modified Alternating Copolymers. Part 1: The Influence of the Grafting. <i>Journal of Physical Chemistry C</i> , 2010, 114, 21900-21907.	1.5	38
297	Hydrophilization of Magnetic Nanoparticles with Modified Alternating Copolymers. Part 2: Behavior in Solution. <i>Journal of Physical Chemistry C</i> , 2010, 114, 21908-21913.	1.5	19
298	Identification and Functional Characterization of a Novel Acetylcholine-Binding Protein from the Marine Annelid <i>Capitella teleta</i> . <i>Biochemistry</i> , 2010, 49, 2279-2287.	1.2	28
299	Vaults Are Dynamically Unconstrained Cytoplasmic Nanoparticles Capable of Half Vault Exchange. <i>ACS Nano</i> , 2010, 4, 7229-7240.	7.3	27
300	Extensive Small-Angle X-ray Scattering Studies of Blood Coagulation Factor VIIa Reveal Interdomain Flexibility. <i>Biochemistry</i> , 2010, 49, 9739-9745.	1.2	11
301	Combination of SAXS and NMR Techniques as a Tool for the Determination of Peptide Structure in Solution. <i>Journal of Physical Chemistry Letters</i> , 2010, 1, 3128-3131.	2.1	6
302	Conformational Space of Flexible Biological Macromolecules from Average Data. <i>Journal of the American Chemical Society</i> , 2010, 132, 13553-13558.	6.6	155
303	Structural Dynamics and Single-Stranded DNA Binding Activity of the Three N-Terminal Domains of the Large Subunit of Replication Protein A from Small Angle X-ray Scattering. <i>Biochemistry</i> , 2010, 49, 2880-2889.	1.2	44
304	Thermal Effects on the Activity and Structural Conformation of Catechol 2,3-Dioxygenase from <i>Pseudomonas putida</i> SH1. <i>Journal of Physical Chemistry B</i> , 2010, 114, 987-992.	1.2	4
305	Structural and spectroscopic studies of DMPC/cationic surfactant system. <i>Journal of Non-Crystalline Solids</i> , 2010, 356, 747-753.	1.5	5
306	Structure and plasticity of the peptidyl-prolyl isomerase Par27 of <i>Bordetella pertussis</i> revealed by X-ray diffraction and small-angle X-ray scattering. <i>Journal of Structural Biology</i> , 2010, 169, 253-265.	1.3	7

#	ARTICLE	IF	CITATIONS
307	Structural characterization of proteins and complexes using small-angle X-ray solution scattering. <i>Journal of Structural Biology</i> , 2010, 172, 128-141.	1.3	470
308	The Central Portion of Factor H (Modules 10-15) Is Compact and Contains a Structurally Deviant CCP Module. <i>Journal of Molecular Biology</i> , 2010, 395, 105-122.	2.0	51
309	Structural and Biophysical Studies of Human PARP-1 in Complex with Damaged DNA. <i>Journal of Molecular Biology</i> , 2010, 395, 983-994.	2.0	60
310	The Dimeric Structure and the Bivalent Recognition of H3K4me3 by the Tumor Suppressor ING4 Suggests a Mechanism for Enhanced Targeting of the HBO1 Complex to Chromatin. <i>Journal of Molecular Biology</i> , 2010, 396, 1117-1127.	2.0	36
311	Four Distinct Structural Domains in <i>Clostridium difficile</i> Toxin B Visualized Using SAXS. <i>Journal of Molecular Biology</i> , 2010, 396, 1260-1270.	2.0	46
312	Structural and Functional Analysis of the Engineered Type I DNA Methyltransferase EcoR124INT. <i>Journal of Molecular Biology</i> , 2010, 398, 391-399.	2.0	12
313	Structure and Conformational Dynamics of the Metalloregulator MerR upon Binding of Hg(II). <i>Journal of Molecular Biology</i> , 2010, 398, 555-568.	2.0	32
314	Solution Structure and Characterisation of the Human Pyruvate Dehydrogenase Complex Core Assembly. <i>Journal of Molecular Biology</i> , 2010, 399, 71-93.	2.0	52
315	Calmodulin Disrupts the Structure of the HIV-1 MA Protein. <i>Journal of Molecular Biology</i> , 2010, 400, 702-714.	2.0	18
316	Design and Structure of an Equilibrium Protein Folding Intermediate: A Hint into Dynamical Regions of Proteins. <i>Journal of Molecular Biology</i> , 2010, 400, 922-934.	2.0	25
317	The Structure of the FnIII Tandem A77-A78 Points to a Periodically Conserved Architecture in the Myosin-Binding Region of Titin. <i>Journal of Molecular Biology</i> , 2010, 401, 843-853.	2.0	31
318	Structural Characterization of Protein-Protein Complexes by Integrating Computational Docking with Small-angle Scattering Data. <i>Journal of Molecular Biology</i> , 2010, 403, 217-230.	2.0	64
319	The Switch that Does Not Flip: The Blue-Light Receptor YtvA from <i>Bacillus subtilis</i> Adopts an Elongated Dimer Conformation Independent of the Activation State as Revealed by a Combined AUC and SAXS Study. <i>Journal of Molecular Biology</i> , 2010, 403, 78-87.	2.0	35
320	Design, Production and Molecular Structure of a New Family of Artificial Alpha-helical Repeat Proteins (I±Rep) Based on Thermostable HEAT-like Repeats. <i>Journal of Molecular Biology</i> , 2010, 404, 307-327.	2.0	85
321	Nano-structure of the laminin β -1 short arm reveals an extended and curved multidomain assembly. <i>Matrix Biology</i> , 2010, 29, 565-572.	1.5	34
322	Investigation of β -crystallin target protein binding to bovine lens alpha-crystallin by small-angle neutron scattering. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2010, 1800, 392-397.	1.1	8
323	Global structure of HIV-1 neutralizing antibody IgG1 b12 is asymmetric. <i>Biochemical and Biophysical Research Communications</i> , 2010, 391, 947-951.	1.0	20
324	Solution structure of the N-terminal transactivation domain of ERM modified by SUMO-1. <i>Biochemical and Biophysical Research Communications</i> , 2010, 399, 104-110.	1.0	18

#	ARTICLE	IF	CITATIONS
325	Allostery and Intrinsic Disorder Mediate Transcription Regulation by Conditional Cooperativity. <i>Cell</i> , 2010, 142, 101-111.	13.5	226
326	Structural Basis of HIV-1 Tethering to Membranes by the BST-2/Tetherin Ectodomain. <i>Cell Host and Microbe</i> , 2010, 7, 314-323.	5.1	142
327	Homodimerization of the p51 Subunit of HIV-1 Reverse Transcriptase. <i>Biochemistry</i> , 2010, 49, 2821-2833.	1.2	19
328	Evolution of a new enzyme for carbon disulphide conversion by an acidothermophilic archaeon. <i>Nature</i> , 2011, 478, 412-416.	13.7	91
329	A macrocyclic HCV NS3/4A protease inhibitor interacts with protease and helicase residues in the complex with its full-length target. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21052-21056.	3.3	50
330	Dehaloperoxidase-Hemoglobin from <i>Amphitrite ornata</i> Is Primarily a Monomer in Solution. <i>Journal of Physical Chemistry B</i> , 2011, 115, 4266-4272.	1.2	13
331	Ubiquitin in Motion: Structural Studies of the Ubiquitin-Conjugating Enzyme ^{1/4} Ubiquitin Conjugate. <i>Biochemistry</i> , 2011, 50, 1624-1633.	1.2	124
332	The structural plasticity of the human copper chaperone for SOD1: insights from combined size-exclusion chromatographic and solution X-ray scattering studies. <i>Biochemical Journal</i> , 2011, 439, 39-44.	1.7	22
333	Comparison of a PreQ1 Riboswitch Aptamer in Metabolite-bound and Free States with Implications for Gene Regulation. <i>Journal of Biological Chemistry</i> , 2011, 286, 24626-24637.	1.6	114
334	Solution-Based Structural Analysis of the Decaheme Cytochrome, MtrA, by Small-Angle X-ray Scattering and Analytical Ultracentrifugation. <i>Journal of Physical Chemistry B</i> , 2011, 115, 11208-11214.	1.2	32
335	Small Angle X-Ray Scattering Spectroscopy. <i>Methods in Molecular Biology</i> , 2011, 766, 177-189.	0.4	0
336	Polyelectrolyte [~] Surfactant Complexes Formed by Poly[3,5-bis(trimethylammoniummethyl)4-hydroxystyrene iodide]- <i>block</i> -poly(ethylene oxide) and Sodium Dodecyl Sulfate in Aqueous Solutions. <i>Langmuir</i> , 2011, 27, 5275-5281.	1.6	35
337	Molecular Investigations of the Structure and Function of the Protein Phosphatase 1 [~] Spinophilin [~] Inhibitor 2 Heterotrimeric Complex. <i>Biochemistry</i> , 2011, 50, 1238-1246.	1.2	44
338	Engineering a Structure Switching Mechanism into a Steroid-Binding Aptamer and Hydrodynamic Analysis of the Ligand Binding Mechanism. <i>Biochemistry</i> , 2011, 50, 9368-9376.	1.2	25
339	The Mechanism of Linkage-Specific Ubiquitin Chain Elongation by a Single-Subunit E2. <i>Cell</i> , 2011, 144, 769-781.	13.5	241
340	A Mechanism for Tunable Autoinhibition in the Structure of a Human Ca ²⁺ /Calmodulin-Dependent Kinase II Holoenzyme. <i>Cell</i> , 2011, 146, 732-745.	13.5	230
341	Structural Insights into RNA Recognition by RIG-I. <i>Cell</i> , 2011, 147, 409-422.	13.5	337
342	Structural Basis of Wnt Signaling Inhibition by Dickkopf Binding to LRP5/6. <i>Developmental Cell</i> , 2011, 21, 862-873.	3.1	153

#	ARTICLE	IF	CITATIONS
343	SAXS data analysis and modeling of tetravalent neutralizing antibody CD4 ^g /+ HIV-1 gp120 revealed that first two gp120 bind to the same Fab arm. <i>Biochemical and Biophysical Research Communications</i> , 2011, 415, 680-685.	1.0	4
344	Structure and dimerization of translation initiation factor eIF5B in solution. <i>Biochemical and Biophysical Research Communications</i> , 2011, 416, 140-145.	1.0	1
345	The Interface between Catalytic and Hemopexin Domains in Matrix Metalloproteinase-1 Conceals a Collagen Binding Exosite. <i>Journal of Biological Chemistry</i> , 2011, 286, 45073-45082.	1.6	49
346	Macromolecular docking restrained by a small angle X-ray scattering profile. <i>Journal of Structural Biology</i> , 2011, 173, 461-471.	1.3	97
347	Structural and functional insights into a dodecameric molecular machine – The RuvBL1/RuvBL2 complex. <i>Journal of Structural Biology</i> , 2011, 176, 279-291.	1.3	98
348	Synergy, Structure and Conformational Flexibility of Hybrid Cellulosomes Displaying Various Inter-cohesins Linkers. <i>Journal of Molecular Biology</i> , 2011, 405, 143-157.	2.0	33
349	A Novel Structure of an Antikinase and its Inhibitor. <i>Journal of Molecular Biology</i> , 2011, 405, 214-226.	2.0	21
350	Tuning Riboswitch Regulation through Conformational Selection. <i>Journal of Molecular Biology</i> , 2011, 405, 926-938.	2.0	48
351	Molecular Basis of Bacterial Defense against Host Lysozymes: X-ray Structures of Periplasmic Lysozyme Inhibitors Plil and PlIc. <i>Journal of Molecular Biology</i> , 2011, 405, 1233-1245.	2.0	28
352	Structural Analysis of an Equilibrium Folding Intermediate in the Apoflavodoxin Native Ensemble by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2011, 406, 604-619.	2.0	27
353	Structural Investigation of PsbO from Plant and Cyanobacterial Photosystem II. <i>Journal of Molecular Biology</i> , 2011, 407, 125-137.	2.0	14
354	Small-angle X-ray Scattering Study of a Rex Family Repressor: Conformational Response to NADH and NAD ⁺ Binding in Solution. <i>Journal of Molecular Biology</i> , 2011, 408, 670-683.	2.0	23
355	Structural Analysis of a Novel Class of M Controller Proteins: C.Csp231I from <i>Citrobacter</i> sp. RFL231. <i>Journal of Molecular Biology</i> , 2011, 409, 177-188.	2.0	12
356	Probing Dimerization and Structural Flexibility of Mammalian Lipoxygenases by Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2011, 409, 654-668.	2.0	37
357	Three-Dimensional Structure of β -Crystallin Domain Dimers of Human Small Heat Shock Proteins HSPB1 and HSPB6. <i>Journal of Molecular Biology</i> , 2011, 411, 110-122.	2.0	107
358	The Overall Architecture and Receptor Binding of Pneumococcal Carbohydrate-Antigen-Hydrolyzing Enzymes. <i>Journal of Molecular Biology</i> , 2011, 411, 1017-1036.	2.0	24
359	The Nonlinear Structure of the Desmoplakin Plakin Domain and the Effects of Cardiomyopathy-Linked Mutations. <i>Journal of Molecular Biology</i> , 2011, 411, 1049-1061.	2.0	26
360	Structural Characterization of Intramolecular Hg ²⁺ Transfer between Flexibly Linked Domains of Mercuric Ion Reductase. <i>Journal of Molecular Biology</i> , 2011, 413, 639-656.	2.0	24

#	ARTICLE	IF	CITATIONS
361	Human Cardiac Myosin Binding Protein C: Structural Flexibility within an Extended Modular Architecture. <i>Journal of Molecular Biology</i> , 2011, 414, 735-748.	2.0	37
362	Oligomerization Propensity and Flexibility of Yeast Frataxin Studied by X-ray Crystallography and Small-Angle X-ray Scattering. <i>Journal of Molecular Biology</i> , 2011, 414, 783-797.	2.0	21
363	GPCR stabilization using the bicelle-like architecture of mixed sterol-detergent micelles. <i>Methods</i> , 2011, 55, 310-317.	1.9	80
364	Structural basis of RNA recognition and activation by innate immune receptor RIG-I. <i>Nature</i> , 2011, 479, 423-427.	13.7	364
365	Human mitochondrial transcription factor A induces a U-turn structure in the light strand promoter. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 1281-1289.	3.6	168
366	Modulation of the Pharmacological Activities of Secretory Phospholipase A2 from <i>Crotalus durissus cascavella</i> Induced by Naringin. <i>Molecules</i> , 2011, 16, 738-761.	1.7	5
367	Variation in the organization and subunit composition of the mammalian pyruvate dehydrogenase complex E2/E3BP core assembly. <i>Biochemical Journal</i> , 2011, 437, 565-574.	1.7	27
368	The modular structure of haemagglutinin/adhesin regions in gingipains of <i>Porphyromonas gingivalis</i> . <i>Molecular Microbiology</i> , 2011, 81, 1358-1373.	1.2	20
369	Characterization of the elongasome core PBP2 ϵ :MreC complex of <i>Helicobacter pylori</i> . <i>Molecular Microbiology</i> , 2011, 82, 68-86.	1.2	34
370	The <i>Leishmania</i> nicotinamidase is essential for NAD ⁺ production and parasite proliferation. <i>Molecular Microbiology</i> , 2011, 82, 21-38.	1.2	47
371	ABC ATPase signature helices in Rad50 link nucleotide state to Mre11 interface for DNA repair. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 423-431.	3.6	149
372	Common architecture of nuclear receptor heterodimers on DNA direct repeat elements with different spacings. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 564-570.	3.6	176
373	Effect of phosphorylation on the interaction of calcium with leucine-rich amelogenin peptide. <i>European Journal of Oral Sciences</i> , 2011, 119, 97-102.	0.7	18
374	Structural Characterization of the Multidomain Regulatory Protein Rv1364c from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2011, 19, 56-69.	1.6	19
375	The Conformation and Function of a Multimodular Glycogen-Degrading Pneumococcal Virulence Factor. <i>Structure</i> , 2011, 19, 640-651.	1.6	42
376	Extracellular Complexes of the Hematopoietic Human and Mouse CSF-1 Receptor Are Driven by Common Assembly Principles. <i>Structure</i> , 2011, 19, 1762-1772.	1.6	36
377	A structural basis for Staphylococcal complement subversion: X-ray structure of the complement-binding domain of <i>Staphylococcus aureus</i> protein Sbi in complex with ligand C3d. <i>Molecular Immunology</i> , 2011, 48, 452-462.	1.0	32
378	Structural studies of the PARP-1 BRCT domain. <i>BMC Structural Biology</i> , 2011, 11, 37.	2.3	41

#	ARTICLE	IF	CITATIONS
379	The structure of the unliganded extracellular domain of the interleukin-6 signal transducer gp130 in solution. <i>European Journal of Cell Biology</i> , 2011, 90, 515-520.	1.6	4
380	Flexibility in the PP1:spinophilin holoenzyme. <i>FEBS Letters</i> , 2011, 585, 36-40.	1.3	21
381	Essential role of the metal-ion in the IPM-assisted domain closure of 3-isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 2011, 585, 3297-3302.	1.3	4
382	Retention of gold nanoparticles in the structure of quasinematic layers formed by DNA molecules. <i>Biochemistry (Moscow) Supplement Series A: Membrane and Cell Biology</i> , 2011, 5, 191-197.	0.3	8
383	Synthesis of Ag and Cu-chitosan metal-polymer nanocomposites in supercritical carbon dioxide medium and study of their structure and antimicrobial activity. <i>Nanotechnologies in Russia</i> , 2011, 6, 341-352.	0.7	21
384	Small-angle X-ray scattering, synchrotron radiation, and the structure of bio- and nanosystems. <i>Crystallography Reports</i> , 2011, 56, 725-750.	0.1	18
385	The Low Resolution Structure of ApoA1 in Spherical High Density Lipoprotein Revealed by Small Angle Neutron Scattering. <i>Journal of Biological Chemistry</i> , 2011, 286, 12495-12508.	1.6	50
386	Structural Insights on Two Hypothetical Secretion Chaperones from <i>Xanthomonas axonopodis</i> pv. <i>citri</i> . <i>Protein Journal</i> , 2011, 30, 324-333.	0.7	7
387	Biophysical characterization of recombinant HIV-1 subtype C virus infectivity factor. <i>Amino Acids</i> , 2011, 40, 981-989.	1.2	11
388	Protein loop compaction and the origin of the effect of arginine and glutamic acid mixtures on solubility, stability and transient oligomerization of proteins. <i>European Biophysics Journal</i> , 2011, 40, 1327-1338.	1.2	15
389	Small-angle X-ray scattering study of the ATP modulation of the structural features of the nucleotide binding domains of the CFTR in solution. <i>European Biophysics Journal</i> , 2011, 40, 811-824.	1.2	13
390	Structural insights into the membrane-extracted dimeric form of the ATPase TraB from the <i>Escherichia coli</i> pKM101 conjugation system. <i>BMC Structural Biology</i> , 2011, 11, 4.	2.3	21
391	Octuple cuvette for small-angle X-ray solution scattering. <i>Journal of Applied Crystallography</i> , 2011, 44, 1294-1296.	1.9	1
392	X-ray crystal structure and small-angle X-ray scattering of sheep liver sorbitol dehydrogenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 440-446.	2.5	11
393	Structural studies on the enzyme complex isopropylmalate isomerase (LeuCD) from <i>Mycobacterium tuberculosis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 35-49.	1.5	26
394	Crystal structure of a bacterial phosphoglucomutase, an enzyme involved in the virulence of multiple human pathogens. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1215-1229.	1.5	29
395	Structure of the C-terminal domain of <i>Saccharomyces cerevisiae</i> Nup133, a component of the nuclear pore complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1672-1677.	1.5	16
396	Structural memory of natively unfolded tau protein detected by small angle X-ray scattering. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2122-2131.	1.5	52

#	ARTICLE	IF	CITATIONS
397	The N ⁰ -binding region of the vesicular stomatitis virus phosphoprotein is globally disordered but contains transient α -helices. <i>Protein Science</i> , 2011, 20, 542-556.	3.1	49
398	T-shaped arrangement of the recombinant agrin G3 α IgG Fc protein. <i>Protein Science</i> , 2011, 20, 931-940.	3.1	16
399	Small angle X-ray scattering as a complementary tool for high-throughput structural studies. <i>Biopolymers</i> , 2011, 95, 517-530.	1.2	69
400	Characterizing flexible and intrinsically unstructured biological macromolecules by SAS using the Porod-Debye law. <i>Biopolymers</i> , 2011, 95, 559-571.	1.2	440
401	Engineered Synthetic Virus-Like Particles and Their Use in Vaccine Delivery. <i>ChemBioChem</i> , 2011, 12, 100-109.	1.3	52
402	Structure and Scm3-mediated assembly of budding yeast centromeric nucleosomes. <i>Nature Communications</i> , 2011, 2, 313.	5.8	111
403	Structural context for mobilization of a human tRNA synthetase from its cytoplasmic complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8239-8244.	3.3	33
404	First Structural Glimpse of CCN3 and CCN5 Multifunctional Signaling Regulators Elucidated by Small Angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2011, 286, 22243-22249.	1.6	13
405	Mutational and biochemical analysis of the DNA-entry nuclease EndA from <i>Streptococcus pneumoniae</i> . <i>Nucleic Acids Research</i> , 2011, 39, 623-634.	6.5	24
406	Structural and Immunologic Characterization of Ara h 1, a Major Peanut Allergen. <i>Journal of Biological Chemistry</i> , 2011, 286, 39318-39327.	1.6	89
407	The Dimer Interface of the Membrane Type 1 Matrix Metalloproteinase Hemopexin Domain. <i>Journal of Biological Chemistry</i> , 2011, 286, 7587-7600.	1.6	52
408	A Structural Model of the Sgt2 Protein and Its Interactions with Chaperones and the Get4/Get5 Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 34325-34334.	1.6	58
409	Structural insights into the dynamics and function of the C-terminus of the <i>E. coli</i> RNA chaperone Hfq. <i>Nucleic Acids Research</i> , 2011, 39, 4900-4915.	6.5	74
410	The structural basis for partitioning of the XRCC1/DNA ligase III- β BRCT-mediated dimer complexes. <i>Nucleic Acids Research</i> , 2011, 39, 7816-7827.	6.5	56
411	The structural basis for recognition of base J containing DNA by a novel DNA binding domain in JBP1. <i>Nucleic Acids Research</i> , 2011, 39, 5715-5728.	6.5	32
412	A Spring-loaded Release Mechanism Regulates Domain Movement and Catalysis in Phosphoglycerate Kinase. <i>Journal of Biological Chemistry</i> , 2011, 286, 14040-14048.	1.6	53
413	Structure of the Lassa Virus Nucleoprotein Revealed by X-ray Crystallography, Small-angle X-ray Scattering, and Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2011, 286, 38748-38756.	1.6	47
414	Electrostatic Interactions Involving the Extreme C Terminus of Nuclear Export Factor CRM1 Modulate Its Affinity for Cargo. <i>Journal of Biological Chemistry</i> , 2011, 286, 29325-29335.	1.6	26

#	ARTICLE	IF	CITATIONS
415	Evidence on How a Conserved Glycine in the Hinge Region of HapR Regulates Its DNA Binding Ability. <i>Journal of Biological Chemistry</i> , 2011, 286, 15043-15049.	1.6	30
416	Structure of the Periplasmic Stress Response Protein CpxP. <i>Journal of Bacteriology</i> , 2011, 193, 2149-2157.	1.0	41
417	Solution structures of DNA-bound gyrase. <i>Nucleic Acids Research</i> , 2011, 39, 755-766.	6.5	36
418	Biophysical analysis and small-angle X-ray scattering-derived structures of MeCP2 nucleosome complexes. <i>Nucleic Acids Research</i> , 2011, 39, 4122-4135.	6.5	49
419	Molecular basis of the recognition of the ap65-1 gene transcription promoter elements by a Myb protein from the protozoan parasite <i>Trichomonas vaginalis</i> . <i>Nucleic Acids Research</i> , 2011, 39, 8992-9008.	6.5	20
420	Insights into the Molecular Activation Mechanism of the RhoA-specific Guanine Nucleotide Exchange Factor, PDZRhoGEF. <i>Journal of Biological Chemistry</i> , 2011, 286, 35163-35175.	1.6	23
421	Small-angle X-ray Scattering Studies of the Oligomeric State and Quaternary Structure of the Trifunctional Proline Utilization A (PutA) Flavoprotein from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 43144-43153.	1.6	17
422	Fission Yeast Swi5-Sfr1 Protein Complex, an Activator of Rad51 Recombinase, Forms an Extremely Elongated Dogleg-shaped Structure. <i>Journal of Biological Chemistry</i> , 2011, 286, 43569-43576.	1.6	22
423	A Dual Effect of Au-Nanoparticles on Nucleic Acid Cholesteric Liquid-Crystalline Particles. <i>Journal of Biomaterials and Nanobiotechnology</i> , 2011, 02, 461-471.	1.0	9
424	Solution conformation of the response regulator proteins from <i>Deinococcus radiodurans</i> studied by SAXS. <i>Chinese Physics C</i> , 2011, 35, 974-977.	1.5	3
425	Structural model of the p14/SF3b155 branch duplex complex. <i>Rna</i> , 2011, 17, 155-165.	1.6	21
426	Copper Alters Aggregation Behavior of Prion Protein and Induces Novel Interactions between Its N- and C-terminal Regions. <i>Journal of Biological Chemistry</i> , 2011, 286, 38533-38545.	1.6	66
427	Solution Structure of the Soluble Receptor for Advanced Glycation End Products (sRAGE). <i>Journal of Biological Chemistry</i> , 2011, 286, 37525-37534.	1.6	32
428	Visual Insight into How Low pH Alone Can Induce Actin-severing Ability in Gelsolin under Calcium-free Conditions. <i>Journal of Biological Chemistry</i> , 2011, 286, 20387-20397.	1.6	20
429	ATP Induces Conformational Changes in the Carboxyl-terminal Region of Clc-5. <i>Journal of Biological Chemistry</i> , 2011, 286, 6733-6741.	1.6	18
430	Activation of the Retroviral Budding Factor ALIX. <i>Journal of Virology</i> , 2011, 85, 9222-9226.	1.5	47
431	Structure of Human Na ⁺ /H ⁺ Exchanger NHE1 Regulatory Region in Complex with Calmodulin and Ca ²⁺ . <i>Journal of Biological Chemistry</i> , 2011, 286, 40954-40961.	1.6	47
432	Low-resolution structure of a vesicle disrupting I α -synuclein oligomer that accumulates during fibrillation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3246-3251.	3.3	222

#	ARTICLE	IF	CITATIONS
433	The translational repressor 4E-BP called to order by eIF4E: new structural insights by SAXS. <i>Nucleic Acids Research</i> , 2011, 39, 3496-3503.	6.5	42
434	Solution structure of RNase P RNA. <i>Rna</i> , 2011, 17, 1159-1171.	1.6	43
435	Dimerization of Plasmodium vivax DBP is induced upon receptor binding and drives recognition of DARC. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 908-914.	3.6	128
436	Evidence for ATP-dependent Structural Rearrangement of Nuclease Catalytic Site in DNA Mismatch Repair Endonuclease MutL. <i>Journal of Biological Chemistry</i> , 2011, 286, 42337-42348.	1.6	21
437	Shape of tropoelastin, the highly extensible protein that controls human tissue elasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4322-4327.	3.3	170
438	Antagonists Induce a Conformational Change in cIAP1 That Promotes Autoubiquitination. <i>Science</i> , 2011, 334, 376-380.	6.0	196
439	Structure of the Vesicular Stomatitis Virus N0-P Complex. <i>PLoS Pathogens</i> , 2011, 7, e1002248.	2.1	111
440	Assembly of a Filamin Four-domain Fragment and the Influence of Splicing Variant-1 on the Structure. <i>Journal of Biological Chemistry</i> , 2011, 286, 26921-26930.	1.6	17
441	Indirect DNA Readout by an H-NS Related Protein: Structure of the DNA Complex of the C-Terminal Domain of Ler. <i>PLoS Pathogens</i> , 2011, 7, e1002380.	2.1	53
442	Structural and functional characterization of the Mycobacterium tuberculosis uridine monophosphate kinase: insights into the allosteric regulation. <i>Nucleic Acids Research</i> , 2011, 39, 3458-3472.	6.5	13
443	Ligand Binding Induces an Ammonia Channel in 2-Amino-2-desoxyisochorismate (ADIC) Synthase PhzE. <i>Journal of Biological Chemistry</i> , 2011, 286, 18213-18221.	1.6	49
444	Structural Basis for Partial Redundancy in a Class of Transcription Factors, the LIM Homeodomain Proteins, in Neural Cell Type Specification. <i>Journal of Biological Chemistry</i> , 2011, 286, 42971-42980.	1.6	35
445	Solution Structures of PPAR β /RXR β Complexes. <i>PPAR Research</i> , 2012, 2012, 1-8.	1.1	19
446	A flexible brace maintains the assembly of a hexameric replicative helicase during DNA unwinding. <i>Nucleic Acids Research</i> , 2012, 40, 2271-2283.	6.5	12
447	DNA binding by the plant-specific NAC transcription factors in crystal and solution: a firm link to WRKY and GCM transcription factors. <i>Biochemical Journal</i> , 2012, 444, 395-404.	1.7	77
448	Solution structure of the natively assembled yeast ribosomal stalk determined by small-angle X-ray scattering. <i>Biochemical Journal</i> , 2012, 444, 205-209.	1.7	10
449	Tail-anchor targeting by a Get3 tetramer: the structure of an archaeal homologue. <i>EMBO Journal</i> , 2012, 31, 707-719.	3.5	37
450	Superhelical Architecture of the Myosin Filament-Linking Protein Myomesin with Unusual Elastic Properties. <i>PLoS Biology</i> , 2012, 10, e1001261.	2.6	35

#	ARTICLE	IF	CITATIONS
451	Ligand-Binding Properties and Conformational Dynamics of Autolysin Repeat Domains in Staphylococcal Cell Wall Recognition. <i>Journal of Bacteriology</i> , 2012, 194, 3789-3802.	1.0	72
452	Structures of inactive retinoblastoma protein reveal multiple mechanisms for cell cycle control. <i>Genes and Development</i> , 2012, 26, 1156-1166.	2.7	111
453	Structural Analysis of the Plasmodium falciparum Erythrocyte Membrane Protein 1 (PfEMP1) Intracellular Domain Reveals a Conserved Interaction Epitope. <i>Journal of Biological Chemistry</i> , 2012, 287, 7182-7189.	1.6	53
454	Tropoelastin bridge region positions the cell-interactive C terminus and contributes to elastic fiber assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2878-2883.	3.3	51
455	Structural and Functional Insight into How the Plasmodium falciparum VAR2CSA Protein Mediates Binding to Chondroitin Sulfate A in Placental Malaria. <i>Journal of Biological Chemistry</i> , 2012, 287, 23332-23345.	1.6	154
456	Structure of the Cyanobacterial Magnesium Chelatase H Subunit Determined by Single Particle Reconstruction and Small-angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2012, 287, 4946-4956.	1.6	19
457	Crystal Structures and Small-angle X-ray Scattering Analysis of UDP-galactopyranose Mutase from the Pathogenic Fungus Aspergillus fumigatus. <i>Journal of Biological Chemistry</i> , 2012, 287, 9041-9051.	1.6	33
458	The Extracellular Protein Factor Epf from Streptococcus pyogenes Is a Cell Surface Adhesin That Binds to Cells through an N-terminal Domain Containing a Carbohydrate-binding Module. <i>Journal of Biological Chemistry</i> , 2012, 287, 38178-38189.	1.6	18
459	Structure of the heterodimer of human NONO and paraspeckle protein component 1 and analysis of its role in subnuclear body formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4846-4850.	3.3	132
460	Nonstructural Proteins 7 and 8 of Feline Coronavirus Form a 2:1 Heterotrimer That Exhibits Primer-Independent RNA Polymerase Activity. <i>Journal of Virology</i> , 2012, 86, 4444-4454.	1.5	73
461	Crystal and Solution Structures of Plasmodium falciparum Erythrocyte-binding Antigen 140 Reveal Determinants of Receptor Specificity during Erythrocyte Invasion. <i>Journal of Biological Chemistry</i> , 2012, 287, 36830-36836.	1.6	48
462	ATP-dependent conformational dynamics underlie the functional asymmetry of the replicative helicase from a minimalist eukaryote. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11999-12004.	3.3	65
463	A Flexible Multidomain Structure Drives the Function of the Urokinase-type Plasminogen Activator Receptor (uPAR)*. <i>Journal of Biological Chemistry</i> , 2012, 287, 34304-34315.	1.6	43
464	Biophysical and Mechanistic Insights into Novel Allosteric Inhibitor of Spleen Tyrosine Kinase. <i>Journal of Biological Chemistry</i> , 2012, 287, 7717-7727.	1.6	10
465	Biophysical Analysis of Kindlin-3 Reveals an Elongated Conformation and Maps Integrin Binding to the Membrane-distal β^2 -Subunit NPXY Motif. <i>Journal of Biological Chemistry</i> , 2012, 287, 37715-37731.	1.6	33
466	Low-resolution solution structures of Munc18:Syntaxin protein complexes indicate an open binding mode driven by the Syntaxin N-peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9816-9821.	3.3	59
467	Modulation of the Pyrococcus abyssi NucS Endonuclease Activity by Replication Clamp at Functional and Structural Levels. <i>Journal of Biological Chemistry</i> , 2012, 287, 15648-15660.	1.6	20
468	Biophysical and Functional Analyses Suggest That Adenovirus E4-ORF3 Protein Requires Higher-order Multimerization to Function against Promyelocytic Leukemia Protein Nuclear Bodies. <i>Journal of Biological Chemistry</i> , 2012, 287, 22573-22583.	1.6	14

#	ARTICLE	IF	CITATIONS
469	The low-resolution solution structure of <i>Vibrio cholerae</i> Hfq in complex with Qrr1 sRNA. <i>Nucleic Acids Research</i> , 2012, 40, 8698-8710.	6.5	25
470	Phosphorylation of CRN2 by CK2 regulates F-actin and Arp2/3 interaction and inhibits cell migration. <i>Scientific Reports</i> , 2012, 2, 241.	1.6	34
471	Small-Angle X-Ray Scattering Analysis of the Bifunctional Antibiotic Resistance Enzyme Aminoglycoside (6â€²) Acetyltransferase-Ie/Aminoglycoside (2â€³) Phosphotransferase-Ia Reveals a Rigid Solution Structure. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 1899-1906.	1.4	23
472	Interaction Surface and Topology of Get3-Get4-Get5 Protein Complex, Involved in Targeting Tail-anchored Proteins to Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2012, 287, 4783-4789.	1.6	12
473	Get5 Carboxyl-terminal Domain Is a Novel Dimerization Motif That Tethers an Extended Get4/Get5 Complex. <i>Journal of Biological Chemistry</i> , 2012, 287, 8310-8317.	1.6	26
474	Biophysical and Structural Characterization of a Sequence-diverse Set of Solute-binding Proteins for Aromatic Compounds. <i>Journal of Biological Chemistry</i> , 2012, 287, 23748-23756.	1.6	15
475	Structural Insights into the Regulatory Mechanism of the Response Regulator RocR from <i>Pseudomonas aeruginosa</i> in Cyclic Di-GMP Signaling. <i>Journal of Bacteriology</i> , 2012, 194, 4837-4846.	1.0	57
476	Structural flexibility of RNA as molecular basis for Hfq chaperone function. <i>Nucleic Acids Research</i> , 2012, 40, 8072-8084.	6.5	29
477	The multiple Tudor domain-containing protein TDRD1 is a molecular scaffold for mouse Piwi proteins and piRNA biogenesis factors. <i>Rna</i> , 2012, 18, 2056-2072.	1.6	41
478	Juxtanodin is an intrinsically disordered F-actin-binding protein. <i>Scientific Reports</i> , 2012, 2, 899.	1.6	30
479	Heat-induced structural transitions of alpha-crystallin studied by small-angle neutron scattering. <i>Journal of Physics: Conference Series</i> , 2012, 351, 012008.	0.3	0
480	Structural characterization of recombinant crustacyanin subunits from the lobster <i>Homarus americanus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 846-853.	0.7	16
481	Solution Structure of CCP Modules 10â€“12 Illuminates Functional Architecture of the Complement Regulator, Factor H. <i>Journal of Molecular Biology</i> , 2012, 424, 295-312.	2.0	24
482	Structure and function of proteins in hydrated choline dihydrogen phosphate ionic liquid. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 790-801.	1.3	86
483	Characterization of Enzymes from <i>Legionella pneumophila</i> Involved in Reversible Adenylation of Rab1 Protein. <i>Journal of Biological Chemistry</i> , 2012, 287, 35036-35046.	1.6	28
484	Scaffoldin Conformation and Dynamics Revealed by a Ternary Complex from the <i>Clostridium thermocellum</i> Cellulosome. <i>Journal of Biological Chemistry</i> , 2012, 287, 26953-26961.	1.6	33
485	Architecture of the Atg17 Complex as a Scaffold for Autophagosome Biogenesis. <i>Cell</i> , 2012, 151, 1501-1512.	13.5	205
486	Characterization of a novel copper-haem <i>Ralstonia pickettii</i> dissimilatory nitrite reductase from <i>Ralstonia pickettii</i> . <i>Biochemical Journal</i> , 2012, 444, 219-226.	1.7	15

#	ARTICLE	IF	CITATIONS
487	Structural characterization of the PlIG lysozyme inhibitor family. <i>Journal of Structural Biology</i> , 2012, 180, 235-242.	1.3	12
488	Tripod facial surfactants with benzene as the central core: design, synthesis and self-assembly study. <i>New Journal of Chemistry</i> , 2012, 36, 1170.	1.4	1
489	Conformational Characterization of Synapse-Associated Protein 97 by Nuclear Magnetic Resonance and Small-Angle X-ray Scattering Shows Compact and Elongated Forms. <i>Biochemistry</i> , 2012, 51, 899-908.	1.2	9
490	Large Multimeric Assemblies of Nucleosome Assembly Protein and Histones Revealed by Small-angle X-ray Scattering and Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2012, 287, 26657-26665.	1.6	12
491	Dengue Virus Nonstructural Protein 5 Adopts Multiple Conformations in Solution. <i>Biochemistry</i> , 2012, 51, 5921-5931.	1.2	54
492	G503 Is Obligatory for Coupling of Regulatory Domains in NCX Proteins. <i>Biochemistry</i> , 2012, 51, 7313-7320.	1.2	14
493	Macromolecular HPMA-Based Nanoparticles with Cholesterol for Solid-Tumor Targeting: Detailed Study of the Inner Structure of a Highly Efficient Drug Delivery System. <i>Biomacromolecules</i> , 2012, 13, 2594-2604.	2.6	51
494	A bimodular mechanism of calcium control in eukaryotes. <i>Nature</i> , 2012, 491, 468-472.	13.7	110
495	First Structural Model of Full-Length Human Tissue-Plasminogen Activator: A SAXS Data-Based Modeling Study. <i>Journal of Physical Chemistry B</i> , 2012, 116, 496-502.	1.2	23
496	Influence of the Cosolute Environment on IgG Solution Structure Analyzed by Small-Angle X-ray Scattering. <i>Journal of Physical Chemistry B</i> , 2012, 116, 9611-9618.	1.2	61
497	A Novel DNA Binding Mechanism for maf Basic Region-Leucine Zipper Factors Inferred from a MafA-DNA Complex Structure and Binding Specificities. <i>Biochemistry</i> , 2012, 51, 9706-9717.	1.2	18
498	Unusual Structural Morphology of Dendrimer/CdS Nanocomposites Revealed by Synchrotron X-ray Scattering. <i>Journal of Physical Chemistry C</i> , 2012, 116, 8069-8078.	1.5	12
499	Revisiting the Role of Glycosylation in the Structure of Human IgG Fc. <i>ACS Chemical Biology</i> , 2012, 7, 1596-1602.	1.6	128
500	Non-Ionic Amphiphilic Homopolymers: Synthesis, Solution Properties, and Biochemical Validation. <i>Langmuir</i> , 2012, 28, 4625-4639.	1.6	64
501	Two ZnF-UBP Domains in Isopeptidase T (USP5). <i>Biochemistry</i> , 2012, 51, 1188-1198.	1.2	49
502	High Ionic Liquid Concentration-Induced Structural Change of Protein in Aqueous Solution: A Case Study of Lysozyme. <i>Journal of Physical Chemistry B</i> , 2012, 116, 11092-11097.	1.2	93
503	Studying the structure of nanocomposites obtained via the chemical decomposition of metal siloxanes in polymer matrices. <i>Bulletin of the Russian Academy of Sciences: Physics</i> , 2012, 76, 1005-1008.	0.1	2
504	The effect of ionic strength on the mechanical, structural and transport properties of peptide hydrogels. <i>Soft Matter</i> , 2012, 8, 11723.	1.2	46

#	ARTICLE	IF	CITATIONS
505	Effects of hydrostatic pressure on the quaternary structure and enzymatic activity of a large peptidase complex from <i>Pyrococcus horikoshii</i> . <i>Archives of Biochemistry and Biophysics</i> , 2012, 517, 104-110.	1.4	28
506	Direct intracellular selection and biochemical characterization of a recombinant anti-proNGF single chain antibody fragment. <i>Archives of Biochemistry and Biophysics</i> , 2012, 522, 26-36.	1.4	9
507	Three RNA Recognition Motifs Participate in RNA Recognition and Structural Organization by the Pro-Apoptotic Factor TIA-1. <i>Journal of Molecular Biology</i> , 2012, 415, 727-740.	2.0	35
508	Disease-Associated Polyglutamine Stretches in Monomeric Huntingtin Adopt a Compact Structure. <i>Journal of Molecular Biology</i> , 2012, 421, 587-600.	2.0	51
509	Crystal Structure of <i>Pseudomonas aeruginosa</i> Tsi2 Reveals a Stably Folded Superhelical Antitoxin. <i>Journal of Molecular Biology</i> , 2012, 417, 351-361.	2.0	11
510	The Role of Hydration in Protein Stability: Comparison of the Cold and Heat Unfolded States of Yfh1. <i>Journal of Molecular Biology</i> , 2012, 417, 413-424.	2.0	52
511	Characterization of <i>Vibrio cholerae</i> Hfq Provides Novel Insights into the Role of the Hfq C-Terminal Region. <i>Journal of Molecular Biology</i> , 2012, 420, 56-69.	2.0	27
512	Determination of a molecular shape for netrin-4 from hydrodynamic and small angle X-ray scattering measurements. <i>Matrix Biology</i> , 2012, 31, 135-140.	1.5	20
513	Crystal and solution structures of methyltransferase RsmH provide basis for methylation of C1402 in 16S rRNA. <i>Journal of Structural Biology</i> , 2012, 179, 29-40.	1.3	31
514	The structure of monoacylglycerol lipase from <i>Bacillus</i> sp. H257 reveals unexpected conservation of the cap architecture between bacterial and human enzymes. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2012, 1821, 1012-1021.	1.2	40
515	The structural basis of the response regulator DrRRA from <i>Deinococcus radiodurans</i> . <i>Biochemical and Biophysical Research Communications</i> , 2012, 417, 1206-1212.	1.0	2
516	Crystal and solution structures disclose a putative transient state of mitogen-activated protein kinase kinase 4. <i>Biochemical and Biophysical Research Communications</i> , 2012, 425, 195-200.	1.0	11
517	Small-angle X-ray scattering reveals structural dynamics of the botulinum neurotoxin associating protein, nontoxic nonhemagglutinin. <i>Biochemical and Biophysical Research Communications</i> , 2012, 425, 256-260.	1.0	12
518	Concerted action of the PHD, chromo and motor domains regulates the human chromatin remodelling ATPase CHD4. <i>FEBS Letters</i> , 2012, 586, 2513-2521.	1.3	33
519	Structural and SAXS analysis of the budding yeast SHU complex proteins. <i>FEBS Letters</i> , 2012, 586, 2306-2312.	1.3	18
520	The X-ray Crystal Structure of Full-Length Human Plasminogen. <i>Cell Reports</i> , 2012, 1, 185-190.	2.9	189
521	Transient B ₁₂ -Dependent Methyltransferase Complexes Revealed by Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2012, 134, 17945-17954.	6.6	18
522	Modulation of Structure and Dynamics by Disulfide Bond Formation in Unfolded States. <i>Journal of the American Chemical Society</i> , 2012, 134, 6846-6854.	6.6	33

#	ARTICLE	IF	CITATIONS
523	Integrative structural modeling with small angle X-ray scattering profiles. <i>BMC Structural Biology</i> , 2012, 12, 17.	2.3	92
524	Nucleic Acid Structure Characterization by Small Angle X-ray Scattering (SAXS). <i>Current Protocols in Nucleic Acid Chemistry</i> , 2012, 51, Unit7.18.	0.5	24
525	Comparative study on low resolution structures of apoferritin via SANS and SAXS. <i>Journal of Physics: Conference Series</i> , 2012, 351, 012009.	0.3	5
526	Sample Preparation, Data Collection, and Preliminary Data Analysis in Biomolecular Solution X-ray Scattering. <i>Current Protocols in Protein Science</i> , 2012, 70, Unit17.14.	2.8	27
527	Structural Characterization of Prefibrillar Intermediates and Amyloid Fibrils by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2012, 849, 137-155.	0.4	10
528	ATP-dependent DNA ligase from <i>Thermococcus</i> sp. 1519 displays a new arrangement of the OB-fold domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1440-1447.	0.7	16
529	Dimeric Smac mimetics/IAP inhibitors as in vivo-active pro-apoptotic agents. Part II: Structural and biological characterization. <i>Bioorganic and Medicinal Chemistry</i> , 2012, 20, 6709-6723.	1.4	29
530	Conformational Analysis of a Genetically Encoded FRET Biosensor by SAXS. <i>Biophysical Journal</i> , 2012, 102, 2866-2875.	0.2	19
531	Dynamical Coupling of Intrinsically Disordered Proteins and Their Hydration Water: Comparison with Folded Soluble and Membrane Proteins. <i>Biophysical Journal</i> , 2012, 103, 129-136.	0.2	79
532	Structural and Functional Characterization of an SMC-like Protein RecN: New Insights into Double-Strand Break Repair. <i>Structure</i> , 2012, 20, 2076-2089.	1.6	43
533	Ensemble Structure of the Modular and Flexible Full-Length Vesicular Stomatitis Virus Phosphoprotein. <i>Journal of Molecular Biology</i> , 2012, 423, 182-197.	2.0	37
534	Conservation of Functionally Important Global Motions in an Enzyme Superfamily across Varying Quaternary Structures. <i>Journal of Molecular Biology</i> , 2012, 423, 831-846.	2.0	13
535	Insights into the Catalytic Mechanism of 16S rRNA Methyltransferase RsmE (m3U1498) from Crystal and Solution Structures. <i>Journal of Molecular Biology</i> , 2012, 423, 576-589.	2.0	13
536	Small Angle Neutron Scattering for the Structural Study of Intrinsically Disordered Proteins in Solution: A Practical Guide. , 2012, 896, 123-135.		10
537	Structural analysis of intrinsically disordered proteins by small-angle X-ray scattering. <i>Molecular BioSystems</i> , 2012, 8, 151-167.	2.9	291
538	A potentiator induces conformational changes on the recombinant CFTR nucleotide binding domains in solution. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 3701-3713.	2.4	10
539	Characterization of the Self-Assembly of <i>meso</i> -Tetra(4-sulfonatophenyl)porphyrin (H ₂ TPPS ⁴⁻) in Aqueous Solutions. <i>Biomacromolecules</i> , 2012, 13, 60-72.	2.6	75
540	Defining the Nature of Thermal Intermediate in 3 State Folding Proteins: Apoflavodoxin, a Study Case. <i>PLoS Computational Biology</i> , 2012, 8, e1002647.	1.5	14

#	ARTICLE	IF	CITATIONS
541	Structural Analysis of the C-Terminal Region (Modules 18â€“20) of Complement Regulator Factor H (FH). PLoS ONE, 2012, 7, e32187.	1.1	39
542	Structural Characterisation of Tpx from <i>Yersinia pseudotuberculosis</i> Reveals Insights into the Binding of Salicylidene Acylhydrazide Compounds. PLoS ONE, 2012, 7, e32217.	1.1	17
543	Myelin 2â€²,3â€²-Cyclic Nucleotide 3â€²-Phosphodiesterase: Active-Site Ligand Binding and Molecular Conformation. PLoS ONE, 2012, 7, e32336.	1.1	31
544	Lack of Evidence from Studies of Soluble Protein Fragments that Knops Blood Group Polymorphisms in Complement Receptor-Type 1 Are Driven by Malaria. PLoS ONE, 2012, 7, e34820.	1.1	25
545	Structural and Functional Analysis of the Symmetrical Type I Restriction Endonuclease R.EcoR124INT. PLoS ONE, 2012, 7, e35263.	1.1	9
546	Conformational States of a Bacterial Î±2-Macroglobulin Resemble Those of Human Complement C3. PLoS ONE, 2012, 7, e35384.	1.1	25
547	Altering APP Proteolysis: Increasing sAPPalpha Production by Targeting Dimerization of the APP Ectodomain. PLoS ONE, 2012, 7, e40027.	1.1	12
548	Characterisation of the First Enzymes Committed to Lysine Biosynthesis in <i>Arabidopsis thaliana</i> . PLoS ONE, 2012, 7, e40318.	1.1	45
549	The Internal Organization of Mycobacterial Partition Assembly: Does the DNA Wrap a Protein Core?. PLoS ONE, 2012, 7, e52690.	1.1	9
550	Expression, purification and preliminary structural analysis of the head domain of <i>Deinococcus radiodurans</i> RecN. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 81-84.	0.7	2
551	Expression, purification and preliminary structural analysis of the coiled-coil domain of <i>Deinococcus radiodurans</i> RecN. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 218-221.	0.7	2
552	Modulated nicking endonuclease function by the Nâ€¢terminal extended region of the smr domain in human Bclâ€² binding protein. Proteins: Structure, Function and Bioinformatics, 2012, 80, 327-332.	1.5	1
553	Ligandâ€¢induced formation of transient dimers of mammalian 12/15â€¢lipoxygenase: A key to allosteric behavior of this class of enzymes?. Proteins: Structure, Function and Bioinformatics, 2012, 80, 703-712.	1.5	33
554	The conserved arginine 380 of Hsp90 is not a catalytic residue, but stabilizes the closed conformation required for ATP hydrolysis. Protein Science, 2012, 21, 1162-1171.	3.1	56
555	Solution structure studies of monomeric human TIP47/perilipinâ€² reveal a highly extended conformation. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2046-2055.	1.5	15
556	Atomic structure of the nuclear pore complex targeting domain of a Nup116 homologue from the yeast, <i>Candida glabrata</i> . Proteins: Structure, Function and Bioinformatics, 2012, 80, 2110-2116.	1.5	7
557	Uncovering of a Short Internal Peptide Activates a tRNA Synthetase Procytokine. Journal of Biological Chemistry, 2012, 287, 20504-20508.	1.6	10
558	Chirality-Mediated Mechanical and Structural Properties of Oligopeptide Hydrogels. Chemistry of Materials, 2012, 24, 2299-2310.	3.2	26

