

Pavel E Volynsky

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

57
papers

1,528
citations

24
h-index

38
g-index

70
ext. papers

1,761
ext. citations

3.9
avg, IF

4.27
L-index

#	Paper	IF	Citations
57	All-Enantiomeric Peptide D3 Designed for Alzheimer's Disease Treatment Dynamically Interacts with Membrane-Bound Amyloid- β -Precursors. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 16464-16479	8.3	0
56	The Membrane-Water Partition Coefficients of Antifungal, but Not Antibacterial, Membrane-Active Compounds Are Similar. <i>Frontiers in Microbiology</i> , 2021 , 12, 756408	5.7	
55	Phospholipase A2 way to hydrolysis: Dint formation, hydrophobic mismatch, and lipid exclusion. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2021 , 1863, 183481	3.8	3
54	Structure of Supramers Formed by the Amphiphile Biotin-CMG-DOPE. <i>ChemistryOpen</i> , 2020 , 9, 641-648	2.3	2
53	Cyclopentane rings in hydrophobic chains of a phospholipid enhance the bilayer stability to electric breakdown. <i>Soft Matter</i> , 2020 , 16, 3216-3223	3.6	0
52	Probing temperature and capsaicin-induced activation of TRPV1 channel via computationally guided point mutations in its pore and TRP domains. <i>International Journal of Biological Macromolecules</i> , 2020 , 158, 1175-1175	7.9	1
51	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. <i>Journal of Applied Crystallography</i> , 2020 , 53, 236-243	3.8	4
50	Specific refolding pathway of viscumin A chain in membrane-like medium reveals a possible mechanism of toxin entry into cell. <i>Scientific Reports</i> , 2019 , 9, 413	4.9	2
49	Familial L723P Mutation Can Shift the Distribution between the Alternative APP Transmembrane Domain Cleavage Cascades by Local Unfolding of the β -Cleavage Site Suggesting a Straightforward Mechanism of Alzheimer's Disease Pathogenesis. <i>ACS Chemical Biology</i> , 2019 , 14, 1573-1582	4.9	8
48	Effects of Sterols on the Interaction of SDS, Benzalkonium Chloride, and A Novel Compound, Kor105, with Membranes. <i>Biomolecules</i> , 2019 , 9,	5.9	3
47	Structural basis of the signal transduction via transmembrane domain of the human growth hormone receptor. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018 , 1862, 1410-1420	4	17
46	Impact of membrane partitioning on the spatial structure of an S-type cobra cytotoxin. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 3463-3478	3.6	8
45	Behavior of Doxorubicin Lipophilic Conjugates in Liposomal Lipid Bilayers. <i>Russian Journal of Bioorganic Chemistry</i> , 2018 , 44, 732-739	1	
44	Improving therapeutic potential of antibacterial spider venom peptides: coarse-grain molecular dynamics guided approach. <i>Future Medicinal Chemistry</i> , 2018 , 10, 2309-2322	4.1	4
43	The Conformation of the Epidermal Growth Factor Receptor Transmembrane Domain Dimer Dynamically Adapts to the Local Membrane Environment. <i>Biochemistry</i> , 2017 , 56, 1697-1705	3.2	26
42	Pore formation in lipid membrane II: Energy landscape under external stress. <i>Scientific Reports</i> , 2017 , 7, 12509	4.9	55
41	Pore formation in lipid membrane I: Continuous reversible trajectory from intact bilayer through hydrophobic defect to transversal pore. <i>Scientific Reports</i> , 2017 , 7, 12152	4.9	67

40	Spatial structure of TLR4 transmembrane domain in bicelles provides the insight into the receptor activation mechanism. <i>Scientific Reports</i> , 2017 , 7, 6864	4.9	14
39	Why human anti-Gal α -4Gal α -4Glc natural antibodies do not recognize the trisaccharide on erythrocyte membrane? Molecular dynamics and immunochemical investigation. <i>Molecular Immunology</i> , 2017 , 90, 87-97	4.3	6
38	Temperature-sensitive gating of TRPV1 channel as probed by atomistic simulations of its trans- and juxtamembrane domains. <i>Scientific Reports</i> , 2016 , 6, 33112	4.9	35
37	HER2 Transmembrane Domain Dimerization Coupled with Self-Association of Membrane-Embedded Cytoplasmic Juxtamembrane Regions. <i>Journal of Molecular Biology</i> , 2016 , 428, 52-61	6.5	39
36	Adaptable Lipid Matrix Promotes Protein-Protein Association in Membranes. <i>Journal of Chemical Theory and Computation</i> , 2015 , 11, 4415-26	6.4	16
35	Liquid but durable: molecular dynamics simulations explain the unique properties of archaeal-like membranes. <i>Scientific Reports</i> , 2014 , 4, 7462	4.9	28
34	PREDDIMER: a web server for prediction of transmembrane helical dimers. <i>Bioinformatics</i> , 2014 , 30, 889-90	4.9	49
33	Secretory phospholipase A2 activity in blood serum: the challenge to sense. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 454, 178-82	3.4	7
32	Role of dimerization efficiency of transmembrane domains in activation of fibroblast growth factor receptor 3. <i>Journal of the American Chemical Society</i> , 2013 , 135, 8105-8	16.4	19
31	Multistate organization of transmembrane helical protein dimers governed by the host membrane. <i>Journal of the American Chemical Society</i> , 2012 , 134, 14390-400	16.4	45
30	The role of chain rigidity in lipid self-association: comparative study of dihexanoyl- and disorbyl-phosphatidylcholines. <i>Chemistry and Physics of Lipids</i> , 2012 , 165, 382-6	3.7	1
29	Structural, dynamic, and functional aspects of helix association in membranes: a computational view. <i>Advances in Protein Chemistry and Structural Biology</i> , 2011 , 83, 129-61	5.3	10
28	Structure elucidation of dimeric transmembrane domains of bitopic proteins. <i>Cell Adhesion and Migration</i> , 2010 , 4, 284-98	3.2	29
27	Left-handed dimer of EphA2 transmembrane domain: Helix packing diversity among receptor tyrosine kinases. <i>Biophysical Journal</i> , 2010 , 98, 881-9	2.9	87
26	Antimicrobial Peptides Induce Growth of Phosphatidylglycerol Domains in a Model Bacterial Membrane. <i>Journal of Physical Chemistry Letters</i> , 2010 , 1, 3108-3111	6.4	56
25	Computer simulations and modeling-assisted ToxR screening in deciphering 3D structures of transmembrane alpha-helical dimers: ephrin receptor A1. <i>Physical Biology</i> , 2010 , 7, 16014	3	10
24	N-terminal amphipathic helix as a trigger of hemolytic activity in antimicrobial peptides: a case study in laticins. <i>FEBS Letters</i> , 2009 , 583, 2425-8	3.8	27
23	Adaptation of a membrane-active peptide to heterogeneous environment. II. The role of mosaic nature of the membrane surface. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 1120-6	3.4	21

