Roman G Efremov

List of Publications by Year
in descending order

197	4,501	94433 37	149698 56
papers	citations	h-index	g-index

205	205	205	4198
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Spatial Structure of the Dimeric Transmembrane Domain of the Growth Factor Receptor ErbB2 Presumably Corresponding to the Receptor Active State. Journal of Biological Chemistry, 2008, 283, 6950-6956.	3.4	189
2	PLATINUM: a web tool for analysis of hydrophobic/hydrophilic organization of biomolecular complexes. Bioinformatics, 2009, 25, 1201-1202.	4.1	159
3	Molecular Lipophilicity in Protein Modeling and Drug Design. Current Medicinal Chemistry, 2007, 14, 393-415.	2.4	128
4	Unique Dimeric Structure of BNip3 Transmembrane Domain Suggests Membrane Permeabilization as a Cell Death Trigger. Journal of Biological Chemistry, 2007, 282, 16256-16266.	3.4	121
5	Surface-enhanced Raman spectroscopy of biomolecules. Part I.-water-soluble proteins, dipeptides and amino acids. Journal of Raman Spectroscopy, 1990, 21, 43-48.	2.5	109
6	Spatial Structure and pH-dependent Conformational Diversity of Dimeric Transmembrane Domain of the Receptor Tyrosine Kinase EphA1. Journal of Biological Chemistry, 2008, 283, 29385-29395.	3.4	100
7	Left-Handed Dimer of EphA2 Transmembrane Domain: Helix Packing Diversity among Receptor Tyrosine Kinases. Biophysical Journal, 2010, 98, 881-889.	0.5	100
8	Insulin Receptor-Related Receptor as an Extracellular Alkali Sensor. Cell Metabolism, 2011, 13, 679-689.	16.2	92
9	PREDDIMER: a web server for prediction of transmembrane helical dimers. Bioinformatics, 2014, 30, 889-890.	4.1	77
10	Structural mechanism of heat-induced opening of a temperature-sensitive TRP channel. Nature Structural and Molecular Biology, 2021, 28, 564-572.	8.2	76
11	Helix-helix interactions in membrane domains of bitopic proteins: Specificity and role of lipid environment. Biochimica Et Biophysica Acta - Biomembranes, 2017, 1859, 561-576.	2.6	72
12	The Role of the Invariant His-1069 in Folding and Function of the Wilson's Disease Protein, the Human Copper-transporting ATPase ATP7B. Journal of Biological Chemistry, 2003, 278, 13302-13308.	3.4	66
13	Antimicrobial Peptides Induce Growth of Phosphatidylglycerol Domains in a Model Bacterial Membrane. Journal of Physical Chemistry Letters, 2010, 1, 3108-3111.	4.6	65
14	How broadly tuned olfactory receptors equally recognize their agonists. Human OR1G1 as a test case. Cellular and Molecular Life Sciences, 2012, 69, 4205-4213.	5.4	64
15	A Solvent Model for Simulations of Peptides in Bilayers. I. Membrane-Promoting Î±-Helix Formation. Biophysical Journal, 1999, 76, 2448-2459.	0.5	63
16	Multistate Organization of Transmembrane Helical Protein Dimers Governed by the Host Membrane. Journal of the American Chemical Society, 2012, 134, 14390-14400.	13.7	63
17	Human copper-transporting ATPase ATP7B (the Wilson's disease protein): biochemical properties and regulation. Journal of Bioenergetics and Biomembranes, 2002, 34, 351-362.	2.3	61
18	Pyrenemethyl ara-Uridine-2â€²-carbamate: A Strong Interstrand Excimer in the Major Groove of a DNA Duplex. ChemBioChem, 2003, 4, 841-847.	2.6	61

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19	Interaction of three-finger toxins with phospholipid membranes: comparison of S- and P-type cytotoxins. Biochemical Journal, 2005, 387, 807-815.	3.7	59
20	Structure and Dynamics of Cardiotoxins. Current Protein and Peptide Science, 2012, 13, 570-584.	1.4	58