#	ARTICLE	IF	CITATIONS
559	SbsB structure and lattice reconstruction unveil Ca ²⁺ triggered S-layer assembly. <i>Nature</i> , 2012, 487, 119-122.	13.7	125
560	Kinetic and Stoichiometric Characterisation of Streptavidin- β -Binding Aptamers. <i>ChemBioChem</i> , 2012, 13, 829-836.	1.3	24
561	Disentangling the Coil: Modulation of Conformational and Dynamic Properties by Site-Directed Mutation in the Non-Native State of Hen Egg White Lysozyme. <i>Biochemistry</i> , 2012, 51, 3361-3372.	1.2	22
562	Plant UVR8 Photoreceptor Senses UV-B by Tryptophan-Mediated Disruption of Cross-Dimer Salt Bridges. <i>Science</i> , 2012, 335, 1492-1496.	6.0	397
563	High Concentration Formulation Studies of an IgG2 Antibody Using Small Angle X-ray Scattering. <i>Pharmaceutical Research</i> , 2012, 29, 2225-2235.	1.7	44
564	Catalytically active filaments of pyruvate decarboxylase from <i>Neurospora crassa</i> . pH-controlled oligomer structure and catalytic function. <i>FEBS Journal</i> , 2012, 279, 275-284.	2.2	2
565	The catalytic core of an archaeal oxoacid dehydrogenase multienzyme complex is a 42mer protein assembly. <i>FEBS Journal</i> , 2012, 279, 713-723.	2.2	14
566	Structural role of the active-site metal in the conformation of <i>Trypanosoma brucei</i> phosphoglycerate mutase. <i>FEBS Journal</i> , 2012, 279, 2012-2021.	2.2	18
567	Porous zirconium and tin phosphonates incorporating 2,2'-bipyridine as supports for palladium nanoparticles. <i>Microporous and Mesoporous Materials</i> , 2012, 149, 172-180.	2.2	18
568	New developments in the <i>ATSAS</i> program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2012, 45, 342-350.	1.9	1,551
569	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 521-530.	2.5	24
570	Expression, purification and preliminary structural analysis of <i>Escherichia coli</i> MatP in complex with the matSDNA site. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 638-643.	0.7	4
571	A structural study of biocompatible magnetic nanofluid with synchrotron radiation-based X-ray scattering techniques. <i>Moscow University Physics Bulletin (English Translation of Vestnik Tj ETQq0 0 0 rgBT /Overlook 10 Tf 50 257 Td</i>		
572	Autocovariance structures for radial averages in small-angle X-ray scattering experiments. <i>Journal of Time Series Analysis</i> , 2012, 33, 704-717.	0.7	4
573	White Wine Proteins: How Does the pH Affect Their Conformation at Room Temperature?. <i>Langmuir</i> , 2013, 29, 10475-10482.	1.6	24
574	Structural effects induced by gold nanoparticles in particles of cholesteric liquid-crystalline dispersion of double-stranded nucleic acids. <i>Pharmaceutical Chemistry Journal</i> , 2013, 47, 71-79.	0.3	4
575	The Yeast Alix Homolog Bro1 Functions as a Ubiquitin Receptor for Protein Sorting into Multivesicular Endosomes. <i>Developmental Cell</i> , 2013, 25, 520-533.	3.1	83
576	Redox-Linked Domain Movements in the Catalytic Cycle of Cytochrome P450 Reductase. <i>Structure</i> , 2013, 21, 1581-1589.	1.6	68

#	ARTICLE	IF	CITATIONS
577	Combining NMR and small angle X-ray and neutron scattering in the structural analysis of a ternary protein-RNA complex. <i>Journal of Biomolecular NMR</i> , 2013, 56, 17-30.	1.6	48
578	Self-assembly of three bacterially-derived bioactive lipopeptides. <i>Soft Matter</i> , 2013, 9, 9572.	1.2	50
579	Short-block polyurea-polydimethylsiloxane block copolymers based on secondary diamines. <i>Polymer Science - Series B</i> , 2013, 55, 226-232.	0.3	0
580	MgATP Regulates Allostery and Fiber Formation in IMPDHs. <i>Structure</i> , 2013, 21, 975-985.	1.6	72
581	Linear clusters of gold nanoparticles in quasinematic layers of DNA liquid-crystalline dispersion particles. <i>Biophysics (Russian Federation)</i> , 2013, 58, 148-156.	0.2	10
582	Structural characterization of <i>Staphylococcus aureus</i> biotin protein ligase and interaction partners: An antibiotic target. <i>Protein Science</i> , 2013, 22, 762-773.	3.1	32
583	Diagnostics of gold-containing surgical-dressing materials with X-ray and synchrotron radiation. <i>Journal of Surface Investigation</i> , 2013, 7, 509-514.	0.1	5
584	Human IL-34 and CSF-1 Establish Structurally Similar Extracellular Assemblies with Their Common Hematopoietic Receptor. <i>Structure</i> , 2013, 21, 528-539.	1.6	65
585	Solution Structure of Clostridial Collagenase H and Its Calcium-Dependent Global Conformation Change. <i>Biophysical Journal</i> , 2013, 104, 1538-1545.	0.2	18
586	Hexamers of the Type II Secretion ATPase GspE from <i>Vibrio cholerae</i> with Increased ATPase Activity. <i>Structure</i> , 2013, 21, 1707-1717.	1.6	60
587	Visualizing the elusive open shape of G-actin in solution by SAXS data analysis. <i>Biochemical and Biophysical Research Communications</i> , 2013, 435, 740-744.	1.0	7
588	Quaternary structure of human, <i>Drosophila melanogaster</i> and <i>Caenorhabditis elegans</i> MFE ϵ 2 in solution from synchrotron small-angle X-ray scattering. <i>FEBS Letters</i> , 2013, 587, 305-310.	1.3	5
589	Assessing the Conformational Changes of pb5, the Receptor-binding Protein of Phage T5, upon Binding to Its <i>Escherichia coli</i> Receptor FhuA. <i>Journal of Biological Chemistry</i> , 2013, 288, 30763-30772.	1.6	40
590	Shape Matters: A Gold Nanoparticle Enabled Shape Memory Polymer Triggered by Laser Irradiation. <i>Particle and Particle Systems Characterization</i> , 2013, 30, 338-345.	1.2	54
591	Conformational states and recognition of amyloidogenic peptides of human insulin-degrading enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13827-13832.	3.3	52
592	Binding of the N-Terminal Domain of the Lactococcal Bacteriophage TP901-1 CI Repressor to Its Target DNA: A Crystallography, Small Angle Scattering, and Nuclear Magnetic Resonance Study. <i>Biochemistry</i> , 2013, 52, 6892-6904.	1.2	12
593	Reconstruction of Quaternary Structure from X-ray Scattering by Equilibrium Mixtures of Biological Macromolecules. <i>Biochemistry</i> , 2013, 52, 6844-6855.	1.2	24
594	Hydrolytically Degradable Polymer Micelles for Drug Delivery: A SAXS/SANS Kinetic Study. <i>Biomacromolecules</i> , 2013, 14, 4061-4070.	2.6	39

#	ARTICLE	IF	CITATIONS
595	NMR reveals the allosteric opening and closing of Abelson tyrosine kinase by ATP-site and myristoyl pocket inhibitors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4437-45.	3.3	106
596	Solution study of novel diblock copolymers: Morphology and structural transition. Polymer, 2013, 54, 6971-6978.	1.8	1
597	The structure of the box C/D enzyme reveals regulation of RNA methylation. Nature, 2013, 502, 519-523.	13.7	154
598	TssK Is a Trimeric Cytoplasmic Protein Interacting with Components of Both Phage-like and Membrane Anchoring Complexes of the Type VI Secretion System. Journal of Biological Chemistry, 2013, 288, 27031-27041.	1.6	100
599	The Molecular Basis of Iron-induced Oligomerization of Frataxin and the Role of the Ferroxidation Reaction in Oligomerization. Journal of Biological Chemistry, 2013, 288, 8156-8167.	1.6	21
600	Solution Small Angle X-ray Scattering (SAXS) Studies of RecQ from Deinococcus radiodurans and Its Complexes with Junction DNA Substrates. Journal of Biological Chemistry, 2013, 288, 32414-32423.	1.6	4
601	Modern X-ray scattering studies of complex biological systems. Current Opinion in Biotechnology, 2013, 24, 716-723.	3.3	20
602	Small-angle X-ray Solution Scattering Study of the Multi-aminoacyl-tRNA Synthetase Complex Reveals an Elongated and Multi-armed particle. Journal of Biological Chemistry, 2013, 288, 23979-23989.	1.6	28
603	Structural studies of the Trypanosoma cruzi Old Yellow Enzyme: Insights into enzyme dynamics and specificity. Biophysical Chemistry, 2013, 184, 44-53.	1.5	18
604	Structural Insights into Functional Overlapping and Differentiation among Myosin V Motors. Journal of Biological Chemistry, 2013, 288, 34131-34145.	1.6	29
605	Characterization and Solution Structure of the Factor VIII C2 Domain in a Ternary Complex with Classical and Non-classical Inhibitor Antibodies. Journal of Biological Chemistry, 2013, 288, 9905-9914.	1.6	14
606	The Structure of Yeast Glutaminyl-tRNA Synthetase and Modeling of Its Interaction with tRNA. Journal of Molecular Biology, 2013, 425, 2480-2493.	2.0	13
607	Danio rerio Î±E-catenin Is a Monomeric F-actin Binding Protein with Distinct Properties from Mus musculus Î±E-catenin. Journal of Biological Chemistry, 2013, 288, 22324-22332.	1.6	31
608	An Autoinhibited Structure of Î±-Catenin and Its Implications for Vinculin Recruitment to Adherens Junctions. Journal of Biological Chemistry, 2013, 288, 15913-15925.	1.6	110
609	Crystal Structures of the First Condensation Domain of CDA Synthetase Suggest Conformational Changes during the Synthetic Cycle of Nonribosomal Peptide Synthetases. Journal of Molecular Biology, 2013, 425, 3137-3150.	2.0	79
610	Structureâ€“function studies of <i><sc>E</sc>scherichia coli</i>â€™...<sc>RnlA</sc> reveal a novel toxin structure involved in bacteriophage resistance. Molecular Microbiology, 2013, 90, 956-965.	1.2	21
611	Influence of Hydrophobic Micelle Structure on Crystallization of the Photosynthetic RC-LH1-PufX Complex from Rhodobacter blasticus. Journal of Physical Chemistry B, 2013, 117, 8770-8781.	1.2	10
612	Solution structure of hyperactive type I antifreeze protein. RSC Advances, 2013, 3, 5903-5908.	1.7	12

#	ARTICLE	IF	CITATIONS
613	Structural analysis of monomeric retroviral reverse transcriptase in complex with an RNA/DNA hybrid. <i>Nucleic Acids Research</i> , 2013, 41, 3874-3887.	6.5	42
614	<i>Aspergillus niger</i> β -Glucosidase Has a Cellulase-like Tadpole Molecular Shape. <i>Journal of Biological Chemistry</i> , 2013, 288, 32991-33005.	1.6	60
615	Small-Angle X-Ray Scattering on Biological Macromolecules and Nanocomposites in Solution. <i>Annual Review of Physical Chemistry</i> , 2013, 64, 37-54.	4.8	173
616	Light-Induced Subunit Dissociation by a Light-Oxygen-Voltage Domain Photoreceptor from <i>Rhodobacter sphaeroides</i> . <i>Biochemistry</i> , 2013, 52, 378-391.	1.2	67
617	Architecture of the Soluble Receptor Aer2 Indicates an In-Line Mechanism for PAS and HAMP Domain Signaling. <i>Journal of Molecular Biology</i> , 2013, 425, 886-901.	2.0	43
618	Structural characterization of a eukaryotic chaperone-the ribosome-associated complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 23-28.	3.6	79
619	Solution structures of polyclonal Phl p 7 in three ligation states: Apo, hemic-bound, and fully Ca ²⁺ -bound. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 300-315.	1.5	12
620	Self-Assembly and Conformational Heterogeneity of the AXH Domain of Ataxin-1: An Unusual Example of a Chameleon Fold. <i>Biophysical Journal</i> , 2013, 104, 1304-1313.	0.2	19
621	Structural peculiarities of the (MHF1-MHF2) ₄ octamer provide a long DNA binding patch to anchor the MHF-FANCM complex to chromatin: A solution SAXS study. <i>FEBS Letters</i> , 2013, 587, 2912-2917.	1.3	3
622	Correlation of thermostability and conformational changes of catechol 2, 3-dioxygenases from two disparate micro-organisms. <i>Biophysical Chemistry</i> , 2013, 180-181, 145-152.	1.5	0
623	Structure of a Truncation Mutant of the Nuclear Export Factor CRM1 Provides Insights into the Auto-Inhibitory Role of Its C-Terminal Helix. <i>Structure</i> , 2013, 21, 1338-1349.	1.6	15
624	Structural Determinants of Oligomerization of β -1-Pyrroline-5-Carboxylate Dehydrogenase: Identification of a Hexamerization Hot Spot. <i>Journal of Molecular Biology</i> , 2013, 425, 3106-3120.	2.0	24
625	Amino-acid substitutions at the domain interface affect substrate and allosteric inhibitor binding in β -isopropylmalate synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2013, 433, 249-254.	1.0	7
626	The Differential Regulation of p38 β by the Neuronal Kinase Interaction Motif Protein Tyrosine Phosphatases, a Detailed Molecular Study. <i>Structure</i> , 2013, 21, 1612-1623.	1.6	20
627	Recombinant production of <i>Yersinia enterocolitica</i> pyruvate kinase isoenzymes PykA and PykF. <i>Protein Expression and Purification</i> , 2013, 88, 243-247.	0.6	6
628	Biochemical and structural studies of the oligomerization domain of the Nipah virus phosphoprotein: Evidence for an elongated coiled-coil homotrimer. <i>Virology</i> , 2013, 446, 162-172.	1.1	23
629	The structural organization of the N-terminus domain of SopB, a virulence factor of <i>Salmonella</i> , depends on the nature of its protein partners. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 2564-2572.	1.1	7
630	Structural Flexibility of CaV1.2 and CaV2.2 I-II Proximal Linker Fragments in Solution. <i>Biophysical Journal</i> , 2013, 104, 2392-2400.	0.2	5

#	ARTICLE	IF	CITATIONS
631	Structural Mechanism of GAF-Regulated γ 54 Activators from Aquifex aeolicus. <i>Journal of Molecular Biology</i> , 2013, 425, 156-170.	2.0	16
632	A T3R3 hexamer of the human insulin variant B28Asp. <i>Biophysical Chemistry</i> , 2013, 173-174, 1-7.	1.5	17
633	Structural Principles of RNA Catalysis in a $2\text{â}^2\text{â}^5$ Lariat-Forming Ribozyme. <i>Journal of the American Chemical Society</i> , 2013, 135, 4403-4411.	6.6	16
634	Impact of macromolecular crowding on DNA replication. <i>Nature Communications</i> , 2013, 4, 1615.	5.8	134
635	SOCS3 binds specific receptorâ€”JAK complexes to control cytokine signaling by direct kinase inhibition. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 469-476.	3.6	229
636	Molecular Model of a Soluble Guanylyl Cyclase Fragment Determined by Small-Angle X-ray Scattering and Chemical Cross-Linking. <i>Biochemistry</i> , 2013, 52, 1568-1582.	1.2	56
637	Self-Assembling Semiconducting Polymersâ€”Rods and Gels from Electronic Materials. <i>ACS Nano</i> , 2013, 7, 962-977.	7.3	25
638	The Bacterial DnaC Helicase Loader Is a DnaB Ring Breaker. <i>Cell</i> , 2013, 153, 438-448.	13.5	89
639	Low temperature synthesis of monodisperse nanoscaled ZrO_2 with a large specific surface area. <i>Dalton Transactions</i> , 2013, 42, 432-440.	1.6	19
640	Small Angle X-ray Scattering-Based Elucidation of the Self-Association Mechanism of Human Insulin Analogue Lys ^{B29} (N ¹ μ -carboxyheptadecanoyl) des(B30). <i>Biochemistry</i> , 2013, 52, 282-294.	1.2	17
641	Multimeric and differential binding of $\langle \text{CIN} \rangle_{85} \langle \text{CD} \rangle_2 \langle \text{AP} \rangle$ with two atypical prolineâ€”rich sequences from $\langle \text{CD} \rangle_2$ and Cblâ€”*. <i>FEBS Journal</i> , 2013, 280, 3399-3415.	2.2	9
642	Monoclonal Antibody Self-Association, Cluster Formation, and Rheology at High Concentrations. <i>Journal of Physical Chemistry B</i> , 2013, 117, 6373-6384.	1.2	135
643	Human UDP- β -xylose Synthase Forms a Catalytically Important Tetramer That Has Not Been Observed in Crystal Structures. <i>Biochemistry</i> , 2013, 52, 3888-3898.	1.2	6
644	Developing advanced X-ray scattering methods combined with crystallography and computation. <i>Methods</i> , 2013, 59, 363-371.	1.9	22
645	All-Atom Ensemble Modeling to Analyze Small-Angle X-Ray Scattering of Glycosylated Proteins. <i>Structure</i> , 2013, 21, 321-331.	1.6	77
646	Applications of small-angle X-ray scattering to biomacromolecular solutions. <i>International Journal of Biochemistry and Cell Biology</i> , 2013, 45, 429-437.	1.2	94
647	A structural model of PpoA derived from SAXS-analysisâ€”Implications for substrate conversion. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013, 1831, 1449-1457.	1.2	9
648	Ligand-Controlled Assembly of Hexamers, Dihexamers, and Linear Multihexamer Structures by the Engineered Acylated Insulin Degludec. <i>Biochemistry</i> , 2013, 52, 295-309.	1.2	72

#	ARTICLE	IF	CITATIONS
649	Structure and Conformational Dynamics of DMPC/Dicationic Surfactant and DMPC/Dicationic Surfactant/DNA Systems. <i>International Journal of Molecular Sciences</i> , 2013, 14, 7642-7659.	1.8	27
650	Interactions of a cationic surfactant " (benzyloxymethyl) dodecyldimethylammonium chloride with model biomembrane systems. <i>Colloids and Surfaces B: Biointerfaces</i> , 2013, 108, 212-218.	2.5	1
651	Insights into Degron Recognition by APC/C Coactivators from the Structure of an Acm1-Cdh1 Complex. <i>Molecular Cell</i> , 2013, 50, 649-660.	4.5	115
652	Synthesis of β -Glucan in Mycobacteria Involves a Hetero-octameric Complex of Trehalose Synthase TreS and Maltokinase Pep2. <i>ACS Chemical Biology</i> , 2013, 8, 2245-2255.	1.6	27
653	Effect of Poly(propylene imine) Glycodendrimers on β -Amyloid Aggregation in Vitro and in APP/PS1 Transgenic Mice, as a Model of Brain Amyloid Deposition and Alzheimer's Disease. <i>Biomacromolecules</i> , 2013, 14, 3570-3580.	2.6	64
654	The Denatured State Ensemble Contains Significant Local and Long-Range Structure under Native Conditions: Analysis of the N-Terminal Domain of Ribosomal Protein L9. <i>Biochemistry</i> , 2013, 52, 2662-2671.	1.2	29
655	Solution conformations of early intermediates in Mos1 transposition. <i>Nucleic Acids Research</i> , 2013, 41, 2020-2033.	6.5	27
656	Renewal of the Air-Water Interface as a Critical System Parameter of Protein Stability: Aggregation of the Human Growth Hormone and Its Prevention by Surface-Active Compounds. <i>Langmuir</i> , 2013, 29, 15240-15250.	1.6	72
657	The Structure of Integrin β 11 Domain in Complex with a Collagen-mimetic Peptide. <i>Journal of Biological Chemistry</i> , 2013, 288, 36796-36809.	1.6	22
658	Biophysical analysis of the putative acetyltransferase SACOL2570 from methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 97-108.	1.2	9
659	Cooperative Cold Denaturation: The Case of the C-Terminal Domain of Ribosomal Protein L9. <i>Biochemistry</i> , 2013, 52, 2402-2409.	1.2	31
660	Intrinsic Flexibility of West Nile Virus Protease in Solution Characterized Using Small-Angle X-ray Scattering. <i>Biochemistry</i> , 2013, 52, 6856-6865.	1.2	5
661	Shape evolution with temperature of a thermotolerant protein (PeaT1) in solution detected by small angle X-ray scattering. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 53-62.	1.5	3
662	Unique Features of a <i>Pseudomonas aeruginosa</i> β 2-Macroglobulin Homolog. <i>MBio</i> , 2013, 4, .	1.8	24
663	Hfq binding changes the structure of <i>Escherichia coli</i> small noncoding RNAs OxyS and RprA, which are involved in the riboregulation of <i>rpoS</i> . <i>Rna</i> , 2013, 19, 1089-1104.	1.6	38
664	Structural insights into protein-only RNase P complexed with tRNA. <i>Nature Communications</i> , 2013, 4, 1353.	5.8	62
665	Ligand binding and aggregation of pathogenic SOD1. <i>Nature Communications</i> , 2013, 4, 1758.	5.8	90
666	A molecular explanation for the recessive nature of parkin-linked Parkinson's disease. <i>Nature Communications</i> , 2013, 4, 1983.	5.8	123

#	ARTICLE	IF	CITATIONS
667	The Truncated C-terminal RNA Recognition Motif of TDP-43 Protein Plays a Key Role in Forming Proteinaceous Aggregates. <i>Journal of Biological Chemistry</i> , 2013, 288, 9049-9057.	1.6	84
668	The Geminin and Idas Coiled Coils Preferentially Form a Heterodimer That Inhibits Geminin Function in DNA Replication Licensing. <i>Journal of Biological Chemistry</i> , 2013, 288, 31624-31634.	1.6	22
669	Structural insights into the inhibition of type A β effector Tae3 by its immunity protein Tai3. <i>Biochemical Journal</i> , 2013, 454, 59-68.	1.7	26
670	Tensile properties of in-situ precipitated polydimethylsiloxane networks. <i>EXPRESS Polymer Letters</i> , 2013, 7, 863-872.	1.1	1
671	Characterization of a pre-export enzyme-chaperone complex on the twin-arginine transport pathway. <i>Biochemical Journal</i> , 2013, 452, 57-66.	1.7	16
672	Structural and Functional Basis for Inhibition of Erythrocyte Invasion by Antibodies that Target Plasmodium falciparum EBA-175. <i>PLoS Pathogens</i> , 2013, 9, e1003390.	2.1	55
673	A new structural framework for integrating replication protein A into DNA processing machinery. <i>Nucleic Acids Research</i> , 2013, 41, 2313-2327.	6.5	88
674	Using stable MutS dimers and tetramers to quantitatively analyze DNA mismatch recognition and sliding clamp formation. <i>Nucleic Acids Research</i> , 2013, 41, 8166-8181.	6.5	36
675	Design, purification and characterization of a soluble variant of the integral membrane protein MotB for structural studies. <i>Journal of the Royal Society Interface</i> , 2013, 10, 20120717.	1.5	4
676	Conformational Plasticity of the Essential Membrane-associated Mannosyltransferase PimA from Mycobacteria. <i>Journal of Biological Chemistry</i> , 2013, 288, 29797-29808.	1.6	24
677	Asymmetric recognition of the HIV-1 trimer by broadly neutralizing antibody PG9. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4351-4356.	3.3	236
678	SASET: a program for series analysis of small-angle scattering data. <i>Journal of Applied Crystallography</i> , 2013, 46, 1187-1195.	1.9	20
679	Characterization of Anopheles gambiae Transglutaminase 3 (AgTG3) and Its Native Substrate Plugin. <i>Journal of Biological Chemistry</i> , 2013, 288, 4844-4853.	1.6	14
680	Structure of Severe Fever with Thrombocytopenia Syndrome Virus Nucleocapsid Protein in Complex with Suramin Reveals Therapeutic Potential. <i>Journal of Virology</i> , 2013, 87, 6829-6839.	1.5	67
681	Structure-Informed Design of an Enzymatically Inactive Vaccine Component for Group A Streptococcus. <i>MBio</i> , 2013, 4, .	1.8	18
682	Structure, phosphorylation and U2AF65 binding of the N-terminal domain of splicing factor 1 during splice site recognition. <i>Nucleic Acids Research</i> , 2013, 41, 1343-1354.	6.5	61
683	Structural Basis for the Regulation of the Mitogen-activated Protein (MAP) Kinase p38 β by the Dual Specificity Phosphatase 16 MAP Kinase Binding Domain in Solution. <i>Journal of Biological Chemistry</i> , 2013, 288, 28347-28356.	1.6	13
684	Quaternary structure of the yeast Arc1p-aminoacyl-tRNA synthetase complex in solution and its compaction upon binding of tRNAs. <i>Nucleic Acids Research</i> , 2013, 41, 667-676.	6.5	12

#	ARTICLE	IF	CITATIONS
685	Small-angle X-ray Scattering of Apolipoprotein A-IV Reveals the Importance of Its Termini for Structural Stability. <i>Journal of Biological Chemistry</i> , 2013, 288, 4854-4866.	1.6	10
686	Small Oligomers of Ribulose-bisphosphate Carboxylase/Oxygenase (Rubisco) Activase Are Required for Biological Activity. <i>Journal of Biological Chemistry</i> , 2013, 288, 20607-20615.	1.6	30
687	Interaction of Aryl Hydrocarbon Receptor-interacting Protein-like 1 with the Farnesyl Moiety. <i>Journal of Biological Chemistry</i> , 2013, 288, 21320-21328.	1.6	32
688	The Role of Nonconserved Residues of <i>Archaeoglobus fulgidus</i> Ferritin on Its Unique Structure and Biophysical Properties. <i>Journal of Biological Chemistry</i> , 2013, 288, 32663-32672.	1.6	43
689	Structural characterization of gephyrin by AFM and SAXS reveals a mixture of compact and extended states. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2050-2060.	2.5	43
690	<i>Staphylococcus aureus</i> thiaminase II: oligomerization warrants proteolytic protection against serine proteases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2320-2329.	2.5	6
691	Structural basis of SUFU-Gli interaction in human Hedgehog signalling regulation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2563-2579.	2.5	54
692	Crystallization and preliminary structure determination of the transfer protein TraM from the Gram-positive conjugative plasmid pIP501. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 178-183.	0.7	6
693	High-resolution structure of the Tiam1 PH _n -CC-Ex domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 744-752.	0.7	5
694	Difference in hydration structures between F-actin and myosin subfragment-1 detected by small-angle X-ray and neutron scattering. <i>Biophysics (Nagoya-shi, Japan)</i> , 2013, 9, 99-106.	0.4	10
695	Isolate-Specific Differences in the Conformational Dynamics and Antigenicity of HIV-1 gp120. <i>Journal of Virology</i> , 2013, 87, 10855-10873.	1.5	29
696	Structure of the Type VI Effector-Immunity Complex (Tae4-Tai4) Provides Novel Insights into the Inhibition Mechanism of the Effector by Its Immunity Protein*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5928-5939.	1.6	65
697	An interplay between electrostatic and polar interactions in peptide hydrogels. <i>Biopolymers</i> , 2013, 100, 174-183.	1.2	17
698	Conformational transitions in human translin enable nucleic acid binding. <i>Nucleic Acids Research</i> , 2013, 41, 9956-9966.	6.5	11
699	Kinetic analysis of cytokine-mediated receptor assembly using engineered FC heterodimers. <i>Protein Science</i> , 2013, 22, 1100-1108.	3.1	12
700	Low-Resolution Structure of Vaccinia Virus DNA Replication Machinery. <i>Journal of Virology</i> , 2013, 87, 1679-1689.	1.5	37
701	Molecular Architecture of a Complex between an Adhesion Protein from the Malaria Parasite and Intracellular Adhesion Molecule 1. <i>Journal of Biological Chemistry</i> , 2013, 288, 5992-6003.	1.6	37
702	Examination of Matrix Metalloproteinase-1 in Solution. <i>Journal of Biological Chemistry</i> , 2013, 288, 30659-30671.	1.6	68

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703	NrdH-redoxin of <i>Mycobacterium tuberculosis</i> and <i>Corynebacterium glutamicum</i> Dimerizes at High Protein Concentration and Exclusively Receives Electrons from Thioredoxin Reductase. <i>Journal of Biological Chemistry</i> , 2013, 288, 7942-7955.	1.6	14
704	Population Shift Underlies Ca ²⁺ -induced Regulatory Transitions in the Sodium-Calcium Exchanger (NCX). <i>Journal of Biological Chemistry</i> , 2013, 288, 23141-23149.	1.6	26
705	Global Shapes of F-actin Depolymerization-competent Minimal Gelsolins. <i>Journal of Biological Chemistry</i> , 2013, 288, 28266-28282.	1.6	20
706	Structural Analysis of Collagen Type I Interactions with Human Fibronectin Reveals a Cooperative Binding Mode. <i>Journal of Biological Chemistry</i> , 2013, 288, 17441-17450.	1.6	67
707	The Fic protein Doc uses an inverted substrate to phosphorylate and inactivate EF-Tu. <i>Nature Chemical Biology</i> , 2013, 9, 811-817.	3.9	159
708	Characterization of MicA interactions suggests a potential novel means of gene regulation by small non-coding RNAs. <i>Nucleic Acids Research</i> , 2013, 41, 3386-3397.	6.5	20
709	A UDP-X Diphosphatase from <i>Streptococcus pneumoniae</i> Hydrolyzes Precursors of Peptidoglycan Biosynthesis. <i>PLoS ONE</i> , 2013, 8, e64241.	1.1	2
710	Low Resolution Structural Studies Indicate that the Activator of Hsp90 ATPase 1 (Aha1) of <i>Leishmania braziliensis</i> Has an Elongated Shape Which Allows Its Interaction with Both N- and M-Domains of Hsp90. <i>PLoS ONE</i> , 2013, 8, e66822.	1.1	22
711	The Inhibitory Helix Controls the Intramolecular Conformational Switching of the C-Terminus of STIM1. <i>PLoS ONE</i> , 2013, 8, e74735.	1.1	40
712	Substitution of Glutamate Residue by Lysine in the Dimerization Domain Affects DNA Binding Ability of HapR by Inducing Structural Deformity in the DNA Binding Domain. <i>PLoS ONE</i> , 2013, 8, e76033.	1.1	22
713	Ceruloplasmin: Macromolecular Assemblies with Iron-Containing Acute Phase Proteins. <i>PLoS ONE</i> , 2013, 8, e67145.	1.1	82
714	Structural Analysis of Influenza A Virus Matrix Protein M1 and Its Self-Assemblies at Low pH. <i>PLoS ONE</i> , 2013, 8, e82431.	1.1	60
715	Flexibility of the Linker between the Domains of DNA Methyltransferase SsoII Revealed by Small-Angle X-Ray Scattering: Implications for Transcription Regulation in SsoII Restriction-Modification System. <i>PLoS ONE</i> , 2014, 9, e93453.	1.1	7
716	The C-Terminal Random Coil Region Tunes the Ca ²⁺ -Binding Affinity of S100A4 through Conformational Activation. <i>PLoS ONE</i> , 2014, 9, e97654.	1.1	11
717	Crystal Structure of Arginine Methyltransferase 6 from <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2014, 9, e87267.	1.1	21
718	Interaction of Kinase-Interaction-Motif Protein Tyrosine Phosphatases with the Mitogen-Activated Protein Kinase ERK2. <i>PLoS ONE</i> , 2014, 9, e91934.	1.1	13
719	Structural Insight into the Tetramerization of an Iterative Ketoreductase SiaM through Aromatic Residues in the Interfaces. <i>PLoS ONE</i> , 2014, 9, e97996.	1.1	4
720	Structural and Biophysical Characterization of <i>Bacillus thuringiensis</i> Insecticidal Proteins Cry34Ab1 and Cry35Ab1. <i>PLoS ONE</i> , 2014, 9, e112555.	1.1	62

#	ARTICLE	IF	CITATIONS
721	RNA-guided assembly of Rev-RRE nuclear export complexes. <i>ELife</i> , 2014, 3, e03656.	2.8	81
722	Promotion of Enzyme Flexibility by Dephosphorylation and Coupling to the Catalytic Mechanism of a Phosphohexomutase. <i>Journal of Biological Chemistry</i> , 2014, 289, 4674-4682.	1.6	16
723	A Novel Structural Unit in the N-terminal Region of Filamins. <i>Journal of Biological Chemistry</i> , 2014, 289, 8588-8598.	1.6	18
724	The palindromic DNA-bound USP/EcR nuclear receptor adopts an asymmetric organization with allosteric domain positioning. <i>Nature Communications</i> , 2014, 5, 4139.	5.8	33
725	Molecular functions of the TLE tetramerization domain in Wnt target gene repression. <i>EMBO Journal</i> , 2014, 33, 719-731.	3.5	77
726	A new calmodulin-binding motif for inositol 1,4,5-trisphosphate 3-kinase regulation. <i>Biochemical Journal</i> , 2014, 463, 319-328.	1.7	8
727	A Negatively Charged Residue Stabilizes the Tropoelastin N-terminal Region for Elastic Fiber Assembly. <i>Journal of Biological Chemistry</i> , 2014, 289, 34815-34826.	1.6	22
728	Global Shape and Ligand Binding Efficiency of the HIV-1-neutralizing Antibodies Differ from Those of Antibodies That Cannot Neutralize HIV-1. <i>Journal of Biological Chemistry</i> , 2014, 289, 34780-34800.	1.6	19
729	Dimerization Is Not a Determining Factor for Functional High Affinity Human Plasminogen Binding by the Group A Streptococcal Virulence Factor PAM and Is Mediated by Specific Residues within the PAM a1a2 Domain. <i>Journal of Biological Chemistry</i> , 2014, 289, 21684-21693.	1.6	17
730	Structural Model for Covalent Adhesion of the <i>Streptococcus pyogenes</i> Pilus through a Thioester Bond. <i>Journal of Biological Chemistry</i> , 2014, 289, 177-189.	1.6	41
731	Conserved Distal Loop Residues in the Hsp104 and ClpB Middle Domain Contact Nucleotide-binding Domain 2 and Enable Hsp70-dependent Protein Disaggregation. <i>Journal of Biological Chemistry</i> , 2014, 289, 848-867.	1.6	42
732	Oleoyl Coenzyme A Regulates Interaction of Transcriptional Regulator RaaS (Rv1219c) with DNA in <i>Mycobacteria</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 25241-25249.	1.6	8
733	Conformational Itinerary of <i>Pseudomonas aeruginosa</i> 1,6-Anhydro-N-acetylmuramic Acid Kinase during Its Catalytic Cycle. <i>Journal of Biological Chemistry</i> , 2014, 289, 4504-4514.	1.6	7
734	Disease causing mutants of TDP-43 nucleic acid binding domains are resistant to aggregation and have increased stability and half-life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 4309-4314.	3.3	68
735	Structural Insights into the Activation of the RhoA GTPase by the Lymphoid Blast Crisis (Lbc) Oncoprotein. <i>Journal of Biological Chemistry</i> , 2014, 289, 23992-24004.	1.6	10
737	Cu(I)-mediated Allosteric Switching in a Copper-sensing Operon Repressor (CsoR). <i>Journal of Biological Chemistry</i> , 2014, 289, 19204-19217.	1.6	50
738	Insights into the evolution of divergent nucleotide-binding mechanisms among pseudokinases revealed by crystal structures of human and mouse MLKL. <i>Biochemical Journal</i> , 2014, 457, 369-377.	1.7	92
739	Why are the 2-oxoacid dehydrogenase complexes so large? Generation of an active trimeric complex. <i>Biochemical Journal</i> , 2014, 463, 405-412.	1.7	18

#	ARTICLE	IF	CITATIONS
740	RNA Mimicry by the Fap7 Adenylate Kinase in Ribosome Biogenesis. <i>PLoS Biology</i> , 2014, 12, e1001860.	2.6	37
741	Conformational transition of a non-associative fluorinated amphiphile in aqueous solution. <i>RSC Advances</i> , 2014, 4, 54565-54575.	1.7	13
742	The CD27L and CTP1L Endolysins Targeting Clostridia Contain a Built-in Trigger and Release Factor. <i>PLoS Pathogens</i> , 2014, 10, e1004228.	2.1	37
743	The Structure and Regulation of Human Muscle β -Actinin. <i>Cell</i> , 2014, 159, 1447-1460.	13.5	178
744	Mechanistic insights into activation and SOCS3-mediated inhibition of myeloproliferative neoplasm-associated JAK2 mutants from biochemical and structural analyses. <i>Biochemical Journal</i> , 2014, 458, 395-405.	1.7	33
745	Lectin-Like Bacteriocins from <i>Pseudomonas</i> spp. Utilise D-Rhamnose Containing Lipopolysaccharide as a Cellular Receptor. <i>PLoS Pathogens</i> , 2014, 10, e1003898.	2.1	56
746	Structural Insights into SraP-Mediated <i>Staphylococcus aureus</i> Adhesion to Host Cells. <i>PLoS Pathogens</i> , 2014, 10, e1004169.	2.1	85
747	Structural Data on the Periplasmic Aldehyde Oxidoreductase PaoABC from <i>Escherichia coli</i> : SAXS and Preliminary X-ray Crystallography Analysis. <i>International Journal of Molecular Sciences</i> , 2014, 15, 2223-2236.	1.8	13
748	Crystal structure of the mouse interleukin-3 β -receptor: insights into interleukin-3 binding and receptor activation. <i>Biochemical Journal</i> , 2014, 463, 393-403.	1.7	5
749	Ca ²⁺ -stabilized adhesin helps an Antarctic bacterium reach out and bind ice. <i>Bioscience Reports</i> , 2014, 34, .	1.1	32
750	The Structural Characteristics Features of the Nanocomposite Systems of CdS Quantum Dots in the Gel Matrix Obtained by the Method of Small-Angle X-Ray Scattering. <i>Solid State Phenomena</i> , 0, 213, 216-221.	0.3	0
751	Non-stop mRNA decay: a special attribute of trans-translation mediated ribosome rescue. <i>Frontiers in Microbiology</i> , 2014, 5, 93.	1.5	17
752	Characterization of the Conformational Fluctuations in the Josephin Domain of Ataxin-3. <i>Biophysical Journal</i> , 2014, 107, 2932-2940.	0.2	15
753	The structural basis for receptor recognition of human interleukin-18. <i>Nature Communications</i> , 2014, 5, 5340.	5.8	107
754	Structural analysis of poly-SUMO chain recognition by the RNF4-SIMs domain. <i>Biochemical Journal</i> , 2014, 462, 53-65.	1.7	29
755	Structural Basis of a Kv7.1 Potassium Channel Gating Module: Studies of the Intracellular C-Terminal Domain in Complex with Calmodulin. <i>Structure</i> , 2014, 22, 1582-1594.	1.6	88
756	Structural Basis of the pH-Dependent Assembly of a Botulinum Neurotoxin Complex. <i>Journal of Molecular Biology</i> , 2014, 426, 3773-3782.	2.0	28
757	Ultra-high resolution crystal structure of recombinant caprine β -lactoglobulin. <i>FEBS Letters</i> , 2014, 588, 3816-3822.	1.3	16

#	ARTICLE	IF	CITATIONS
758	Crystal structure of a <i>ε</i> -AMP riboswitch reveals an internally pseudo-dimeric RNA. <i>EMBO Journal</i> , 2014, 33, 2692-2703.	3.5	53
759	The 2'-5'-Oligoadenylate Synthetase 3 Enzyme Potently Synthesizes the 2'-5'-Oligoadenylates Required for RNase L Activation. <i>Journal of Virology</i> , 2014, 88, 14222-14231.	1.5	59
760	The Structure of the Catalytic Domain of a Plant Cellulose Synthase and Its Assembly into Dimers. <i>Plant Cell</i> , 2014, 26, 2996-3009.	3.1	61
761	Flexibility of truncated and full-length glucanase GTF180 enzymes from <i>Lactobacillus reuteri</i> . <i>FEBS Journal</i> , 2014, 281, 2159-2171.	2.2	21
762	Protein grafting of p53TAD onto a leucine zipper scaffold generates a potent HDM dual inhibitor. <i>Nature Communications</i> , 2014, 5, 3814.	5.8	8
763	Characterization and assembly of a GFP-tagged cylindrical silk into hexameric complexes. <i>Biopolymers</i> , 2014, 101, 378-390.	1.2	4
764	Structural basis for adaptation of lactobacilli to gastrointestinal mucus. <i>Environmental Microbiology</i> , 2014, 16, 888-903.	1.8	102
765	Towards strain-independent anti-influenza peptides: a SAXS- and modeling-based study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1720-1733.	2.0	4
766	Integrative Structure-Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2911-2926.	2.5	67
767	Susceptibility to HLA-DM Protein Is Determined by a Dynamic Conformation of Major Histocompatibility Complex Class II Molecule Bound with Peptide. <i>Journal of Biological Chemistry</i> , 2014, 289, 23449-23464.	1.6	49
768	A conformational switch in collybistin determines the differentiation of inhibitory postsynapses. <i>EMBO Journal</i> , 2014, 33, 2113-2133.	3.5	75
769	Characterization and Structure of the Vaccinia Virus NF-B Antagonist A46. <i>Journal of Biological Chemistry</i> , 2014, 289, 3749-3762.	1.6	28
770	Regulation of the catalytic activity of the human phosphatase PTPN4 by its PDZ domain. <i>FEBS Journal</i> , 2014, 281, 4852-4865.	2.2	19
771	Structural Asymmetry of the Terminal Catalytic Complex in Selenocysteine Synthesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 28783-28794.	1.6	11
772	Structure of the Hemoglobin-IsoD Hemoglobin Complex Reveals the Molecular Basis of Iron Capture by <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 6728-6738.	1.6	58
773	Homodimerization of RBPMS2 through a new RRM-interaction motif is necessary to control smooth muscle plasticity. <i>Nucleic Acids Research</i> , 2014, 42, 10173-10184.	6.5	39
774	A unique octameric structure of Axe2, an intracellular acetyl-xylooligosaccharide esterase from <i>Geobacillus stearothermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 261-278.	2.5	30
775	The histone chaperones Vps75 and Nap1 form ring-like, tetrameric structures in solution. <i>Nucleic Acids Research</i> , 2014, 42, 6038-6051.	6.5	37

#	ARTICLE	IF	CITATIONS
776	Gene regulation by substoichiometric heterocomplex formation of undecameric TRAP and trimeric anti-TRAP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3442-3447.	3.3	13
777	Structure, dynamics and RNA binding of the multi-domain splicing factor TIA-1. <i>Nucleic Acids Research</i> , 2014, 42, 5949-5966.	6.5	77
778	ModBase, a database of annotated comparative protein structure models and associated resources. <i>Nucleic Acids Research</i> , 2014, 42, D336-D346.	6.5	275
779	Crystal structure of tRNA m1G9 methyltransferase Trm10: insight into the catalytic mechanism and recognition of tRNA substrate. <i>Nucleic Acids Research</i> , 2014, 42, 509-525.	6.5	46
780	Organization of the human mitochondrial transcription initiation complex. <i>Nucleic Acids Research</i> , 2014, 42, 4100-4112.	6.5	39
781	Periaxin and AHNAK Nucleoprotein 2 Form Intertwined Homodimers through Domain Swapping. <i>Journal of Biological Chemistry</i> , 2014, 289, 14121-14131.	1.6	30
782	Structure-specificity relationships in Abp, a GH27 β -arabinopyranosidase from <i>Geobacillus stearothermophilus</i> T6. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2994-3012.	2.5	9
783	Endophilin-A1 BAR domain interaction with arachidonyl CoA. <i>Frontiers in Molecular Biosciences</i> , 2014, 1, 20.	1.6	3
784	Characterization of spinach ribulose-1,5-bisphosphate carboxylase/oxygenase activase isoforms reveals hexameric assemblies with increased thermal stability. <i>Biochemical Journal</i> , 2014, 464, 413-423.	1.7	36
785	Structure, mechanism and ensemble formation of the alkylhydroperoxide reductase subunits AhpC and AhpF from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2848-2862.	2.5	47
786	SAXS analysis of the tRNA-modifying enzyme complex MnmE/MnmG reveals a novel interaction mode and GTP-induced oligomerization. <i>Nucleic Acids Research</i> , 2014, 42, 5978-5992.	6.5	27
787	Structural and biophysical characterization of <i>Staphylococcus aureus</i> SaMazF shows conservation of functional dynamics. <i>Nucleic Acids Research</i> , 2014, 42, 6709-6725.	6.5	33
788	Small-angle neutron scattering reveals the assembly mode and oligomeric architecture of TET, a large, dodecameric aminopeptidase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2983-2993.	2.5	19
789	Domain mobility as probed by small-angle X-ray scattering may account for substrate access to the active site of two copper-dependent amine oxidases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2101-2110.	2.5	8
790	Structural insight into arginine methylation by the mouse protein arginine methyltransferase 7: a zinc finger freezes the mimic of the dimeric state into a single active site. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2401-2412.	2.5	32
791	Structural insights into the human RyR2 N-terminal region involved in cardiac arrhythmias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2897-2912.	2.5	25
792	The structure of vanin 1: a key enzyme linking metabolic disease and inflammation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3320-3329.	2.5	37
793	Structural and functional insights into an archaeal α -asparaginase obtained through the linker-less assembly of constituent domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 3187-3197.	2.5	25

#	ARTICLE	IF	CITATIONS
794	Production and characterization of a retinoic acid receptor RAR β construction encompassing the DNA binding domain and the disordered N-terminal proline rich domain. Protein Expression and Purification, 2014, 95, 113-120.	0.6	4
795	Solution conformation of adenovirus virus associated RNA-I and its interaction with PKR. Journal of Structural Biology, 2014, 185, 48-57.	1.3	21
796	A quantitative assay for binding and inhibition of Plasmodium falciparum Erythrocyte Binding Antigen 175 reveals high affinity binding depends on both DBL domains. Protein Expression and Purification, 2014, 95, 188-194.	0.6	20
797	p15PAF Is an Intrinsically Disordered Protein with Nonrandom Structural Preferences at Sites of Interaction with Other Proteins. Biophysical Journal, 2014, 106, 865-874.	0.2	54
798	Global analysis of riboswitches by small-angle X-ray scattering and calorimetry. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1020-1029.	0.9	34
799	Guanidine hydrochloride denaturation of dopamine-induced α -synuclein oligomers: A small-angle X-ray scattering study. Proteins: Structure, Function and Bioinformatics, 2014, 82, 10-21.	1.5	9
800	Structural elucidation of full-length nidogen and the laminin α 5-nidogen complex in solution. Matrix Biology, 2014, 33, 60-67.	1.5	32
801	Interactions of ataxin-3 with its molecular partners in the protein machinery that sorts protein aggregates to the aggresome. International Journal of Biochemistry and Cell Biology, 2014, 51, 58-64.	1.2	18
802	Weak protein α 5-ligand interactions studied by small α 5-angle X-ray scattering. FEBS Journal, 2014, 281, 1974-1987.	2.2	35
803	Chemical inhibition of prometastatic lysyl-tRNA synthetase α 5-laminin receptor interaction. Nature Chemical Biology, 2014, 10, 29-34.	3.9	55
804	The Salmonella enterica ZinT structure, zinc affinity and interaction with the high-affinity uptake protein ZnuA provide insight into the management of periplasmic zinc. Biochimica Et Biophysica Acta - General Subjects, 2014, 1840, 535-544.	1.1	46
805	Structural Basis for Assembly and Function of a Heterodimeric Plant Immune Receptor. Science, 2014, 344, 299-303.	6.0	300
806	Signal amplification and transduction in phytochrome photosensors. Nature, 2014, 509, 245-248.	13.7	303
807	Peroxiredoxin is a Versatile Self-Assembling Tecton for Protein Nanotechnology. Biomacromolecules, 2014, 15, 1871-1881.	2.6	43
808	Mechanism of Bacterial Interference with TLR4 Signaling by Brucella Toll/Interleukin-1 Receptor Domain-containing Protein TcpB. Journal of Biological Chemistry, 2014, 289, 654-668.	1.6	73
809	Product formation controlled by substrate dynamics in leukotriene A4 hydrolase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 439-446.	1.1	8
810	How a Viscoelastic Solution of Wormlike Micelles Transforms into a Microemulsion upon Absorption of Hydrocarbon: New Insight. Langmuir, 2014, 30, 3705-3714.	1.6	71
811	Aspects of nonviral gene therapy: Correlation of molecular parameters with lipoplex structure and transfection efficacy in pyridinium-based cationic lipids. International Journal of Pharmaceutics, 2014, 461, 145-156.	2.6	19

