

David N Langelaan

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

572
citations

687363

13
h-index

677142

22
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24
all docs

24
docs citations

24
times ranked

852
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Insight into G-Protein Coupled Receptor Binding by Apelin. <i>Biochemistry</i> , 2009, 48, 537-548.	2.5	87
2	Structure of a 1.5-MDa adhesin that binds its Antarctic bacterium to diatoms and ice. <i>Science Advances</i> , 2017, 3, e1701440.	10.3	83
3	Improved Helix and Kink Characterization in Membrane Proteins Allows Evaluation of Kink Sequence Predictors. <i>Journal of Chemical Information and Modeling</i> , 2010, 50, 2213-2220.	5.4	59
4	Periodicity in Structure, Bonding, and Reactivity for β -block Complexes of a Geometry Constraining Triamide Ligand. <i>Chemistry - A European Journal</i> , 2019, 25, 16414-16424.	3.3	41
5	Headgroup-Dependent Membrane Catalysis of Apelin ¹⁻³⁶ Receptor Interactions Is Likely. <i>Journal of Physical Chemistry B</i> , 2009, 113, 10465-10471.	2.6	35
6	Structural features of the apelin receptor N-terminal tail and first transmembrane segment implicated in ligand binding and receptor trafficking. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 1471-1483.	2.6	34
7	Characterization of a Basidiomycota hydrophobin reveals the structural basis for a high-similarity Class I subdivision. <i>Scientific Reports</i> , 2017, 7, 45863.	3.3	32
8	Membrane catalysis of peptide ¹⁻³⁶ receptor bindingThis paper is one of a selection of papers published in this special issue entitled "Canadian Society of Biochemistry, Molecular & Cellular Biology 52nd Annual Meeting" Protein Folding: Principles and Diseases and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 203-210.	2.0	27
9	Identification of the first transcriptional activator of an archaeal operon in a euryarchaeon. <i>Molecular Microbiology</i> , 2016, 102, 54-70.	2.5	26
10	Functional redundancy between the transcriptional activation domains of E2A is mediated by binding to the KIX domain of CBP/p300. <i>Nucleic Acids Research</i> , 2014, 42, 7370-7382.	14.5	23
11	Properties of a family 56 carbohydrate-binding module and its role in the recognition and hydrolysis of β -1,3-glucan. <i>Journal of Biological Chemistry</i> , 2017, 292, 16955-16968.	3.4	19
12	Reovirus FAST Proteins Drive Pore Formation and Syncytiogenesis Using a Novel Helix-Loop-Helix Fusion-Inducing Lipid Packing Sensor. <i>PLoS Pathogens</i> , 2015, 11, e1004962.	4.7	18
13	Conserved structural features anchor biofilm-associated RTX adhesins to the outer membrane of bacteria. <i>FEBS Journal</i> , 2018, 285, 1812-1826.	4.7	18
14	Rhodoquinone in bacteria and animals: Two distinct pathways for biosynthesis of this key electron transporter used in anaerobic bioenergetics. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2020, 1861, 148278.	1.0	16
15	Biophysical characterization of G-protein coupled receptor ¹⁻³⁶ peptide ligand bindingThis paper is one of a selection of papers published in a Special Issue entitled CSBMCB 53rd Annual Meeting "Membrane Proteins in Health and Disease, and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2011, 89, 98-105.	2.0	13
16	Peptide backbone circularization enhances antifreeze protein thermostability. <i>Protein Science</i> , 2017, 26, 1932-1941.	7.6	11
17	Structure of the Single-lobe Myosin Light Chain C in Complex with the Light Chain-binding Domains of Myosin-1C Provides Insights into Divergent IQ Motif Recognition. <i>Journal of Biological Chemistry</i> , 2016, 291, 19607-19617.	3.4	10
18	Structural insights into TAZ2 domain-mediated CBP/p300 recruitment by transactivation domain 1 of the lymphopoietic transcription factor E2A. <i>Journal of Biological Chemistry</i> , 2020, 295, 4303-4315.	3.4	9

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19	Preserved Transmembrane Segment Topology, Structure, and Dynamics in Disparate Micellar Environments. <i>Journal of Physical Chemistry Letters</i> , 2017, 8, 2381-2386.	4.6	4
20	Expression, purification, and refolding of diverse class IB hydrophobins. <i>Protein Expression and Purification</i> , 2020, 176, 105732.	1.3	3
21	Characterization of Protein-Carbohydrate Interactions by NMR Spectroscopy. <i>Methods in Molecular Biology</i> , 2017, 1588, 143-156.	0.9	2
22	The N-terminal tail of the hydrophobin SC16 is not required for rodlet formation. <i>Scientific Reports</i> , 2022, 12, 366.	3.3	2
23	Backbone ¹ H, ¹³ C, and ¹⁵ N NMR resonance assignments of the KrÄ1/4ppel-like factor 4 activation domain. <i>Biomolecular NMR Assignments</i> , 2017, 11, 95-98.	0.8	0
24	The Microphthalmia-Associated Transcription Factor Associates with Multiple Domains of CBP/P300, Including the E1A Binding Face of TAZ2. <i>Biophysical Journal</i> , 2019, 116, 471a-472a.	0.5	0