21	The Distinct Functional Properties of the Nucleotide-binding Domain of ATP7B, the Human Copper-transporting ATPase. Journal of Biological Chemistry, 2004, 279, 36363-36371.	3.4	56
22	Lipid-II forms potential â€œlanding terrainâ€•for lantibiotics in simulated bacterial membrane. Scientific Reports, 2013, 3, 1678.	3.3	56
23	Peptides and Proteins in Membranes: What Can We Learn via Computer Simulations?. Current Medicinal Chemistry, 2004, 11, 2421-2442.	2.4	54
24	Latarcins: versatile spider venom peptides. Cellular and Molecular Life Sciences, 2015, 72, 4501-4522.	5.4	54
25	Snake Cytotoxins Bind to Membranes via Interactions with Phosphatidylserine Head Groups of Lipids. PLoS ONE, 2011, 6, e19064.	2.5	53
26	Interaction between the Elastin Peptide VGVAPG and Human Elastin Binding Protein. Journal of Biological Chemistry, 2013, 288, 1317-1328.	3.4	50
27	Temperature-sensitive gating of TRPV1 channel as probed by atomistic simulations of its trans- and juxtamembrane domains. Scientific Reports, 2016, 6, 33112.	3.3	49
28	Cobra Cardiotoxins: Membrane Interactions and Pharmacological Potential. Current Medicinal Chemistry, 2013, 21, 270-287.	2.4	48
29	Interaction of Cardiotoxins with Membranes: A Molecular Modeling Study. Biophysical Journal, 2002, 83, 144-153.	0.5	46
30	New Insights into Molecular Organization of Human Neuraminidase-1: Transmembrane Topology and Dimerization Ability. Scientific Reports, 2016, 6, 38363.	3.3	44
31	Hydrophobic Nature of Membrane-Spanning .alpha.-Helical Peptides as Revealed by Monte Carlo Simulations and Molecular Hydrophobicity Potential Analysis. The Journal of Physical Chemistry, 1995, 99, 10658-10666.	2.9	42
32	Spatial Structure of Zervamicin IIB Bound to DPC Micelles: Implications for Voltage-Gating. Biophysical Journal, 2002, 82, 762-771.	0.5	42
33	Liquid but Durable: Molecular Dynamics Simulations Explain the Unique Properties of Archaeal-Like Membranes. Scientific Reports, 2014, 4, 7462.	3.3	42
34	Factors important for fusogenic activity of peptides: molecular modeling study of analogs of fusion peptide of influenza virus hemagglutinin. FEBS Letters, 1999, 462, 205-210.	2.8	40
35	Role of Lipid Charge in Organization of Water/Lipid Bilayer Interface:Â Insights via Computer Simulations. Journal of Physical Chemistry B, 2005, 109, 15052-15059.	2.6	40
36	Environmental Characteristics of Residues in Proteins: Three-Dimensional Molecular Hydrophobicity Potential Approach. Journal of Biomolecular Structure and Dynamics, 1993, 11, 483-507.	3.5	39

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37	A cytochrome c mutant with high electron transfer and antioxidant activities but devoid of apoptogenic effect. Biochemical Journal, 2002, 362, 749.	3.7	39
38	The Conformation of the Epidermal Growth Factor Receptor Transmembrane Domain Dimer Dynamically Adapts to the Local Membrane Environment. Biochemistry, 2017, 56, 1697-1705.	2.5	39
39	Three-Dimensional Structure/Hydrophobicity of Latarcins Specifies Their Mode of Membrane Activity[,]. Biochemistry, 2008, 47, 3525-3533.	2.5	38
40	Linker and/or transmembrane regions of influenza A/Group-1, A/Group-2, and type B virus hemagglutinins are packed differently within trimers. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 1843-1854.	2.6	38
41	Surface-enhanced Raman spectroscopy of biomolecules. Part II. Application of short- and long-range components of SERS to the study of the structure and function of membrane proteins. Journal of Raman Spectroscopy, 1990, 21, 49-53.	2.5	37
