Robbie P Joosten

List of Publications by Year in descending order

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	Towards Consistency in Geometry Restraints for Carbohydrates in the Pyranose form: Modern Dictionary Generators Reviewed. Current Medicinal Chemistry, 2022, 29, 1193-1207.	1.2	7
2	Tryptophan depletion results in tryptophan-to-phenylalanine substitutants. Nature, 2022, 603, 721-727.	13.7	47
3	Updated restraint dictionaries for carbohydrates in the pyranose form. Acta Crystallographica Section D: Structural Biology, 2022, 78, 455-465.	1.1	6
4	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. Journal of Molecular Biology, 2022, 434, 167599.	2.0	39
5	LAHMA: structure analysis through local annotation of homology-matched amino acids. Acta Crystallographica Section D: Structural Biology, 2021, 77, 28-40.	1.1	5
6	Modelling covalent linkages in CCP4. Acta Crystallographica Section D: Structural Biology, 2021, 77, 712-726.	1.1	10
7	The missing link: covalent linkages in structural models. Acta Crystallographica Section D: Structural Biology, 2021, 77, 727-745.	1.1	10
8	New restraints and validation approaches for nucleic acid structures in PDB-REDO. Acta Crystallographica Section D: Structural Biology, 2021, 77, 1127-1141.	1.1	6
9	Facilities that make the PDB data collection more powerful. Protein Science, 2020, 29, 330-344.	3.1	7
10	A Global Ramachandran Score Identifies Protein Structures with Unlikely Stereochemistry. Structure, 2020, 28, 1249-1258.e2.	1.6	86
11	A crystal structure of the human protein kinase Mps1 reveals an ordered conformation of the activation loop. Proteins: Structure, Function and Bioinformatics, 2019, 87, 348-352.	1.5	3
12	West-Life: A Virtual Research Environment for structural biology. Journal of Structural Biology: X, 2019, 1, 100006.	0.7	2
13	Building and rebuilding N-glycans in protein structure models. Acta Crystallographica Section D: Structural Biology, 2019, 75, 416-425.	1.1	19
14	Homologyâ€based hydrogen bond information improves crystallographic structures in the <scp>PDB</scp>. Protein Science, 2018, 27, 798-808.	3.1	41
15	An allosteric binding site of the Î±7 nicotinic acetylcholine receptor revealed in a humanized acetylcholine-binding protein. Journal of Biological Chemistry, 2018, 293, 2534-2545.	1.6	34
16	Characterization and structure determination of a llama-derived nanobody targeting the J-base binding protein 1. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 690-695.	0.4	1
17	Making glycoproteins a little bit sweeter withPDB-REDO. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 463-472.	0.4	18
18	Homology-based loop modeling yields more complete crystallographic protein structures. IUCrJ, 2018, 5, 585-594.	1.0	27

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19	On the information content of X-ray diffraction data. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, a301-a301.	0.0	0
20	Understanding inhibitor resistance in Mps1 kinase through novel biophysical assays and structures. Journal of Biological Chemistry, 2017, 292, 14496-14504.	1.6	23
21	Carbohydrate 3D structure validation. Current Opinion in Structural Biology, 2017, 44, 9-17.	2.6	25
22	Validation and correction of Znâ€“Cys _x His _y complexes. Acta Crystallographica Section D: Structural Biology, 2016, 72, 1110-1118.	1.1	27
23	The impact of crystallization conditions on structureâ€based drug design: A case study on the methylene blue/acetylcholinesterase complex. Protein Science, 2016, 25, 1096-1114.	3.1	31
24	Data Mining of Macromolecular Structures. Methods in Molecular Biology, 2016, 1415, 107-138.	0.4	12
25	Steroid binding to Autotaxin links bile salts and lysophosphatidic acid signalling. Nature Communications, 2016, 7, 11248.	5.8	74
26	Structural basis of reversine selectivity in inhibiting Mps1 more potently than aurora B kinase. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1761-1766.	1.5	23
27	Structural snapshots of the catalytic cycle of the phosphodiesterase Autotaxin. Journal of Structural Biology, 2016, 195, 199-206.	1.3	18
28	New Biological Insights from Better Structure Models. Journal of Molecular Biology, 2016, 428, 1375-1393.	2.0	28
29	Detection oftransâ€“cisflips and peptide plane flips in protein structures. Acta Crystallographica Section A: Foundations and Advances, 2015, 71, s270-s270.	0.0	1
30	Detection oftransâ€“cisflips and peptide-plane flips in protein structures. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1604-1614.	2.5	25
31	The first step of peptide selection in antigen presentation by MHC class I molecules. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1505-1510.	3.3	85
32	A series of PDB-related databanks for everyday needs. Nucleic Acids Research, 2015, 43, D364-D368.	6.5	757
33	ThePDB_REDOserver for macromolecular structure model optimization. IUCrJ, 2014, 1, 213-220.	1.0	709
34	High-resolution structure of the M14-type cytosolic carboxypeptidase fromBurkholderia cenocepaciarefined exploitingPDB_REDOstrategies. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 279-289.	2.5	8
35	The good, the bad and the dubious: VHELIBS, a validation helper for ligands and binding sites. Journal of Cheminformatics, 2013, 5, 36.	2.8	42
36	Timely deposition of macromolecular structures is necessary for peer review. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2293-2295.	2.5	3

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37	Structure of NPP1, an Ectonucleotide Pyrophosphatase/Phosphodiesterase Involved in Tissue Calcification. Structure, 2012, 20, 1948-1959.	1.6	75
38	PDB_REDO: constructive validation, more than just looking for errors. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 484-496.	2.5	195
39	A New Generation of Crystallographic Validation Tools for the Protein Data Bank. Structure, 2011, 19, 1395-1412.	1.6	405
40	The structural basis for recognition of base J containing DNA by a novel DNA binding domain in JBP1. Nucleic Acids Research, 2011, 39, 5715-5728.	6.5	32
41	Automatic rebuilding and optimization of crystallographic structures in the Protein Data Bank. Bioinformatics, 2011, 27, 3392-3398.	1.8	91
42	A series of PDB related databases for everyday needs. Nucleic Acids Research, 2011, 39, D411-D419.	6.5	837
43	Homology modelling and spectroscopy, a never-ending love story. European Biophysics Journal, 2010, 39, 551-563.	1.2	51
44	Re-refinement from deposited X-ray data can deliver improved models for most PDB entries. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 176-185.	2.5	71
45	PDB_REDO: automated re-refinement of X-ray structure models in the PDB. Journal of Applied Crystallography, 2009, 42, 376-384.	1.9	204
46	Challenges in structure validation - going beyond the protein. Acta Crystallographica Section A: Foundations and Advances, 2009, 65, s38-s38.	0.3	2
47	PDB Improvement Starts with Data Deposition. Science, 2007, 317, 195-196.	6.0	41
48	Structure of a calcium-deficient form of influenza virus neuraminidase: implications for substrate binding. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 947-952.	2.5	36