

Dmitri I Svergun

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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	PRIMUS: a Windows PC-based system for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2003 , 36, 1277-1282	3.8	2249
219	Uniqueness of ab initio shape determination in small-angle scattering. <i>Journal of Applied Crystallography</i> , 2003 , 36, 860-864	3.8	1542
218	New developments in the program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2012 , 45, 342-350	3.8	1316
217	PRIMUS, a program for rapid shape determination in small-angle scattering. <i>Journal of Applied Crystallography</i> , 2009 , 42, 342-346	3.8	1148
216	Determination of domain structure of proteins from X-ray solution scattering. <i>Biophysical Journal</i> , 2001 , 80, 2946-53	2.9	1133
215	Structural characterization of flexible proteins using small-angle X-ray scattering. <i>Journal of the American Chemical Society</i> , 2007 , 129, 5656-64	16.4	900
214	Global rigid body modeling of macromolecular complexes against small-angle scattering data. <i>Biophysical Journal</i> , 2005 , 89, 1237-50	2.9	770
213	ATSAS2.1, a program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2006 , 39, 277-286	3.8	499
212	Small-angle scattering: a view on the properties, structures and structural changes of biological macromolecules in solution. <i>Quarterly Reviews of Biophysics</i> , 2003 , 36, 147-227	7	427
211	Structural characterization of proteins and complexes using small-angle X-ray solution scattering. <i>Journal of Structural Biology</i> , 2010 , 172, 128-41	3.4	406
210	ATSAS 2.1: towards automated and web-supported small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2007 , 40, s223-s228	3.8	355
209	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. <i>IUCrJ</i> , 2015 , 2, 207-17	4.7	353
208	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> , 2015 , 48, 431-443	3.8	350
207	A practical guide to small angle X-ray scattering (SAXS) of flexible and intrinsically disordered proteins. <i>FEBS Letters</i> , 2015 , 589, 2570-7	3.8	312
206	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	3.8	296
205	Automated acquisition and analysis of small angle X-ray scattering data. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2012 , 689, 52-59	1.2	212
204	SASBDB, a repository for biological small-angle scattering data. <i>Nucleic Acids Research</i> , 2015 , 43, D357-63	0.1	211

203	A helical structural nucleus is the primary elongating unit of insulin amyloid fibrils. <i>PLoS Biology</i> , 2007 , 5, e134	9.7	206
202	Low-resolution structure of a vesicle disrupting α -synuclein oligomer that accumulates during fibrillation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 3246-51	11.5	194
201	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014 , 42, D326-35	20.1	159
200	Small Angle X-Ray and Neutron Scattering from Solutions of Biological Macromolecules 2013 ,		153
199	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	5.5	145
198	Impact and progress in small and wide angle X-ray scattering (SAXS and WAXS). <i>Current Opinion in Structural Biology</i> , 2013 , 23, 748-54	8.1	143
197	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012 , 10, 743-767	4.2	142
196	Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. <i>Nature Methods</i> , 2015 , 12, 419-22	21.6	141
195	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> , 2015 , 71, 67-75		140
194	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> , 2017 , 114, E6342-E6351	11.5	136
193	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015 , 23, 1156-67	5.2	131
192	: expanded functionality and new tools for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2021 , 54, 343-355	3.8	120
191	The structure and regulation of human muscle β -actinin. <i>Cell</i> , 2014 , 159, 1447-60	56.2	118
190	Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012 , 68, 620-6		107
189	CHROMIXS: automatic and interactive analysis of chromatography-coupled small-angle X-ray scattering data. <i>Bioinformatics</i> , 2018 , 34, 1944-1946	7.2	104
188	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. <i>Nature Protocols</i> , 2016 , 11, 2122-2153	18.8	98
187	Deciphering conformational transitions of proteins by small angle X-ray scattering and normal mode analysis. <i>Physical Chemistry Chemical Physics</i> , 2016 , 18, 5707-19	3.6	96
186	Limiting radiation damage for high-brilliance biological solution scattering: practical experience at the EMBL P12 beamline PETRAIII. <i>Journal of Synchrotron Radiation</i> , 2015 , 22, 273-9	2.4	92

