

# Dmitri I Svergun

## List of Publications by Year in descending order

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216  
papers

24,246  
citations

22099

59  
h-index

8370

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. <i>Journal of Applied Crystallography</i> , 2003, 36, 1277-1282.	1.9	2,672
2	Uniqueness of ab initio shape determination in small-angle scattering. <i>Journal of Applied Crystallography</i> , 2003, 36, 860-864.	1.9	1,759
3	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
4	<i>DAMMIF</i> , a program for rapid <i>ab-initio</i> shape determination in small-angle scattering. <i>Journal of Applied Crystallography</i> , 2009, 42, 342-346.	1.9	1,431
5	Determination of Domain Structure of Proteins from X-Ray Solution Scattering. <i>Biophysical Journal</i> , 2001, 80, 2946-2953.	0.2	1,309
6	Structural Characterization of Flexible Proteins Using Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2007, 129, 5656-5664.	6.6	1,080
7	Global Rigid Body Modeling of Macromolecular Complexes against Small-Angle Scattering Data. <i>Biophysical Journal</i> , 2005, 89, 1237-1250.	0.2	846
8	ATSAS2.1, a program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2006, 39, 277-286.	1.9	557
9	Advanced ensemble modelling of flexible macromolecules using X-ray solution scattering. <i>IUCr</i> , 2015, 2, 207-217.	1.0	516
10	<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
11	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.	1.9	508
12	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.	2.4	476
13	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
14	A practical guide to small angle X-ray scattering (SAXS) of flexible and intrinsically disordered proteins. <i>FEBS Letters</i> , 2015, 589, 2570-2577.	1.3	461
15	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
16	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
17	SASBDB, a repository for biological small-angle scattering data. <i>Nucleic Acids Research</i> , 2015, 43, D357-D363.	6.5	279
18	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.	0.7	272

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19	A Helical Structural Nucleus Is the Primary Elongating Unit of Insulin Amyloid Fibrils. <i>PLoS Biology</i> , 2007, 5, e134.	2.6	229
20	Low-resolution structure of a vesicle disrupting $\hat{\alpha}$ -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
21	CHROMIXS: automatic and interactive analysis of chromatography-coupled small-angle X-ray scattering data. <i>Bioinformatics</i> , 2018, 34, 1944-1946.	1.8	219
22	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
23	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , 2014, 42, D326-D335.	6.5	195
24	Correlation Map, a goodness-of-fit test for one-dimensional X-ray scattering spectra. <i>Nature Methods</i> , 2015, 12, 419-422.	9.0	195
25	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.	3.3	195
26	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.	2.5	181
27	The Structure and Regulation of Human Muscle $\hat{\alpha}$ -Actinin. <i>Cell</i> , 2014, 159, 1447-1460.	13.5	178
28	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	2.5	170
29	Deciphering conformational transitions of proteins by small angle X-ray scattering and normal mode analysis. <i>Physical Chemistry Chemical Physics</i> , 2016, 18, 5707-5719.	1.3	161
30	Impact and progress in small and wide angle X-ray scattering (SAXS and WAXS). <i>Current Opinion in Structural Biology</i> , 2013, 23, 748-754.	2.6	160
31	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	1.6	159
32	SASBDB: Towards an automatically curated and validated repository for biological scattering data. <i>Protein Science</i> , 2020, 29, 66-75.	3.1	158
33	Consensus Bayesian assessment of protein molecular mass from solution X-ray scattering data. <i>Scientific Reports</i> , 2018, 8, 7204.	1.6	154
34	Preparing monodisperse macromolecular samples for successful biological small-angle X-ray and neutron-scattering experiments. <i>Nature Protocols</i> , 2016, 11, 2122-2153.	5.5	142
35	Selection, biophysical and structural analysis of synthetic nanobodies that effectively neutralize SARS-CoV-2. <i>Nature Communications</i> , 2020, 11, 5588.	5.8	132
36	Publication guidelines for structural modelling of small-angle scattering data from biomolecules in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 620-626.	2.5	125