#	ARTICLE	IF	CITATIONS
812	Common Mechanism for RNA Encapsidation by Negative-Strand RNA Viruses. <i>Journal of Virology</i> , 2014, 88, 3766-3775.	1.5	37
813	Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors. <i>Cell</i> , 2014, 156, 577-589.	13.5	348
814	Characterization of a periplasmic nitrate reductase in complex with its biosynthetic chaperone. <i>FEBS Journal</i> , 2014, 281, 246-260.	2.2	11
815	High-resolution crystal structure reveals a HEPN domain at the C-terminal region of <i>S. cerevisiae</i> RNA endonuclease Swt1. <i>Biochemical and Biophysical Research Communications</i> , 2014, 453, 826-832.	1.0	2
816	The SH2 domain of Abl kinases regulates kinase autophosphorylation by controlling activation loop accessibility. <i>Nature Communications</i> , 2014, 5, 5470.	5.8	36
817	The Roles of the RII ² Linker and N-terminal Cyclic Nucleotide-binding Domain in Determining the Unique Structures of the Type III ² Protein Kinase A. <i>Journal of Biological Chemistry</i> , 2014, 289, 28505-28512.	1.6	5
818	Tuning Micelle Dimensions and Properties with Binary Surfactant Mixtures. <i>Langmuir</i> , 2014, 30, 13353-13361.	1.6	20
819	Internal motions prime cIAP1 for rapid activation. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1068-1074.	3.6	20
820	Conformational Analysis of the <i>Streptococcus pneumoniae</i> Hyaluronate Lyase and Characterization of Its Hyaluronan-specific Carbohydrate-binding Module. <i>Journal of Biological Chemistry</i> , 2014, 289, 27264-27277.	1.6	17
821	Synthesis and properties of a rod-g-rod bottlebrush with a semirigid mesogen-jacketed polymer as the side chain. <i>Polymer Chemistry</i> , 2014, 5, 4948-4956.	1.9	11
822	Laser-induced photodynamic effects at silica nanocomposite based on cadmium sulphide quantum dots. <i>Optics Express</i> , 2014, 22, 2105.	1.7	7
823	Insights into the function of trans-acyl transferase polyketide synthases from the SAXS structure of a complete module. <i>Chemical Science</i> , 2014, 5, 3081-3095.	3.7	33
824	A Fusion Intermediate gp41 Immunogen Elicits Neutralizing Antibodies to HIV-1. <i>Journal of Biological Chemistry</i> , 2014, 289, 29912-29926.	1.6	32
825	Probing the determinants of phosphorylated sugar-substrate binding for human sialic acid synthase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 2257-2264.	1.1	4
826	Structural basis for glucose tolerance in GH1 β -glucosidases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1631-1639.	2.5	115
827	An16-resilin: An advanced multi-stimuli-responsive resilin-mimetic protein polymer. <i>Acta Biomaterialia</i> , 2014, 10, 4768-4777.	4.1	43
828	Crystal and Solution Structure Analysis of FhuD2 from <i>Staphylococcus aureus</i> in Multiple Unliganded Conformations and Bound to Ferrioxamine-B. <i>Biochemistry</i> , 2014, 53, 2017-2031.	1.2	31
829	Low pH Overrides the Need of Calcium Ions for the Shape-Function Relationship of Calmodulin: Resolving Prevailing Debates. <i>Journal of Physical Chemistry B</i> , 2014, 118, 5059-5074.	1.2	18

#	ARTICLE	IF	CITATIONS
830	Role of the EF-hand-like Motif in the 14-3-3 Protein-mediated Activation of Yeast Neutral Trehalase Nth1. <i>Journal of Biological Chemistry</i> , 2014, 289, 13948-13961.	1.6	23
831	Characterization of Protein Flexibility Using Small-Angle X-Ray Scattering and Amplified Collective Motion Simulations. <i>Biophysical Journal</i> , 2014, 107, 956-964.	0.2	20
832	Glycosylation of Skp1 Affects Its Conformation and Promotes Binding to a Model F-Box Protein. <i>Biochemistry</i> , 2014, 53, 1657-1669.	1.2	42
833	Probing the Conformation of FhaC with Small-Angle Neutron Scattering and Molecular Modeling. <i>Biophysical Journal</i> , 2014, 107, 185-196.	0.2	16
834	Study of Complex Thermosensitive Amphiphilic Polyoxazolines and Their Interaction with Ionic Surfactants. Are Hydrophobic, Thermosensitive, and Hydrophilic Moieties Equally Important?. <i>Journal of Physical Chemistry B</i> , 2014, 118, 4940-4950.	1.2	25
835	Structural Basis of hAT Transposon End Recognition by Hermes, an Octameric DNA Transposase from <i>Musca domestica</i> . <i>Cell</i> , 2014, 158, 353-367.	13.5	63
836	Synchrotron-based small-angle X-ray scattering of proteins in solution. <i>Nature Protocols</i> , 2014, 9, 1727-1739.	5.5	156
837	Structural Insight into How <i>Streptomyces coelicolor</i> Maltosyl Transferase GlgE Binds α -Maltose 1-Phosphate and Forms a Maltosyl-enzyme Intermediate. <i>Biochemistry</i> , 2014, 53, 2494-2504.	1.2	33
838	Structural basis for the recruitment and activation of the <i>Legionella</i> phospholipase VipD by the host GTPase Rab5. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3514-23.	3.3	46
839	Tailoring of Clay/Poly(ethylene oxide) Hydrogel Properties by Chitosan Incorporation. <i>Industrial & Engineering Chemistry Research</i> , 2014, 53, 13690-13698.	1.8	22
840	Differential Role of HAMP-like Linkers in Regulating the Functionality of the Group III Histidine Kinase DhNik1p. <i>Journal of Biological Chemistry</i> , 2014, 289, 20245-20258.	1.6	14
841	Structure of malaria invasion protein RH5 with erythrocyte basigin and blocking antibodies. <i>Nature</i> , 2014, 515, 427-430.	13.7	180
842	Structure of the <i>C.Âlegans</i> ZYG-1 Cryptic Polo Box Suggests a Conserved Mechanism for Centriolar Docking of Plk4 Kinases. <i>Structure</i> , 2014, 22, 1090-1104.	1.6	45
843	The Statistical Conformation of a Highly Flexible Protein: Small-Angle X-Ray Scattering of <i>S.Âaureus</i> Protein A. <i>Structure</i> , 2014, 22, 1184-1195.	1.6	19
844	Mechanistic Insights in Glycation-Induced Protein Aggregation. <i>Biomacromolecules</i> , 2014, 15, 3449-3462.	2.6	51
845	Multicore Iron Oxide Mesocrystals Stabilized by a Poly(phenylene-pyridyl) Dendron and Dendrimer: Role of the Dendron/Dendrimer Self-Assembly. <i>Langmuir</i> , 2014, 30, 8543-8550.	1.6	12
846	Novel thermosensitive telechelic PEGs with antioxidant activity: synthesis, molecular properties and conformational behaviour. <i>RSC Advances</i> , 2014, 4, 41763-41771.	1.7	17
847	Applications of Synchrotron-Based Spectroscopic Techniques in Studying Nucleic Acids and Nucleic Acid-Functionalized Nanomaterials. <i>Advanced Materials</i> , 2014, 26, 7849-7872.	11.1	19

#	ARTICLE	IF	CITATIONS
848	Observation of the Early Structural Changes Leading to the Formation of Protein Superstructures. <i>Journal of Physical Chemistry Letters</i> , 2014, 5, 3254-3258.	2.1	22
849	Structural basis for activity of highly efficient RNA mimics of green fluorescent protein. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 658-663.	3.6	299
850	DNA binding properties of human Cdc45 suggest a function as molecular wedge for DNA unwinding. <i>Nucleic Acids Research</i> , 2014, 42, 2308-2319.	6.5	30
851	Interaction of Bovine Serum Albumin (BSA) with Novel Gemini Surfactants Studied by Synchrotron Radiation Scattering (SR-SAXS), Circular Dichroism (CD), and Nuclear Magnetic Resonance (NMR). <i>Journal of Physical Chemistry B</i> , 2014, 118, 8652-8661.	1.2	35
852	Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , 2014, 5, 616-630.	4.8	27
853	Vernier-templated Synthesis, Crystal Structure, and Supramolecular Chemistry of a 12-porphyrin Nanoring. <i>Chemistry - A European Journal</i> , 2014, 20, 12826-12834.	1.7	46
854	Formation of Inverse Topology Lyotropic Phases in Dioleoylphosphatidylcholine/Oleic Acid and Dioleoylphosphatidylethanolamine/Oleic Acid Binary Mixtures. <i>Langmuir</i> , 2014, 30, 3337-3344.	1.6	24
855	Structural basis for the assembly of the Sxl-Unr translation regulatory complex. <i>Nature</i> , 2014, 515, 287-290.	13.7	102
856	The Crystal Structure of Netrin-1 in Complex with DCC Reveals the Bifunctionality of Netrin-1 As a Guidance Cue. <i>Neuron</i> , 2014, 83, 839-849.	3.8	103
857	Hydrophobic Periphery Tails of Polyphenylenepyridyl Dendrons Control Nanoparticle Formation and Catalytic Properties. <i>Chemistry of Materials</i> , 2014, 26, 5654-5663.	3.2	20
858	Conformational Activation of Poly(ADP-ribose) Polymerase-1 upon DNA Binding Revealed by Small-Angle X-ray Scattering. <i>Biochemistry</i> , 2014, 53, 1779-1788.	1.2	20
859	Measuring the Molecular Dimensions of Wine Tannins: Comparison of Small-Angle X-ray Scattering, Gel-Permeation Chromatography and Mean Degree of Polymerization. <i>Journal of Agricultural and Food Chemistry</i> , 2014, 62, 7216-7224.	2.4	5
860	Structure of the double-stranded DNA-binding type IV secretion protein TraN from <i>Enterococcus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2376-2389.	2.5	11
861	Evidence That the C-Terminal Domain of a Type B PutA Protein Contributes to Aldehyde Dehydrogenase Activity and Substrate Channeling. <i>Biochemistry</i> , 2014, 53, 5661-5673.	1.2	18
862	Denatured State Ensembles with the Same Radii of Gyration Can Form Significantly Different Long-Range Contacts. <i>Biochemistry</i> , 2014, 53, 39-47.	1.2	14
863	Structural Studies of Yeast β -Pyrroline-5-carboxylate Dehydrogenase (ALDH4A1): Active Site Flexibility and Oligomeric State. <i>Biochemistry</i> , 2014, 53, 1350-1359.	1.2	30
864	Structural Determinants for the Strict Monomethylation Activity by <i>Trypanosoma brucei</i> Protein Arginine Methyltransferase 7. <i>Structure</i> , 2014, 22, 756-768.	1.6	43
865	Structural basis for recognition of the type VI spike protein VgrG3 by a cognate immunity protein. <i>FEBS Letters</i> , 2014, 588, 1891-1898.	1.3	6

#	ARTICLE	IF	CITATIONS
866	Architectures of Whole-Module and Bimodular Proteins from the 6-Deoxyerythronolide B Synthase. <i>Journal of Molecular Biology</i> , 2014, 426, 2229-2245.	2.0	60
867	Protein arginine methyltransferase 7 has a novel homodimer-like structure formed by tandem repeats. <i>FEBS Letters</i> , 2014, 588, 1942-1948.	1.3	42
868	Novel cationic polyene glycol phospholipids as DNA transfer reagents—Lack of a structure–activity relationship due to uncontrolled self-assembling processes. <i>Chemistry and Physics of Lipids</i> , 2014, 183, 117-136.	1.5	9
869	Analysis of the solution structure of <i>Thermosynechococcus elongatus</i> photosystem I in n-dodecyl- β -D-maltoside using small-angle neutron scattering and molecular dynamics simulation. <i>Archives of Biochemistry and Biophysics</i> , 2014, 550-551, 50-57.	1.4	23
870	Structure of the atypical bacteriocin pectocin $\langle \text{scp} \rangle \text{M} \langle / \text{scp} \rangle 2$ implies a novel mechanism of protein uptake. <i>Molecular Microbiology</i> , 2014, 93, 234-246.	1.2	23
871	Coiled-coil deformations in crystal structures: the measles virus phosphoprotein multimerization domain as an illustrative example. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1589-1603.	2.5	29
872	Transient Electrostatic Interactions Dominate the Conformational Equilibrium Sampled by Multidomain Splicing Factor U2AF65: A Combined NMR and SAXS Study. <i>Journal of the American Chemical Society</i> , 2014, 136, 7068-7076.	6.6	79
873	Structural and Mechanistic Paradigm of Leptin Receptor Activation Revealed by Complexes with Wild-Type and Antagonist Leptins. <i>Structure</i> , 2014, 22, 866-877.	1.6	37
874	Reciprocal allosteric regulation of p38 β and PTPN3 involves a PDZ domain–modulated complex formation. <i>Science Signaling</i> , 2014, 7, ra98.	1.6	25
875	Methods for SAXS-Based Structure Determination of Biomolecular Complexes. <i>Advanced Materials</i> , 2014, 26, 7902-7910.	11.1	40
876	The structure of a purple acid phosphatase involved in plant growth and pathogen defence exhibits a novel immunoglobulin-like fold. <i>IUCr</i> , 2014, 1, 101-109.	1.0	26
877	Substrate-Induced Allosteric Change in the Quaternary Structure of the Spermidine N-Acetyltransferase SpeG. <i>Journal of Molecular Biology</i> , 2015, 427, 3538-3553.	2.0	12
878	Identification of two p23 co-chaperone isoforms in <i>Leishmania braziliensis</i> exhibiting similar structures and Hsp90 interaction properties despite divergent stabilities. <i>FEBS Journal</i> , 2015, 282, 388-406.	2.2	19
879	Active site coupling in <i>Plasmodium falciparum</i> GMP synthetase is triggered by domain rotation. <i>Nature Communications</i> , 2015, 6, 8930.	5.8	24
880	Phosphoregulation of the <i>C. elegans</i> cadherin–catenin complex. <i>Biochemical Journal</i> , 2015, 472, 339-352.	1.7	15
881	Structural basis for cpSRP43 chromodomain selectivity and dynamics in Alb3 insertase interaction. <i>Nature Communications</i> , 2015, 6, 8875.	5.8	24
882	Asymmetric ring structure of Vps4 required for ESCRT-III disassembly. <i>Nature Communications</i> , 2015, 6, 8781.	5.8	45
883	sAPP \pm is a Potent Endogenous Inhibitor of $\text{A}\beta$ ACE1. <i>Journal of Alzheimer's Disease</i> , 2015, 47, 545-555.	1.2	46

#	ARTICLE	IF	CITATIONS
884	The structure of <i>Legionella pneumophila</i> LegK4 type four secretion system (T4SS) effector reveals a novel dimeric eukaryotic-like kinase. <i>Scientific Reports</i> , 2015, 5, 14602.	1.6	15
885	Structural analysis of <i>Clostridium botulinum</i> neurotoxin type D as a platform for the development of targeted secretion inhibitors. <i>Scientific Reports</i> , 2015, 5, 13397.	1.6	12
886	Small-angle X-ray scattering method to characterize molecular interactions: Proof of concept. <i>Scientific Reports</i> , 2015, 5, 12085.	1.6	33
887	Structural characterization of the principal mRNA-export factor Mex67/Mtr2 from <i>Chaetomium thermophilum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 876-888.	0.4	8
888	Solution study of the <i>Escherichia coli</i> DNA polymerase III clamp loader reveals the location of the dynamic β' heterodimer. <i>Structural Dynamics</i> , 2015, 2, 054701.	0.9	5
889	Considerably Unfolded Transthyretin Monomers Precede and Exchange with Dynamically Structured Amyloid Protofibrils. <i>Scientific Reports</i> , 2015, 5, 11443.	1.6	36
890	SAXS fingerprints of aldehyde dehydrogenase oligomers. <i>Data in Brief</i> , 2015, 5, 745-751.	0.5	7
891	Structure of the Helicase Domain of DNA Polymerase Theta Reveals a Possible Role in the Microhomology-Mediated End-Joining Pathway. <i>Structure</i> , 2015, 23, 2319-2330.	1.6	64
892	Maturation of 6S regulatory γ -RNA to a highly elongated structure. <i>FEBS Journal</i> , 2015, 282, 4548-4564.	2.2	4
893	1 H-NMR studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial γ -Cys peroxidase machinery. <i>FEBS Journal</i> , 2015, 282, 4620-4638.	2.2	9
894	Synthesis and double-hierarchical structure of MoS ₂ /C nanospheres. <i>Physica Status Solidi (A) Applications and Materials Science</i> , 2015, 212, 2309-2314.	0.8	9
895	Oligomerization state and pigment binding strength of the peridinin-chlorophyll <i>a</i> protein. <i>FEBS Letters</i> , 2015, 589, 2713-2719.	1.3	1
896	Designing Artificial 3D Helicates: Unprecedented Self-Assembly of Homo-octanuclear Tetrapods with Europium. <i>Chemistry - A European Journal</i> , 2015, 21, 6695-6699.	1.7	19
897	Unique Role of the WD-40 Repeat Protein 5 (WDR5) Subunit within the Mixed Lineage Leukemia 3 (MLL3) Histone Methyltransferase Complex. <i>Journal of Biological Chemistry</i> , 2015, 290, 25819-25833.	1.6	25
898	Advances in Understanding Carboxysome Assembly in <i>Prochlorococcus</i> and <i>Synechococcus</i> Implicate CsoS2 as a Critical Component. <i>Life</i> , 2015, 5, 1141-1171.	1.1	82
899	Stability of the Octameric Structure Affects Plasminogen-Binding Capacity of Streptococcal Enolase. <i>PLoS ONE</i> , 2015, 10, e0121764.	1.1	14
900	<i>a posteriori</i> determination of the useful data range for small-angle scattering experiments on dilute monodisperse systems. <i>IUCr</i> , 2015, 2, 352-360.	1.0	78
901	Formation of a Trimeric Xpo1-Ran[GTP]-Ded1 Exportin Complex Modulates ATPase and Helicase Activities of Ded1. <i>PLoS ONE</i> , 2015, 10, e0131690.	1.1	10

#	ARTICLE	IF	CITATIONS
902	Dimerization-Induced Allosteric Changes of the Oxyanion-Hole Loop Activate the Pseudorabies Virus Assemblin pUL26N, a Herpesvirus Serine Protease. <i>PLoS Pathogens</i> , 2015, 11, e1005045.	2.1	15
903	Structure and inhibition of subunit I of the anthranilate synthase complex of <i>Mycobacterium tuberculosis</i> and expression of the active complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2297-2308.	2.5	17
904	Domain organization within the nuclear export factor Mex67:Mtr2 generates an extended mRNA binding surface. <i>Nucleic Acids Research</i> , 2015, 43, 1927-1936.	6.5	21
905	Structural ensembles reveal intrinsic disorder for the multi-stimuli responsive bio-mimetic protein Rec1-resilin. <i>Scientific Reports</i> , 2015, 5, 10896.	1.6	34
906	Allosteric regulation of deubiquitylase activity through ubiquitination. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 2.	1.6	15
907	Small-angle X-ray scattering: a bridge between RNA secondary structures and three-dimensional topological structures. <i>Current Opinion in Structural Biology</i> , 2015, 30, 147-160.	2.6	40
908	Coat Protein-Dependent Behavior of Poly(ethylene glycol) Tails in Iron Oxide Core Virus-like Nanoparticles. <i>ACS Applied Materials & Interfaces</i> , 2015, 7, 12089-12098.	4.0	17
909	Kirkwood's Buff Approach Rescues Overcollapse of a Disordered Protein in Canonical Protein Force Fields. <i>Journal of Physical Chemistry B</i> , 2015, 119, 7975-7984.	1.2	70
910	Structure of a bacterial toxin-activating acyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3058-66.	3.3	33
911	The Cryo-EM structure of the CorA channel from <i>Methanocaldococcus jannaschii</i> in low magnesium conditions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 2206-2215.	1.4	12
912	Structure of a BAG6 (Bcl-2-associated Athanogene 6)-Ubl4a (Ubiquitin-like Protein 4a) Complex Reveals a Novel Binding Interface That Functions in Tail-anchored Protein Biogenesis. <i>Journal of Biological Chemistry</i> , 2015, 290, 9387-9398.	1.6	29
913	Bipartite Topology of <i>Treponema pallidum</i> Repeat Proteins C/D and I. <i>Journal of Biological Chemistry</i> , 2015, 290, 12313-12331.	1.6	30
914	Structure and Mechanism of Dimer-to-Monomer Transition of a Plant Poly(A)-Binding Protein upon RNA Interaction: Insights into Its Poly(A) Tail Assembly. <i>Journal of Molecular Biology</i> , 2015, 427, 2491-2506.	2.0	5
915	The solution structure of the pentatricopeptide repeat protein PPR10 upon binding atpH RNA. <i>Nucleic Acids Research</i> , 2015, 43, 1918-1926.	6.5	56
916	Constrained Maximum Likelihood Estimation of Relative Abundances of Protein Conformation in a Heterogeneous Mixture From Small Angle X-Ray Scattering Intensity Measurements. <i>IEEE Transactions on Signal Processing</i> , 2015, 63, 5383-5394.	3.2	10
917	Structural Studies of Geosmin Synthase, a Bifunctional Sesquiterpene Synthase with $\hat{\pm}\hat{\pm}$ Domain Architecture That Catalyzes a Unique Cyclization-to-Fragmentation Reaction Sequence. <i>Biochemistry</i> , 2015, 54, 7142-7155.	1.2	36
918	The principal mRNA nuclear export factor NXF1:NXT1 forms a symmetric binding platform that facilitates export of retroviral CTE-RNA. <i>Nucleic Acids Research</i> , 2015, 43, 1883-1893.	6.5	43
919	Crystal structures of the Gon7/Pcc1 and Bud32/Cgi121 complexes provide a model for the complete yeast KEOPS complex. <i>Nucleic Acids Research</i> , 2015, 43, 3358-3372.	6.5	43

#	ARTICLE	IF	CITATIONS
920	Crystal structure of the Bloom's syndrome helicase indicates a role for the HRDC domain in conformational changes. <i>Nucleic Acids Research</i> , 2015, 43, 5221-5235.	6.5	74
921	Evidence that avian reovirus NS is an RNA chaperone: implications for genome segment assortment. <i>Nucleic Acids Research</i> , 2015, 43, 7044-7057.	6.5	26
922	The sliding clamp tethers the endonuclease domain of MutL to DNA. <i>Nucleic Acids Research</i> , 2015, 43, 10746-10759.	6.5	45
923	Maximum a posteriori estimation of relative abundances of protein conformations. , 2015, , .		0
924	Structure and primase-mediated activation of a bacterial dodecameric replicative helicase. <i>Nucleic Acids Research</i> , 2015, 43, 8564-8576.	6.5	42
925	Intrinsically disordered cytoplasmic domains of two cytokine receptors mediate conserved interactions with membranes. <i>Biochemical Journal</i> , 2015, 468, 495-506.	1.7	68
926	Crystal Structures of the Extracellular Domain from PepT1 and PepT2 Provide Novel Insights into Mammalian Peptide Transport. <i>Structure</i> , 2015, 23, 1889-1899.	1.6	40
927	Solvent-induced structural transitions of lysozyme in an electrospray ionization source. <i>Analyst</i> , 2015, 140, 3573-3580.	1.7	4
928	Exploring the structure of biological macromolecules in solution using Quokka, the small angle neutron scattering instrument, at ANSTO. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2015, 798, 44-51.	0.7	4
929	The Redox State Regulates the Conformation of Rv2466c to Activate the Antitubercular Prodrug TP053. <i>Journal of Biological Chemistry</i> , 2015, 290, 31077-31089.	1.6	17
930	Insights into the Hendra virus N TAIL -XD complex: Evidence for a parallel organization of the helical MoRE at the XD surface stabilized by a combination of hydrophobic and polar interactions. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 1038-1053.	1.1	15
931	Structural basis of <i>Deer</i> pox virus-mediated inhibition of apoptosis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1593-1603.	2.5	25
932	Calcium-controlled conformational choreography in the N-terminal half of adseverin. <i>Nature Communications</i> , 2015, 6, 8254.	5.8	13
933	The Activator of Apoptosis Smac-DIABLO Acts as a Tetramer in Solution. <i>Biophysical Journal</i> , 2015, 108, 714-723.	0.2	12
934	Effects of Macromolecular Crowding on the Structure of a Protein Complex: A Small-Angle Scattering Study of Superoxide Dismutase. <i>Biophysical Journal</i> , 2015, 108, 967-974.	0.2	17
935	Crystal Structure of Subunits D and F in Complex Gives Insight into Energy Transmission of the Eukaryotic V-ATPase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 3183-3196.	1.6	38
936	Biochemical and structural investigation of two paralogous glycoside hydrolases from <i>Zobellia galactanivorans</i> : novel insights into the evolution, dimerization plasticity and catalytic mechanism of the GH117 family. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 209-223.	2.5	18
937	Dimerization and phosphatase activity of calcyclin-binding protein/Siah1 interacting protein: the influence of oxidative stress. <i>FASEB Journal</i> , 2015, 29, 1711-1724.	0.2	20

#	ARTICLE	IF	CITATIONS
938	The Conundrum of the High-Affinity NGF Binding Site Formation Unveiled?. <i>Biophysical Journal</i> , 2015, 108, 687-697.	0.2	20
939	Glutamate 270 plays an essential role in K ⁺ activation and domain closure of <i>Thermus thermophilus</i> isopropylmalate dehydrogenase. <i>FEBS Letters</i> , 2015, 589, 240-245.	1.3	5
940	Human Adenosine A2A Receptor Binds Calmodulin with High Affinity in a Calcium-Dependent Manner. <i>Biophysical Journal</i> , 2015, 108, 903-917.	0.2	12
941	Insights into the coiled-coil organization of the Hendra virus phosphoprotein from combined biochemical and SAXS studies. <i>Virology</i> , 2015, 477, 42-55.	1.1	12
942	Supramolecular Aggregation in Organic Solvents of Discrete Copper Complexes Formed with Organosiloxane Ligands. <i>Soft Materials</i> , 2015, 13, 93-105.	0.8	9
943	A Salmonella Type Three Secretion Effector/Chaperone Complex Adopts a Hexameric Ring-Like Structure. <i>Journal of Bacteriology</i> , 2015, 197, 688-698.	1.0	8
944	The solution structure of the transducin α 119 protein complex suggests occlusion of the G β 1 γ 13 binding sites. <i>FEBS Journal</i> , 2015, 282, 550-561.	2.2	4
945	Micellar and biochemical properties of a propyl-ended fluorinated surfactant designed for membrane protein study. <i>Journal of Colloid and Interface Science</i> , 2015, 445, 127-136.	5.0	30
946	Structural heterogeneity of milk casein micelles: a SANS contrast variation study. <i>Soft Matter</i> , 2015, 11, 389-399.	1.2	32
947	RXR Agonist Modulates TR: Corepressor Dissociation Upon 9-cis Retinoic Acid Treatment. <i>Molecular Endocrinology</i> , 2015, 29, 258-273.	3.7	20
948	Stabilization of Nontoxic A β -Oligomers: Insights into the Mechanism of Action of Hydroxyquinolines in Alzheimer's Disease. <i>Journal of Neuroscience</i> , 2015, 35, 2871-2884.	1.7	67
949	X-Ray Structure of the Amidase Domain of AtzF, the Allophanate Hydrolase from the Cyanuric Acid-Mineralizing Multienzyme Complex. <i>Applied and Environmental Microbiology</i> , 2015, 81, 470-480.	1.4	18
950	Expression, Receptor Binding, and Biophysical Characterization of Guinea Pig Insulin desB30: A Monomeric Insulin Variant. <i>ChemBioChem</i> , 2015, 16, 954-958.	1.3	2
951	A Dimer Interface Mutation in Glyceraldehyde-3-Phosphate Dehydrogenase Regulates Its Binding to AU-rich RNA. <i>Journal of Biological Chemistry</i> , 2015, 290, 1770-1785.	1.6	47
952	Structural Model of the Cytosolic Domain of the Plant Ethylene Receptor 1 (ETR1). <i>Journal of Biological Chemistry</i> , 2015, 290, 2644-2658.	1.6	35
953	Structures of Human CCL18, CCL3, and CCL4 Reveal Molecular Determinants for Quaternary Structures and Sensitivity to Insulin-Degrading Enzyme. <i>Journal of Molecular Biology</i> , 2015, 427, 1345-1358.	2.0	21
954	A Tail of Two Sites: A Bipartite Mechanism for Recognition of Notch Ligands by Mind Bomb E3 Ligases. <i>Molecular Cell</i> , 2015, 57, 912-924.	4.5	33
955	Crystallographic and solution studies of NAD ⁺ - and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from <i>Escherichia coli</i> provide insight into sequential enzymatic steps. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 1139-1152.	0.5	12

#	ARTICLE	IF	CITATIONS
956	Quercetin-3-rutinoside Inhibits Protein Disulfide Isomerase by Binding to Its β_2 Domain. <i>Journal of Biological Chemistry</i> , 2015, 290, 23543-23552.	1.6	90
957	Bending Rigidities and Interdomain Forces in Membranes with Coexisting Lipid Domains. <i>Biophysical Journal</i> , 2015, 108, 2833-2842.	0.2	35
958	The Structure of the PanD/PanZ Protein Complex Reveals Negative Feedback Regulation of Pantothenate Biosynthesis by Coenzyme A. <i>Chemistry and Biology</i> , 2015, 22, 492-503.	6.2	30
959	The Pentameric Nucleoplasmin Fold Is Present in <i>Drosophila</i> FKBP39 and a Large Number of Chromatin-Related Proteins. <i>Journal of Molecular Biology</i> , 2015, 427, 1949-1963.	2.0	29
960	Interaction of two imidazolium gemini surfactants with two model proteins BSA and HEWL. <i>Colloid and Polymer Science</i> , 2015, 293, 2855-2866.	1.0	26
961	Preformed Soluble Chemoreceptor Trimers That Mimic Cellular Assembly States and Activate CheA Autophosphorylation. <i>Biochemistry</i> , 2015, 54, 3454-3468.	1.2	14
962	Structure and mechanism of the Rubisco-assembly chaperone Raf1. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 720-728.	3.6	61
963	Structural Insights into Ca^{2+} -Calmodulin Regulation of Plectin 1 α -Integrin β_4 Interaction in Hemidesmosomes. <i>Structure</i> , 2015, 23, 558-570.	1.6	28
964	X-Ray Structure of the Pestivirus NS3 Helicase and Its Conformation in Solution. <i>Journal of Virology</i> , 2015, 89, 4356-4371.	1.5	11
965	Biochemical and structural characterization of the apicoplast dihydrolipoamide dehydrogenase of <i>Plasmodium falciparum</i> . <i>Bioscience Reports</i> , 2015, 35, .	1.1	12
966	Investigating acid-induced structural transitions of lysozyme in an electrospray ionization source. <i>Analyst</i> , 2015, 140, 661-669.	1.7	19
967	Combination of X-ray crystallography, SAXS and DEER to obtain the structure of the FnIII-3,4 domains of integrin β_4 . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 969-985.	2.5	38
968	Protein kinase C (PKC)-mediated phosphorylation of PACSIN2 triggers the removal of caveolae from the plasma membrane. <i>Journal of Cell Science</i> , 2015, 128, 2766-80.	1.2	39
969	Biogenesis and structure of a type VI secretion membrane core complex. <i>Nature</i> , 2015, 523, 555-560.	13.7	241
970	Automated Pipeline for Purification, Biophysical and X-Ray Analysis of Biomacromolecular Solutions. <i>Scientific Reports</i> , 2015, 5, 10734.	1.6	99
971	Identification of large channels in cationic PEGylated cubosome nanoparticles by synchrotron radiation SAXS and Cryo-TEM imaging. <i>Soft Matter</i> , 2015, 11, 3686-3692.	1.2	92
972	Composite materials based on poly(<i>N</i> -isopropylacrylamide-co-methacrylic acid) hydrogels and calcium carbonate. <i>High Performance Polymers</i> , 2015, 27, 516-525.	0.8	5
973	Structural basis for cellobiose dehydrogenase action during oxidative cellulose degradation. <i>Nature Communications</i> , 2015, 6, 7542.	5.8	187

#	ARTICLE	IF	CITATIONS
974	Methods for analysis of size-exclusion chromatography–small-angle X-ray scattering and reconstruction of protein scattering. <i>Journal of Applied Crystallography</i> , 2015, 48, 1102-1113.	1.9	46
975	Differential ultracentrifugation coupled to small-angle X-ray scattering on macromolecular complexes. <i>Journal of Applied Crystallography</i> , 2015, 48, 769-775.	1.9	6
976	Molecular mechanism for the action of the anti-CD44 monoclonal antibody MEM-85. <i>Journal of Structural Biology</i> , 2015, 191, 214-223.	1.3	13
977	Structure-dynamic determinants governing a mode of regulatory response and propagation of allosteric signal in splice variants of Na ⁺ /Ca ²⁺ exchange (NCX) proteins. <i>Biochemical Journal</i> , 2015, 465, 489-501.	1.7	25
978	Structural and functional characterization of TesB from <i>Yersinia pestis</i> reveals a unique octameric arrangement of hotdog domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 986-995.	2.5	8
979	The VPS-20 subunit of the endosomal sorting complex ESCRT-III exhibits an open conformation in the absence of upstream activation. <i>Biochemical Journal</i> , 2015, 466, 625-637.	1.7	20
980	Light-induced Changes in the Dimerization Interface of Bacteriophytochromes. <i>Journal of Biological Chemistry</i> , 2015, 290, 16383-16392.	1.6	48
981	Crystal structures reveal transient <i>scp</i> PERK/ <i>scp</i> luminal domain tetramerization in endoplasmic reticulum stress signaling. <i>EMBO Journal</i> , 2015, 34, 1589-1600.	3.5	69
982	Random-Coil Behavior of Chemically Denatured Topologically Knotted Proteins Revealed by Small-Angle X-ray Scattering. <i>Journal of Physical Chemistry B</i> , 2015, 119, 5437-5443.	1.2	20
983	Role of Conserved Proline Residues in Human Apolipoprotein A-IV Structure and Function. <i>Journal of Biological Chemistry</i> , 2015, 290, 10689-10702.	1.6	11
984	Effects of Precursor Solution Aging and Other Parameters on Synthesis of Ordered Mesoporous Titania Powders. <i>Journal of Physical Chemistry C</i> , 2015, 119, 7172-7183.	1.5	9
985	SAXS Data Based Global Shape Analysis of Trigger Factor (TF) Proteins from <i>E. coli</i> , <i>V. cholerae</i> , and <i>P. frigidicola</i> : Resolving the Debate on the Nature of Monomeric and Dimeric Forms. <i>Journal of Physical Chemistry B</i> , 2015, 119, 6101-6112.	1.2	6
986	One-pot refolding of core histones from bacterial inclusion bodies allows rapid reconstitution of histone octamer. <i>Protein Expression and Purification</i> , 2015, 110, 89-94.	0.6	23
987	Characterization of the termini of the West Nile virus genome and their interactions with the small isoform of the 5' 5'-oligoadenylate synthetase family. <i>Journal of Structural Biology</i> , 2015, 190, 236-249.	1.3	21
988	In vitro effect of temperature on the conformational structure and collagen binding of SdrF, a <i>Staphylococcus epidermidis</i> adhesin. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5593-5603.	1.7	4
989	Small-angle X-ray scattering analysis reveals the ATP-bound monomeric state of the ATPase domain from the homodimeric MutL endonuclease, a GHKL phosphotransferase superfamily protein. <i>Extremophiles</i> , 2015, 19, 643-656.	0.9	6
990	Solution structure and biophysical characterization of the multifaceted signalling effector protein growth arrest specific-1. <i>BMC Biochemistry</i> , 2015, 16, 8.	4.4	7
991	High-resolution structure of a type IV pilin from the metal-reducing bacterium <i>Shewanella oneidensis</i> . <i>BMC Structural Biology</i> , 2015, 15, 4.	2.3	15

#	ARTICLE	IF	CITATIONS
992	Salts employed in hydrophobic interaction chromatography can change protein structure – insights from protein–ligand interaction thermodynamics, circular dichroism spectroscopy and small angle X-ray scattering. <i>Biotechnology Journal</i> , 2015, 10, 417-426.	1.8	3
993	PqqD Is a Novel Peptide Chaperone That Forms a Ternary Complex with the Radical S-Adenosylmethionine Protein PqqE in the Pyrroloquinoline Quinone Biosynthetic Pathway. <i>Journal of Biological Chemistry</i> , 2015, 290, 12908-12918.	1.6	72
994	Hidden disorder propensity of the N-terminal segment of universal adapter protein 14-3-3 is manifested in its monomeric form: Novel insights into protein dimerization and multifunctionality. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 492-504.	1.1	22
995	Conformational Analysis and Chemical Reactivity of the Multidomain Sulfurtransferase, <i>Staphylococcus aureus</i> CstA. <i>Biochemistry</i> , 2015, 54, 2385-2398.	1.2	36
996	Heme binds to an intrinsically disordered region of Bach2 and alters its conformation. <i>Archives of Biochemistry and Biophysics</i> , 2015, 565, 25-31.	1.4	31
997	Dynamic Changes during Acid-Induced Activation of Influenza Hemagglutinin. <i>Structure</i> , 2015, 23, 665-676.	1.6	60
998	Small angle X-ray scattering analysis of Cu ²⁺ -induced oligomers of the Alzheimer's amyloid β peptide. <i>Metallomics</i> , 2015, 7, 536-543.	1.0	25
999	The influence of novel gemini surfactants containing cycloalkyl side-chains on the structural phases of DNA in solution. <i>Colloids and Surfaces B: Biointerfaces</i> , 2015, 131, 83-92.	2.5	16
1000	Probing the Interactions of Intrinsically Disordered Proteins Using Nanoparticle Tags. <i>Nano Letters</i> , 2015, 15, 3080-3087.	4.5	14
1001	Ambiguity assessment of small-angle scattering curves from monodisperse systems. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1051-1058.	2.5	118
1002	Controlling Clusters of Colloidal Platelets: Effects of Edge and Face Surface Chemistries on the Behavior of Montmorillonite Suspensions. <i>Langmuir</i> , 2015, 31, 4377-4385.	1.6	20
1003	Anthranoyl-CoA monooxygenase/reductase from <i>Azoarcus evansii</i> possesses both FMN and FAD in two distinct and independent active sites. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 890-896.	1.1	4
1004	Dimeric WH2 repeats of VopF sequester actin monomers into non-nucleating linear string conformations: An X-ray scattering study. <i>Journal of Structural Biology</i> , 2015, 190, 192-199.	1.3	14
1005	HrpG and HrpV proteins from the Type III secretion system of <i>Erwinia amylovora</i> form a stable heterodimer. <i>FEMS Microbiology Letters</i> , 2015, 362, 1-8.	0.7	9
1006	Solution Structure of the Atg1 Complex: Implications for the Architecture of the Phagophore Assembly Site. <i>Structure</i> , 2015, 23, 809-818.	1.6	35
1007	A Mechanism of Global Shape-dependent Recognition and Phosphorylation of Filamin by Protein Kinase A. <i>Journal of Biological Chemistry</i> , 2015, 290, 8527-8538.	1.6	14
1008	Cadherin flexibility provides a key difference between desmosomes and adherens junctions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5395-5400.	3.3	37
1009	Structure and catalytic mechanism of the evolutionarily unique bacterial chalcone isomerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 907-917.	2.5	21

#	ARTICLE	IF	CITATIONS
1010	Escherichia coli antitoxin MazE as transcription factor: insights into MazE-DNA binding. <i>Nucleic Acids Research</i> , 2015, 43, 1241-1256.	6.5	35
1011	The architecture of amyloid-like peptide fibrils revealed by X-ray scattering, diffraction and electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 882-895.	2.5	50
1012	Small-angle X-ray scattering probe of intermolecular interaction in red blood cells. <i>Chinese Physics C</i> , 2015, 39, 038001.	1.5	1
1013	Mapping the Binding Site of a Cross-Reactive <i>Plasmodium falciparum</i> PfEMP1 Monoclonal Antibody Inhibitory of ICAM-1 Binding. <i>Journal of Immunology</i> , 2015, 195, 3273-3283.	0.4	25
1014	Structural Basis for Antigen Recognition by Transglutaminase 2-specific Autoantibodies in Celiac Disease. <i>Journal of Biological Chemistry</i> , 2015, 290, 21365-21375.	1.6	27
1015	Conformational Transitions that Enable Histidine Kinase Autophosphorylation and Receptor Array Integration. <i>Journal of Molecular Biology</i> , 2015, 427, 3890-3907.	2.0	25
1016	Superparamagnetic cobalt ferrite nanoparticles – the spatial ordering of double-stranded DNA molecules. <i>Biophysics (Russian Federation)</i> , 2015, 60, 341-347.	0.2	4
1017	Structural insight and flexible features of NS5 proteins from all four serotypes of <i>Dengue virus</i> in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2309-2327.	2.5	34
1018	Molecular Mechanism of CCAAT-Enhancer Binding Protein Recruitment by the TRIB1 Pseudokinase. <i>Structure</i> , 2015, 23, 2111-2121.	1.6	93
1019	Assembly of Simple Epithelial Keratin Filaments: Deciphering the Ion Dependence in Filament Organization. <i>Biomacromolecules</i> , 2015, 16, 3313-3321.	2.6	20
1020	Structural Basis of Substrate Recognition by Aldehyde Dehydrogenase 7A1. <i>Biochemistry</i> , 2015, 54, 5513-5522.	1.2	36
1021	The Substrate-free and -bound Crystal Structures of the Duplicated Taurocyamine Kinase from the Human Parasite <i>Schistosoma mansoni</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 12951-12963.	1.6	9
1022	Olfactomedin-1 Has a V-shaped Disulfide-linked Tetrameric Structure. <i>Journal of Biological Chemistry</i> , 2015, 290, 15092-15101.	1.6	18
1023	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015, 6, 7271.	5.8	52
1024	Structural, Functional, and Immunogenic Insights on Cu,Zn Superoxide Dismutase Pathogenic Virulence Factors from <i>Neisseria meningitidis</i> and <i>Brucella abortus</i> . <i>Journal of Bacteriology</i> , 2015, 197, 3834-3847.	1.0	24
1025	Application of SAXS for the Structural Characterization of IDPs. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 261-289.	0.8	33
1026	The First Crystal Structure of the UP1 Domain of hnRNP A1 Bound to RNA Reveals a New Look for an Old RNA Binding Protein. <i>Journal of Molecular Biology</i> , 2015, 427, 3241-3257.	2.0	35
1027	Ligand regulation of a constitutively dimeric EGF receptor. <i>Nature Communications</i> , 2015, 6, 7380.	5.8	31

#	ARTICLE	IF	CITATIONS
1028	Structure and properties of enamatically ordered aerogels. JETP Letters, 2015, 101, 556-561.	0.4	42
1029	Structural Ensembles of Intrinsically Disordered Proteins Depend Strongly on Force Field: A Comparison to Experiment. Journal of Chemical Theory and Computation, 2015, 11, 5513-5524.	2.3	368
1030	Hydrodynamic and Membrane Binding Properties of Purified Rous Sarcoma Virus Gag Protein. Journal of Virology, 2015, 89, 10371-10382.	1.5	17
1031	A Three-protein Charge Zipper Stabilizes a Complex Modulating Bacterial Gene Silencing. Journal of Biological Chemistry, 2015, 290, 21200-21212.	1.6	18
1032	Prion Protein Antibody Complexes Characterized by Chromatography-Coupled Small-Angle X-Ray Scattering. Biophysical Journal, 2015, 109, 793-805.	0.2	33
1033	Oligomerization of a Glucagon-like Peptide 1 Analog: Bridging Experiment and Simulations. Biophysical Journal, 2015, 109, 1202-1213.	0.2	35
1034	A practical guide to small angle X-ray scattering (SAXS) of flexible and intrinsically disordered proteins. FEBS Letters, 2015, 589, 2570-2577.	1.3	461
1035	Mechanistic Implications of the Unique Structural Features and Dimerization of the Cytoplasmic Domain of the <i>Pseudomonas</i> Sigma Regulator, PupR. Biochemistry, 2015, 54, 5867-5877.	1.2	6
1036	Next generation macrocyclic and acyclic cationic lipids for gene transfer: Synthesis and in vitro evaluation. Bioorganic and Medicinal Chemistry, 2015, 23, 6364-6378.	1.4	4
1037	Local and global structural drivers for the photoactivation of the orange carotenoid protein. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5567-74.	3.3	121
1038	Histone Core Phosphorylation Regulates DNA Accessibility. Journal of Biological Chemistry, 2015, 290, 22612-22621.	1.6	76
1039	Unravelling the shape and structural assembly of the photosynthetic GAPDH-CP12-PRK complex from <i>Arabidopsis thaliana</i> by small-angle X-ray scattering analysis. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2372-2385.	2.5	13
1040	SdsA polymorph isolation and improvement of their crystal quality using nonconventional crystallization techniques. Journal of Applied Crystallography, 2015, 48, 1551-1559.	1.9	5
1041	NADH oxidase and alkyl hydroperoxide reductase subunit C (peroxiredoxin) from <i>Amphibacillus xylanus</i> form an oligomeric assembly. FEBS Open Bio, 2015, 5, 124-131.	1.0	6
1042	Anti-PolyQ Antibodies Recognize a Short PolyQ Stretch in Both Normal and Mutant Huntingtin Exon 1. Journal of Molecular Biology, 2015, 427, 2507-2519.	2.0	31
1043	Structural characterization and modeling of the <i>Borrelia burgdorferi</i> hybrid histidine kinase Hk1 periplasmic sensor: A system for sensing small molecules associated with tick feeding. Journal of Structural Biology, 2015, 192, 48-58.	1.3	24
1044	Protein-protein interactions within the ensemble, eukaryotic V-ATPase, and its concerted interactions with cellular machineries. Progress in Biophysics and Molecular Biology, 2015, 119, 84-93.	1.4	2
1045	Structural and Functional Highlights of Vacuolar Soluble Protein 1 from Pathogen <i>Trypanosoma brucei brucei</i> . Journal of Biological Chemistry, 2015, 290, 30498-30513.	1.6	10

#	ARTICLE	IF	CITATIONS
1046	Allosteric Activation of Bacterial Swi2/Snf2 (Switch/Sucrose Non-fermentable) Protein RapA by RNA Polymerase. <i>Journal of Biological Chemistry</i> , 2015, 290, 23656-23669.	1.6	8
1047	A coiled-coil domain acts as a molecular ruler to regulate O-antigen chain length in lipopolysaccharide. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 50-56.	3.6	55
1048	Viruslike Nanoparticles with Maghemite Cores Allow for Enhanced MRI Contrast Agents. <i>Chemistry of Materials</i> , 2015, 27, 327-335.	3.2	32
1049	The $\hat{\iota}^2$ -Lactamase Gene Regulator AmpR Is a Tetramer That Recognizes and Binds the d-Ala-d-Ala Motif of Its Repressor UDP-N-acetylmuramic Acid (MurNAc)-pentapeptide. <i>Journal of Biological Chemistry</i> , 2015, 290, 2630-2643.	1.6	77
1050	Ion-Specific Control of the Self-Assembly Dynamics of a Nanostructured Protein Lattice. <i>ACS Nano</i> , 2015, 9, 180-190.	7.3	37
1051	Pressure-induced molten globule state of human acetylcholinesterase: structural and dynamical changes monitored by neutron scattering. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 3157-3163.	1.3	34
1052	The C-terminal region of the human p23 chaperone modulates its structure and function. <i>Archives of Biochemistry and Biophysics</i> , 2015, 565, 57-67.	1.4	16
1053	Alpha-synuclein oligomers and fibrils originate in two distinct conformer pools: a small angle X-ray scattering and ensemble optimisation modelling study. <i>Molecular BioSystems</i> , 2015, 11, 190-196.	2.9	24
1054	Impact of Matrix Dynamic Properties on Stem Cell Viability. , 2016, , 203-214.		0
1055	Protein Structure and Folding. , 2016, , 47-48.		0
1056	SEC-SANS: size exclusion chromatography combined <i>in situ</i> with small-angle neutron scattering. <i>Journal of Applied Crystallography</i> , 2016, 49, 2015-2020.	1.9	60
1057	X-Ray Solution Scattering Study of Four Escherichia coli Enzymes Involved in Stationary-Phase Metabolism. <i>PLoS ONE</i> , 2016, 11, e0156105.	1.1	2
1058	Comprehensive characterization of ligand-induced plasticity changes in a dimeric enzyme. <i>FEBS Journal</i> , 2016, 283, 3029-3038.	2.2	4
1059	Modeling RNA topological structures using small angle X-ray scattering. <i>Methods</i> , 2016, 103, 18-24.	1.9	9
1060	Structure of chromatin remodeler Swi2/Snf2 in the resting state. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 722-729.	3.6	55
1061	Estradiol protective role in atherogenesis through LDL structure modification. <i>Journal Physics D: Applied Physics</i> , 2016, 49, 285402.	1.3	2
1062	Structure and mechanism of a molecular rheostat, an RNA thermometer that modulates immune evasion by <i>Neisseria meningitidis</i> . <i>Nucleic Acids Research</i> , 2016, 44, gkw584.	6.5	40
1063	Structure of UBE2Z Enzyme Provides Functional Insight into Specificity in the FAT10 Protein Conjugation Machinery. <i>Journal of Biological Chemistry</i> , 2016, 291, 630-639.	1.6	26

