Andrei L Lomize

List of Publications by Year
in descending order

39 papers	3,964 citations	331670 21 h-index	315739 38 g-index
39 all docs	39 docs citations	39 times ranked	5927 citing authors

#	Article	IF	Citations
1	Spatial arrangement of proteins in planar and curved membranes by <scp>PPM</scp> 3.0. Protein Science, 2022, 31, 209-220.	7.6	89
2	Comparative Molecular Dynamics Simulation Studies of Realistic Eukaryotic, Prokaryotic, and Archaeal Membranes. Journal of Chemical Information and Modeling, 2022, 62, 1036-1051.	5.4	32
3	Membranome 3.0: Database of singleâ€pass membrane proteins with <scp>AlphaFold</scp> models. Protein Science, 2022, 31, e4318.	7.6	20
4	Thermodynamics-Based Molecular Modeling of Î±-Helices in Membranes and Micelles. Journal of Chemical Information and Modeling, 2021, 61, 2884-2896.	5.4	6
5	TMPfold: A Web Tool for Predicting Stability of Transmembrane Î±-Helix Association. Journal of Molecular Biology, 2020, 432, 3388-3394.	4.2	4
6	PerMM: A Web Tool and Database for Analysis of Passive Membrane Permeability and Translocation Pathways of Bioactive Molecules. Journal of Chemical Information and Modeling, 2019, 59, 3094-3099.	5.4	41
7	Physics-Based Method for Modeling Passive Membrane Permeability and Translocation Pathways of Bioactive Molecules. Journal of Chemical Information and Modeling, 2019, 59, 3198-3213.	5.4	41
8	Membranome 2.0: database for proteome-wide profiling of bitopic proteins and their dimers. Bioinformatics, 2018, 34, 1061-1062.	4.1	28
9	Evolution and adaptation of single-pass transmembrane proteins. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 364-377.	2.6	16
10	PerMM: Web Server and Database for Prediction of Membrane Permeability and Translocation Pathways of Molecules. Biophysical Journal, 2018, 114, 343a-344a.	0.5	1
11	Prediction of Passive Membrane Permeability and Translocation Pathways of Biologically Active Molecules. Biophysical Journal, 2017, 112, 525a.	0.5	3
12	Proteome-Wide Modeling of Transmembrane Alpha-Helical Homodimers by TMDOCK. Biophysical Journal, 2017, 112, 358a.	0.5	2
13	TMDOCK: An Energy-Based Method for Modeling Î±-Helical Dimers in Membranes. Journal of Molecular Biology, 2017, 429, 390-398.	4.2	35
14	Membranome: a database for proteome-wide analysis of single-pass membrane proteins. Nucleic Acids Research, 2017, 45, D250-D255.	14.5	52
15	Membranome: A Database of Single-Spanning Transmembrane Proteins. Biophysical Journal, 2015, 108, 249a-250a.	0.5	2
16	Life at the border: Adaptation of proteins to anisotropic membrane environment. Protein Science, 2014, 23, 1165-1196.	7.6	21
17	Structural adaptations of proteins to different biological membranes. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2592-2608.	2.6	54
18	Solvation Models and Computational Prediction of Orientations of Peptides and Proteins in Membranes. Methods in Molecular Biology, 2013, 1063, 125-142.	0.9	8

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19	Antimicrobial Action of the Cyclic Peptide Bactenecin on Burkholderia pseudomallei Correlates with Efficient Membrane Permeabilization. PLoS Neglected Tropical Diseases, 2013, 7, e2267.	3.0	37
20	OPM database and PPM web server: resources for positioning of proteins in membranes. Nucleic Acids Research, 2012, 40, D370-D376.	14.5	1,572
21	Thermodynamic Approach to Large-Scale Modeling of Alpha-Helices in Membranes. Biophysical Journal, 2012, 102, 490a-491a.	0.5	2
22	Anisotropic Solvent Model of the Lipid Bilayer. 2. Energetics of Insertion of Small Molecules, Peptides, and Proteins in Membranes. Journal of Chemical Information and Modeling, 2011, 51, 930-946.	5.4	131
23	Membrane Topology of the Colicin E1 Channel Using Genetically Encoded Fluorescence. Biochemistry, 2011, 50, 4830-4842.	2.5	12
24	Anisotropic Solvent Model of the Lipid Bilayer. 1. Parameterization of Long-Range Electrostatics and First Solvation Shell Effects. Journal of Chemical Information and Modeling, 2011, 51, 918-929.	5.4	38
25	The Contribution of Surface Residues to Membrane Binding and Ligand Transfer by the Î±-Tocopherol Transfer Protein (Î±-TTP). Journal of Molecular Biology, 2011, 405, 972-988.	4.2	29
26	Cytotoxic potency of small macrocyclic knot proteins: Structureâ€“activity and mechanistic studies of native and chemically modified cyclotides. Organic and Biomolecular Chemistry, 2011, 9, 4306.	2.8	41
27	Open and closed conformations of two SpoIIAA-like proteins (YP_749275.1 and YP_001095227.1) provide insights into membrane association and ligand binding. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1245-1253.	0.7	8
28	Quantification of helix-helix binding affinities in micelles and lipid bilayers. Protein Science, 2009, 13, 2600-2612.	7.6	27
29	Carnitine palmitoyltransferase 2: Analysis of membrane association and complex structure with a substrate analog. FEBS Letters, 2007, 581, 3247-3252.	2.8	20
30	The role of hydrophobic interactions in positioning of peripheral proteins in membranes. BMC Structural Biology, 2007, 7, 44.	2.3	107
31	Positioning of proteins in membranes: A computational approach. Protein Science, 2006, 15, 1318-1333.	7.6	218
32	OPM: Orientations of Proteins in Membranes database. Bioinformatics, 2006, 22, 623-625.	4.1	1,064
33	Interatomic potentials and solvation parameters from protein engineering data for buried residues. Protein Science, 2002, 11, 1984-2000.	7.6	33
34	Structural organization of G-protein-coupled receptors. Journal of Computer-Aided Molecular Design, 1999, 13, 325-353.	2.9	50
35	Prediction of protein structure: The problem of fold multiplicity. Proteins: Structure, Function and Bioinformatics, 1999, 37, 199-203.	2.6	20
36	Development of a model for the Î´-opioid receptor pharmacophore: 3. Comparison of the cyclic tetrapeptide Tyr-c[D-Cys-Phe-D-Pen] OH with other conformationally constrained Î´-receptor selective ligands. Biopolymers, 1998, 38, 221-234.	2.4	26

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37	Development of a model for the Î´-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
38	Thermodynamic model of secondary structure for Î±-helical peptides and proteins. Biopolymers, 1997, 42, 239-269.	2.4	30
39	Development of a model for the Î´â€opioid receptor pharmacophore: 3. Comparison of the cyclic tetrapeptide Tyrâ€c[Dâ€Cysâ€Pheâ€Dâ€Pen] OH with other conformationally constrained Î´â€receptor selective ligands. Biopolymers, 1996, 38, 221-234.	2.4	13