Marie Chabbert

List of Publications by Year in descending order

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1163117 1199594 13 172 8 12 citations h-index g-index papers 14 14 14 289 citing authors docs citations times ranked all docs

#	Article	IF	Citations
1	Evolutionary information helps understand distinctive features of the angiotensin II receptors AT1 and AT2 in amniota. PLoS Computational Biology, 2022, 18, e1009732.	3.2	О
2	Bios2cor: an R package integrating dynamic and evolutionary correlations to identify functionally important residues in proteins. Bioinformatics, 2021, 37, 2483-2484.	4.1	5
3	Homology Modeling of Class A G-Protein-Coupled Receptors in the Age of the Structure Boom. Methods in Molecular Biology, 2021, 2315, 73-97.	0.9	3
4	Deciphering collaborative sidechain motions in proteins during molecular dynamics simulations. Scientific Reports, 2020, 10, 15901.	3.3	7
5	Evolution of chemokine receptors is driven by mutations in the sodium binding site. PLoS Computational Biology, 2018, 14, e1006209.	3.2	18
6	The G Protein-Coupled Receptor UT of the Neuropeptide Urotensin II Displays Structural and Functional Chemokine Features. Frontiers in Endocrinology, 2017, 8, 76.	3.5	22
7	Molecular Insights into the Transmembrane Domain of the Thyrotropin Receptor. PLoS ONE, 2015, 10, e0142250.	2.5	12
8	Comparative analysis of sequence covariation methods to mine evolutionary hubs: Examples from selected GPCR families. Proteins: Structure, Function and Bioinformatics, 2014, 82, 2141-2156.	2.6	11
9	Structural Evolution of G-Protein-Coupled Receptors. Methods in Enzymology, 2013, 520, 49-66.	1.0	1
10	Multidimensional Scaling Reveals the Main Evolutionary Pathways of Class A G-Protein-Coupled Receptors. PLoS ONE, 2011, 6, e19094.	2.5	32
11	Structural determinants stabilizing helical distortions related to proline. Journal of Structural Biology, 2010, 171, 266-276.	2.8	14
12	An Indel in Transmembrane Helix 2 Helps to Trace the Molecular Evolution of Class A G-Protein-Coupled Receptors. Journal of Molecular Evolution, 2009, 68, 475-489.	1.8	29
13	Comprehensive analysis of the helixâ€Xâ€helix motif in soluble proteins. Proteins: Structure, Function and Bioinformatics, 2008, 72, 115-135.	2.6	18