Pavel E Volynsky

List of Publications by Year
in descending order

68	1,826	279701 23	276775 41
papers	citations	h-index	g-index

70	70	70	1827
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.	1.6	189
2	Unique Dimeric Structure of BNip3 Transmembrane Domain Suggests Membrane Permeabilization as a Cell Death Trigger. Journal of Biological Chemistry, 2007, 282, 16256-16266.	1.6	121
3	Pore formation in lipid membrane I: Continuous reversible trajectory from intact bilayer through hydrophobic defect to transversal pore. Scientific Reports, 2017, 7, 12152.	1.6	102
4	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.	1.6	100
5	Left-Handed Dimer of EphA2 Transmembrane Domain: Helix Packing Diversity among Receptor Tyrosine Kinases. Biophysical Journal, 2010, 98, 881-889.	0.2	100
6	PREDDIMER: a web server for prediction of transmembrane helical dimers. Bioinformatics, 2014, 30, 889-890.	1.8	77
7	Pore formation in lipid membrane II: Energy landscape under external stress. Scientific Reports, 2017, 7, 12509.	1.6	73
8	Antimicrobial Peptides Induce Growth of Phosphatidylglycerol Domains in a Model Bacterial Membrane. Journal of Physical Chemistry Letters, 2010, 1, 3108-3111.	2.1	65
9	Multistate Organization of Transmembrane Helical Protein Dimers Governed by the Host Membrane. Journal of the American Chemical Society, 2012, 134, 14390-14400.	6.6	63
10	Pyrenemethyl ara-Uridine-2â€²-carbamate: A Strong Interstrand Excimer in the Major Groove of a DNA Duplex. ChemBioChem, 2003, 4, 841-847.	1.3	61
11	HER2 Transmembrane Domain Dimerization Coupled with Self-Association of Membrane-Embedded Cytoplasmic Juxtamembrane Regions. Journal of Molecular Biology, 2016, 428, 52-61.	2.0	55
12	Temperature-sensitive gating of TRPV1 channel as probed by atomistic simulations of its trans- and juxtamembrane domains. Scientific Reports, 2016, 6, 33112.	1.6	49
13	Interaction of Cardiotoxins with Membranes: A Molecular Modeling Study. Biophysical Journal, 2002, 83, 144-153.	0.2	46
14	Liquid but Durable: Molecular Dynamics Simulations Explain the Unique Properties of Archaeal-Like Membranes. Scientific Reports, 2014, 4, 7462.	1.6	42
15	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.	1.3	40
16	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.	1.2	40
17	The Conformation of the Epidermal Growth Factor Receptor Transmembrane Domain Dimer Dynamically Adapts to the Local Membrane Environment. Biochemistry, 2017, 56, 1697-1705.	1.2	39
18	Three-Dimensional Structure/Hydrophobicity of Latarcins Specifies Their Mode of Membrane Activity[,]. Biochemistry, 2008, 47, 3525-3533.	1.2	38

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19	Spatial Structure and Activity Mechanism of a Novel Spider Antimicrobial Peptide,. Biochemistry, 2006, 45, 10759-10767.	1.2	37
20	Adaptation of a Membrane-active Peptide to Heterogeneous Environment. I. Structural Plasticity of the Peptide. Journal of Physical Chemistry B, 2009, 113, 1107-1119.	1.2	36
21	Nâ€terminal amphipathic helix as a trigger of hemolytic activity in antimicrobial peptides: A case study in latarcins. FEBS Letters, 2009, 583, 2425-2428.	1.3	34
22	Structure elucidation of dimeric transmembrane domains of bitopic proteins. Cell Adhesion and Migration, 2010, 4, 284-298.	1.1	34
23	Effect of Lipid Composition on the â€œMembrane Responseâ€•Induced by a Fusion Peptideâ€. Biochemistry, 2005, 44, 14626-14637.	1.2	31
24	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.	1.1	28
25	Association of transmembrane helices: what determines assembling of a dimer?. Journal of Computer-Aided Molecular Design, 2006, 20, 27-45.	1.3	23
26	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.	1.2	23
27	Spatial structure of TLR4 transmembrane domain in bicelles provides the insight into the receptor activation mechanism. Scientific Reports, 2017, 7, 6864.	1.6	23
28	Adaptable Lipid Matrix Promotes Proteinâ€“Protein Association in Membranes. Journal of Chemical Theory and Computation, 2015, 11, 4415-4426.	2.3	21
29	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.	6.6	20
30	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.	0.5	18
31	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.	1.5	15
32	Helix Interactions in Membranes:Â Lessons from Unrestrained Monte Carlo Simulations. Journal of Chemical Theory and Computation, 2005, 1, 1252-1264.	2.3	13
33	Impact of membrane partitioning on the spatial structure of an S-type cobra cytotoxin. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3463-3478.	2.0	13
34	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.	1.6	13
35	Structural, dynamic, and functional aspects of helix association in membranes. Advances in Protein Chemistry and Structural Biology, 2011, 83, 129-161.	1.0	12
36	Computer simulations and modeling-assisted ToxR screening in deciphering 3D structures of transmembrane Î±-helical dimers: ephrin receptor A1. Physical Biology, 2010, 7, 016014.	0.8	11