185	Ambiguity assessment of small-angle scattering curves from monodisperse systems. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 1051-8		89
184	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, 6395-403	16.4	86
183	Calcium-Driven Folding of RTX Domain \square -Rolls Ratchets Translocation of RTX Proteins through Type I Secretion Ducts. <i>Molecular Cell</i> , 2016 , 62, 47-62	17.6	86
182	Applications of small-angle X-ray scattering to biomacromolecular solutions. <i>International Journal of Biochemistry and Cell Biology</i> , 2013 , 45, 429-37	5.6	83
181	Potent and selective bivalent inhibitors of BET bromodomains. <i>Nature Chemical Biology</i> , 2016 , 12, 1097-1104		82
180	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. <i>Scientific Reports</i> , 2018 , 8, 7204	4.9	82
179	A map of protein-rRNA distribution in the 70 S Escherichia coli ribosome. <i>Journal of Biological Chemistry</i> , 2000 , 275, 14432-9	5.4	82
178	Automated pipeline for purification, biophysical and x-ray analysis of biomacromolecular solutions. <i>Scientific Reports</i> , 2015 , 5, 10734	4.9	77
177	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, 173-81	2.9	77
176	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017 , 2, 17047	26.6	74
175	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. <i>Nature Communications</i> , 2020 , 11, 5588	17.4	73
174	Resolution of shapes determined from small-angle scattering. <i>IUCrJ</i> , 2016 , 3, 440-447	4.7	69
173	Large differences are observed between the crystal and solution quaternary structures of allosteric aspartate transcarbamylase in the R state. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997 , 27, 110-117	4.2	68
172	A posteriori determination of the useful data range for small-angle scattering experiments on dilute monodisperse systems. <i>IUCrJ</i> , 2015 , 2, 352-60	4.7	65
171	Report of the wwPDB Small-Angle Scattering Task Force: data requirements for biomolecular modeling and the PDB. <i>Structure</i> , 2013 , 21, 875-81	5.2	65
170	SASBDB: Towards an automatically curated and validated repository for biological scattering data. <i>Protein Science</i> , 2020 , 29, 66-75	6.3	65
169	Conformational variability of nucleo-cytoplasmic transport factors. <i>Journal of Biological Chemistry</i> , 2004 , 279, 2176-81	5.4	63
168	Instrumental setup for high-throughput small- and wide-angle solution scattering at the X33 beamline of EMBL Hamburg. <i>Journal of Applied Crystallography</i> , 2012 , 45, 489-495	3.8	61

167	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, 4444-54	6.6	59
166	Structure of ATP citrate lyase and the origin of citrate synthase in the Krebs cycle. <i>Nature</i> , 2019 , 568, 571-575	50.4	58
165	A conformational switch in collybistin determines the differentiation of inhibitory postsynapses. <i>EMBO Journal</i> , 2014 , 33, 2113-33	13	57
164	Conformation of full-length Bruton tyrosine kinase (Btk) from synchrotron X-ray solution scattering. <i>EMBO Journal</i> , 2003 , 22, 4616-24	13	56
163	pyDockSAXS: protein-protein complex structure by SAXS and computational docking. <i>Nucleic Acids Research</i> , 2015 , 43, W356-61	20.1	55
162	Low-resolution structures of transient protein-protein complexes using small-angle X-ray scattering. <i>Journal of the American Chemical Society</i> , 2009 , 131, 4378-86	16.4	55
161	Progress in small-angle scattering from biological solutions at high-brilliance synchrotrons. <i>IUCrJ</i> , 2017 , 4, 518-528	4.7	49
160	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 76-85		45
159	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	17.6	45
158	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	6.5	45
157	Molecular basis of histone tail recognition by human TIP5 PHD finger and bromodomain of the chromatin remodeling complex NoRC. <i>Structure</i> , 2015 , 23, 80-92	5.2	44
156	Studies on the conformational changes in the bacterial cell wall biosynthetic enzyme UDP-N-acetylglucosamine enolpyruvyltransferase (MurA). <i>FEBS Journal</i> , 1998 , 253, 406-12		44
155	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	5.2	44
154	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, 882-95		42
153	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. <i>ELife</i> , 2017 , 6,	8.9	41
152	Saposin Lipid Nanoparticles: A Highly Versatile and Modular Tool for Membrane Protein Research. <i>Structure</i> , 2018 , 26, 345-355.e5	5.2	40
151	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	5.4	40
150	Escherichia coli SecA shape and dimensions. <i>FEBS Letters</i> , 1998 , 436, 277-82	3.8	40