42	Spatial Structure and Activity Mechanism of a Novel Spider Antimicrobial Peptide,. Biochemistry, 2006, 45, 10759-10767.	2.5	37
43	Structural Insight into Specificity of Interactions between Nonconventional Three-finger Weak Toxin from Naja kaouthia (WTX) and Muscarinic Acetylcholine Receptors. Journal of Biological Chemistry, 2015, 290, 23616-23630.	3.4	37
44	Dimeric Structure of the Transmembrane Domain of Glycophorin A in Lipidic and Detergent Environments. Acta Naturae, 2011, 3, 90-98.	1.7	37
45	A Solvent Model for Simulations of Peptides in Bilayers. II. Membrane-Spanning Î±-Helices. Biophysical Journal, 1999, 76, 2460-2471.	0.5	36
46	Adaptation of a Membrane-active Peptide to Heterogeneous Environment. I. Structural Plasticity of the Peptide. Journal of Physical Chemistry B, 2009, 113, 1107-1119.	2.6	36
47	Nâ€terminal amphipathic helix as a trigger of hemolytic activity in antimicrobial peptides: A case study in latarcins. FEBS Letters, 2009, 583, 2425-2428.	2.8	34
48	Structure elucidation of dimeric transmembrane domains of bitopic proteins. Cell Adhesion and Migration, 2010, 4, 284-298.	2.7	34
49	Nontrivial Behavior of Water in the Vicinity and Inside Lipid Bilayers As Probed by Molecular Dynamics Simulations. ACS Nano, 2013, 7, 9428-9442.	14.6	34
50	Secreted Isoform of Human Lynx1 (SLURP-2): Spatial Structure and Pharmacology of Interactions with Different Types of Acetylcholine Receptors. Scientific Reports, 2016, 6, 30698.	3.3	34
51	Effect of Lipid Composition on the â€œMembrane Responseâ€•Induced by a Fusion Peptideâ€. Biochemistry, 2005, 44, 14626-14637.	2.5	31
52	Specific Membrane Binding of Neurotoxin II Can Facilitate Its Delivery to Acetylcholine Receptor. Biophysical Journal, 2009, 97, 2089-2097.	0.5	31
53	Modular Organization of Î±-Toxins from Scorpion Venom Mirrors Domain Structure of Their Targets, Sodium Channels. Journal of Biological Chemistry, 2013, 288, 19014-19027.	3.4	31
54	Application of three-dimensional molecular hydrophobicity potential to the analysis of spatial organization of membrane domains in proteins: I. Hydrophobic properties of transmembrane segments of Na+, K+-ATPase. The Protein Journal, 1992, 11, 665-675.	1.1	30

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55	Effect of hydrophobic environment on the resonance Raman spectra of tryptophan residues in proteins. Journal of Raman Spectroscopy, 1992, 23, 69-73.	2.5	29
56	Spatial structure of the M2 transmembrane segment of the nicotinic acetylcholine receptor Î±-subunit. FEBS Letters, 1999, 457, 117-121.	2.8	28
57	Deciphering Fine Molecular Details of Proteinsâ€™ Structure and Function with a Protein Surface Topography (PST) Method. Journal of Chemical Information and Modeling, 2014, 54, 1189-1199.	5.4	28
58	Structural basis of the signal transduction via transmembrane domain of the human growth hormone receptor. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1410-1420.	2.4	28
59	Kalium 2.0, a comprehensive database of polypeptide ligands of potassium channels. Scientific Data, 2019, 6, 73.	5.3	28
60	Differentiated analysis of the secondary structure of hydrophilic and hydrophobic regions in Î±- and Î²-subunits of Na+,K+-ATPase by Raman spectroscopy. FEBS Letters, 1988, 227, 235-239.	2.8	27
61	Atomic-scale lateral heterogeneity and dynamics of two-component lipid bilayers composed of saturated and unsaturated phosphatidylcholines. Soft Matter, 2011, 7, 2569.	2.7	27
62	Elastic fibers and elastin receptor complex: Neuraminidase-1 takes the center stage. Matrix Biology, 2019, 84, 57-67.	3.6	27