#	ARTICLE	IF	CITATIONS
1064	<scp>SAXS</scp> studies of <scp>RNA</scp>: structures, dynamics, and interactions with partners. Wiley Interdisciplinary Reviews RNA, 2016, 7, 512-526.	3.2	60
1065	Heterogeneity of Collagen VI Microfibrils. Journal of Biological Chemistry, 2016, 291, 5247-5258.	1.6	24
1066	Characterization of the structure and catalytic activity of <i>Legionella pneumophila</i> VipF. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1422-1430.	1.5	5
1067	Redox cofactors insertion in prokaryotic molybdoenzymes occurs via a conserved folding mechanism. Scientific Reports, 2016, 6, 37743.	1.6	4
1068	The dynamic organization of fungal acetyl-CoA carboxylase. Nature Communications, 2016, 7, 11196.	5.8	39
1069	Rifampin phosphotransferase is an unusual antibiotic resistance kinase. Nature Communications, 2016, 7, 11343.	5.8	36
1070	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. Scientific Reports, 2016, 6, 20915.	1.6	11
1071	The solution configurations of inactive and activated DntR have implications for the sliding dimer mechanism of LysR transcription factors. Scientific Reports, 2016, 6, 19988.	1.6	36
1072	A small-angle X-ray scattering study of alpha-synuclein from human red blood cells. Scientific Reports, 2016, 6, 30473.	1.6	30
1073	Transparent and fluorescent thin films of polysilane-SiQD nanocomposite: cellulose acetate. Cellulose, 2016, 23, 3847-3860.	2.4	8
1074	Tick receptor for outer surface protein A from Ixodes ricinus – the first intrinsically disordered protein involved in vector-microbe recognition. Scientific Reports, 2016, 6, 25205.	1.6	4
1075	Interactive graphical system for small-angle scattering analysis of polydisperse systems. Journal of Physics: Conference Series, 2016, 747, 012036.	0.3	5
1076	Structural basis for early-onset neurological disorders caused by mutations in human selenocysteine synthase. Scientific Reports, 2016, 6, 32563.	1.6	13
1077	Structural basis of myelin-associated glycoprotein adhesion and signalling. Nature Communications, 2016, 7, 13584.	5.8	94
1078	Restriction endonuclease AgeI is a monomer which dimerizes to cleave DNA. Nucleic Acids Research, 2016, 45, gkw1310.	6.5	11
1079	Structural and dynamics studies of a truncated variant of CI repressor from bacteriophage TP901-1. Scientific Reports, 2016, 6, 29574.	1.6	13
1080	The system with zwitterionic lactose-based surfactant for complexation and delivery of small interfering ribonucleic acid – A structural and spectroscopic study. Applied Physics Letters, 2016, 108, .	1.5	4
1081	Destabilization of the PCNA trimer mediated by its interaction with the NEIL1 DNA glycosylase. Nucleic Acids Research, 2016, 45, gkw1282.	6.5	11

#	ARTICLE	IF	CITATIONS
1082	Functional architecture of the Reb1-Ter complex of <i>Schizosaccharomyces pombe</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2267-76.	3.3	30
1083	Structural and Functional Consequences of Three Cancer-Associated Mutations of the Oncogenic Phosphatase SHP2. Biochemistry, 2016, 55, 2269-2277.	1.2	55
1084	Probing the Impact of Local Structural Dynamics of Conformational Epitopes on Antibody Recognition. Biochemistry, 2016, 55, 2197-2213.	1.2	23
1085	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. MABs, 2016, 8, 928-940.	2.6	42
1086	Regulation of Microtubule Assembly by Tau and not by Pin1. Journal of Molecular Biology, 2016, 428, 1742-1759.	2.0	20
1087	Modulating the Cascade architecture of a minimal Type I-F CRISPR-Cas system. Nucleic Acids Research, 2016, 44, 5872-5882.	6.5	57
1088	Heterotrimeric G-Protein Alpha ($\hat{\pm}$) Subunit from <i>a. Thaliana</i> Forms Trimeric Structures in Solution. Biophysical Journal, 2016, 110, 380a.	0.2	0
1089	Mechanism of increased clearance of glycated albumin by proximal tubule cells. American Journal of Physiology - Renal Physiology, 2016, 310, F1089-F1102.	1.3	28
1090	The N Terminus of the Vaccinia Virus Protein F1L Is an Intrinsically Unstructured Region That Is Not Involved in Apoptosis Regulation. Journal of Biological Chemistry, 2016, 291, 14600-14608.	1.6	11
1091	The unexpected structure of the designed protein Octarellin V.1 forms a challenge for protein structure prediction tools. Journal of Structural Biology, 2016, 195, 19-30.	1.3	15
1092	SAXS/SANS on Supercharged Proteins Reveals Residue-Specific Modifications of the Hydration Shell. Biophysical Journal, 2016, 110, 2185-2194.	0.2	32
1093	Structural Analysis of the Myo1c and Neph1 Complex Provides Insight into the Intracellular Movement of Neph1. Molecular and Cellular Biology, 2016, 36, 1639-1654.	1.1	34
1094	Beeswax organogels: Influence of gelator concentration and oil type in the gelation process. Food Research International, 2016, 84, 170-179.	2.9	119
1095	Use of complementary nucleobase-containing synthetic polymers to prepare complex self-assembled morphologies in water. Polymer Chemistry, 2016, 7, 2836-2846.	1.9	29
1096	Structural basis for oligomerization and glycosaminoglycan binding of CCL5 and CCL3. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5000-5005.	3.3	72
1097	Crystal Structure of an Engineered LRRTM2 Synaptic Adhesion Molecule and a Model for Neurexin Binding. Biochemistry, 2016, 55, 914-926.	1.2	17
1098	Dimerization of Bacterial Diaminopimelate Decarboxylase Is Essential for Catalysis. Journal of Biological Chemistry, 2016, 291, 9785-9795.	1.6	31
1100	Dual Role of the Active Site Residues of <i>Thermus thermophilus</i> 3-Isopropylmalate Dehydrogenase: Chemical Catalysis and Domain Closure. Biochemistry, 2016, 55, 560-574.	1.2	2

#	ARTICLE	IF	CITATIONS
1101	Molecular studies on structural changes and oligomerisation of violaxanthin de-epoxidase associated with the pH-dependent activation. <i>Photosynthesis Research</i> , 2016, 129, 29-41.	1.6	16
1102	Apolipoprotein C-II Adopts Distinct Structures in Complex with Micellar and Submicellar Forms of the Amyloid-Inhibiting Lipid-Mimetic Dodecylphosphocholine. <i>Biophysical Journal</i> , 2016, 110, 85-94.	0.2	4
1103	Thermal modification of optical properties of silicate nanocomposites based on cadmium sulfide quantum dots. <i>Journal of Nanophotonics</i> , 2016, 10, 033510.	0.4	2
1104	Combined pressure and temperature denaturation of ribonuclease A produces alternate denatured states. <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 834-839.	1.0	3
1105	The Potassium Binding Protein Kbp Is a Cytoplasmic Potassium Sensor. <i>Structure</i> , 2016, 24, 741-749.	1.6	38
1106	Sister Chromatid Cohesion Establishment Factor ESCO1 Operates by Substrate-Assisted Catalysis. <i>Structure</i> , 2016, 24, 789-796.	1.6	14
1107	A Novel Fic (Filamentation Induced by cAMP) Protein from <i>Clostridium difficile</i> Reveals an Inhibitory Motif-independent Adenylation/AMPylation Mechanism. <i>Journal of Biological Chemistry</i> , 2016, 291, 13286-13300.	1.6	14
1108	Structural Mechanism of Allosteric Activity Regulation in a Ribonucleotide Reductase with Double ATP Cones. <i>Structure</i> , 2016, 24, 906-917.	1.6	28
1109	Features of polyelectrolyte behavior and structure of sodium polyacrylamido-2-methyl-1-propanesulfonate cryogels. <i>Polymer</i> , 2016, 96, 1-5.	1.8	2
1110	The Use of Small-Angle Scattering for the Characterization of Multi Subunit Complexes. <i>Advances in Experimental Medicine and Biology</i> , 2016, 896, 329-350.	0.8	1
1111	A small protein inhibits proliferating cell nuclear antigen by breaking the DNA clamp. <i>Nucleic Acids Research</i> , 2016, 44, 6232-6241.	6.5	11
1112	The Sac3 TPR-like region in the <i>Saccharomyces cerevisiae</i> TREX-2 complex is more extensive but independent of the CID region. <i>Journal of Structural Biology</i> , 2016, 195, 316-324.	1.3	3
1113	Sulfmyoglobin conformational change: A role in the decrease of oxy-myoglobin functionality. <i>Biochemistry and Biophysics Reports</i> , 2016, 7, 386-393.	0.7	8
1114	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016, 131, 106-114.	1.3	6
1115	Domain Organization in the 54-kDa Subunit of the Chloroplast Signal Recognition Particle. <i>Biophysical Journal</i> , 2016, 111, 1151-1162.	0.2	7
1116	Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from <i>Burkholderia pseudomallei</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 19387-19400.	1.6	28
1117	Structural Insight into the 14-3-3 Protein-dependent Inhibition of Protein Kinase ASK1 (Apoptosis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	45
1118	Enzymatic hydrolysis by transition-metal-dependent nucleophilic aromatic substitution. <i>Nature Chemical Biology</i> , 2016, 12, 1031-1036.	3.9	12

#	ARTICLE	IF	CITATIONS
1119	Small-angle x-ray scattering study of polymer structure: Carbosilane dendrimers in hexane solution. <i>Crystallography Reports</i> , 2016, 61, 815-825.	0.1	6
1120	The Human Centriolar Protein CEP135 Contains a Two-Stranded Coiled-Coil Domain Critical for Microtubule Binding. <i>Structure</i> , 2016, 24, 1358-1371.	1.6	27
1121	Succinyl-5-aminoimidazole-4-carboxamide-1-ribose 5-Phosphate (SAICAR) Activates Pyruvate Kinase Isoform M2 (PKM2) in Its Dimeric Form. <i>Biochemistry</i> , 2016, 55, 4731-4736.	1.2	24
1122	Changes in Structure and Antigenicity of HIV-1 Env Trimers Resulting from Removal of a Conserved CD4 Binding Site-Proximal Glycan. <i>Journal of Virology</i> , 2016, 90, 9224-9236.	1.5	25
1123	Redox chemistry of Mycobacterium tuberculosis alkylhydroperoxide reductase E (AhpE): Structural and mechanistic insight into a mycoredoxin-1 independent reductive pathway of AhpE via mycothiol. <i>Free Radical Biology and Medicine</i> , 2016, 97, 588-601.	1.3	19
1124	Discovery, characterization and <i>in vivo</i> activity of pyocin SD2, a protein antibiotic from <i>Pseudomonas aeruginosa</i> . <i>Biochemical Journal</i> , 2016, 473, 2345-2358.	1.7	42
1125	Structure and target interaction of a G-quadruplex RNA-aptamer. <i>RNA Biology</i> , 2016, 13, 973-987.	1.5	20
1126	Independent catalysis of the short form HisG from <i>Lactococcus lactis</i> . <i>FEBS Letters</i> , 2016, 590, 2603-2610.	1.3	12
1127	Apo- and Antagonist-Binding Structures of Vitamin D Receptor Ligand-Binding Domain Revealed by Hybrid Approach Combining Small-Angle X-ray Scattering and Molecular Dynamics. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 7888-7900.	2.9	25
1128	Structural Insights into the M-Channel Proximal C-Terminus/Calmodulin Complex. <i>Biochemistry</i> , 2016, 55, 5353-5365.	1.2	26
1129	The role of conformational flexibility in Baeyer-Villiger monooxygenase catalysis and structure. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1641-1648.	1.1	21
1130	Structural Basis of Host Autophagy-related Protein 8 (ATG8) Binding by the Irish Potato Famine Pathogen Effector Protein PexRD54. <i>Journal of Biological Chemistry</i> , 2016, 291, 20270-20282.	1.6	74
1131	The Structure of the Antibiotic Deactivating, N-hydroxylating Rifampicin Monooxygenase. <i>Journal of Biological Chemistry</i> , 2016, 291, 21553-21562.	1.6	36
1132	Protein encapsulation in SBA-15 with expanded pores. <i>Microporous and Mesoporous Materials</i> , 2016, 235, 59-68.	2.2	22
1133	pH-Dependent Interactions in Dimers Govern the Mechanics and Structure of von Willebrand Factor. <i>Biophysical Journal</i> , 2016, 111, 312-322.	0.2	18
1134	CARP interacts with titin at a unique helical N2A sequence and at the domain Ig81 to form a structured complex. <i>FEBS Letters</i> , 2016, 590, 3098-3110.	1.3	22
1135	Solution Structures of Complement C2 and Its C4 Complexes Propose Pathway-specific Mechanisms for Control and Activation of the Complement Proconvertases. <i>Journal of Biological Chemistry</i> , 2016, 291, 16494-16507.	1.6	24
1136	Crystal structure of FabZ-ACP complex reveals a dynamic seesaw-like catalytic mechanism of dehydratase in fatty acid biosynthesis. <i>Cell Research</i> , 2016, 26, 1330-1344.	5.7	31

#	ARTICLE	IF	CITATIONS
1137	Molecular mechanisms of substrate-controlled ring dynamics and substepping in a nucleic acid-dependent hexameric motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7691-E7700.	3.3	48
1138	Two crystal structures reveal design for repurposing the C-Ala domain of human AlaRS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14300-14305.	3.3	21
1139	Virus Matryoshka: A Bacteriophage Particle-Guided Molecular Assembly Approach to a Monodisperse Model of the Immature Human Immunodeficiency Virus. <i>Small</i> , 2016, 12, 5862-5872.	5.2	8
1140	Biosynthesis of Violacein, Structure and Function of L-Tryptophan Oxidase VioA from <i>Chromobacterium violaceum</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 20068-20084.	1.6	45
1141	A conserved two-step binding for the UAF1 regulator to the USP12 deubiquitinating enzyme. <i>Journal of Structural Biology</i> , 2016, 196, 437-447.	1.3	27
1142	Structural characterization suggests models for monomeric and dimeric forms of full-length ezrin. <i>Biochemical Journal</i> , 2016, 473, 2763-2782.	1.7	27
1143	FAK Forms a Complex with MEF2 to Couple Biomechanical Signaling to Transcription in Cardiomyocytes. <i>Structure</i> , 2016, 24, 1301-1310.	1.6	30
1144	Structures of mammalian ER β -glucosidase II capture the binding modes of broad-spectrum iminosugar antivirals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4630-8.	3.3	65
1145	Structural studies of the formation of lipoplexes between siRNA and selected bis-imidazolium gemini surfactants. <i>Colloids and Surfaces B: Biointerfaces</i> , 2016, 146, 598-606.	2.5	9
1146	Identification of BECN1 and ATG14 Coiled-Coil Interface Residues That Are Important for Starvation-Induced Autophagy. <i>Biochemistry</i> , 2016, 55, 4239-4253.	1.2	25
1147	Noncovalent PEGylation via Lectin-Glycopolymer Interactions. <i>Biomacromolecules</i> , 2016, 17, 2719-2725.	2.6	21
1148	Effects of Crowding and Environment on the Evolution of Conformational Ensembles of the Multi-Stimuli-Responsive Intrinsically Disordered Protein, Rec1-Resilin: A Small-Angle Scattering Investigation. <i>Journal of Physical Chemistry B</i> , 2016, 120, 6490-6503.	1.2	22
1149	Homodimerization of the Lymph Vessel Endothelial Receptor LYVE-1 through a Redox-labile Disulfide Is Critical for Hyaluronan Binding in Lymphatic Endothelium. <i>Journal of Biological Chemistry</i> , 2016, 291, 25004-25018.	1.6	28
1150	Structural and mechanistic insights into regulation of the retromer coat by TBC1d5. <i>Nature Communications</i> , 2016, 7, 13305.	5.8	88
1151	An elastic element in the protocadherin-15 tip link of the inner ear. <i>Nature Communications</i> , 2016, 7, 13458.	5.8	39
1152	Structural characterization of the N-terminal part of the MERS-CoV nucleocapsid by X-ray diffraction and small-angle X-ray scattering. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 192-202.	1.1	25
1153	Structure and inhibition of N-acetylneuraminidase from methicillin-resistant <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2016, 590, 4414-4428.	1.3	18
1154	Taste substance binding elicits conformational change of taste receptor T1r heterodimer extracellular domains. <i>Scientific Reports</i> , 2016, 6, 25745.	1.6	36

#	ARTICLE	IF	CITATIONS
1155	Interdomain Conformational Changes Provide Allosteric Regulation en Route to Chorismate. <i>Journal of Biological Chemistry</i> , 2016, 291, 21836-21847.	1.6	22
1156	Casitas B-lineage lymphoma linker helix mutations found in myeloproliferative neoplasms affect conformation. <i>BMC Biology</i> , 2016, 14, 76.	1.7	16
1157	In vivo epidermal migration requires focal adhesion targeting of ACF7. <i>Nature Communications</i> , 2016, 7, 11692.	5.8	49
1158	Characterization of the DNA dependent activation of human ARTD2/PARP2. <i>Scientific Reports</i> , 2016, 6, 34487.	1.6	34
1159	Early nucleation events in the polymerization of actin, probed by time-resolved small-angle x-ray scattering. <i>Scientific Reports</i> , 2016, 6, 34539.	1.6	18
1160	Structural basis of GM-CSF and IL-2 sequestration by the viral decoy receptor GIF. <i>Nature Communications</i> , 2016, 7, 13228.	5.8	15
1161	Crystal structures of the human elongation factor eEFSec suggest a non-canonical mechanism for selenocysteine incorporation. <i>Nature Communications</i> , 2016, 7, 12941.	5.8	22
1162	Stable preparations of tyrosine hydroxylase provide the solution structure of the full-length enzyme. <i>Scientific Reports</i> , 2016, 6, 30390.	1.6	24
1163	Structural basis for misregulation of kinesin KIF21A autoinhibition by CFEOM1 disease mutations. <i>Scientific Reports</i> , 2016, 6, 30668.	1.6	26
1164	Saccharification of thermochemically pretreated cellulosic biomass using native and engineered cellulosomal enzyme systems. <i>Reaction Chemistry and Engineering</i> , 2016, 1, 616-628.	1.9	8
1165	Structure and dynamics of concentrated micellar solutions of sodium dodecyl sulfate. <i>Russian Chemical Bulletin</i> , 2016, 65, 158-166.	0.4	17
1166	Sequence Determinants of the Conformational Properties of an Intrinsically Disordered Protein Prior to and upon Multisite Phosphorylation. <i>Journal of the American Chemical Society</i> , 2016, 138, 15323-15335.	6.6	217
1167	Molecular characterization of a family 5 glycoside hydrolase suggests an induced-fit enzymatic mechanism. <i>Scientific Reports</i> , 2016, 6, 23473.	1.6	25
1168	Mechanism of intermediate filament recognition by plakin repeat domains revealed by envoplakin targeting of vimentin. <i>Nature Communications</i> , 2016, 7, 10827.	5.8	28
1169	New structural insights into Golgi Reassembly and Stacking Protein (GRASP) in solution. <i>Scientific Reports</i> , 2016, 6, 29976.	1.6	24
1170	Structural Insights into the Tetrameric State of Aspartate- β -semialdehyde Dehydrogenases from Fungal Species. <i>Scientific Reports</i> , 2016, 6, 21067.	1.6	9
1171	VirB8-like protein TraH is crucial for DNA transfer in <i>Enterococcus faecalis</i> . <i>Scientific Reports</i> , 2016, 6, 24643.	1.6	23
1172	Subtle balance of tropoelastin molecular shape and flexibility regulates dynamics and hierarchical assembly. <i>Science Advances</i> , 2016, 2, e1501145.	4.7	43

#	ARTICLE	IF	CITATIONS
1173	Engineering a trifunctional proline utilization A chimaera by fusing a DNA-binding domain to a bifunctional PutA. <i>Bioscience Reports</i> , 2016, 36, .	1.1	6
1174	Oligomeric interface modulation causes misregulation of purine 5 ^Å -nucleotidase in relapsed leukemia. <i>BMC Biology</i> , 2016, 14, 91.	1.7	9
1175	Combined small angle X-ray solution scattering with atomic force microscopy for characterizing radiation damage on biological macromolecules. <i>BMC Structural Biology</i> , 2016, 16, 18.	2.3	13
1176	Structural investigations of E. Coli dihydrolipoamide dehydrogenase in solution: Small-angle X-ray scattering and molecular docking. <i>Crystallography Reports</i> , 2016, 61, 414-420.	0.1	1
1177	Effect of hybrid nanoparticles on glass transition temperature of polymer nanocomposites. <i>Polymer Composites</i> , 2016, 37, 1978-1990.	2.3	18
1178	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , 2016, 291, 14430-14446.	1.6	16
1179	Dicationic Surfactants with Glycine Counter Ions for Oligonucleotide Transportation. <i>ChemPhysChem</i> , 2016, 17, 2424-2433.	1.0	6
1180	Micellar nanoparticles with tuneable morphologies through interactions between nucleobase-containing synthetic polymers in aqueous solution. <i>Polymer Chemistry</i> , 2016, 7, 4254-4262.	1.9	35
1181	SAXS Combined with UV-vis Spectroscopy and QELS: Accurate Characterization of Silver Sols Synthesized in Polymer Matrices. <i>Nanoscale Research Letters</i> , 2016, 11, 35.	3.1	19
1182	Flexibility of KorA, a plasmid-encoded, global transcription regulator, in the presence and the absence of its operator. <i>Nucleic Acids Research</i> , 2016, 44, 4947-4956.	6.5	6
1183	Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t ^{sup>6</sup>A biosynthesis. <i>Nucleic Acids Research</i>, 2016, 44, 6971-6980.}	6.5	26
1184	A crystallographic study of human NONO (p54 ^{sup>nrb</sup>): overcoming pathological problems with purification, data collection and noncrystallographic symmetry. <i>Acta Crystallographica Section D: Structural Biology</i>, 2016, 72, 761-769.}	1.1	11
1185	Analysis of biostructural changes, dynamics, and interactions â€“ Small-angle X-ray scattering to the rescue. <i>Archives of Biochemistry and Biophysics</i> , 2016, 602, 69-79.	1.4	28
1186	Novel helical assembly in arginine methyltransferase 8. <i>Journal of Molecular Biology</i> , 2016, 428, 1197-1208.	2.0	19
1187	Biochemical properties and crystal structure of the flavin reductase FerA from <i>Paracoccus denitrificans</i> . <i>Microbiological Research</i> , 2016, 188-189, 9-22.	2.5	14
1188	Solution structure of an â€œopenâ€•E. coli Pol III clamp loader sliding clamp complex. <i>Journal of Structural Biology</i> , 2016, 194, 272-281.	1.3	4
1189	Impact of the crystallization condition on importin-Î² conformation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 705-717.	1.1	12
1190	Dimer conformation of soluble PECAM-1, an endothelial marker. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 77, 102-108.	1.2	11

#	ARTICLE	IF	CITATIONS
1191	Low sequence identity but high structural and functional conservation: The case of Hsp70/Hsp90 organizing protein (Hop/Sti1) of <i>Leishmania braziliensis</i> . <i>Archives of Biochemistry and Biophysics</i> , 2016, 600, 12-22.	1.4	8
1192	Structure-Dynamic Determinants Governing a Mode of Regulatory Response and Propagation of Allosteric Signal in Splice Variants of Na ⁺ /Ca ²⁺ Exchange (NCX) Proteins. <i>Biophysical Journal</i> , 2016, 110, 45a.	0.2	7
1193	Structural characterization of twisted gastrulation provides insights into opposing functions on the BMP signalling pathway. <i>Matrix Biology</i> , 2016, 55, 49-62.	1.5	15
1194	The Disulfide Bonds within BST-2 Enhance Tensile Strength during Viral Tethering. <i>Biochemistry</i> , 2016, 55, 940-947.	1.2	8
1195	The epigenetic regulator Smchd1 contains a functional GHKL-type ATPase domain. <i>Biochemical Journal</i> , 2016, 473, 1733-1744.	1.7	25
1196	Biophysical Characterization of Chromatin Remodeling Protein CHD4. <i>Methods in Molecular Biology</i> , 2016, 1431, 175-193.	0.4	1
1197	Structural insights and membrane binding properties of MGD1, the major galactolipid synthase in plants. <i>Plant Journal</i> , 2016, 85, 622-633.	2.8	22
1198	Structural model of the dimeric Parkinson's protein LRRK2 reveals a compact architecture involving distant interdomain contacts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4357-E4366.	3.3	130
1199	Identification of the critical linker residues conferring differences in the compactness of NS5 from Dengue virus serotype 4 and NS5 from Dengue virus serotypes 1-3. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 795-807.	1.1	14
1200	Active-Site-Directed Inhibitors of Prolyl Oligopeptidase Abolish Its Conformational Dynamics. <i>ChemBioChem</i> , 2016, 17, 913-917.	1.3	14
1201	Structural characterization of a <i>Vatairea macrocarpa</i> lectin in complex with a tumor-associated antigen: A new tool for cancer research. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 72, 27-39.	1.2	12
1202	Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. <i>Journal of Biological Chemistry</i> , 2016, 291, 4882-4893.	1.6	36
1203	Structural and Functional Characterization of the Paal Thioesterase from <i>Streptococcus pneumoniae</i> Reveals a Dual Specificity for Phenylacetyl-CoA and Medium-chain Fatty Acyl-CoAs and a Novel CoA-induced Fit Mechanism. <i>Journal of Biological Chemistry</i> , 2016, 291, 1866-1876.	1.6	6
1204	Insights into open/closed conformations of the catalytically active human guanylate kinase as investigated by small-angle X-ray scattering. <i>European Biophysics Journal</i> , 2016, 45, 81-89.	1.2	8
1205	Characterization of Intersubunit Communication in the Virginiamycin <i>trans</i> -Acyl Transferase Polyketide Synthase. <i>Journal of the American Chemical Society</i> , 2016, 138, 4155-4167.	6.6	42
1206	Solution Structure of the HIV-1 Intron Splicing Silencer and Its Interactions with the UP1 Domain of Heterogeneous Nuclear Ribonucleoprotein (hnRNP) A1. <i>Journal of Biological Chemistry</i> , 2016, 291, 2331-2344.	1.6	25
1207	Structural characterization of a dimer of RNA duplexes composed of 8-bromoguanosine modified CCG trinucleotide repeats: a novel architecture of RNA quadruplexes. <i>Nucleic Acids Research</i> , 2016, 44, 2409-2416.	6.5	22
1208	C-terminal region of bacterial Ku controls DNA bridging, DNA threading and recruitment of DNA ligase D for double strand breaks repair. <i>Nucleic Acids Research</i> , 2016, 44, 4785-4806.	6.5	37

#	ARTICLE	IF	CITATIONS
1209	Molecular Mechanism of Pin1â€™Tau Recognition and Catalysis. <i>Journal of Molecular Biology</i> , 2016, 428, 1760-1775.	2.0	22
1210	Force sensing by the vascular protein von Willebrand factor is tuned by a strong intermonomer interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1208-1213.	3.3	51
1211	Fabrication and study of properties of magnetite nanoparticles in hybrid micelles of polystyrene-block-polyethylene oxide and sodium dodecyl sulfate. <i>Crystallography Reports</i> , 2016, 61, 77-83.	0.1	1
1212	<i>Helicobacter pylori</i> cell binding factor 2: Insights into domain motion. <i>Journal of Structural Biology</i> , 2016, 194, 90-101.	1.3	3
1213	Interaction of TAPBPR, a tapasin homolog, with MHC-I molecules promotes peptide editing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1006-15.	3.3	73
1214	Biophysical Characterization and Activity of Lymphostatin, a Multifunctional Virulence Factor of Attaching and Effacing <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 5803-5816.	1.6	9
1215	Structures of <i>Xenopus</i> Embryonic Epidermal Lectin Reveal a Conserved Mechanism of Microbial Glycan Recognition. <i>Journal of Biological Chemistry</i> , 2016, 291, 5596-5610.	1.6	33
1216	The hinge domain of the epigenetic repressor Smchd1 adopts an unconventional homodimeric configuration. <i>Biochemical Journal</i> , 2016, 473, 733-742.	1.7	19
1217	Priming and polymerization of a bacterial contractile tail structure. <i>Nature</i> , 2016, 531, 59-63.	13.7	127
1218	Domain Organization of Vaccinia Virus Helicase-Primase D5. <i>Journal of Virology</i> , 2016, 90, 4604-4613.	1.5	22
1219	Investigation of the Initial Crystallization Stage in Lysozyme Solutions by Small-Angle X-ray Scattering. <i>Crystal Growth and Design</i> , 2016, 16, 1792-1797.	1.4	48
1220	RNF8 E3 Ubiquitin Ligase Stimulates Ubc13 E2 Conjugating Activity That Is Essential for DNA Double Strand Break Signaling and BRCA1 Tumor Suppressor Recruitment. <i>Journal of Biological Chemistry</i> , 2016, 291, 9396-9410.	1.6	26
1221	Solution Behavior of the Intrinsically Disordered N-Terminal Domain of Retinoid X Receptor $\hat{\pm}$ in the Context of the Full-Length Protein. <i>Biochemistry</i> , 2016, 55, 1741-1748.	1.2	19
1222	In situ study of the state of lysozyme molecules at the very early stage of the crystallization process by small-angle X-ray scattering. <i>Crystallography Reports</i> , 2016, 61, 5-10.	0.1	29
1223	Conformational Flexibility Enables the Function of a BECN1 Region Essential for Starvation-Mediated Autophagy. <i>Biochemistry</i> , 2016, 55, 1945-1958.	1.2	28
1224	Quaternary Structure of Fur Proteins, a New Subfamily of Tetrameric Proteins. <i>Biochemistry</i> , 2016, 55, 1503-1515.	1.2	22
1225	Structural Basis of Stereospecificity in the Bacterial Enzymatic Cleavage of $\hat{\text{I}}^2$ -Aryl Ether Bonds in Lignin. <i>Journal of Biological Chemistry</i> , 2016, 291, 5234-5246.	1.6	40
1226	Conformational Disorder of the Most Immature Cu, Zn-Superoxide Dismutase Leading to Amyotrophic Lateral Sclerosis. <i>Journal of Biological Chemistry</i> , 2016, 291, 4144-4155.	1.6	42

#	ARTICLE	IF	CITATIONS
1227	Tetramerization and interdomain flexibility of the replication initiation controller YabA enables simultaneous binding to multiple partners. <i>Nucleic Acids Research</i> , 2016, 44, 449-463.	6.5	96
1228	Low resolution solution structure of an enzymatic active AhpC 10 :AhpF 2 ensemble of the Escherichia coli Alkyl hydroperoxide Reductase. <i>Journal of Structural Biology</i> , 2016, 193, 13-22.	1.3	10
1229	Combination Therapy of LysGH15 and Apigenin as a New Strategy for Treating Pneumonia Caused by Staphylococcus aureus. <i>Applied and Environmental Microbiology</i> , 2016, 82, 87-94.	1.4	51
1230	E-selectin ligand complexes adopt an extended high-affinity conformation. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 62-72.	1.5	50
1231	The PRE-Derived NMR Model of the 38.8-kDa Tri-Domain IsdH Protein from Staphylococcus aureus Suggests That It Adaptively Recognizes Human Hemoglobin. <i>Journal of Molecular Biology</i> , 2016, 428, 1107-1129.	2.0	20
1232	Application of advanced X-ray methods in life sciences. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3671-3685.	1.1	14
1233	Tumor delivery of liposomal doxorubicin prepared with poly-L-glutamic acid as a drug-trapping agent. <i>Journal of Liposome Research</i> , 2017, 27, 99-107.	1.5	10
1234	Inter-molecular crosslinking activity is engendered by the dimeric form of transglutaminase 2. <i>Amino Acids</i> , 2017, 49, 461-471.	1.2	13
1235	Nucleoplasmin-like domain of FKBP39 from Drosophila melanogaster forms a tetramer with partly disordered tentacle-like C-terminal segments. <i>Scientific Reports</i> , 2017, 7, 40405.	1.6	7
1236	SAXS Structural Studies of Dps from Deinococcus radiodurans Highlights the Conformation of the Mobile N-Terminal Extensions. <i>Journal of Molecular Biology</i> , 2017, 429, 667-687.	2.0	13
1237	Probing the internal and external micelle structures of differently sized casein micelles from individual cows milk by dynamic light and small-angle X-ray scattering. <i>Food Hydrocolloids</i> , 2017, 69, 150-163.	5.6	42
1238	Coupling High Throughput Microfluidics and Small-Angle X-ray Scattering to Study Protein Crystallization from Solution. <i>Analytical Chemistry</i> , 2017, 89, 2282-2287.	3.2	49
1239	Time-resolved neutron scattering provides new insight into protein substrate processing by a AAA+ unfoldase. <i>Scientific Reports</i> , 2017, 7, 40948.	1.6	32
1240	Uridine as a new scavenger for synchrotron-based structural biology techniques. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 53-62.	1.0	19
1241	The Matrix protein M1 from influenza C virus induces tubular membrane invaginations in an in vitro cell membrane model. <i>Scientific Reports</i> , 2017, 7, 40801.	1.6	21
1242	Insights on the structural dynamics of Leishmania braziliensis Hsp90 molecular chaperone by small angle X-ray scattering. <i>International Journal of Biological Macromolecules</i> , 2017, 97, 503-512.	3.6	13
1243	esoscopic structure of pectin in solution. <i>Biopolymers</i> , 2017, 107, e23016.	1.2	26
1244	Solution structure and excitation energy transfer in phycobiliproteins of Acaryochloris marina investigated by small angle scattering. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 318-324.	0.5	15

#	ARTICLE	IF	CITATIONS
1245	Cloning, heterologous expression and biochemical characterization of a non-specific endoglucanase family 12 from <i>Aspergillus terreus</i> NIH2624. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 395-403.	1.1	32
1246	Calcium modulates calmodulin/Î±-actinin 1 interaction with and agonist-dependent internalization of the adenosine A _{2A} receptor. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017, 1864, 674-686.	1.9	4
1247	The Functional Cycle of Rnt1p: Five Consecutive Steps of Double-Stranded RNA Processing by a Eukaryotic RNase III. <i>Structure</i> , 2017, 25, 353-363.	1.6	15
1248	Force interacts with macromolecular structure in activation of TGF-Î². <i>Nature</i> , 2017, 542, 55-59.	13.7	222
1249	Assembly of the elongated collagen prolyl 4-hydroxylase Î±2Î²2 heterotetramer around a central Î±2 dimer. <i>Biochemical Journal</i> , 2017, 474, 751-769.	1.7	17
1250	Stoichiometry and structure of a lantibiotic maturation complex. <i>Scientific Reports</i> , 2017, 7, 42163.	1.6	17
1251	Oxidation of F-actin controls the terminal steps of cytokinesis. <i>Nature Communications</i> , 2017, 8, 14528.	5.8	130
1252	Structural analyses combined with small-angle X-ray scattering reveals that the retention of heme is critical for maintaining the structure of horseradish peroxidase under denaturing conditions. <i>Amino Acids</i> , 2017, 49, 715-723.	1.2	4
1253	Structure of the <i>Escherichia coli</i> ProQ RNA-binding protein. <i>Rna</i> , 2017, 23, 696-711.	1.6	50
1254	Structural features of Zika virus non-structural proteins 3 and -5 and its individual domains in solution as well as insights into NS3 inhibition. <i>Antiviral Research</i> , 2017, 141, 73-90.	1.9	24
1255	Functional and structural insight into properdin control of complement alternative pathway amplification. <i>EMBO Journal</i> , 2017, 36, 1084-1099.	3.5	69
1256	Nature of impurities during protein crystallization. <i>Crystallography Reports</i> , 2017, 62, 148-156.	0.1	2
1257	Structural basis of homo- and heterotrimerization of collagen I. <i>Nature Communications</i> , 2017, 8, 14671.	5.8	79
1258	Structural studies of <i>Neurospora crassa</i> LPMO9D and redox partner CDH1A using neutron crystallography and small-angle scattering. <i>Carbohydrate Research</i> , 2017, 448, 200-204.	1.1	19
1259	Structural Insights into a Unique Dimeric DEAD-Box Helicase CshA that Promotes RNA Decay. <i>Structure</i> , 2017, 25, 469-481.	1.6	19
1260	Structural basis of autoregulatory scaffolding by apoptosis signal-regulating kinase 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2096-E2105.	3.3	34
1261	Stability, structural and functional properties of a monomeric, calcium-loaded adenylate cyclase toxin, CyaA, from <i>Bordetella pertussis</i> . <i>Scientific Reports</i> , 2017, 7, 42065.	1.6	38
1262	A Transition Metal-Binding, Trimeric Î² ³ -Crystallin from Methane-Producing Thermophilic Archaea, <i>Methanosaeta thermophila</i> . <i>Biochemistry</i> , 2017, 56, 1299-1310.	1.2	7

#	ARTICLE	IF	CITATIONS
1263	Significance of Individual Residues at the Regulatory Site of Yeast Pyruvate Decarboxylase for Allosteric Substrate Activation. <i>Biochemistry</i> , 2017, 56, 1285-1298.	1.2	2
1264	Structural insights into POT1-TPP1 interaction and POT1 C-terminal mutations in human cancer. <i>Nature Communications</i> , 2017, 8, 14929.	5.8	71
1265	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017, 2, 17047.	5.9	102
1266	Quantitative determining interface information of nano composite by synchrotron radiation small-angle X-ray scattering. <i>Composites Part B: Engineering</i> , 2017, 120, 92-96.	5.9	17
1267	Probing the Complex Architecture of Multimodular Carbohydrate-Active Enzymes Using a Combination of Small Angle X-Ray Scattering and X-Ray Crystallography. <i>Methods in Molecular Biology</i> , 2017, 1588, 239-253.	0.4	3
1268	The severe impact of in vivo-like microfluidic flow and the influence of gemini surfactants on amyloid aggregation of hen egg white lysozyme. <i>RSC Advances</i> , 2017, 7, 10973-10984.	1.7	5
1269	Essential role of the flexible linker on the conformational equilibrium of bacterial peroxiredoxin reductase for effective regeneration of peroxiredoxin. <i>Journal of Biological Chemistry</i> , 2017, 292, 6667-6679.	1.6	5
1270	Twitchin kinase inhibits muscle activity. <i>Molecular Biology of the Cell</i> , 2017, 28, 1591-1600.	0.9	16
1271	Analysis of Novel Interactions between Components of the Selenocysteine Biosynthesis Pathway, SEPHS1, SEPHS2, SEPSECS, and SECp43. <i>Biochemistry</i> , 2017, 56, 2261-2270.	1.2	20
1272	Structural basis of apoptosis inhibition by the fowlpox virus protein FPV039. <i>Journal of Biological Chemistry</i> , 2017, 292, 9010-9021.	1.6	30
1273	The uniqueness of subunit $\hat{\iota}$ of mycobacterial F-ATP synthases: An evolutionary variant for niche adaptation. <i>Journal of Biological Chemistry</i> , 2017, 292, 11262-11279.	1.6	33
1274	Structural heterogeneity in the intrinsically disordered RNA polymerase II C-terminal domain. <i>Nature Communications</i> , 2017, 8, 15231.	5.8	58
1275	Determining Atomistic SAXS Models of Tri-Ubiquitin Chains from Bayesian Analysis of Accelerated Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 2418-2429.	2.3	16
1276	Structural and mechanistic insights into Mycothiol Disulphide Reductase and the Mycoredoxin-1-alkylhydroperoxide reductase E assembly of <i>Mycobacterium tuberculosis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2354-2366.	1.1	9
1277	Structural Insight into Ubiquitin-Like Protein Recognition and Oligomeric States of JAMM/MPN+ Proteases. <i>Structure</i> , 2017, 25, 823-833.e6.	1.6	16
1278	Structural features of NS3 of Dengue virus serotypes 2 and 4 in solution and insight into RNA binding and the inhibitory role of quercetin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 402-419.	1.1	12
1279	Structural and biochemical analyses reveal insights into covalent flavinylation of the <i>Escherichia coli</i> Complex II homolog quinol:fumarate reductase. <i>Journal of Biological Chemistry</i> , 2017, 292, 12921-12933.	1.6	15
1280	The effect of solution pH on the structural stability of magnetoferritin. <i>Colloids and Surfaces B: Biointerfaces</i> , 2017, 156, 375-381.	2.5	13

#	ARTICLE	IF	CITATIONS
1281	Effective Interactions and Colloidal Stability of Bovine \hat{I}^3 -Globulin in Solution. <i>Journal of Physical Chemistry B</i> , 2017, 121, 5759-5769.	1.2	26
1282	The origin and evolution of human glutaminases and their atypical C-terminal ankyrin repeats. <i>Journal of Biological Chemistry</i> , 2017, 292, 11572-11585.	1.6	19
1283	Investigation of calcium-dependent activity and conformational dynamics of zebra fish 12-lipoxygenase. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2099-2111.	1.1	6
1284	Wing phosphorylation is a major functional determinant of the Lrs14-type biofilm and motility regulator AbfR1 in <i>Sulfolobus acidocaldarius</i> . <i>Molecular Microbiology</i> , 2017, 105, 777-793.	1.2	32
1285	Three-dimensional structure of the 3'-X-tail of hepatitis C virus RNA in monomeric and dimeric states. <i>Rna</i> , 2017, 23, 1465-1476.	1.6	21
1286	HnRNP A1 Alters the Structure of a Conserved Enterovirus IRES Domain to Stimulate Viral Translation. <i>Journal of Molecular Biology</i> , 2017, 429, 2841-2858.	2.0	56
1287	Structural and Biochemical Characterization of Poly-ADP-ribose Polymerase from <i>Trypanosoma brucei</i> . <i>Scientific Reports</i> , 2017, 7, 3642.	1.6	7
1288	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017, 25, 1079-1088.e3.	1.6	34
1289	Bacterial protease uses distinct thermodynamic signatures for substrate recognition. <i>Scientific Reports</i> , 2017, 7, 2848.	1.6	14
1290	Solution structure of human steroidogenic acute regulatory protein STARD1 studied by small-angle X-ray scattering. <i>Biochemical and Biophysical Research Communications</i> , 2017, 489, 445-450.	1.0	12
1291	Contrast-Matched Isotropic Bicelles: A Versatile Tool to Specifically Probe the Solution Structure of Peripheral Membrane Proteins Using SANS. <i>Langmuir</i> , 2017, 33, 6572-6580.	1.6	19
1292	Characterization of the oligomeric states of the CK2 \hat{I}^2 holoenzyme in solution. <i>Biochemical Journal</i> , 2017, 474, 2405-2416.	1.7	17
1293	Small-angle X-ray scattering study of conditions for the formation of growth units of protein crystals in lysozyme solutions. <i>Crystallography Reports</i> , 2017, 62, 364-369.	0.1	21
1294	Alternative stable conformation capable of protein misinteraction links tRNA synthetase to peripheral neuropathy. <i>Nucleic Acids Research</i> , 2017, 45, 8091-8104.	6.5	38
1295	Overall Structural Model of NS5A Protein from Hepatitis C Virus and Modulation by Mutations Confering Resistance of Virus Replication to Cyclosporin A. <i>Biochemistry</i> , 2017, 56, 3029-3048.	1.2	29
1296	Insulin fibrillation: The influence and coordination of Zn ²⁺ . <i>Journal of Structural Biology</i> , 2017, 199, 27-38.	1.3	34
1297	Zinc and the iron donor frataxin regulate oligomerization of the scaffold protein to form new Fe-S cluster assembly centers. <i>Metallomics</i> , 2017, 9, 773-801.	1.0	6
1298	The study of complexation between dicationic surfactants and the DNA duplex using structural and spectroscopic methods. <i>RSC Advances</i> , 2017, 7, 26006-26018.	1.7	11

#	ARTICLE	IF	CITATIONS
1299	X-ray Scattering Studies of Protein Structural Dynamics. <i>Chemical Reviews</i> , 2017, 117, 7615-7672.	23.0	83
1300	The POTRA domains of Toc75 exhibit chaperone-like function to facilitate import into chloroplasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4868-E4876.	3.3	40
1301	Triazolopyrimidines Are Microtubule-Stabilizing Agents that Bind the Vinca Inhibitor Site of Tubulin. <i>Cell Chemical Biology</i> , 2017, 24, 737-750.e6.	2.5	58
1302	Computational design of trimeric influenza-neutralizing proteins targeting the hemagglutinin receptor binding site. <i>Nature Biotechnology</i> , 2017, 35, 667-671.	9.4	108
1303	Neutron scattering shows a droplet of oleic acid at the center of the BAMLET complex. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1371-1378.	1.5	7
1304	Overall conformation of covalently stabilized domain-swapped dimer of human cystatin C in solution. <i>Nuclear Instruments & Methods in Physics Research B</i> , 2017, 411, 136-140.	0.6	1
1305	Structural Analysis of the Flagellar Component Proteins in Solution by Small Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2017, 1593, 105-117.	0.4	0
1306	Disulfide Bond Formation and N-Glycosylation Modulate Protein-Protein Interactions in GPI-Transamidase (GPIT). <i>Scientific Reports</i> , 2017, 7, 45912.	1.6	10
1307	A Combined NMR and SAXS Analysis of the Partially Folded Cataract-Associated V75D $\hat{\text{I}}^{\text{D}}$ -Crystallin. <i>Biophysical Journal</i> , 2017, 112, 1135-1146.	0.2	15
1308	The crystal structure of a multidomain protease inhibitor (HA1-1) reveals the mechanism of its auto-inhibition. <i>Journal of Biological Chemistry</i> , 2017, 292, 8412-8423.	1.6	10
1309	Solution structure of monomeric and trimeric photosystem I of <i>Thermosynechococcus elongatus</i> investigated by small-angle X-ray scattering. <i>Photosynthesis Research</i> , 2017, 133, 163-173.	1.6	18
1310	Phosphorylation-induced conformational dynamics in an intrinsically disordered protein and potential role in phenotypic heterogeneity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2644-E2653.	3.3	72
1311	The Unique Domain Forms a Fuzzy Intramolecular Complex in Src Family Kinases. <i>Structure</i> , 2017, 25, 630-640.e4.	1.6	72
1312	Structural basis of outer dynein arm intraflagellar transport by the transport adaptor protein ODA16 and the intraflagellar transport protein IFT46. <i>Journal of Biological Chemistry</i> , 2017, 292, 7462-7473.	1.6	48
1313	Structural and functional characterization of <i>Caenorhabditis elegans</i> $\hat{\text{I}}^{\text{z}}$ -catenin reveals constitutive binding to $\hat{\text{I}}^{\text{2}}$ -catenin and F-actin. <i>Journal of Biological Chemistry</i> , 2017, 292, 7077-7086.	1.6	26
1314	Using Small Angle X-Ray Scattering (SAXS) to Characterize the Solution Conformation and Flexibility of Matrix Metalloproteinases (MMPs). <i>Methods in Molecular Biology</i> , 2017, 1579, 87-108.	0.4	0
1315	Structural model of dodecameric heat-shock protein Hsp21: Flexible N-terminal arms interact with client proteins while C-terminal tails maintain the dodecamer and chaperone activity. <i>Journal of Biological Chemistry</i> , 2017, 292, 8103-8121.	1.6	24
1316	Molecular determinants of KA1 domain-mediated autoinhibition and phospholipid activation of MARK1 kinase. <i>Biochemical Journal</i> , 2017, 474, 385-398.	1.7	21

#	ARTICLE	IF	CITATIONS
1317	The Human RecQ4 Helicase Contains a Functional RecQ C-terminal Region (RQC) That Is Essential for Activity. <i>Journal of Biological Chemistry</i> , 2017, 292, 4176-4184.	1.6	15
1318	Modeling Protein Excited-state Structures from ϵ -Over-length ϵ -Chemical Cross-links. <i>Journal of Biological Chemistry</i> , 2017, 292, 1187-1196.	1.6	48
1319	Re-entrant cholesteric phase in DNA liquid-crystalline dispersion particles. <i>Journal of Biological Physics</i> , 2017, 43, 45-68.	0.7	12
1320	The <i>Streptococcus gordonii</i> Adhesin CshA Protein Binds Host Fibronectin via a Catch-Clamp Mechanism. <i>Journal of Biological Chemistry</i> , 2017, 292, 1538-1549.	1.6	26
1321	Small-Angle X-ray Scattering Study of Protein Complexes with Tea Polyphenols. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 656-665.	2.4	28
1322	A misfolded dimer of Cu/Zn ϵ -superoxide dismutase leading to pathological oligomerization in amyotrophic lateral sclerosis. <i>Protein Science</i> , 2017, 26, 484-496.	3.1	28
1323	Recombinant Expression of the Full-length Ectodomain of LDL Receptor-related Protein 1 (LRP1) Unravels pH-dependent Conformational Changes and the Stoichiometry of Binding with Receptor-associated Protein (RAP). <i>Journal of Biological Chemistry</i> , 2017, 292, 912-924.	1.6	17
1324	Structural studies of RNA-protein complexes: A hybrid approach involving hydrodynamics, scattering, and computational methods. <i>Methods</i> , 2017, 118-119, 146-162.	1.9	39
1325	Evidence for M1-Linked Polyubiquitin-Mediated Conformational Change in NEMO. <i>Journal of Molecular Biology</i> , 2017, 429, 3793-3800.	2.0	27
1326	Structural analysis of variant of <i>Helicobacter pylori</i> MotB in its activated form, engineered as chimera of MotB and leucine zipper. <i>Scientific Reports</i> , 2017, 7, 13435.	1.6	12
1327	Structural analysis of aqueous ferrofluids with cobalt ferrite particles stabilized with lauric acid and sodium n-dodecyl sulphate. <i>Journal of Physics: Conference Series</i> , 2017, 848, 012026.	0.3	2
1328	The Crystal Structure and Conformations of an Unbranched Mixed Tri-Ubiquitin Chain Containing K48 and K63 Linkages. <i>Journal of Molecular Biology</i> , 2017, 429, 3801-3813.	2.0	3
1329	Insights into the Structure of Dimeric RNA Helicase CsdA and Indispensable Role of Its C-Terminal Regions. <i>Structure</i> , 2017, 25, 1795-1808.e5.	1.6	23
1330	Structural Characterization of Whirlin Reveals an Unexpected and Dynamic Supramodule Conformation of Its PDZ Tandem. <i>Structure</i> , 2017, 25, 1645-1656.e5.	1.6	22
1331	The Henipavirus V protein is a prevalently unfolded protein with a zinc-finger domain involved in binding to DDB1. <i>Molecular BioSystems</i> , 2017, 13, 2254-2267.	2.9	18
1332	Structural Basis for EarP-Mediated Arginine Glycosylation of Translation Elongation Factor EF-P. <i>MBio</i> , 2017, 8, .	1.8	24
1333	Molecular basis of human CD22 function and therapeutic targeting. <i>Nature Communications</i> , 2017, 8, 764.	5.8	114
1334	EGFR Ligands Differentially Stabilize Receptor Dimers to Specify Signaling Kinetics. <i>Cell</i> , 2017, 171, 683-695.e18.	13.5	276