149	Multiple assembly states of lumazine synthase: a model relating catalytic function and molecular assembly. <i>Journal of Molecular Biology</i> , 2006 , 362, 753-70	6.5	40
148	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015 , 6, 7271	17.4	38
147	An NAD Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. <i>Molecular Cell</i> , 2019 , 73, 1282-1291.e8	17.6	37
146	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. <i>MAbs</i> , 2016 , 8, 928-40	6.6	36
145	Scanning tunneling microscopy and small angle neutron scattering study of mixed monolayer protected gold nanoparticles in organic solvents. <i>Chemical Science</i> , 2014 , 5, 1232	9.4	35
144	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	6.5	35
143	LabDisk for SAXS: a centrifugal microfluidic sample preparation platform for small-angle X-ray scattering. <i>Lab on A Chip</i> , 2016 , 16, 1161-70	7.2	34
142	The CD27L and CTP1L endolysins targeting <i>Clostridia</i> contain a built-in trigger and release factor. <i>PLoS Pathogens</i> , 2014 , 10, e1004228	7.6	34
141	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. <i>Biophysical Journal</i> , 2018 , 114, 2485-2492	2.9	33
140	Quantitative 3D determination of self-assembled structures on nanoparticles using small angle neutron scattering. <i>Nature Communications</i> , 2018 , 9, 1343	17.4	32
139	The histone chaperones Vps75 and Nap1 form ring-like, tetrameric structures in solution. <i>Nucleic Acids Research</i> , 2014 , 42, 6038-51	20.1	31
138	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021 , 49, D404-D411	20.1	31
137	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, 4882-93	5.4	29
136	Weak protein-ligand interactions studied by small-angle X-ray scattering. <i>FEBS Journal</i> , 2014 , 281, 1974-87	9.7	29
135	Combining NMR and small angle X-ray scattering for the study of biomolecular structure and dynamics. <i>Archives of Biochemistry and Biophysics</i> , 2017 , 628, 33-41	4.1	28
134	The SH2 domain of Abl kinases regulates kinase autophosphorylation by controlling activation loop accessibility. <i>Nature Communications</i> , 2014 , 5, 5470	17.4	28
133	Structural Modeling Using Solution Small-Angle X-ray Scattering (SAXS). <i>Journal of Molecular Biology</i> , 2020 , 432, 3078-3092	6.5	27
132	Epsin and Sla2 form assemblies through phospholipid interfaces. <i>Nature Communications</i> , 2018 , 9, 328	17.4	26

131	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017 , 25, 1079-1088.e3	5.2	24
130	Structural Basis for Antigen Recognition by Transglutaminase 2-specific Autoantibodies in Celiac Disease. <i>Journal of Biological Chemistry</i> , 2015 , 290, 21365-75	5.4	24
129	Application of SAXS for the Structural Characterization of IDPs. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 870, 261-89	3.6	23
128	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , 2018 , 361,	33.3	23
127	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , 2018 , 9, 164	17.4	22
126	Structure of the <i>C. elegans</i> ZYG-1 cryptic polo box suggests a conserved mechanism for centriolar docking of Plk4 kinases. <i>Structure</i> , 2014 , 22, 1090-1104	5.2	22
125	RAID3--An interleukin-6 receptor-binding aptamer with post-selective modification-resistant affinity. <i>RNA Biology</i> , 2015 , 12, 1043-53	4.8	21
124	SASpy: a PyMOL plugin for manipulation and refinement of hybrid models against small angle X-ray scattering data. <i>Bioinformatics</i> , 2016 , 32, 2062-4	7.2	21
123	Reconstruction of quaternary structure from X-ray scattering by equilibrium mixtures of biological macromolecules. <i>Biochemistry</i> , 2013 , 52, 6844-55	3.2	20
122	Rapid automated superposition of shapes and macromolecular models using spherical harmonics. <i>Journal of Applied Crystallography</i> , 2016 , 49, 953-960	3.8	20
121	Structural basis for activation of plasma-membrane Ca-ATPase by calmodulin. <i>Communications Biology</i> , 2018 , 1, 206	6.7	20
120	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	3.5	20
119	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	5.4	19
118	Smaller capillaries improve the small-angle X-ray scattering signal and sample consumption for biomacromolecular solutions. <i>Journal of Synchrotron Radiation</i> , 2018 , 25, 1113-1122	2.4	19
117	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	4.9	17
116	Studying Conformational Changes of the <i>Yersinia</i> Type-III-Secretion Effector YopO in Solution by Integrative Structural Biology. <i>Structure</i> , 2019 , 27, 1416-1426.e3	5.2	16
115	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, 1304-13	2.9	16
114	Methods, development and applications of small-angle X-ray scattering to characterize biological macromolecules in solution. <i>Current Research in Structural Biology</i> , 2020 , 2, 164-170	2.8	16