63	Molecular modelling of the nucleotide-binding domain of Wilson's disease protein: location of the ATP-binding site, domain dynamics and potential effects of the major disease mutations. Biochemical Journal, 2004, 382, 293-305.	3.7	23
64	Association of transmembrane helices: what determines assembling of a dimer?. Journal of Computer-Aided Molecular Design, 2006, 20, 27-45.	2.9	23
65	Homology modeling of MT1 and MT2 receptors. European Journal of Medicinal Chemistry, 2008, 43, 1926-1944.	5.5	23
66	Adaptation of a Membrane-active Peptide to Heterogeneous Environment. II. The Role of Mosaic Nature of the Membrane Surface. Journal of Physical Chemistry B, 2009, 113, 1120-1126.	2.6	23
67	High-Affinity Î±-Conotoxin PnIA Analogs Designed on the Basis of the Protein Surface Topography Method. Scientific Reports, 2016, 6, 36848.	3.3	23
68	Dimeric structure of the transmembrane domain of glycophorin a in lipidic and detergent environments. Acta Naturae, 2011, 3, 90-8.	1.7	23
69	The chromophore-binding site of bacteriorhodopsin. Resonance Raman and surface-enhanced resonance Raman spectroscopy and quantum chemical study. Journal of Biosciences, 1985, 8, 363-374.	1.1	22
70	Complementarity of hydrophobic properties in ATP-protein binding: A new criterion to rank docking solutions. Proteins: Structure, Function and Bioinformatics, 2006, 66, 388-398.	2.6	21
71	Adaptable Lipid Matrix Promotes Proteinâ€“Protein Association in Membranes. Journal of Chemical Theory and Computation, 2015, 11, 4415-4426.	5.3	21
72	Environmental and dynamic effects explain how nisin captures membrane-bound lipid II. Scientific Reports, 2020, 10, 8821.	3.3	21

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73	Transmembrane Peptides as Inhibitors of Protein-Protein Interactions: An Efficient Strategy to Target Cancer Cells?. Frontiers in Oncology, 2020, 10, 519.	2.8	21
74	Role of Dimerization Efficiency of Transmembrane Domains in Activation of Fibroblast Growth Factor Receptor 3. Journal of the American Chemical Society, 2013, 135, 8105-8108.	13.7	20
75	KV1.2 channel-specific blocker from Mesobuthus eupeus scorpion venom: Structural basis of selectivity. Neuropharmacology, 2018, 143, 228-238.	4.1	20
76	Atomic Solvation Parameters for Proteins in a Membrane Environment. Application to Transmembrane Î±-Helices. Journal of Biomolecular Structure and Dynamics, 1997, 15, 1-18.	3.5	19
77	Recent Advances in Computational Modeling of α.-Helical Membrane- Active Peptides. Current Protein and Peptide Science, 2012, 13, 644-657.	1.4	19
78	Implicit two-phase solvation model as a tool to assess conformation and energetics of proteins in membrane-mimetic media. Theoretical Chemistry Accounts, 2001, 106, 48-54.	1.4	18
79	The X-ray structure ofSalmonella typhimuriumuridine nucleoside phosphorylase complexed with 2,2â€²-anhydrouridine, phosphate and potassium ions at 1.86â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 51-60.	2.5	18
80	Central loop of non-conventional toxin WTX from Naja kaouthia is important for interaction with nicotinic acetylcholine receptors. Toxicon, 2016, 119, 274-279.	1.6	18
81	The Role of Stacking Interactions in Complexes of Proteins with Adenine and Guanine Fragments of Ligands. Acta Naturae, 2009, 1, 124-127.	1.7	17
82	Binding of monovalent cations induces large changes in the secondary structure of Na+,K+-ATPase as probed by Raman spectroscopy. FEBS Letters, 1988, 236, 235-239.	2.8	16
