Marc F Lensink

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9075988/publications.pdf

Version: 2024-02-01

76 papers	3,406 citations	201674 27 h-index	149698 56 g-index
83 all docs	83 docs citations	83 times ranked	3635 citing authors

#	Article	IF	Citations
1	TRPM8-Rap1A Interaction Sites as Critical Determinants for Adhesion and Migration of Prostate and Other Epithelial Cancer Cells. Cancers, 2022, 14, 2261.	3.7	6
2	O-GlcNAcylation Prediction: An Unattained Objective. Advances and Applications in Bioinformatics and Chemistry, 2021, Volume 14, 87-102.	2.6	5
3	Centrality Measures in Residue Interaction Networks to Highlight Amino Acids in Proteinâ€“Protein Binding. Frontiers in Bioinformatics, 2021, 1, .	2.1	9
4	DNA Aptamers Block the Receptor Binding Domain at the Spike Protein of SARS-CoV-2. Frontiers in Molecular Biosciences, 2021, 8, 713003.	3.5	11
5	Prediction of protein assemblies, the next frontier: The <scp>CASP14â€CAPRI</scp> experiment. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1800-1823.	2.6	73
6	Modeling proteinâ€protein, proteinâ€peptide, and proteinâ€oligosaccharide complexes: CAPRI 7th edition. Proteins: Structure, Function and Bioinformatics, 2020, 88, 916-938.	2.6	96
7	Cover Image, Volume 88, Issue 8. Proteins: Structure, Function and Bioinformatics, 2020, 88, C1.	2.6	1
8	Assembly of B4GALT1/ST6GAL1 heteromers in the Golgi membranes involves lateral interactions via highly charged surface domains. Journal of Biological Chemistry, 2019, 294, 14383-14393.	3.4	29
9	Blind prediction of homoâ€and heteroâ€protein complexes: The CASP13â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1200-1221.	2.6	99
10	Identification of Novel Interaction Partners of Ets-1: Focus on DNA Repair. Genes, 2019, 10, 206.	2.4	1
11	Identification of Key Residues in Proteins Through Centrality Analysis and Flexibility Prediction with RINspector. Current Protocols in Bioinformatics, 2019, 65, e66.	25.8	13
12	Asymmetrical diversification of the receptor-ligand interaction controlling self-incompatibility in Arabidopsis. ELife, 2019, 8, .	6.0	11
13	Coiled-Coil Antagonism Regulates Activity of Venus Flytrap-Domain-Containing Sensor Kinases of the BvgS Family. MBio, 2018, 9, .	4.1	23
14	RINspector: a Cytoscape app for centrality analyses and DynaMine flexibility prediction. Bioinformatics, 2018, 34, 294-296.	4.1	23
15	The challenge of modeling protein assemblies: the CASP12â€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 257-273.	2.6	85
16	A Novel Integrated Way for Deciphering the Glycan Code for the FimH Lectin. Molecules, 2018, 23, 2794.	3.8	13
17	The Inclusion of Water Molecules in Residue Interaction Networks Identifies Additional Central Residues. Frontiers in Molecular Biosciences, 2018, 5, 88.	3.5	9
18	Structure and dynamics of a human myelin protein P2 portal region mutant indicate opening of the Î² barrel in fatty acid binding proteins. BMC Structural Biology, 2018, 18, 8.	2.3	19

