Geraldo Rodrigues Sartori

List of Publications by Year
in descending order

14 papers	90 citations	1937685 4 h-index	1372567 10 g-index
14 all docs	14 docs citations	14 times ranked	209 citing authors

#	Article	IF	Citations
1	Investigation of Unprecedented Sites and Proposition of New Ligands for Programmed Cell Death Protein I through Molecular Dynamics with Probes and Virtual Screening. Journal of Chemical Information and Modeling, 2022, 62, 1236-1248.	5.4	2
2	Development of New Potential Inhibitors of Î²1 Integrins through In Silico Methodsâ€"Screening and Computational Validation. Life, 2022, 12, 932.	2.4	4
3	Computationally-obtained structural insights into the molecular interactions between Pidilizumab and binding partners DLL1 and PD-1. Journal of Biomolecular Structure and Dynamics, 2021, , 1-13.	3.5	2
4	Guidelines To Predict Binding Poses of Antibodyâ€"Integrin Complexes. ACS Omega, 2020, 5, 16379-16385.	3.5	1
5	Ligand-induced conformational selection predicts the selectivity of cysteine protease inhibitors. PLoS ONE, 2019, 14, e0222055.	2.5	6
6	Polymorphisms in plastoquinol oxidase (PTOX) from Arabidopsis accessions indicate SNP-induced structural variants associated with altitude and rainfall. Journal of Bioenergetics and Biomembranes, 2019, 51, 151-164.	2.3	3
7	Ligand-induced conformational selection predicts the selectivity of cysteine protease inhibitors. , 2019, 14, e0222055.		0
8	Ligand-induced conformational selection predicts the selectivity of cysteine protease inhibitors. , 2019, 14, e0222055.		0
9	Ligand-induced conformational selection predicts the selectivity of cysteine protease inhibitors. , 2019, 14, e0222055.		0
10	Ligand-induced conformational selection predicts the selectivity of cysteine protease inhibitors. , 2019, 14, e0222055.		0
11	Highly predictive hologram QSAR models of nitrile-containing cruzain inhibitors. Journal of Biomolecular Structure and Dynamics, 2017, 35, 3232-3249.	3.5	4
12	Hydrogen Bond Basicity Prediction for Medicinal Chemistry Design. Journal of Medicinal Chemistry, 2016, 59, 4278-4288.	6.4	48
13	Integration of methods in cheminformatics and biocalorimetry for the design of trypanosomatid enzyme inhibitors. Future Medicinal Chemistry, 2014, 6, 17-33.	2.3	10
14	Small-angle X-ray scattering and structural modeling of full-length: cellobiohydrolase I from Trichoderma harzianum. Cellulose, 2013, 20, 1573-1585.	4.9	10