113	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> , 2019 , 20,	6.3	16
112	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	2.3	15
111	Solution Behavior of the Intrinsically Disordered N-Terminal Domain of Retinoid X Receptor in the Context of the Full-Length Protein. <i>Biochemistry</i> , 2016 , 55, 1741-1748	3.2	15
110	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	5.6	15
109	Direct shape determination of intermediates in evolving macromolecular solutions from small-angle scattering data. <i>IUCrJ</i> , 2018 , 5, 402-409	4.7	15
108	Molecular Organization of Soluble Type III Secretion System Sorting Platform Complexes. <i>Journal of Molecular Biology</i> , 2019 , 431, 3787-3803	6.5	15
107	Novel thermosensitive telechelic PEGs with antioxidant activity: synthesis, molecular properties and conformational behaviour. <i>RSC Advances</i> , 2014 , 4, 41763-41771	3.7	15
106	The conundrum of the high-affinity NGF binding site formation unveiled?. <i>Biophysical Journal</i> , 2015 , 108, 687-97	2.9	15
105	Interactions of ataxin-3 with its molecular partners in the protein machinery that sorts protein aggregates to the aggresome. <i>International Journal of Biochemistry and Cell Biology</i> , 2014 , 51, 58-64	5.6	15
104	Designing a multimer allergen for diagnosis and immunotherapy of dog allergic patients. <i>PLoS ONE</i> , 2014 , 9, e111041	3.7	15
103	Small-angle X-ray and neutron scattering. <i>Nature Reviews Methods Primers</i> , 2021 , 1,		15
102	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , 2020 , 28, 348-354.e3	5.2	15
101	Small-angle X-ray solution scattering study on the dimerization of the FKBP25mem from <i>Legionella pneumophila</i> . <i>FEBS Letters</i> , 1995 , 372, 169-72	3.8	14
100	DARA: a web server for rapid search of structural neighbours using solution small angle X-ray scattering data. <i>Bioinformatics</i> , 2016 , 32, 616-8	7.2	14
99	Structure and target interaction of a G-quadruplex RNA-aptamer. <i>RNA Biology</i> , 2016 , 13, 973-987	4.8	14
98	Analysis of self-assembly of S-layer protein slp-B53 from <i>Lysinibacillus sphaericus</i> . <i>European Biophysics Journal</i> , 2017 , 46, 77-89	1.9	13
97	Extension of the sasCIF format and its applications for data processing and deposition. <i>Journal of Applied Crystallography</i> , 2016 , 49, 302-310	3.8	13
96	KSHV but not MHV-68 LANA induces a strong bend upon binding to terminal repeat viral DNA. <i>Nucleic Acids Research</i> , 2015 , 43, 10039-54	20.1	13

