

Robbie P Joosten

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3507761/publications.pdf>

Version: 2024-02-01

48
papers

4,340
citations

257357

24
h-index

206029

48
g-index

64
all docs

64
docs citations

64
times ranked

7327
citing authors

#	ARTICLE	IF	CITATIONS
1	A series of PDB related databases for everyday needs. <i>Nucleic Acids Research</i> , 2011, 39, D411-D419.	6.5	837
2	A series of PDB-related databanks for everyday needs. <i>Nucleic Acids Research</i> , 2015, 43, D364-D368.	6.5	757
3	The <i>PDB_REDO</i> server for macromolecular structure model optimization. <i>IUCr</i> , 2014, 1, 213-220.	1.0	709
4	A New Generation of Crystallographic Validation Tools for the Protein Data Bank. <i>Structure</i> , 2011, 19, 1395-1412.	1.6	405
5	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. <i>Journal of Applied Crystallography</i> , 2009, 42, 376-384.	1.9	204
6	<i>PDB_REDO</i> : constructive validation, more than just looking for errors. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 484-496.	2.5	195
7	Automatic rebuilding and optimization of crystallographic structures in the Protein Data Bank. <i>Bioinformatics</i> , 2011, 27, 3392-3398.	1.8	91
8	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. <i>Structure</i> , 2020, 28, 1249-1258.e2.	1.6	86
9	The first step of peptide selection in antigen presentation by MHC class I molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1505-1510.	3.3	85
10	Structure of NPP1, an Ectonucleotide Pyrophosphatase/Phosphodiesterase Involved in Tissue Calcification. <i>Structure</i> , 2012, 20, 1948-1959.	1.6	75
11	Steroid binding to Autotaxin links bile salts and lysophosphatidic acid signalling. <i>Nature Communications</i> , 2016, 7, 11248.	5.8	74
12	Re-refinement from deposited X-ray data can deliver improved models for most PDB entries. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 176-185.	2.5	71
13	Homology modelling and spectroscopy, a never-ending love story. <i>European Biophysics Journal</i> , 2010, 39, 551-563.	1.2	51
14	Tryptophan depletion results in tryptophan-to-phenylalanine substituents. <i>Nature</i> , 2022, 603, 721-727.	13.7	47
15	The good, the bad and the dubious: VHELIBS, a validation helper for ligands and binding sites. <i>Journal of Cheminformatics</i> , 2013, 5, 36.	2.8	42
16	PDB Improvement Starts with Data Deposition. <i>Science</i> , 2007, 317, 195-196.	6.0	41
17	Homology-based hydrogen bond information improves crystallographic structures in the <i>PDB</i> . <i>Protein Science</i> , 2018, 27, 798-808.	3.1	41
18	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	2.0	39

#	ARTICLE	IF	CITATIONS
19	Structure of a calcium-deficient form of influenza virus neuraminidase: implications for substrate binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 947-952.	2.5	36
20	An allosteric binding site of the $\alpha 7$ nicotinic acetylcholine receptor revealed in a humanized acetylcholine-binding protein. <i>Journal of Biological Chemistry</i> , 2018, 293, 2534-2545.	1.6	34
21	The structural basis for recognition of base J containing DNA by a novel DNA binding domain in JBP1. <i>Nucleic Acids Research</i> , 2011, 39, 5715-5728.	6.5	32
22	The impact of crystallization conditions on structure-based drug design: A case study on the methylene blue/acetylcholinesterase complex. <i>Protein Science</i> , 2016, 25, 1096-1114.	3.1	31
23	New Biological Insights from Better Structure Models. <i>Journal of Molecular Biology</i> , 2016, 428, 1375-1393.	2.0	28
24	Validation and correction of Zn ²⁺ -Cys ^x -His ^y complexes. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1110-1118.	1.1	27
25	Homology-based loop modeling yields more complete crystallographic protein structures. <i>IUCr</i> , 2018, 5, 585-594.	1.0	27
26	Detection of trans-cis flips and peptide-plane flips in protein structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1604-1614.	2.5	25
27	Carbohydrate 3D structure validation. <i>Current Opinion in Structural Biology</i> , 2017, 44, 9-17.	2.6	25
28	Structural basis of reversine selectivity in inhibiting Mps1 more potently than aurora B kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1761-1766.	1.5	23
29	Understanding inhibitor resistance in Mps1 kinase through novel biophysical assays and structures. <i>Journal of Biological Chemistry</i> , 2017, 292, 14496-14504.	1.6	23
30	Building and rebuilding N-glycans in protein structure models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 416-425.	1.1	19
31	Structural snapshots of the catalytic cycle of the phosphodiesterase Autotaxin. <i>Journal of Structural Biology</i> , 2016, 195, 199-206.	1.3	18
32	Making glycoproteins a little bit sweeter with PDB-REDO. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 463-472.	0.4	18
33	Data Mining of Macromolecular Structures. <i>Methods in Molecular Biology</i> , 2016, 1415, 107-138.	0.4	12
34	Modelling covalent linkages in CCP4. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 712-726.	1.1	10
35	The missing link: covalent linkages in structural models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 727-745.	1.1	10
36	High-resolution structure of the M14-type cytosolic carboxypeptidase from <i>Burkholderia cenocepacia</i> refined exploiting PDB_REDO strategies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 279-289.	2.5	8

#	ARTICLE	IF	CITATIONS
37	Facilities that make the PDB data collection more powerful. <i>Protein Science</i> , 2020, 29, 330-344.	3.1	7
38	Towards Consistency in Geometry Restraints for Carbohydrates in the Pyranose form: Modern Dictionary Generators Reviewed. <i>Current Medicinal Chemistry</i> , 2022, 29, 1193-1207.	1.2	7
39	New restraints and validation approaches for nucleic acid structures in <i>PDB-REDO</i>. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1127-1141.	1.1	6
40	Updated restraint dictionaries for carbohydrates in the pyranose form. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 455-465.	1.1	6
41	<i>LAHMA</i>: structure analysis through local annotation of homology-matched amino acids. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 28-40.	1.1	5
42	Timely deposition of macromolecular structures is necessary for peer review. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2293-2295.	2.5	3
43	A crystal structure of the human protein kinase Mps1 reveals an ordered conformation of the activation loop. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 348-352.	1.5	3
44	West-Life: A Virtual Research Environment for structural biology. <i>Journal of Structural Biology: X</i> , 2019, 1, 100006.	0.7	2
45	Challenges in structure validation - going beyond the protein. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2009, 65, s38-s38.	0.3	2
46	Detection of<i>trans</i>“<i>cis</i>flips and peptide plane flips in protein structures. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2015, 71, s270-s270.	0.0	1
47	Characterization and structure determination of a llama-derived nanobody targeting the J-base binding protein 1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 690-695.	0.4	1
48	On the information content of X-ray diffraction data. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, a301-a301.	0.0	0