Rich Olson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Social evolution of shared biofilm matrix components. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	14
2	Protein yoga: Conformational versatility of the Hemolysin II Câ€ŧerminal domain detailed by NMR structures for multiple states. Protein Science, 2021, 30, 990-1005.	3.1	7
3	Searching for the Secret of Stickiness: How Biofilms Adhere to Surfaces. Frontiers in Microbiology, 2021, 12, 686793.	1.5	24
4	The 1.9 Ã crystal structure of the extracellular matrix protein Bap1 from Vibrio cholerae provides insights into bacterial biofilm adhesion. Journal of Biological Chemistry, 2019, 294, 14499-14511.	1.6	13
5	Structural basis of mammalian glycan targeting by Vibrio cholerae cytolysin and biofilm proteins. PLoS Pathogens, 2018, 14, e1006841.	2.1	11
6	NMR structure of the Bacillus cereus hemolysin II C-terminal domain reveals a novel fold. Scientific Reports, 2017, 7, 3277.	1.6	10
7	Conserved SecA Signal Peptide-Binding Site Revealed by Engineered Protein Chimeras and Förster Resonance Energy Transfer. Biochemistry, 2016, 55, 1291-1300.	1.2	7
8	The Relationship between Glycan Binding and Direct Membrane Interactions in Vibrio cholerae Cytolysin, a Channel-forming Toxin. Journal of Biological Chemistry, 2015, 290, 28402-28415.	1.6	11
9	Key Residues in Vibrio Cholerae Cytolysin Involved in Membrane Binding. Biophysical Journal, 2015, 108, 81a-82a.	0.2	0
10	NMR assignments for the cis and trans forms of the hemolysin II C-terminal domain. Biomolecular NMR Assignments, 2014, 8, 419-423.	0.4	8
11	Structure and Glycan-Binding Properties of the Vibrio Vulnificus Hemolysin B-Trefoil Lectin. Biophysical Journal, 2014, 106, 87a.	0.2	1
12	Glycan Specificity of the Vibrio vulnificus Hemolysin Lectin Outlines Evolutionary History of Membrane Targeting by a Toxin Family. Journal of Molecular Biology, 2014, 426, 2800-2812.	2.0	31
13	Understanding the Carbohydrate Specificity of Vibrio Cholerae Cytolysin. Biophysical Journal, 2013, 104, 240a.	0.2	0
14	Identification and Characterization of the Glycan Binding Site of Vibrio Cholerae Cytolysin. Biophysical Journal, 2013, 104, 238a.	0.2	0
15	Vibrio cholerae Cytolysin Recognizes the Heptasaccharide Core of Complex N-Glycans with Nanomolar Affinity. Journal of Molecular Biology, 2013, 425, 944-957.	2.0	38
16	Determination of the Carbohydrate-Binding Specificity of Lectin-Like Domains in Vibrio Cholerae Cytolysin. Biophysical Journal, 2012, 102, 461a-462a.	0.2	2
17	High-Resolution Structure of the Vibrio Cholerae Cytolysin Heptamer. Biophysical Journal, 2011, 100, 382a.	0.2	0
18	Crystal Structure of the VIBRIO Cholerae Cytolysin Heptameric Pore. Biophysical Journal, 2011, 100, 8a.	0.2	0

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19	Crystal structure of the <i>Vibrio cholerae</i> cytolysin heptamer reveals common features among disparate pore-forming toxins. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7385-7390.	3.3	117
20	Three-dimensional structure of the detergent-solubilized Vibrio cholerae cytolysin (VCC) heptamer by electron cryomicroscopy. Journal of Structural Biology, 2010, 169, 6-13.	1.3	14
21	The Crystal Structure of CHIR-AB1: A Primordial Avian Classical Fc Receptor. Journal of Molecular Biology, 2008, 381, 1012-1024.	2.0	30
22	MHC homologs in the nervous system — they haven't lost their groove. Current Opinion in Neurobiology, 2006, 16, 351-357.	2.0	26
23	Structure of a Pheromone Receptor-Associated MHC Molecule with an Open and Empty Groove. PLoS Biology, 2005, 3, e257.	2.6	43
24	Crystal Structure of the Vibrio cholerae Cytolysin (VCC) Pro-toxin and its Assembly into a Heptameric Transmembrane Pore. Journal of Molecular Biology, 2005, 350, 997-1016.	2.0	122
25	Structural basis for modulation and agonist specificity of HCN pacemaker channels. Nature, 2003, 425, 200-205.	13.7	540
26	Vibrio cholerae cytolysin is composed of an alpha-hemolysin-like core. Protein Science, 2003, 12, 379-383.	3.1	42
27	STATs Dimerize in the Absence of Phosphorylation. Journal of Biological Chemistry, 2003, 278, 34133-34140.	1.6	182
28	Mechanism of glutamate receptor desensitization. Nature, 2002, 417, 245-253.	13.7	650
29	Mechanisms for ligand binding to GluR0 ion channels: crystal structures of the glutamate and serine complexes and a closed apo state. Journal of Molecular Biology, 2001, 311, 815-836.	2.0	141
30	Crystal structure of staphylococcal LukF delineates conformational changes accompanying formation of a transmembrane channel. Nature Structural Biology, 1999, 6, 134-140.	9.7	220