

# Dmitri I Svergun

## List of Publications by Year in descending order

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216  
papers

24,246  
citations

20817

60  
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8396

147  
g-index

240  
all docs

240  
docs citations

240  
times ranked

20165  
citing authors

#	ARTICLE	IF	CITATIONS
1	PRIMUS: a Windows PC-based system for small-angle scattering data analysis. Journal of Applied Crystallography, 2003, 36, 1277-1282.	4.5	2,672
2	Uniqueness of <i>ab initio</i> shape determination in small-angle scattering. Journal of Applied Crystallography, 2003, 36, 860-864.	4.5	1,759
3	New developments in the <i>ATSAS</i> program package for small-angle scattering data analysis. Journal of Applied Crystallography, 2012, 45, 342-350.	4.5	1,551
4	<i>DAMMIF</i> , a program for rapid <i>ab-initio</i> shape determination in small-angle scattering. Journal of Applied Crystallography, 2009, 42, 342-346.	4.5	1,431
5	Determination of Domain Structure of Proteins from X-Ray Solution Scattering. Biophysical Journal, 2001, 80, 2946-2953.	0.5	1,309
6	Structural Characterization of Flexible Proteins Using Small-Angle X-ray Scattering. Journal of the American Chemical Society, 2007, 129, 5656-5664.	13.7	1,080
7	Global Rigid Body Modeling of Macromolecular Complexes against Small-Angle Scattering Data. Biophysical Journal, 2005, 89, 1237-1250.	0.5	846
8	ATSAS2.1, a program package for small-angle scattering data analysis. Journal of Applied Crystallography, 2006, 39, 277-286.	4.5	557
9	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. IUCr, 2015, 2, 207-217.	2.2	516
10	<i>ATSAS 3.0</i> : expanded functionality and new tools for small-angle scattering data analysis. Journal of Applied Crystallography, 2021, 54, 343-355.	4.5	512
11	Versatile sample environments and automation for biological solution X-ray scattering experiments at the P12 beamline (PETRA III, DESY). Journal of Applied Crystallography, 2015, 48, 431-443.	4.5	508
12	Small-angle scattering: a view on the properties, structures and structural changes of biological macromolecules in solution. Quarterly Reviews of Biophysics, 2003, 36, 147-227.	5.7	476
13	Structural characterization of proteins and complexes using small-angle X-ray solution scattering. Journal of Structural Biology, 2010, 172, 128-141.	2.8	470
14	A practical guide to small angle X-ray scattering (SAXS) of flexible and intrinsically disordered proteins. FEBS Letters, 2015, 589, 2570-2577.	2.8	461
15	ATSAS 2.1 – towards automated and web-supported small-angle scattering data analysis. Journal of Applied Crystallography, 2007, 40, s223-s228.	4.5	404
16	Accuracy of molecular mass determination of proteins in solution by small-angle X-ray scattering. Journal of Applied Crystallography, 2007, 40, s245-s249.	4.5	328
17	SASBDB, a repository for biological small-angle scattering data. Nucleic Acids Research, 2015, 43, D357-D363.	14.5	279
18	Automated acquisition and analysis of small angle X-ray scattering data. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 2012, 689, 52-59.	1.6	272

