

Marie Chabbert

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

172
citations

1163117

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1199594

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14
docs citations

14
times ranked

289
citing authors

#	ARTICLE	IF	CITATIONS
1	Multidimensional Scaling Reveals the Main Evolutionary Pathways of Class A G-Protein-Coupled Receptors. <i>PLoS ONE</i> , 2011, 6, e19094.	2.5	32
2	An Indel in Transmembrane Helix 2 Helps to Trace the Molecular Evolution of Class A G-Protein-Coupled Receptors. <i>Journal of Molecular Evolution</i> , 2009, 68, 475-489.	1.8	29
3	The G Protein-Coupled Receptor UT of the Neuropeptide Urotensin II Displays Structural and Functional Chemokine Features. <i>Frontiers in Endocrinology</i> , 2017, 8, 76.	3.5	22
4	Comprehensive analysis of the helix-ex-helix motif in soluble proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 115-135.	2.6	18
5	Evolution of chemokine receptors is driven by mutations in the sodium binding site. <i>PLoS Computational Biology</i> , 2018, 14, e1006209.	3.2	18
6	Structural determinants stabilizing helical distortions related to proline. <i>Journal of Structural Biology</i> , 2010, 171, 266-276.	2.8	14
7	Molecular Insights into the Transmembrane Domain of the Thyrotropin Receptor. <i>PLoS ONE</i> , 2015, 10, e0142250.	2.5	12
8	Comparative analysis of sequence covariation methods to mine evolutionary hubs: Examples from selected GPCR families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2141-2156.	2.6	11
9	Deciphering collaborative sidechain motions in proteins during molecular dynamics simulations. <i>Scientific Reports</i> , 2020, 10, 15901.	3.3	7
10	Bios2cor: an R package integrating dynamic and evolutionary correlations to identify functionally important residues in proteins. <i>Bioinformatics</i> , 2021, 37, 2483-2484.	4.1	5
11	Homology Modeling of Class A G-Protein-Coupled Receptors in the Age of the Structure Boom. <i>Methods in Molecular Biology</i> , 2021, 2315, 73-97.	0.9	3
12	Structural Evolution of G-Protein-Coupled Receptors. <i>Methods in Enzymology</i> , 2013, 520, 49-66.	1.0	1
13	Evolutionary information helps understand distinctive features of the angiotensin II receptors AT1 and AT2 in amniota. <i>PLoS Computational Biology</i> , 2022, 18, e1009732.	3.2	0