

# Dmitri I Svergun

## List of Publications by Year in Descending Order

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

220  
papers

18,844  
citations

56  
h-index

135  
g-index

240  
ext. papers

21,936  
ext. citations

7.4  
avg, IF

7.15  
L-index

#	Paper	IF	Citations
220	The prion protein and its ligands: Insights into structure-function relationships.. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2022</b> , 1869, 119240	4.9	0
219	EFAMIX, a tool to decompose inline chromatography SAXS data from partially overlapping components. <i>Protein Science</i> , <b>2021</b> ,	6.3	8
218	Probing the existence of non-thermal Terahertz radiation induced changes of the protein solution structure. <i>Scientific Reports</i> , <b>2021</b> , 11, 22311	4.9	2
217	Ligands binding to the prion protein induce its proteolytic release with therapeutic potential in neurodegenerative proteinopathies. <i>Science Advances</i> , <b>2021</b> , 7, eabj1826	14.3	4
216	Clustering in ferronematics-The effect of magnetic collective ordering.. <i>IScience</i> , <b>2021</b> , 24, 103493	6.1	
215	Small-angle X-ray and neutron scattering. <i>Nature Reviews Methods Primers</i> , <b>2021</b> , 1,		15
214	The USR domain of USF1 mediates NF-Y interactions and cooperative DNA binding. <i>International Journal of Biological Macromolecules</i> , <b>2021</b> , 193, 401-413	7.9	
213	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> , <b>2021</b> , 11,	3.8	1
212	The Disease Associated Tau35 Fragment has an Increased Propensity to Aggregate Compared to Full-Length Tau. <i>Frontiers in Molecular Biosciences</i> , <b>2021</b> , 8, 779240	5.6	1
211	Limitations of the iterative electron density reconstruction algorithm from solution scattering data. <i>Nature Methods</i> , <b>2021</b> , 18, 244-245	21.6	2
210	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> , <b>2021</b> , 17, 2014-2021	6.4	2
209	Hallmarks of and non-structural protein 7+8 complexes. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	9
208	Anomalous SAXS at P12 beamline EMBL Hamburg: instrumentation and applications. <i>Journal of Synchrotron Radiation</i> , <b>2021</b> , 28, 812-823	2.4	5
207	Molecular basis of F-actin regulation and sarcomere assembly via myotilin. <i>PLoS Biology</i> , <b>2021</b> , 19, e3001448	14.8	3
206	Structural analysis of the SRP Alu domain from Plasmodium falciparum reveals a non-canonical open conformation. <i>Communications Biology</i> , <b>2021</b> , 4, 600	6.7	0
205	Molecular model of a sensor of two-component signaling system. <i>Scientific Reports</i> , <b>2021</b> , 11, 10774	4.9	2
204	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. <i>Nature Communications</i> , <b>2021</b> , 12, 2889	17.4	5

203	ASAXS measurements on ferritin and apoferritin at the bioSAXS beamline P12 (PETRA III, DESY). <i>Journal of Applied Crystallography</i> , <b>2021</b> , 54, 830-838	3.8	4
202	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with $\beta$ -actinin. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	1
201	Autism-associated missense point mutations impact conformational fluctuations and protein turnover at synapses. <i>ELife</i> , <b>2021</b> , 10,	8.9	5
200	Capturing the Conformational Ensemble of the Mixed Folded Polyglutamine Protein Ataxin-3. <i>Structure</i> , <b>2021</b> , 29, 70-81.e5	5.2	3
199	The allosteric modulation of complement C5 by knob domain peptides. <i>ELife</i> , <b>2021</b> , 10,	8.9	5
198	Restoring structural parameters of lipid mixtures from small-angle X-ray scattering data. <i>Journal of Applied Crystallography</i> , <b>2021</b> , 54, 169-179	3.8	6
197	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules. <i>Nature Communications</i> , <b>2021</b> , 12, 939	17.4	6
196	: expanded functionality and new tools for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , <b>2021</b> , 54, 343-355	3.8	120
195	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009824	7.6	4
194	Mechanism of activation and regulation of deubiquitinase activity in MINDY1 and MINDY2. <i>Molecular Cell</i> , <b>2021</b> , 81, 4176-4190.e6	17.6	2
193	Structure and dynamics of UBA5-UFM1 complex formation showing new insights in the UBA5 activation mechanism. <i>Journal of Structural Biology</i> , <b>2021</b> , 213, 107796	3.4	0
192	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D404-D411	20.1	31
191	Self-assembly and cellular effect of tau35, a disease-associated tau fragment.. <i>Alzheimer's and Dementia</i> , <b>2021</b> , 17 Suppl 3, e052072	1.2	
190	Adding Size Exclusion Chromatography (SEC) and Light Scattering (LS) Devices to Obtain High-Quality Small Angle X-Ray Scattering (SAXS) Data. <i>Crystals</i> , <b>2020</b> , 10, 975	2.3	15
189	A Giant Extracellular Matrix Binding Protein of Binds Surface-Immobilized Fibronectin via a Novel Mechanism. <i>MBio</i> , <b>2020</b> , 11,	7.8	1
188	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. <i>Nature Communications</i> , <b>2020</b> , 11, 5588	17.4	73
187	An automated data processing and analysis pipeline for transmembrane proteins in detergent solutions. <i>Scientific Reports</i> , <b>2020</b> , 10, 8081	4.9	9
186	Btk SH2-kinase interface is critical for allosteric kinase activation and its targeting inhibits B-cell neoplasms. <i>Nature Communications</i> , <b>2020</b> , 11, 2319	17.4	12

