Rasmus Fonseca

List of Publications by Year in descending order

19 papers	740 citations	1162367 8 h-index	839053 18 g-index
22 all docs	22 docs citations	22 times ranked	1462 citing authors

#	Article	IF	Citations
1	Structural insights into the activation of metabotropic glutamate receptors. Nature, 2019, 566, 79-84.	13.7	233
2	Conformational transitions of a neurotensin receptorÂ1â€“Gi1Âcomplex. Nature, 2019, 572, 80-85.	13.7	199
3	Diverse GPCRs exhibit conserved water networks for stabilization and activation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3288-3293.	3.3	116
4	qFit-ligand Reveals Widespread Conformational Heterogeneity of Drug-Like Molecules in X-Ray Electron Density Maps. Journal of Medicinal Chemistry, 2018, 61, 11183-11198.	2.9	44
5	Characterizing RNA ensembles from NMR data with kinematic models. Nucleic Acids Research, 2014, 42, 9562-9572.	6.5	25
6	Protein Structure Prediction Using Bee Colony Optimization Metaheuristic. Mathematical Modelling and Algorithms, 2010, 9, 181-194.	0.5	16
7	Predicting dihedral angle probability distributions for protein coil residues from primary sequence using neural networks. BMC Bioinformatics, 2009, 10, 338.	1.2	13
8	Coupled Motions in Î²₂AR:GÎ±s Conformational Ensembles. Journal of Chemical Theory and Computation, 2016, 12, 946-956.	2.3	12
9	Ranking Beta Sheet Topologies with Applications to Protein Structure Prediction. Mathematical Modelling and Algorithms, 2011, 10, 357-369.	0.5	7
10	Frustration-guided motion planning reveals conformational transitions in proteins. Proteins: Structure, Function and Bioinformatics, 2017, 85, 1795-1807.	1.5	7
11	Driving Structural Transitions in Molecular Simulations Using the Nonequilibrium Candidate Monte Carlo. Journal of Physical Chemistry B, 2018, 122, 1195-1204.	1.2	7
12	Bounding Volumes for Proteins: A Comparative Study. Journal of Computational Biology, 2012, 19, 1203-1213.	0.8	5
13	Collisionâ€free poisson motion planning in ultra highâ€dimensional molecular conformation spaces. Journal of Computational Chemistry, 2018, 39, 711-720.	1.5	5
14	KGSrna: Efficient 3D Kinematics-Based Sampling for Nucleic Acids. Lecture Notes in Computer Science, 2015, , 80-95.	1.0	4
15	Probing RNA Native Conformational Ensembles with Structural Constraints. Journal of Computational Biology, 2016, 23, 362-371.	0.8	4
16	Fast, clash-free RNA conformational morphing using molecular junctions. Bioinformatics, 2017, 33, 2114-2122.	1.8	4
17	Adjustable Chain Trees for Proteins. Journal of Computational Biology, 2012, 19, 83-99.	0.8	1
18	Protein Packing Quality Using Delaunay Complexes. , 2011, , .		0

#	Article	IF	Citations
19	Fast, Clash-Free RNA Conformational Morphing using Molecular Junctions. , 2017, , .		0