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19	A Helical Structural Nucleus Is the Primary Elongating Unit of Insulin Amyloid Fibrils. PLoS Biology, 2007, 5, e134.	5.6	229
20	Low-resolution structure of a vesicle disrupting $\alpha$ -synuclein oligomer that accumulates during fibrillation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3246-3251.	7.1	222
21	CHROMIXS: automatic and interactive analysis of chromatography-coupled small-angle X-ray scattering data. Bioinformatics, 2018, 34, 1944-1946.	4.1	219
22	2017 publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution: an update. Acta Crystallographica Section D: Structural Biology, 2017, 73, 710-728.	2.3	205
23	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. Nucleic Acids Research, 2014, 42, D326-D335.	14.5	195
24	Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. Nature Methods, 2015, 12, 419-422.	19.0	195
25	Decoupling of size and shape fluctuations in heteropolymeric sequences reconciles discrepancies in SAXS vs. FRET measurements. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6342-E6351.	7.1	195
26	BioSAXS Sample Changer: a robotic sample changer for rapid and reliable high-throughput X-ray solution scattering experiments. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 67-75.	2.5	181
27	The Structure and Regulation of Human Muscle $\alpha$ -Actinin. Cell, 2014, 159, 1447-1460.	28.9	178
28	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	3.9	170
29	Deciphering conformational transitions of proteins by small angle X-ray scattering and normal mode analysis. Physical Chemistry Chemical Physics, 2016, 18, 5707-5719.	2.8	161
30	Impact and progress in small and wide angle X-ray scattering (SAXS and WAXS). Current Opinion in Structural Biology, 2013, 23, 748-754.	5.7	160
31	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. Structure, 2015, 23, 1156-1167.	3.3	159
32	SASBDB: Towards an automatically curated and validated repository for biological scattering data. Protein Science, 2020, 29, 66-75.	7.6	158
33	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. Scientific Reports, 2018, 8, 7204.	3.3	154
34	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. Nature Protocols, 2016, 11, 2122-2153.	12.0	142
35	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. Nature Communications, 2020, 11, 5588.	12.8	132
36	Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 620-626.	2.5	125

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37	Ambiguity assessment of small-angle scattering curves from monodisperse systems. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1051-1058.	2.5	118
38	Limiting radiation damage for high-brilliance biological solution scattering: practical experience at the EMBL P12 beamline PETRAIII. Journal of Synchrotron Radiation, 2015, 22, 273-279.	2.4	112
39	Calcium-Driven Folding of RTX Domain $\hat{1}^2$ -Rolls Ratchets Translocation of RTX Proteins through Type I Secretion Ducts. Molecular Cell, 2016, 62, 47-62.	9.7	110
40	Potent and selective bivalent inhibitors of BET bromodomains. Nature Chemical Biology, 2016, 12, 1097-1104.	8.0	109
41	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. Nature Microbiology, 2017, 2, 17047.	13.3	102
42	Structure of ATP citrate lyase and the origin of citrate synthase in the Krebs cycle. Nature, 2019, 568, 571-575.	27.8	101
43	Automated Pipeline for Purification, Biophysical and X-Ray Analysis of Biomacromolecular Solutions. Scientific Reports, 2015, 5, 10734.	3.3	99
44	Dynamics in a Pure Encounter Complex of Two Proteins Studied by Solution Scattering and Paramagnetic NMR Spectroscopy. Journal of the American Chemical Society, 2008, 130, 6395-6403.	13.7	96
45	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. Nucleic Acids Research, 2021, 49, D404-D411.	14.5	95
46	Applications of small-angle X-ray scattering to biomacromolecular solutions. International Journal of Biochemistry and Cell Biology, 2013, 45, 429-437.	2.8	94
47	A Map of Protein-rRNA Distribution in the 70 S Escherichia coli Ribosome. Journal of Biological Chemistry, 2000, 275, 14432-14439.	3.4	92
48	Resolution of <i>ab initio</i> shapes determined from small-angle scattering. IUCr, 2016, 3, 440-447.	2.2	88
49	Solution Structure of Poly(ethylene) Glycol-Conjugated Hemoglobin Revealed by Small-Angle X-Ray Scattering: Implications for a New Oxygen Therapeutic. Biophysical Journal, 2008, 94, 173-181.	0.5	80
50	<i>A posteriori</i> determination of the useful data range for small-angle scattering experiments on dilute monodisperse systems. IUCr, 2015, 2, 352-360.	2.2	78
51	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. Structure, 2013, 21, 875-881.	3.3	77
52	Small-angle X-ray and neutron scattering. Nature Reviews Methods Primers, 2021, 1, .	21.2	77
53	Large differences are observed between the crystal and solution quaternary structures of allosteric aspartate transcarbamylase in the R state. Proteins: Structure, Function and Bioinformatics, 1997, 27, 110-117.	2.6	76
54	A conformational switch in collybistin determines the differentiation of inhibitory postsynapses. EMBO Journal, 2014, 33, 2113-2133.	7.8	75