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37	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
38	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, 273-279.	1.0	112
39	Calcium-Driven Folding of RTX Domain $\hat{1}^2$ -Rolls Ratchets Translocation of RTX Proteins through Type I Secretion Ducts. <i>Molecular Cell</i> , 2016, 62, 47-62.	4.5	110
40	Potent and selective bivalent inhibitors of BET bromodomains. <i>Nature Chemical Biology</i> , 2016, 12, 1097-1104.	3.9	109
41	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
42	Structure of ATP citrate lyase and the origin of citrate synthase in the Krebs cycle. <i>Nature</i> , 2019, 568, 571-575.	13.7	101
43	Automated Pipeline for Purification, Biophysical and X-Ray Analysis of Biomacromolecular Solutions. <i>Scientific Reports</i> , 2015, 5, 10734.	1.6	99
44	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
45	PED in 2021: a major update of the protein ensemble database for intrinsically disordered proteins. <i>Nucleic Acids Research</i> , 2021, 49, D404-D411.	6.5	95
46	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
47	A Map of Protein-rRNA Distribution in the 70 <i>Escherichia coli</i> Ribosome. <i>Journal of Biological Chemistry</i> , 2000, 275, 14432-14439.	1.6	92
48	Resolution of <i>ab initio</i> shapes determined from small-angle scattering. <i>IUCr</i> , 2016, 3, 440-447.	1.0	88
49	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
50	<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
51	Report of the wwPDB Small-Angle Scattering Task Force: Data Requirements for Biomolecular Modeling and the PDB. <i>Structure</i> , 2013, 21, 875-881.	1.6	77
52	Small-angle X-ray and neutron scattering. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	77
53	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.	1.5	76
54	A conformational switch in collybistin determines the differentiation of inhibitory postsynapses. <i>EMBO Journal</i> , 2014, 33, 2113-2133.	3.5	75

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55	Conformational Variability of Nucleo-cytoplasmic Transport Factors. <i>Journal of Biological Chemistry</i> , 2004, 279, 2176-2181.	1.6	74
56	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
57	Machine Learning Methods for X-Ray Scattering Data Analysis from Biomacromolecular Solutions. <i>Biophysical Journal</i> , 2018, 114, 2485-2492.	0.2	71
58	Conformation of full-length Bruton tyrosine kinase (Btk) from synchrotron X-ray solution scattering. <i>EMBO Journal</i> , 2003, 22, 4616-4624.	3.5	69
59	Saposin Lipid Nanoparticles: A Highly Versatile and Modular Tool for Membrane Protein Research. <i>Structure</i> , 2018, 26, 345-355.e5.	1.6	69
60	Progress in small-angle scattering from biological solutions at high-brilliance synchrotrons. <i>IUCr</i> , 2017, 4, 518-528.	1.0	67
61	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.	1.9	65
62	pyDockSAXS: protein-protein complex structure by SAXS and computational docking. <i>Nucleic Acids Research</i> , 2015, 43, W356-W361.	6.5	61
63	Structural Modeling Using Solution Small-Angle X-ray Scattering (SAXS). <i>Journal of Molecular Biology</i> , 2020, 432, 3078-3092.	2.0	61
64	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
65	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.	1.6	59
66	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
67	An NAD <sup>+</sup> Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. <i>Molecular Cell</i> , 2019, 73, 1282-1291.e8.	4.5	58
68	ISPyB for BioSAXS, the gateway to user autonomy in solution scattering experiments. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 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. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 50-56.	3.6	55
70	Quantitative 3D determination of self-assembled structures on nanoparticles using small angle neutron scattering. <i>Nature Communications</i> , 2018, 9, 1343.	5.8	54
71	Cooperative folding of intrinsically disordered domains drives assembly of a strong elongated protein. <i>Nature Communications</i> , 2015, 6, 7271.	5.8	52
72	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. <i>ELife</i> , 2017, 6, .	2.8	51

