Jakob P Ulmschneider

List of Publications by Year
in descending order

32	1,536	331670 21	434195 31
papers	citations	h-index	g-index

34	34	34	1786
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Predicting Membrane-Active Peptide Dynamics in Fluidic Lipid Membranes. Methods in Molecular Biology, 2022, 2405, 115-136.	0.9	0
2	Integrated Design of a Membraneâ€Lytic Peptideâ€Based Intravenous Nanotherapeutic Suppresses Tripleâ€Negative Breast Cancer. Advanced Science, 2022, 9, e2105506.	11.2	7
3	Tuning of a Membrane-Perforating Antimicrobial Peptide to Selectively Target Membranes of Different Lipid Composition. Journal of Membrane Biology, 2021, 254, 75-96.	2.1	13
4	Understanding and modelling the interactions of peptides with membranes: from partitioning to self-assembly. Current Opinion in Structural Biology, 2020, 61, 160-166.	5.7	31
5	Mechanisms of a Small Membrane-Active Antimicrobial Peptide from Hyla punctata. Australian Journal of Chemistry, 2020, 73, 236.	0.9	12
6	Simulation-Guided Rational de Novo Design of a Small Pore-Forming Antimicrobial Peptide. Journal of the American Chemical Society, 2019, 141, 4839-4848.	13.7	80
7	Computed Free Energies of Peptide Insertion into Bilayers are Independent of Computational Method. Journal of Membrane Biology, 2018, 251, 345-356.	2.1	22
8	Molecular Dynamics Simulations Are Redefining Our View of Peptides Interacting with Biological Membranes. Accounts of Chemical Research, 2018, 51, 1106-1116.	15.6	94
9	The importance of the membrane interface as the reference state for membrane protein stability. Biochimica Et Biophysica Acta - Biomembranes, 2018, 1860, 2539-2548.	2.6	13
10	Role of the Interaction Motif in Maintaining the Open Gate of an Open Sodium Channel. Biophysical Journal, 2018, 115, 1920-1930.	0.5	13
11	Transmembrane helices containing a charged arginine are thermodynamically stable. European Biophysics Journal, 2017, 46, 627-637.	2.2	21
12	Charged Antimicrobial Peptides Can Translocate across Membranes without Forming Channel-like Pores. Biophysical Journal, 2017, 113, 73-81.	0.5	91
13	Spontaneous formation of structurally diverse membrane channel architectures from a single antimicrobial peptide. Nature Communications, 2016, 7, 13535.	12.8	99
14	Insights from Micro-second Atomistic Simulations of Melittin in Thin Lipid Bilayers. Journal of Membrane Biology, 2015, 248, 497-503.	2.1	26
15	How reliable are molecular dynamics simulations of membrane active antimicrobial peptides?. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 2280-2288.	2.6	83
16	Spontaneous transmembrane helix insertion thermodynamically mimics translocon-guided insertion. Nature Communications, 2014, 5, 4863.	12.8	91
17	Molecular dynamics of ion transport through the open conformation of a bacterial voltage-gated sodium channel. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 6364-6369.	7.1	149
18	Conformational States of Melittin at a Bilayer Interface. Biophysical Journal, 2013, 104, L12-L14.	0.5	48

#	Article	IF	Citations
19	Reorientation and Dimerization of the Membrane-Bound Antimicrobial Peptide PGLa from Microsecond All-Atom MD Simulations. Biophysical Journal, 2012, 103, 472-482.	0.5	51
20	In Silico Partitioning and Transmembrane Insertion of Hydrophobic Peptides under Equilibrium Conditions. Journal of the American Chemical Society, 2011, 133, 15487-15495.	13.7	92
21	Determining Peptide Partitioning Properties via Computer Simulation. Journal of Membrane Biology, 2011, 239, 15-26.	2.1	25
22	Mechanism and Kinetics of Peptide Partitioning into Membranes from All-Atom Simulations of Thermostable Peptides. Journal of the American Chemical Society, 2010, 132, 3452-3460.	13.7	80
23	Peptide Partitioning Properties from Direct Insertion Studies. Biophysical Journal, 2010, 98, L60-L62.	0.5	26
24	Sampling efficiency in explicit and implicit membrane environments studied by peptide folding simulations. Proteins: Structure, Function and Bioinformatics, 2009, 75, 586-597.	2.6	25
25	United Atom Lipid Parameters for Combination with the Optimized Potentials for Liquid Simulations All-Atom Force Field. Journal of Chemical Theory and Computation, 2009, 5, 1803-1813.	5.3	104
26	Peptide Partitioning and Folding into Lipid Bilayers. Journal of Chemical Theory and Computation, 2009, 5, 2202-2205.	5.3	17
27	Membrane adsorption, folding, insertion and translocation of synthetic trans-membrane peptides. Molecular Membrane Biology, 2008, 25, 245-257.	2.0	20
28	Folding Peptides into Lipid Bilayer Membranes. Journal of Chemical Theory and Computation, 2008, 4, 1807-1809.	5.3	28
29	Folding Simulations of the Transmembrane Helix of Virus Protein U in an Implicit Membrane Model. Journal of Chemical Theory and Computation, 2007, 3, 2335-2346.	5.3	30
30	A Generalized Born Implicit-Membrane Representation Compared to Experimental Insertion Free Energies. Biophysical Journal, 2007, 92, 2338-2349.	0.5	74
31	Monte carlo folding of trans-membrane helical peptides in an implicit generalized Born membrane. Proteins: Structure, Function and Bioinformatics, 2007, 69, 297-308.	2.6	21
32	Monte Carlo vs Molecular Dynamics for All-Atom Polypeptide Folding Simulations. Journal of Physical Chemistry B, 2006, 110, 16733-16742.	2.6	49