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55	Conformational Variability of Nucleo-cytoplasmic Transport Factors. Journal of Biological Chemistry, 2004, 279, 2176-2181.	3.4	74
56	Nonstructural Proteins 7 and 8 of Feline Coronavirus Form a 2:1 Heterotrimer That Exhibits Primer-Independent RNA Polymerase Activity. Journal of Virology, 2012, 86, 4444-4454.	3.4	73
57	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. Biophysical Journal, 2018, 114, 2485-2492.	0.5	71
58	Conformation of full-length Bruton tyrosine kinase (Btk) from synchrotron X-ray solution scattering. EMBO Journal, 2003, 22, 4616-4624.	7.8	69
59	Saposin Lipid Nanoparticles: A Highly Versatile and Modular Tool for Membrane Protein Research. Structure, 2018, 26, 345-355.e5.	3.3	69
60	Progress in small-angle scattering from biological solutions at high-brilliance synchrotrons. IUCr, 2017, 4, 518-528.	2.2	67
61	Instrumental setup for high-throughput small- and wide-angle solution scattering at the X33 beamline of EMBL Hamburg. Journal of Applied Crystallography, 2012, 45, 489-495.	4.5	65
62	pyDockSAXS: protein-protein complex structure by SAXS and computational docking. Nucleic Acids Research, 2015, 43, W356-W361.	14.5	61
63	Structural Modeling Using Solution Small-Angle X-ray Scattering (SAXS). Journal of Molecular Biology, 2020, 432, 3078-3092.	4.2	61
64	Low-Resolution Structures of Transient Protein-Protein Complexes Using Small-Angle X-ray Scattering. Journal of the American Chemical Society, 2009, 131, 4378-4386.	13.7	59
65	Molecular Basis of Histone Tail Recognition by Human TIP5 PHD Finger and Bromodomain of the Chromatin Remodeling Complex NoRC. Structure, 2015, 23, 80-92.	3.3	59
66	Conformational States of ABC Transporter MsbA in a Lipid Environment Investigated by Small-Angle Scattering Using Stealth Carrier Nanodiscs. Structure, 2018, 26, 1072-1079.e4.	3.3	58
67	An NAD+ Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. Molecular Cell, 2019, 73, 1282-1291.e8.	9.7	58
68	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 76-85.	2.5	56
69	A coiled-coil domain acts as a molecular ruler to regulate O-antigen chain length in lipopolysaccharide. Nature Structural and Molecular Biology, 2015, 22, 50-56.	8.2	55
70	Quantitative 3D determination of self-assembled structures on nanoparticles using small angle neutron scattering. Nature Communications, 2018, 9, 1343.	12.8	54
71	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. Nature Communications, 2015, 6, 7271.	12.8	52
72	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. ELife, 2017, 6, .	6.0	51