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37	Development of the force field parameters for phosphoimidazole and phosphohistidine. Journal of Computational Chemistry, 2004, 25, 1313-1321.	1.5	10
38	Effects of Sterols on the Interaction of SDS, Benzalkonium Chloride, and A Novel Compound, Kor105, with Membranes. Biomolecules, 2019, 9, 627.	1.8	10
39	Phospholipase A2 way to hydrolysis: Dint formation, hydrophobic mismatch, and lipid exclusion. Biochimica Et Biophysica Acta - Biomembranes, 2021, 1863, 183481.	1.4	10
40	COMPUTER SIMULATIONS OF MEMBRANE-LYTIC PEPTIDES: PERSPECTIVES IN DRUG DESIGN. Journal of Bioinformatics and Computational Biology, 2007, 05, 611-626.	0.3	9
41	Secretory phospholipase A2 activity in blood serum: The challenge to sense. Biochemical and Biophysical Research Communications, 2014, 454, 178-182.	1.0	9
42	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.	1.0	8
43	Monte Carlo simulations of voltage-driven translocation of a signal sequence. FEBS Letters, 2002, 526, 97-100.	1.3	7
44	Improving therapeutic potential of antibacterial spider venom peptides: coarse-grain molecular dynamics guided approach. Future Medicinal Chemistry, 2018, 10, 2309-2322.	1.1	7
45	BILMIX: a new approach to restore the size polydispersity and electron density profiles of lipid bilayers from liposomes using small-angle X-ray scattering data. Journal of Applied Crystallography, 2020, 53, 236-243.	1.9	7
46	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.	2.9	7
47	Structure of Supramers Formed by the Amphiphile Biotinâ€CMGâ€DOPE. ChemistryOpen, 2020, 9, 641-648.	0.9	5
48	Recognizing misfolded and distorted protein structures by the assumption-based similarity score. Protein Engineering, Design and Selection, 1999, 12, 31-40.	1.0	4
49	Assessment of conformation and energetics of the N-terminal part of elafin via computer simulations. Theoretical Chemistry Accounts, 2001, 106, 55-61.	0.5	4
50	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.	1.6	3
51	Cyclopentane rings in hydrophobic chains of a phospholipid enhance the bilayer stability to electric breakdown. Soft Matter, 2020, 16, 3216-3223.	1.2	3
52	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.	3.6	3
53	Modeling of Peptides in Implicit Membrane-Mimetic Media. Molecular Simulation, 2000, 24, 275-291.	0.9	2
54	The Membrane-proximal Fusion Domain of HIV-1 GP41 Reveals Sequence-specific and Fine-tuning Mechanism of Membrane Binding. Journal of Biomolecular Structure and Dynamics, 2007, 25, 195-205.	2.0	2

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55	Structural Aspects of Transmembrane Domain Interactions of Receptor Tyrosine Kinases. Biophysical Journal, 2011, 100, 207a.	0.2	1
56	Structure-Functional Insight into Transmembrane Helix Dimerization byÂProtein Engineering, Molecular Modeling and Heteronuclear NMR Spectroscopy. Biophysical Journal, 2012, 102, 470a.	0.2	1
57	The role of chain rigidity in lipid self-association: Comparative study of dihexanoyl- and disorbyl-phosphatidylcholines. Chemistry and Physics of Lipids, 2012, 165, 382-386.	1.5	1
58	Dynamic Structural/Amphiphilic â€œPortraitâ€•of Biomembranes as their Fundamental Property Relevant to Function: Results of Atomistic Simulations. Biophysical Journal, 2015, 108, 78a.	0.2	1
59	Protein-Membrane Interactions: Lessons from In Silico Studies. , 2007, , 19-39.		1
60	The Membrane-Water Partition Coefficients of Antifungal, but Not Antibacterial, Membrane-Active Compounds Are Similar. Frontiers in Microbiology, 2021, 12, 756408.	1.5	1
61	Differences in Medium-Induced Conformational Plasticity Presumably Underlie Different Cytotoxic Activity of Ricin and Viscumin. Biomolecules, 2022, 12, 295.	1.8	1
62	Recognition Specificity of Proteins and Biomembranes: A Computational View. Biophysical Journal, 2012, 102, 434a.	0.2	0
63	Influence of Ether Bonds and Branched Lipid Tails on Stability of Membranes to Pore Formation. Biophysical Journal, 2015, 108, 238a-239a.	0.2	0
64	Temperature-Sensitive Gating of TRPV1 Channel as Probed by Atomistic Simulations. Biophysical Journal, 2017, 112, 506a.	0.2	0
65	Energy Landscape of Pore Formation in Bilayer Lipid Membrane. Biophysical Journal, 2017, 112, 468a.	0.2	0
66	Behavior of Doxorubicin Lipophilic Conjugates in Liposomal Lipid Bilayers. Russian Journal of Bioorganic Chemistry, 2018, 44, 732-739.	0.3	0
67	Dynamic â€œMolecular Portraitsâ€•of Proteins and Cell Membranes: A Computational View. Biophysical Journal, 2019, 116, 205a.	0.2	0
68	Computer Simulations of Anionic Unsaturated Lipid Bilayerâ€”A Suitable Model to Study Membrane Interactions with A Cell-Penetrating Peptide. , 2006, , 235-246.		0