95	Crystal structures of substrate-bound chitinase from the psychrophilic bacterium <i>Moritella marina</i> and its structure in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 676-84		13
94	Btk SH2-kinase interface is critical for allosteric kinase activation and its targeting inhibits B-cell neoplasms. <i>Nature Communications</i> , 2020 , 11, 2319	17.4	12
93	Macromolecular pHPMA-Based Nanoparticles with Cholesterol for Solid Tumor Targeting: Behavior in HSA Protein Environment. <i>Biomacromolecules</i> , 2018 , 19, 470-480	6.9	12
92	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016 , 24, 851-61	5.2	12
91	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	2.4	12
90	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> , 2018 , 1866, 292-306	4	12
89	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> , 2018 , 25, 361-372	2.4	12
88	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	4.6	11
87	Disease Variants of FGFR3 Reveal Molecular Basis for the Recognition and Additional Roles for Cdc37 in Hsp90 Chaperone System. <i>Structure</i> , 2018 , 26, 446-458.e8	5.2	11
86	Prp19/Pso4 Is an Autoinhibited Ubiquitin Ligase Activated by Stepwise Assembly of Three Splicing Factors. <i>Molecular Cell</i> , 2018 , 69, 979-992.e6	17.6	11
85	The F1 loop of the talin head domain acts as a gatekeeper in integrin activation and clustering. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	11
84	Structural properties of [2Fe-2S] ISCA2-IBA57: a complex of the mitochondrial iron-sulfur cluster assembly machinery. <i>Scientific Reports</i> , 2019 , 9, 18986	4.9	11
83	The <i>Shigella</i> Virulence Factor IcsA Relieves N-WASP Autoinhibition by Displacing the Verprolin Homology/Cofilin/Acidic (VCA) Domain. <i>Journal of Biological Chemistry</i> , 2017 , 292, 134-145	5.4	10
82	A small and robust active beamstop for scattering experiments on high-brilliance undulator beamlines. <i>Journal of Synchrotron Radiation</i> , 2015 , 22, 461-4	2.4	10
81	Highly selective tungstate transporter protein TupA from <i>Desulfovibrio alaskensis</i> G20. <i>Scientific Reports</i> , 2017 , 7, 5798	4.9	10
80	The Redox State Regulates the Conformation of Rv2466c to Activate the Antitubercular Prodrug TP053. <i>Journal of Biological Chemistry</i> , 2015 , 290, 31077-89	5.4	10
79	Molecular mechanism for the action of the anti-CD44 monoclonal antibody MEM-85. <i>Journal of Structural Biology</i> , 2015 , 191, 214-23	3.4	9
78	An automated data processing and analysis pipeline for transmembrane proteins in detergent solutions. <i>Scientific Reports</i> , 2020 , 10, 8081	4.9	9

77	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. <i>Scientific Reports</i> , 2018 , 8, 4326	4.9	9
76	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , 2016 , 291, 14430-46	5.4	9
75	A structural model of PpoA derived from SAXS-analysis-implications for substrate conversion. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013 , 1831, 1449-57	5	9
74	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite Plasmodium falciparum. <i>Cell Reports</i> , 2020 , 31, 107817	10.6	9
73	Hallmarks of and non-structural protein 7+8 complexes. <i>Science Advances</i> , 2021 , 7,	14.3	9
72	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. <i>Scientific Reports</i> , 2016 , 6, 20915	4.9	9
71	The dimeric ectodomain of the alkali-sensing insulin receptor-related receptor (ectoIRR) has a droplike shape. <i>Journal of Biological Chemistry</i> , 2019 , 294, 17790-17798	5.4	8
70	The C-terminal random coil region tunes the Ca ²⁺ -binding affinity of S100A4 through conformational activation. <i>PLoS ONE</i> , 2014 , 9, e97654	3.7	8
69	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> , 2020 , 53, 1169-1180	3.8	8
68	EFAMIX, a tool to decompose inline chromatography SAXS data from partially overlapping components. <i>Protein Science</i> , 2021 ,	6.3	8
67	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> , 2020 , 117, 317-327	11.5	8
66	Molecular Mechanisms of the Interactions of -(2-Hydroxypropyl)methacrylamide Copolymers Designed for Cancer Therapy with Blood Plasma Proteins. <i>Pharmaceutics</i> , 2020 , 12,	6.4	7
65	Solution structure and flexibility of the condensin HEAT-repeat subunit Ycg1. <i>Journal of Biological Chemistry</i> , 2019 , 294, 13822-13829	5.4	7
64	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR-RXR. <i>Nucleic Acids Research</i> , 2020 , 48, 9969-9985	20.1	7
63	Probing the Architecture of a Multi-PDZ Domain Protein: Structure of PDZK1 in Solution. <i>Structure</i> , 2018 , 26, 1522-1533.e5	5.2	7
62	Structure-specific recognition protein-1 (SSRP1) is an elongated homodimer that binds histones. <i>Journal of Biological Chemistry</i> , 2018 , 293, 10071-10083	5.4	7
61	Utilization of Staphylococcal Immune Evasion Protein Sbi as a Novel Vaccine Adjuvant. <i>Frontiers in Immunology</i> , 2018 , 9, 3139	8.4	6
60	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> , 2019 , 9, 5822	4.9	6

