Andreas Kukol

List of Publications by Year
in descending order

46	1,760	304743 22	265206 42
papers	citations	h-index	g-index

48	48	48	2008
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrating molecular modelling methods to advance influenza A virus drug discovery. Drug Discovery Today, 2021, 26, 503-510.	6.4	11
2	Prediction of ligands to universally conserved binding sites of the influenza a virus nuclear export protein. Virology, 2019, 537, 97-103.	2.4	8
3	Genomic evidence for genes encoding leucine-rich repeat receptors linked to resistance against the eukaryotic extra- and intracellular Brassica napus pathogens Leptosphaeria maculans and Plasmodiophora brassicae. PLoS ONE, 2018, 13, e0198201.	2.5	13
4	Evolutionary conservation of influenza A PB2 sequences reveals potential target sites for small molecule inhibitors. Virology, 2017, 509, 112-120.	2.4	16
5	L30A Mutation of Phospholemman Mimics Effects of Cardiac Glycosides in Isolated Cardiomyocytes. Biochemistry, 2016, 55, 6196-6204.	2.5	5
6	Evaluation of a novel virtual screening strategy using receptor decoy binding sites. Journal of Negative Results in BioMedicine, 2016, 15, 15.	1.4	5
7	Recent discoveries of influenza A drug target sites to combat virus replication. Biochemical Society Transactions, 2016, 44, 932-936.	3.4	4
8	Lipid Membranes for Membrane Proteins. Methods in Molecular Biology, 2015, 1215, 73-90.	0.9	4
9	A cellulose-based bioassay for the colorimetric detection of pathogen DNA. Analytical and Bioanalytical Chemistry, 2014, 406, 7887-7898.	3.7	14
10	Large-scale analysis of influenza A virus nucleoprotein sequence conservation reveals potential drug-target sites. Virology, 2014, 454-455, 40-47.	2.4	29
11	G-quadruplex formation of FXYD1 pre-mRNA indicates the possibility of regulating expression of its protein product. Archives of Biochemistry and Biophysics, 2014, 560, 52-58.	3.0	8
12	Influenza A nucleoprotein binding sites for antivirals: current research and future potential. Future Virology, 2014, 9, 625-627.	1.8	1
13	How the amyloid-Î² peptide and membranes affect each other: An extensive simulation study. Biochimica Et Biophysica Acta - Biomembranes, 2013, 1828, 327-339.	2.6	66
14	Structure and dynamics of the kinase IKK-Î² â€“ A key regulator of the NF-kappa B transcription factor. Journal of Structural Biology, 2011, 176, 133-142.	2.8	11
15	Lipid models for united-atom molecular dynamics simulations of protein. Nature Precedings, 2011, , .	0.1	1
16	Consensus virtual screening approaches to predict protein ligands. Nature Precedings, 2011, , .	0.1	0
17	Consensus virtual screening approaches to predict protein ligands. European Journal of Medicinal Chemistry, 2011, 46, 4661-4664.	5.5	53
18	Large-scale analysis of influenza A virus sequences reveals potential drug target sites of non-structural proteins. Journal of General Virology, 2009, 90, 2124-2133.	2.9	53

