

Ronald E Stenkamp

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38
papers

7,765
citations

23
h-index

39
g-index

39
ext. papers

8,169
ext. citations

8.6
avg, IF

4.93
L-index

#	Paper	IF	Citations
38	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	7.6	0
37	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	5.4	6
36	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	4.2	4
35	The Evolution of SlyA/RovA Transcription Factors from Repressors to Countersilencers in. <i>MBio</i> , 2019 , 10,	7.8	12
34	Identifying G protein-coupled receptor dimers from crystal packings. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018 , 74, 655-670	5.5	13
33	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, 669-77	4	7
32	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, 5201-3	3.2	5
31	The structure of rice weevil pectin methylesterase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 1480-4	1.1	11
30	Structural consequences of cutting a binding loop: two circularly permuted variants of streptavidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 968-77		5
29	Streptavidin and its biotin complex at atomic resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 813-21		62
28	The bacterial fimbrial tip acts as a mechanical force sensor. <i>PLoS Biology</i> , 2011 , 9, e1000617	9.7	61
27	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, 4568-70	3.2	9
26	Structural basis for mechanical force regulation of the adhesin FimH via finger trap-like beta sheet twisting. <i>Cell</i> , 2010 , 141, 645-55	56.2	204
25	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, 6971-85	3.4	30
24	Simulations of a protein crystal: explicit treatment of crystallization conditions links theory and experiment in the streptavidin-biotin complex. <i>Biochemistry</i> , 2008 , 47, 12065-77	3.2	32
23	Alternative models for two crystal structures of bovine rhodopsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , D64, 902-4		46
22	X-ray structure and designed evolution of an artificial transfer hydrogenase. <i>Angewandte Chemie - International Edition</i> , 2008 , 47, 1400-4	16.4	125

21	Crystal packing analysis of Rhodopsin crystals. <i>Journal of Structural Biology</i> , 2007 , 158, 455-62	3-4	40
20	Reprint of "Crystal packing analysis of Rhodopsin crystals" [J. Struct. Biol. 158 (2007) 455-462]. <i>Journal of Structural Biology</i> , 2007 , 159, 253-60	3-4	1
19	Crystal structure of a photoactivated deprotonated intermediate of rhodopsin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 16123-8	11.5	391
18	Crystal structure and mutational analysis of the DaaE adhesin of Escherichia coli. <i>Journal of Biological Chemistry</i> , 2006 , 281, 22367-22377	5-4	23
17	Cooperative hydrogen bond interactions in the streptavidin-biotin system. <i>Protein Science</i> , 2006 , 15, 459-67	6.3	110
16	Crystallographic analysis of a full-length streptavidin with its C-terminal polypeptide bound in the biotin binding site. <i>Journal of Molecular Biology</i> , 2006 , 356, 738-45	6.5	35
15	Improvements in G protein-coupled receptor purification yield light stable rhodopsin crystals. <i>Journal of Structural Biology</i> , 2006 , 156, 497-504	3-4	48
14	The high-resolution structure of (+)-epi-biotin bound to streptavidin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 576-81		5
13	Rhodopsin: a structural primer for G-protein coupled receptors. <i>Archiv Der Pharmazie</i> , 2005 , 338, 209-16	4.3	30
12	Anatomy of a trans-cis peptide transition during least-squares refinement of rubrerythrin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1599-602		3
11	G protein-coupled receptor rhodopsin: a prospectus. <i>Annual Review of Physiology</i> , 2003 , 65, 851-79	23.1	202
10	Early mechanistic events in biotin dissociation from streptavidin. <i>Nature Structural Biology</i> , 2002 , 9, 582-5		23
9	Advances in determination of a high-resolution three-dimensional structure of rhodopsin, a model of G-protein-coupled receptors (GPCRs). <i>Biochemistry</i> , 2001 , 40, 7761-72	3.2	597
8	Ser45 plays an important role in managing both the equilibrium and transition state energetics of the streptavidin-biotin system. <i>Protein Science</i> , 2000 , 9, 878-85	6.3	68
7	Crystal structure of rhodopsin: A G protein-coupled receptor. <i>Science</i> , 2000 , 289, 739-45	33.3	5015
6	Streptavidin-biotin binding energetics. <i>New Biotechnology</i> , 1999 , 16, 39-44		87
5	X-ray crystallographic studies of streptavidin mutants binding to biotin. <i>New Biotechnology</i> , 1999 , 16, 13-9		26
4	Thermodynamic and structural consequences of flexible loop deletion by circular permutation in the streptavidin-biotin system. <i>Protein Science</i> , 1998 , 7, 848-59	6.3	65

- 3 Structural studies of binding site tryptophan mutants in the high-affinity streptavidin-biotin complex. *Journal of Molecular Biology*, **1998**, 279, 211-21 6.5 70
- 2 Structural studies of the streptavidin binding loop. *Protein Science*, **1997**, 6, 1157-66 6.3 162
- 1 Transglutaminase factor XIII uses proteinase-like catalytic triad to crosslink macromolecules. *Protein Science*, **1994**, 3, 1131-5 6.3 132