#	ARTICLE	IF	CITATIONS
1335	<i>Bacillus anthracis</i> Prolyl 4-Hydroxylase Interacts with and Modifies Elongation Factor Tu. <i>Biochemistry</i> , 2017, 56, 5771-5785.	1.2	9
1336	Structure of Sgk223 pseudokinase reveals novel mechanisms of homotypic and heterotypic association. <i>Nature Communications</i> , 2017, 8, 1157.	5.8	40
1337	Structural insights into the interaction of the conserved mammalian proteins GAPR-1 and Beclin 1, a key autophagy protein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 775-792.	1.1	14
1338	Structural basis for enzyme bifunctionality – the case of Gan1D from <i>Geobacillus stearothermophilus</i> . <i>FEBS Journal</i> , 2017, 284, 3931-3953.	2.2	9
1339	Pyrazinoic Acid Inhibits Mycobacterial Coenzyme A Biosynthesis by Binding to Aspartate Decarboxylase PanD. <i>ACS Infectious Diseases</i> , 2017, 3, 807-819.	1.8	52
1340	Fortified beeswax oleogels: effect of β -carotene on the gel structure and oxidative stability. <i>Food and Function</i> , 2017, 8, 4241-4250.	2.1	87
1341	Self-association of a highly charged arginine-rich cell-penetrating peptide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11428-11433.	3.3	63
1342	A homodimer interface without base pairs in an RNA mimic of red fluorescent protein. <i>Nature Chemical Biology</i> , 2017, 13, 1195-1201.	3.9	111
1343	Novel insights into the vancomycin-resistant <i>Enterococcus faecalis</i> (V583) alkylhydroperoxide reductase subunit F. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3201-3214.	1.1	2
1344	Design of coiled-coil protein-origami cages that self-assemble in vitro and in vivo. <i>Nature Biotechnology</i> , 2017, 35, 1094-1101.	9.4	143
1345	A homologue of the Parkinson's disease-associated protein LRRK2 undergoes a monomer-dimer transition during GTP turnover. <i>Nature Communications</i> , 2017, 8, 1008.	5.8	53
1346	Importance of the C-Terminus of Aldehyde Dehydrogenase 7A1 for Oligomerization and Catalytic Activity. <i>Biochemistry</i> , 2017, 56, 5910-5919.	1.2	7
1347	Molecular dissection of protein-protein interactions between integrin $\alpha 5 \beta 1$ and the <i>Helicobacter pylori</i> Cag type IV secretion system. <i>FEBS Journal</i> , 2017, 284, 4143-4157.	2.2	29
1348	A Broad-Spectrum Inhibitor of CRISPR-Cas9. <i>Cell</i> , 2017, 170, 1224-1233.e15.	13.5	211
1349	Intrinsic disorder in the partitioning protein KorB persists after co-operative complex formation with operator DNA and KorA. <i>Biochemical Journal</i> , 2017, 474, 3121-3135.	1.7	6
1350	Structural analyses of the bacterial primosomal protein DnaB reveal that it is a tetramer and forms a complex with a primosomal re-initiation protein. <i>Journal of Biological Chemistry</i> , 2017, 292, 15744-15757.	1.6	8
1351	The Tiam1 guanine nucleotide exchange factor is auto-inhibited by its pleckstrin homology coiled-coil extension domain. <i>Journal of Biological Chemistry</i> , 2017, 292, 17777-17793.	1.6	19
1352	Cardiolipin mediates membrane and channel interactions of the mitochondrial TIM23 protein import complex receptor Tim50. <i>Science Advances</i> , 2017, 3, e1700532.	4.7	50

#	ARTICLE	IF	CITATIONS
1353	Structural and molecular comparison of bacterial and eukaryotic trigger factors. <i>Scientific Reports</i> , 2017, 7, 10680.	1.6	24
1354	Structural basis for the shielding function of the dynamic trypanosome variant surface glycoprotein coat. <i>Nature Microbiology</i> , 2017, 2, 1523-1532.	5.9	48
1355	Orchestrated Domain Movement in Catalysis by Cytochrome P450 Reductase. <i>Scientific Reports</i> , 2017, 7, 9741.	1.6	24
1356	The open architecture of HD-PTP phosphatase provides new insights into the mechanism of regulation of ESCRT function. <i>Scientific Reports</i> , 2017, 7, 9151.	1.6	22
1357	Structural analysis of Wss1 protein from <i>saccharomyces cerevisiae</i> . <i>Scientific Reports</i> , 2017, 7, 8270.	1.6	10
1358	Periplasmic Binding Protein Dimer Has a Second Allosteric Event Tied to Ligand Binding. <i>Biochemistry</i> , 2017, 56, 5328-5337.	1.2	14
1359	Conformational plasticity and evolutionary analysis of the myotilin tandem Ig domains. <i>Scientific Reports</i> , 2017, 7, 3993.	1.6	11
1360	Structure-based analysis of the guanine nucleotide exchange factor SmgGDS reveals armadillo-repeat motifs and key regions for activity and GTPase binding. <i>Journal of Biological Chemistry</i> , 2017, 292, 13441-13448.	1.6	17
1361	The Unique Protein-to-Protein Carotenoid Transfer Mechanism. <i>Biophysical Journal</i> , 2017, 113, 402-414.	0.2	40
1362	A nucleotide-controlled conformational switch modulates the activity of eukaryotic IMP dehydrogenases. <i>Scientific Reports</i> , 2017, 7, 2648.	1.6	36
1363	The re-entrant cholesteric phase of DNA. <i>Optics and Spectroscopy (English Translation of Optika)</i> Tj ETQq0 0 0 rgBT./Overlock 10 Tf 50 80.2 7	0.2	7
1364	The butyrophilin 3A1 intracellular domain undergoes a conformational change involving the juxtamembrane region. <i>FASEB Journal</i> , 2017, 31, 4697-4706.	0.2	41
1365	Biophysical investigation of type A PutAs reveals a conserved core oligomeric structure. <i>FEBS Journal</i> , 2017, 284, 3029-3049.	2.2	14
1366	Crystallographic and solution structure of the N-terminal domain of the Rel protein from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2017, 591, 2323-2337.	1.3	27
1367	Structural and dynamic properties of the C-terminal region of the Escherichia coli RNA chaperone Hfq: integrative experimental and computational studies. <i>Physical Chemistry Chemical Physics</i> , 2017, 19, 21152-21164.	1.3	15
1368	Conformational variability of the stationary phase survival protein E from <i>Xylella fastidiosa</i> revealed by X-ray crystallography, small-angle X-ray scattering studies, and normal mode analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 1931-1943.	1.5	0
1369	Structure-based dynamic arrays in regulatory domains of sodium-calcium exchanger (NCX) isoforms. <i>Scientific Reports</i> , 2017, 7, 993.	1.6	21
1370	Biochemical characterization of Arabidopsis thaliana starch branching enzyme 2.2 reveals an enzymatic positive cooperativity. <i>Biochimie</i> , 2017, 140, 146-158.	1.3	9

#	ARTICLE	IF	CITATIONS
1371	Structural and SAXS analysis of Tle5â€“Tli5 complex reveals a novel inhibition mechanism of H2â€“T6SS in <i>Pseudomonas aeruginosa</i> . <i>Protein Science</i> , 2017, 26, 2083-2091.	3.1	6
1372	Characterization of New Detergents and Detergent Mimetics by Scattering Techniques for Membrane Protein Crystallization. <i>Methods in Molecular Biology</i> , 2017, 1635, 169-193.	0.4	2
1373	Microchip Circulation Drastically Accelerates Amyloid Aggregation of 1â€“42 Î²-amyloid Peptide from <i>Felis catus</i> . <i>ACS Chemical Neuroscience</i> , 2017, 8, 2558-2567.	1.7	5
1374	Conformational switch of harmonin, a submembrane scaffold protein of the hair cell mechano-electrical transduction machinery. <i>FEBS Letters</i> , 2017, 591, 2299-2310.	1.3	9
1375	Structural flexibility of human Î±â€“dystroglycan. <i>FEBS Open Bio</i> , 2017, 7, 1064-1077.	1.0	12
1376	A PDZ-like domain mediates the dimerization of 11R-lipoxygenase. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2017, 1862, 1121-1128.	1.2	3
1377	Effects of Catalytic Action and Ligand Binding on Conformational Ensembles of Adenylate Kinase. <i>Biochemistry</i> , 2017, 56, 4559-4567.	1.2	13
1378	Glucagon-like Peptide 1 Conjugated to Recombinant Human Serum Albumin Variants with Modified Neonatal Fc Receptor Binding Properties. Impact on Molecular Structure and Half-Life. <i>Biochemistry</i> , 2017, 56, 4860-4870.	1.2	18
1379	Structural transitions in conserved, ordered Beclin 1 domains essential to regulating autophagy. <i>Journal of Biological Chemistry</i> , 2017, 292, 16235-16248.	1.6	10
1380	Synthesis and characterization of chitosanâ€“copper nanocomposites and their fungicidal activity against two sclerotia-forming plant pathogenic fungi. <i>Journal of Nanostructure in Chemistry</i> , 2017, 7, 249-258.	5.3	63
1381	Search for non-lactam inhibitors of mtb Î²-lactamase led to its open shape in apo state: new concept for antibiotic design. <i>Scientific Reports</i> , 2017, 7, 6204.	1.6	11
1382	SAS-Based Studies of Protein Fibrillation. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 149-165.	0.8	0
1383	The repeat region of cortactin is intrinsically disordered in solution. <i>Scientific Reports</i> , 2017, 7, 16696.	1.6	9
1384	Small-angle X-ray scattering study of the influence of solvent replacement (from H2O to D2O) on the initial crystallization stage of tetragonal lysozyme. <i>Crystallography Reports</i> , 2017, 62, 837-842.	0.1	24
1385	Disulfide driven folding for a conditionally disordered protein. <i>Scientific Reports</i> , 2017, 7, 16994.	1.6	14
1386	What Can We Learn from Wide-Angle Solution Scattering?. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 131-147.	0.8	5
1387	Influenza virus Matrix Protein M1 preserves its conformation with pH, changing multimerization state at the priming stage due to electrostatics. <i>Scientific Reports</i> , 2017, 7, 16793.	1.6	25
1388	Natural Parasite Exposure Induces Protective Human Anti-Malarial Antibodies. <i>Immunity</i> , 2017, 47, 1197-1209.e10.	6.6	129

#	ARTICLE	IF	CITATIONS
1389	Small-angle X-Ray analysis of macromolecular structure: the structure of protein NS2 (NEP) in solution. <i>Crystallography Reports</i> , 2017, 62, 894-902.	0.1	4
1390	Structure and Misfolding of the Flexible Tripartite Coiled-Coil Domain of Glaucoma-Associated Myocilin. <i>Structure</i> , 2017, 25, 1697-1707.e5.	1.6	26
1391	The Two-State Prehensile Tail of the Antibacterial Toxin Colicin N. <i>Biophysical Journal</i> , 2017, 113, 1673-1684.	0.2	18
1392	Structure and function of yeast Atg20, a sorting nexin that facilitates autophagy induction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10112-E10121.	3.3	34
1393	The structure of the tetanus toxin reveals pH-mediated domain dynamics. <i>EMBO Reports</i> , 2017, 18, 1306-1317.	2.0	61
1394	Localisation of alkaline phosphatase in the pore structure of paper. <i>Colloid and Polymer Science</i> , 2017, 295, 1293-1304.	1.0	4
1395	Linking functions: an additional role for an intrinsically disordered linker domain in the transcriptional coactivator CBP. <i>Scientific Reports</i> , 2017, 7, 4676.	1.6	39
1396	On the effect of alkaline pH and cofactor availability in the conformational and oligomeric state of <i>Escherichia coli</i> glutamate decarboxylase. <i>Protein Engineering, Design and Selection</i> , 2017, 30, 235-244.	1.0	3
1397	ATSAS 2.8: a comprehensive data analysis suite for small-angle scattering from macromolecular solutions. <i>Journal of Applied Crystallography</i> , 2017, 50, 1212-1225.	1.9	1,205
1398	Structural similarities and functional differences clarify evolutionary relationships between tRNA healing enzymes and the myelin enzyme CNPase. <i>BMC Biochemistry</i> , 2017, 18, 7.	4.4	1
1399	Structural evaluation of an amyloid fibril model using small-angle x-ray scattering. <i>Physical Biology</i> , 2017, 14, 046001.	0.8	15
1400	Skeletal Dysplasia Mutations Effect on Human Filamins TM Structure and Mechanosensing. <i>Scientific Reports</i> , 2017, 7, 4218.	1.6	13
1401	Engineering a monomeric variant of macrophage colony-stimulating factor (M-CSF) that antagonizes the c-FMS receptor. <i>Biochemical Journal</i> , 2017, 474, 2601-2617.	1.7	11
1402	Phosphorylation regulates the secondary structure and function of dentin phosphoprotein peptides. <i>Bone</i> , 2017, 95, 65-75.	1.4	18
1403	Targeted Modulation of Tropoelastin Structure and Assembly. <i>ACS Biomaterials Science and Engineering</i> , 2017, 3, 2832-2844.	2.6	16
1404	Structural studies of protein arginine methyltransferase 2 reveal its interactions with potential substrates and inhibitors. <i>FEBS Journal</i> , 2017, 284, 77-96.	2.2	25
1405	Crystallographic analysis of the laminin Î2 short arm reveals how the LF domain is inserted into a regular array of LE domains. <i>Matrix Biology</i> , 2017, 57-58, 204-212.	1.5	8
1406	Structural characterization of human aminoacyl-tRNA synthetases for translational and nontranslational functions. <i>Methods</i> , 2017, 113, 83-90.	1.9	18

#	ARTICLE	IF	CITATIONS
1407	Structural Basis for the Subversion of MAP Kinase Signaling by an Intrinsically Disordered Parasite Secreted Agonist. <i>Structure</i> , 2017, 25, 16-26.	1.6	41
1408	Preliminary small-angle X-ray scattering and X-ray diffraction studies of the BTB domain of lola protein from <i>Drosophila melanogaster</i> . <i>Crystallography Reports</i> , 2017, 62, 912-915.	0.1	0
1409	Nanoscale Assembly of High-Mobility Group AT-Hook 2 Protein with DNA Replication Fork. <i>Biophysical Journal</i> , 2017, 113, 2609-2620.	0.2	16
1410	Structural disorder and induced folding within two cereal, ABA stress and ripening (ASR) proteins. <i>Scientific Reports</i> , 2017, 7, 15544.	1.6	47
1411	Structural dissection of human metapneumovirus phosphoprotein using small angle x-ray scattering. <i>Scientific Reports</i> , 2017, 7, 14865.	1.6	20
1412	Biochemical and structural studies of <i>Mycobacterium smegmatis</i> MutT1, a sanitization enzyme with unusual modes of association. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 349-364.	1.1	14
1413	Nogo Receptor crystal structures with a native disulfide pattern suggest a novel mode of self-interaction. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 860-876.	1.1	3
1414	Octamer formation in lysozyme solutions at the initial crystallization stage detected by small-angle neutron scattering. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 591-599.	1.1	22
1415	Crystal structure of the <i>Thermoplasma acidophilum</i> protein Ta1207. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 328-335.	0.4	0
1416	<i>Toscana virus</i> nucleoprotein oligomer organization observed in solution. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 650-659.	1.1	8
1417	Progress in small-angle scattering from biological solutions at high-brilliance synchrotrons. <i>IUCr</i> , 2017, 4, 518-528.	1.0	67
1418	A conformational switch regulates the ubiquitin ligase HUWE1. <i>ELife</i> , 2017, 6, .	2.8	62
1419	Crystallographic and SAXS studies of <i>S</i> -adenosyl-L-homocysteine hydrolase from <i>Bradyrhizobium elkanii</i> . <i>IUCr</i> , 2017, 4, 271-282.	1.0	11
1420	Analysis of Functional Dynamics of Modular Multidomain Proteins by SAXS and NMR. <i>Methods in Enzymology</i> , 2017, 592, 49-76.	0.4	10
1421	<i>BioXTAS RAW</i> : improvements to a free open-source program for small-angle X-ray scattering data reduction and analysis. <i>Journal of Applied Crystallography</i> , 2017, 50, 1545-1553.	1.9	451
1422	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 710-728.	1.1	205
1423	SAXS and stability studies of iron-induced oligomers of bacterial frataxin CyaY. <i>PLoS ONE</i> , 2017, 12, e0184961.	1.1	1
1424	A novel <i>Porphyromonas gingivalis</i> enzyme: An atypical dipeptidyl peptidase III with an ARM repeat domain. <i>PLoS ONE</i> , 2017, 12, e0188915.	1.1	8

#	ARTICLE	IF	CITATIONS
1425	Structural insights into reptarenavirus cap-snatching machinery. <i>PLoS Pathogens</i> , 2017, 13, e1006400.	2.1	32
1426	The effect of the pathological V72I, D109N and T190M missense mutations on the molecular structure of Î±-dystroglycan. <i>PLoS ONE</i> , 2017, 12, e0186110.	1.1	4
1427	Calmodulin fishing with a structurally disordered bait triggers CyaA catalysis. <i>PLoS Biology</i> , 2017, 15, e2004486.	2.6	31
1428	Structural insights into dynamics of RecUâ€“HJ complex formation elucidates key role of NTR and stalk region toward formation of reactive state. <i>Nucleic Acids Research</i> , 2017, 45, 975-986.	6.5	5
1429	Disentangling polydispersity in the PCNAâ€“p15PAF complex, a disordered, transient and multivalent macromolecular assembly. <i>Nucleic Acids Research</i> , 2017, 45, 1501-1515.	6.5	33
1430	Monomeric green fluorescent protein as a protein standard for small angle scattering. <i>Biomedical Spectroscopy and Imaging</i> , 2017, 6, 123-134.	1.2	8
1431	Evaluation of solution stability for two-component polydisperse systems by small-angle scattering. <i>Journal of Physics: Conference Series</i> , 2017, 941, 012069.	0.3	3
1432	The effects of osmolytes and crowding on the pressure-induced dissociation and inactivation of dimeric LADH. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 7093-7104.	1.3	13
1433	The C-terminal tail of the NEIL1 DNA glycosylase interacts with the human mitochondrial single-stranded DNA binding protein. <i>DNA Repair</i> , 2018, 65, 11-19.	1.3	21
1434	Solution Structure of an Intramembrane Aspartyl Protease via Small Angle Neutron Scattering. <i>Biophysical Journal</i> , 2018, 114, 602-608.	0.2	11
1435	Active site CP-loop dynamics modulate substrate binding, catalysis, oligomerization, stability, over-oxidation and recycling of 2-Cys Peroxiredoxins. <i>Free Radical Biology and Medicine</i> , 2018, 118, 59-70.	1.3	7
1436	Solution structure of the cytochrome P450 reductaseâ€“cytochrome c complex determined by neutron scattering. <i>Journal of Biological Chemistry</i> , 2018, 293, 5210-5219.	1.6	15
1437	Self-interaction of NPM1 modulates multiple mechanisms of liquidâ€“liquid phase separation. <i>Nature Communications</i> , 2018, 9, 842.	5.8	285
1438	Functional interaction of low-homology FRPs from different cyanobacteria with <i>Synechocystis</i> OCP. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 382-393.	0.5	13
1439	Ethanol Controls the Self-Assembly and Mesoscopic Properties of Human Insulin Amyloid Spherulites. <i>Journal of Physical Chemistry B</i> , 2018, 122, 3101-3112.	1.2	28
1440	Study of the Solution Stability in the Analysis of Polydisperse Systems by Small-Angle Scattering. <i>Crystallography Reports</i> , 2018, 63, 26-31.	0.1	6
1441	Integrating NMR, SAXS, and Atomistic Simulations: Structure and Dynamics of a Two-Domain Protein. <i>Biophysical Journal</i> , 2018, 114, 839-855.	0.2	20
1442	Exploring modular allostery via interchangeable regulatory domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3006-3011.	3.3	27

#	ARTICLE	IF	CITATIONS
1443	Disulfide isomerase activity of the dynamic, trimeric ScsC protein is primed by the tandem immunoglobulin-fold domain of ScsB. <i>Journal of Biological Chemistry</i> , 2018, 293, 5793-5805.	1.6	19
1444	Structural Basis of the Molecular Switch between Phosphatase and Mutase Functions of Human Phosphomannomutase 1 under Ischemic Conditions. <i>Biochemistry</i> , 2018, 57, 3480-3492.	1.2	7
1445	Structural insights into the RNA methyltransferase domain of METTL16. <i>Scientific Reports</i> , 2018, 8, 5311.	1.6	80
1446	Structural modeling of an outer membrane electron conduit from a metal-reducing bacterium suggests electron transfer via periplasmic redox partners. <i>Journal of Biological Chemistry</i> , 2018, 293, 8103-8112.	1.6	51
1447	Structural basis of epilepsy-related ligand-receptor complex LGI1-ADAM22. <i>Nature Communications</i> , 2018, 9, 1546.	5.8	54
1448	Structural investigation of cellobiose dehydrogenase IIA: Insights from small angle scattering into intra- and intermolecular electron transfer mechanisms. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1031-1039.	1.1	26
1449	Conformational sampling of the intrinsically disordered dsRBD-1 domain from <i>Arabidopsis thaliana</i> DCL1. <i>Physical Chemistry Chemical Physics</i> , 2018, 20, 11237-11246.	1.3	5
1450	The effect of fatty acid binding in the acid isomerizations of albumin investigated with a continuous acidification method. <i>Colloids and Surfaces B: Biointerfaces</i> , 2018, 168, 109-116.	2.5	3
1451	Architecture of the complete oxygen-sensing FixL-FixJ two-component signal transduction system. <i>Science Signaling</i> , 2018, 11, .	1.6	38
1452	14-3-3 protein directly interacts with the kinase domain of calcium/calmodulin-dependent protein kinase kinase (CaMKK2). <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1612-1625.	1.1	29
1453	Molecular Basis of Unusually High Neutralization Resistance in Tier 3 HIV-1 Strain 253-11. <i>Journal of Virology</i> , 2018, 92, .	1.5	16
1456	Tudor staphylococcal nuclease is a structure-specific ribonuclease that degrades RNA at unstructured regions during microRNA decay. <i>Rna</i> , 2018, 24, 739-748.	1.6	13
1457	Structural Architecture of the Nucleosome Remodeler ISWI Determined from Cross-Linking, Mass Spectrometry, SAXS, and Modeling. <i>Structure</i> , 2018, 26, 282-294.e6.	1.6	11
1458	Effect of diamond nanoparticle chains on rheological properties of hydrosol. <i>Diamond and Related Materials</i> , 2018, 83, 141-145.	1.8	22
1459	Tuning the associative properties and micelles geometry by stepwise quaternization of PDMAEMA. <i>Reactive and Functional Polymers</i> , 2018, 124, 171-180.	2.0	9
1460	An optimized SEC-SAXS system enabling high X-ray dose for rapid SAXS assessment with correlated UV measurements for biomolecular structure analysis. <i>Journal of Applied Crystallography</i> , 2018, 51, 97-111.	1.9	61
1461	The brace helices of MLKL mediate interdomain communication and oligomerisation to regulate cell death by necroptosis. <i>Cell Death and Differentiation</i> , 2018, 25, 1567-1580.	5.0	66
1462	Assembly of an atypical β -macroglobulin complex from <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2018, 8, 527.	1.6	1

#	ARTICLE	IF	CITATIONS
1463	Crystal structure of thermospermine synthase from <i>Medicago truncatula</i> and substrate discriminatory features of plant aminopropyltransferases. <i>Biochemical Journal</i> , 2018, 475, 787-802.	1.7	16
1464	Investigation into the Mechanism of Homo- and Heterodimerization of Angiotensin-Converting Enzyme. <i>Molecular Pharmacology</i> , 2018, 93, 344-354.	1.0	4
1465	Structure and stability of the Human respiratory syncytial virus M ¹ RNA-binding core domain reveals a compact and cooperative folding unit. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 23-30.	0.4	5
1466	Substrate-induced structural alterations of Mycobacterial mycothione reductase and critical residues involved. <i>FEBS Letters</i> , 2018, 592, 568-585.	1.3	4
1467	Crystal structure of the mammalian lipopolysaccharide detoxifier. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E896-E905.	3.3	24
1468	Cluster Size and Quinary Structure Determine the Rheological Effects of Antibody Self-Association at High Concentrations. <i>Journal of Physical Chemistry B</i> , 2018, 122, 2138-2154.	1.2	33
1469	An N-Terminal Retention Module Anchors the Giant Adhesin LapA of <i>Pseudomonas fluorescens</i> at the Cell Surface: a Novel Subfamily of Type I Secretion Systems. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	44
1470	A Calmodulin C-Lobe Ca ²⁺ -Dependent Switch Governs Kv7 Channel Function. <i>Neuron</i> , 2018, 97, 836-852.e6.	3.8	63
1471	Structural and Biophysical Characterization of Human EXTL3: Domain Organization, Glycosylation, and Solution Structure. <i>Biochemistry</i> , 2018, 57, 1166-1177.	1.2	7
1472	Structural Study of the C-Terminal Domain of Nonstructural Protein 1 from Japanese Encephalitis Virus. <i>Journal of Virology</i> , 2018, 92, .	1.5	24
1473	Determination of protein oligomeric structure from small-angle X-ray scattering. <i>Protein Science</i> , 2018, 27, 814-824.	3.1	40
1474	The structure of serum resistance-associated protein and its implications for human African trypanosomiasis. <i>Nature Microbiology</i> , 2018, 3, 295-301.	5.9	21
1475	Multiple Conformational States Contribute to the 3D Structure of a Glucan Decasaccharide: A Combined SAXS and MD Simulation Study. <i>Journal of Physical Chemistry B</i> , 2018, 122, 1169-1175.	1.2	9
1476	Structural analysis of mtEXO mitochondrial RNA degradosome reveals tight coupling of nuclease and helicase components. <i>Nature Communications</i> , 2018, 9, 97.	5.8	23
1477	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , 2018, 9, 164.	5.8	36
1478	Characterization of human small heat shock protein HSPB1 $\hat{\pm}$ -crystallin domain localized mutants associated with hereditary motor neuron diseases. <i>Scientific Reports</i> , 2018, 8, 688.	1.6	34
1479	A dimeric catalytic core relates the short and long forms of ATP-phosphoribosyltransferase. <i>Biochemical Journal</i> , 2018, 475, 247-260.	1.7	12
1480	Structure and mechanism of a bacterial t6A biosynthesis system. <i>Nucleic Acids Research</i> , 2018, 46, 1395-1411.	6.5	25

#	ARTICLE	IF	CITATIONS
1481	Monoclonal antibody higher order structure analysis by high throughput protein conformational array. <i>MAbs</i> , 2018, 10, 397-405.	2.6	11
1482	Electrochemical generation and observation by magnetic resonance of superparamagnetic cobalt nanoparticles. <i>Electrochimica Acta</i> , 2018, 260, 324-329.	2.6	13
1483	Structural Dynamics Control Allosteric Activation of Cytohesin Family Arf GTPase Exchange Factors. <i>Structure</i> , 2018, 26, 106-117.e6.	1.6	11
1484	CDC42 binds PAK4 via an extended GTPase-effector interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 531-536.	3.3	29
1485	Transferrin receptor 1 is a reticulocyte-specific receptor for <i>Plasmodium vivax</i> . <i>Science</i> , 2018, 359, 48-55.	6.0	158
1486	Robo1 Forms a Compact Dimer-of-Dimers Assembly. <i>Structure</i> , 2018, 26, 320-328.e4.	1.6	28
1487	Interferons type II and their receptors R1 and R2 in fish species: Evolution, structure, and function. <i>Fish and Shellfish Immunology</i> , 2018, 79, 140-152.	1.6	19
1488	Structural basis of the bacteriophage λ CI repressor dimerization and interaction with DNA. <i>FEBS Letters</i> , 2018, 592, 1738-1750.	1.3	5
1489	Daidzein reductase of <i>Eggerthella</i> sp. YY7918, its octameric subunit structure containing FMN/FAD/4Fe-4S, and its enantioselective production of R-dihydroisoflavones. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 301-309.	1.1	10
1490	The L^{β} Phase of Pulmonary Surfactant. <i>Langmuir</i> , 2018, 34, 6601-6611.	1.6	10
1491	Structure and hydrodynamics of a DNA G-quadruplex with a cytosine bulge. <i>Nucleic Acids Research</i> , 2018, 46, 5319-5331.	6.5	44
1492	An N-terminally truncated form of cyclic GMP-dependent protein kinase $\hat{I}\pm$ (PKG $\hat{I}\pm$) is monomeric and autoinhibited and provides a model for activation. <i>Journal of Biological Chemistry</i> , 2018, 293, 7916-7929.	1.6	11
1493	Structure-function analyses reveal the molecular architecture and neutralization mechanism of a bacterial HEPN-MNT toxin-antitoxin system. <i>Journal of Biological Chemistry</i> , 2018, 293, 6812-6823.	1.6	24
1494	A trapped human PPM1A-phosphopeptide complex reveals structural features critical for regulation of PPM protein phosphatase activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 7993-8008.	1.6	19
1495	A Pseudoisostuctural Type II DAH7PS Enzyme from <i>Pseudomonas aeruginosa</i> : Alternative Evolutionary Strategies to Control Shikimate Pathway Flux. <i>Biochemistry</i> , 2018, 57, 2667-2678.	1.2	14
1496	Prp19/Pso4 Is an Autoinhibited Ubiquitin Ligase Activated by Stepwise Assembly of Three Splicing Factors. <i>Molecular Cell</i> , 2018, 69, 979-992.e6.	4.5	28
1497	The invasin D protein from <i>Yersinia pseudotuberculosis</i> selectively binds the Fab region of host antibodies and affects colonization of the intestine. <i>Journal of Biological Chemistry</i> , 2018, 293, 8672-8690.	1.6	573
1498	Structural modelling of the DNAJB6 oligomeric chaperone shows a peptide-binding cleft lined with conserved S/T-residues at the dimer interface. <i>Scientific Reports</i> , 2018, 8, 5199.	1.6	43

#	ARTICLE	IF	CITATIONS
1499	High-Pressure NMR and SAXS Reveals How Capping Modulates Folding Cooperativity of the pp32 Leucine-rich Repeat Protein. <i>Journal of Molecular Biology</i> , 2018, 430, 1336-1349.	2.0	7
1500	Mechanism of formation of a toroid around DNA by the mismatch sensor protein. <i>Nucleic Acids Research</i> , 2018, 46, 256-266.	6.5	10
1501	The C-terminal region of translesion synthesis DNA polymerase $\hat{\nu}$ is partially unstructured and has high conformational flexibility. <i>Nucleic Acids Research</i> , 2018, 46, 2107-2120.	6.5	17
1502	Optical and Structural Characterization of a Chronic Myeloid Leukemia DNA Biosensor. <i>ACS Chemical Biology</i> , 2018, 13, 1235-1242.	1.6	3
1503	The GDP-switched GAF domain of DcpA modulates the concerted synthesis/hydrolysis of c-di-GMP in <i>Mycobacterium smegmatis</i> . <i>Biochemical Journal</i> , 2018, 475, 1295-1308.	1.7	13
1504	Utilizing Coarse-Grained Modeling and Monte Carlo Simulations to Evaluate the Conformational Ensemble of Intrinsically Disordered Proteins and Regions. <i>Journal of Molecular Biology</i> , 2018, 430, 2478-2492.	2.0	43
1505	Structural evolution of photocrosslinked silk fibroin and silk fibroin-based hybrid hydrogels: A small angle and ultra-small angle scattering investigation. <i>International Journal of Biological Macromolecules</i> , 2018, 114, 998-1007.	3.6	35
1506	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. <i>Cell</i> , 2018, 173, 208-220.e20.	13.5	51
1507	Interaction studies of a protein and carbohydrate system using an integrated approach: a case study of the miniagrinâ€“heparin system. <i>European Biophysics Journal</i> , 2018, 47, 751-759.	1.2	1
1508	Dirichlet Priors for MAP Inference of Protein Conformation Abundances from SAXS. <i>Journal of Signal Processing Systems</i> , 2018, 90, 167-174.	1.4	1
1509	Allosteric control of a bacterial stress response system by an anti- σ^f factor. <i>Molecular Microbiology</i> , 2018, 107, 164-179.	1.2	9
1510	Solution scattering approaches to dynamical ordering in biomolecular systems. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 253-274.	1.1	39
1511	Reversible Self-Assembly of Water-Soluble Gold(I) Complexes. <i>Inorganic Chemistry</i> , 2018, 57, 1017-1028.	1.9	29
1512	Ferromagnetic iron oxideâ€“cellulose nanocomposites prepared by ultrasonication. <i>Polymer Chemistry</i> , 2018, 9, 860-868.	1.9	48
1513	Structural insights of Rm Xyn10A â€“ A prebiotic-producing GH10 xylanase with a non-conserved aglycone binding region. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 292-306.	1.1	14
1514	Cyclic olefin copolymer as an X-ray compatible material for microfluidic devices. <i>Lab on A Chip</i> , 2018, 18, 171-178.	3.1	33
1515	Crystal and solution structures of human protein-disulfide isomerase-like protein of the testis (PDILT) provide insight into its chaperone activity. <i>Journal of Biological Chemistry</i> , 2018, 293, 1192-1202.	1.6	7
1516	Structure and interaction of silk fibroin and graphene oxide in concentrated solution under shear. <i>International Journal of Biological Macromolecules</i> , 2018, 107, 2590-2597.	3.6	14

#	ARTICLE	IF	CITATIONS
1517	Metal-dependent allosteric activation and inhibition on the same molecular scaffold: the copper sensor CopY from <i>Streptococcus pneumoniae</i> . <i>Chemical Science</i> , 2018, 9, 105-118.	3.7	27
1518	Insights into Biofilm Dispersal Regulation from the Crystal Structure of the PAS-GGDEF-EAL Region of RbdA from <i>Pseudomonas aeruginosa</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	37
1519	Tuning magnetic relaxation properties of hard cores in core-shell colloids by modification of soft shell. <i>Colloids and Surfaces B: Biointerfaces</i> , 2018, 162, 52-59.	2.5	19
1520	Prediction of protein structure with the coarse-grained UNRES force field assisted by small X-ray scattering data and knowledge-based information. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 228-239.	1.5	26
1521	A dystroglycan mutation (p.Cys667Phe) associated to muscle-eye-brain disease with multicystic leucodystrophy results in ER-retention of the mutant protein. <i>Human Mutation</i> , 2018, 39, 266-280.	1.1	8
1522	Investigation of the Pre-crystallization Stage of Proteinase K in Solution (Influence of Temperature) T_j $ETQq1$ 1 0.784314 $rgBT$ / 10 $Overlock$	0.1	10
1523	Molecular comparison of Neanderthal and Modern Human adenylsuccinate lyase. <i>Scientific Reports</i> , 2018, 8, 18008.	1.6	6
1524	Oil-induced formation of branched wormlike micelles in an alcohol propoxysulfate extended surfactant system. <i>Soft Matter</i> , 2018, 14, 8378-8389.	1.2	18
1525	Calculation of Small-Angle Scattering Patterns. , 2018, , .		3
1526	Structural Parameters of Ordered Nanocomposites Based on Opal Matrices in Accordance with the Data of Small-Angle X-ray and Neutron Scattering: Simulation of Structural and Size Dispersion Characteristics of Nanocomposites. Part II. <i>Nanotechnologies in Russia</i> , 2018, 13, 565-577.	0.7	3
1527	Effect of Composition and Molecular Structure of Poly(<i>l</i> -lactic acid)/Poly(ethylene oxide) Block Copolymers on Micellar Morphology in Aqueous Solution. <i>Langmuir</i> , 2018, 34, 15470-15482.	1.6	22
1528	Structural basis for activation of plasma-membrane Ca ²⁺ -ATPase by calmodulin. <i>Communications Biology</i> , 2018, 1, 206.	2.0	30
1529	Structure and oligomerization of the periplasmic domain of GspL from the type II secretion system of <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2018, 8, 16760.	1.6	12
1530	Structure and Function Studies of Asian Corn Borer <i>Ostrinia furnacalis</i> Pheromone Binding Protein2. <i>Scientific Reports</i> , 2018, 8, 17105.	1.6	9
1531	Intrinsic disorder in the regulatory N-terminal domain of diacylglycerol acyltransferase 1 from <i>Brassica napus</i> . <i>Scientific Reports</i> , 2018, 8, 16665.	1.6	10
1532	β 2-Type Amyloidlike Fibrils of Poly-L-glutamic Acid Convert into Long, Highly Ordered Helices upon Dissolution in Dimethyl Sulfoxide. <i>Journal of Physical Chemistry B</i> , 2018, 122, 11895-11905.	1.2	7
1533	Nanostructure Evolution of Biomimetic Hydrogel from Silk Fibroin and Poly(<i>N</i> -Vinylcaprolactam): A Small Angle Neutron Scattering Study. <i>ACS Symposium Series</i> , 2018, , 71-89.	0.5	0
1534	Hybrid Methods for Modeling Protein Structures Using Molecular Dynamics Simulations and Small-Angle X-Ray Scattering Data. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1105, 237-258.	0.8	9

#	ARTICLE	IF	CITATIONS
1535	Silk fibroin hydrogels for potential applications in photodynamic therapy. <i>Biopolymers</i> , 2018, 110, e23245.	1.2	16
1536	Structural basis of meiotic telomere attachment to the nuclear envelope by MAJIN-TERB2-TERB1. <i>Nature Communications</i> , 2018, 9, 5355.	5.8	37
1537	Structure of Potato Virus A Coat Protein Particles and Their Dissociation. <i>Molecular Biology</i> , 2018, 52, 913-921.	0.4	3
1538	A Mechanically Weak Extracellular Membrane-Adjacent Domain Induces Dimerization of Protocadherin-15. <i>Biophysical Journal</i> , 2018, 115, 2368-2385.	0.2	27
1539	Self-Interaction of Human Serum Albumin: A Formulation Perspective. <i>ACS Omega</i> , 2018, 3, 16105-16117.	1.6	24
1540	A Study of Beryllium-Based Materials and Comparison of Their X-Ray Homogeneities According to Small-Angle Scattering Data. <i>Crystallography Reports</i> , 2018, 63, 874-882.	0.1	1
1541	Crystal structure of intraflagellar transport protein 80 reveals a homo-dimer required for ciliogenesis. <i>ELife</i> , 2018, 7, .	2.8	36
1542	Sulfonated Thiophene Derivative Stabilized Aqueous Poly(3-hexylthiophene):Phenyl-C ₆₁ -butyric Acid Methyl Ester Nanoparticle Dispersion for Organic Solar Cell Applications. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 44116-44125.	4.0	18
1543	Small but large enough: structural properties of armless mitochondrial tRNAs from the nematode <i>Romanomermis culicivorax</i> . <i>Nucleic Acids Research</i> , 2018, 46, 9170-9180.	6.5	35
1544	A bidentate Polycomb Repressive-Deubiquitinase complex is required for efficient activity on nucleosomes. <i>Nature Communications</i> , 2018, 9, 3932.	5.8	25
1545	High-affinity heterotetramer formation between the large myelin-associated glycoprotein and the dynein light chain <i>DYNLL1</i> . <i>Journal of Neurochemistry</i> , 2018, 147, 764-783.	2.1	24
1546	Recent developments in small-angle X-ray scattering and hybrid method approaches for biomacromolecular solutions. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 69-79.	1.1	29
1547	Microfluidic Cell for Studying the Precrystallization Stage Structure of Protein Solutions by Small-Angle X-Ray Scattering. <i>Crystallography Reports</i> , 2018, 63, 713-718.	0.1	1
1548	14-3-3 protein masks the nuclear localization sequence of caspase-2. <i>FEBS Journal</i> , 2018, 285, 4196-4213.	2.2	17
1549	Reduced Activity of Geranylgeranyl Diphosphate Synthase Mutant Is Involved in Bisphosphonate-Induced Atypical Fractures. <i>Molecular Pharmacology</i> , 2018, 94, 1391-1400.	1.0	10
1550	Self-assembly of Gd ³⁺ -bound keplerate polyanions into nanoparticles as a route for the synthesis of positive MRI contrast agents. Impact of the structure on the magnetic relaxivity. <i>Soft Matter</i> , 2018, 14, 7916-7925.	1.2	11
1551	Characterization of a nontypeable <i>Haemophilus influenzae</i> thermonuclease. <i>PLoS ONE</i> , 2018, 13, e0197010.	1.1	1
1552	OCP ⁺ FRP protein complex topologies suggest a mechanism for controlling high light tolerance in cyanobacteria. <i>Nature Communications</i> , 2018, 9, 3869.	5.8	42

#	ARTICLE	IF	CITATIONS
1553	Molecular Basis for Membrane Recruitment by the PX and C2 Domains of Class II Phosphoinositide 3-Kinase-C2 $\hat{\pm}$. <i>Structure</i> , 2018, 26, 1612-1625.e4.	1.6	25
1554	Structural analysis of human NHLRC2, mutations of which are associated with FINCA disease. <i>PLoS ONE</i> , 2018, 13, e0202391.	1.1	15
1555	Conformational Flexibility of Ubiquitin-Modified and SUMO-Modified PCNA Shown by Full-Ensemble Hybrid Methods. <i>Journal of Molecular Biology</i> , 2018, 430, 5294-5303.	2.0	5
1556	Crystal Structure of a Tetrameric DNA Fold-Back Quadruplex. <i>Journal of the American Chemical Society</i> , 2018, 140, 16291-16298.	6.6	13
1557	Structural basis for activation of fluorogenic dyes by an RNA aptamer lacking a G-quadruplex motif. <i>Nature Communications</i> , 2018, 9, 4542.	5.8	37
1558	Disruptive effect of tocopherol oxalate on DPPC liposome structure: DSC, SAXS, and fluorescence anisotropy studies. <i>Chemistry and Physics of Lipids</i> , 2018, 216, 104-113.	1.5	26
1559	Direct observation of conformational dynamics of the PH domain in phospholipases CÉ and Î ² may contribute to subfamily-specific roles in regulation. <i>Journal of Biological Chemistry</i> , 2018, 293, 17477-17490.	1.6	16
1560	The multicatalytic compartment of propionyl-CoA synthase sequesters a toxic metabolite. <i>Nature Chemical Biology</i> , 2018, 14, 1127-1132.	3.9	34
1561	Characterization of a New Glyoxal Oxidase from the Thermophilic Fungus <i>Myceliophthora thermophila</i> M77: Hydrogen Peroxide Production Retained in 5-Hydroxymethylfurfural Oxidation. <i>Catalysts</i> , 2018, 8, 476.	1.6	24
1562	Metal-free ribonucleotide reduction powered by a DOPA radical in <i>Mycoplasma</i> pathogens. <i>Nature</i> , 2018, 563, 416-420.	13.7	50
1563	Crystal structure of an Lrs14-like archaeal biofilm regulator from <i>Sulfolobus acidocaldarius</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1105-1114.	1.1	4
1564	Structural and Functional Insights Into Lysostaphinâ€™Substrate Interaction. <i>Frontiers in Molecular Biosciences</i> , 2018, 5, 60.	1.6	32
1565	Structure of an H1-Bound 6-Nucleosome Array Reveals an Untwisted Two-Start Chromatin Fiber Conformation. <i>Molecular Cell</i> , 2018, 72, 902-915.e7.	4.5	93
1566	Structure and function of <i>Mycobacterium</i> -specific components of F-ATP synthase subunits Î± and Îµ. <i>Journal of Structural Biology</i> , 2018, 204, 420-434.	1.3	9
1567	Resonant Soft X-Ray Scattering Provides Protein Structure with Chemical Specificity. <i>Structure</i> , 2018, 26, 1513-1521.e3.	1.6	10
1568	Probing the Architecture of a Multi-PDZ Domain Protein: Structure of PDZK1 in Solution. <i>Structure</i> , 2018, 26, 1522-1533.e5.	1.6	10
1569	NAD ⁺ promotes assembly of the active tetramer of aldehyde dehydrogenase 7A1. <i>FEBS Letters</i> , 2018, 592, 3229-3238.	1.3	11
1570	High-performance small- and wide-angle X-ray scattering (SAXS/WAXS) experiments on a multi-functional laboratory goniometer platform with easily exchangeable X-ray modules. <i>Review of Scientific Instruments</i> , 2018, 89, 085115.	0.6	14

#	ARTICLE	IF	CITATIONS
1571	Structure of a Novel Dimeric SET Domain Methyltransferase that Regulates Cell Motility. <i>Journal of Molecular Biology</i> , 2018, 430, 4209-4229.	2.0	3
1572	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. <i>Structure</i> , 2018, 26, 948-959.e5.	1.6	5
1573	Structure-specific recognition protein-1 (SSRP1) is an elongated homodimer that binds histones. <i>Journal of Biological Chemistry</i> , 2018, 293, 10071-10083.	1.6	9
1574	VirB8 homolog TraE from plasmid pKM101 forms a hexameric ring structure and interacts with the VirB6 homolog TraD. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5950-5955.	3.3	16
1575	Structural basis of ubiquitin modification by the Legionella effector SdeA. <i>Nature</i> , 2018, 557, 674-678.	13.7	69
1576	Adsorption of lysozyme on pH-responsive PnBA-b-PAA polymeric nanoparticles: studies by stopped-flow SAXS and ITC. <i>Colloid and Polymer Science</i> , 2018, 296, 1183-1191.	1.0	5
1577	Glycogen-nucleic acid constructs for gene silencing in multicellular tumor spheroids. <i>Biomaterials</i> , 2018, 176, 34-49.	5.7	35
1578	Stability of local secondary structure determines selectivity of viral RNA chaperones. <i>Nucleic Acids Research</i> , 2018, 46, 7924-7937.	6.5	28
1579	Fluorinated diglucose detergents for membrane-protein extraction. <i>Methods</i> , 2018, 147, 84-94.	1.9	18
1580	<i>Helicobacter pylori</i> adhesin HopQ disrupts trans dimerization in human CEACAM s. <i>EMBO Journal</i> , 2018, 37, .	3.5	73
1581	Unbiased Combinatorial Screening Identifies a Bispecific IgG1 that Potently Inhibits HER3 Signaling via HER2-Guided Ligand Blockade. <i>Cancer Cell</i> , 2018, 33, 922-936.e10.	7.7	78
1582	Structural Basis for Polyamine Binding at the dCACHE Domain of the McpU Chemoreceptor from <i>Pseudomonas putida</i> . <i>Journal of Molecular Biology</i> , 2018, 430, 1950-1963.	2.0	33
1583	Temperature-Induced Self-Assembly of the Group B Streptococcus (GBS) Fusion Antigen GBS-NN. <i>Molecular Pharmaceutics</i> , 2018, 15, 2584-2593.	2.3	5
1584	Gold nanocrystal labels provide a sequence-3D structure map in SAXS reconstructions. <i>Science Advances</i> , 2018, 4, eaar4418.	4.7	11
1585	CK1/Doubletime activity delays transcription activation in the circadian clock. <i>ELife</i> , 2018, 7, .	2.8	24
1586	Ensemble cryoEM elucidates the mechanism of insulin capture and degradation by human insulin degrading enzyme. <i>ELife</i> , 2018, 7, .	2.8	45
1587	Structural and functional studies of the <i>Leishmania braziliensis</i> SGT co-chaperone indicate that it shares structural features with HIP and can interact with both Hsp90 and Hsp70 with similar affinities. <i>International Journal of Biological Macromolecules</i> , 2018, 118, 693-706.	3.6	11
1588	Crystal structure of the flavin reductase of <i>Acinetobacter baumannii</i> p-hydroxyphenylacetate 3-hydroxylase (HPAH) and identification of amino acid residues underlying its regulation by aromatic ligands. <i>Archives of Biochemistry and Biophysics</i> , 2018, 653, 24-38.	1.4	6

#	ARTICLE	IF	CITATIONS
1589	Conformational States of ABC Transporter MsbA in a Lipid Environment Investigated by Small-Angle Scattering Using Stealth Carrier Nanodiscs. <i>Structure</i> , 2018, 26, 1072-1079.e4.	1.6	58
1590	Compact Seahorse-Shape Cell-Activating Antibody for Cancer Therapy. <i>Advanced Therapeutics</i> , 2018, 1, 1700031.	1.6	4
1591	Migration of Type III Secretion System Transcriptional Regulators Links Gene Expression to Secretion. <i>MBio</i> , 2018, 9, .	1.8	9
1592	Small-Angle X-ray Scattering Study of Macrophage Migration Inhibitory Factor Complexed with Albumin. <i>Crystallography Reports</i> , 2018, 63, 589-593.	0.1	0
1593	Solution scattering study of the <i>Bacillus subtilis</i> PgdS enzyme involved in poly- β -glutamic acids degradation. <i>PLoS ONE</i> , 2018, 13, e0195355.	1.1	2
1594	<i>Staphylococcus epidermidis</i> small basic protein (Sbp) forms amyloid fibrils, consistent with its function as a scaffolding protein in biofilms. <i>Journal of Biological Chemistry</i> , 2018, 293, 14296-14311.	1.6	23
1595	Structural plasticity of the HHD 2 domain of whirlin. <i>FEBS Journal</i> , 2018, 285, 3738-3752.	2.2	9
1596	CaMKK2 kinase domain interacts with the autoinhibitory region through the N-terminal lobe including the RP insert. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2304-2313.	1.1	4
1597	Crystal Structures of R-Type Bacteriocin Sheath and Tube Proteins CD1363 and CD1364 From <i>Clostridium difficile</i> in the Pre-assembled State. <i>Frontiers in Microbiology</i> , 2018, 9, 1750.	1.5	14
1598	The oligomeric assembly of the phosphodiesterase-5 is a mixture of dimers and tetramers: A putative role in the regulation of function. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2183-2190.	1.1	7
1599	The multi-ligand binding first family 35 Carbohydrate Binding Module (CBM35) of <i>Clostridium thermocellum</i> targets rhamnogalacturonan I. <i>Archives of Biochemistry and Biophysics</i> , 2018, 654, 194-208.	1.4	5
1600	FusC, a member of the M16 protease family acquired by bacteria for iron piracy against plants. <i>PLoS Biology</i> , 2018, 16, e2006026.	2.6	17
1601	Formation of a Secretion-Competent Protein Complex by a Dynamic Wrap-around Binding Mechanism. <i>Journal of Molecular Biology</i> , 2018, 430, 3157-3169.	2.0	5
1602	The Molecular Bases of the Dual Regulation of Bacterial Iron Sulfur Cluster Biogenesis by CyaY and IscX. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 97.	1.6	25
1603	Structural and functional characterization of suramin-bound MjTX-I from <i>Bothrops moojeni</i> suggests a particular myotoxic mechanism. <i>Scientific Reports</i> , 2018, 8, 10317.	1.6	26
1604	Structural and functional studies of the metalloregulator Fur identify a promoter-binding mechanism and its role in <i>Francisella tularensis</i> virulence. <i>Communications Biology</i> , 2018, 1, 93.	2.0	19
1605	Tough Photocrosslinked Silk Fibroin/Graphene Oxide Nanocomposite Hydrogels. <i>Langmuir</i> , 2018, 34, 9238-9251.	1.6	54
1606	Hop-family <i>Helicobacter</i> outer membrane adhesins form a novel class of Type V-like secretion proteins with an interrupted β -barrel domain. <i>Molecular Microbiology</i> , 2018, 110, 33-46.	1.2	24