185	Molecular Mechanisms of the Interactions of -(2-Hydroxypropyl)methacrylamide Copolymers Designed for Cancer Therapy with Blood Plasma Proteins. <i>Pharmaceutics</i> , <b>2020</b> , 12,	6.4	7
184	Structural Modeling Using Solution Small-Angle X-ray Scattering (SAXS). <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 3078-3092	6.5	27
183	Tetrameric Structures of Inorganic CBS-Pyrophosphatases from Various Bacterial Species Revealed by Small-Angle X-ray Scattering in Solution. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	2
182	Simulation of small-angle X-ray scattering data of biological macromolecules in solution. <i>Journal of Applied Crystallography</i> , <b>2020</b> , 53, 536-539	3.8	6
181	Rapid screening of grown protein crystals via a small-angle X-ray scattering/X-ray powder diffraction synergistic approach. <i>Journal of Applied Crystallography</i> , <b>2020</b> , 53, 1169-1180	3.8	8
180	A beginner's guide to solution small-angle X-ray scattering (SAXS). <i>Biochemist</i> , <b>2020</b> , 42, 36-42	0.5	2
179	SASBDB: Towards an automatically curated and validated repository for biological scattering data. <i>Protein Science</i> , <b>2020</b> , 29, 66-75	6.3	65
178	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , <b>2020</b> , 28, 348-354.e3	5.2	15
177	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. <i>Journal of Applied Crystallography</i> , <b>2020</b> , 53, 236-243	3.8	4
176	Effect of the concentration of protein and nanoparticles on the structure of biohybrid nanocomposites. <i>Biopolymers</i> , <b>2020</b> , 111, e23342	2.2	3
175	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR-RXR. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 9969-9985	20.1	7
174	Methods, development and applications of small-angle X-ray scattering to characterize biological macromolecules in solution. <i>Current Research in Structural Biology</i> , <b>2020</b> , 2, 164-170	2.8	16
173	The F1 loop of the talin head domain acts as a gatekeeper in integrin activation and clustering. <i>Journal of Cell Science</i> , <b>2020</b> , 133,	5.3	11
172	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , <b>2020</b> , 31, 107817	10.6	9
171	Molecular mechanism of leukocidin GH-integrin CD11b/CD18 recognition and species specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 317-327	11.5	8
170	The basics of small-angle neutron scattering (SANS for new users of structural biology). <i>EPJ Web of Conferences</i> , <b>2020</b> , 236, 03001	0.3	1
169	Anomeric Selectivity of Trehalose Transferase with Rare l-Sugars. <i>ACS Catalysis</i> , <b>2020</b> , 10, 8835-8839	13.1	1
168	RovC - a novel type of hexameric transcriptional activator promoting type VI secretion gene expression. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008552	7.6	3

