Linda Columbus

List of Publications by Year
in descending order

68	3,021	249298 26	198040 52
papers	citations	h-index	g-index

91	91	91	4265
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The role of globins in cardiovascular physiology. Physiological Reviews, 2022, 102, 859-892.	13.1	16
2	Human CEACAM1 N-domain dimerization is independent from glycan modifications. Structure, 2022, 30, 658-670.e5.	1.6	4
3	Variable Expression of Opa Proteins by Neisseria gonorrhoeae Influences Bacterial Association and Phagocytic Killing by Human Neutrophils. Journal of Bacteriology, 2022, 204, e0003522.	1.0	8
4	TM1385 from Thermotoga maritima functions as a phosphoglucose isomerase via cis-enediol-based mechanism with active site redundancy. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140602.	1.1	1
5	Imaging Flow Cytometry Analysis of <scp>CEACAM</scp> Binding to Opaâ€Expressing <scp><i>Neisseria gonorrhoeae</i></scp>. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 1081-1089.	1.1	10
6	Quantifying Carcinoembryonic Antigen-like Cell Adhesion Molecule-Targeted Liposome Delivery Using Imaging Flow Cytometry. Molecular Pharmaceutics, 2019, 16, 2354-2363.	2.3	6
7	The Fluidity of Phosphocholine and Maltoside Micelles and the Effect of CHAPS. Biophysical Journal, 2019, 116, 1682-1691.	0.2	1
8	Heterocellular Contact Can Dictate Arterial Function. Circulation Research, 2019, 124, 1473-1481.	2.0	30
9	Quantifying CEACAM Targeted Liposome Delivery Using Imaging Flow Cytometry. Biophysical Journal, 2019, 116, 93a.	0.2	0
10	A Molecular Model of the Alpha Globin/eNOS Complex. FASEB Journal, 2019, 33, 481.3.	0.2	0
11	Heterocellular contact can dictate arterial function. FASEB Journal, 2019, 33, .	0.2	0
12	Refinement of Highly Flexible Protein Structures using Simulationâ€Guided Spectroscopy. Angewandte Chemie, 2018, 130, 17356-17360.	1.6	1
13	Refinement of Highly Flexible Protein Structures using Simulationâ€Guided Spectroscopy. Angewandte Chemie - International Edition, 2018, 57, 17110-17114.	7.2	10
14	Low-<i>q</i> Bicelles Are Mixed Micelles. Journal of Physical Chemistry Letters, 2018, 9, 4469-4473.	2.1	33
15	Mapping the interface of alpha globin and eNOS: implications for increasing endogenous NO therapeutically. FASEB Journal, 2018, 32, 652.34.	0.2	0
16	Conformation transitions of the polypeptide-binding pocket support an active substrate release from Hsp70s. Nature Communications, 2017, 8, 1201.	5.8	55
17	Leading Change in Undergraduate STEM Education. ACS Symposium Series, 2017, , 1-13.	0.5	1
18	Throwing Away the Cookbook: Implementing Course-Based Undergraduate Research Experiences (CUREs) in Chemistry. ACS Symposium Series, 2017, , 33-63.	0.5	37