#	ARTICLE	IF	CITATIONS
1607	Estimation of degree of polymerization of poly-acrylonitrile-grafted carbon nanotubes using Guinier plot of small angle x-ray scattering. <i>Nanotechnology</i> , 2018, 29, 275708.	1.3	4
1608	Conformational response to charge clustering in synthetic intrinsically disordered proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 2204-2214.	1.1	16
1609	Evaluating Anti-CD32b F(ab) Conformation Using Molecular Dynamics and Small-Angle X-Ray Scattering. <i>Biophysical Journal</i> , 2018, 115, 289-299.	0.2	4
1610	Characterization of recombinant dihydrodipicolinate synthase from the bread wheat <i>Triticum aestivum</i> . <i>Planta</i> , 2018, 248, 381-391.	1.6	6
1611	Quantitative 3D determination of self-assembled structures on nanoparticles using small angle neutron scattering. <i>Nature Communications</i> , 2018, 9, 1343.	5.8	54
1612	Inherent flexibility of CLIC6 revealed by crystallographic and solution studies. <i>Scientific Reports</i> , 2018, 8, 6882.	1.6	18
1613	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. <i>Scientific Reports</i> , 2018, 8, 7204.	1.6	154
1614	FSDH2- and BAMS-associated mutations confer opposing effects on SMCHD1 function. <i>Journal of Biological Chemistry</i> , 2018, 293, 9841-9853.	1.6	33
1615	Analysis of the natively unstructured RNA/protein-recognition core in the Escherichia coli RNA degradosome and its interactions with regulatory RNA/Hfq complexes. <i>Nucleic Acids Research</i> , 2018, 46, 387-402.	6.5	66
1616	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. <i>Nature Communications</i> , 2018, 9, 1820.	5.8	124
1617	Differential Conformational Dynamics Encoded by the Linker between Quasi RNA Recognition Motifs of Heterogeneous Nuclear Ribonucleoprotein H. <i>Journal of the American Chemical Society</i> , 2018, 140, 11661-11673.	6.6	11
1618	Integrated beamline control and data acquisition for small-angle X-ray scattering at the P12 BioSAXS beamline at PETRAIII storage ring DESY. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 906-914.	1.0	30
1619	The Escherichia coli SRP Receptor Forms a Homodimer at the Membrane. <i>Structure</i> , 2018, 26, 1440-1450.e5.	1.6	4
1620	Bonsai Gelsolin Survives Heat Induced Denaturation by Forming β^2 -Amyloids which Leach Out Functional Monomer. <i>Scientific Reports</i> , 2018, 8, 12602.	1.6	14
1621	Heparin assisted assembly of somatostatin amyloid nanofibrils results in disordered precipitates by hindrance of protofilaments interactions. <i>Nanoscale</i> , 2018, 10, 18195-18204.	2.8	18
1622	Functionally specific binding regions of microtubule-associated protein 2c exhibit distinct conformations and dynamics. <i>Journal of Biological Chemistry</i> , 2018, 293, 13297-13309.	1.6	13
1623	Structural Aspects of Fe ₃ O ₄ /CoFe ₂ O ₄ Magnetic Nanoparticles According to X-Ray and Neutron Scattering. <i>Journal of Surface Investigation</i> , 2018, 12, 737-743.	0.1	8
1624	Structural rearrangements in the C-terminal domain homolog of Orange Carotenoid Protein are crucial for carotenoid transfer. <i>Communications Biology</i> , 2018, 1, 125.	2.0	39

#	ARTICLE	IF	CITATIONS
1625	Structural insights into SorCS2â€“Nerve Growth Factor complex formation. <i>Nature Communications</i> , 2018, 9, 2979.	5.8	24
1626	The 3-D structure of VNG0258H/RosR â€“ A haloarchaeal DNA-binding protein in its ionic shell. <i>Journal of Structural Biology</i> , 2018, 204, 191-198.	1.3	7
1627	Molecular architecture of the multifunctional collagen lysyl hydroxylase and glycosyltransferase LH3. <i>Nature Communications</i> , 2018, 9, 3163.	5.8	46
1628	Insights into the structure and dynamics of lysyl oxidase propeptide, a flexible protein with numerous partners. <i>Scientific Reports</i> , 2018, 8, 11768.	1.6	39
1629	Evaluation of the Solution Stability When Reconstructing the Volume Particle Size Distribution from Small-Angle X-Ray Scattering Data for a Silicasol Solution. <i>Crystallography Reports</i> , 2018, 63, 531-535.	0.1	5
1630	Nanoconjugates of a calixresorcinarene derivative with methoxy poly(ethylene glycol) fragments for drug encapsulation. <i>Beilstein Journal of Nanotechnology</i> , 2018, 9, 2057-2070.	1.5	8
1631	Biological Small-Angle X-Ray Scattering (SAXS). , 2018, , 277-293.		0
1632	Viscoelasticity and structure of blood clots generated in-vitro by rheometry: A comparison between human, horse, rat, and camel. <i>Clinical Hemorheology and Microcirculation</i> , 2018, 69, 515-531.	0.9	6
1633	NCAM2 Fibronectin type-III domains form a rigid structure that binds and activates the Fibroblast Growth Factor Receptor. <i>Scientific Reports</i> , 2018, 8, 8957.	1.6	16
1634	Noninvasive Structural Analysis of Intermediate Species During Fibrillation: An Application of Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2018, 1779, 209-239.	0.4	5
1635	Direct shape determination of intermediates in evolving macromolecular solutions from small-angle scattering data. <i>IUCr</i> , 2018, 5, 402-409.	1.0	20
1636	Conformational switching of the pseudokinase domain promotes human MLKL tetramerization and cell death by necroptosis. <i>Nature Communications</i> , 2018, 9, 2422.	5.8	154
1637	Redox Modulation of Oligomeric State in Proline Utilization A. <i>Biophysical Journal</i> , 2018, 114, 2833-2843.	0.2	2
1638	Structural basis of meiotic chromosome synapsis through SYCP1 self-assembly. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 557-569.	3.6	67
1639	Solvothermal hot injection synthesis of core-shell AgNi nanoparticles. <i>Journal of Alloys and Compounds</i> , 2019, 770, 377-385.	2.8	16
1640	Orientational order in the splay nematic ground state. <i>Physical Chemistry Chemical Physics</i> , 2019, 21, 18769-18772.	1.3	34
1641	Magnetite Nanoparticles in Hybrid Micelles of Polylactide-block-polyethylene Oxide and Sodium Dodecyl Sulfate in Water. <i>Crystallography Reports</i> , 2019, 64, 128-133.	0.1	2
1642	Mechanistic and Structural Insights into Cysteine-Mediated Inhibition of Pyruvate Kinase Muscle Isoform 2. <i>Biochemistry</i> , 2019, 58, 3669-3682.	1.2	11

#	ARTICLE	IF	CITATIONS
1643	ATP/ADP modulates gp16â€™pRNA conformational change in the Phi29 DNA packaging motor. <i>Nucleic Acids Research</i> , 2019, 47, 9818-9828.	6.5	10
1644	Histone chaperone exploits intrinsic disorder to switch acetylation specificity. <i>Nature Communications</i> , 2019, 10, 3435.	5.8	21
1645	Comparison of the Size and Properties of the Cytochrome c/Cardiolipin Nanospheres in a Sediment and Non-polar Medium. <i>Biochemistry (Moscow)</i> , 2019, 84, 923-930.	0.7	4
1646	The quaternary structure of insulin glargine and glulisine under formulation conditions. <i>Biophysical Chemistry</i> , 2019, 253, 106226.	1.5	9
1647	Structural Adaptation in Its Orphan Domain Engenders Betaglycan with an Alternate Mode of Growth Factor Binding Relative to Endoglin. <i>Structure</i> , 2019, 27, 1427-1442.e4.	1.6	12
1648	Conformational communication mediates the reset step in t6A biosynthesis. <i>Nucleic Acids Research</i> , 2019, 47, 6551-6567.	6.5	21
1649	A biophysical and structural study of two chitinases from <i>AgaveÂtequilana</i> and their potential role as defense proteins. <i>FEBS Journal</i> , 2019, 286, 4778-4796.	2.2	8
1650	The archaeal LDH-like malate dehydrogenase from <i>Ignicoccus islandicus</i> displays dual substrate recognition, hidden allostery and a non-canonical tetrameric oligomeric organization. <i>Journal of Structural Biology</i> , 2019, 208, 7-17.	1.3	13
1651	The mechanism of RNA duplex recognition and unwinding by DEAD-box helicase DDX3X. <i>Nature Communications</i> , 2019, 10, 3085.	5.8	77
1652	Lanthanide-dependent methanol dehydrogenase from the legume symbiotic nitrogen-fixing bacterium <i>Bradyrhizobium diazoefficiens</i> strain USDA110. <i>Enzyme and Microbial Technology</i> , 2019, 130, 109371.	1.6	18
1653	Interplay of Protein Disorder in Retinoic Acid Receptor Heterodimer and Its Corepressor Regulates Gene Expression. <i>Structure</i> , 2019, 27, 1270-1285.e6.	1.6	50
1654	Structure and biochemical characterization of glucose tolerant Î²-1,4 glucosidase (HtBgl) of family 1 glycoside hydrolase from <i>Hungateiclostridium thermocellum</i> . <i>Carbohydrate Research</i> , 2019, 483, 107750.	1.1	15
1655	Solution structure and flexibility of the condensin HEAT-repeat subunit Ycg1. <i>Journal of Biological Chemistry</i> , 2019, 294, 13822-13829.	1.6	9
1656	PrP (58â€™93) peptide from unstructured N-terminal domain of human prion protein forms amyloid-like fibrillar structures in the presence of Zn ²⁺ ions. <i>RSC Advances</i> , 2019, 9, 22211-22219.	1.7	9
1657	A structural and biochemical comparison of Ribonuclease E homologues from pathogenic bacteria highlights species-specific properties. <i>Scientific Reports</i> , 2019, 9, 7952.	1.6	6
1658	Solution Structure of SpoIVB Reveals Mechanism of PDZ Domain-Regulated Protease Activity. <i>Frontiers in Microbiology</i> , 2019, 10, 1232.	1.5	3
1659	The domain swapping of human cystatin C induced by synchrotron radiation. <i>Scientific Reports</i> , 2019, 9, 8548.	1.6	13
1660	Modelling of multicomponent polydisperse systems using small-angle scattering data. <i>Journal of Physics: Conference Series</i> , 2019, 1238, 012004.	0.3	0

#	ARTICLE	IF	CITATIONS
1661	DNA processing by the MOBH family relaxase Tral encoded within the gonococcal genetic island. <i>Nucleic Acids Research</i> , 2019, 47, 8136-8153.	6.5	2
1662	Morphology Control in AgCu Nanoalloy Synthesis by Molecular Cu(I) Precursors. <i>Inorganic Chemistry</i> , 2019, 58, 15246-15254.	1.9	4
1663	A nitric oxide-binding heterodimeric cytochrome c complex from the anammox bacterium <i>Kuenenia stuttgartiensis</i> binds to hydrazine synthase. <i>Journal of Biological Chemistry</i> , 2019, 294, 16712-16728.	1.6	16
1664	Concatenation of 14-3-3 with partner phosphoproteins as a tool to study their interaction. <i>Scientific Reports</i> , 2019, 9, 15007.	1.6	15
1665	A Proximal Operator for Multispectral Phase Retrieval Problems. <i>SIAM Journal on Optimization</i> , 2019, 29, 2594-2607.	1.2	7
1666	Small angle X-ray scattering-assisted protein structure prediction in CASP13 and emergence of solution structure differences. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 1298-1314.	1.5	24
1667	Structure and membrane-targeting of a <i>Bordetella pertussis</i> effector N-terminal domain. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019, 1861, 183054.	1.4	10
1668	Protease-associated import systems are widespread in Gram-negative bacteria. <i>PLoS Genetics</i> , 2019, 15, e1008435.	1.5	15
1669	Critical Structural Defects Explain Filamin A Mutations Causing Mitral Valve Dysplasia. <i>Biophysical Journal</i> , 2019, 117, 1467-1475.	0.2	2
1670	Molecular recognition of ubiquitin and Lys63-linked diubiquitin by STAM2 UIM-SH3 dual domain: the effect of its linker length and flexibility. <i>Scientific Reports</i> , 2019, 9, 14645.	1.6	3
1671	A theoretical and experimental investigation of the effect of sodium dodecyl sulfate on the structural and conformational properties of bovine β -casein. <i>Soft Matter</i> , 2019, 15, 1551-1561.	1.2	11
1672	Crystal structure, epitope, and functional impact of an antibody against a superactive FVII provide insights into allosteric mechanism. <i>Research and Practice in Thrombosis and Haemostasis</i> , 2019, 3, 412-419.	1.0	0
1673	Ammonium Gemini Surfactants Form Complexes with Model Oligomers of siRNA and dsDNA. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5546.	1.8	6
1674	How BamA recruits OMP substrates via poly-POTRA domain. <i>FASEB Journal</i> , 2019, 33, 14690-14702.	0.2	3
1675	Experimental determination of second virial coefficients by small-angle X-ray scattering: a problem revisited. <i>European Biophysics Journal</i> , 2019, 48, 781-787.	1.2	0
1676	Small-angle X-ray scattering intensity of multiscale models of spheres. <i>Journal of Applied Crystallography</i> , 2019, 52, 1348-1357.	1.9	5
1677	A Sustainable Biomineralization Approach for the Synthesis of Highly Fluorescent Ultra-Small Pt Nanoclusters. <i>Biosensors</i> , 2019, 9, 128.	2.3	15
1678	Structural Organization and Dynamics of Homodimeric Cytohesin Family Arf GTPase Exchange Factors in Solution and on Membranes. <i>Structure</i> , 2019, 27, 1782-1797.e7.	1.6	14

#	ARTICLE	IF	CITATIONS
1679	Structural characterization of the RH1-LZI tandem of JIP3/4 highlights RH1 domains as a cytoskeletal motor-binding motif. <i>Scientific Reports</i> , 2019, 9, 16036.	1.6	22
1680	Structures of a dimodular nonribosomal peptide synthetase reveal conformational flexibility. <i>Science</i> , 2019, 366, .	6.0	99
1681	Dynamic structural determinants underlie the neurotoxicity of the N-terminal tau 26-44 peptide in Alzheimer's disease and other human tauopathies. <i>International Journal of Biological Macromolecules</i> , 2019, 141, 278-289.	3.6	16
1682	Distinctive Low-Resolution Structural Features of Dimers of Antibody-Drug Conjugates and Parent Antibody Determined by Small-Angle X-ray Scattering. <i>Molecular Pharmaceutics</i> , 2019, 16, 4902-4912.	2.3	0
1683	Structural and Mechanistic Insights into Caffeine Degradation by the Bacterial N-Demethylase Complex. <i>Journal of Molecular Biology</i> , 2019, 431, 3647-3661.	2.0	26
1684	Rapid Rock Nanoporosity Analysis Using Small Angle Scattering Fused with Imaging Data Based on Stochastic Reconstructions. , 2019, , .		2
1685	Conformation and mechanical property of rpoS mRNA inhibitory stem studied by optical tweezers and X-ray scattering. <i>PLoS ONE</i> , 2019, 14, e0222938.	1.1	3
1686	The flagellotropic bacteriophage YSD1 targets <i>Salmonella</i> Typhi with a Chi-like protein tail fibre. <i>Molecular Microbiology</i> , 2019, 112, 1831-1846.	1.2	24
1687	The activity of <i>Saccharomyces cerevisiae</i> Na ⁺ , K ⁺ /H ⁺ antiporter Nha1 is negatively regulated by 14-3-3 protein binding at serine 481. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2019, 1866, 118534.	1.9	9
1688	Development of novel subunit vaccine based on truncated fiber protein of egg drop syndrome virus and its immunogenicity in chickens. <i>Virus Research</i> , 2019, 272, 197728.	1.1	5
1689	Dynamic tuning of FRET in a green fluorescent protein biosensor. <i>Science Advances</i> , 2019, 5, eaaw4988.	4.7	28
1690	Studying Excipient Modulated Physical Stability and Viscosity of Monoclonal Antibody Formulations Using Small-Angle Scattering. <i>Molecular Pharmaceutics</i> , 2019, 16, 4319-4338.	2.3	36
1691	The Bateman domain of IMP dehydrogenase is a binding target for dinucleoside polyphosphates. <i>Journal of Biological Chemistry</i> , 2019, 294, 14768-14775.	1.6	16
1692	CMT disease severity correlates with mutation-induced open conformation of histidyl-tRNA synthetase, not aminoacylation loss, in patient cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19440-19448.	3.3	28
1693	Molecular basis for metabolite channeling in a ring opening enzyme of the phenylacetate degradation pathway. <i>Nature Communications</i> , 2019, 10, 4127.	5.8	14
1694	<i>Streptomyces</i> IHF uses multiple interfaces to bind DNA. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 129405.	1.1	2
1695	Human immunoglobulin G hinge regulates agonistic anti-CD40 immunostimulatory and antitumour activities through biophysical flexibility. <i>Nature Communications</i> , 2019, 10, 4206.	5.8	21
1696	Structural characterization of transfection nanosystems based on tricationic surfactants and short double stranded oligonucleotides. <i>Biochemical and Biophysical Research Communications</i> , 2019, 518, 706-711.	1.0	4

#	ARTICLE	IF	CITATIONS
1697	Consensus model of a cyanobacterial light-dependent protochlorophyllide oxidoreductase in its pigment-free apo-form and photoactive ternary complex. <i>Communications Biology</i> , 2019, 2, 351.	2.0	9
1698	<i>Arabidopsis</i> immunity regulator EDS1 in a PAD4/SAG101-unbound form is a monomer with an inherently inactive conformation. <i>Journal of Structural Biology</i> , 2019, 208, 107390.	1.3	19
1699	Solution Structure and Conformational Flexibility in the Active State of the Orange Carotenoid Protein: Part I. Small-Angle Scattering. <i>Journal of Physical Chemistry B</i> , 2019, 123, 9525-9535.	1.2	17
1700	Structure of full-length wild-type human phenylalanine hydroxylase by small angle X-ray scattering reveals substrate-induced conformational stability. <i>Scientific Reports</i> , 2019, 9, 13615.	1.6	13
1701	Biochemical and structural characterization of two variants of uncertain significance in the PMS2 gene. <i>Human Mutation</i> , 2019, 40, 458-471.	1.1	6
1702	Structural insights into the tyrosine phosphorylation-mediated inhibition of SH3 domain-ligand interactions. <i>Journal of Biological Chemistry</i> , 2019, 294, 4608-4620.	1.6	12
1703	Biochemical characterization of the respiratory syncytial virus N0-P complex in solution. <i>Journal of Biological Chemistry</i> , 2019, 294, 3647-3660.	1.6	22
1704	Exploring the minimal structure of a functional ADAMTS13 by mutagenesis and small-angle X-ray scattering. <i>Blood</i> , 2019, 133, 1909-1918.	0.6	23
1705	A vesicle-to-sponge transition via the proliferation of membrane-linking pores in 1%-3 polyunsaturated fatty acid-containing lipid assemblies. <i>Journal of Molecular Liquids</i> , 2019, 279, 518-523.	2.3	26
1706	Domain cross-talk within a bifunctional enzyme provides catalytic and allosteric functionality in the biosynthesis of aromatic amino acids. <i>Journal of Biological Chemistry</i> , 2019, 294, 4828-4842.	1.6	8
1707	Quantitative live-cell imaging and 3D modeling reveal critical functional features in the cytosolic complex of phagocyte NADPH oxidase. <i>Journal of Biological Chemistry</i> , 2019, 294, 3824-3836.	1.6	25
1708	Lysyl oxidase-like 2 (LOXL2)-mediated crosslinking of tropoelastin. <i>FASEB Journal</i> , 2019, 33, 5468-5481.	0.2	53
1709	A flap motif in human serine hydroxymethyltransferase is important for structural stabilization, ligand binding, and control of product release. <i>Journal of Biological Chemistry</i> , 2019, 294, 10490-10502.	1.6	11
1710	Low-resolution SAXS and structural dynamics analysis on <i>M. tuberculosis</i> GmhB enzyme involved in GDP-heptose biosynthetic pathway. <i>International Journal of Biological Macromolecules</i> , 2019, 136, 676-685.	3.6	7
1711	Convergent allostery in ribonucleotide reductase. <i>Nature Communications</i> , 2019, 10, 2653.	5.8	27
1712	Insights into the full-length SRPK2 structure and its hydrodynamic behavior. <i>International Journal of Biological Macromolecules</i> , 2019, 137, 205-214.	3.6	1
1713	Structural Characterization of <i>Arabidopsis thaliana</i> NAP1-Related Protein 2 (AtNRP2) and Comparison with its Homolog AtNRP1. <i>Molecules</i> , 2019, 24, 2258.	1.7	6
1714	Static and dynamic properties of nano-confined water in room-temperature ionic liquids. <i>Journal of Molecular Liquids</i> , 2019, 290, 111216.	2.3	14

#	ARTICLE	IF	CITATIONS
1715	Complementary substrate specificity and distinct quaternary assembly of the <i>Escherichia coli</i> aerobic and anaerobic β^2 -oxidation trifunctional enzyme complexes. <i>Biochemical Journal</i> , 2019, 476, 1975-1994.	1.7	8
1716	The role of gelsolin domain 3 in familial amyloidosis (Finnish type). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13958-13963.	3.3	14
1717	The Effect of Cationic Polylysine on the Release of an Encapsulated Substance from pH-Sensitive Anionic Liposomes. <i>Polymer Science - Series A</i> , 2019, 61, 308-316.	0.4	4
1718	Solution structures of long-acting insulin analogues and their complexes with albumin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 272-282.	1.1	10
1719	Modeling Conformationally Flexible Proteins With X-ray Scattering and Molecular Simulations. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 570-578.	1.9	8
1720	Comparison of lipidic carrier systems for integral membrane proteins – MsbA as case study. <i>Biological Chemistry</i> , 2019, 400, 1509-1518.	1.2	15
1721	A direct approach to estimate the anisotropy of protein structures from small-angle X-ray scattering. <i>Journal of Applied Crystallography</i> , 2019, 52, 274-283.	1.9	5
1722	Temperature Driven Transformation in Dextran-Graft-PNIPAM/Embedded Silver Nanoparticle Hybrid System. <i>International Journal of Polymer Science</i> , 2019, 2019, 1-7.	1.2	6
1723	How much can we trust polysorbates as food protein stabilizers - The case of bovine casein. <i>Food Hydrocolloids</i> , 2019, 96, 81-92.	5.6	15
1724	Preparation and characterization of biomedical collagen-chitosan scaffolds with entrapped ibuprofen and silver nanoparticles. <i>Polymer Engineering and Science</i> , 2019, 59, 2479-2487.	1.5	27
1725	Protective Dps-DNA co-crystallization in stressed cells: an <i>in vitro</i> structural study by small-angle X-ray scattering and cryo-electron tomography. <i>FEBS Letters</i> , 2019, 593, 1360-1371.	1.3	28
1726	Zika virus nonstructural protein 5 residue R681 is critical for dimer formation and enzymatic activity. <i>FEBS Letters</i> , 2019, 593, 1272-1291.	1.3	6
1727	Study of the Influence of a Precipitant Cation on the Formation of Oligomers in Crystallization Solutions of Lysozyme Protein. <i>Crystallography Reports</i> , 2019, 64, 11-15.	0.1	13
1728	The Capsid Domain of Arc Changes Its Oligomerization Propensity through Direct Interaction with the NMDA Receptor. <i>Structure</i> , 2019, 27, 1071-1081.e5.	1.6	31
1729	Investigation of the Structure of Crystal-Forming Solutions of Potassium Dihydrogen Phosphate K(H ₂ PO ₄) (KDP type) on the Basis of Modeling Precursor Clusters and According to Small-Angle X-Ray Scattering Data. <i>Crystallography Reports</i> , 2019, 64, 6-10.	0.1	19
1730	Topology and enzymatic properties of a canonical Polycomb repressive complex 1 isoform. <i>FEBS Letters</i> , 2019, 593, 1837-1848.	1.3	4
1731	Structural Basis for YjbH Adaptor-Mediated Recognition of Transcription Factor Spx. <i>Structure</i> , 2019, 27, 923-936.e6.	1.6	16
1732	Structure and oligomerization state of the C-terminal region of the Middle East respiratory syndrome coronavirus nucleoprotein. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 8-15.	1.1	32

#	ARTICLE	IF	CITATIONS
1733	Robust and Tunable Hybrid Hydrogels from Photo-Cross-Linked Soy Protein Isolate and Regenerated Silk Fibroin. <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 9257-9271.	3.2	44
1734	Unique structural features of a bacterial autotransporter adhesin suggest mechanisms for interaction with host macromolecules. <i>Nature Communications</i> , 2019, 10, 1967.	5.8	22
1735	New approach to the synthesis of polymethylsilsesquioxane dendrimers. <i>Polymer</i> , 2019, 174, 159-169.	1.8	17
1736	Supramolecular tripodal Au(μ_3) assemblies in water. Interactions with a pyrene fluorescent probe. <i>New Journal of Chemistry</i> , 2019, 43, 8279-8289.	1.4	12
1737	Domain structure of HelD, an interaction partner of <i>Bacillus subtilis</i> RNA polymerase. <i>FEBS Letters</i> , 2019, 593, 996-1005.	1.3	7
1738	The Tumor Suppressor ING5 Is a Dimeric, Bivalent Recognition Molecule of the Histone H3K4me3 Mark. <i>Journal of Molecular Biology</i> , 2019, 431, 2298-2319.	2.0	18
1739	A molecular model for self-assembly of the synaptonemal complex protein SYCE3. <i>Journal of Biological Chemistry</i> , 2019, 294, 9260-9275.	1.6	27
1740	Structural characteristics of lysozyme Langmuir layers grown on a liquid surface from an oligomeric mixture formed during the early stages of lysozyme crystallization. <i>Thin Solid Films</i> , 2019, 677, 13-21.	0.8	8
1741	Scalable Geometrically Designed Protein Cages Assembled via Genetically Encoded Split Inteins. <i>Structure</i> , 2019, 27, 776-784.e4.	1.6	9
1742	The MurG glycosyltransferase provides an oligomeric scaffold for the cytoplasmic steps of peptidoglycan biosynthesis in the human pathogen <i>Bordetella pertussis</i> . <i>Scientific Reports</i> , 2019, 9, 4656.	1.6	15
1743	Restoring silicasol structural parameters using gradient and simulation annealing optimization schemes from small-angle X-ray scattering data. <i>Journal of Molecular Liquids</i> , 2019, 283, 221-224.	2.3	6
1744	Preparation and Antitumoral Activity of Au-Based Inorganic-Organometallic Nanocomposites. <i>Frontiers in Chemistry</i> , 2019, 7, 60.	1.8	4
1745	Zika Virus NS5 Forms Supramolecular Nuclear Bodies That Sequester Importin- β and Modulate the Host Immune and Pro-Inflammatory Response in Neuronal Cells. <i>ACS Infectious Diseases</i> , 2019, 5, 932-948.	1.8	34
1746	Structures of Class Id Ribonucleotide Reductase Catalytic Subunits Reveal a Minimal Architecture for Deoxynucleotide Biosynthesis. <i>Biochemistry</i> , 2019, 58, 1845-1860.	1.2	10
1747	Efficacy of aldose reductase inhibitors is affected by oxidative stress induced under X-ray irradiation. <i>Scientific Reports</i> , 2019, 9, 3177.	1.6	11
1748	Structural Characterization of N-WASP Domain V Using MD Simulations with NMR and SAXS Data. <i>Biophysical Journal</i> , 2019, 116, 1216-1227.	0.2	18
1749	The carbon monoxide dehydrogenase accessory protein CooJ is a histidine-rich multidomain dimer containing an unexpected Ni(II)-binding site. <i>Journal of Biological Chemistry</i> , 2019, 294, 7601-7614.	1.6	16
1750	Borrelia outer surface protein C is capable of human fibrinogen binding. <i>FEBS Journal</i> , 2019, 286, 2415-2428.	2.2	13

#	ARTICLE	IF	CITATIONS
1751	Crystal structure and activation mechanism of DR3 death domain. <i>FEBS Journal</i> , 2019, 286, 2593-2610.	2.2	6
1752	Thermodynamic Stability of the Transcription Regulator PaaR2 from <i>Escherichia coli</i> O157:H7. <i>Biophysical Journal</i> , 2019, 116, 1420-1431.	0.2	4
1753	A Tail-Based Mechanism Drives Nucleosome Demethylation by the LSD2/NPAC Multimeric Complex. <i>Cell Reports</i> , 2019, 27, 387-399.e7.	2.9	31
1754	The novel calix[4]resorcinarene-PEG conjugate: Synthesis, self-association and encapsulation properties. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2019, 570, 182-190.	2.3	15
1755	C9orf72 Poly(PR) Dipeptide Repeats Disturb Biomolecular Phase Separation and Disrupt Nucleolar Function. <i>Molecular Cell</i> , 2019, 74, 713-728.e6.	4.5	128
1756	Structure–function analyses of two plant meso-diaminopimelate decarboxylase isoforms reveal that active-site gating provides stereochemical control. <i>Journal of Biological Chemistry</i> , 2019, 294, 8505-8515.	1.6	6
1757	Biochemical characterization of the Lassa virus L protein. <i>Journal of Biological Chemistry</i> , 2019, 294, 8088-8100.	1.6	35
1758	Molecular basis for feedback inhibition of tyrosine-regulated 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase from <i>Escherichia coli</i> . <i>Journal of Structural Biology</i> , 2019, 206, 322-334.	1.3	11
1759	Supramolecular arrangement of the full-length Zika virus NS5. <i>PLoS Pathogens</i> , 2019, 15, e1007656.	2.1	38
1760	Octa-repeat domain of the mammalian prion protein mRNA forms stable A-helical hairpin structure rather than G-quadruplexes. <i>Scientific Reports</i> , 2019, 9, 2465.	1.6	3
1761	Evolution of the Interfacial Structure of a Catalyst Ink with the Quality of the Dispersing Solvent: A Contrast Variation Small-Angle and Ultrasmall-Angle Neutron Scattering Investigation. <i>ACS Applied Materials & Interfaces</i> , 2019, 11, 9934-9946.	4.0	65
1762	NADPH-dependent sulfite reductase flavoprotein adopts an extended conformation unique to this diflavin reductase. <i>Journal of Structural Biology</i> , 2019, 205, 170-179.	1.3	12
1763	Overall Structures of <i>Mycobacterium tuberculosis</i> DNA Gyrase Reveal the Role of a Corynebacteriales GyrB-Specific Insert in ATPase Activity. <i>Structure</i> , 2019, 27, 579-589.e5.	1.6	24
1764	Impact of Macromolecular Crowding and Compression on Protein–Protein Interactions and Liquid–Liquid Phase Separation Phenomena. <i>Macromolecules</i> , 2019, 52, 1772-1784.	2.2	34
1765	Elucidating the Mechanism of Absorption of Fast-Acting Insulin Aspart: The Role of Niacinamide. <i>Pharmaceutical Research</i> , 2019, 36, 49.	1.7	60
1766	The Membrane Proximal Domain of TRPV1 and TRPV2 Channels Mediates Protein–Protein Interactions and Lipid Binding In Vitro. <i>International Journal of Molecular Sciences</i> , 2019, 20, 682.	1.8	4
1767	<i>D+i>: software for high-resolution hierarchical modeling of solution X-ray scattering from complex structures. <i>Journal of Applied Crystallography</i> , 2019, 52, 219-242.	1.9	26
1768	Defining the remarkable structural malleability of a bacterial surface protein Rib domain implicated in infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26540-26548.	3.3	15

#	ARTICLE	IF	CITATIONS
1769	Optical and structural characteristics of PMMA films doped with a new anisometric Eu ^{III} complex. <i>Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials</i> , 2019, 75, 570-577.	0.5	7
1771	Combination of Minimization Schemes for Improving the Efficiency of Volume Particle Size Distribution Reconstructions from Silicasol Solutions by Small-Angle X-Ray Scattering. <i>Physics of Atomic Nuclei</i> , 2019, 82, 1576-1581.	0.1	1
1772	Crystal Structure of IlvC, a Ketol-Acid Reductoisomerase, from <i>Streptococcus Pneumoniae</i> . <i>Crystals</i> , 2019, 9, 551.	1.0	5
1774	Structural insights into Acyl-Coenzyme A binding domain containing 3 (ACBD3) protein hijacking by picornaviruses. <i>Protein Science</i> , 2019, 28, 2073-2079.	3.1	7
1775	Design and structural characterisation of olfactomedin-1 variants as tools for functional studies. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 50.	1.0	2
1776	Conformational flexibility of fork-remodeling helicase Rad5 shown by full-ensemble hybrid methods. <i>PLoS ONE</i> , 2019, 14, e0223875.	1.1	7
1777	Application of Experimental Design to Hydrogen Storage: Optimisation of Lignin-Derived Carbons. <i>Journal of Carbon Research</i> , 2019, 5, 82.	1.4	6
1778	Artificial covalent linkage of bacterial acyl carrier proteins for fatty acid production. <i>Scientific Reports</i> , 2019, 9, 16011.	1.6	2
1779	Structural insights into diverse modes of ICAM-1 binding by <i>Plasmodium falciparum</i> -infected erythrocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 20124-20134.	3.3	24
1780	Raptor-Mediated Proteasomal Degradation of Deamidated 4E-BP2 Regulates Postnatal Neuronal Translation and NF- κ B Activity. <i>Cell Reports</i> , 2019, 29, 3620-3635.e7.	2.9	8
1781	Nano-encapsulated <i>Escherichia coli</i> Divisome Anchor ZipA, and in Complex with FtsZ. <i>Scientific Reports</i> , 2019, 9, 18712.	1.6	16
1782	Structure and flexibility of non-structural proteins 3 and -5 of Dengue- and Zika viruses in solution. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 143, 67-77.	1.4	4
1783	Structural and Biochemical Characterization of Aldehyde Dehydrogenase 12, the Last Enzyme of Proline Catabolism in Plants. <i>Journal of Molecular Biology</i> , 2019, 431, 576-592.	2.0	20
1784	Crystal Structure of Aldehyde Dehydrogenase 16 Reveals Trans-Hierarchical Structural Similarity and a New Dimer. <i>Journal of Molecular Biology</i> , 2019, 431, 524-541.	2.0	15
1785	The Structure and Stability of the Disulfide-Linked β S-Crystallin Dimer Provide Insight into Oxidation Products Associated with Lens Cataract Formation. <i>Journal of Molecular Biology</i> , 2019, 431, 483-497.	2.0	35
1786	YB-1, an abundant core mRNA-binding protein, has the capacity to form an RNA nucleoprotein filament: a structural analysis. <i>Nucleic Acids Research</i> , 2019, 47, 3127-3141.	6.5	32
1787	Solution Structure, Self-Assembly, and Membrane Interactions of the Matrix Protein from Newcastle Disease Virus at Neutral and Acidic pH. <i>Journal of Virology</i> , 2019, 93, .	1.5	13
1788	The Structure of the Pro-domain of Mouse proNGF in Contact with the NGF Domain. <i>Structure</i> , 2019, 27, 78-89.e3.	1.6	15

#	ARTICLE	IF	CITATIONS
1789	I-Asparaginase from <i>Erwinia carotovora</i> : insights about its stability and activity. <i>Molecular Biology Reports</i> , 2019, 46, 1313-1316.	1.0	1
1790	Structural Variability of EspG Chaperones from Mycobacterial ESX-1, ESX-3, and ESX-5 Type VII Secretion Systems. <i>Journal of Molecular Biology</i> , 2019, 431, 289-307.	2.0	21
1791	Analysis of styrene maleic acid alternating copolymer supramolecular assemblies in solution by small angle X-ray scattering. <i>European Polymer Journal</i> , 2019, 111, 178-184.	2.6	14
1792	Studies on the effect of the J-domain on the substrate binding domain (SBD) of Hsp70 using a chimeric human J-SBD polypeptide. <i>International Journal of Biological Macromolecules</i> , 2019, 124, 111-120.	3.6	3
1793	Water loading driven size, shape, and composition of cetyltrimethylammonium/hexanol/pentane reverse micelles. <i>Journal of Colloid and Interface Science</i> , 2019, 540, 207-217.	5.0	14
1794	Unusual magnetic relaxation behavior of hydrophilic colloids based on gadolinium(III) octabutoxyphthalocyaninate. <i>Journal of Nanoparticle Research</i> , 2019, 21, 1.	0.8	23
1795	N-glycan Utilization by <i>Bifidobacterium</i> Gut Symbionts Involves a Specialist β -Mannosidase. <i>Journal of Molecular Biology</i> , 2019, 431, 732-747.	2.0	18
1796	Calicivirus VP2 forms a portal-like assembly following receptor engagement. <i>Nature</i> , 2019, 565, 377-381.	13.7	103
1797	Structure of the UHRF1 Tandem Tudor Domain Bound to a Methylated Non-histone Protein, LIG1, Reveals Rules for Binding and Regulation. <i>Structure</i> , 2019, 27, 485-496.e7.	1.6	41
1798	Unraveling the structural basis for the exceptional stability of RNA G-quadruplexes capped by a uridine tetrad at the 3' terminus. <i>Rna</i> , 2019, 25, 121-134.	1.6	8
1799	Influence of energy bandwidth of pink beam on small angle X-ray scattering. <i>Radiation Detection Technology and Methods</i> , 2019, 3, 1.	0.4	5
1800	Non-syndromic Mitral Valve Dysplasia Mutation Changes the Force Resilience and Interaction of Human Filamin A. <i>Structure</i> , 2019, 27, 102-112.e4.	1.6	12
1801	3D structure of the natural tetrameric form of human butyrylcholinesterase as revealed by cryoEM, SAXS and MD. <i>Biochimie</i> , 2019, 156, 196-205.	1.3	26
1802	Disruption of amyloid aggregates by artificial ferritins. <i>Journal of Magnetism and Magnetic Materials</i> , 2019, 473, 215-220.	1.0	5
1803	Structure and Dynamics of a Promiscuous Xanthan Lyase from <i>Paenibacillus nanensis</i> and the Design of Variants with Increased Stability and Activity. <i>Cell Chemical Biology</i> , 2019, 26, 191-202.e6.	2.5	13
1804	Regulation of Human Hsc70 ATPase and Chaperone Activities by Apg2: Role of the Acidic Subdomain. <i>Journal of Molecular Biology</i> , 2019, 431, 444-461.	2.0	16
1805	Human MICAL1: Activation by the small GTPase Rab8 and small angle X-ray scattering studies on the oligomerization state of MICAL1 and its complex with Rab8. <i>Protein Science</i> , 2019, 28, 150-166.	3.1	7
1806	Revealing the interaction mode of the highly flexible <i>Sorghum bicolor</i> Hsp70/Hsp90 organizing protein (Hop): A conserved carboxylate clamp confers high affinity binding to Hsp90. <i>Journal of Proteomics</i> , 2019, 191, 191-201.	1.2	2

#	ARTICLE	IF	CITATIONS
1807	Structure and dynamics analysis of a new member heparinase II/III of family 12 polysaccharide lyase from <i>Pseudopedobacter saltans</i> by computational modeling and small-angle X-ray scattering. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2007-2020.	2.0	2
1808	Quaternary structures of Vac8 differentially regulate the Cvt and PMN pathways. <i>Autophagy</i> , 2020, 16, 991-1006.	4.3	17
1809	Structural studies of the Hsp70/Hsp90 organizing protein of <i>Plasmodium falciparum</i> and its modulation of Hsp70 and Hsp90 ATPase activities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140282.	1.1	13
1810	Small-angle X-ray scattering based structure, modeling and molecular dynamics analyses of a family 5 glycoside hydrolase first endo-mannanase named as <i>RfGH5_7</i> from <i>Ruminococcus flavefaciens</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4371-4384.	2.0	3
1811	Glycerol induced stability enhancement and conformational changes of β^2 -lactoglobulin. <i>Food Chemistry</i> , 2020, 308, 125596.	4.2	12
1812	Tetramerization at Low pH Licenses DNA Methylation Activity of M.HpyAXI in the Presence of Acid Stress. <i>Journal of Molecular Biology</i> , 2020, 432, 324-342.	2.0	7
1813	Farnesylation of human guanylate-binding protein 1 as safety mechanism preventing structural rearrangements and uninduced dimerization. <i>FEBS Journal</i> , 2020, 287, 496-514.	2.2	8
1814	Dodecamers derived from the crystal structure were found in the pre-crystallization solution of the transaminase from the thermophilic bacterium <i>Thermobaculum terrenum</i> by small-angle X-ray scattering. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2939-2944.	2.0	9
1815	Structural basis of the strong cell-cell junction formed by cadherin-23. <i>FEBS Journal</i> , 2020, 287, 2328-2347.	2.2	6
1816	Structural analysis of pathogenic mutations targeting Glu427 of ALDH7A1, the hot spot residue of pyridoxine-dependent epilepsy. <i>Journal of Inherited Metabolic Disease</i> , 2020, 43, 635-644.	1.7	6
1817	On the structure and function of <i>Escherichia coli</i> YjhC: An oxidoreductase involved in bacterial sialic acid metabolism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 654-668.	1.5	13
1818	Ensemble structural analyses depict the regulatory mechanism of non-phosphorylated human MAP2K4. <i>Biochemical and Biophysical Research Communications</i> , 2020, 521, 106-112.	1.0	3
1819	Structural and functional characterization of D109H and R69C mutant versions of human β -crystallin: The biochemical pathomechanism underlying cataract and myopathy development. <i>International Journal of Biological Macromolecules</i> , 2020, 146, 1142-1160.	3.6	23
1820	Asparagine-84, a regulatory allosteric site residue, helps maintain the quaternary structure of <i>Campylobacter jejuni</i> dihydrodipicolinate synthase. <i>Journal of Structural Biology</i> , 2020, 209, 107409.	1.3	4
1821	Drug-templated mesoporous silica nanocontainers with extra high payload and controlled release rate. <i>Colloids and Surfaces B: Biointerfaces</i> , 2020, 185, 110577.	2.5	12
1822	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , 2020, 28, 348-354.e3.	1.6	28
1823	Structure and regulation of human epithelial cell transforming 2 protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1027-1035.	3.3	37
1824	Small angle X-ray scattering and molecular dynamic simulations provide molecular insight for stability of recombinant human transferrin. <i>Journal of Structural Biology: X</i> , 2020, 4, 100017.	0.7	9

#	ARTICLE	IF	CITATIONS
1825	Structure and activity of PPX/GppA homologs from <i>Escherichia coli</i> and <i>Helicobacter pylori</i> . FEBS Journal, 2020, 287, 1865-1885.	2.2	19
1826	Novel inter-domain Ca ²⁺ -binding site in the gelsolin superfamily protein fragmin. Journal of Muscle Research and Cell Motility, 2020, 41, 153-162.	0.9	7
1827	Molecular characterization of a ghrelin-ligand complex. Journal of Molecular Structure, 2020, 1204, 127510.	1.8	4
1828	Structural insights into the mechanism of c-di-GMP-bound YcgR regulating flagellar motility in <i>Escherichia coli</i> . Journal of Biological Chemistry, 2020, 295, 808-821.	1.6	17
1829	New hydrogels in the poly-N-vinylpyrrolidone RE(NO ₃) ₃ ·xH ₂ O (RE=La, Gd, Yb) system: Fabrication, structure, bactericidal properties. Polymer, 2020, 186, 122079.	1.8	4
1830	BILMIX: a new approach to restore the size polydispersity and electron density profiles of lipid bilayers from liposomes using small-angle X-ray scattering data. Journal of Applied Crystallography, 2020, 53, 236-243.	1.9	7
1831	Investigations of Albumin-Insulin Detemir Complexes Using Molecular Dynamics Simulations and Free Energy Calculations. Molecular Pharmaceutics, 2020, 17, 132-144.	2.3	8
1832	Aggregation induced emission of a new naphthyridine-ethynyl-gold complex as a potential tool for sensing guanosine nucleotides in aqueous media. Dalton Transactions, 2020, 49, 171-178.	1.6	9
1833	Synthesis and physico-chemical properties of poly(N-vinyl pyrrolidone)-based hydrogels with titania nanoparticles. Journal of Materials Science, 2020, 55, 3005-3021.	1.7	22
1834	Characterization of Native Reversible Self-Association of a Monoclonal Antibody Mediated by Fab-Fab Interaction. Journal of Pharmaceutical Sciences, 2020, 109, 443-451.	1.6	17
1835	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR-RXR. Nucleic Acids Research, 2020, 48, 9969-9985.	6.5	17
1836	Molecular determinants of MED1 interaction with the DNA bound VDR-RXR heterodimer. Nucleic Acids Research, 2020, 48, 11199-11213.	6.5	17
1837	Interdomain Flexibility within NADPH Oxidase Suggested by SANS Using LMNG Stealth Carrier. Biophysical Journal, 2020, 119, 605-618.	0.2	9
1838	Water oxidation electrocatalysis using ruthenium coordination oligomers adsorbed on multiwalled carbon nanotubes. Nature Chemistry, 2020, 12, 1060-1066.	6.6	54
1839	Continuous Assembly of β -Roll Structures Is Implicated in the Type I-Dependent Secretion of Large Repeat-in-Toxins (RTX) Proteins. Journal of Molecular Biology, 2020, 432, 5696-5710.	2.0	15
1840	Mechanism of efficient double-strand break repair by a long non-coding RNA. Nucleic Acids Research, 2020, 48, 10953-10972.	6.5	43
1841	Development of efficient luminescent soft media by incorporation of a hetero-ligand macrocyclic terbium complex into a lyomesophase. Russian Chemical Bulletin, 2020, 69, 1763-1770.	0.4	2
1842	Structural role of essential light chains in the apicomplexan glideosome. Communications Biology, 2020, 3, 568.	2.0	10

#	ARTICLE	IF	CITATIONS
1843	Deciphering the Unexpected Binding Capacity of the Third PDZ Domain of Whirlin to Various Cochlear Hair Cell Partners. <i>Journal of Molecular Biology</i> , 2020, 432, 5920-5937.	2.0	7
1844	Carnitine metabolism in the human gut: characterization of the two-component carnitine monooxygenase CntAB from <i>Acinetobacter baumannii</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 13065-13078.	1.6	15
1845	Inactivation of the dimeric RappLS20 anti-repressor of the conjugation operon is mediated by peptide-induced tetramerization. <i>Nucleic Acids Research</i> , 2020, 48, 8113-8127.	6.5	4
1846	Structural peculiarities of lysozyme-PLURONIC complexes at the aqueous-air and liquid-liquid interfaces and in the bulk of aqueous solution. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 721-731.	3.6	8
1847	The Polyglutamine Expansion at the N-Terminal of Huntingtin Protein Modulates the Dynamic Configuration and Phosphorylation of the C-Terminal HEAT Domain. <i>Structure</i> , 2020, 28, 1035-1050.e8.	1.6	24
1848	Solution structure of <i>Plasmodium falciparum</i> Hsp90 indicates a high flexible dimer. <i>Archives of Biochemistry and Biophysics</i> , 2020, 690, 108468.	1.4	6
1849	Optimization of Molecular Dynamics Simulations of c-MYC1-88-An Intrinsically Disordered System. <i>Life</i> , 2020, 10, 109.	1.1	10
1850	Structural and enzymatic characterisation of the Type III effector NopAA (=GunA) from <i>Sinorhizobium fredii</i> USDA257 reveals a Xyloglucan hydrolase activity. <i>Scientific Reports</i> , 2020, 10, 9932.	1.6	6
1851	Structural Characterization of Non-structural Protein 9 Complexed With Specific Nanobody Pinpoints Two Important Residues Involved in Porcine Reproductive and Respiratory Syndrome Virus Replication. <i>Frontiers in Microbiology</i> , 2020, 11, 581856.	1.5	8
1852	Crystallographic structure of wild-type SARS-CoV-2 main protease acyl-enzyme intermediate with physiological C-terminal autoprocessing site. <i>Nature Communications</i> , 2020, 11, 5877.	5.8	141
1853	Functional and structural characterization of allosteric activation of phospholipase C μ by Rap1A. <i>Journal of Biological Chemistry</i> , 2020, 295, 16562-16571.	1.6	3
1854	Controlling Protein Nanocage Assembly with Hydrostatic Pressure. <i>Journal of the American Chemical Society</i> , 2020, 142, 20640-20650.	6.6	17
1855	Ligand-induced conformational rearrangements regulate the switch between membrane-proximal and distal functions of Rho kinase 2. <i>Communications Biology</i> , 2020, 3, 721.	2.0	3
1856	Effect of Ligands on HP-Induced Unfolding and Oligomerization of β^2 -Lactoglobulin. <i>Biophysical Journal</i> , 2020, 119, 2262-2274.	0.2	10
1857	In Vivo Biogenesis of a De Novo Designed Iron-Sulfur Protein. <i>ACS Synthetic Biology</i> , 2020, 9, 3400-3407.	1.9	10
1858	Engineered chemotaxis core signaling units indicate a constrained kinase-off state. <i>Science Signaling</i> , 2020, 13, .	1.6	10
1859	Electrochemical Synthesis of Mesoporous Architected Ru Films Using Supramolecular Templates. <i>Small</i> , 2020, 16, e2002489.	5.2	7
1860	A THz transparent 3D printed microfluidic cell for small angle x-ray scattering. <i>Review of Scientific Instruments</i> , 2020, 91, 084101.	0.6	5

