

Ronald E Stenkamp

List of Publications by Year in descending order

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8,588
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257450

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docs citations

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times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	Toggle switch residues control allosteric transitions in bacterial adhesins by participating in a concerted repacking of the protein core. <i>PLoS Pathogens</i> , 2021, 17, e1009440.	4.7	6
2	Structure of 3-mercaptopropionic acid dioxygenase with a substrate analog reveals bidentate substrate binding at the iron center. <i>Journal of Biological Chemistry</i> , 2021, 296, 100492.	3.4	12
3	RMSD analysis of structures of the bacterial protein FimH identifies five conformations of its lectin domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020, 88, 593-603.	2.6	12
4	The Evolution of SlyA/RovA Transcription Factors from Repressors to Countersilencers in <i>Enterobacteriaceae</i> . <i>MBio</i> , 2019, 10, .	4.1	26
5	Identifying G protein-coupled receptor dimers from crystal packings. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 655-670.	2.3	18
6	A Streptavidin Binding Site Mutation Yields an Unexpected Result: An Ionized Asp128 Residue Is Not Essential for Strong Biotin Binding. <i>Biochemistry</i> , 2016, 55, 5201-5203.	2.5	5
7	The role of cytochrome P450 BM3 phenylalanine-87 and threonine-268 in binding organic hydroperoxides. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2016, 1860, 669-677.	2.4	8
8	The structure of rice weevil pectin methylesterase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1480-1484.	0.8	15
9	Structural consequences of cutting a binding loop: two circularly permuted variants of streptavidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 968-977.	2.5	6
10	Streptavidin and its biotin complex at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 813-821.	2.5	83
11	The Bacterial Fimbrial Tip Acts as a Mechanical Force Sensor. <i>PLoS Biology</i> , 2011, 9, e1000617.	5.6	72
12	A Distal Point Mutation in the Streptavidin~Biotin Complex Preserves Structure but Diminishes Binding Affinity: Experimental Evidence of Electronic Polarization Effects?. <i>Biochemistry</i> , 2010, 49, 4568-4570.	2.5	9
13	Structural Basis for Mechanical Force Regulation of the Adhesin FimH via Finger Trap-like β^2 Sheet Twisting. <i>Cell</i> , 2010, 141, 645-655.	28.9	239
14	Dynamics of the Streptavidin~Biotin Complex in Solution and in Its Crystal Lattice: Distinct Behavior Revealed by Molecular Simulations. <i>Journal of Physical Chemistry B</i> , 2009, 113, 6971-6985.	2.6	37
15	Alternative models for two crystal structures of bovine rhodopsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008, 64, 902-904.	2.5	55
16	X-ray Structure and Designed Evolution of an Artificial Transfer Hydrogenase. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 1400-1404.	13.8	138
17	Simulations of a Protein Crystal: Explicit Treatment of Crystallization Conditions Links Theory and Experiment in the Streptavidin~Biotin Complex. <i>Biochemistry</i> , 2008, 47, 12065-12077.	2.5	46
18	Crystal packing analysis of Rhodopsin crystals. <i>Journal of Structural Biology</i> , 2007, 158, 455-462.	2.8	42

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19	Reprint of "Crystal packing analysis of Rhodopsin crystals". J. Struct. Biol. 158 (2007) 455-462. Journal of Structural Biology, 2007, 159, 253-260.	2.8	1
20	Cooperative hydrogen bond interactions in the streptavidin-biotin system. Protein Science, 2006, 15, 459-467.	7.6	123
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	Improvements in G protein-coupled receptor purification yield light stable rhodopsin crystals. Journal of Structural Biology, 2006, 156, 497-504.	2.8	52
23	The high-resolution structure of (+)-epi-biotin bound to streptavidin. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 576-581.	2.5	6
24	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
25	Crystal Structure and Mutational Analysis of the DaaE Adhesin of Escherichia coli. Journal of Biological Chemistry, 2006, 281, 22367-22377.	3.4	24
26	Rhodopsin: A Structural Primer for G-Protein Coupled Receptors. Archiv Der Pharmazie, 2005, 338, 209-216.	4.1	34
27	Anatomy of a trans-cis peptide transition during least-squares refinement of rubrerythrin. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1599-1602.	2.5	3
28	G Protein-Coupled Receptor Rhodopsin: A Prospectus. Annual Review of Physiology, 2003, 65, 851-879.	13.1	237
29	Early mechanistic events in biotin dissociation from streptavidin. Nature Structural Biology, 2002, 9, 582-5.	9.7	27
30	Advances in Determination of a High-Resolution Three-Dimensional Structure of Rhodopsin, a Model of G-Protein-Coupled Receptors (GPCRs). Biochemistry, 2001, 40, 7761-7772.	2.5	627
31	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
32	Crystal Structure of Rhodopsin: A G Protein-Coupled Receptor. Science, 2000, 289, 739-745.	12.6	5,486
33	Streptavidin-biotin binding energetics. New Biotechnology, 1999, 16, 39-44.	2.7	99
34	X-ray crystallographic studies of streptavidin mutants binding to biotin. New Biotechnology, 1999, 16, 13-19.	2.7	29
35	Thermodynamic and structural consequences of flexible loop deletion by circular permutation in the streptavidin-biotin system. Protein Science, 1998, 7, 848-859.	7.6	70
36	Structural studies of binding site tryptophan mutants in the high-affinity streptavidin-biotin complex 1 Edited by I. A. Wilson. Journal of Molecular Biology, 1998, 279, 211-221.	4.2	77

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37	Structural studies of the streptavidin binding loop. Protein Science, 1997, 6, 1157-1166.	7.6	180
38	Transglutaminase factor XIII uses proteinase-like catalytic triad to crosslink macromolecules. Protein Science, 1994, 3, 1131-1135.	7.6	142