

# Maxim V Petoukhov

## List of Publications by Year in descending order

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74  
papers

10,201  
citations

126708

33  
h-index

82410

72  
g-index

76  
all docs

76  
docs citations

76  
times ranked

12242  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Determination of Domain Structure of Proteins from X-Ray Solution Scattering. <i>Biophysical Journal</i> , 2001, 80, 2946-2953.	0.2	1,309
3	<i>ATSAS 2.8</i> : a comprehensive data analysis suite for small-angle scattering from macromolecular solutions. <i>Journal of Applied Crystallography</i> , 2017, 50, 1212-1225.	1.9	1,205
4	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
5	Global Rigid Body Modeling of Macromolecular Complexes against Small-Angle Scattering Data. <i>Biophysical Journal</i> , 2005, 89, 1237-1250.	0.2	846
6	ATSAS2.1, a program package for small-angle scattering data analysis. <i>Journal of Applied Crystallography</i> , 2006, 39, 277-286.	1.9	557
7	<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
8	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
9	Analysis of X-ray and neutron scattering from biomacromolecular solutions. <i>Current Opinion in Structural Biology</i> , 2007, 17, 562-571.	2.6	201
10	Structural basis of hepatocyte growth factor/scatter factor and MET signalling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4046-4051.	3.3	193
11	Conformational Space of Flexible Biological Macromolecules from Average Data. <i>Journal of the American Chemical Society</i> , 2010, 132, 13553-13558.	6.6	155
12	MASSHA – a graphics system for rigid-body modelling of macromolecular complexes against solution scattering data. <i>Journal of Applied Crystallography</i> , 2001, 34, 527-532.	1.9	136
13	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
14	Addition of Missing Loops and Domains to Protein Models by X-Ray Solution Scattering. <i>Biophysical Journal</i> , 2002, 83, 3113-3125.	0.2	96
15	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
16	Chemical Basis of Peptidoglycan Discrimination by PrkC, a Key Kinase Involved in Bacterial Resuscitation from Dormancy. <i>Journal of the American Chemical Society</i> , 2011, 133, 20676-20679.	6.6	89
17	The Active Conformation of Glutamate Synthase and its Binding to Ferredoxin. <i>Journal of Molecular Biology</i> , 2003, 330, 113-128.	2.0	85
18	Ceruloplasmin: Macromolecular Assemblies with Iron-Containing Acute Phase Proteins. <i>PLoS ONE</i> , 2013, 8, e67145.	1.1	82

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19	X-Ray Scattering Study of Activated Arp2/3 Complex with Bound Actin-WCA. <i>Structure</i> , 2008, 16, 695-704.	1.6	71
20	A Common Structural Basis for pH- and Calmodulin-mediated Regulation in Plant Glutamate Decarboxylase. <i>Journal of Molecular Biology</i> , 2009, 392, 334-351.	2.0	71
21	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
22	Joint use of small-angle X-ray and neutron scattering to study biological macromolecules in solution. <i>European Biophysics Journal</i> , 2006, 35, 567-576.	1.2	68
23	Quaternary structure of the human Cdt1-Geminin complex regulates DNA replication licensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19807-19812.	3.3	67
24	Conformation of Polypyrimidine Tract Binding Protein in Solution. <i>Structure</i> , 2006, 14, 1021-1027.	1.6	60
25	Triticum durum Metallothionein. <i>Journal of Biological Chemistry</i> , 2005, 280, 13701-13711.	1.6	54
26	Structural reorganization of the chromatin remodeling enzyme Chd1 upon engagement with nucleosomes. <i>ELife</i> , 2017, 6, .	2.8	51
27	New methods for domain structure determination of proteins from solution scattering data. <i>Journal of Applied Crystallography</i> , 2003, 36, 540-544.	1.9	47
28	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
29	Interaction between the C-terminal region of human myelin basic protein and calmodulin: analysis of complex formation and solution structure. <i>BMC Structural Biology</i> , 2008, 8, 10.	2.3	43
30	Flexible segments modulate co-folding of dUTPase and nucleocapsid proteins. <i>Nucleic Acids Research</i> , 2006, 35, 495-505.	6.5	42
31	Crystal Versus Solution Structures of Thiamine Diphosphate-dependent Enzymes. <i>Journal of Biological Chemistry</i> , 2000, 275, 297-302.	1.6	40
32	Engineering the NK1 Fragment of Hepatocyte Growth Factor/Scatter Factor as a MET Receptor Antagonist. <i>Journal of Molecular Biology</i> , 2008, 377, 616-622.	2.0	38
33	Rapid automated superposition of shapes and macromolecular models using spherical harmonics. <i>Journal of Applied Crystallography</i> , 2016, 49, 953-960.	1.9	37
34	MaxOcc: a web portal for maximum occurrence analysis. <i>Journal of Biomolecular NMR</i> , 2012, 53, 271-280.	1.6	36
35	Using stable MutS dimers and tetramers to quantitatively analyze DNA mismatch recognition and sliding clamp formation. <i>Nucleic Acids Research</i> , 2013, 41, 8166-8181.	6.5	36
36	X-ray and Neutron Small-Angle Scattering Analysis of the Complex Formed by the Met Receptor and the <i>Listeria monocytogenes</i> Invasion Protein InlB. <i>Journal of Molecular Biology</i> , 2008, 377, 489-500.	2.0	34