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73	Studies on the conformational changes in the bacterial cell wall biosynthetic enzyme UDP-N-acetylglucosamine enolpyruvyltransferase (MurA). FEBS Journal, 1998, 253, 406-412.	0.2	50
74	The architecture of amyloid-like peptide fibrils revealed by X-ray scattering, diffraction and electron microscopy. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 882-895.	2.5	50
75	Structural Characterization of the Active and Inactive States of Src Kinase in Solution by Small-Angle X-ray Scattering. Journal of Molecular Biology, 2008, 376, 492-505.	4.2	49
76	Adding Size Exclusion Chromatography (SEC) and Light Scattering (LS) Devices to Obtain High-Quality Small Angle X-Ray Scattering (SAXS) Data. Crystals, 2020, 10, 975.	2.2	48
77	Structure of the Lassa Virus Nucleoprotein Revealed by X-ray Crystallography, Small-angle X-ray Scattering, and Electron Microscopy. Journal of Biological Chemistry, 2011, 286, 38748-38756.	3.4	47
78	Epsin and Sla2 form assemblies through phospholipid interfaces. Nature Communications, 2018, 9, 328.	12.8	47
79	Escherichia coli SecA shape and dimensions. FEBS Letters, 1998, 436, 277-282.	2.8	46
80	Combining NMR and small angle X-ray scattering for the study of biomolecular structure and dynamics. Archives of Biochemistry and Biophysics, 2017, 628, 33-41.	3.0	46
81	Structure of the C.Âelegans ZYG-1 Cryptic Polo Box Suggests a Conserved Mechanism for Centriolar Docking of Plk4 Kinases. Structure, 2014, 22, 1090-1104.	3.3	45
82	LabDisk for SAXS: a centrifugal microfluidic sample preparation platform for small-angle X-ray scattering. Lab on A Chip, 2016, 16, 1161-1170.	6.0	44
83	Multiple Assembly States of Lumazine Synthase: A Model Relating Catalytic Function and Molecular Assembly. Journal of Molecular Biology, 2006, 362, 753-770.	4.2	43
84	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. MABs, 2016, 8, 928-940.	5.2	42
85	Methods, development and applications of small-angle X-ray scattering to characterize biological macromolecules in solution. Current Research in Structural Biology, 2020, 2, 164-170.	2.2	41
86	The CD27L and CTP1L Endolysins Targeting Clostridia Contain a Built-in Trigger and Release Factor. PLoS Pathogens, 2014, 10, e1004228.	4.7	37
87	The histone chaperones Vps75 and Nap1 form ring-like, tetrameric structures in solution. Nucleic Acids Research, 2014, 42, 6038-6051.	14.5	37
88	Rapid automated superposition of shapes and macromolecular models using spherical harmonics. Journal of Applied Crystallography, 2016, 49, 953-960.	4.5	37
89	The SH2 domain of Abl kinases regulates kinase autophosphorylation by controlling activation loop accessibility. Nature Communications, 2014, 5, 5470.	12.8	36
90	Scanning tunneling microscopy and small angle neutron scattering study of mixed monolayer protected gold nanoparticles in organic solvents. Chemical Science, 2014, 5, 1232.	7.4	36

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91	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.	3.4	36
92	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , 2018, 9, 164.	12.8	36
93	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.	4.2	35
94	Weak proteinâ€“ligand interactions studied by smallâ€“angle X-ray scattering. <i>FEBS Journal</i> , 2014, 281, 1974-1987.	4.7	35
95	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017, 25, 1079-1088.e3.	3.3	34
96	Application of SAXS for the Structural Characterization of IDPs. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 261-289.	1.6	33
97	SASpy: a PyMOL plugin for manipulation and refinement of hybrid models against small angle X-ray scattering data. <i>Bioinformatics</i> , 2016, 32, 2062-2064.	4.1	30
98	Structural basis for activation of plasma-membrane Ca <sup>2+</sup> -ATPase by calmodulin. <i>Communications Biology</i> , 2018, 1, 206.	4.4	30
99	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	30
100	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.	2.6	29
101	Prp19/Pso4 Is an Autoinhibited Ubiquitin Ligase Activated by Stepwise Assembly of Three Splicing Factors. <i>Molecular Cell</i> , 2018, 69, 979-992.e6.	9.7	28
102	Molecular Organization of Soluble Type III Secretion System Sorting Platform Complexes. <i>Journal of Molecular Biology</i> , 2019, 431, 3787-3803.	4.2	28
103	Structural Kinetics of MsbA Investigated by Stopped-Flow Time-Resolved Small-Angle X-Ray Scattering. <i>Structure</i> , 2020, 28, 348-354.e3.	3.3	28
104	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules. <i>Nature Communications</i> , 2021, 12, 939.	12.8	28
105	Structural Basis for Antigen Recognition by Transglutaminase 2-specific Autoantibodies in Celiac Disease. <i>Journal of Biological Chemistry</i> , 2015, 290, 21365-21375.	3.4	27
106	Comment on “Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water”. <i>Science</i> , 2018, 361, .	12.6	27
107	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	27
108	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.	3.3	25



