

# Oleg V Sobolev

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

8,094  
citations

623188

14  
h-index

752256

20  
g-index

30  
all docs

30  
docs citations

30  
times ranked

12074  
citing authors

#	ARTICLE	IF	CITATIONS
1	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	2.0	39
2	Protein identification from electron cryomicroscopy maps by automated model building and side-chain matching. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 457-462.	1.1	9
3	Macromolecular refinement of X-ray and cryoelectron microscopy structures with Phenix/OPLS3e for improved structure and ligand quality. <i>Structure</i> , 2021, 29, 913-921.e4.	1.6	29
4	Cryo-EM map interpretation and protein model building using iterative map segmentation. <i>Protein Science</i> , 2020, 29, 87-99.	3.1	27
5	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , 2020, 28, 1249-1258.e2.	1.6	86
6	Density modification of cryo-EM maps. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 912-925.	1.1	28
7	Real-space quantum-based refinement for cryo-EM: <i>Q</i>   <i>R</i> #3. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1184-1191.	1.1	7
8	Cryo_fit: Democratization of flexible fitting for cryo-EM. <i>Journal of Structural Biology</i> , 2019, 208, 1-6.	1.3	30
9	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	1.1	46
10	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	1.1	4,060
11	A fully automatic method yielding initial models from high-resolution cryo-electron microscopy maps. <i>Nature Methods</i> , 2018, 15, 905-908.	9.0	137
12	Map segmentation, automated model-building and their application to the Cryo-EM Model Challenge. <i>Journal of Structural Biology</i> , 2018, 204, 338-343.	1.3	6
13	Automated map sharpening by maximization of detail and connectivity. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 545-559.	1.1	218
14	Real-space refinement in <i>PHENIX</i> for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	1.1	2,065
15	New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 814-840.	1.1	575
16	Polder maps: improving OMIT maps by excluding bulk solvent. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 148-157.	1.1	500
17	Programming new geometry restraints: parallelity of atomic groups. <i>Journal of Applied Crystallography</i> , 2015, 48, 1130-1141.	1.9	13
18	FEM: feature-enhanced map. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 646-666.	2.5	157

#	ARTICLE	IF	CITATIONS
19	Detection of alternative conformations:Shift_plotandAC_predictionprograms. Journal of Applied Crystallography, 2013, 46, 554-559.	1.9	0
20	Detection of alternative conformations by unrestrained refinement. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1118-1127.	2.5	5
21	Online resource for theoretical study of hydration of biopolymers. SAR and QSAR in Environmental Research, 2008, 19, 303-315.	1.0	2