83	Study of ATP binding in the active site of Na+ ,K+ -ATPase as probed by ultraviolet resonance Raman spectroscopy. FEBS Letters, 1990, 260, 257-260.	2.8	16
84	Differences in Binding Sites of Two Melatonin Receptors Help to Explain Their Selectivity to Some Melatonin Analogs: A Molecular Modeling Study. Journal of Biomolecular Structure and Dynamics, 2006, 24, 91-107.	3.5	16
85	Specificity of helix packing in transmembrane dimer of the cell death factor BNIP3: A molecular modeling study. Proteins: Structure, Function and Bioinformatics, 2007, 69, 309-325.	2.6	15
86	Cardiotoxins: Functional Role of Local Conformational Changes. Journal of Chemical Information and Modeling, 2017, 57, 2799-2810.	5.4	15
87	Normal coordinate treatment of 1-methylthymine in the crystalline state: Use of the ultraviolet resonance Raman intensities to improve the vibrational force field. Spectrochimica Acta Part A: Molecular Spectroscopy, 1994, 50, 961-971.	0.1	14
88	Protonâ€independent activation of acidâ€sensing ion channel 3 by an alkaloid, lindoldhamine, from Laurus nobilis. British Journal of Pharmacology, 2018, 175, 924-937.	5.4	14
89	Application of three-dimensional molecular hydrophobicity potential to the analysis of spatial organization of membrane protein domains. II. Optimization of hydrophobic contacts in transmembrane hairpin structures of Na+, K+-ATPase. The Protein Journal, 1992, 11, 699-708.	1.1	13
90	Helix Interactions in Membranes:Â Lessons from Unrestrained Monte Carlo Simulations. Journal of Chemical Theory and Computation, 2005, 1, 1252-1264.	5.3	13

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91	Impact of membrane partitioning on the spatial structure of an S-type cobra cytotoxin. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3463-3478.	3.5	13
92	Familial L723P Mutation Can Shift the Distribution between the Alternative APP Transmembrane Domain Cleavage Cascades by Local Unfolding of the Î•-Cleavage Site Suggesting a Straightforward Mechanism of Alzheimerâ€™s Disease Pathogenesis. ACS Chemical Biology, 2019, 14, 1573-1582.	3.4	13
93	Retinal Schiff base position relative to the surfaces of photoreceptor disk. FEBS Letters, 1987, 213, 113-118.	2.8	12
94	Structural, dynamic, and functional aspects of helix association in membranes. Advances in Protein Chemistry and Structural Biology, 2011, 83, 129-161.	2.3	12
95	Dynamic clustering of lipids in hydrated two-component membranes: results of computer modeling and putative biological impact. Journal of Biomolecular Structure and Dynamics, 2013, 31, 87-95.	3.5	12
96	Amino acid residue: is it structural or functional?. FEBS Letters, 1995, 375, 162-166.	2.8	11
97	Hydrophobic organization of Î±-helix membrane bundle in bacteriorhodopsin. The Protein Journal, 1996, 15, 63-76.	1.1	11
98	Docking of ATP to Ca-ATPase:â€‰ Considering Protein Domain Motions. Journal of Chemical Information and Modeling, 2007, 47, 1171-1181.	5.4	11
99	Ligand-specific scoring functions: improved ranking of docking solutions. SAR and QSAR in Environmental Research, 2008, 19, 91-99.	2.2	11
100	Computer simulations and modeling-assisted ToxR screening in deciphering 3D structures of transmembrane Î±-helical dimers: ephrin receptor A1. Physical Biology, 2010, 7, 016014.	1.8	11
101	Complex approach for analysis of snake venom Î±-neurotoxins binding to HAP, the high-affinity peptide. Scientific Reports, 2020, 10, 3861.	3.3	11
102	Transmembrane Peptides as a New Strategy to Inhibit Neuraminidase-1 Activation. Frontiers in Cell and Developmental Biology, 2020, 8, 611121.	3.7	11
