Pavel E Volynsky

List of Publications by Citations

57	1,528	24	38
papers	citations	h-index	g-index
70	1,761	3.9	4.27
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
57	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, 6950-6	5.4	164
56	Unique dimeric structure of BNip3 transmembrane domain suggests membrane permeabilization as a cell death trigger. *Journal of Biological Chemistry*, **2007**, 282, 16256-66	5.4	106
55	Left-handed dimer of EphA2 transmembrane domain: Helix packing diversity among receptor tyrosine kinases. *Biophysical Journal*, **2010**, 98, 881-9	2.9	87
54	Spatial structure and pH-dependent conformational diversity of dimeric transmembrane domain of the receptor tyrosine kinase EphA1. *Journal of Biological Chemistry*, **2008**, 283, 29385-95	5.4	86
53	Pore formation in lipid membrane I: Continuous reversible trajectory from intact bilayer through hydrophobic defect to transversal pore. *Scientific Reports*, **2017**, 7, 12152	4.9	67
52	Antimicrobial Peptides Induce Growth of Phosphatidylglycerol Domains in a Model Bacterial Membrane. *Journal of Physical Chemistry Letters*, **2010**, 1, 3108-3111	6.4	56
51	Pore formation in lipid membrane II: Energy landscape under external stress. *Scientific Reports*, **2017**, 7, 12509	4.9	55
50	Pyrenemethyl ara-uridine-2U-carbamate: a strong interstrand excimer in the major groove of a DNA duplex. *ChemBioChem*, **2003**, 4, 841-7	3.8	54
49	PREDDIMER: a web server for prediction of transmembrane helical dimers. *Bioinformatics*, **2014**, 30, 889-90	7.2	49
48	Multistate organization of transmembrane helical protein dimers governed by the host membrane. *Journal of the American Chemical Society*, **2012**, 134, 14390-400	16.4	45
47	Interaction of cardiotoxins with membranes: a molecular modeling study. *Biophysical Journal*, **2002**, 83, 144-53	2.9	43
46	HER2 Transmembrane Domain Dimerization Coupled with Self-Association of Membrane-Embedded Cytoplasmic Juxtamembrane Regions. *Journal of Molecular Biology*, **2016**, 428, 52-61	6.5	39
45	Role of lipid charge in organization of water/lipid bilayer interface: insights via computer simulations. *Journal of Physical Chemistry B*, **2005**, 109, 15052-9	3.4	37
44	Factors important for fusogenic activity of peptides: molecular modeling study of analogs of fusion peptide of influenza virus hemagglutinin. *FEBS Letters*, **1999**, 462, 205-10	3.8	37
43	Temperature-sensitive gating of TRPV1 channel as probed by atomistic simulations of its trans- and juxtamembrane domains. *Scientific Reports*, **2016**, 6, 33112	4.9	35
42	Spatial structure and activity mechanism of a novel spider antimicrobial peptide. *Biochemistry*, **2006**, 45, 10759-67	3.2	34
41	Adaptation of a membrane-active peptide to heterogeneous environment. I. Structural plasticity of the peptide. *Journal of Physical Chemistry B*, **2009**, 113, 1107-19	3.4	30

40	Three-dimensional structure/hydrophobicity of latarcins specifies their mode of membrane activity. *Biochemistry*, **2008**, 47, 3525-33	3.2	30
39	Structure elucidation of dimeric transmembrane domains of bitopic proteins. *Cell Adhesion and Migration*, **2010**, 4, 284-98	3.2	29
38	Liquid but durable: molecular dynamics simulations explain the unique properties of archaeal-like membranes. *Scientific Reports*, **2014**, 4, 7462	4.9	28
37	N-terminal amphipathic helix as a trigger of hemolytic activity in antimicrobial peptides: a case study in latarcins. *FEBS Letters*, **2009**, 583, 2425-8	3.8	27
36	Effect of lipid composition on the "membrane response" induced by a fusion peptide. *Biochemistry*, **2005**, 44, 14626-37	3.2	27
35	The Conformation of the Epidermal Growth Factor Receptor Transmembrane Domain Dimer Dynamically Adapts to the Local Membrane Environment. *Biochemistry*, **2017**, 56, 1697-1705	3.2	26
34	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, 1120-6	3.4	21
33	Role of dimerization efficiency of transmembrane domains in activation of fibroblast growth factor receptor 3. *Journal of the American Chemical Society*, **2013**, 135, 8105-8	16.4	19
32	Association of transmembrane helices: what determines assembling of a dimer?. *Journal of Computer-Aided Molecular Design*, **2006**, 20, 27-45	4.2	19
31	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	4	17
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	1.9	17
29	Adaptable Lipid Matrix Promotes Protein-Protein Association in Membranes. *Journal of Chemical Theory and Computation*, **2015**, 11, 4415-26	6.4	16
28	Spatial structure of TLR4 transmembrane domain in bicelles provides the insight into the receptor activation mechanism. *Scientific Reports*, **2017**, 7, 6864	4.9	14
27	Specificity of helix packing in transmembrane dimer of the cell death factor BNIP3: a molecular modeling study. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 309-25	4.2	13
26	Helix Interactions in Membranes: Lessons from Unrestrained Monte Carlo Simulations. *Journal of Chemical Theory and Computation*, **2005**, 1, 1252-64	6.4	11
25	Computer simulations and modeling-assisted ToxR screening in deciphering 3D structures of transmembrane alpha-helical dimers: ephrin receptor A1. *Physical Biology*, **2010**, 7, 16014	3	10
24	Structural, dynamic, and functional aspects of helix association in membranes: a computational view. *Advances in Protein Chemistry and Structural Biology*, **2011**, 83, 129-61	5.3	10
23	Development of the force field parameters for phosphoimidazole and phosphohistidine. *Journal of Computational Chemistry*, **2004**, 25, 1313-21	3.5	9

