## Ronald E Stenkamp

List of Publications by Year in descending order

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38 papers 8,588 citations

257450 24 h-index 315739 38 g-index

39 all docs 39 docs citations

39 times ranked 7003 citing authors

#	Article	IF	CITATIONS
1	Crystal Structure of Rhodopsin: A G Protein-Coupled Receptor. Science, 2000, 289, 739-745.	12.6	5,486
2	Advances in Determination of a High-Resolution Three-Dimensional Structure of Rhodopsin, a Model of G-Protein-Coupled Receptors (GPCRs)â€,‡. Biochemistry, 2001, 40, 7761-7772.	2.5	627
3	Crystal structure of a photoactivated deprotonated intermediate of rhodopsin. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 16123-16128.	7.1	431
4	Structural Basis for Mechanical Force Regulation of the Adhesin FimH via Finger Trap-like $\hat{l}^2$ Sheet Twisting. Cell, 2010, 141, 645-655.	28.9	239
5	G Protein-Coupled Receptor Rhodopsin: A Prospectus. Annual Review of Physiology, 2003, 65, 851-879.	13.1	237
6	Structural studies of the streptavidin binding loop. Protein Science, 1997, 6, 1157-1166.	7.6	180
7	Transglutaminase factor XIII uses proteinaseâ€ike catalytic triad to crosslink macromolecules. Protein Science, 1994, 3, 1131-1135.	7.6	142
8	Xâ€Ray Structure and Designed Evolution of an Artificial Transfer Hydrogenase. Angewandte Chemie - International Edition, 2008, 47, 1400-1404.	13.8	138
9	Cooperative hydrogen bond interactions in the streptavidin-biotin system. Protein Science, 2006, 15, 459-467.	7.6	123
10	Streptavidin–biotin binding energetics. New Biotechnology, 1999, 16, 39-44.	2.7	99
11	Streptavidin and its biotin complex at atomic resolution. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 813-821.	2.5	83
12	Structural studies of binding site tryptophan mutants in the high-affinity streptavidin-biotin complex 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 1998, 279, 211-221.	4.2	77
13	Ser45 plays an important role in managing both the equilibrium and transition state energetics of the streptavidin—biotin system. Protein Science, 2000, 9, 878-885.	7.6	75
14	The Bacterial Fimbrial Tip Acts as a Mechanical Force Sensor. PLoS Biology, 2011, 9, e1000617.	5.6	72
15	Thermodynamic and structural consequences of flexible loop deletion by circular permutation in the streptavidinâ€biotin system. Protein Science, 1998, 7, 848-859.	7.6	70
16	Alternative models for two crystal structures of bovine rhodopsin. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 902-904.	2.5	55
17	Improvements in G protein-coupled receptor purification yield light stable rhodopsin crystals. Journal of Structural Biology, 2006, 156, 497-504.	2.8	52
18	Simulations of a Protein Crystal: Explicit Treatment of Crystallization Conditions Links Theory and Experiment in the Streptavidinâ 'Biotin Complex. Biochemistry, 2008, 47, 12065-12077.	2.5	46

#	Article	IF	CITATIONS
19	Crystal packing analysis of Rhodopsin crystals. Journal of Structural Biology, 2007, 158, 455-462.	2.8	42
20	Dynamics of the Streptavidinâ^'Biotin Complex in Solution and in Its Crystal Lattice: Distinct Behavior Revealed by Molecular Simulations. Journal of Physical Chemistry B, 2009, 113, 6971-6985.	2.6	37
21	Crystallographic Analysis of a Full-length Streptavidin with Its C-terminal Polypeptide Bound in the Biotin Binding Site. Journal of Molecular Biology, 2006, 356, 738-745.	4.2	36
22	Rhodopsin: A Structural Primer for G-Protein Coupled Receptors. Archiv Der Pharmazie, 2005, 338, 209-216.	4.1	34
23	X-ray crystallographic studies of streptavidin mutants binding to biotin. New Biotechnology, 1999, 16, 13-19.	2.7	29
24	Early mechanistic events in biotin dissociation from streptavidin. Nature Structural Biology, 2002, 9, 582-5.	9.7	27
25	The Evolution of SlyA/RovA Transcription Factors from Repressors to Countersilencers in <i>Enterobacteriaceae</i> MBio, 2019, 10, .	4.1	26
26	Crystal Structure and Mutational Analysis of the DaaE Adhesin of Escherichia coli. Journal of Biological Chemistry, 2006, 281, 22367-22377.	3.4	24
27	Identifying G protein-coupled receptor dimers from crystal packings. Acta Crystallographica Section D: Structural Biology, 2018, 74, 655-670.	2.3	18
28	The structure of rice weevil pectin methylesterase. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 1480-1484.	0.8	15
29	RMSD analysis of structures of the bacterial protein FimH identifies five conformations of its lectin domain. Proteins: Structure, Function and Bioinformatics, 2020, 88, 593-603.	2.6	12
30	Structure of 3-mercaptopropionic acid dioxygenase with a substrate analog reveals bidentate substrate binding at the iron center. Journal of Biological Chemistry, 2021, 296, 100492.	3.4	12
31	A Distal Point Mutation in the Streptavidinâ 'Biotin Complex Preserves Structure but Diminishes Binding Affinity: Experimental Evidence of Electronic Polarization Effects?. Biochemistry, 2010, 49, 4568-4570.	2.5	9
32	The role of cytochrome P450 BM3 phenylalanine-87 and threonine-268 in binding organic hydroperoxides. Biochimica Et Biophysica Acta - General Subjects, 2016, 1860, 669-677.	2.4	8
33	The high-resolution structure of (+)-epi-biotin bound to streptavidin. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 576-581.	2.5	6
34	Structural consequences of cutting a binding loop: two circularly permuted variants of streptavidin. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 968-977.	2.5	6
35	Toggle switch residues control allosteric transitions in bacterial adhesins by participating in a concerted repacking of the protein core. PLoS Pathogens, 2021, 17, e1009440.	4.7	6
36	A Streptavidin Binding Site Mutation Yields an Unexpected Result: An Ionized Asp128 Residue Is Not Essential for Strong Biotin Binding. Biochemistry, 2016, 55, 5201-5203.	2.5	5

#	Article	lF	CITATIONS
37	Anatomy of atrans–cispeptide transition during least-squares refinement of rubrerythrin. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1599-1602.	2.5	3
38	Reprint of "Crystal packing analysis of Rhodopsin crystals―[J. Struct. Biol. 158 (2007) 455–462]â~†. Journ of Structural Biology, 2007, 159, 253-260.	al 2.8	1