#	Article	IF	Citations
19	Neisserial Opa Proteinâ€"CEACAM Interactions: Competition for Receptors as a Means of Bacterial Invasion and Pathogenesis. Biochemistry, 2016, 55, 4286-4294.	1.2	20
20	Modulating Vascular Hemodynamics With an Alpha Globin Mimetic Peptide (HbÎ±X). Hypertension, 2016, 68, 1494-1503.	1.3	26
21	Known structure, unknown function: An inquiryâ€based undergraduate biochemistry laboratory course. Biochemistry and Molecular Biology Education, 2015, 43, 245-262.	0.5	36
22	Opa+<i>N</i><i>eisseria gonorrhoeae</i>exhibits reduced survival in human neutrophils via Src family kinase-mediated bacterial trafficking into mature phagolysosomes. Cellular Microbiology, 2015, 17, 648-665.	1.1	33
23	Solution NMR Structure Determination of Polytopic Î±-Helical Membrane Proteins. Methods in Enzymology, 2015, 557, 329-348.	0.4	4
24	Endothelial nitric oxide synthase in the microcirculation. Cellular and Molecular Life Sciences, 2015, 72, 4561-4575.	2.4	89
25	Tuning Micelle Dimensions and Properties for Stabilizing Membrane Protein Fold and Function. Biophysical Journal, 2015, 108, 43a.	0.2	1
26	Post-expression strategies for structural investigations of membrane proteins. Current Opinion in Structural Biology, 2015, 32, 131-138.	2.6	14
27	Identification of a novel mitochondrial uncoupler that does not depolarize the plasma membrane. Molecular Metabolism, 2014, 3, 114-123.	3.0	168
28	Cottrell Scholars Collaborative New Faculty Workshop: Professional Development for New Chemistry Faculty and Initial Assessment of Its Efficacy. Journal of Chemical Education, 2014, 91, 1874-1881.	1.1	38
29	Tuning Micelle Dimensions and Properties with Binary Surfactant Mixtures. Langmuir, 2014, 30, 13353-13361.	1.6	20
30	Hemoglobin Î±/eNOS Coupling at Myoendothelial Junctions Is Required for Nitric Oxide Scavenging During Vasoconstriction. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 2594-2600.	1.1	72
31	Structure of the Neisserial Outer Membrane Protein Opa₆₀:ÂLoop Flexibility Essential to Receptor Recognition and Bacterial Engulfment. Journal of the American Chemical Society, 2014, 136, 9938-9946.	6.6	52
32	Mapping Membrane Protein Backbone Dynamics: A Comparison of Site-Directed Spin Labeling with NMR 15N-Relaxation Measurements. Biophysical Journal, 2014, 107, 1697-1702.	0.2	6
33	Hemoglobin Î± in the blood vessel wall. Free Radical Biology and Medicine, 2014, 73, 136-142.	1.3	31
34	Backbone 1H, 13C and 15N resonance assignments of the Î±-helical membrane protein TM0026 from Thermotoga maritima. Biomolecular NMR Assignments, 2013, 7, 203-206.	0.4	2
35	Solution NMR resonance assignment strategies for Î²â€barrel membrane proteins. Protein Science, 2013, 22, 1133-1140.	3.1	14
36	Modulating the Physical Properties of Micelles for Membrane Protein Investigations. Biophysical Journal, 2013, 104, 44a.	0.2	0

#	Article	IF	Citations
37	NMR Solution Structure of Opa60: A Neisserial Membrane Protein that Mediates Host Phagocytosis. Biophysical Journal, 2013, 104, 179a-180a.	0.2	0
38	Label-Free Method for Cell Counting in Crude Biological Samples via Paramagnetic Bead Aggregation. Analytical Chemistry, 2013, 85, 11233-11239.	3.2	9
39	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54
40	Dependence of Micelle Size and Shape on Detergent Alkyl Chain Length and Head Group. PLoS ONE, 2013, 8, e62488.	1.1	182
41	A broad specificity nucleoside kinase from <i>Thermoplasma acidophilum</i>. Proteins: Structure, Function and Bioinformatics, 2013, 81, 568-582.	1.5	10
42	MAPK Phosphorylation of Connexin 43 Promotes Binding of Cyclin E and Smooth Muscle Cell Proliferation. Circulation Research, 2012, 111, 201-211.	2.0	89
43	Strategies for the Solution NMR Structure Determination of Beta-Barrel Membrane Proteins. Biophysical Journal, 2012, 102, 422a-423a.	0.2	0
44	Endothelial cell expression of haemoglobin Î± regulates nitric oxide signalling. Nature, 2012, 491, 473-477.	13.7	261
45	Identification and removal of nitroxide spin label contaminant: Impact on PRE studies of Î±â€helical membrane proteins in detergent. Protein Science, 2012, 21, 589-595.	3.1	6
46	MAPK phosphorylation of connexin 43 promotes binding of cyclin E and smooth muscle cell proliferation. FASEB Journal, 2012, 26, 870.15.	0.2	0
47	Investigating the Relationship Between Physical Properties of Detergents and Membrane Protein Structure Determination. Biophysical Journal, 2011, 100, 385a.	0.2	0
48	Nitroxide Spin Label Side Chain Dynamics of Solvent Exposed Sites on Membrane Proteins. Biophysical Journal, 2011, 100, 143a-144a.	0.2	0
49	Physical Determinants of Î²-Barrel Membrane Protein Folding in Lipid Vesicles. Biophysical Journal, 2011, 100, 2131-2140.	0.2	34
50	NMR Backbone Assignment of Opai: A Mediator of Host:Neisseria Interactions. Biophysical Journal, 2011, 100, 385a.	0.2	0
51	Structural Investigations of Inclusion Membrane Protein a (INCA) of Chlamydia Trachomatis. Biophysical Journal, 2011, 100, 381a.	0.2	0
52	Structural Origins of Nitroxide Side Chain Dynamics on Membrane Protein Î±-Helical Sites,. Biochemistry, 2010, 49, 10045-10060.	1.2	74
53	Structure of the GLD-1 Homodimerization Domain: Insights into STAR Protein-Mediated Translational Regulation. Structure, 2010, 18, 377-389.	1.6	23
54	The Spontaneous Refolding of Opacity-Associated Proteins into Lipid Membranes. Biophysical Journal, 2010, 98, 624a.	0.2	0

