Hui Wen Ng

List of Publications by Year
in descending order

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21 papers	760 citations	567281 15 h-index	713466 21 g-index
21 all docs	21 docs citations	21 times ranked	1322 citing authors

#	Article	IF	Citations
1	Competitive docking model for prediction of the human nicotinic acetylcholine receptor Î±7 binding of tobacco constituents. Oncotarget, 2018, 9, 16899-16916.	1.8	7
2	A Rat Î±-Fetoprotein Binding Activity Prediction Model to Facilitate Assessment of the Endocrine Disruption Potential of Environmental Chemicals. International Journal of Environmental Research and Public Health, 2016, 13, 372.	2.6	15
3	Pathway Analysis Revealed Potential Diverse Health Impacts of Flavonoids that Bind Estrogen Receptors. International Journal of Environmental Research and Public Health, 2016, 13, 373.	2.6	9
4	Experimental Data Extraction and in Silico Prediction of the Estrogenic Activity of Renewable Replacements for Bisphenol A. International Journal of Environmental Research and Public Health, 2016, 13, 705.	2.6	73
5	sNebula, a network-based algorithm to predict binding between human leukocyte antigens and peptides. Scientific Reports, 2016, 6, 32115.	3.3	34
6	Structures of androgen receptor bound with ligands: advancing understanding of biological functions and drug discovery. Expert Opinion on Therapeutic Targets, 2016, 20, 1267-1282.	3.4	26
7	QSAR Models at the US FDA/NCTR. Methods in Molecular Biology, 2016, 1425, 431-459.	0.9	19
8	Applying network analysis and Nebula (neighbor-edges based and unbiased leverage algorithm) to ToxCast data. Environment International, 2016, 89-90, 81-92.	10.0	6
9	Homology Model and Ligand Binding Interactions of the Extracellular Domain of the Human <i>Î±</i>4<i>Î²</i>2 Nicotinic Acetylcholine Receptor. Journal of Biomedical Science and Engineering, 2016, 09, 41-100.	0.4	5
10	Machine Learning Methods for Predicting HLA-Peptide Binding Activity. Bioinformatics and Biology Insights, 2015, 9s3, BBI.S29466.	2.0	68
11	Understanding and predicting binding between human leukocyte antigens (HLAs) and peptides by network analysis. BMC Bioinformatics, 2015, 16, S9.	2.6	19
12	Development and Validation of Decision Forest Model for Estrogen Receptor Binding Prediction of Chemicals Using Large Data Sets. Chemical Research in Toxicology, 2015, 28, 2343-2351.	3.3	47
13	Comparing genetic variants detected in the 1000 genomes project with SNPs determined by the International HapMap Consortium. Journal of Genetics, 2015, 94, 731-740.	0.7	20
14	Human Sex Hormone-Binding Globulin Binding Affinities of 125 Structurally Diverse Chemicals and Comparison with Their Binding to Androgen Receptor, Estrogen Receptor, and Î±-Fetoprotein. Toxicological Sciences, 2015, 143, 333-348.	3.1	69
15	Estrogenic Activity Data Extraction and in Silico Prediction Show the Endocrine Disruption Potential of Bisphenol A Replacement Compounds. Chemical Research in Toxicology, 2015, 28, 1784-1795.	3.3	68
16	Versatility or Promiscuity: The Estrogen Receptors, Control of Ligand Selectivity and an Update on Subtype Selective Ligands. International Journal of Environmental Research and Public Health, 2014, 11, 8709-8742.	2.6	61
17	Molecular Dynamics Simulations of the Adenosine A2a Receptor in POPC and POPE Lipid Bilayers: Effects of Membrane on Protein Behavior. Journal of Chemical Information and Modeling, 2014, 54, 573-581.	5.4	33
18	Competitive molecular docking approach for predicting estrogen receptor subtype Î± agonists and antagonists. BMC Bioinformatics, 2014, 15, S4.	2.6	58

#	Article	IF	Citations
19	Whole genome sequencing of 35 individuals provides insights into the genetic architecture of Korean population. BMC Bioinformatics, 2014, 15, S6.	2.6	34
20	Conversion of a non-selective adenosine receptor antagonist into A3-selective high affinity fluorescent probes using peptide-based linkers. Organic and Biomolecular Chemistry, 2013, 11, 5673.	2.8	47
21	Molecular Dynamics Simulations of the Adenosine A2a Receptor: Structural Stability, Sampling, and Convergence. Journal of Chemical Information and Modeling, 2013, 53, 1168-1178.	5.4	42