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37	The Asymmetric Binding of PGC-1 $\beta$ to the ERR $\alpha$ and ERR $\beta$ Nuclear Receptor Homodimers Involves a Similar Recognition Mechanism. <i>PLoS ONE</i> , 2013, 8, e67810.	1.1	34
38	A Spring-Loaded Mechanism Governs the Clamp-like Dynamics of the Skp Chaperone. <i>Structure</i> , 2017, 25, 1079-1088.e3.	1.6	34
39	The Subnanometer Resolution Structure of the Glutamate Synthase 1.2-MDa Hexamer by Cryoelectron Microscopy and Its Oligomerization Behavior in Solution. <i>Journal of Biological Chemistry</i> , 2008, 283, 8237-8249.	1.6	30
40	Low Resolution Structure Determination Shows Procollagen C-Proteinase Enhancer to be an Elongated Multidomain Glycoprotein. <i>Journal of Biological Chemistry</i> , 2003, 278, 7199-7205.	1.6	29
41	Small Angle X-Ray Scattering Studies of Mitochondrial Glutaminase C Reveal Extended Flexible Regions, and Link Oligomeric State with Enzyme Activity. <i>PLoS ONE</i> , 2013, 8, e74783.	1.1	29
42	Robo1 Forms a Compact Dimer-of-Dimers Assembly. <i>Structure</i> , 2018, 26, 320-328.e4.	1.6	28
43	Protective Dps DNA co-crystallization in stressed cells: an <i>in vitro</i> structural study by small angle X-ray scattering and cryo-electron tomography. <i>FEBS Letters</i> , 2019, 593, 1360-1371.	1.3	28
44	Evidence for a dimeric assembly of two titin/telethonin complexes induced by the telethonin C-terminus. <i>Journal of Structural Biology</i> , 2006, 155, 239-250.	1.3	25
45	Reconstruction of Quaternary Structure from X-ray Scattering by Equilibrium Mixtures of Biological Macromolecules. <i>Biochemistry</i> , 2013, 52, 6844-6855.	1.2	24
46	Molecular shape and prominent role of $\beta$ -strand swapping in organization of dUTPase oligomers. <i>FEBS Letters</i> , 2009, 583, 865-871.	1.3	23
47	Kinetic and mechanistic characterization of <i>Mycobacterium tuberculosis</i> glutamyl-tRNA synthetase and determination of its oligomeric structure in solution. <i>FEBS Journal</i> , 2009, 276, 1398-1417.	2.2	23
48	Quaternary Structure of <i>Azospirillum brasilense</i> NADPH-dependent Glutamate Synthase in Solution as Revealed by Synchrotron Radiation X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2003, 278, 29933-29939.	1.6	21
49	Structural characterization of the nonameric assembly of an Archaeal $\beta$ -l-fucosidase by synchrotron small angle X-ray scattering. <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 176-182.	1.0	21
50	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
51	The solution structure and dynamics of the DH $\alpha$ PH module of PDZRhoGEF in isolation and in complex with nucleotide-free RhoA. <i>Protein Science</i> , 2009, 18, 2067-2079.	3.1	18
52	Hybrid Polycarbosilane-Siloxane Dendrimers: Synthesis and Properties. <i>Polymers</i> , 2021, 13, 606.	2.0	17
53	Spatial organization of Dps and DNA-Dps complexes. <i>Journal of Molecular Biology</i> , 2021, 433, 166930.	2.0	17
54	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