22	Adaptation of a membrane-active peptide to heterogeneous environment. I. Structural plasticity of the peptide. <i>Journal of Physical Chemistry B</i> , 2009 , 113, 1107-19	3.4	30
21	Spatial structure of the dimeric transmembrane domain of the growth factor receptor ErbB2 presumably corresponding to the receptor active state. <i>Journal of Biological Chemistry</i> , 2008 , 283, 6950-6	5.4	164
20	Three-dimensional structure/hydrophobicity of laticins specifies their mode of membrane activity. <i>Biochemistry</i> , 2008 , 47, 3525-33	3.2	30
19	Spatial structure and pH-dependent conformational diversity of dimeric transmembrane domain of the receptor tyrosine kinase EphA1. <i>Journal of Biological Chemistry</i> , 2008 , 283, 29385-95	5.4	86
18	Specificity of helix packing in transmembrane dimer of the cell death factor BNIP3: a molecular modeling study. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 309-25	4.2	13
17	Computer simulations of membrane-lytic peptides: perspectives in drug design. <i>Journal of Bioinformatics and Computational Biology</i> , 2007 , 5, 611-26	1	8
16	Unique dimeric structure of BNip3 transmembrane domain suggests membrane permeabilization as a cell death trigger. <i>Journal of Biological Chemistry</i> , 2007 , 282, 16256-66	5.4	106
15	The membrane-proximal fusion domain of HIV-1 GP41 reveals sequence-specific and fine-tuning mechanism of membrane binding. <i>Journal of Biomolecular Structure and Dynamics</i> , 2007 , 25, 195-205	3.6	2
14	Spatial structure and activity mechanism of a novel spider antimicrobial peptide. <i>Biochemistry</i> , 2006 , 45, 10759-67	3.2	34
13	Association of transmembrane helices: what determines assembling of a dimer?. <i>Journal of Computer-Aided Molecular Design</i> , 2006 , 20, 27-45	4.2	19
12	Effect of lipid composition on the "membrane response" induced by a fusion peptide. <i>Biochemistry</i> , 2005 , 44, 14626-37	3.2	27
11	Helix Interactions in Membranes: Lessons From Unrestrained Monte Carlo Simulations. <i>Journal of Chemical Theory and Computation</i> , 2005 , 1, 1252-64	6.4	11
10	Role of lipid charge in organization of water/lipid bilayer interface: insights via computer simulations. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 15052-9	3.4	37
9	Development of the force field parameters for phosphoimidazole and phosphohistidine. <i>Journal of Computational Chemistry</i> , 2004 , 25, 1313-21	3.5	9
8	Pyrenemethyl ara-uridine-2Ucarbamate: a strong interstrand excimer in the major groove of a DNA duplex. <i>ChemBioChem</i> , 2003 , 4, 841-7	3.8	54
7	Monte Carlo simulations of voltage-driven translocation of a signal sequence. <i>FEBS Letters</i> , 2002 , 526, 97-100	3.8	7
6	Interaction of cardiotoxins with membranes: a molecular modeling study. <i>Biophysical Journal</i> , 2002 , 83, 144-53	2.9	43
5	Implicit two-phase solvation model as a tool to assess conformation and energetics of proteins in membrane-mimetic media. <i>Theoretical Chemistry Accounts</i> , 2001 , 106, 48-54	1.9	17

4	Assessment of conformation and energetics of the N-terminal part of elafin via computer simulations. <i>Theoretical Chemistry Accounts</i> , 2001 , 106, 55-61	1.9	4
3	Modeling of Peptides in Implicit Membrane-Mimetic Media. <i>Molecular Simulation</i> , 2000 , 24, 275-291	2	2
2	Recognizing misfolded and distorted protein structures by the assumption-based similarity score. <i>Protein Engineering, Design and Selection</i> , 1999 , 12, 31-40	1.9	3
1	Factors important for fusogenic activity of peptides: molecular modeling study of analogs of fusion peptide of influenza virus hemagglutinin. <i>FEBS Letters</i> , 1999 , 462, 205-10	3.8	37