59	The quaternary structure of insulin glargine and glulisine under formulation conditions. <i>Biophysical Chemistry</i> , 2019 , 253, 106226	3.5	6
58	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	3.7	6
57	Simulation of small-angle X-ray scattering data of biological macromolecules in solution. <i>Journal of Applied Crystallography</i> , 2020 , 53, 536-539	3.8	6
56	Restoring structural parameters of lipid mixtures from small-angle X-ray scattering data. <i>Journal of Applied Crystallography</i> , 2021 , 54, 169-179	3.8	6
55	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules. <i>Nature Communications</i> , 2021 , 12, 939	17.4	6
54	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> , 2017 , 7, 40408	4.9	5
53	Structural complexity of the co-chaperone SGTA: a conserved C-terminal region is implicated in dimerization and substrate quality control. <i>BMC Biology</i> , 2018 , 16, 76	7.3	5
52	Structural Insights into Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering 2010 , 451-476		5
51	Anomalous SAXS at P12 beamline EMBL Hamburg: instrumentation and applications. <i>Journal of Synchrotron Radiation</i> , 2021 , 28, 812-823	2.4	5
50	Structure of the endocytic adaptor complex reveals the basis for efficient membrane anchoring during clathrin-mediated endocytosis. <i>Nature Communications</i> , 2021 , 12, 2889	17.4	5
49	Autism-associated missense point mutations impact conformational fluctuations and protein turnover at synapses. <i>ELife</i> , 2021 , 10,	8.9	5
48	The flexibility of a homeodomain transcription factor heterodimer and its allosteric regulation by DNA binding. <i>FEBS Journal</i> , 2016 , 283, 3134-54	5.7	5
47	The allosteric modulation of complement C5 by knob domain peptides. <i>ELife</i> , 2021 , 10,	8.9	5
46	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> , 2018 , 122, 11895-11905	3.4	5
45	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, 240-5	3.8	4
44	Structural characterization of recombinant catalase-peroxidase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical Society Transactions</i> , 1997 , 25, S617	5.1	4
43	Ligands binding to the prion protein induce its proteolytic release with therapeutic potential in neurodegenerative proteinopathies. <i>Science Advances</i> , 2021 , 7, eabj1826	14.3	4
42	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> , 2020 , 53, 236-243	3.8	4

41	ASAXS measurements on ferritin and apoferritin at the bioSAXS beamline P12 (PETRA III, DESY). <i>Journal of Applied Crystallography</i> , 2021 , 54, 830-838	3.8	4
40	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016 , 131, 106-114	4.6	4
39	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021 , 17, e1009824	7.6	4
38	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	4.9	3
37	Maturation of 6S regulatory RNA to a highly elongated structure. <i>FEBS Journal</i> , 2015 , 282, 4548-64	5.7	3
36	Advances in Small- and Wide-Angle X-ray Scattering SAXS and WAXS of Proteins 2014 , 1-34		3
35	Conformational characterization of full-length X-chromosome-linked inhibitor of apoptosis protein (XIAP) through an integrated approach. <i>IUCrJ</i> , 2019 , 6, 948-957	4.7	3
34	Effect of the concentration of protein and nanoparticles on the structure of biohybrid nanocomposites. <i>Biopolymers</i> , 2020 , 111, e23342	2.2	3
33	RovC - a novel type of hexameric transcriptional activator promoting type VI secretion gene expression. <i>PLoS Pathogens</i> , 2020 , 16, e1008552	7.6	3
32	Structure of a collagen VI B chain VWA domain array: adaptability and functional implications of myopathy causing mutations. <i>Journal of Biological Chemistry</i> , 2020 , 295, 12755-12771	5.4	3
31	Molecular basis of F-actin regulation and sarcomere assembly via myotilin. <i>PLoS Biology</i> , 2021 , 19, e3001448	4.8	3
30	Capturing the Conformational Ensemble of the Mixed Folded Polyglutamine Protein Ataxin-3. <i>Structure</i> , 2021 , 29, 70-81.e5	5.2	3
29	Tetrameric Structures of Inorganic CBS-Pyrophosphatases from Various Bacterial Species Revealed by Small-Angle X-ray Scattering in Solution. <i>Biomolecules</i> , 2020 , 10,	5.9	2
28	Probing the existence of non-thermal Terahertz radiation induced changes of the protein solution structure. <i>Scientific Reports</i> , 2021 , 11, 22311	4.9	2
27	A beginner's guide to solution small-angle X-ray scattering (SAXS). <i>Biochemist</i> , 2020 , 42, 36-42	0.5	2
26	Structural role of essential light chains in the apicomplexan glideosome		2
25	Limitations of the iterative electron density reconstruction algorithm from solution scattering data. <i>Nature Methods</i> , 2021 , 18, 244-245	21.6	2
24	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	6.4	2