103	Quantitative Treatment of UV Resonance Raman Spectra of Biological Molecules: Application to the Study of Membrane-Bound Proteins. Applied Spectroscopy, 1991, 45, 272-278.	2.2	10
104	Development of the force field parameters for phosphoimidazole and phosphohistidine. Journal of Computational Chemistry, 2004, 25, 1313-1321.	3.3	10
105	Probing the effect of membrane contents on transmembrane protein-protein interaction using solution NMR and computer simulations. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 2486-2498.	2.6	10
106	Protein surface topography as a tool to enhance the selective activity of a potassium channel blocker. Journal of Biological Chemistry, 2019, 294, 18349-18359.	3.4	10
107	Human Three-Finger Protein Lypd6 Is a Negative Modulator of the Cholinergic System in the Brain. Frontiers in Cell and Developmental Biology, 2021, 9, 662227.	3.7	10
108	COMPUTER SIMULATIONS OF MEMBRANE-LYTIC PEPTIDES: PERSPECTIVES IN DRUG DESIGN. Journal of Bioinformatics and Computational Biology, 2007, 05, 611-626.	0.8	9

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109	A Fragment-Based Scoring Function to Re-rank ATP Docking Results. International Journal of Molecular Sciences, 2007, 8, 1083-1094.	4.1	9
110	A Single Missense Mutation in a Coiled-Coil Domain of Escherichia coli Ribosomal Protein S2 Confers a Thermosensitive Phenotype That Can Be Suppressed by Ribosomal Protein S1. Journal of Bacteriology, 2013, 195, 95-104.	2.2	9
111	libxtc: an efficient library for reading XTC-compressed MD trajectory data. BMC Research Notes, 2021, 14, 124.	1.4	9
112	Molecular Dynamics Insight into the Lipid II Recognition by Type A Lantibiotics: Nisin, Epidermin, and Gallidermin. Micromachines, 2021, 12, 1169.	2.9	9
113	Anionic Lipids: Determinants of Binding Cytotoxins from Snake Venom on the Surface of Cell Membranes. Acta Naturae, 2010, 2, 88-95.	1.7	9
114	Application of three-dimensional molecular hydrophobicity potential to the analysis of spatial organization of membrane domains in proteins. III. Modeling of intramembrane moiety of Na+, K+-ATPase. The Protein Journal, 1993, 12, 143-152.	1.1	8
115	Correlation of Local Changes in the Temperature-Dependent Conformational Flexibility of Thioredoxins with Their Thermostability. Russian Journal of Bioorganic Chemistry, 2004, 30, 421-430.	1.0	8
116	Analysis of hydrophobic interactions of antagonists with the beta2-adrenergic receptor. SAR and QSAR in Environmental Research, 2010, 21, 37-55.	2.2	8
117	C-Terminal residues in small potassium channel blockers OdK1 and OSK3 from scorpion venom fine-tune the selectivity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2017, 1865, 465-472.	2.3	8
118	Structural and Dynamic â€œPortraitsâ€•of Recombinant and Native Cytotoxin I from Naja oxiana: How Close Are They?. Biochemistry, 2017, 56, 4468-4477.	2.5	8
119	Why human anti-GalÎ±1â€“4GalÎ²1â€“4Glc natural antibodies do not recognize the trisaccharide on erythrocyte membrane? Molecular dynamics and immunochemical investigation. Molecular Immunology, 2017, 90, 87-97.	2.2	8
120	The role of hydrophobic /hydrophilic balance in the activity of structurally flexible vs. rigid cytolytic polypeptides and analogs developed on their basis. Expert Review of Proteomics, 2018, 15, 873-886.	3.0	8
121	Dielectric-Dependent Strength of Interlipid Hydrogen Bonding in Biomembranes: Model Case Study. Journal of Chemical Information and Modeling, 2019, 59, 2765-2775.	5.4	8