#	ARTICLE	IF	CITATIONS
1861	Conserved cysteine dioxidation enhances membrane interaction of human Cl ^{<sup>â</sup>} intracellular channel 5. <i>FASEB Journal</i> , 2020, 34, 9925-9940.	0.2	4
1862	Synthetic Tuning of Coll-Doped Silica Nanoarchitecture Towards Electrochemical Sensing Ability. <i>Nanomaterials</i> , 2020, 10, 1338.	1.9	9
1863	Towards improved understanding of intersubunit interactions in modular polyketide biosynthesis: Docking in the enacyloxin Ila polyketide synthase. <i>Journal of Structural Biology</i> , 2020, 212, 107581.	1.3	9
1864	Dissecting the Structural and Chemical Determinants of the "Open-to-Closed" Motion in the Mannosyltransferase PimA from <i>Mycobacteria</i> . <i>Biochemistry</i> , 2020, 59, 2934-2945.	1.2	5
1865	Structural analysis of the LDL receptor-interacting FERM domain in the E3 ubiquitin ligase IDOL reveals an obscured substrate-binding site. <i>Journal of Biological Chemistry</i> , 2020, 295, 13570-13583.	1.6	7
1866	Application of X-Ray Methods for Determining the Dimensions of Nanoparticles in the Nanosized Anatase-Poly(N-vinylcaprolactam) System. <i>Crystallography Reports</i> , 2020, 65, 631-640.	0.1	0
1867	Inhibition, crystal structures, and in-solution oligomeric structure of aldehyde dehydrogenase 9A1. <i>Archives of Biochemistry and Biophysics</i> , 2020, 691, 108477.	1.4	15
1868	The architecture and stabilisation of flagellotropic tailed bacteriophages. <i>Nature Communications</i> , 2020, 11, 3748.	5.8	28
1869	Integrated Structural Modeling of Full-Length LRH-1 Reveals Inter-domain Interactions Contribute to Receptor Structure and Function. <i>Structure</i> , 2020, 28, 830-846.e9.	1.6	22
1870	Molecular mechanisms underlying the extreme mechanical anisotropy of the flaviviral exoribonuclease-resistant RNAs (xrRNAs). <i>Nature Communications</i> , 2020, 11, 5496.	5.8	9
1871	Molecular characterization of the RNA-protein complex directing $\hat{2}/\hat{1}$ programmed ribosomal frameshifting during arterivirus replicase expression. <i>Journal of Biological Chemistry</i> , 2020, 295, 17904-17921.	1.6	10
1872	Small-angle X-ray scattering studies of emergent polyoxometalates in solution. <i>Journal of Coordination Chemistry</i> , 2020, 73, 2365-2372.	0.8	3
1873	Insight into human Miro1/2 domain organization based on the structure of its N-terminal GTPase. <i>Journal of Structural Biology</i> , 2020, 212, 107656.	1.3	17
1874	The allosteric activation mechanism of a phospholipase A2-like toxin from <i>Bothrops jararacussu</i> venom: a dynamic description. <i>Scientific Reports</i> , 2020, 10, 16252.	1.6	14
1875	Structural insights into rice SaltTol QTL located SALT protein. <i>Scientific Reports</i> , 2020, 10, 16589.	1.6	5
1876	Characterization of the nucleotide-binding domain NsrF from the BceAB-type ABC-transporter NsrFP from the human pathogen <i>Streptococcus agalactiae</i> . <i>Scientific Reports</i> , 2020, 10, 15208.	1.6	6
1877	IM30 IDPs form a membrane-protective carpet upon super-complex disassembly. <i>Communications Biology</i> , 2020, 3, 595.	2.0	16
1878	Small-Angle X-ray Scattering Study of Changes in the Quaternary Structure of Nucleotide-Regulated Pyrophosphatase from <i>Desulfitobacterium hafniense</i> upon Ligand Binding in Solution. <i>Crystallography Reports</i> , 2020, 65, 749-754.	0.1	1

#	ARTICLE	IF	CITATIONS
1879	Pearl-necklace assembly of human serum albumin with the poly(acrylic acid) polyelectrolyte investigated using small angle X-ray scattering (SAXS). <i>Soft Matter</i> , 2020, 16, 9964-9974.	1.2	4
1880	RovC - a novel type of hexameric transcriptional activator promoting type VI secretion gene expression. <i>PLoS Pathogens</i> , 2020, 16, e1008552.	2.1	6
1881	The Aggregation of β -Crystallin under Crowding Conditions Is Prevented by α -Crystallin: Implications for β -Crystallin Stability and Lens Transparency. <i>Journal of Molecular Biology</i> , 2020, 432, 5593-5613.	2.0	12
1882	The influence of proline isomerization on potency and stability of anti-HIV antibody 10E8. <i>Scientific Reports</i> , 2020, 10, 14313.	1.6	12
1883	Structure of phospholipase C μ reveals an integrated RA1 domain and previously unidentified regulatory elements. <i>Communications Biology</i> , 2020, 3, 445.	2.0	9
1884	Solution Structures and Dynamic Assembly of the 24-Meric Plasmodial Pdx1 α -Pdx2 Complex. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5971.	1.8	3
1885	Crystal structure of GCN5 PCAF N-terminal domain reveals atypical ubiquitin ligase structure. <i>Journal of Biological Chemistry</i> , 2020, 295, 14630-14639.	1.6	8
1886	Structural Characterization of Covalently Stabilized Human Cystatin C Oligomers. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5860.	1.8	3
1887	A novel function of Mycobacterium α -tuberculosis chaperonin paralog GroEL1 in copper homeostasis. <i>FEBS Letters</i> , 2020, 594, 3305-3323.	1.3	9
1888	Structural insights of the enzymes from the chitin utilization locus of <i>Flavobacterium johnsoniae</i> . <i>Scientific Reports</i> , 2020, 10, 13775.	1.6	9
1889	Posttranscriptional site-directed spin labeling of large RNAs with an unnatural base pair system under non-denaturing conditions. <i>Chemical Science</i> , 2020, 11, 9655-9664.	3.7	16
1890	BAK core dimers bind lipids and can be bridged by them. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 1024-1031.	3.6	49
1891	Hybrid Biopolymer and Lipid Nanoparticles with Improved Transfection Efficacy for mRNA. <i>Cells</i> , 2020, 9, 2034.	1.8	57
1892	Evidence that immunization with TP0751, a bipartite <i>Treponema pallidum</i> lipoprotein with an intrinsically disordered region and lipocalin fold, fails to protect in the rabbit model of experimental syphilis. <i>PLoS Pathogens</i> , 2020, 16, e1008871.	2.1	16
1893	Allosteric regulation of lysosomal enzyme recognition by the cation-independent mannose 6-phosphate receptor. <i>Communications Biology</i> , 2020, 3, 498.	2.0	20
1894	A rationally identified marine GH1 β -glucosidase has distinguishing functional features for simultaneous saccharification and fermentation. <i>Biofuels, Bioproducts and Biorefining</i> , 2020, 14, 1163-1179.	1.9	5
1895	Solution Structure of the Detergent α -Photosystem II Core Complex Investigated by Small-Angle Scattering Techniques. <i>Journal of Physical Chemistry B</i> , 2020, 124, 8583-8592.	1.2	13
1896	The Non-Fibrillating N-Terminal of β -Synuclein Binds and Co-Fibrillates with Heparin. <i>Biomolecules</i> , 2020, 10, 1192.	1.8	6

#	ARTICLE	IF	CITATIONS
1897	Heat induces end to end repetitive association in <i>P. furiosus</i> l-asparaginase which enables its thermophilic property. <i>Scientific Reports</i> , 2020, 10, 21702.	1.6	8
1898	New exploration of the β -gliadin structure through its partial hydrolysis. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 654-664.	3.6	6
1899	Oligomers, fibrils and aggregates formed by alpha-synuclein: role of solution conditions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, , 1-10.	2.0	2
1900	Modulation of Guanylate Cyclase Activating Protein 1 (GCAP1) Dimeric Assembly by Ca ²⁺ or Mg ²⁺ : Hints to Understand Protein Activity. <i>Biomolecules</i> , 2020, 10, 1408.	1.8	11
1901	Adding Size Exclusion Chromatography (SEC) and Light Scattering (LS) Devices to Obtain High-Quality Small Angle X-Ray Scattering (SAXS) Data. <i>Crystals</i> , 2020, 10, 975.	1.0	48
1902	The intrinsically disordered region of GCE protein adopts a more fixed structure by interacting with the LBD of the nuclear receptor FTZ-F1. <i>Cell Communication and Signaling</i> , 2020, 18, 180.	2.7	8
1903	Structure and functional analysis of the <i>Legionella pneumophila</i> chitinase ChiA reveals a novel mechanism of metal-dependent mucin degradation. <i>PLoS Pathogens</i> , 2020, 16, e1008342.	2.1	29
1904	Structural basis of substrate recognition and catalysis by fucosyltransferase 8. <i>Journal of Biological Chemistry</i> , 2020, 295, 6677-6688.	1.6	19
1905	Btk SH2-kinase interface is critical for allosteric kinase activation and its targeting inhibits B-cell neoplasms. <i>Nature Communications</i> , 2020, 11, 2319.	5.8	23
1906	Structure-Function Studies of the Antibiotic Target <i>l</i> -Diaminopimelate Aminotransferase from <i>Verrucomicrobium spinosum</i> Reveal an Unusual Oligomeric Structure. <i>Biochemistry</i> , 2020, 59, 2274-2288.	1.2	0
1907	Structure of Supramers Formed by the Amphiphile Biotin- <i>CMC</i> -DOPE. <i>ChemistryOpen</i> , 2020, 9, 641-648.	0.9	5
1908	Molecular assemblies built with the artificial protein Pizza. <i>Journal of Structural Biology: X</i> , 2020, 4, 100027.	0.7	10
1909	Structural Analysis of an <i>l</i> -Cysteine Desulfurase from an Ssp DNA Phosphorothioation System. <i>MBio</i> , 2020, 11, .	1.8	8
1910	Different views of the dynamic landscape covered by the 5'-hairpin of the 7SK small nuclear RNA. <i>Rna</i> , 2020, 26, 1184-1197.	1.6	10
1911	Synthesis and Characterization of Novel Nanoporous GI-POSS-Branched Polymeric Gas Separation Membranes. <i>Membranes</i> , 2020, 10, 110.	1.4	9
1912	Silver Composites of Ultradisperse Polytetrafluoroethylene and Its Fractions in Supercritical Carbon Dioxide: Synthesis and Structural Study. <i>Polymer Science - Series B</i> , 2020, 62, 125-136.	0.3	2
1913	Noncanonical inhibition of caspase-3 by a nuclear microRNA confers endothelial protection by autophagy in atherosclerosis. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	88
1914	Crystal structure of the hinge domain of Smchd1 reveals its dimerization mode and nucleic acid-binding residues. <i>Science Signaling</i> , 2020, 13, .	1.6	12

#	ARTICLE	IF	CITATIONS
1915	Structural Diversity of Native Major Ampullate, Minor Ampullate, Cylindriform, and Flagelliform Silk Proteins in Solution. <i>Biomacromolecules</i> , 2020, 21, 3387-3393.	2.6	5
1916	Biotinylated non-ionic amphipols for GPCR ligands screening. <i>Methods</i> , 2020, 180, 69-78.	1.9	6
1917	Exolysin (ExlA) from <i>Pseudomonas aeruginosa</i> Punctures Holes into Target Membranes Using a Molten Globule Domain. <i>Journal of Molecular Biology</i> , 2020, 432, 4466-4480.	2.0	8
1918	Structure and Dynamics of N-Glycosylated Human Ribonuclease 1. <i>Biochemistry</i> , 2020, 59, 3148-3156.	1.2	8
1919	Conformational dynamics modulate the catalytic activity of the molecular chaperone Hsp90. <i>Nature Communications</i> , 2020, 11, 1410.	5.8	50
1920	Structural basis of cell-surface signaling by a conserved sigma regulator in Gram-negative bacteria. <i>Journal of Biological Chemistry</i> , 2020, 295, 5795-5806.	1.6	3
1921	Structural analysis of TIFA: Insight into TIFA-dependent signal transduction in innate immunity. <i>Scientific Reports</i> , 2020, 10, 5152.	1.6	7
1922	Inter- β -inhibitor heavy chain-1 has an integrin-like 3D structure mediating immune regulatory activities and matrix stabilization during ovulation. <i>Journal of Biological Chemistry</i> , 2020, 295, 5278-5291.	1.6	18
1923	A single amino acid substitution uncouples catalysis and allostery in an essential biosynthetic enzyme in <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 6252-6262.	1.6	13
1924	The dimeric organization that enhances the microtubule end-binding affinity of EB1 is susceptible to phosphorylation. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	9
1925	Thermal properties of Ag@Ni core-shell nanoparticles. <i>Calphad: Computer Coupling of Phase Diagrams and Thermochemistry</i> , 2020, 69, 101741.	0.7	8
1926	The Dual PDZ Domain from Postsynaptic Density Protein 95 Forms a Scaffold with Peptide Ligand. <i>Biophysical Journal</i> , 2020, 119, 667-689.	0.2	9
1927	Self-Assembly of Model Amphiphilic Peptides in Nonaqueous Solvents: Changing the Driving Force for Aggregation Does Not Change the Fibril Structure. <i>Langmuir</i> , 2020, 36, 8451-8460.	1.6	7
1928	Characterisation of the Effect of the Spatial Organisation of Hemicellulases on the Hydrolysis of Plant Biomass Polymer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4360.	1.8	5
1929	Missense mutations affecting Ca ²⁺ -coordination in GCAP1 lead to cone-rod dystrophies by altering protein structural and functional properties. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118794.	1.9	7
1930	Structural and Hydrodynamic Characterization of Dimeric Human Oligoadenylate Synthetase 2. <i>Biophysical Journal</i> , 2020, 118, 2726-2740.	0.2	4
1931	Architecture and functional dynamics of the pentafunctional AROM complex. <i>Nature Chemical Biology</i> , 2020, 16, 973-978.	3.9	8
1932	A partially disordered region connects gene repression and activation functions of EZH2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16992-17002.	3.3	36

#	ARTICLE	IF	CITATIONS
1933	Probing remote residues important for catalysis in Escherichia coli ornithine transcarbamoylase. PLoS ONE, 2020, 15, e0228487.	1.1	4
1934	Structural Insights Into the Transcriptional Regulation of HigBA Toxin Antitoxin System by Antitoxin HigA in Pseudomonas aeruginosa. Frontiers in Microbiology, 2019, 10, 3158.	1.5	16
1935	The structural basis of fungal glucuronoyl esterase activity on natural substrates. Nature Communications, 2020, 11, 1026.	5.8	16
1936	Room temperature crystallization of amorphous polysiloxane using photodimerization. Chemical Science, 2020, 11, 3081-3088.	3.7	5
1937	N-terminal domain of the architectural protein CTCF has similar structural organization and ability to self-association in bilaterian organisms. Scientific Reports, 2020, 10, 2677.	1.6	20
1938	Crystal Structure of the Mannose-6-Phosphate Uncovering Enzyme. Structure, 2020, 28, 426-436.e3.	1.6	6
1939	Polymorphic Self-Organization of Lauroyl Peptide in Response to pH and Concentration. Langmuir, 2020, 36, 3941-3951.	1.6	7
1940	Structural basis of the zinc-induced cytoplasmic aggregation of the RNA-binding protein SFPO. Nucleic Acids Research, 2020, 48, 3356-3365.	6.5	19
1941	Nanoscale Structure Determination of Murray Valley Encephalitis and Powassan Virus Non-Coding RNAs. Viruses, 2020, 12, 190.	1.5	12
1942	Tunable Biomimetic Hydrogels from Silk Fibroin and Nanocellulose. ACS Sustainable Chemistry and Engineering, 2020, 8, 2375-2389.	3.2	84
1943	Structural and Biophysical Analysis of the CLCA1 VWA Domain Suggests Mode of TMEM16A Engagement. Cell Reports, 2020, 30, 1141-1151.e3.	2.9	10
1944	Digging deeper: structural background of PEGylated fibrin gels in cell migration and lumenogenesis. RSC Advances, 2020, 10, 4190-4200.	1.7	25
1945	Combined SAXS and computational approaches for structure determination and binding characteristics of Chimera (CtGH1-L1-CtGH5-F194A) generated by assembling β -glucosidase (CtGH1) and a mutant endoglucanase (CtGH5-F194A) from Clostridium thermocellum. International Journal of Biological Macromolecules, 2020, 148, 364-377.	3.6	15
1946	The antioxidant vitamin E as a membrane raft modulator: Tocopherols do not abolish lipid domains. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183189.	1.4	20
1947	Molecular Mechanisms of the Interactions of N-(2-Hydroxypropyl)methacrylamide Copolymers Designed for Cancer Therapy with Blood Plasma Proteins. Pharmaceutics, 2020, 12, 106.	2.0	12
1948	Structural Modeling Using Solution Small-Angle X-ray Scattering (SAXS). Journal of Molecular Biology, 2020, 432, 3078-3092.	2.0	61
1949	Biophysical analysis of Plasmodium falciparum Hsp70-Hsp90 organising protein (PfHop) reveals a monomer that is characterised by folded segments connected by flexible linkers. PLoS ONE, 2020, 15, e0226657.	1.1	12
1950	The BRCA2-MEILB2-BRME1 complex governs meiotic recombination and impairs the mitotic BRCA2-RAD51 function in cancer cells. Nature Communications, 2020, 11, 2055.	5.8	42

#	ARTICLE	IF	CITATIONS
1951	Tetrameric Structures of Inorganic CBS-Pyrophosphatases from Various Bacterial Species Revealed by Small-Angle X-ray Scattering in Solution. <i>Biomolecules</i> , 2020, 10, 564.	1.8	4
1952	Structural features of composite protein-polysaccharide hydrogel in the presence of a carbon nanomaterial. <i>Russian Chemical Bulletin</i> , 2020, 69, 581-589.	0.4	12
1953	Interaction between the scaffold proteins CBP by IQGAP1 provides an interface between gene expression and cytoskeletal activity. <i>Scientific Reports</i> , 2020, 10, 5753.	1.6	6
1954	Solution structure and assembly of Î ² -amylase 2 from <i>Arabidopsis thaliana</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 357-365.	1.1	9
1955	Covalent immobilization of delipidated human serum albumin on poly(pyrrole-2-carboxylic) acid film for the impedimetric detection of perfluorooctanoic acid. <i>Bioelectrochemistry</i> , 2020, 134, 107540.	2.4	16
1956	Quasi-Atomistic Approach to Modeling of Liposomes. <i>Crystallography Reports</i> , 2020, 65, 258-263.	0.1	5
1957	Heat shock protein 90ÅkDa (Hsp90) from <i>Aedes aegypti</i> has an open conformation and is expressed under heat stress. <i>International Journal of Biological Macromolecules</i> , 2020, 156, 522-530.	3.6	5
1958	Avidity within the N-terminal anchor drives Î±synuclein membrane interaction and insertion. <i>FASEB Journal</i> , 2020, 34, 7462-7482.	0.2	28
1959	Photocatalytic properties of supramolecular nanoassociates based on gold and platinum nanoparticles, capped by amphiphilic calix[4]resorcinarenes, towards organic dyes. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2020, 596, 124700.	2.3	9
1960	Allosteric regulation accompanied by oligomeric state changes of <i>Trypanosoma brucei</i> GMP reductase through cystathionine-Î ² -synthase domain. <i>Nature Communications</i> , 2020, 11, 1837.	5.8	10
1961	Structural and functional characterization of the severe fever with thrombocytopenia syndrome virus L protein. <i>Nucleic Acids Research</i> , 2020, 48, 5749-5765.	6.5	44
1962	Structure-based mechanism of preferential complex formation by apoptosis signal-regulating kinases. <i>Science Signaling</i> , 2020, 13, .	1.6	18
1963	Characterization of Tobacco Mosaic Virus Virions and Repolymerized Coat Protein Aggregates in Solution by Small-Angle X-Ray Scattering. <i>Biochemistry (Moscow)</i> , 2020, 85, 310-317.	0.7	6
1964	Structural dynamics in the La-module of La-related proteins. <i>RNA Biology</i> , 2021, 18, 194-206.	1.5	10
1965	Cold and distant: structural features of the nucleoprotein complex of a cold-adapted influenza A virus strain. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 4375-4384.	2.0	1
1966	Shape-function insights into bifunctional <i>O</i> -GlcNAc transferase of <i>Listeria monocytogenes</i> EGD-e. <i>Glycobiology</i> , 2021, 31, 275-287.	1.3	3
1967	PfKsgA1 functions as a transcription initiation factor and interacts with the N-terminal region of the mitochondrial RNA polymerase of <i>Plasmodium falciparum</i> . <i>International Journal for Parasitology</i> , 2021, 51, 23-37.	1.3	2
1968	Recombinant expression, purification and SAXS analysis of <i>Arabidopsis thaliana</i> ClpC1. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 1273-1280.	3.6	1

#	ARTICLE	IF	CITATIONS
1969	A structure-function study of ZraP and ZraS provides new insights into the two-component system Zra. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2021, 1865, 129810.	1.1	6
1970	In-solution structural studies involving a phospholipase A2-like myotoxin and a natural inhibitor: Plasticity of oligomeric assembly affects mechanisms of inhibition. <i>Biochimie</i> , 2021, 181, 145-153.	1.3	7
1971	Ion type and valency differentially drive vimentin tetramers into intermediate filaments or higher order assemblies. <i>Soft Matter</i> , 2021, 17, 870-878.	1.2	8
1973	Structural Characterization and Modeling of a Respiratory Syncytial Virus Fusion Glycoprotein Nanoparticle Vaccine in Solution. <i>Molecular Pharmaceutics</i> , 2021, 18, 359-376.	2.3	12
1974	Multicolor Fluorescent Graphene Oxide Quantum Dots for Sensing Cancer Cell Biomarkers. <i>ACS Applied Nano Materials</i> , 2021, 4, 211-219.	2.4	16
1975	Atomic structure of and valine binding to the regulatory ACT domain of the Mycobacterium tuberculosis Rel protein. <i>FEBS Journal</i> , 2021, 288, 2377-2397.	2.2	4
1977	Structure of the Complete Dimeric Human GDAP1 Core Domain Provides Insights into Ligand Binding and Clustering of Disease Mutations. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 631232.	1.6	11
1979	Comparison of angiotensin-like protein 3 and 4 reveals structural and mechanistic similarities. <i>Journal of Biological Chemistry</i> , 2021, 296, 100312.	1.6	8
1981	In Cellulo Analysis of Huntingtin Inclusion Bodies by Cryogenic Nanoprobe SAXS. <i>ChemSystemsChem</i> , 2021, 3, e2000050.	1.1	4
1982	Unique Structural Features of Mammalian NEIL2 DNA Glycosylase Prime Its Activity for Diverse DNA Substrates and Environments. <i>Structure</i> , 2021, 29, 29-42.e4.	1.6	19
1983	Linker histone defines structure and self-association behaviour of the 177Åbp human chromatosome. <i>Scientific Reports</i> , 2021, 11, 380.	1.6	16
1984	A molecular mechanism for LINC complex branching by structurally diverse SUN-KASH 6:6 assemblies. <i>ELife</i> , 2021, 10, .	2.8	25
1986	Poly(Ethylene Glycol)-b-Poly(D,L-Lactide) Nanoparticles as Potential Carriers for Anticancer Drug Oxaliplatin. <i>Molecules</i> , 2021, 26, 602.	1.7	22
1987	A combined evolutionary and structural approach to disclose the primary structural determinants essential for proneurotrophins biological functions. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2891-2904.	1.9	4
1989	Structure of the Mycobacterium tuberculosis cPknF and conformational changes induced in forkhead-associated regulatory domains. <i>Current Research in Structural Biology</i> , 2021, 3, 165-178.	1.1	2
1990	Capturing the Conformational Ensemble of the Mixed Folded Polyglutamine Protein Ataxin-3. <i>Structure</i> , 2021, 29, 70-81.e5.	1.6	8
1991	<i>REGALS</i>: a general method to deconvolve X-ray scattering data from evolving mixtures. <i>IUCr</i> , 2021, 8, 225-237.	1.0	23
1993	Probing Protein Folding with Sequence-Reversed α -Helical Bundles. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1955.	1.8	8

#	ARTICLE	IF	CITATIONS
1994	The allosteric modulation of complement C5 by knob domain peptides. <i>ELife</i> , 2021, 10, .	2.8	21
1995	Structural mechanism of DNA recognition by the p204 HIN domain. <i>Nucleic Acids Research</i> , 2021, 49, 2959-2972.	6.5	11
1996	EGCG binds intrinsically disordered N-terminal domain of p53 and disrupts p53-MDM2 interaction. <i>Nature Communications</i> , 2021, 12, 986.	5.8	77
1997	Structure and mechanism of a phage-encoded SAM lyase revises catalytic function of enzyme family. <i>ELife</i> , 2021, 10, .	2.8	15
1998	Structural analyses of PCNA from the fungal pathogen <i>Candida albicans</i> identify three regions with species-specific conformations. <i>FEBS Letters</i> , 2021, 595, 1328-1349.	1.3	5
1999	Designed folding pathway of modular coiled-coil-based proteins. <i>Nature Communications</i> , 2021, 12, 940.	5.8	14
2000	The Structure of the Potato Virus A Particles Elucidated by Small Angle X-Ray Scattering and Complementary Techniques. <i>Biochemistry (Moscow)</i> , 2021, 86, 230-240.	0.7	3
2001	Granulovirus PK-1 kinase activity relies on a side-to-side dimerization mode centered on the regulatory I±C helix. <i>Nature Communications</i> , 2021, 12, 1002.	5.8	7
2002	The lytic polysaccharide monooxygenase CbpD promotes <i>Pseudomonas aeruginosa</i> virulence in systemic infection. <i>Nature Communications</i> , 2021, 12, 1230.	5.8	57
2003	Restoring size of detonation nanodiamonds from small-angle x-ray scattering of polychromatic synchrotron radiation beam. <i>Journal of Physics: Conference Series</i> , 2021, 1787, 012029.	0.3	2
2004	Thermodynamic stability of <i>hnRNP A1</i> low complexity domain revealed by high-pressure NMR. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 781-791.	1.5	1
2005	Insights into Solution Structures of Photosynthetic Protein Complexes from Small-Angle Scattering Methods. <i>Crystals</i> , 2021, 11, 203.	1.0	11
2006			
2007	An Eight Amino Acid Segment Controls Oligomerization and Preferred Conformation of the two Non-visual Arrestins. <i>Journal of Molecular Biology</i> , 2021, 433, 166790.	2.0	15
2008	The protealysin operon encodes emfourin, a prototype of a novel family of protein metalloprotease inhibitors. <i>International Journal of Biological Macromolecules</i> , 2021, 169, 583-596.	3.6	5
2009	<i>ATSAS 3.0</i> : expanded functionality and new tools for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2021, 54, 343-355.	1.9	512
2010	Dynamics and stability in the maturation of a eukaryotic virus: a paradigm for chemically programmed large-scale macromolecular reorganization. <i>Archives of Virology</i> , 2021, 166, 1547-1563.	0.9	4
2013	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2014-2021.	2.3	13

#	ARTICLE	IF	CITATIONS
2014	Structure of <i>Arabidopsis</i> CESA3 catalytic domain with its substrate UDP-glucose provides insight into the mechanism of cellulose synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	22
2015	Gene Expression, Biochemical Characterization of a sn-1, 3 Extracellular Lipase From <i>Aspergillus niger</i> GZUF36 and Its Model-Structure Analysis. Frontiers in Microbiology, 2021, 12, 633489.	1.5	6
2017	Hallmarks of <i>Alpha-</i> and <i>Betacoronavirus</i> non-structural protein 7+8 complexes. Science Advances, 2021, 7, .	4.7	20
2018	Inference of molecular structure for characterization and improvement of clinical grade immunocytokines. Journal of Structural Biology, 2021, 213, 107696.	1.3	2
2019	Modulation of Human Phenylalanine Hydroxylase by 3-Hydroxyquinolin-2(1H)-One Derivatives. Biomolecules, 2021, 11, 462.	1.8	5
2020	The Interaction Mechanism of Intrinsically Disordered PP2A Inhibitor Proteins ARPP-16 and ARPP-19 With PP2A. Frontiers in Molecular Biosciences, 2021, 8, 650881.	1.6	5
2021	Mechanism of NanR gene repression and allosteric induction of bacterial sialic acid metabolism. Nature Communications, 2021, 12, 1988.	5.8	16
2022	Computational and SAXS-based structure insights of pectin acetyl esterase (CtPae12B) of family 12 carbohydrate esterase from <i>Clostridium thermocellum</i> ATCC 27405. Journal of Biomolecular Structure and Dynamics, 2021, , 1-18.	2.0	3
2023	Simultaneous binding of Guidance Cues NET1 and RGM blocks extracellular NEO1 signaling. Cell, 2021, 184, 2103-2120.e31.	13.5	20
2025	Biophysical characterization of two commercially available preparations of the drug containing <i>Escherichia coli</i> L-Asparaginase 2. Biophysical Chemistry, 2021, 271, 106554.	1.5	9
2026	Elicitation of potent serum neutralizing antibody responses in rabbits by immunization with an HIV-1 clade C trimeric Env derived from an Indian elite neutralizer. PLoS Pathogens, 2021, 17, e1008977.	2.1	4
2027	Structural Insights of <i>Shigella</i> Translocator IpaB and Its Chaperone IpgC in Solution. Frontiers in Cellular and Infection Microbiology, 2021, 11, 673122.	1.8	8
2028	The SARS-CoV-2 unique domain (SUD) of SARS-CoV and SARS-CoV-2 interacts with human Paip1 to enhance viral RNA translation. EMBO Journal, 2021, 40, e102277.	3.5	26
2029	Molecular basis of F-actin regulation and sarcomere assembly via myotilin. PLoS Biology, 2021, 19, e3001148.	2.6	9
2030	Solution and Membrane Interaction Dynamics of <i>Mycobacterium tuberculosis</i> Fatty Acyl-CoA Synthetase FadD13. Biochemistry, 2021, 60, 1520-1532.	1.2	1
2032	Heterologous Expression and Biochemical Characterization of the Human Zinc Transporter 1 (ZnT1) and Its Soluble C-Terminal Domain. Frontiers in Chemistry, 2021, 9, 667803.	1.8	9
2034	Polymer Coatings on Virus-like Particle Nanoreactors at Low Ionic Strength Charge Reversal and Substrate Access. Biomacromolecules, 2021, 22, 2107-2118.	2.6	14
2035	Structural basis for allosteric regulation of Human Topoisomerase α . Nature Communications, 2021, 12, 2962.	5.8	38

#	ARTICLE	IF	CITATIONS
2036	Structural analysis of the SRP Alu domain from <i>Plasmodium falciparum</i> reveals a non-canonical open conformation. <i>Communications Biology</i> , 2021, 4, 600.	2.0	5
2038	Expression and analysis of the SAM-dependent RNA methyltransferase Rsm22 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 840-853.	1.1	7
2039	The DNA binding domain of the <i>Vibrio vulnificus</i> SmcR transcription factor is flexible and binds diverse DNA sequences. <i>Nucleic Acids Research</i> , 2021, 49, 5967-5984.	6.5	7
2040	Structural model of the M7G46 Methyltransferase TrmB in complex with tRNA. <i>RNA Biology</i> , 2021, 18, 2466-2479.	1.5	8
2041	Molecular model of a sensor of two-component signaling system. <i>Scientific Reports</i> , 2021, 11, 10774.	1.6	14
2042	Phylogenetic and Structural Analysis of NIN-Like Proteins With a Type I/II PB1 Domain That Regulates Oligomerization for Nitrate Response. <i>Frontiers in Plant Science</i> , 2021, 12, 672035.	1.7	7
2044	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. <i>Nature Communications</i> , 2021, 12, 2889.	5.8	13
2046	Mechanism for DPY30 and ASH2L intrinsically disordered regions to modulate the MLL/SET1 activity on chromatin. <i>Nature Communications</i> , 2021, 12, 2953.	5.8	21
2047	Structural mechanism for modulation of functional amyloid and biofilm formation by Staphylococcal Bap protein switch. <i>EMBO Journal</i> , 2021, 40, e107500.	3.5	22
2048	3D architecture and structural flexibility revealed in the subfamily of large glutamate dehydrogenases by a mycobacterial enzyme. <i>Communications Biology</i> , 2021, 4, 684.	2.0	3
2049	The <i>Komagataeibacter europaeus</i> GqqA is the prototype of a novel bifunctional N-Acyl-homoserine lactone acylase with prephenate dehydratase activity. <i>Scientific Reports</i> , 2021, 11, 12255.	1.6	4
2050	Small-angle neutron scattering solution structures of NADPH-dependent sulfite reductase. <i>Journal of Structural Biology</i> , 2021, 213, 107724.	1.3	10
2051	Comprehensive and comparative studies on nanocytotoxicity of glyceryl monooleate- and phytantriol-based lipid liquid crystalline nanoparticles. <i>Journal of Nanobiotechnology</i> , 2021, 19, 168.	4.2	7
2052	Structural and Functional Analysis of a Multimodular Hyperthermostable Xylanase-Glucuronoyl Esterase from <i>Caldicellulosiruptor kristjansonii</i> . <i>Biochemistry</i> , 2021, 60, 2206-2220.	1.2	7
2053	Periscope Proteins are variable-length regulators of bacterial cell surface interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
2054	The Molecular Basis for <i>Escherichia coli</i> O157:H7 Phage FAHEc1 Endolysin Function and Protein Engineering to Increase Thermal Stability. <i>Viruses</i> , 2021, 13, 1101.	1.5	10
2055	Structural Rearrangement of Dps-DNA Complex Caused by Divalent Mg and Fe Cations. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6056.	1.8	12
2057	Structural basis for the coiled-coil architecture of human CtIP. <i>Open Biology</i> , 2021, 11, 210060.	1.5	11

#	ARTICLE	IF	CITATIONS
2059	Cross-linked polymer networks based on polysiloxane and nickel \hat{I}^2 -diketonate precursors. <i>Reactive and Functional Polymers</i> , 2021, 164, 104896.	2.0	7
2060	Structural analysis of <i>Mycobacterium tuberculosis</i> M13 metalloprotease Zmp1 open states. <i>Structure</i> , 2021, 29, 709-720.e3.	1.6	3
2061	PlzA is a bifunctional c-di-GMP biosensor that promotes tick and mammalian host-adaptation of <i>Borrelia burgdorferi</i> . <i>PLoS Pathogens</i> , 2021, 17, e1009725.	2.1	8
2062	Analysis of ligand binding and resulting conformational changes in pyrophosphatase NUDT9. <i>FEBS Journal</i> , 2021, 288, 6769-6782.	2.2	4
2063	Surface modification of silica nanoparticles by hexarhenium anionic cluster complexes for pH-sensing and staining of cell nuclei. <i>Journal of Colloid and Interface Science</i> , 2021, 594, 759-769.	5.0	9
2064	14-3-3-protein regulates Nedd4-2 by modulating interactions between HECT and WW domains. <i>Communications Biology</i> , 2021, 4, 899.	2.0	27
2065	Structural Modeling of the <i>Treponema pallidum</i> Outer Membrane Protein Repertoire: a Road Map for Deconvolution of Syphilis Pathogenesis and Development of a Syphilis Vaccine. <i>Journal of Bacteriology</i> , 2021, 203, e0008221.	1.0	20
2066	SMCHD1's ubiquitin-like domain is required for N-terminal dimerization and chromatin localization. <i>Biochemical Journal</i> , 2021, 478, 2555-2569.	1.7	2
2067	Solution Structure of the dATP-Inactivated Class I Ribonucleotide Reductase From <i>Leeuwenhoekella blandensis</i> by SAXS and Cryo-Electron Microscopy. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 713608.	1.6	2
2068	Notchâ€“Jagged signaling complex defined by an interaction mosaic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	12
2069	Almost half of the RTX domain is dispensable for complement receptor 3 binding and cell-invasive activity of the <i>Bordetella adenylate cyclase</i> toxin. <i>Journal of Biological Chemistry</i> , 2021, 297, 100833.	1.6	7
2071	The Ambiguity Issue in Solving Inverse Problems of Small-Angle Scattering: A Consistent Approach Using an Insulin Receptor-Related Receptor as an Example. <i>Methods for Interpreting SAXS Data. Biochemistry (Moscow) Supplement Series A: Membrane and Cell Biology</i> , 2021, 15, 270-283.	0.3	0
2073	Conformational flexibility of EptA driven by an interdomain helix provides insights for enzymeâ€“substrate recognition. <i>IUCr</i> , 2021, 8, 732-746.	1.0	5
2074	TSC1 binding to lysosomal PIPs is required for TSC complex translocation and mTORC1 regulation. <i>Molecular Cell</i> , 2021, 81, 2705-2721.e8.	4.5	25
2075	<i>Salmonella enterica</i> BcfH Is a Trimeric Thioredoxin-Like Bifunctional Enzyme with Both Thiol Oxidase and Disulfide Isomerase Activities. <i>Antioxidants and Redox Signaling</i> , 2021, 35, 21-39.	2.5	7
2076	Structure and dynamics of the quaternary <i>hunchback</i> mRNA translation repression complex. <i>Nucleic Acids Research</i> , 2021, 49, 8866-8885.	6.5	4
2077	14-3-3 proteins inactivate DAPK2 by promoting its dimerization and protecting key regulatory phosphosites. <i>Communications Biology</i> , 2021, 4, 986.	2.0	19
2078	A Structural and Dynamic Analysis of the Partially Disordered Polymerase-Binding Domain in RSV Phosphoprotein. <i>Biomolecules</i> , 2021, 11, 1225.	1.8	6

#	ARTICLE	IF	CITATIONS
2079	Osmosensing by WNK Kinases. <i>Molecular Biology of the Cell</i> , 2021, 32, 1614-1623.	0.9	16
2080	Structural basis of meiotic chromosome synaptic elongation through hierarchical fibrous assembly of SYCE2-TEX12. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 681-693.	3.6	23
2081	Transient and stabilized complexes of Nsp7, Nsp8, and Nsp12 in SARS-CoV-2 replication. <i>Biophysical Journal</i> , 2021, 120, 3152-3165.	0.2	39
2082	Interaction mechanism of endogenous PP2A inhibitor protein ENSA with PP2A. <i>FEBS Journal</i> , 2022, 289, 519-534.	2.2	3
2083	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	2.1	19
2084	A fragment-based approach identifies an allosteric pocket that impacts malate dehydrogenase activity. <i>Communications Biology</i> , 2021, 4, 949.	2.0	2
2085	BonA from <i>Acinetobacter baumannii</i> Forms a Divisome-Localized Decamer That Supports Outer Envelope Function. <i>MBio</i> , 2021, 12, e0148021.	1.8	5
2086	Dependence of the Nanoscale Composite Morphology of Fe ₃ O ₄ Nanoparticle-Infused Lysozyme Amyloid Fibrils on Timing of Infusion: A Combined SAXS and AFM Study. <i>Molecules</i> , 2021, 26, 4864.	1.7	2
2087	X-shaped structure of bacterial heterotetrameric tRNA synthetase suggests cryptic prokaryote functions and a rationale for synthetase classifications. <i>Nucleic Acids Research</i> , 2021, 49, 10106-10119.	6.5	12
2088	Choice of force fields and water models for sampling solution conformations of bacteriophage T4 lysozyme. <i>Chinese Journal of Chemical Physics</i> , 2021, 34, 487-496.	0.6	0
2089	Structural basis for ALK2/BMP2 receptor complex signaling through kinase domain oligomerization. <i>Nature Communications</i> , 2021, 12, 4950.	5.8	15
2090	The effect of chemical structure of carboxylate molecules on hydroxyapatite nanoparticles. A structural and morphological study. <i>Bioactive Materials</i> , 2021, 6, 2360-2371.	8.6	6
2091	Structural basis for diguanylate cyclase activation by its binding partner in <i>Pseudomonas aeruginosa</i> . <i>ELife</i> , 2021, 10, .	2.8	8
2092	Reciprocal allostery arising from a bienzyme assembly controls aromatic amino acid biosynthesis in <i>Prevotella nigrescens</i> . <i>Journal of Biological Chemistry</i> , 2021, 297, 101038.	1.6	2
2094	Molecular mechanism of quorum sensing inhibition in <i>Streptococcus</i> by the phage protein paratox. <i>Journal of Biological Chemistry</i> , 2021, 297, 100992.	1.6	1
2095	Structure and thermodynamics of transient protein-protein complexes by chemometric decomposition of SAXS datasets. <i>Structure</i> , 2021, 29, 1074-1090.e4.	1.6	7
2096	Molecular mechanism of interactions between ACAD9 and binding partners in mitochondrial respiratory complex I assembly. <i>IScience</i> , 2021, 24, 103153.	1.9	13
2097	A Structural Study of the Cytoplasmic Chaperone Effect of 14-3-3 Proteins on Ataxin-1. <i>Journal of Molecular Biology</i> , 2021, 433, 167174.	2.0	7

#	ARTICLE	IF	CITATIONS
2098	High Conformational Flexibility of the E2F1/DP1/DNA Complex. <i>Journal of Molecular Biology</i> , 2021, 433, 167119.	2.0	4
2099	Mechanism of activation and regulation of deubiquitinase activity in MINDY1 and MINDY2. <i>Molecular Cell</i> , 2021, 81, 4176-4190.e6.	4.5	18
2100	Structure and SAXS studies unveiled a novel inhibition mechanism of the <i>Pseudomonas aeruginosa</i> T6SS TseT-TsiT complex. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 450-459.	3.6	4
2101	The Jo-In protein welding system is a relevant tool to create CBM-containing plant cell wall degrading enzymes. <i>New Biotechnology</i> , 2021, 65, 31-41.	2.4	5
2102	Conformational Changes of ROR β During Response Element Recognition and Coregulator Engagement. <i>Journal of Molecular Biology</i> , 2021, 433, 167258.	2.0	4
2103	BthTX-II from <i>Bothrops jararacussu</i> venom has variants with different oligomeric assemblies: An example of snake venom phospholipases A2 versatility. <i>International Journal of Biological Macromolecules</i> , 2021, 191, 255-266.	3.6	6
2104	Unveiling the structure of the primary caseinate particle using small-angle X-ray scattering and simulation methodologies. <i>Food Research International</i> , 2021, 149, 110653.	2.9	9
2105	Structure and dynamics of UBA5-UFM1 complex formation showing new insights in the UBA5 activation mechanism. <i>Journal of Structural Biology</i> , 2021, 213, 107796.	1.3	2
2106	First electrochemical synthesis of mesoporous RhNi alloy films for an alkali-mediated hydrogen evolution reaction. <i>Journal of Materials Chemistry A</i> , 2021, 9, 2754-2763.	5.2	25
2107	Structure of transmembrane prolyl 4-hydroxylase reveals unique organization of EF and dioxygenase domains. <i>Journal of Biological Chemistry</i> , 2021, 296, 100197.	1.6	7
2108	A Dimerization Site at SCR-17/18 in Factor H Clarifies a New Mechanism for Complement Regulatory Control. <i>Frontiers in Immunology</i> , 2020, 11, 601895.	2.2	3
2109	Crystal structures of the EVE-HNH endonuclease VcaM4I in the presence and absence of DNA. <i>Nucleic Acids Research</i> , 2021, 49, 1708-1723.	6.5	4
2110	Small-Angle Neutron Scattering of RNA-Protein Complexes. <i>Methods in Molecular Biology</i> , 2020, 2113, 165-188.	0.4	10
2111	Use of Small-Angle X-ray Scattering to Investigate the Structure and Function of Dengue Virus NS3 and NS5. <i>Methods in Molecular Biology</i> , 2014, 1138, 241-252.	0.4	8
2112	Small-Angle X-Ray Scattering to Obtain Models of Multivalent Lectin-Glycan Complexes. <i>Methods in Molecular Biology</i> , 2014, 1200, 511-526.	0.4	4
2113	High-Throughput Studies of Protein Shapes and Interactions by Synchrotron Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2015, 1261, 277-301.	0.4	7
2114	Small Angle X-ray Scattering (SAXS) Characterization of the POTRA Domains of BamA. <i>Methods in Molecular Biology</i> , 2015, 1329, 149-155.	0.4	1
2115	Small-Angle Scattering and Neutron Contrast Variation for Studying Bio-Molecular Complexes. <i>Methods in Molecular Biology</i> , 2009, 544, 307-323.	0.4	45

#	ARTICLE	IF	CITATIONS
2116	Exploring RNA Oligomerization and Ligand Binding by Fluorescence Correlation Spectroscopy and Small Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2014, 1086, 321-334.	0.4	1
2117	Synchrotron Small-Angle X-Ray Scattering on Biological Macromolecules in Solution. , 2020, , 1645-1672.		2
2118	Protein Shape and Assembly Studied with X-Ray Solution Scattering: Fundamentals and Practice. <i>Lecture Notes in Physics</i> , 2009, , 245-263.	0.3	2
2119	Current limits of structural biology: The transient interaction between cytochrome c and photosystem I. <i>Current Research in Structural Biology</i> , 2020, 2, 171-179.	1.1	13
2120	Exaptation of two ancient immune proteins into a new dimeric pore-forming toxin in snails. <i>Journal of Structural Biology</i> , 2020, 211, 107531.	1.3	5
2121	Structural characterization of aqueous magnetic fluids with nanomagnetite of different origin stabilized by sodium oleate. <i>Journal of Molecular Liquids</i> , 2020, 312, 113430.	2.3	10
2122	On the structure and function of Sorghum bicolor CHIP (carboxyl terminus of Hsc70-interacting) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 5	1.7	2
2123	Structural insights into the mechanism of c-di-GMPâ€‘bound YcgR regulating flagellar motility in Escherichia coli. <i>Journal of Biological Chemistry</i> , 2020, 295, 808-821.	1.6	11
2124	Marfan Syndrome-causing Mutations in Fibrillin-1 Result in Gross Morphological Alterations and Highlight the Structural Importance of the Second Hybrid Domain. <i>Journal of Biological Chemistry</i> , 2006, 281, 31854-31862.	1.6	7
2125	Crystal structures of fukutin-related protein (FKRP), a ribitol-phosphate transferase related to muscular dystrophy. <i>Nature Communications</i> , 2020, 11, 303.	5.8	21
2126	Structure of KCNH2 cyclic nucleotide-binding homology domain reveals a functionally vital salt-bridge. <i>Journal of General Physiology</i> , 2020, 152, .	0.9	7
2127	Self-association and conformational variation of NS5A domain 1 of hepatitis C virus. <i>Journal of General Virology</i> , 2018, 99, 194-208.	1.3	2
2146	The type IV secretion protein TraK from the <i>Enterococcus</i> conjugative plasmid pIP501 exhibits a novel fold. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1124-1135.	2.5	9
2147	The high-intensity option of the SANS diffractometer KWS-2 at JCMS â€‘ characterization and performance of the new multi-megahertz detection system. <i>Journal of Applied Crystallography</i> , 2018, 51, 323-336.	1.9	13
2148	Model-free classification of X-ray scattering signals applied to image segmentation. <i>Journal of Applied Crystallography</i> , 2018, 51, 1378-1386.	1.9	11
2149	Simulation of small-angle X-ray scattering data of biological macromolecules in solution. <i>Journal of Applied Crystallography</i> , 2020, 53, 536-539.	1.9	7
2150	Rapid screening of <i>in cellulo</i> grown protein crystals via a small-angle X-ray scattering/X-ray powder diffraction synergistic approach. <i>Journal of Applied Crystallography</i> , 2020, 53, 1169-1180.	1.9	17
2151	Concentrated protein solutions investigated using acoustic levitation and small-angle X-ray scattering. <i>Journal of Synchrotron Radiation</i> , 2020, 27, 396-404.	1.0	3

