Isaiah T Arkin

List of Publications by Year
in descending order

74 papers	3,386 citations	182225 30 h-index	182931 54 g-index
76 all docs	76 docs citations	76 times ranked	3141 citing authors

#	Article	IF	Citations
1	Zika Mâ€"A Potential Viroporin: Mutational Study and Drug Repurposing. Biomedicines, 2022, 10, 641.	1.4	6
2	Targeting Viral Ion Channels: A Promising Strategy to Curb SARS-CoV-2. Pharmaceuticals, 2022, 15, 396.	1.7	4
3	MutagenPred-GCNNs: A Graph Convolutional Neural Network-Based Classification Model for Mutagenicity Prediction with Data-Driven Molecular Fingerprints. Interdisciplinary Sciences, Computational Life Sciences, 2021, 13, 25-33.	2.2	18
4	Blockers of the SARS-CoV-2 3a Channel Identified by Targeted Drug Repurposing. Viruses, 2021, 13, 532.	1.5	18
5	Identification of SARS-CoV-2 E Channel Blockers from a Repurposed Drug Library. Pharmaceuticals, 2021, 14, 604.	1.7	7
6	Isotope-Edited Amide II Mode: A New Label for Site-Specific Vibrational Spectroscopy. Journal of Physical Chemistry Letters, 2021, 12, 6634-6638.	2.1	4
7	Quantitative Analysis of Multiplex H-Bonds. Journal of the American Chemical Society, 2020, 142, 14150-14157.	6.6	24
8	The balance between sideâ€chain and backboneâ€driven association in folding of the Î±â€helical influenza A transmembrane peptide. Journal of Computational Chemistry, 2020, 41, 2177-2188.	1.5	3
9	SARS-CoV-2 E protein is a potential ion channel that can be inhibited by Gliclazide and Memantine. Biochemical and Biophysical Research Communications, 2020, 530, 10-14.	1.0	94
10	Potential Viroporin Candidates From Pathogenic Viruses Using Bacteria-Based Bioassays. Viruses, 2019, 11, 632.	1.5	14
11	Random Mutagenesis Analysis of the Influenza A M2 Proton Channel Reveals Novel Resistance Mutants. Biochemistry, 2018, 57, 5957-5968.	1.2	11
12	A Robust Proton Flux (pHlux) Assay for Studying the Function and Inhibition of the Influenza A M2 Proton Channel. Biochemistry, 2018, 57, 5949-5956.	1.2	15
13	Site-Specific Hydrogen Exchange in a Membrane Environment Analyzed by Infrared Spectroscopy. Journal of Physical Chemistry Letters, 2018, 9, 4059-4065.	2.1	9
14	Mapping the Resistance Potential of Influenza's H+ Channel against an Antiviral Blocker. Journal of Molecular Biology, 2016, 428, 4209-4217.	2.0	11
15	Mechanistic studies of the apical sodium-dependent bile acid transporter. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1107-1117.	1.5	11
16	Bacteria-Based Analysis of HIV-1 Vpu Channel Activity. PLoS ONE, 2014, 9, e105387.	1.1	14
17	Strength of a bifurcated H bond. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4085-4090.	3.3	110
18	Computational and experimental analysis of drug binding to the Influenza M2 channel. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 1068-1073.	1.4	23