22	Familial L723P Mutation Can Shift the Distribution between the Alternative APP Transmembrane Domain Cleavage Cascades by Local Unfolding of the ε-Cleavage Site Suggesting a Straightforward Mechanism of Alzheimer's Disease Pathogenesis. *ACS Chemical Biology*, **2019**, 14, 1573-1582	4.9	8
21	Impact of membrane partitioning on the spatial structure of an S-type cobra cytotoxin. *Journal of Biomolecular Structure and Dynamics*, **2018**, 36, 3463-3478	3.6	8
20	Computer simulations of membrane-lytic peptides: perspectives in drug design. *Journal of Bioinformatics and Computational Biology*, **2007**, 5, 611-26	1	8
19	Secretory phospholipase A2 activity in blood serum: the challenge to sense. *Biochemical and Biophysical Research Communications*, **2014**, 454, 178-82	3.4	7
18	Monte Carlo simulations of voltage-driven translocation of a signal sequence. *FEBS Letters*, **2002**, 526, 97-100	3.8	7
17	Why human anti-Galα1-4Galβ1-4Glc natural antibodies do not recognize the trisaccharide on erythrocyte membrane? Molecular dynamics and immunochemical investigation. *Molecular Immunology*, **2017**, 90, 87-97	4.3	6
16	Assessment of conformation and energetics of the N-terminal part of elafin via computer simulations. *Theoretical Chemistry Accounts*, **2001**, 106, 55-61	1.9	4
15	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	3.8	4
14	Improving therapeutic potential of antibacterial spider venom peptides: coarse-grain molecular dynamics guided approach. *Future Medicinal Chemistry*, **2018**, 10, 2309-2322	4.1	4
13	Effects of Sterols on the Interaction of SDS, Benzalkonium Chloride, and A Novel Compound, Kor105, with Membranes. *Biomolecules*, **2019**, 9,	5.9	3
12	Recognizing misfolded and distorted protein structures by the assumption-based similarity score. *Protein Engineering, Design and Selection*, **1999**, 12, 31-40	1.9	3
11	Phospholipase A2 way to hydrolysis: Dint formation, hydrophobic mismatch, and lipid exclusion. *Biochimica Et Biophysica Acta - Biomembranes*, **2021**, 1863, 183481	3.8	3
10	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	4.9	2
9	Structure of Supramers Formed by the Amphiphile Biotin-CMG-DOPE. *ChemistryOpen*, **2020**, 9, 641-648	2.3	2
8	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	3.6	2
7	Modeling of Peptides in Implicit Membrane-Mimetic Media. *Molecular Simulation*, **2000**, 24, 275-291	2	2
6	The role of chain rigidity in lipid self-association: comparative study of dihexanoyl- and disorbyl-phosphatidylcholines. *Chemistry and Physics of Lipids*, **2012**, 165, 382-6	3.7	1
5	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, 1175-1175	7.9	1

4	Cyclopentane rings in hydrophobic chains of a phospholipid enhance the bilayer stability to electric breakdown. *Soft Matter*, **2020**, 16, 3216-3223	3.6	0
3	AlldEnantiomeric Peptide D3 Designed for Alzheimer's Disease Treatment Dynamically Interacts with Membrane-Bound Amyloid- Precursors. *Journal of Medicinal Chemistry*, **2021**, 64, 16464-16479	8.3	0
2	The Membrane-Water Partition Coefficients of Antifungal, but Not Antibacterial, Membrane-Active Compounds Are Similar. *Frontiers in Microbiology*, **2021**, 12, 756408	5.7	
1	Behavior of Doxorubicin Lipophilic Conjugates in Liposomal Lipid Bilayers. *Russian Journal of Bioorganic Chemistry*, **2018**, 44, 732-739	1	