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109	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.	3.5	25
110	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, 860.	4.1	25
111	Reconstruction of Quaternary Structure from X-ray Scattering by Equilibrium Mixtures of Biological Macromolecules. <i>Biochemistry</i> , 2013, 52, 6844-6855.	2.5	24
112	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.	3.4	23
113	RAID3 - An interleukin-6 receptor-binding aptamer with post-selective modification-resistant affinity. <i>RNA Biology</i> , 2015, 12, 1043-1053.	3.1	23
114	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2020, 31, 107817.	6.4	23
115	Btk SH2-kinase interface is critical for allosteric kinase activation and its targeting inhibits B-cell neoplasms. <i>Nature Communications</i> , 2020, 11, 2319.	12.8	23
116	Structural properties of [2Fe-2S] ISCA2-IBA57: a complex of the mitochondrial iron-sulfur cluster assembly machinery. <i>Scientific Reports</i> , 2019, 9, 18986.	3.3	22
117	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016, 24, 851-861.	3.3	21
118	The allosteric modulation of complement C5 by knob domain peptides. <i>ELife</i> , 2021, 10, .	6.0	21
119	The Conundrum of the High-Affinity NGF Binding Site Formation Unveiled?. <i>Biophysical Journal</i> , 2015, 108, 687-697.	0.5	20
120	Structure and target interaction of a G-quadruplex RNA-aptamer. <i>RNA Biology</i> , 2016, 13, 973-987.	3.1	20
121	Direct shape determination of intermediates in evolving macromolecular solutions from small-angle scattering data. <i>IUCr</i> , 2018, 5, 402-409.	2.2	20
122	Hallmarks of $\alpha$ - and $\beta$ -coronavirus non-structural protein 7+8 complexes. <i>Science Advances</i> , 2021, 7, .	10.3	20
123	Designing a Multimer Allergen for Diagnosis and Immunotherapy of Dog Allergic Patients. <i>PLoS ONE</i> , 2014, 9, e111041.	2.5	20
124	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.	0.5	19
125	Solution Behavior of the Intrinsically Disordered N-Terminal Domain of Retinoid X Receptor $\hat{1}$ in the Context of the Full-Length Protein. <i>Biochemistry</i> , 2016, 55, 1741-1748.	2.5	19
126	Analysis of self-assembly of S-layer protein slp-B53 from <i>Lysinibacillus sphaericus</i> . <i>European Biophysics Journal</i> , 2017, 46, 77-89.	2.2	19