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73	Studies on the conformational changes in the bacterial cell wall biosynthetic enzyme UDP-N-acetylglucosamine enolpyruvyltransferase (MurA). <i>FEBS Journal</i> , 1998, 253, 406-412.	0.2	50
74	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
75	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
76	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
77	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
78	Epsin and Sla2 form assemblies through phospholipid interfaces. <i>Nature Communications</i> , 2018, 9, 328.	5.8	47
79	Escherichia coli SecA shape and dimensions. <i>FEBS Letters</i> , 1998, 436, 277-282.	1.3	46
80	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.	1.4	46
81	Structure of the C.Âlegans 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
82	LabDisk for SAXS: a centrifugal microfluidic sample preparation platform for small-angle X-ray scattering. <i>Lab on A Chip</i> , 2016, 16, 1161-1170.	3.1	44
83	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
84	Characterization of mAb dimers reveals predominant dimer forms common in therapeutic mAbs. <i>MABs</i> , 2016, 8, 928-940.	2.6	42
85	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.	1.1	41
86	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
87	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
88	Rapid automated superposition of shapes and macromolecular models using spherical harmonics. <i>Journal of Applied Crystallography</i> , 2016, 49, 953-960.	1.9	37
89	The SH2 domain of Abl kinases regulates kinase autophosphorylation by controlling activation loop accessibility. <i>Nature Communications</i> , 2014, 5, 5470.	5.8	36
90	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.	3.7	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.	1.6	36
92	Signaling ammonium across membranes through an ammonium sensor histidine kinase. <i>Nature Communications</i> , 2018, 9, 164.	5.8	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.	2.0	35
94	Weak protein-ligand interactions studied by small-angle X-ray scattering. <i>FEBS Journal</i> , 2014, 281, 1974-1987.	2.2	35
95	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017, 25, 1079-1088.e3.	1.6	34
96	Application of SAXS for the Structural Characterization of IDPs. <i>Advances in Experimental Medicine and Biology</i> , 2015, 870, 261-289.	0.8	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.	1.8	30
98	Structural basis for activation of plasma-membrane Ca <sup>2+</sup> -ATPase by calmodulin. <i>Communications Biology</i> , 2018, 1, 206.	2.0	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.	1.0	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.	1.1	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.	4.5	28
102	Molecular Organization of Soluble Type III Secretion System Sorting Platform Complexes. <i>Journal of Molecular Biology</i> , 2019, 431, 3787-3803.	2.0	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.	1.6	28
104	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules. <i>Nature Communications</i> , 2021, 12, 939.	5.8	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.	1.6	27
106	Comment on "Innovative scattering analysis shows that hydrophobic disordered proteins are expanded in water". <i>Science</i> , 2018, 361, .	6.0	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.	1.0	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.	1.6	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.	1.6	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.	1.8	25
111	Reconstruction of Quaternary Structure from X-ray Scattering by Equilibrium Mixtures of Biological Macromolecules. <i>Biochemistry</i> , 2013, 52, 6844-6855.	1.2	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.	1.6	23
113	RAID3 - An interleukin-6 receptor-binding aptamer with post-selective modification-resistant affinity. <i>RNA Biology</i> , 2015, 12, 1043-1053.	1.5	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.	2.9	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.	5.8	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.	1.6	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.	1.6	21
118	The allosteric modulation of complement C5 by knob domain peptides. <i>ELife</i> , 2021, 10, .	2.8	21
119	The Conundrum of the High-Affinity NGF Binding Site Formation Unveiled?. <i>Biophysical Journal</i> , 2015, 108, 687-697.	0.2	20
120	Structure and target interaction of a G-quadruplex RNA-aptamer. <i>RNA Biology</i> , 2016, 13, 973-987.	1.5	20
121	Direct shape determination of intermediates in evolving macromolecular solutions from small-angle scattering data. <i>IUCr</i> , 2018, 5, 402-409.	1.0	20
122	Hallmarks of $\alpha$ - and $\beta$ -coronavirus non-structural protein 7+8 complexes. <i>Science Advances</i> , 2021, 7, .	4.7	20
123	Designing a Multimer Allergen for Diagnosis and Immunotherapy of Dog Allergic Patients. <i>PLoS ONE</i> , 2014, 9, e111041.	1.1	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.	0.2	19
125	Solution Behavior of the Intrinsically Disordered N-Terminal Domain of Retinoid X Receptor $\beta$ in the Context of the Full-Length Protein. <i>Biochemistry</i> , 2016, 55, 1741-1748.	1.2	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.	1.2	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.	1.6	19
128	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	2.1	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.	1.2	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.	1.9	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, .	1.2	18
132	Mechanism of activation and regulation of deubiquitinase activity in MINDY1 and MINDY2. <i>Molecular Cell</i> , 2021, 81, 4176-4190.e6.	4.5	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.	4.7	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.	1.3	17
135	Novel thermosensitive telechelic PEGs with antioxidant activity: synthesis, molecular properties and conformational behaviour. <i>RSC Advances</i> , 2014, 4, 41763-41771.	1.7	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.	1.6	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.	1.8	17
138	Macromolecular <i>HPMA</i> -Based Nanoparticles with Cholesterol for Solid Tumor Targeting: Behavior in HSA Protein Environment. <i>Biomacromolecules</i> , 2018, 19, 470-480.	2.6	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.	6.5	17
140	Molecular mechanism of leukocidin <i>GH</i> -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.	3.3	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.	1.9	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.	1.9	17
143	Structural Insights into the Polyphyletic Origins of Glycyl tRNA Synthetases. <i>Journal of Biological Chemistry</i> , 2016, 291, 14430-14446.	1.6	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.	1.6	16

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145	<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
146	KSHV but not MHV-68 LANA induces a strong bend upon binding to terminal repeat viral DNA. <i>Nucleic Acids Research</i> , 2015, 43, gkv987.	6.5	15
147	Structural model of human dUTPase in complex with a novel proteinaceous inhibitor. <i>Scientific Reports</i> , 2018, 8, 4326.	1.6	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. <i>Journal of Synchrotron Radiation</i> , 2018, 25, 361-372.	1.0	15
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