#	Article	IF	Citations
19	Targeting Dynamical Binding Processes in the Design of Non-Antibiotic Anti-Adhesives by Molecular Simulationâ€"The Example of FimH. Molecules, 2018, 23, 1641.	3.8	15
20	Computational characterization of the binding mode between oncoprotein Etsâ€1 and DNAâ€repair enzymes. Proteins: Structure, Function and Bioinformatics, 2018, 86, 1055-1063.	2.6	4
21	Comparing protein structures with RINspector automation in Cytoscape. F1000Research, 2018, 7, 563.	1.6	9
22	Comparing protein structures with RINspector automation in Cytoscape. F1000Research, 2018, 7, 563.	1.6	15
23	Cover Image, Volume 85, Issue 3. Proteins: Structure, Function and Bioinformatics, 2017, 85, C1.	2.6	0
24	FlexPepDock lessons from CAPRI peptideâ€"protein rounds and suggested new criteria for assessment of model quality and utility. Proteins: Structure, Function and Bioinformatics, 2017, 85, 445-462.	2.6	19
25	Mutation of Tyr137 of the universalEscherichia colifimbrial adhesin FimH relaxes the tyrosine gate prior to mannose binding. IUCrJ, 2017, 4, 7-23.	2.2	19
26	Modeling proteinâ€"protein and proteinâ€"peptide complexes: CAPRI 6th edition. Proteins: Structure, Function and Bioinformatics, 2017, 85, 359-377.	2.6	198
27	Sites for Dynamic Protein-Carbohydrate Interactions of O- and C-Linked Mannosides on the E. coli FimH Adhesin. Molecules, 2017, 22, 1101.	3.8	23
28	CLUB-MARTINI: Selecting Favourable Interactions amongst Available Candidates, a Coarse-Grained Simulation Approach to Scoring Docking Decoys. PLoS ONE, 2016, 11, e0155251.	2.5	20
29	Introducing a Clustering Step in a Consensus Approach for the Scoring of Protein-Protein Docking Models. PLoS ONE, 2016, 11, e0166460.	2.5	20
30	Molecular docking as a popular tool in drug design, an in silico travel. Advances and Applications in Bioinformatics and Chemistry, 2016, Volume 9, 1-11.	2.6	182
31	Balance between Coiled-Coil Stability and Dynamics Regulates Activity of BvgS Sensor Kinase in Bordetella. MBio, 2016, 7, e02089.	4.1	32
32	Prediction of homoprotein and heteroprotein complexes by protein docking and templateâ€based modeling: A CASPâ€CAPRI experiment. Proteins: Structure, Function and Bioinformatics, 2016, 84, 323-348.	2.6	148
33	On the ability of molecular dynamics simulation and continuum electrostatics to treat interfacial water molecules in protein-protein complexes. Scientific Reports, 2016, 6, 38259.	3.3	11
34	The Antiadhesive Strategy in Crohnâ€²s Disease: Orally Active Mannosides to Decolonize Pathogenic Escherichia coli from the Gut. ChemBioChem, 2016, 17, 936-952.	2.6	46
35	Structures ofC-mannosylated anti-adhesives bound to the type 1 fimbrial FimH adhesin. IUCrJ, 2016, 3, 163-167.	2.2	16
36	Regulatory motifs on ISWI chromatin remodelers: molecular mechanisms and kinetic proofreading. Journal of Physics Condensed Matter, 2015, 27, 064108.	1.8	3

#	Article	IF	Citations
37	Virulence Regulation with Venus Flytrap Domains: Structure and Function of the Periplasmic Moiety of the Sensor-Kinase BvgS. PLoS Pathogens, 2015, 11, e1004700.	4.7	51
38	Signal Transduction by BvgS Sensor Kinase. Journal of Biological Chemistry, 2015, 290, 23307-23319.	3.4	19
39	Kinetic proofreading of chromatin remodeling: from gene activation to gene repression and back. AIMS Biophysics, 2015, 2, 398-411.	0.6	3
40	Membrane-Associated Proteins and Peptides. Methods in Molecular Biology, 2015, 1215, 109-124.	0.9	1
41	Score_set: A CAPRI benchmark for scoring protein complexes. Proteins: Structure, Function and Bioinformatics, 2014, 82, 3163-3169.	2.6	72
42	Blind prediction of interfacial water positions in CAPRI. Proteins: Structure, Function and Bioinformatics, 2014, 82, 620-632.	2.6	50
43	Probing the Conformation of FhaC with Small-Angle Neutron Scattering and Molecular Modeling. Biophysical Journal, 2014, 107, 185-196.	0.5	16
44	The structure of the CD3Î¶Î¶ transmembrane dimer in lipid bilayers. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 739-746.	2.6	5
45	Docking, scoring, and affinity prediction in CAPRI. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2082-2095.	2.6	216
46	On the Molecular Basis of D-Bifunctional Protein Deficiency Type III. PLoS ONE, 2013, 8, e53688.	2.5	7
47	Oligoarginine vectors for intracellular delivery: Role of arginine side-chain orientation in chain length-dependent destabilization of lipid membranes. Chemistry and Physics of Lipids, 2012, 165, 89-96.	3.2	5
48	Unexpected wide substrate specificity of C. perfringens Î±-toxin phospholipase C. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 2618-2627.	2.6	25
49	Fusogenic activity of cationic lipids and lipid shape distribution. Cellular and Molecular Life Sciences, 2010, 67, 483-494.	5.4	29
50	Docking and scoring protein interactions: CAPRI 2009. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3073-3084.	2.6	210
51	Blind predictions of protein interfaces by docking calculations in CAPRI. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3085-3095.	2.6	77
52	Identification of Specific Lipid-binding Sites in Integral Membrane Proteins. Journal of Biological Chemistry, 2010, 285, 10519-10526.	3.4	33
53	Spotlight on Human LL-37, an Immunomodulatory Peptide with Promising Cell-Penetrating Properties. Pharmaceuticals, 2010, 3, 3435-3460.	3.8	31
54	Lipid Membrane Destabilisation By Arginine Peptides Is Chain Length Dependent. Biophysical Journal, 2010, 98, 82a-83a.	0.5	0