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127	Studying Conformational Changes of the Yersinia Type-III-Secretion Effector YopO in Solution by Integrative Structural Biology. <i>Structure</i> , 2019, 27, 1416-1426.e3.	3.3	19
128	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	4.7	19
129	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.	2.8	18
130	Extension of the sasCIF format and its applications for data processing and deposition. <i>Journal of Applied Crystallography</i> , 2016, 49, 302-310.	4.5	18
131	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, .	2.0	18
132	Mechanism of activation and regulation of deubiquitinase activity in MINDY1 and MINDY2. <i>Molecular Cell</i> , 2021, 81, 4176-4190.e6.	9.7	18
133	Ligands binding to the prion protein induce its proteolytic release with therapeutic potential in neurodegenerative proteinopathies. <i>Science Advances</i> , 2021, 7, eabj1826.	10.3	18
134	Small-angle X-ray solution scattering study on the dimerization of the FKBP25mem from <i>Legionella pneumophila</i> . <i>FEBS Letters</i> , 1995, 372, 169-172.	2.8	17
135	Novel thermosensitive telechelic PEGs with antioxidant activity: synthesis, molecular properties and conformational behaviour. <i>RSC Advances</i> , 2014, 4, 41763-41771.	3.6	17
136	The Redox State Regulates the Conformation of Rv2466c to Activate the Antitubercular Prodrug TP053. <i>Journal of Biological Chemistry</i> , 2015, 290, 31077-31089.	3.4	17
137	DARA: a web server for rapid search of structural neighbours using solution small angle X-ray scattering data. <i>Bioinformatics</i> , 2016, 32, 616-618.	4.1	17
138	Macromolecular <i>p</i> -HPMA-Based Nanoparticles with Cholesterol for Solid Tumor Targeting: Behavior in HSA Protein Environment. <i>Biomacromolecules</i> , 2018, 19, 470-480.	5.4	17
139	Structural basis for DNA recognition and allosteric control of the retinoic acid receptors RAR/RXR. <i>Nucleic Acids Research</i> , 2020, 48, 9969-9985.	14.5	17
140	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.	7.1	17
141	Restoring structural parameters of lipid mixtures from small-angle X-ray scattering data. <i>Journal of Applied Crystallography</i> , 2021, 54, 169-179.	4.5	17
142	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.	4.5	17
143	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , 2016, 291, 14430-14446.	3.4	16
144	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.	3.4	16

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145	<sc>EFAMIX</sc>, a tool to decompose inline chromatography <sc>SAXS</sc> data from partially overlapping components. Protein Science, 2022, 31, 269-282.	7.6	16
146	KSHV but not MHV-68 LANA induces a strong bend upon binding to terminal repeat viral DNA. Nucleic Acids Research, 2015, 43, gkv987.	14.5	15
147	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. Scientific Reports, 2018, 8, 4326.	3.3	15
148	Multi-channel<i>in situ</i> dynamic light scattering instrumentation enhancing biological small-angle X-ray scattering experiments at the PETRA III beamline P12. Journal of Synchrotron Radiation, 2018, 25, 361-372.	2.4	15
149	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with $\beta$ -actinin. Science Advances, 2021, 7, .	10.3	15
150	Structural insights of Rm Xyn10A – A prebiotic-producing GH10 xylanase with a non-conserved aglycone binding region. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 292-306.	2.3	14
151	Molecular model of a sensor of two-component signaling system. Scientific Reports, 2021, 11, 10774.	3.3	14
152	Autism-associated SHANK3 missense point mutations impact conformational fluctuations and protein turnover at synapses. ELife, 2021, 10, .	6.0	14
153	Crystal structures of substrate-bound chitinase from the psychrophilic bacterium <i>Moritella marina</i> and its structure in solution. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 676-684.	2.5	13
154	Molecular mechanism for the action of the anti-CD44 monoclonal antibody MEM-85. Journal of Structural Biology, 2015, 191, 214-223.	2.8	13
155	A small and robust active beamstop for scattering experiments on high-brilliance undulator beamlines. Journal of Synchrotron Radiation, 2015, 22, 461-464.	2.4	13
156	Functional interaction of low-homology FRPs from different cyanobacteria with Synechocystis OCP. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, 382-393.	1.0	13
157	Disease Variants of FGFR3 Reveal Molecular Basis for the Recognition and Additional Roles for Cdc37 in Hsp90 Chaperone System. Structure, 2018, 26, 446-458.e8.	3.3	13
158	Utilization of Staphylococcal Immune Evasion Protein Sbi as a Novel Vaccine Adjuvant. Frontiers in Immunology, 2018, 9, 3139.	4.8	13
159	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. Journal of Chemical Theory and Computation, 2021, 17, 2014-2021.	5.3	13
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