167	Structure of a collagen VI B chain VWA domain array: adaptability and functional implications of myopathy causing mutations. <i>Journal of Biological Chemistry</i> , <b>2020</b> , 295, 12755-12771	5.4	3
166	Structural Analyses of Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2141, 249-269	1.4	2
165	The free energy landscape of the oncogene protein E7 of human papillomavirus type 16 reveals a complex interplay between ordered and disordered regions. <i>Scientific Reports</i> , <b>2019</b> , 9, 5822	4.9	6
164	Structure of ATP citrate lyase and the origin of citrate synthase in the Krebs cycle. <i>Nature</i> , <b>2019</b> , 568, 571-575	50.4	58
163	Octa-repeat domain of the mammalian prion protein mRNA forms stable A-helical hairpin structure rather than G-quadruplexes. <i>Scientific Reports</i> , <b>2019</b> , 9, 2465	4.9	3
162	The quaternary structure of insulin glargine and glulisine under formulation conditions. <i>Biophysical Chemistry</i> , <b>2019</b> , 253, 106226	3.5	6
161	Molecular Organization of Soluble Type III Secretion System Sorting Platform Complexes. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 3787-3803	6.5	15
160	Studying Conformational Changes of the Yersinia Type-III-Secretion Effector YopO in Solution by Integrative Structural Biology. <i>Structure</i> , <b>2019</b> , 27, 1416-1426.e3	5.2	16
159	Solution structure and flexibility of the condensin HEAT-repeat subunit Ycg1. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 13822-13829	5.4	7
158	The dimeric ectodomain of the alkali-sensing insulin receptor-related receptor (ectoIRR) has a droplike shape. <i>Journal of Biological Chemistry</i> , <b>2019</b> , 294, 17790-17798	5.4	8
157	Conformational characterization of full-length X-chromosome-linked inhibitor of apoptosis protein (XIAP) through an integrated approach. <i>IUCrJ</i> , <b>2019</b> , 6, 948-957	4.7	3
156	An NAD Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. <i>Molecular Cell</i> , <b>2019</b> , 73, 1282-1291.e8	17.6	37
155	Shedding Light on the Interaction of Human Anti-Apoptotic Bcl-2 Protein with Ligands through Biophysical and in Silico Studies. <i>International Journal of Molecular Sciences</i> , <b>2019</b> , 20,	6.3	16
154	Application of Small-Angle X-Ray Scattering in Studies of Biological Macromolecules <b>2019</b> , 1-22		
153	Advances in Small and Wide-Angle X-Ray Scattering from Proteins and Macromolecular Solutions <b>2019</b> , 1-39		
152	Structural properties of [2Fe-2S] ISCA2-IBA57: a complex of the mitochondrial iron-sulfur cluster assembly machinery. <i>Scientific Reports</i> , <b>2019</b> , 9, 18986	4.9	11
151	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> , <b>2019</b> , 28, 150-166	6.3	2
150	Utilization of Staphylococcal Immune Evasion Protein Sbi as a Novel Vaccine Adjuvant. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 3139	8.4	6

149	Functional interaction of low-homology FRPs from different cyanobacteria with Synechocystis OCP. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2018</b> , 1859, 382-393	4.6	11
148	Disease Variants of FGFR3 Reveal Molecular Basis for the Recognition and Additional Roles for Cdc37 in Hsp90 Chaperone System. <i>Structure</i> , <b>2018</b> , 26, 446-458.e8	5.2	11
147	Epsin and Sla2 form assemblies through phospholipid interfaces. <i>Nature Communications</i> , <b>2018</b> , 9, 328	17.4	26
146	Sapoin Lipid Nanoparticles: A Highly Versatile and Modular Tool for Membrane Protein Research. <i>Structure</i> , <b>2018</b> , 26, 345-355.e5	5.2	40
145	Macromolecular pHPMA-Based Nanoparticles with Cholesterol for Solid Tumor Targeting: Behavior in HSA Protein Environment. <i>Biomacromolecules</i> , <b>2018</b> , 19, 470-480	6.9	12
144	CHROMIXS: automatic and interactive analysis of chromatography-coupled small-angle X-ray scattering data. <i>Bioinformatics</i> , <b>2018</b> , 34, 1944-1946	7.2	104
143	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , <b>2018</b> , 9, 164	17.4	22
142	Prp19/Pso4 Is an Autoinhibited Ubiquitin Ligase Activated by Stepwise Assembly of Three Splicing Factors. <i>Molecular Cell</i> , <b>2018</b> , 69, 979-992.e6	17.6	11
141	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. <i>Scientific Reports</i> , <b>2018</b> , 8, 4326	4.9	9
140	Optical and Structural Characterization of a Chronic Myeloid Leukemia DNA Biosensor. <i>ACS Chemical Biology</i> , <b>2018</b> , 13, 1235-1242	4.9	1
139	Structural complexity of the co-chaperone SGTA: a conserved C-terminal region is implicated in dimerization and substrate quality control. <i>BMC Biology</i> , <b>2018</b> , 16, 76	7.3	5
138	Quantitative 3D determination of self-assembled structures on nanoparticles using small angle neutron scattering. <i>Nature Communications</i> , <b>2018</b> , 9, 1343	17.4	32
137	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. <i>Scientific Reports</i> , <b>2018</b> , 8, 7204	4.9	82
136	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> , <b>2018</b> , 25, 906-914	2.4	12
135	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. <i>Biophysical Journal</i> , <b>2018</b> , 114, 2485-2492	2.9	33
134	Direct shape determination of intermediates in evolving macromolecular solutions from small-angle scattering data. <i>IUCrJ</i> , <b>2018</b> , 5, 402-409	4.7	15
133	Smaller capillaries improve the small-angle X-ray scattering signal and sample consumption for biomacromolecular solutions. <i>Journal of Synchrotron Radiation</i> , <b>2018</b> , 25, 1113-1122	2.4	19
132	Structural insights of RmXyn10A - A prebiotic-producing GH10 xylanase with a non-conserved aglycone binding region. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2018</b> , 1866, 292-306	4	12

