Kranthi Kumar Konidala

List of Publications by Year
in descending order

16	173	1162367 8	1125271 13
papers	citations	h-index	g-index

16	16	16	296
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integration of in silico methods to determine endocrine-disrupting tobacco pollutants binding potency with steroidogenic genes: comprehensive QSAR modeling and ensemble docking strategies. Environmental Science and Pollution Research, 2022, 29, 65806-65825.	2.7	3
2	Gene microarray expression profile analysis of differentially expressed genes of potential alternative pathways in nonâ€“small cell lung cancer: In search of biomarkers. Gene Reports, 2020, 19, 100633.	0.4	0
3	Applications of in silico methods to analyze the toxicity and estrogen receptor-mediated properties of plant-derived phytochemicals. Food and Chemical Toxicology, 2019, 125, 361-369.	1.8	6
4	QSAR modeling, pharmacophore-based virtual screening, and ensemble docking insights into predicting potential epigallocatechin gallate (EGCG) analogs against epidermal growth factor receptor. Journal of Receptor and Signal Transduction Research, 2019, 39, 18-27.	1.3	10
5	Structural Probing, Screening and Structure-Based Drug Repositioning Insights into the Identification of Potential Cox-2 Inhibitors from Selective Coxibs. Interdisciplinary Sciences, Computational Life Sciences, 2019, 11, 153-169.	2.2	9
6	Molecular activities and ligand-binding specificities of StAR-related lipid transfer domains: exploring integrated in silico methods and ensemble-docking approaches. SAR and QSAR in Environmental Research, 2018, 29, 483-501.	1.0	8
7	Computational screening, ensemble docking and pharmacophore analysis of potential gefitinib analogues against epidermal growth factor receptor. Journal of Receptor and Signal Transduction Research, 2018, 38, 48-60.	1.3	10
8	In silico insights into the identification of potential novel angiogenic inhibitors against human VEGFR-2: a new SAR-based hierarchical clustering approach. Journal of Receptor and Signal Transduction Research, 2018, 38, 372-383.	1.3	5
9	Elucidation of endocrineâ€disrupting polychlorinated biphenyls binding potency with steroidogenic genes: Integration of in silico methods and ensemble docking approaches. Ecotoxicology and Environmental Safety, 2018, 165, 194-201.	2.9	9
10	In silico insights into prediction andÂanalysis of potentialÂnovel pyrrolopyridine analogs against human MAPKAPK-2: a new SAR-based hierarchical clustering approach. 3 Biotech, 2018, 8, 385.	1.1	2
11	Ligand-based virtual screening, molecular docking, QSAR and pharmacophore analysis of quercetin-associated potential novel analogs against epidermal growth factor receptor. Journal of Receptor and Signal Transduction Research, 2017, 37, 600-610.	1.3	12
12	Integration of in silico approaches to determination of endocrine-disrupting perfluorinated chemicals binding potency with steroidogenic acute regulatory protein. Biochemical and Biophysical Research Communications, 2017, 491, 1007-1014.	1.0	17
13	Isolation, characterization and in silico docking studies of synergistic estrogen receptor and #945; (ER and #945;) anticancer polyphenols from Syzygium alternifolium (Wt.) walp.. Journal of Intercultural Ethnopharmacology, 2017, 6, 296.	0.9	19
14	Modeling, molecular dynamics, and docking assessment of transcription factor rho: a potential drug target in Brucella melitensis 16M. Drug Design, Development and Therapy, 2015, 9, 1897.	2.0	41
15	Complete genome-wide screening and subtractive genomic approach revealed new virulence factors, potential drug targets against bio-war pathogen Brucella melitensis 16M. Drug Design, Development and Therapy, 2015, 9, 1691.	2.0	16
16	CGMD: An integrated database of cancer genes and markers. Scientific Reports, 2015, 5, 12035.	1.6	6