

# Przemyslaw Jerzy Porebski

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1443083/publications.pdf>

Version: 2024-02-01

30  
papers

1,940  
citations

471509

17  
h-index

477307

29  
g-index

34  
all docs

34  
docs citations

34  
times ranked

3667  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural and immunologic characterization of bovine, horse, and rabbit serum albumins. <i>Molecular Immunology</i> , 2012, 52, 174-182.	2.2	756
2	<i>CheckMyMetal</i> : a macromolecular metal-binding validation tool. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 223-233.	2.3	268
3	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1181-1193.	2.3	103
4	<i>Alternaria alternata</i> allergen Alt a 1: A unique $\beta$ -barrel protein dimer found exclusively in fungi. <i>Journal of Allergy and Clinical Immunology</i> , 2012, 130, 241-247.e9.	2.9	99
5	Serum albumins—Unusual allergens. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 5375-5381.	2.4	89
6	Molecular Determinants for Antibody Binding on Group 1 House Dust Mite Allergens. <i>Journal of Biological Chemistry</i> , 2012, 287, 7388-7398.	3.4	75
7	X-ray crystallography: assessment and validation of protein—small molecule complexes for drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2011, 6, 771-782.	5.0	53
8	Molecular basis for phosphospecific recognition of histone H3 tails by Survivin paralogues at inner centromeres. <i>Molecular Biology of the Cell</i> , 2012, 23, 1457-1466.	2.1	53
9	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	4.7	49
10	Protein purification and crystallization artifacts: The tale usually not told. <i>Protein Science</i> , 2016, 25, 720-733.	7.6	46
11	Refining the macromolecular model—achieving the best agreement with the data from X-ray diffraction experiment. <i>Crystallography Reviews</i> , 2018, 24, 236-262.	1.5	43
12	Testosterone meets albumin—the molecular mechanism of sex hormone transport by serum albumins. <i>Chemical Science</i> , 2019, 10, 1607-1618.	7.4	38
13	Molstack—Interactive visualization tool for presentation, interpretation, and validation of macromolecules and electron density maps. <i>Protein Science</i> , 2018, 27, 86-94.	7.6	31
14	<i>Fitmunk</i> : improving protein structures by accurate, automatic modeling of side-chain conformations. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 266-280.	2.3	25
15	The Integrated Resource for Reproducibility in Macromolecular Crystallography: Experiences of the first four years. <i>Structural Dynamics</i> , 2019, 6, 064301.	2.3	25
16	Crystal structure of thebaine 6-O-demethylase from the morphine biosynthesis pathway. <i>Journal of Structural Biology</i> , 2018, 202, 229-235.	2.8	24
17	Automatic recognition of ligands in electron density by machine learning. <i>Bioinformatics</i> , 2019, 35, 452-461.	4.1	22
18	Projected resurgence of COVID-19 in the United States in July—December 2021 resulting from the increased transmissibility of the Delta variant and faltering vaccination. <i>ELife</i> , 0, 11, .	6.0	22

#	ARTICLE	IF	CITATIONS
19	Structural Analysis of a Putative Aminoglycoside N-Acetyltransferase from <i>Bacillus anthracis</i> . <i>Journal of Molecular Biology</i> , 2011, 410, 411-423.	4.2	17
20	Structural characterization of <i>Helicobacter pylori</i> dethiobiotin synthetase reveals differences between family members. <i>FEBS Journal</i> , 2012, 279, 1093-1105.	4.7	15
21	Regioselectivity of hyoscyamine 6 <sup>β</sup> -hydroxylase-catalysed hydroxylation as revealed by high-resolution structural information and QM/MM calculations. <i>Dalton Transactions</i> , 2020, 49, 4454-4469.	3.3	15
22	A Gcn5-Related N-Acetyltransferase (GNAT) Capable of Acetylating Polymyxin B and Colistin Antibiotics in Vitro. <i>Biochemistry</i> , 2018, 57, 7011-7020.	2.5	11
23	Molstack: A platform for interactive presentations of electron density and cryo-EM maps and their interpretations. <i>Protein Science</i> , 2020, 29, 120-127.	7.6	9
24	Recognizing and validating ligands with CheckMyBlob. <i>Nucleic Acids Research</i> , 2021, 49, W86-W92.	14.5	9
25	Detecting anomalies in X-ray diffraction images using convolutional neural networks. <i>Expert Systems With Applications</i> , 2021, 174, 114740.	7.6	9
26	Crystal structures of putative phosphoglycerate kinases from <i>B. anthracis</i> and <i>C. jejuni</i> . <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 15-26.	1.2	7
27	Databases, Repositories, and Other Data Resources in Structural Biology. <i>Methods in Molecular Biology</i> , 2017, 1607, 643-665.	0.9	6
28	A study on the structure, mechanism, and biochemistry of kanamycin B dioxygenase (KanJ) an enzyme with a broad range of substrates. <i>FEBS Journal</i> , 2021, 288, 1366-1386.	4.7	5
29	State-of-the-Art Data Management: Improving the Reproducibility, Consistency, and Traceability of Structural Biology and in Vitro Biochemical Experiments. <i>Methods in Molecular Biology</i> , 2021, 2199, 209-236.	0.9	5
30	Structure of anabolic ornithine carbamoyltransferase from <i>Campylobacter jejuni</i> at 2.7 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1018-1024.	0.7	4