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19	Use of Isotope-Edited FTIR to Derive a Backbone Structure of a Transmembrane Protein. Journal of Physical Chemistry Letters, 2014, 5, 2573-2579.	2.1	12
20	Gaining insight into membrane protein structure using isotope-edited FTIR. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2256-2264.	1.4	12
21	Preface. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 2255.	1.4	2
22	Environment Polarity in Proteins Mapped Noninvasively by FTIR Spectroscopy. Journal of Physical Chemistry Letters, 2012, 3, 939-944.	2.1	22
23	Computational Studies of Na+/H+ Antiporter: Structure, Dynamics and Function. , 2011, , 131-149.		0
24	Resistance characteristics of influenza to amino-adamantyls. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 547-553.	1.4	24
25	Quantitative analysis of influenza M2 channel blockers. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 394-398.	1.4	21
26	How Do Aminoadamantanes Block the Influenza M2 Channel, and How Does Resistance Develop?. Journal of the American Chemical Society, 2011, 133, 9903-9911.	6.6	73
27	Characterization of the Na+/H+ Antiporter from Yersinia pestis. PLoS ONE, 2011, 6, e26115.	1.1	8
28	Computational study of the Na+/H+ antiporter from Vibrio parahaemolyticus. Journal of Molecular Modeling, 2011, 17, 1877-1890.	0.8	5
29	Promiscuous Binding in a Selective Protein: The Bacterial Na+/H+ Antiporter. PLoS ONE, 2011, 6, e25182.	1.1	8
30	pH-driven helix rotations in the influenza M2 H+ channel: a potential gating mechanism. European Biophysics Journal, 2010, 39, 1043-1049.	1.2	5
31	Gating Mechanism of the Influenza A M2 Channel Revealed by 1D and 2D IR Spectroscopies. Structure, 2009, 17, 247-254.	1.6	116
32	Structure and dynamics of the influenza A M2 Channel: a comparison of three structures. Journal of Molecular Modeling, 2009, 15, 1317-1328.	0.8	11
33	Mechanism of Na ⁺ /H ⁺ Antiporting. Science, 2007, 317, 799-803.	6.0	141
34	Structural Disorder of the CD3Î¶ Transmembrane Domain Studied with 2D IR Spectroscopy and Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2006, 110, 24740-24749.	1.2	64
35	A Trimerizing GxxxG Motif Is Uniquely Inserted in the Severe Acute Respiratory Syndrome (SARS) Coronavirus Spike Protein Transmembrane Domainâ€. Biochemistry, 2006, 45, 11349-11356.	1.2	32
36	Isotope-edited IR spectroscopy for the study of membrane proteins. Current Opinion in Chemical Biology, 2006, 10, 394-401.	2.8	75

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37	How pH Opens a H+ Channel: The Gating Mechanism of Influenza A M2. Structure, 2005, 13, 1789-1798.	1.6	60
38	Disorder Influence on Linear Dichroism Analyses of Smectic Phases. Biophysical Journal, 2005, 89, 563-571.	0.2	7
39	FTIR Studies of Viral Ion Channels. , 2005, , 91-100.		0
40	Site-specific vibrational dynamics of the CD3Î¶ membrane peptide using heterodyned two-dimensional infrared photon echo spectroscopy. Journal of Chemical Physics, 2004, 120, 10215-10224.	1.2	110
41	A novel method of resistance for influenza against a channel-blocking antiviral drug. Proteins: Structure, Function and Bioinformatics, 2004, 55, 251-257.	1.5	60
42	A Highly Unusual Palindromic Transmembrane Helical Hairpin Formed by SARS Coronavirus E Protein. Journal of Molecular Biology, 2004, 341, 769-779.	2.0	89
43	Modeling Sample Disorder in Site-Specific Dichroism Studies of Uniaxial Systems. Biophysical Journal, 2004, 86, 2502-2507.	0.2	8
44	Site-Specific Dichroism Analysis Utilizing Transmission FTIR. Biophysical Journal, 2003, 85, 2476-2483.	0.2	5
45	Multiple site-specific infrared dichroism of CD3-Î¶, a transmembrane helix bundle. Journal of Molecular Biology, 2002, 316, 365-374.	2.0	42
46	Convergence of experimental, computational and evolutionary approaches predicts the presence of a tetrameric form for CD3-Î¶. Journal of Molecular Biology, 2002, 316, 375-384.	2.0	35
47	Structural aspects of oligomerization taking place between the transmembrane Î±-helices of bitopic membrane proteins. Biochimica Et Biophysica Acta - Biomembranes, 2002, 1565, 347-363.	1.4	52
48	A Structure for the Trimeric MHC Class II-associated Invariant Chain Transmembrane Domain. Journal of Molecular Biology, 2002, 320, 1109-1117.	2.0	43
49	C-Deuterated Alanine: A New Label to Study Membrane Protein Structure Using Site-Specific Infrared Dichroism. Biophysical Journal, 2002, 82, 1068-1075.	0.2	30
50	Contribution of Energy Values to the Analysis of Global Searching Molecular Dynamics Simulations of Transmembrane Helical Bundles. Biophysical Journal, 2002, 82, 3063-3071.	0.2	24
51	Hydrogen/deuterium exchange of hydrophobic peptides in model membranes by electrospray ionization mass spectrometry. Journal of the American Society for Mass Spectrometry, 2002, 13, 1376-1387.	1.2	30
52	Mapping the Energy Surface of Transmembrane Helix-Helix Interactions. Biophysical Journal, 2001, 81, 2681-2692.	0.2	29
53	A new method to model membrane protein structure based on silent amino acid substitutions. Proteins: Structure, Function and Bioinformatics, 2001, 44, 370-375.	1.5	46
54	Site-specific examination of secondary structure and orientation determination in membrane proteins: The peptidic13C?18O group as a novel infrared probe. Biopolymers, 2001, 59, 396-401.	1.2	104