#	Article	IF	Citations
55	Mixing and Matching Detergents for Membrane Protein NMR Structure Determination. Journal of the American Chemical Society, 2009, 131, 7320-7326.	6.6	79
56	Molecular Determinants of Neisserial Pathogenesis: Mapping the Interaction Between Opa I and a Human Binding Partner CEACAM1. Biophysical Journal, 2009, 96, 338a.	0.2	0
57	Structure and ligand binding of the soluble domain of a <i>Thermotoga maritima</i> membrane protein of unknown function TM1634. Protein Science, 2008, 17, 869-877.	3.1	4
58	NMR structural characterization of the homodimerization domain of the translational repressor GLDâ€1. FASEB Journal, 2008, 22, 783.1.	0.2	0
59	Analysis of small-angle X-ray scattering data of proteinâ€“detergent complexes by singular value decomposition. Journal of Applied Crystallography, 2007, 40, s235-s239.	1.9	17
60	Size and Shape of Detergent Micelles Determined by Small-Angle X-ray Scattering. Journal of Physical Chemistry B, 2007, 111, 12427-12438.	1.2	219
61	Expression, purification, and characterization ofThermotoga maritimamembrane proteins for structure determination. Protein Science, 2006, 15, 961-975.	3.1	46
62	NMR structure determination of the conserved hypothetical protein TM1816 from Thermotoga maritima. Proteins: Structure, Function and Bioinformatics, 2005, 60, 552-557.	1.5	7
63	A Multifrequency Electron Spin Resonance Study of T4 Lysozyme Dynamics Using the Slowly Relaxing Local Structure Model. Journal of Physical Chemistry B, 2004, 108, 17649-17659.	1.2	66
64	Mapping Backbone Dynamics in Solution with Site-Directed Spin Labeling:Â GCN4â^’58 bZip Free and Bound to DNAâ€. Biochemistry, 2004, 43, 7273-7287.	1.2	128
65	A new spin on protein dynamics. Trends in Biochemical Sciences, 2002, 27, 288-295.	3.7	403
66	Molecular Motion of Spin Labeled Side Chains in Î±-Helices:â€‰ Analysis by Variation of Side Chain Structure. Biochemistry, 2001, 40, 3828-3846.	1.2	266
67	Protein global fold determination using siteâ€directed spin and isotope labeling. Protein Science, 2000, 9, 302-309.	3.1	81
68	Structure of the KcsA Potassium Channel fromStreptomyces lividans:Â A Site-Directed Spin Labeling Study of the Second Transmembrane Segmentâ€. Biochemistry, 1999, 38, 10324-10335.	1.2	122