131	Structural basis for activation of plasma-membrane Ca-ATPase by calmodulin. <i>Communications Biology</i> , <b>2018</b> , 1, 206	6.7	20
130	β-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> , <b>2018</b> , 122, 11895-11905	3.4	5
129	Recent developments in small-angle X-ray scattering and hybrid method approaches for biomacromolecular solutions. <i>Emerging Topics in Life Sciences</i> , <b>2018</b> , 2, 69-79	3.5	20
128	Probing the Architecture of a Multi-PDZ Domain Protein: Structure of PDZK1 in Solution. <i>Structure</i> , <b>2018</b> , 26, 1522-1533.e5	5.2	7
127	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , <b>2018</b> , 361,	33.3	23
126	Structure-specific recognition protein-1 (SSRP1) is an elongated homodimer that binds histones. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 10071-10083	5.4	7
125	Multi-channel in situ dynamic light scattering instrumentation enhancing biological small-angle X-ray scattering experiments at the PETRA III beamline P12. <i>Journal of Synchrotron Radiation</i> , <b>2018</b> , 25, 361-372	2.4	12
124	Conformational States of ABC Transporter MsbA in a Lipid Environment Investigated by Small-Angle Scattering Using Stealth Carrier Nanodiscs. <i>Structure</i> , <b>2018</b> , 26, 1072-1079.e4	5.2	44
123	Analysis of self-assembly of S-layer protein slp-B53 from <i>Lysinibacillus sphaericus</i> . <i>European Biophysics Journal</i> , <b>2017</b> , 46, 77-89	1.9	13
122	Structural basis of the interaction between the putative adhesion-involved and iron-regulated FrpD and FrpC proteins of <i>Neisseria meningitidis</i> . <i>Scientific Reports</i> , <b>2017</b> , 7, 40408	4.9	5
121	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17047	26.6	74
120	Combining NMR and small angle X-ray scattering for the study of biomolecular structure and dynamics. <i>Archives of Biochemistry and Biophysics</i> , <b>2017</b> , 628, 33-41	4.1	28
119	The Shigella Virulence Factor IcsA Relieves N-WASP Autoinhibition by Displacing the Verprolin Homology/Cofilin/Acidic (VCA) Domain. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 134-145	5.4	10
118	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , <b>2017</b> , 25, 1079-1088.e3	5.2	24
117	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> , <b>2017</b> , 73, 710-728	5.5	145
116	The Molecular Bases of the Dual Regulation of Bacterial Iron Sulfur Cluster Biogenesis by CyaY and IscX. <i>Frontiers in Molecular Biosciences</i> , <b>2017</b> , 4, 97	5.6	15
115	Decoupling of size and shape fluctuations in heteropolymeric sequences reconciles discrepancies in SAXS vs. FRET measurements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E6342-E6351	11.5	136
114	Highly selective tungstate transporter protein TupA from <i>Desulfovibrio alaskensis</i> G20. <i>Scientific Reports</i> , <b>2017</b> , 7, 5798	4.9	10