122	Atomistic mechanism of the constitutive activation of PDGFRA via its transmembrane domain. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 82-95.	2.4	8
123	Tuning Scorpion Toxin Selectivity: Switching From KV1.1 to KV1.3. Frontiers in Pharmacology, 2020, 11, 1010.	3.5	8
124	Small Amphiphilic Peptides: Activity Against a Broad Range of Drug-Resistant Bacteria and Structural Insight into Membranolytic Properties. Journal of Medicinal Chemistry, 2022, 65, 665-687.	6.4	8
125	Architecture of the Sodium Pump Molecule.. Annals of the New York Academy of Sciences, 1992, 671, 134-146.	3.8	7
126	Recognition of transmembrane Î±-helical segments with environmental profiles. Protein Engineering, Design and Selection, 1996, 9, 253-263.	2.1	7

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127	Molecular Modeling of HIV-1 Coreceptor CCR5 and Exploring of Conformational Space of its Extracellular Domain in Molecular Dynamics Simulation. Journal of Biomolecular Structure and Dynamics, 1998, 16, 77-90.	3.5	7
128	Monte Carlo simulations of voltage-driven translocation of a signal sequence. FEBS Letters, 2002, 526, 97-100.	2.8	7
129	Method To Assess Packing Quality of Transmembrane Î±-Helices in Proteins. 1. Parametrization Using Structural Data. Journal of Chemical Information and Modeling, 2007, 47, 1150-1162.	5.4	7
130	Method To Assess Packing Quality of Transmembrane Î±-Helices in Proteins. 2. Validation by â€œCorrect vs Misleadingâ€•Test. Journal of Chemical Information and Modeling, 2007, 47, 1163-1170.	5.4	7
131	Interaction of linear cationic peptides with phospholipid membranes and polymers of sialic acid. Biochemistry (Moscow), 2014, 79, 459-468.	1.5	7
132	Improving therapeutic potential of antibacterial spider venom peptides: coarse-grain molecular dynamics guided approach. Future Medicinal Chemistry, 2018, 10, 2309-2322.	2.3	7
133	Role of the Lipid Environment in the Dimerization of Transmembrane Domains of Glycophorin A. Acta Naturae, 2015, 7, 122-127.	1.7	7
134	All-d-Enantiomeric Peptide D3 Designed for Alzheimerâ€™s Disease Treatment Dynamically Interacts with Membrane-Bound Amyloid-Î² Precursors. Journal of Medicinal Chemistry, 2021, 64, 16464-16479.	6.4	7
135	Detailed Assessment of Spatial Hydrophobic and Electrostatic Properties of 2D NMR-Derived Models of Neurotoxin II. Journal of Biomolecular Structure and Dynamics, 1995, 12, 971-991.	3.5	6
136	Cobra cytotoxins: determinants of antibacterial activity. Mendeleev Communications, 2015, 25, 70-71.	1.6	6
137	Dimeric states of transmembrane domains of insulin and IGF-1R receptors: Structures and possible role in activation. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183417.	2.6	6
138	Tuning of Molecular Electrostatic Potential Enables Efficient Charge Transport in Crystalline Azaacenes: A Computational Study. International Journal of Molecular Sciences, 2020, 21, 5654.	4.1	6
139	Stepwise Insertion of Cobra Cardiotoxin CT2 into a Lipid Bilayer Occurs as an Interplay of Protein and Membrane â€œDynamic Molecular Portraitsâ€• Journal of Chemical Information and Modeling, 2021, 61, 385-399.	5.4	6
140	The role of stacking interactions in complexes of proteins with adenine and Guanine fragments of ligands. Acta Naturae, 2009, 1, 124-7.	1.7	6
141	Variability in the Spatial Structure of the Central Loop in Cobra Cytotoxins Revealed by X-ray Analysis and Molecular Modeling. Toxins, 2022, 14, 149.	3.4	6
