Luis P B Scott

List of Publications by Year
in descending order

19	262	933447 10	996975 15
papers	citations	h-index	g-index

22	22	22	942
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	PINK1 Interacts with VCP/p97 and Activates PKA to Promote NSFL1C/p47 Phosphorylation and Dendritic Arborization in Neurons. ENeuro, 2018, 5, ENEURO.0466-18.2018.	1.9	34
2	UDP-glucuronosyltransferases: Structure, Function and Drug Design Studies. Current Medicinal Chemistry, 2018, 25, 3247-3255.	2.4	33
3	Towards gaining sight of multiscale events: utilizing network models and normal modes in hybrid methods. Current Opinion in Structural Biology, 2020, 64, 34-41.	5.7	32
4	Self-Assembly of Argâ€“Phe Nanostructures via the Solidâ€“Vapor Phase Method. Journal of Physical Chemistry B, 2013, 117, 733-740.	2.6	27
5	Structural Dynamics of DPP-4 and Its Influence on the Projection of Bioactive Ligands. Molecules, 2018, 23, 490.	3.8	25
6	A cell-based reporter assay for screening for EcR agonist/antagonist activity of natural ecdysteroids in Lepidoptera (Bm5) and Diptera (S2) cell cultures, followed by modeling of ecdysteroid-EcR interactions and normal mode analysis. Pesticide Biochemistry and Physiology, 2013, 107, 309-320.	3.6	16
7	Interaction between 1-pyrenesulfonic acid and albumin: Moving inside the protein. Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy, 2019, 208, 243-254.	3.9	14
8	Sampling of Protein Conformational Space Using Hybrid Simulations: A Critical Assessment of Recent Methods. Frontiers in Molecular Biosciences, 2022, 9, 832847.	3.5	14
9	Relation between flexibility and positively selected HIVâ€1 protease mutants against inhibitors. Proteins: Structure, Function and Bioinformatics, 2012, 80, 2680-2691.	2.6	13
10	Structure and functional dynamics characterization of the ion channel of the human respiratory syncytial virus (hRSV) small hydrophobic protein (SH) transmembrane domain by combining molecular dynamics with excited normal modes. Journal of Molecular Modeling, 2016, 22, 286.	1.8	13
11	Predicting regions prone to protein aggregation based on SVM algorithm. Applied Mathematics and Computation, 2019, 359, 502-511.	2.2	9
12	The Role of QSAR and Virtual Screening Studies in Type 2 Diabetes Drug Discovery. Medicinal Chemistry, 2017, 13, 706-720.	1.5	7
13	Methyl divanillate: redox properties and binding affinity with albumin of an antioxidant and potential NADPH oxidase inhibitor. RSC Advances, 2019, 9, 19983-19992.	3.6	6
14	Unveiling functional motions based on point mutations in biased signaling systems: A normal mode study on nerve growth factor bound to TrkA. PLoS ONE, 2020, 15, e0231542.	2.5	5
15	Structural modelling and thermostability of a serine protease inhibitor belonging to the Kunitz-BPTI family from the Rhipicephalus microplus tick. Biochimie, 2021, 181, 226-233.	2.6	4
16	Recovery of the wild type atomic flexibility in the HIV-1 protease double mutants. Journal of Molecular Graphics and Modelling, 2015, 59, 107-116.	2.4	3
17	Nifuroxazide as JAK2 inhibitor: A binding mode proposal and Hel cell proliferation assay. European Journal of Pharmaceutical Sciences, 2021, 162, 105822.	4.0	3
18	Integrated Protocol to Design Potential Inhibitors of Dipeptidyl Peptidase- 4 (DPP-4). Current Topics in Medicinal Chemistry, 2020, 20, 209-226.	2.1	2

#	Article	IF	Citations
19	Virtual screening and inÂvitro assays of novel hits as promising DPP-4 inhibitors. Biochimie, 2022, 194, 43-50.	2.6	2