#	Article	IF	Citations
55	Fusogenic Activity of Cationic Lipids Correlates with Lipid Shape Distribution. Biophysical Journal, 2010, 98, 671a.	0.5	0
56	Characterization of the Cationic DiC14-amidine Bilayer by Mixed DMPC/DiC14-amidine Molecular Dynamics Simulations Shows an Interdigitated Nonlamellar Bilayer Phase. Langmuir, 2009, 25, 5230-5238.	3.5	11
57	Cationic lipids activate cellular cascades. Which receptors are involved?. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 425-430.	2.4	22
58	Interaction Between Cationic Lipids and Endotoxin Receptors. Biophysical Journal, 2009, 96, 675a.	0.5	0
59	Homology-based modeling of 3D structures of proteinâ€“protein complexes using alignments of modified sequence profiles. International Journal of Biological Macromolecules, 2008, 43, 198-208.	7.5	39
60	Membrane-Associated Proteins and Peptides. Methods in Molecular Biology, 2008, 443, 161-179.	0.9	4
61	Recognition-induced Conformational Changes in Protein-Protein Docking. Current Pharmaceutical Biotechnology, 2008, 9, 77-86.	1.6	25
62	LigASite a database of biologically relevant binding sites in proteins with known apo-structures. Nucleic Acids Research, 2007, 36, D667-D673.	14.5	79
63	Docking and scoring protein complexes: CAPRI 3rd Edition. Proteins: Structure, Function and Bioinformatics, 2007, 69, 704-718.	2.6	301
64	Relating destabilizing regions to known functional sites in proteins. BMC Bioinformatics, 2007, 8, 141.	2.6	26
65	Predictions of Protein-Protein Interactions at the Atomic Scale. , 2007, , 1-20.		1
66	Assessment of CAPRI predictions in rounds 3-5 shows progress in docking procedures. Proteins: Structure, Function and Bioinformatics, 2005, 60, 150-169.	2.6	310
67	Penetratin-Membrane Association: W48/R52/W56 Shield the Peptide from the Aqueous Phase. Biophysical Journal, 2005, 88, 939-952.	0.5	65
68	Phosphorylation by Protein Kinase CK2 Modulates the Activity of the ATP Binding Cassette A1 Transporter. Journal of Biological Chemistry, 2004, 279, 37779-37788.	3.4	62
69	Molecular Dynamics Simulation of the Effect of Hydrophobic Cosolutes on the Neutral Hydrolysis of an Activated Ester. Journal of Physical Chemistry B, 2004, 108, 5483-5488.	2.6	11
70	A Conserved Arginine Plays a Role in the Catalytic Cycle of the Protein Disulphide Isomerases. Journal of Molecular Biology, 2004, 335, 283-295.	4.2	125
71	Response of SCP-2L Domain of Human MFE-2 to Ligand Removal: Binding Site Closure and Burial of Peroxisomal Targeting Signal. Journal of Molecular Biology, 2002, 323, 99-113.	4.2	14
72	Signal transduction in the photoactive yellow protein. II. Proton transfer initiates conformational changes. Proteins: Structure, Function and Bioinformatics, 2002, 48, 212-219.	2.6	36

#	Article	IF	Citations
73	Signal transduction in the photoactive yellow protein. I. Photon absorption and the isomerization of the chromophore. Proteins: Structure, Function and Bioinformatics, 2002, 48, 202-211.	2.6	64
74	Simulation of slow reaction with quantum character: Neutral hydrolysis of carboxylic ester. Journal of Computational Chemistry, 1999, 20, 886-895.	3.3	25
75	Simultaneous integration of mixed quantum-classical systems by density matrix evolution equations using interaction representation and adaptive time step integrator. Journal of Computational Chemistry, 1996, 17, 1287-1295.	3.3	3
76	Treatment of inelastic collisions of a particle with a quantum harmonic oscillator by density matrix evolution. Molecular Physics, 1994, 82, 1249-1257.	1.7	12