

Andrei L Lomize

List of Publications by Year in descending order

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39
papers

3,964
citations

331538

21
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315616

38
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39
all docs

39
docs citations

39
times ranked

5927
citing authors

#	ARTICLE	IF	CITATIONS
1	OPM database and PPM web server: resources for positioning of proteins in membranes. <i>Nucleic Acids Research</i> , 2012, 40, D370-D376.	6.5	1,572
2	OPM: Orientations of Proteins in Membranes database. <i>Bioinformatics</i> , 2006, 22, 623-625.	1.8	1,064
3	Positioning of proteins in membranes: A computational approach. <i>Protein Science</i> , 2006, 15, 1318-1333.	3.1	218
4	Anisotropic Solvent Model of the Lipid Bilayer. 2. Energetics of Insertion of Small Molecules, Peptides, and Proteins in Membranes. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 930-946.	2.5	131
5	The role of hydrophobic interactions in positioning of peripheral proteins in membranes. <i>BMC Structural Biology</i> , 2007, 7, 44.	2.3	107
6	Spatial arrangement of proteins in planar and curved membranes by <scp>PPM</scp> 3.0. <i>Protein Science</i> , 2022, 31, 209-220.	3.1	89
7	Structural adaptations of proteins to different biological membranes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2592-2608.	1.4	54
8	Membranome: a database for proteome-wide analysis of single-pass membrane proteins. <i>Nucleic Acids Research</i> , 2017, 45, D250-D255.	6.5	52
9	Structural organization of G-protein-coupled receptors. <i>Journal of Computer-Aided Molecular Design</i> , 1999, 13, 325-353.	1.3	50
10	Cytotoxic potency of small macrocyclic knot proteins: Structure-activity and mechanistic studies of native and chemically modified cyclotides. <i>Organic and Biomolecular Chemistry</i> , 2011, 9, 4306.	1.5	41
11	PerMM: A Web Tool and Database for Analysis of Passive Membrane Permeability and Translocation Pathways of Bioactive Molecules. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3094-3099.	2.5	41
12	Physics-Based Method for Modeling Passive Membrane Permeability and Translocation Pathways of Bioactive Molecules. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3198-3213.	2.5	41
13	Anisotropic Solvent Model of the Lipid Bilayer. 1. Parameterization of Long-Range Electrostatics and First Solvation Shell Effects. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 918-929.	2.5	38
14	Antimicrobial Action of the Cyclic Peptide Bactenecin on <i>Burkholderia pseudomallei</i> Correlates with Efficient Membrane Permeabilization. <i>PLoS Neglected Tropical Diseases</i> , 2013, 7, e2267.	1.3	37
15	TMDOCK: An Energy-Based Method for Modeling α -Helical Dimers in Membranes. <i>Journal of Molecular Biology</i> , 2017, 429, 390-398.	2.0	35
16	Interatomic potentials and solvation parameters from protein engineering data for buried residues. <i>Protein Science</i> , 2002, 11, 1984-2000.	3.1	33
17	Comparative Molecular Dynamics Simulation Studies of Realistic Eukaryotic, Prokaryotic, and Archaeal Membranes. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1036-1051.	2.5	32
18	Development of a model for the μ -opioid receptor pharmacophore. 4. Residue 3 dehydrophenylalanine analogues of Tyr-c[D-Cys-Phe-D-Pen]OH (JOM-13) confirm required gauche orientation of aromatic side chain. , 1998, 39, 287-296.		31

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19	Thermodynamic model of secondary structure for α -helical peptides and proteins. <i>Biopolymers</i> , 1997, 42, 239-269.	1.2	30
20	The Contribution of Surface Residues to Membrane Binding and Ligand Transfer by the α -Tocopherol Transfer Protein (α -TTP). <i>Journal of Molecular Biology</i> , 2011, 405, 972-988.	2.0	29
21	Membranome 2.0: database for proteome-wide profiling of bitopic proteins and their dimers. <i>Bioinformatics</i> , 2018, 34, 1061-1062.	1.8	28
22	Quantification of helix-helix binding affinities in micelles and lipid bilayers. <i>Protein Science</i> , 2009, 13, 2600-2612.	3.1	27
23	Development of a model for the μ -opioid receptor pharmacophore: 3. Comparison of the cyclic tetrapeptide Tyr-c[D-Cys-Phe-D-Pen] OH with other conformationally constrained μ -receptor selective ligands. <i>Biopolymers</i> , 1998, 38, 221-234.	1.2	26
24	Life at the border: Adaptation of proteins to anisotropic membrane environment. <i>Protein Science</i> , 2014, 23, 1165-1196.	3.1	21
25	Prediction of protein structure: The problem of fold multiplicity. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 37, 199-203.	1.5	20
26	Carnitine palmitoyltransferase 2: Analysis of membrane association and complex structure with a substrate analog. <i>FEBS Letters</i> , 2007, 581, 3247-3252.	1.3	20
27	Membranome 3.0: Database of single-pass membrane proteins with α Fold models. <i>Protein Science</i> , 2022, 31, e4318.	3.1	20
28	Evolution and adaptation of single-pass transmembrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2018, 1860, 364-377.	1.4	16
29	Development of a model for the μ -opioid receptor pharmacophore: 3. Comparison of the cyclic tetrapeptide Tyr-c[D-Cys-Phe-D-Pen] OH with other conformationally constrained μ -receptor selective ligands. <i>Biopolymers</i> , 1996, 38, 221-234.	1.2	13
30	Membrane Topology of the Colicin E1 Channel Using Genetically Encoded Fluorescence. <i>Biochemistry</i> , 2011, 50, 4830-4842.	1.2	12
31	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1245-1253.	0.7	8
32	Solvation Models and Computational Prediction of Orientations of Peptides and Proteins in Membranes. <i>Methods in Molecular Biology</i> , 2013, 1063, 125-142.	0.4	8
33	Thermodynamics-Based Molecular Modeling of α -Helices in Membranes and Micelles. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2884-2896.	2.5	6
34	TMPfold: A Web Tool for Predicting Stability of Transmembrane α -Helix Association. <i>Journal of Molecular Biology</i> , 2020, 432, 3388-3394.	2.0	4
35	Prediction of Passive Membrane Permeability and Translocation Pathways of Biologically Active Molecules. <i>Biophysical Journal</i> , 2017, 112, 525a.	0.2	3
36	Thermodynamic Approach to Large-Scale Modeling of Alpha-Helices in Membranes. <i>Biophysical Journal</i> , 2012, 102, 490a-491a.	0.2	2

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37	Membranome: A Database of Single-Spanning Transmembrane Proteins. Biophysical Journal, 2015, 108, 249a-250a.	0.2	2
38	Proteome-Wide Modeling of Transmembrane Alpha-Helical Homodimers by TMDOCK. Biophysical Journal, 2017, 112, 358a.	0.2	2
39	PerMM: Web Server and Database for Prediction of Membrane Permeability and Translocation Pathways of Molecules. Biophysical Journal, 2018, 114, 343a-344a.	0.2	1