142	Molecular Dynamics of DHHC20 Acyltransferase Suggests Principles of Lipid and Protein Substrate Selectivity. International Journal of Molecular Sciences, 2022, 23, 5091.	4.1	6
143	A New Method to Characterize Hydrophobic Organization of Proteins: Application to Rational Protein Engineering of Barnase. Journal of Biomolecular Structure and Dynamics, 1998, 15, 673-687.	3.5	5
144	Human chemokine receptors CCR5, CCR3 and CCR2B share common polarity motif in the first extracellular loop with other human G-protein coupled receptors. Implications for HIV-1 coreceptor function. FEBS Journal, 1999, 263, 746-756.	0.2	5

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145	Modeling of peptides and proteins in a membrane environment: I. A solvation model mimicking a lipid bilayer. Russian Journal of Bioorganic Chemistry, 2000, 26, 115-124.	1.0	5
146	Structure of Supramers Formed by the Amphiphile Biotinâ€CMGâ€DOPE. ChemistryOpen, 2020, 9, 641-648.	1.9	5
147	Impact of external amino acids on fluorescent protein chromophore biosynthesis revealed by molecular dynamics and mutagenesis studies. Journal of Photochemistry and Photobiology B: Biology, 2020, 206, 111853.	3.8	5
148	Dynamic â€œMolecular Portraitsâ€•of Biomembranes Drawn by Their Lateral Nanoscale Inhomogeneities. International Journal of Molecular Sciences, 2021, 22, 6250.	4.1	5
149	Anionic lipids: determinants of binding cytotoxins from snake venom on the surface of cell membranes. Acta Naturae, 2010, 2, 88-96.	1.7	5
150	A new "hydrophobic template" method detects segments forming transmembrane Î±-helical bundles in ion channels. Theoretical Chemistry Accounts, 1999, 101, 73-76.	1.4	4
151	Peptides in membranes: assessment of environmental effects via simulations using an implicit solvation model. Theoretical Chemistry Accounts, 1999, 101, 170-174.	1.4	4
152	Assessment of conformation and energetics of the N-terminal part of elafin via computer simulations. Theoretical Chemistry Accounts, 2001, 106, 55-61.	1.4	4
153	Confined Dynamics of Water in Transmembrane Pore of TRPV1 Ion Channel. International Journal of Molecular Sciences, 2019, 20, 4285.	4.1	4
154	Antibacterial activity of cardiotoxin-like basic polypeptide from cobra venom. Bioorganic and Medicinal Chemistry Letters, 2020, 30, 126890.	2.2	4
155	Artificial Peptide Ligand of Potassium Channel KV1.1 with High Selectivity. Journal of Evolutionary Biochemistry and Physiology, 2021, 57, 386-403.	0.6	4
156	Dissecting structural basis of the unique substrate selectivity of human enteropeptidase catalytic subunit. Journal of Biomolecular Structure and Dynamics, 2012, 30, 62-73.	3.5	3
157	End-group differentiating ozonolysis of furocoumarins. RSC Advances, 2014, 4, 61277-61280.	3.6	3
158	Rational design of new ligands for nicotinic receptors on the basis of Î±-conotoxin PnIA. Doklady Biochemistry and Biophysics, 2015, 461, 106-109.	0.9	3
159	Specific refolding pathway of viscumin A chain in membrane-like medium reveals a possible mechanism of toxin entry into cell. Scientific Reports, 2019, 9, 413.	3.3	3
160	Potassium channel blocker crafted by Î±-hairpinin scaffold engineering. Biophysical Journal, 2021, 120, 2471-2481.	0.5	3
161	Probing temperature and capsaicin-induced activation of TRPV1 channel via computationally guided point mutations in its pore and TRP domains. International Journal of Biological Macromolecules, 2020, 158, 1175-1183.	7.5	3
162	Global and Local Secondary Structures of Globular Proteins: Linking Spectroscopies and Predictions. , 1995, , 89-90.		3

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