23	Molecular model of a sensor of two-component signaling system. <i>Scientific Reports</i> , 2021 , 11, 10774	4.9	2
22	Dual Role of the Active Site Residues of <i>Thermus thermophilus</i> 3-Isopropylmalate Dehydrogenase: Chemical Catalysis and Domain Closure. <i>Biochemistry</i> , 2016 , 55, 560-74	3.2	2
21	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	6.3	2
20	Mechanism of activation and regulation of deubiquitinase activity in MINDY1 and MINDY2. <i>Molecular Cell</i> , 2021 , 81, 4176-4190.e6	17.6	2
19	Structural Analyses of Intrinsically Disordered Proteins by Small-Angle X-Ray Scattering. <i>Methods in Molecular Biology</i> , 2020 , 2141, 249-269	1.4	2
18	A Giant Extracellular Matrix Binding Protein of Binds Surface-Immobilized Fibronectin via a Novel Mechanism. <i>MBio</i> , 2020 , 11,	7.8	1
17	Optical and Structural Characterization of a Chronic Myeloid Leukemia DNA Biosensor. <i>ACS Chemical Biology</i> , 2018 , 13, 1235-1242	4.9	1
16	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,	3.8	1
15	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	5.6	1
14	The basics of small-angle neutron scattering (SANS for new users of structural biology). <i>EPJ Web of Conferences</i> , 2020 , 236, 03001	0.3	1
13	Anomeric Selectivity of Trehalose Transferase with Rare l-Sugars. <i>ACS Catalysis</i> , 2020 , 10, 8835-8839	13.1	1
12	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread		1
11	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with β -actinin. <i>Science Advances</i> , 2021 , 7,	14.3	1
10	Large differences are observed between the crystal and solution quaternary structures of allosteric aspartate transcarbamylase in the R state 1997 , 27, 110		1
9	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	6.7	0
8	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	3.4	0
7	The prion protein and its ligands: Insights into structure-function relationships.. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2022 , 1869, 119240	4.9	0
6	Clustering in ferronematics-The effect of magnetic collective ordering.. <i>IScience</i> , 2021 , 24, 103493	6.1	

- 5 The USR domain of USF1 mediates NF-Y interactions and cooperative DNA binding. *International Journal of Biological Macromolecules*, **2021**, 193, 401-413 7.9
- 4 The SH2 Domain of BCR-ABL1 Regulates Kinase Autophosphorylation By Controlling Activation Loop Accessibility. *Blood*, **2014**, 124, 2209-2209 2.2
- 3 Application of Small-Angle X-Ray Scattering in Studies of Biological Macromolecules **2019**, 1-22
- 2 Advances in Small and Wide-Angle X-Ray Scattering from Proteins and Macromolecular Solutions **2019**, 1-39
- 1 Self-assembly and cellular effect of tau35, a disease-associated tau fragment.. *Alzheimer's and Dementia*, **2021**, 17 Suppl 3, e052072 1.2