113	Influenza virus Matrix Protein M1 preserves its conformation with pH, changing multimerization state at the priming stage due to electrostatics. <i>Scientific Reports</i> , <b>2017</b> , 7, 16793	4.9	17
112	Progress in small-angle scattering from biological solutions at high-brilliance synchrotrons. <i>IUCrJ</i> , <b>2017</b> , 4, 518-528	4.7	49
111	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. <i>ELife</i> , <b>2017</b> , 6,	8.9	41
110	Potent and selective bivalent inhibitors of BET bromodomains. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 1097-1104	11.0	82
109	Extension of the sasCIF format and its applications for data processing and deposition. <i>Journal of Applied Crystallography</i> , <b>2016</b> , 49, 302-310	3.8	13
108	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 14430-46	5.4	9
107	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , <b>2016</b> , 24, 851-61	5.2	12
106	Crystal Structure of the CTP1L Endolysin Reveals How Its Activity Is Regulated by a Secondary Translation Product. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 4882-93	5.4	29
105	SASpy: a PyMOL plugin for manipulation and refinement of hybrid models against small angle X-ray scattering data. <i>Bioinformatics</i> , <b>2016</b> , 32, 2062-4	7.2	21
104	LabDisk for SAXS: a centrifugal microfluidic sample preparation platform for small-angle X-ray scattering. <i>Lab on A Chip</i> , <b>2016</b> , 16, 1161-70	7.2	34
103	Solution Behavior of the Intrinsically Disordered N-Terminal Domain of Retinoid X Receptor in the Context of the Full-Length Protein. <i>Biochemistry</i> , <b>2016</b> , 55, 1741-1748	3.2	15
102	Deciphering conformational transitions of proteins by small angle X-ray scattering and normal mode analysis. <i>Physical Chemistry Chemical Physics</i> , <b>2016</b> , 18, 5707-19	3.6	96
101	Rapid automated superposition of shapes and macromolecular models using spherical harmonics. <i>Journal of Applied Crystallography</i> , <b>2016</b> , 49, 953-960	3.8	20
100	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. <i>Scientific Reports</i> , <b>2016</b> , 6, 20915	4.9	9
99	Resolution of shapes determined from small-angle scattering. <i>IUCrJ</i> , <b>2016</b> , 3, 440-447	4.7	69
98	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. <i>MAbs</i> , <b>2016</b> , 8, 928-40	6.6	36
97	Calcium-Driven Folding of RTX Domain $\square$ -Rolls Ratchets Translocation of RTX Proteins through Type I Secretion Ducts. <i>Molecular Cell</i> , <b>2016</b> , 62, 47-62	17.6	86
96	DARA: a web server for rapid search of structural neighbours using solution small angle X-ray scattering data. <i>Bioinformatics</i> , <b>2016</b> , 32, 616-8	7.2	14



95	Dual Role of the Active Site Residues of <i>Thermus thermophilus</i> 3-Isopropylmalate Dehydrogenase: Chemical Catalysis and Domain Closure. <i>Biochemistry</i> , <b>2016</b> , 55, 560-74	3.2	2
94	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , <b>2016</b> , 131, 106-114	4.6	4
93	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. <i>Nature Protocols</i> , <b>2016</b> , 11, 2122-2153	18.8	98
92	The flexibility of a homeodomain transcription factor heterodimer and its allosteric regulation by DNA binding. <i>FEBS Journal</i> , <b>2016</b> , 283, 3134-54	5.7	5
91	Structure and target interaction of a G-quadruplex RNA-aptamer. <i>RNA Biology</i> , <b>2016</b> , 13, 973-987	4.8	14
90	BioSAXS Sample Changer: a robotic sample changer for rapid and reliable high-throughput X-ray solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 67-75		140
89	Limiting radiation damage for high-brilliance biological solution scattering: practical experience at the EMBL P12 beamline PETRAIII. <i>Journal of Synchrotron Radiation</i> , <b>2015</b> , 22, 273-9	2.4	92
88	Automated pipeline for purification, biophysical and x-ray analysis of biomacromolecular solutions. <i>Scientific Reports</i> , <b>2015</b> , 5, 10734	4.9	77
87	Molecular mechanism for the action of the anti-CD44 monoclonal antibody MEM-85. <i>Journal of Structural Biology</i> , <b>2015</b> , 191, 214-23	3.4	9
86	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , <b>2015</b> , 23, 1156-67	5.2	131
85	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2015</b> , 71, 76-85		45
84	A small and robust active beamstop for scattering experiments on high-brilliance undulator beamlines. <i>Journal of Synchrotron Radiation</i> , <b>2015</b> , 22, 461-4	2.4	10
83	pyDockSAXS: protein-protein complex structure by SAXS and computational docking. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W356-61	20.1	55
82	Versatile sample environments and automation for biological solution X-ray scattering experiments at the P12 beamline (PETRA III, DESY). <i>Journal of Applied Crystallography</i> , <b>2015</b> , 48, 431-443	3.8	350
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