

# John P Rose

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11488747/publications.pdf>

Version: 2024-02-01

35  
papers

1,663  
citations

394421

19  
h-index

414414

32  
g-index

35  
all docs

35  
docs citations

35  
times ranked

1642  
citing authors

#	ARTICLE	IF	CITATIONS
1	The SER-CAT Virtual Beamline: Providing Light when You Need it in Your Home Lab. Nihon Kessho Gakkaishi, 2021, 63, 44-52.	0.0	0
2	Transactions from the 69th Annual Meeting of the American Crystallographic Association: Data best practicesâ€”current state and future needs. Structural Dynamics, 2020, 7, 021301.	2.3	1
3	A Unique Protein Self-Assembling Nanoparticle with Significant Advantages in Vaccine Development and Production. Journal of Nanomaterials, 2020, 2020, 1-10.	2.7	20
4	SAD phasing: History, current impact and future opportunities. Archives of Biochemistry and Biophysics, 2016, 602, 80-94.	3.0	21
5	Native SAD is maturing. IUCrJ, 2015, 2, 431-440.	2.2	50
6	The structure of augmenter of liver regeneration crystallized in the presence of 50â€…mMCdCl2reveals a novel Cd2Cl4O6cluster that aids in crystal packing. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1128-1133.	2.5	4
7	Structure based mechanism of the Ca <sup>2+</sup> -induced release of coelenterazine from the <i>Renilla</i> binding protein. Proteins: Structure, Function and Bioinformatics, 2009, 74, 583-593.	2.6	19
8	The First Agmatine/Cadaverine Aminopropyl Transferase: Biochemical and Structural Characterization of an Enzyme Involved in Polyamine Biosynthesis in the Hyperthermophilic Archaeon Pyrococcus furiosus. Journal of Bacteriology, 2007, 189, 6057-6067.	2.2	31
9	Characterization of a corrinoid protein involved in the C1 metabolism of strict anaerobic bacterium Moorella thermoacetica. Proteins: Structure, Function and Bioinformatics, 2007, 67, 167-176.	2.6	28
10	Structural basis of CoA recognition by the Pyrococcus single-domain CoA-binding proteins. Journal of Structural and Functional Genomics, 2007, 7, 119-129.	1.2	3
11	Structural and transcriptional analyses of a purine nucleotide-binding protein from Pyrococcus furiosus: a component of a novel, membrane-bound multiprotein complex unique to this hyperthermophilic archaeon. Journal of Structural and Functional Genomics, 2007, 8, 1-10.	1.2	0
12	A test of enhancing model accuracy in high-throughput crystallography. Journal of Structural and Functional Genomics, 2005, 6, 1-11.	1.2	45
13	Parameter-space screening: a powerful tool for high-throughput crystal structure determination. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 520-527.	2.5	25
14	Away from the edge II: in-house Se-SAS phasing with chromium radiation. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 960-966.	2.5	10
15	The high-throughput protein-to-structure pipeline at SECSG. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 679-684.	2.5	22
16	Isolation, crystallization and preliminary X-ray analysis of a methanol-induced corrinoid protein from Moorella thermoacetica. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 537-540.	0.7	8
17	Structural genomics of Pyrococcus furiosus: X-ray crystallography reveals 3D domain swapping in rubrerythrin. Proteins: Structure, Function and Bioinformatics, 2004, 57, 878-882.	2.6	18
18	Monitoring the anomalous scattering signal and noise levels in X-ray diffraction of crystals. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 499-506.	2.5	5

#	ARTICLE	IF	CITATIONS
19	The Hyperthermophile Protein Sso10a is a Dimer of Winged Helix DNA-binding Domains Linked by an Antiparallel Coiled Coil Rod. <i>Journal of Molecular Biology</i> , 2004, 341, 73-91.	4.2	35
20	The Southeast Collaboratory for Structural Genomics: A High-Throughput Gene to Structural Factory. <i>ChemInform</i> , 2003, 34, no.	0.0	0
21	The crystal structure of augmeter of liver regeneration: A mammalian FAD-dependent sulfhydryl oxidase. <i>Protein Science</i> , 2003, 12, 1109-1118.	7.6	99
22	The Southeast Collaboratory for Structural Genomics: A High-Throughput Gene to Structure Factory. <i>Accounts of Chemical Research</i> , 2003, 36, 191-198.	15.6	76
23	Violet Bioluminescence and Fast Kinetics from W92F Obelin: A Structure-Based Proposal for the Bioluminescence Triggering and the Identification of the Emitting Species. <i>Biochemistry</i> , 2003, 42, 6013-6024.	2.5	57
24	Structures of an unliganded neurophysin and its vasopressin complex: Implications for binding and allosteric mechanisms. <i>Protein Science</i> , 2001, 10, 1869-1880.	7.6	42
25	Crystal structure of the transcription factor sc-mtTFB offers insights into mitochondrial transcription. <i>Protein Science</i> , 2001, 10, 1980-1988.	7.6	93
26	The 2.0 Å structure of human ferrochelatase, the terminal enzyme of heme biosynthesis. <i>Nature Structural Biology</i> , 2001, 8, 156-160.	9.7	200
27	Crystallization and preliminary X-ray diffraction analysis of the mitochondrial transcription factor sc-mtTFB from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 902-903.	2.5	2
28	Structure of the Ca <sup>2+</sup> -regulated photoprotein obelin at 1.7 Å... resolution determined directly from its sulfur substructure. <i>Protein Science</i> , 2000, 9, 2085-2093.	7.6	170
29	Low-salt crystallization of T7 RNA polymerase: a first step towards the transcription bubble complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1188-1192.	2.5	2
30	Human ferrochelatase: crystallization, characterization of the [2Fe-2S] cluster and determination that the enzyme is a homodimer. <i>BBA - Proteins and Proteomics</i> , 1999, 1435, 191-197.	2.1	60
31	Structural basis of neurophysin hormone specificity: Geometry, polarity, and polarizability in aromatic ring interactions. <i>Protein Science</i> , 1999, 8, 820-831.	7.6	9
32	Crystal structure of the neurophysin-oxytocin complex. <i>Nature Structural Biology</i> , 1996, 3, 163-169.	9.7	94
33	Crystal structure of bacteriophage T7 RNA polymerase at 3.3 Å... resolution. <i>Nature</i> , 1993, 364, 593-599.	27.8	381
34	Crystallographic analysis of the neurophysin-oxytocin complex. <i>Journal of Molecular Biology</i> , 1991, 221, 43-45.	4.2	8
35	Single crystals of bacteriophage T7 RNA polymerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1989, 5, 266-270.	2.6	25