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55	Quaternary Structure of Flavorubredoxin as Revealed by Synchrotron Radiation Small-Angle X-Ray Scattering. <i>Structure</i> , 2008, 16, 1428-1436.	1.6	14
56	Structural insights of Rm Xyn10A – A prebiotic-producing GH10 xylanase with a non-conserved aglycone binding region. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 292-306.	1.1	14
57	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, 676-684.	2.5	13
58	Polymorphic Protective Dps–DNA Co-Crystals by Cryo Electron Tomography and Small Angle X-Ray Scattering. <i>Biomolecules</i> , 2020, 10, 39.	1.8	13
59	Comment on the Optimal Parameters to Derive Intrinsically Disordered Protein Conformational Ensembles from Small-Angle X-ray Scattering Data Using the Ensemble Optimization Method. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2014-2021.	2.3	13
60	The C-Terminal Random Coil Region Tunes the Ca <sup>2+</sup> -Binding Affinity of S100A4 through Conformational Activation. <i>PLoS ONE</i> , 2014, 9, e97654.	1.1	11
61	Conformational plasticity of RepB, the replication initiator protein of promiscuous streptococcal plasmid pMV158. <i>Scientific Reports</i> , 2016, 6, 20915.	1.6	11
62	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.	1.6	10
63	Structural peculiarities of lysozyme – PLURONIC complexes at the aqueous-air and liquid-liquid interfaces and in the bulk of aqueous solution. <i>International Journal of Biological Macromolecules</i> , 2020, 158, 721-731.	3.6	8
64	Fine-tuning of intrinsic N-Oct-3 POU domain allostery by regulatory DNA targets. <i>Nucleic Acids Research</i> , 2007, 35, 4420-4432.	6.5	7
65	Human MICAL1: Activation by the small GTPase Rab8 and small-angle X-ray scattering studies on the oligomerization state of MICAL1 and its complex with Rab8. <i>Protein Science</i> , 2019, 28, 150-166.	3.1	7
66	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.	1.9	7
67	Proteins involved in sleep homeostasis: Biophysical characterization of INC and its partners. <i>Biochimie</i> , 2016, 131, 106-114.	1.3	6
68	The structure of the unliganded extracellular domain of the interleukin-6 signal transducer gp130 in solution. <i>European Journal of Cell Biology</i> , 2011, 90, 515-520.	1.6	4
69	Endophilin-A1 BAR domain interaction with arachidonyl CoA. <i>Frontiers in Molecular Biosciences</i> , 2014, 1, 20.	1.6	3
70	The Structure of the Potato Virus A Particles Elucidated by Small Angle X-Ray Scattering and Complementary Techniques. <i>Biochemistry (Moscow)</i> , 2021, 86, 230-240.	0.7	3
71	SAS-Based Structural Modelling and Model Validation. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1009, 87-105.	0.8	1
72	Formation of Iron Oxide Nanoparticles in the Internal Cavity of Ferritin-Like Dps Protein: Studies by Anomalous X-Ray Scattering. <i>Biochemistry (Moscow)</i> , 2022, 87, 511-523.	0.7	1

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73	Comparative Characterization of Apo-, Reconstituted- and In Vivo-Folded forms of a Durum Wheat Metallothionein. <i>Biophysical Journal</i> , 2013, 104, 396a.	0.2	0
74	ATSAS 2.8 software for small-angle scattering from macromolecular solutions. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C647-C647.	0.0	0