#	Article	IF	Citations
19	Lipid Models for United-Atom Molecular Dynamics Simulations of Proteins. Journal of Chemical Theory and Computation, 2009, 5, 615-626.	5.3	241
20	Label-free electrical detection of DNA hybridization for the example of influenza virus gene sequences. Analytical Biochemistry, 2008, 374, 143-153.	2.4	55
21	Solid-state 17O NMR spectroscopy of a phospholemman transmembrane domain protein: Implications for the limits of detecting dilute 17O sites in biomaterials. Solid State Nuclear Magnetic Resonance, 2008, 33, 72-75.	2.3	22
22	Transmembrane Protein Models Based on High-Throughput Molecular Dynamics Simulations with Experimental Constraints. Methods in Molecular Biology, 2008, 443, 213-227.	0.9	1
23	The Structure of Ghrelin. Vitamins and Hormones, 2007, 77, 1-12.	1.7	6
24	Phospholemman Transmembrane Structure Reveals Potential Interactions with Na+/K+-ATPase. Journal of Biological Chemistry, 2007, 282, 32742-32748.	3.4	14
25	Model of a Putative Pore: The Pentameric Î±-Helical Bundle of SARS Coronavirus E Protein in Lipid Bilayers. Biophysical Journal, 2006, 91, 938-947.	0.5	96
26	Secondary structure, orientation, and oligomerization of phospholemman, a cardiac transmembrane protein. Protein Science, 2006, 15, 1127-1132.	7.6	43
27	Conformational Flexibility of the Peptide Hormone Ghrelin in Solution and Lipid Membrane Bound: A Molecular Dynamics Study. Journal of Biomolecular Structure and Dynamics, 2006, 23, 357-363.	3.5	25
28	The Transmembrane Domain of the Oncogenic Mutant ErbB-2 Receptor: A Structure Obtained from Site-specific Infrared Dichroism and Molecular Dynamics. Journal of Molecular Biology, 2006, 361, 945-953.	4.2	23
29	Enhancing resolution and sensitivity of 17O solid-state NMR through combining double rotation, 1H decoupling and satellite modulation for biomolecular applications. Chemical Physics Letters, 2006, 421, 42-46.	2.6	27
30	Systematic molecular dynamics searching in a lipid bilayer: Application to the glycophorin A and oncogenic ErbB-2 transmembrane domains. Journal of Molecular Graphics and Modelling, 2006, 25, 226-233.	2.4	22
31	Siteâ€'specific IR spectroscopy and molecular modelling combined towards solving transmembrane protein structure. Spectroscopy, 2005, 19, 1-16.	0.8	11
32	Solid-State17O NMR of Amino Acids. Journal of Physical Chemistry B, 2004, 108, 9256-9263.	2.6	81
33	A Structure for the Trimeric MHC Class II-associated Invariant Chain Transmembrane Domain. Journal of Molecular Biology, 2002, 320, 1109-1117.	4.2	43
34	Mapping the Energy Surface of Transmembrane Helix-Helix Interactions. Biophysical Journal, 2001, 81, 2681-2692.	0.5	29
35	The structure of the HIV-1 Vpu ion channel: modelling and simulation studies. Biochimica Et Biophysica Acta - Biomembranes, 2001, 1512, 291-298.	2.6	49
36	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.	2.4	104

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37	Siteâ€specific examination of secondary structure and orientation determination in membrane proteins: The peptidic 13Cï£¾18O group as a novel infrared probe. Biopolymers, 2001, 59, 396-401.	2.4	5
38	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.	3.4	36
39	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.	0.5	52
40	Exploring Models of the Influenza A M2 Channel: MD Simulations in a Phospholipid Bilayer. Biophysical Journal, 2000, 78, 55-69.	0.5	98
41	vpu Transmembrane Peptide Structure Obtained by Site-Specific Fourier Transform Infrared Dichroism and Global Molecular Dynamics Searching. Biophysical Journal, 1999, 77, 1594-1601.	0.5	96
42	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.	4.2	141
43	Electrostatic determinants of the ion channel control of the nicotinic acetylcholine receptor of Torpedo californica. European Biophysics Journal, 1998, 27, 618-625.	2.2	7
44	Incorporation of the acetylcholine receptor dimer from Torpedo californica in a peptide supported lipid membrane investigated by surface plasmon and fluorescence spectroscopy. Biosensors and Bioelectronics, 1998, 13, 585-591.	10.1	108
45	Ion channelsâ€"analysis and simulation embedded in a flexible environment. Computers & Chemistry, 1997, 21, 181-184.	1.2	1
46	Methyl group effect on the proton affinity of methylated acetophenones studied by two mass spectrometric techniques. Organic Mass Spectrometry, 1993, 28, 1107-1110.	1.3	22