#	ARTICLE	IF	CITATIONS
2152	Small-angle neutron scattering studies on the AMPA receptor GluA2 in the resting, AMPA-bound and GYKI-53655-bound states. <i>IUCr</i> , 2018, 5, 780-793.	1.0	9
2153	The structural characterization of a glucosylglycerate hydrolase provides insights into the molecular mechanism of mycobacterial recovery from nitrogen starvation. <i>IUCr</i> , 2019, 6, 572-585.	1.0	16
2154	The atypical thiolâ€“disulfide exchange protein Î±-DsbA2 from <i>Wolbachia pipientis</i> is a homotrimeric disulfide isomerase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 283-295.	1.1	4
2155	Engineered variants provide new insight into the structural properties important for activity of the highly dynamic, trimeric protein disulfide isomerase ScsC from <i>Proteus mirabilis</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 296-307.	1.1	5
2156	Improving data quality and expanding BioSAXS experiments to low-molecular-weight and low-concentration protein samples. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 971-981.	1.1	7
2157	New insights into structure-function relationships of oxalylâ€“CoA decarboxylase from <i>Escherichia coli</i> . <i>FEBS Journal</i> , 2010, 277, 2628-2640.	2.2	18
2158	Effect of Buffer Composition on Conformational Flexibility of N-Terminal Fragments of Dps and the Nature of Interactions with DNA. Small-Angle X-Ray Scattering Study. <i>Crystallography Reports</i> , 2020, 65, 891-899.	0.1	7
2159	The SAXS and Rheological Studies of HEWL Amyloid Formation. <i>Acta Physica Polonica A</i> , 2008, 114, 447-454.	0.2	2
2160	SAXS Study of Influence of Gemini Surfactant, 1,1'-(1,4-butanediyl)bis 3-cyclododecyloxymethylimidazolium di-chloride, on the Fully Hydrated DMPC. <i>Acta Physica Polonica A</i> , 2010, 117, 311-314.	0.2	12
2161	Structural Changes of DPPC Bilayers Induced by Gemini Surfactant. <i>Acta Physica Polonica A</i> , 2012, 121, 893-898.	0.2	4
2162	Structures of the Signal Recognition Particle Receptor from the Archaeon <i>Pyrococcus furiosus</i> : Implications for the Targeting Step at the Membrane. <i>PLoS ONE</i> , 2008, 3, e3619.	1.1	21
2163	The “Phantom Effect” of the Rexinoid LG100754: Structural and Functional Insights. <i>PLoS ONE</i> , 2010, 5, e15119.	1.1	64
2164	Preparation and Characterization of the Extracellular Domain of Human Sid-1. <i>PLoS ONE</i> , 2012, 7, e33607.	1.1	15
2165	Characterization of Multi-Functional Properties and Conformational Analysis of MutS2 from <i>Thermotoga maritima</i> MSB8. <i>PLoS ONE</i> , 2012, 7, e34529.	1.1	7
2166	Crystal, Solution and In silico Structural Studies of Dihydrodipicolinate Synthase from the Common Grapevine. <i>PLoS ONE</i> , 2012, 7, e38318.	1.1	32
2167	Solution Structure of the LIM-Homeodomain Transcription Factor Complex Lhx3/Ldb1 and the Effects of a Pituitary Mutation on Key Lhx3 Interactions. <i>PLoS ONE</i> , 2012, 7, e40719.	1.1	7
2168	Crystal Structure of ATVORF273, a New Fold for a Thermo- and Acido-Stable Protein from the Acidianus Two-Tailed Virus. <i>PLoS ONE</i> , 2012, 7, e45847.	1.1	7
2169	Purification and SAXS Analysis of the Integrin Linked Kinase, PINCH, Parvin (IPP) Heterotrimeric Complex. <i>PLoS ONE</i> , 2013, 8, e55591.	1.1	12

#	ARTICLE	IF	CITATIONS
2170	Structural Insights into the Mechanism of Phosphoregulation of the Retinoblastoma Protein. PLoS ONE, 2013, 8, e58463.	1.1	14
2171	Structural Plasticity in Human Heterochromatin Protein 1 ¹² . PLoS ONE, 2013, 8, e60887.	1.1	24
2172	The Carboxy-Terminal Î±N Helix of the Archaeal XerA Tyrosine Recombinase Is a Molecular Switch to Control Site-Specific Recombination. PLoS ONE, 2013, 8, e63010.	1.1	21
2173	Hinged Plakin Domains Provide Specialized Degrees of Articulation in Envoplakin, Periplakin and Desmoplakin. PLoS ONE, 2013, 8, e69767.	1.1	18
2174	Insights into the Cross-Immunity Mechanism within Effector Families of Bacteria Type VI Secretion System from the Structure of StTae4-EcTat4 Complex. PLoS ONE, 2013, 8, e73782.	1.1	11
2175	Small Angle X-Ray Scattering Studies of Mitochondrial Glutaminase C Reveal Extended Flexible Regions, and Link Oligomeric State with Enzyme Activity. PLoS ONE, 2013, 8, e74783.	1.1	29
2176	Distinct Structural Features of the Peroxide Response Regulator from Group A Streptococcus Drive DNA Binding. PLoS ONE, 2014, 9, e89027.	1.1	13
2177	Activation of 2 ^{â€²} 5 ^{â€²} -Oligoadenylate Synthetase by Stem Loops at the 5 ^{â€²} -End of the West Nile Virus Genome. PLoS ONE, 2014, 9, e92545.	1.1	43
2178	Low-Resolution Structure of the Full-Length Barley (<i>Hordeum vulgare</i>) SGT1 Protein in Solution, Obtained Using Small-Angle X-Ray Scattering. PLoS ONE, 2014, 9, e93313.	1.1	9
2179	The Structural and Functional Basis of Catalysis Mediated by NAD(P)H:acceptor Oxidoreductase (FerB) of <i>Paracoccus denitrificans</i> . PLoS ONE, 2014, 9, e96262.	1.1	22
2180	Calponin-Like Chd64 Is Partly Disordered. PLoS ONE, 2014, 9, e96809.	1.1	10
2181	Structural Studies of an Anti-Inflammatory Lectin from <i>Canavalia boliviana</i> Seeds in Complex with Dimannosides. PLoS ONE, 2014, 9, e97015.	1.1	22
2182	Structural and Biochemical Characterization of Human PR70 in Isolation and in Complex with the Scaffolding Subunit of Protein Phosphatase 2A. PLoS ONE, 2014, 9, e101846.	1.1	14
2183	Structural Characterization of the <i>Saccharomyces cerevisiae</i> THO Complex by Small-Angle X-Ray Scattering. PLoS ONE, 2014, 9, e103470.	1.1	3
2184	Dissecting the Functional Role of the N-Terminal Domain of the Human Small Heat Shock Protein HSPB6. PLoS ONE, 2014, 9, e105892.	1.1	33
2185	Small-Angle X-Ray Scattering Reveals Compact Domain-Domain Interactions in the N-Terminal Region of Filamin C. PLoS ONE, 2014, 9, e107457.	1.1	11
2186	Molecular Insights into the Interaction between <i>Plasmodium falciparum</i> Apical Membrane Antigen 1 and an Invasion-Inhibitory Peptide. PLoS ONE, 2014, 9, e109674.	1.1	10
2187	Flexible Structure of Peptide-Bound Filamin A Mechanosensor Domain Pair 20 ^{â€²} 21. PLoS ONE, 2015, 10, e0136969.	1.1	13

#	ARTICLE	IF	CITATIONS
2188	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. PLoS ONE, 2015, 10, e0140219.	1.1	3
2189	Biophysical Characterization of G-Quadruplex Recognition in the PITX1 mRNA by the Specificity Domain of the Helicase RHAU. PLoS ONE, 2015, 10, e0144510.	1.1	19
2190	Structure of the Intermediate Filament-Binding Region of Desmoplakin. PLoS ONE, 2016, 11, e0147641.	1.1	20
2191	Structures of Two Melanoma-Associated Antigens Suggest Allosteric Regulation of Effector Binding. PLoS ONE, 2016, 11, e0148762.	1.1	26
2192	Structure of a Bacterial Virus DNA-Injection Protein Complex Reveals a Decameric Assembly with a Constricted Molecular Channel. PLoS ONE, 2016, 11, e0149337.	1.1	19
2193	Intrinsic Disorder of the C-Terminal Domain of Drosophila Methoprene-Tolerant Protein. PLoS ONE, 2016, 11, e0162950.	1.1	8
2194	Biophysical Studies of the Induced Dimerization of Human VEGF Receptor 1 Binding Domain by Divalent Metals Competing with VEGF-A. PLoS ONE, 2016, 11, e0167755.	1.1	10
2195	Impact of the structural integrity of the three-way junction of adenovirus VAI RNA on PKR inhibition. PLoS ONE, 2017, 12, e0186849.	1.1	19
2196	Iron-induced oligomerization of human FXN81-210 and bacterial CyaY frataxin and the effect of iron chelators. PLoS ONE, 2017, 12, e0188937.	1.1	16
2197	SAXS studies of X-ray induced disulfide bond damage: Engineering high-resolution insight from a low-resolution technique. PLoS ONE, 2020, 15, e0239702.	1.1	9
2198	Characterization of binding between model protein GA-Z and human serum albumin using asymmetrical flow field-flow fractionation and small angle X-ray scattering. PLoS ONE, 2020, 15, e0242605.	1.1	4
2199	Atomic Structure and Biochemical Characterization of an RNA Endonuclease in the N Terminus of Andes Virus L Protein. PLoS Pathogens, 2016, 12, e1005635.	2.1	31
2200	Long non-coding subgenomic flavivirus RNAs have extended 3D structures and are flexible in solution. EMBO Reports, 2019, 20, e47016.	2.0	33
2201	KAP1 is an antiparallel dimer with a functional asymmetry. Life Science Alliance, 2019, 2, e201900349.	1.3	16
2202	Fluorescence detection system based on silicon quantum dots-polysilane nanocomposites. EXPRESS Polymer Letters, 2016, 10, 990-1002.	1.1	10
2203	Human DDX17 Unwinds Rift Valley Fever Virus Non-Coding RNAs. International Journal of Molecular Sciences, 2021, 22, 54.	1.8	20
2204	Biochemical and Biophysical Characterization of the dsDNA Packaging Motor from the Lactococcus lactis Bacteriophage Ascphi28. Viruses, 2021, 13, 15.	1.5	6
2205	Phospholipases A2 Protein Structure and Natural Products Interactions in Development of New Pharmaceuticals. , 0, , .		2

#	ARTICLE	IF	CITATIONS
2206	Phosphorylation-mediated PTEN conformational closure and deactivation revealed with protein semisynthesis. <i>ELife</i> , 2013, 2, e00691.	2.8	89
2207	Crystal structures of the CPAP/STIL complex reveal its role in centriole assembly and human microcephaly. <i>ELife</i> , 2013, 2, e01071.	2.8	90
2208	Molecular mechanism of Aurora A kinase autophosphorylation and its allosteric activation by TPX2. <i>ELife</i> , 2014, 3, e02667.	2.8	112
2209	Molecular mechanism for Rabex-5 GEF activation by Rabaptin-5. <i>ELife</i> , 2014, 3, .	2.8	47
2210	Structural basis for ligand and innate immunity factor uptake by the trypanosome haptoglobin-haemoglobin receptor. <i>ELife</i> , 2014, 3, e05553.	2.8	49
2211	Coincidence detection and bi-directional transmembrane signaling control a bacterial second messenger receptor. <i>ELife</i> , 2016, 5, .	2.8	23
2212	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. <i>ELife</i> , 2017, 6, .	2.8	51
2213	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. <i>ELife</i> , 2019, 8, .	2.8	47
2214	The guide sRNA sequence determines the activity level of box C/D RNPs. <i>ELife</i> , 2020, 9, .	2.8	10
2215	Structure of dual BON-domain protein DolP identifies phospholipid binding as a new mechanism for protein localisation. <i>ELife</i> , 2020, 9, .	2.8	25
2216	Ammonium hydroxide treatment of Al^{12} produces an aggregate free solution suitable for biophysical and cell culture characterization. <i>PeerJ</i> , 2013, 1, e73.	0.9	93
2217	New insights into human hair: SAXS, SEM, TEM and EDX for Alopecia Areata investigations. <i>PeerJ</i> , 2020, 8, e8376.	0.9	7
2218	Searching for an Efficient Solution Reconstruction Algorithm in the Analysis of Small-Angle Scattering Data from Silicasol Solution. <i>Crystallography Reports</i> , 2021, 66, 758-764.	0.1	0
2219	Formation of High-Order Structures in Solution by CBS-Pyrophosphatase from <i>D. hafniense</i> . <i>Crystallography Reports</i> , 2021, 66, 833-839.	0.1	1
2220	Copper-Induced Oligomerization of Ceruloplasmin. <i>Crystallography Reports</i> , 2021, 66, 828-832.	0.1	3
2221	Influence of Chlorides of Mono- and Divalent Metals on the Oligomeric Composition of Lysozyme Crystallization Solutions and Further Crystal Growth. <i>Crystallography Reports</i> , 2021, 66, 751-757.	0.1	4
2222	Insight into the Binding and Hydrolytic Preferences of hNudt16 Based on Nucleotide Diphosphate Substrates. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10929.	1.8	6
2223	ROR and RYK extracellular region structures suggest that receptor tyrosine kinases have distinct WNT-recognition modes. <i>Cell Reports</i> , 2021, 37, 109834.	2.9	13

#	ARTICLE	IF	CITATIONS
2226	Small-angle X-ray and neutron scattering. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	77
2227	The USR domain of USF1 mediates NF-Y interactions and cooperative DNA binding. <i>International Journal of Biological Macromolecules</i> , 2021, 193, 401-413.	3.6	0
2228	¹¹ C-radiolabeled aptamer for imaging of tumors and metastases using positron emission tomography-computed tomography. <i>Molecular Therapy - Nucleic Acids</i> , 2021, 26, 1159-1172.	2.3	11
2229	The Cytoplasmic Tail of Influenza A Virus Hemagglutinin and Membrane Lipid Composition Change the Mode of M1 Protein Association with the Lipid Bilayer. <i>Membranes</i> , 2021, 11, 772.	1.4	8
2230	DNA crosslinking and recombination-activating genes 1/2 (RAG1/2) are required for oncogenic splicing in acute lymphoblastic leukemia. <i>Cancer Communications</i> , 2021, 41, 1116-1136.	3.7	7
2231	Role of Neto1 extracellular domain in modulation of kainate receptors. <i>International Journal of Biological Macromolecules</i> , 2021, 192, 525-536.	3.6	4
2233	Low Resolution Structure of RAR1-GST-Tag Fusion Protein in Solution. <i>Acta Physica Polonica A</i> , 2010, 117, 307-310.	0.2	0
2234	Investigating RNAs Involved in Translational Control by NMR and SAXS. , 2012, , 141-172.		0
2236	SAXS and SANS Investigation of Synthetic Cholesteric Liquid-Crystal Polymers for Biomedical Applications. <i>Journal of Materials Science and Engineering B</i> , 2013, 3, .	0.2	1
2237	Integrated Structural Biology in Combination with SAXS Analysis for Biological Macromolecules. <i>Nihon Kessho Gakkaishi</i> , 2014, 56, 247-252.	0.0	0
2238	Small Angle X-Ray Scattering (SAXS) with Synchrotron Radiation Sources. , 2015, , 337-359.		5
2239	Structural Studies of a Double-Stranded RNA from Trypanosome RNA Editing by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2015, 1240, 165-189.	0.4	2
2240	Synchrotron Small-Angle X-Ray Scattering on Biological Macromolecules in Solution. , 2015, , 1-25.		0
2241	Synchrotron Small-Angle X-Ray Scattering on Biological Macromolecules in Solution. , 2016, , 1393-1420.		0
2248	Sizes and size distributions of nanoparticles: Causes of differences in results obtained by transmission electron microscopy and small angle X-ray scattering. <i>Nanosystems: Physics, Chemistry, Mathematics</i> , 2017, , 512-522.	0.2	0
2252	Scalable Geometrically Designed Protein Cages Assembled via Genetically Encoded Split Inteins. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2253	Pathogenic TFG Mutations Underlying Hereditary Spastic Paraplegia Impair Secretory Protein Trafficking and Axon Fasciculation. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
2256	Molecular Mechanism of the Strong Cell-Adhesion by Cadherin-23. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1

#	ARTICLE	IF	CITATIONS
2268	Scientific Literature of Small-Angle X-Ray and Neutron Scattering Applied to the Characterization of Materials at the Nanometer Scale. <i>Materials Research</i> , 2019, 22, .	0.6	0
2293	Oligomerization of <i>A. thaliana</i> Heterotrimeric G Protein Subunits AGB1 and AGG2 In Vitro. <i>Protein Journal</i> , 2020, 39, 563-573.	0.7	1
2296	Kinetic proofreading of lipochitooligosaccharides determines signal activation of symbiotic plant receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
2297	Uranyl-Binding Proteins on Silica Nanoparticles for Repeatable Capture of Uranyl Ions. <i>ACS Applied Nano Materials</i> , 2021, 4, 11801-11808.	2.4	3
2298	The Disease Associated Tau35 Fragment has an Increased Propensity to Aggregate Compared to Full-Length Tau. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 779240.	1.6	8
2300	Approaches for improving the quality of particle size distribution reconstructions from small-angle scattering data. <i>Journal of Physics: Conference Series</i> , 2020, 1686, 012059.	0.3	0
2302	Molecular dynamics simulation combined with small-angle X-ray/neutron scattering defining <sc>solution state</sc> protein structures. <i>Journal of the Chinese Chemical Society</i> , 2021, 68, 403-408.	0.8	2
2303	Gain-of-Function Variant p.Pro2555Arg of von Willebrand Factor Increases Aggregate Size through Altering Stem Dynamics. <i>Thrombosis and Haemostasis</i> , 2020, , .	1.8	3
2306	The <i>Candida glabrata</i> glycogen branching enzyme structure reveals unique features of branching enzymes of the <i>Saccharomycetaceae</i> phylum. <i>Glycobiology</i> , 2022, 32, 343-355.	1.3	2
2312	A bacteriophage mimic of the bacterial nucleoid-associated protein Fis. <i>Biochemical Journal</i> , 2020, 477, 1345-1362.	1.7	2
2313	Pseudoknot length modulates the folding, conformational dynamics, and robustness of Xrn1 resistance of flaviviral xrRNAs. <i>Nature Communications</i> , 2021, 12, 6417.	5.8	15
2314	Zn(II) binding causes interdomain changes in the structure and flexibility of the human prion protein. <i>Scientific Reports</i> , 2021, 11, 21703.	1.6	8
2315	Multimerization of small G-protein H-Ras induced by chemical modification at hyper variable region with caged compound. <i>Journal of Biochemistry</i> , 2022, 171, 215-225.	0.9	0
2316	The Structural Features of Native Fibrin and Its Conjugates with Polyethylene Glycol and Vascular Endothelial Growth Factor according to Small-Angle X-Ray Scattering. <i>Reviews and Advances in Chemistry</i> , 2020, 10, 158-163.	0.2	0
2317	3D MACROMOLECULAR STRUCTURE ANALYSES: APPLICATIONS IN PLANT PROTEINS. , 2007, , 141-151.		0
2329	Combined Scheme of Reconstruction of the Particle Size Distribution Function Using Small-Angle Scattering Data. <i>JETP Letters</i> , 2020, 112, 591-595.	0.4	2
2330	A Structural Basis for Inhibition of the Complement Initiator Protease C1r by Lyme Disease Spirochetes. <i>Journal of Immunology</i> , 2021, 207, 2856-2867.	0.4	11
2331	<sc>EFAMIX</sc>, a tool to decompose inline chromatography <sc>SAXS</sc> data from partially overlapping components. <i>Protein Science</i> , 2022, 31, 269-282.	3.1	16

#	ARTICLE	IF	CITATIONS
2332	Probing the existence of non-thermal Terahertz radiation induced changes of the protein solution structure. <i>Scientific Reports</i> , 2021, 11, 22311.	1.6	4
2333	Methods for Small-Angle Scattering Measurements on Peptiplexes of DNA with Cell-Penetrating Peptides. <i>Methods in Molecular Biology</i> , 2022, 2383, 181-196.	0.4	2
2335	Actinobacteria challenge the paradigm: A unique protein architecture for a well-known, central metabolic complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
2336	Combination of high throughput and structural screening to assess protein stability â€“ A screening perspective. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2022, 171, 1-10.	2.0	5
2337	Long-range distance determination in fully deuterated RNA with pulsed EPR spectroscopy. <i>Biophysical Journal</i> , 2022, 121, 37-43.	0.2	12
2338	The catalytic activity of TCPTP is auto-regulated by its intrinsically disordered tail and activated by Integrin alpha-1. <i>Nature Communications</i> , 2022, 13, 94.	5.8	16
2339	Upgrade of the BioMUR beamline at the Kurchatov synchrotron radiation source for serial small-angle X-ray scattering experiments in solutions. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2022, 1025, 166170.	0.7	7
2340	Stable aqueous dispersions of bare and double layer functionalized superparamagnetic iron oxide nanoparticles for biomedical applications. <i>Materials Science-Poland</i> , 2021, 39, 331-345.	0.4	5
2341	Centrosome dysfunction associated with somatic expression of the synaptonemal complex protein TEX12. <i>Communications Biology</i> , 2021, 4, 1371.	2.0	10
2342	Intricate coupling between the transactivation and basic-leucine zipper domains governs phosphorylation of transcription factor ATF4 by casein kinase 2. <i>Journal of Biological Chemistry</i> , 2022, , 101633.	1.6	2
2343	Teneurin4 dimer structures reveal a calciumâ€“stabilized compact conformation supporting homomeric transâ€“interactions. <i>EMBO Journal</i> , 2022, 41, e107505.	3.5	6
2344	The low-resolution structural models of hepatitis C virus RNA subdomain 5BSL3.2 and its distal complex with domain 3â€“X point to conserved regulatory mechanisms within the Flaviviridae family. <i>Nucleic Acids Research</i> , 2022, , .	6.5	8
2345	Binary Silicone Elastomeric Systems with Stepwise Crosslinking as a Tool for Tuning Electromechanical Behavior. <i>Polymers</i> , 2022, 14, 211.	2.0	1
2346	The structure and function of modular <i>Escherichia coli</i> O157:H7 bacteriophage FTBEc1 endolysin, LysT84: defining a new endolysin catalytic subfamily. <i>Biochemical Journal</i> , 2022, 479, 207-223.	1.7	5
2347	Structural and biochemical characterization of the relaxosome auxiliary proteins encoded on the <i>Bacillus subtilis</i> plasmid pLS20. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 757-765.	1.9	0
2348	Open-Bundle Structure as the Unfolding Intermediate of Cytochrome câ€“2 Revealed by Small Angle Neutron Scattering. <i>Biomolecules</i> , 2022, 12, 95.	1.8	0
2349	Oligomerization engineering of the fluorinase enzyme leads to an active trimer that supports synthesis of fluorometabolites <i>in vitro</i> . <i>Microbial Biotechnology</i> , 2022, 15, 1622-1632.	2.0	7
2350	Latent TGFÎ² complexes are transglutaminase cross-linked to fibrillin to facilitate TGFÎ² activation. <i>Matrix Biology</i> , 2022, 107, 24-39.	1.5	9

#	ARTICLE	IF	CITATIONS
2351	A FRET-Based Biosensor for the Src N-Terminal Regulatory Element. <i>Biosensors</i> , 2022, 12, 96.	2.3	1
2353	The first structure–function study of GH151 α -mannosidase uncovers new oligomerization pattern, active site complementation, and selective substrate specificity. <i>FEBS Journal</i> , 2022, 289, 4998-5020.	2.2	3
2354	Identity Determinants of the Translocation Signal for a Type 1 Secretion System. <i>Frontiers in Physiology</i> , 2021, 12, 804646.	1.3	4
2356	X-ray Characterization of Conformational Changes of Human Apo- and Holo-Transferrin. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13392.	1.8	7
2357	Investigation of the pH-dependent aggregation mechanisms of GCSF using low resolution protein characterization techniques and advanced molecular dynamics simulations. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 1439-1455.	1.9	4
2358	Structural Insights into the Catalytic Cycle of a Bacterial Multidrug ABC Efflux Pump. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
2359	Rigid-to-Flexible Transition in a Molecular Brush in a Good Solvent at a Semidilute Concentration. <i>Langmuir</i> , 2022, 38, 5226-5236.	1.6	3
2360	The suppressor of copper sensitivity protein C from <i>Caulobacter crescentus</i> is a trimeric disulfide isomerase that binds copper(I) with subpicomolar affinity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 337-352.	1.1	3
2363	SAXS analysis of the intrinsic tenase complex bound to a lipid nanodisc highlights intermolecular contacts between factors VIIIa/IXa. <i>Blood Advances</i> , 2022, 6, 3240-3254.	2.5	1
2364	The Amphoteric Surfactant <i>N,N</i> -Dimethyldodecylamine N-Oxide Unfolds β -Lactoglobulin above the Critical Micelle Concentration. <i>Langmuir</i> , 2022, 38, 4090-4101.	1.6	4
2365	Mechanism of cooperative N-glycan processing by the multi-modular endoglycosidase EndoE. <i>Nature Communications</i> , 2022, 13, 1137.	5.8	10
2366	Coil-to-helix transition at the Nup358-BicD2 interface activates BicD2 for dynein recruitment. <i>ELife</i> , 2022, 11, .	2.8	10
2368	Identification of the Precursor Cluster in the Crystallization Solution of Proteinase K Protein by Molecular Dynamics Methods. <i>Crystals</i> , 2022, 12, 484.	1.0	4
2369	Impact of Fluorinated Ionic Liquids on Human Phenylalanine Hydroxylase—A Potential Drug Delivery System. <i>Nanomaterials</i> , 2022, 12, 893.	1.9	5
2370	Extracellular endosulfatase Sulf-2 harbors a chondroitin/dermatan sulfate chain that modulates its enzyme activity. <i>Cell Reports</i> , 2022, 38, 110516.	2.9	15
2372	Structural basis for the mechanisms of human presequence protease conformational switch and substrate recognition. <i>Nature Communications</i> , 2022, 13, 1833.	5.8	4
2373	“Invisible” Detergents Enable a Reliable Determination of Solution Structures of Native Photosystems by Small-Angle Neutron Scattering. <i>Journal of Physical Chemistry B</i> , 2022, 126, 2824-2833.	1.2	8
2375	Structural Insights into the Catalytic Cycle of a Bacterial Multidrug ABC Efflux Pump. <i>Journal of Molecular Biology</i> , 2022, 434, 167541.	2.0	13

#	ARTICLE	IF	CITATIONS
2376	Cluster-cluster interaction in nanodiamond hydrosols by small-angle scattering. <i>Journal of Molecular Liquids</i> , 2022, 354, 118816.	2.3	5
2377	Electrostatic molecular effect of differently charged surfactants on the solubilization capacity and physicochemical properties of salt-caged nanosuspensions containing pH-dependent and poorly water-soluble rebamipide. <i>International Journal of Pharmaceutics</i> , 2022, 619, 121686.	2.6	3
2378	Microporosity engineered printable silk/graphene hydrogels and their cytocompatibility evaluations. <i>Materials Today Advances</i> , 2022, 14, 100233.	2.5	4
2379	Poly(C)-binding Protein 2 Regulates the p53 Expression via Interactions with the 5'â€²-Terminal Region of p53 mRNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13306.	1.8	6
2380	Self-Interactions of Two Monoclonal Antibodies: Small-Angle X-ray Scattering, Light Scattering, and Coarse-Grained Modeling. <i>Molecular Pharmaceutics</i> , 2022, 19, 508-519.	2.3	3
2382	Cryoâ€²EM structure of MsbA in saposinâ€²lipid nanoparticles (Salipro) provides insights into nucleotide coordination. <i>FEBS Journal</i> , 2022, 289, 2959-2970.	2.2	12
2383	Structural basis of dimerization and nucleic acid binding of human DBHS proteins NONO and PSPC1. <i>Nucleic Acids Research</i> , 2022, 50, 522-535.	6.5	10
2384	Recent Developments in Data-Assisted Modeling of Flexible Proteins. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 765562.	1.6	8
2385	Dimerization-dependent membrane tethering by Atg23 is essential for yeast autophagy. <i>Cell Reports</i> , 2022, 39, 110702.	2.9	8
2386	Structural Characterization of the Full-Length Anti-CD20 Antibody Rituximab. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, 823174.	1.6	10
2405	A cryptic K48 ubiquitin chain binding site on UCH37 is required for its role in proteasomal degradation. <i>ELife</i> , 2022, 11, .	2.8	9
2407	Development of a First-in-Class Small-Molecule Inhibitor of the C-Terminal Hsp90 Dimerization. <i>ACS Central Science</i> , 2022, 8, 636-655.	5.3	12
2409	Structural insights into Charcotâ€²Marieâ€²Tooth diseaseâ€²linked mutations in human GDAP1. <i>FEBS Open Bio</i> , 2022, 12, 1306-1324.	1.0	6
2410	New structural insights into the <sc>P</sc>â€² pilus from <i>Streptococcus oralis</i>, an early dental plaque colonizer. <i>FEBS Journal</i> , 2022, 289, 6342-6366.	2.2	5
2411	Magnetic field effects on the structure and molecular behavior of pigeon ironâ€²sulfur protein. <i>Protein Science</i> , 2022, 31, .	3.1	6
2412	Effect of preparation conditions on the size of nanoparticles based on poly(D,L-lactide-co-glycolide) synthesized with bismuth subsalicylate. <i>Colloids and Surfaces A: Physicochemical and Engineering Aspects</i> , 2022, 648, 129198.	2.3	6
2413	Ultraporous 2D-channeled graphene-wrapped zeolite molecular sieving membranes for hydrogen separation. <i>Science Advances</i> , 2022, 8, eabl3521.	4.7	21
2415	Full-Length Structure of the Host Targeted Bacterial Effector Bep1 Reveals a Novel Structural Domain Conserved in FIC Effector Proteins From <i>Bartonella</i>. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0

#	ARTICLE	IF	CITATIONS
2417	The Role of Cations and Anions in the Formation of Crystallization Oligomers in Protein Solutions as Revealed by Combination of Small-Angle X-ray Scattering and Molecular Dynamics. <i>Crystals</i> , 2022, 12, 751.	1.0	1
2418	Structural and biophysical properties of farnesylated KRas interacting with the chaperone SmgGDS-558. <i>Biophysical Journal</i> , 2022, , .	0.2	2
2419	VSAS: A smart small-angle scattering data processing tool. , 2022, 1, 100012.		0
2420	Structure of proteins under pressure: Covalent binding effects of biliverdin on β -lactoglobulin. <i>Biophysical Journal</i> , 2022, 121, 2514-2525.	0.2	2
2421	Mapping the deformability of natural and designed cellulosomes in solution. , 2022, 15, .		4
2422	High-affinity anti-Arc nanobodies provide tools for structural and functional studies. <i>PLoS ONE</i> , 2022, 17, e0269281.	1.1	5
2423	Modulation of Molecular Structure and Mechanical Properties of κ -Carrageenan-Gelatin Hydrogel with Multi-Walled Carbon Nanotubes. <i>Polymers</i> , 2022, 14, 2346.	2.0	13
2425	SAXS Analysis and Characterization of Anticancer Activity of PNP-UDP Family Protein from <i>Putranjiva roxburghii</i> . <i>Protein Journal</i> , 2022, 41, 381-393.	0.7	1
2426	Untangling the Conformational Plasticity of V66M Human proBDNF Polymorphism as a Modifier of Psychiatric Disorder Susceptibility. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6596.	1.8	2
2427	Solution structure of the type I polyketide synthase Pks13 from <i>Mycobacterium tuberculosis</i> . <i>BMC Biology</i> , 2022, 20, .	1.7	5
2428	Conformational Effects of a Cancer-Linked Mutation in Pri-miR-30c RNA. <i>Journal of Molecular Biology</i> , 2022, 434, 167705.	2.0	4
2429	Formation of Iron Oxide Nanoparticles in the Internal Cavity of Ferritin-Like Dps Protein: Studies by Anomalous X-Ray Scattering. <i>Biochemistry (Moscow)</i> , 2022, 87, 511-523.	0.7	1
2430	A Mademoiselle domain binding platform links the key RNA transporter to endosomes. <i>PLoS Genetics</i> , 2022, 18, e1010269.	1.5	3
2431	PP2A is activated by cytochrome c upon formation of a diffuse encounter complex with SET/TAF- β . <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3695-3707.	1.9	2
2433	Structure of a 14-3-3 β :FOXO3a ^{pS253} Phosphopeptide Complex Reveals 14-3-3 Isoform-Specific Binding of Forkhead Box Class O Transcription Factor (FOXO) Phosphoproteins. <i>ACS Omega</i> , 2022, 7, 24344-24352.	1.6	4
2434	Discovery of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins. <i>Nature Communications</i> , 2022, 13, .	5.8	17
2435	Small angle neutron scattering and lipidomic analysis of a native, trimeric PSI-SMALP from a thermophilic cyanobacteria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2022, 1863, 148596.	0.5	3
2436	Oligomerization processes limit photoactivation and recovery of the orange carotenoid protein. <i>Biophysical Journal</i> , 2022, 121, 2849-2872.	0.2	6

#	ARTICLE	IF	CITATIONS
2438	Solution Structural Studies of Pre-amyloid Oligomer States of the Biofilm Protein Aap. <i>Journal of Molecular Biology</i> , 2022, 434, 167708.	2.0	6
2440	Novel interaction interfaces mediate the interaction between the NEIL1 DNA glycosylase and mitochondrial transcription factor A. <i>Frontiers in Cell and Developmental Biology</i> , 0, 10, .	1.8	3
2441	Structural and biophysical properties of FopA, a major outer membrane protein of <i>Francisella tularensis</i> . <i>PLoS ONE</i> , 2022, 17, e0267370.	1.1	2
2442	Expanding Structural Space for Immunomodulatory Nucleic Acid Nanoparticles via Spatial Arrangement of Their Therapeutic Moieties. <i>Advanced Functional Materials</i> , 2022, 32, .	7.8	12
2443	Binding stoichiometry and structural model of the HIV-1 Rev/importin \hat{I}^2 complex. <i>Life Science Alliance</i> , 2022, 5, e202201431.	1.3	3
2444	Conformational Changes of \hat{I}^2 -Crystallin Proteins Induced by Heat Stress. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9347.	1.8	1
2445	Dynamics and structural changes of calmodulin upon interaction with the antagonist calmidazolium. <i>BMC Biology</i> , 2022, 20, .	1.7	12
2446	Structure of the human NK cell NKR-P1:LLT1 receptor:ligand complex reveals clustering in the immune synapse. <i>Nature Communications</i> , 2022, 13, .	5.8	4
2447	Heparins mediate the multimer assembly of secreted Noggin. <i>Protein Science</i> , 2022, 31, .	3.1	1
2449	Inâ€solution structure and oligomerization of human histone deacetylase 6 â€“ an integrative approach. <i>FEBS Journal</i> , 2023, 290, 821-836.	2.2	2
2452	Amyloid fibril formation by \hat{I}^1 - and \hat{I}^2 -casein implies that fibril formation is a general property of casein proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140854.	1.1	6
2453	Structural and functional insights into the glycoside hydrolase family 30 xylanase of the rumen bacterium <i>Ruminococcus flavefaciens</i> . <i>Journal of Molecular Structure</i> , 2023, 1272, 134155.	1.8	4
2454	Supramolecular gold(<sc>i</sc>) vesicles: an in-depth study of their aggregation process. <i>Inorganic Chemistry Frontiers</i> , 2022, 9, 6047-6060.	3.0	4
2455	Advanced sample environments and sample requirements for biological SAXS. <i>Methods in Enzymology</i> , 2022, , 1-39.	0.4	2
2456	Protein quaternary structures in solution are a mixture of multiple forms. <i>Chemical Science</i> , 2022, 13, 11680-11695.	3.7	14
2457	High-pressure SAXS, deep life, and extreme biophysics. <i>Methods in Enzymology</i> , 2022, , .	0.4	1
2458	Protein fibrillation from another small angle: Sample preparation and SAXS data collection. <i>Methods in Enzymology</i> , 2022, , .	0.4	1
2461	Coiled-coil structure of meiosis protein TEX12 and conformational regulation by its C-terminal tip. <i>Communications Biology</i> , 2022, 5, .	2.0	4

#	ARTICLE	IF	CITATIONS
2462	Crystallographic and X-ray scattering study of RdfS, a recombination directionality factor from an integrative and conjugative element. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1210-1220.	1.1	1
2463	Plant-specific HDT family histone deacetylases are nucleoplasmins. <i>Plant Cell</i> , 2022, 34, 4760-4777.	3.1	6
2465	Protein Self-Assembly in Crystals and Films. <i>Crystallography Reports</i> , 2022, 67, 772-790.	0.1	0
2467	Structural features of chloroplast trigger factor determined at 2.6 Å resolution. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1259-1272.	1.1	1
2468	Dynamics of the secreted frizzled related protein Sizzled and potential implications for binding to bone morphogenetic protein-1 (BMP-1). <i>Scientific Reports</i> , 2022, 12, .	1.6	0
2469	Comprehensive phylogenetic analysis of the ribonucleotide reductase family reveals an ancestral clade. <i>ELife</i> , 0, 11, .	2.8	9
2470	Structure of the malaria vaccine candidate Pfs48/45 and its recognition by transmission blocking antibodies. <i>Nature Communications</i> , 2022, 13, .	5.8	8
2471	Nanobodies identify an activated state of the TRIB2 pseudokinase. <i>Structure</i> , 2022, , .	1.6	2
2472	Short prokaryotic Argonautes provide defence against incoming mobile genetic elements through NAD ⁺ depletion. <i>Nature Microbiology</i> , 2022, 7, 1857-1869.	5.9	52
2473	Crystal structure of the Phospholipase A and acyltransferase 4 (PLAAT4) catalytic domain. <i>Journal of Structural Biology</i> , 2022, , 107903.	1.3	0
2474	Studying integral membrane protein by SANS using stealth reconstitution systems. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
2475	Stopped-flow-time-resolved SAXS for studies of ligand-driven protein dimerization. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
2476	Computational methods for the analysis of solution small-angle X-ray scattering of biomolecules: ATSAS. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
2477	Disentangling polydisperse biomolecular systems by Chemometrics decomposition of SAS data. <i>Methods in Enzymology</i> , 2022, , .	0.4	1
2478	Deriving RNA topological structure from SAXS. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
2479	Production and characterisation of modularly deuterated UBE2D1-Ub conjugate by small angle neutron and X-ray scattering. <i>European Biophysics Journal</i> , 0, , .	1.2	0
2481	Kinetic and Structural Characterization of a Flavin-Dependent Putrescine N-Hydroxylase from <i>Acinetobacter baumannii</i> . <i>Biochemistry</i> , 2022, 61, 2607-2620.	1.2	4
2482	Molecular dynamics simulations of the adsorption of an intrinsically disordered protein: Force field and water model evaluation in comparison with experiments. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	6

#	ARTICLE	IF	CITATIONS
2483	The periplasmic chaperone Skp prevents misfolding of the secretory lipase A from <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	4
2484	Unravelling the regulation pathway of photosynthetic AB-GAPDH. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1399-1411.	1.1	2
2485	Structural and molecular determinants of <i>Candida glabrata</i> metacaspase maturation and activation by calcium. <i>Communications Biology</i> , 2022, 5, .	2.0	5
2486	Study on internal structure of casein micelles in reconstituted skim milk powder. <i>International Journal of Biological Macromolecules</i> , 2023, 224, 437-452.	3.6	10
2487	Supramolecular Structure and Mechanical Performance of $\hat{\text{I}}^{\text{o}}$ -Carrageenanâ€“Gelatin Gel. <i>Polymers</i> , 2022, 14, 4347.	2.0	12
2488	Glycoside hydrolase subfamily GH5_57 features a highly redesigned catalytic interface to process complex hetero- $\hat{\text{I}}^2$ -mannans. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 1358-1372.	1.1	1
2489	Inline smallâ€“angle Xâ€“ray scatteringâ€“coupled chromatography under extreme hydrostatic pressure. <i>Protein Science</i> , 2022, 31, .	3.1	4
2491	Structural insights into the contactin 1 â€“ neurofascin 155 adhesion complex. <i>Nature Communications</i> , 2022, 13, .	5.8	9
2492	Observing protein degradation in solution by the PAN-20S proteasome complex: A state-of-the-art example of bio-macromolecular TR-SANS. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
2493	Protein fibrillation from another small angleâ€“SAXS data analysis of developing systems. <i>Methods in Enzymology</i> , 2022, , .	0.4	1
2495	Expanding the Toolbox for Bicelle-Forming Surfactantâ€“Lipid Mixtures. <i>Molecules</i> , 2022, 27, 7628.	1.7	4
2498	Oligomerization of Human Cystatin Câ€“An Amyloidogenic Protein: An Analysis of Small Oligomeric Subspecies. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13441.	1.8	2
2500	VOLDIS: A Direct Search for the Size Distribution of Nanoparticles from Small-Angle Scattering Data and Stability of the Solution. <i>Crystals</i> , 2022, 12, 1659.	1.0	2
2501	Recent advances in structural characterization of biomacromolecules in foods via small-angle X-ray scattering. <i>Frontiers in Nutrition</i> , 0, 9, .	1.6	5
2502	Adjuvant effect of mesoporous silica SBA-15 on anti-diphtheria and anti-tetanus humoral immune response. <i>Biologicals</i> , 2022, 80, 18-26.	0.5	3
2503	Structural and dynamical insights into SiIe silver binding from combined analytical probes. <i>Physical Chemistry Chemical Physics</i> , 0, , .	1.3	1
2504	Small-angle X-ray scattering studies of enzymes. <i>Current Opinion in Chemical Biology</i> , 2023, 72, 102232.	2.8	14
2505	Structure-based engineering of minimal Proline dehydrogenase domains for inhibitor discovery. <i>Protein Engineering, Design and Selection</i> , 0, , .	1.0	0

#	ARTICLE	IF	CITATIONS
2506	Integrative analysis reveals structural basis for transcription activation of Nurr1 and Nurr1-RXR β heterodimer. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	1
2507	Antiviral signalling by a cyclic nucleotide activated CRISPR protease. Nature, 2023, 614, 168-174.	13.7	12
2508	Conformational interdomain flexibility in a bacterial β -isopropylmalate synthase is necessary for leucine biosynthesis. Journal of Biological Chemistry, 2022, , 102789.	1.6	0
2509	Tuning the Phytoglycogen Size and Aggregate Structure with Solvent Quality: Influence of Water-Ethanol Mixtures Revealed by X-ray and Light Scattering Techniques. Biomacromolecules, 0, , .	2.6	1
2510	Structural, Thermodynamic and Enzymatic Characterization of N,N-Diacetylchitobiose Deacetylase from Pyrococcus chitonophagus. International Journal of Molecular Sciences, 2022, 23, 15736.	1.8	0
2511	Biomolecular solution X-ray scattering at n2STAR Beamline. Mu α Journal of Science and Technology, 0, , .	0.1	2
2512	Difference in the Inhibitory Effect of Thiol Compounds and Demetallation Rates from the Zn(II) Active Site of Metallo- β -lactamases (IMP-1 and IMP-6) Associated with a Single Amino Acid Substitution. ACS Infectious Diseases, 2023, 9, 65-78.	1.8	2
2514	Structural and functional insights into CST tethering in Tetrahymena thermophila telomerase. Structure, 2022, 30, 1565-1572.e4.	1.6	2
2515	Crowder-directed interactions and conformational dynamics in multistimuli-responsive intrinsically disordered protein. Science Advances, 2022, 8, .	4.7	4
2516	Structural and Functional Insights into the Roles of Potential Metal-Binding Sites in Apostichopus japonicus Ferritin. Polymers, 2022, 14, 5378.	2.0	1
2517	Studies on the Interaction between Model Proteins and Fluorinated Ionic Liquids. Pharmaceutics, 2023, 15, 157.	2.0	4
2518	Rational design of potent ultrashort antimicrobial peptides with programmable assembly into nanostructured hydrogels. Frontiers in Chemistry, 0, 10, .	1.8	3
2519	Solution X-ray scattering highlights discrepancies in <i>Plasmodium</i> multi- ϵ -aminoacyl-tRNA synthetase complexes. Protein Science, 2023, 32, .	3.1	6
2521	Structural maturation of SYCP1-mediated meiotic chromosome synapsis by SYCE3. Nature Structural and Molecular Biology, 2023, 30, 188-199.	3.6	10
2522	Structure of SALL4 zinc finger domain reveals link between AT-rich DNA binding and Okhiro syndrome. Life Science Alliance, 2023, 6, e202201588.	1.3	2
2523	Distinct conformational changes occur within the intrinsically unstructured pro α domain of α -Nerve Growth Factor in the presence of ATP and Mg ²⁺ . Protein Science, 0, , .	3.1	2
2524	The ϵ -AMP-binding protein CbpB modulates the level of ppGpp alarmone in <i>Streptococcus agalactiae</i> . FEBS Journal, 2023, 290, 2968-2992.	2.2	4
2525	Insights into the GSDMB-mediated cellular lysis and its targeting by IpaH7.8. Nature Communications, 2023, 14, .	5.8	18

#	ARTICLE	IF	CITATIONS
2526	Stereochemistry and Intermolecular Interactions Influence Carrier Peptide-Mediated Insulin Delivery. <i>Molecular Pharmaceutics</i> , 0, , .	2.3	5
2527	Structural insights into translation regulation by the THF-II riboswitch. <i>Nucleic Acids Research</i> , 2023, 51, 952-965.	6.5	4
2528	Temperature Behavior of Precursor Clusters at the Pre-Crystallization Phase of K(H ₂ PO ₄) Studied by SAXS. <i>Crystals</i> , 2023, 13, 26.	1.0	1
2530	The structure of MadC from <i>Clostridium maddingleyi</i> reveals new insights into class I lanthipeptide cyclases. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	0
2531	Asymmetric horseshoe-like assembly of peroxisomal yeast oxalyl-CoA synthetase. <i>Biological Chemistry</i> , 2023, 404, 195-207.	1.2	1
2532	Linear ubiquitination induces NEMO phase separation to activate NF- κ B signaling. <i>Life Science Alliance</i> , 2023, 6, e202201607.	1.3	14
2533	Electrospinning of Cyclodextrin- α -Oligolactide Derivatives. <i>Biomolecules</i> , 2023, 13, 203.	1.8	6
2534	Staphylococcal Periscope proteins Aap, SasG, and Pls project noncanonical legume-like lectin adhesin domains from the bacterial surface. <i>Journal of Biological Chemistry</i> , 2023, 299, 102936.	1.6	3
2535	Conformational multiplicity of bacterial ferric binding protein revealed by small angle x-ray scattering and molecular dynamics calculations. <i>Journal of Chemical Physics</i> , 2023, 158, .	1.2	1
2536	Development of Algorithms for Analysis of Small-Angle X-Ray Scattering Data from Polydisperse and Partially Ordered Systems. <i>Physics of Atomic Nuclei</i> , 2022, 85, 2127-2132.	0.1	1
2537	Effect of the Coat Protein N-Terminal Domain Structure on the Structure and Physicochemical Properties of Virions of Potato Virus X and Alternanthera Mosaic Virus. <i>Biochemistry (Moscow)</i> , 2023, 88, 119-130.	0.7	1
2538	Structural Insight into Catalysis by the Flavin-Dependent NADH Oxidase (Pden_5119) of <i>Paracoccus denitrificans</i> . <i>International Journal of Molecular Sciences</i> , 2023, 24, 3732.	1.8	0
2539	Modelling the 3D Structure of PEDOT:PSS Supramolecular Assembly in Aqueous Dispersion Based on SAXS with Synchrotron Light. <i>Chinese Journal of Polymer Science (English Edition)</i> , 0, , .	2.0	0
2541	Structural and functional insights of the catalytic GH5 and Calx- \hat{I}^2 domains from the metagenome-derived endoglucanase CelE2. <i>Enzyme and Microbial Technology</i> , 2023, 165, 110206.	1.6	0
2543	Small-angle X-ray scattering intensity of multiscale models of spheroids. <i>Journal of Applied Crystallography</i> , 2023, 56, 237-246.	1.9	0
2545	Mechanistic insights into RNA surveillance by the canonical poly(A) polymerase Pla1 of the MTREC complex. <i>Nature Communications</i> , 2023, 14, .	5.8	4
2546	A Fijivirus Major Viroplasm Protein Shows RNA-Stimulated ATPase Activity by Adopting Pentameric and Hexameric Assemblies of Dimers. <i>MBio</i> , 0, , .	1.8	0
2547	An Anomalous Small-Angle X-Ray Scattering Study of the Formation of Iron Clusters in the Inner Cavity of the Ferritin-Like Protein Dps. <i>Moscow University Physics Bulletin (English Translation of Tj ETQq1 1 0.784314 rgBT fOverloc</i>	1.0	1

#	ARTICLE	IF	CITATIONS
2548	TRYBEÂ®: an Fc-free antibody format with three monovalent targeting arms engineered for long in vivo half-life. <i>MABs</i> , 2023, 15, .	2.6	1
2549	Stages of OCPâ€“FRP Interactions in the Regulation of Photoprotection in Cyanobacteria, Part 2: Small-Angle Neutron Scattering with Partial Deuteration. <i>Journal of Physical Chemistry B</i> , 2023, 127, 1901-1913.	1.2	3
2550	EndophilinA-dependent coupling between activity-induced calcium influx and synaptic autophagy is disrupted by a Parkinson-risk mutation. <i>Neuron</i> , 2023, 111, 1402-1422.e13.	3.8	7
2551	<i>Sorghum bicolor</i> <i>S</i> has an elongated shape and is able of protecting against aggregation and replacing human <i>HSPH1</i> / <i>HSP110</i> in refolding and disaggregation assays. <i>Biopolymers</i> , 2023, 114, .	1.2	0
2554	YbiB: a novel interactor of the GTPase ObgE. <i>Nucleic Acids Research</i> , 0, , .	6.5	0
2555	Cooperative action of separate interaction domains promotes high-affinity DNA binding of <i>Arabidopsis thaliana</i> ARF transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	5
2556	NMR structure of emfourin, a novel protein metalloprotease inhibitor: Insights into the mechanism of action. <i>Journal of Biological Chemistry</i> , 2023, 299, 104585.	1.6	1
2557	Decrypting the programming of Î²-methylation in virginiamycin M biosynthesis. <i>Nature Communications</i> , 2023, 14, .	5.8	0
2560	Conserved intramolecular networks in GDAP1 are closely connected to CMT-linked mutations and protein stability. <i>PLoS ONE</i> , 2023, 18, e0284532.	1.1	2
2561	Evolution of Gold and Iron Oxide Nanoparticles in Conjugates with Methotrexate: Synthesis and Anticancer Effects. <i>Materials</i> , 2023, 16, 3238.	1.3	4
2562	Hybrid Silver-Containing Materials Based on Various Forms of Bacterial Cellulose: Synthesis, Structure, and Biological Activity. <i>International Journal of Molecular Sciences</i> , 2023, 24, 7667.	1.8	3
2568	Using Small-angle X-ray Scattering to Characterize Biological Systems: A General Overview and Practical Tips. <i>Methods in Molecular Biology</i> , 2023, , 381-403.	0.4	1