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55	Substitution rates in Î±â€helical transmembrane proteins. Protein Science, 2001, 10, 2507-2517.	3.1	30
56	Site-specific examination of secondary structure and orientation determination in membrane proteins: The peptidic 13Cï£¾18O group as a novel infrared probe. , 2001, 59, 396.		5
57	Do more complex organisms have a greater proportion of membrane proteins in their genomes?. , 2000, 39, 417-420.		223
58	Turning an opinion inside-out: Rees and Eisenberg's commentary (Proteins 2000;38:121-122) on ?Are membrane proteins ?inside-out? proteins?? (Proteins 1999;36:135-143). Proteins: Structure, Function and Bioinformatics, 2000, 40, 463-464.	1.5	13
59	Recursive use of evolutionary conservation data in molecular modeling of membrane proteins. FEBS Journal, 2000, 267, 3422-3431.	0.2	14
60	Structure of the Influenza C Virus CM2 Protein Transmembrane Domain Obtained by Site-specific Infrared Dichroism and Global Molecular Dynamics Searching. Journal of Biological Chemistry, 2000, 275, 4225-4229.	1.6	36
61	Use of a New Label, 13Cî—»18O, in the Determination of a Structural Model of Phospholamban in a Lipid Bilayer. Spatial Restraints Resolve the Ambiguity Arising from Interpretations of Mutagenesis Data. Journal of Molecular Biology, 2000, 300, 677-685.	2.0	92
62	Use of a Single Glycine Residue to Determine the Tilt and Orientation of a Transmembrane Helix. A New Structural Label for Infrared Spectroscopy. Biophysical Journal, 2000, 79, 3139-3143.	0.2	52
63	The effect of nucleotide bias upon the composition and prediction of transmembrane helices. Protein Science, 2000, 9, 505-511.	3.1	8
64	Are membrane proteins ?inside-out? proteins?. , 1999, 36, 135-143.		68
65	vpu Transmembrane Peptide Structure Obtained by Site-Specific Fourier Transform Infrared Dichroism and Global Molecular Dynamics Searching. Biophysical Journal, 1999, 77, 1594-1601.	0.2	96
66	Experimentally based orientational refinement of membrane protein models: a structure for the Influenza A M2 H + channel 1 1Edited by G. von Heijne. Journal of Molecular Biology, 1999, 286, 951-962.	2.0	141
67	Statistical analysis of predicted transmembrane Î±-helices. BBA - Proteins and Proteomics, 1998, 1429, 113-128.	2.1	166
68	Helicity, membrane incorporation, orientation and thermal stability of the large conductance mechanosensitive ion channel from E. coli. Biochimica Et Biophysica Acta - Biomembranes, 1998, 1369, 131-140.	1.4	25
69	STRUCTURAL PERSPECTIVES OF PHOSPHOLAMBAN, A HELICAL TRANSMEMBRANE PENTAMER. Annual Review of Biophysics and Biomolecular Structure, 1997, 26, 157-179.	18.3	67
70	Site-Directed Dichroism As a Method for Obtaining Rotational and Orientational Constraints for Oriented Polymers. Journal of the American Chemical Society, 1997, 119, 8973-8980.	6.6	68
71	Are there dominant membrane protein families with a given number of helices?. , 1997, 28, 465-466.		58
72	Determining the Secondary Structure and Orientation of EmrE, a Multi-Drug Transporter, Indicates a Transmembrane Four-Helix Bundle. Biochemistry, 1996, 35, 7233-7238.	1.2	101

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73	Computational searching and mutagenesis suggest a structure for the pentameric transmembrane domain of phospholamban. Nature Structural and Molecular Biology, 1995, 2, 154-162.	3.6	198
74	Structural Model of the Phospholamban Ion Channel Complex in Phospholipid Membranes. Journal of Molecular Biology, 1995, 248, 824-834.	2.0	122