Svetoslav H Slavov

List of Publications by Year
in descending order

19	276	1040056 9	888059 17
papers	citations	h-index	g-index

20	20	20	420
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of structural factors that affect binding to cannabinoid receptor type 1. Journal of Molecular Structure, 2022, 1249, 131589.	3.6	0
2	Determination of structural factors affecting binding to mu, kappa and delta opioid receptors. Archives of Toxicology, 2020, 94, 1215-1227.	4.2	2
3	Quantitative structureâ€“toxicity relationships in translational toxicology. Current Opinion in Toxicology, 2020, 23-24, 46-49.	5.0	4
4	Computational identification of structural factors affecting the mutagenic potential of aromatic amines: study design and experimental validation. Archives of Toxicology, 2018, 92, 2369-2384.	4.2	6
5	3D-SDAR modeling of hERG potassium channel affinity: A case study in model design and toxicophore identification. Journal of Molecular Graphics and Modelling, 2017, 72, 246-255.	2.4	10
6	Rigorous 3-dimensional spectral data activity relationship approach modeling strategy for ToxCast estrogen receptor data classification, validation, and feature extraction. Environmental Toxicology and Chemistry, 2017, 36, 823-830.	4.3	4
7	Why are most phospholipidosis inducers also hERG blockers?. Archives of Toxicology, 2017, 91, 3885-3895.	4.2	22
8	4-Fluoro-3â€²,4â€²,5â€²-trimethoxychalcone as a new anti-invasive agent. From discovery to initial validation in an inÂvivo metastasis model. European Journal of Medicinal Chemistry, 2015, 101, 627-639.	5.5	13
9	Computational identification of a phospholipidosis toxicophore using 13 C and 15 N NMR-distance based fingerprints. Bioorganic and Medicinal Chemistry, 2014, 22, 6706-6714.	3.0	20
10	Identification of a metabolic biomarker panel in rats for prediction of acute and idiosyncratic hepatotoxicity. Computational and Structural Biotechnology Journal, 2014, 10, 78-89.	4.1	18
11	Comprehensive analysis of alterations in lipid and bile acid metabolism by carbon tetrachloride using integrated transcriptomics and metabolomics. Metabolomics, 2014, 10, 1293-1304.	3.0	5
12	Complementary PLS and KNN algorithms for improved 3D-QSDAR consensus modeling of AhR binding. Journal of Cheminformatics, 2013, 5, 47.	6.1	11
13	¹³C NMRâ€“Distance Matrix Descriptors: Optimal Abstract 3D Space Granularity for Predicting Estrogen Binding. Journal of Chemical Information and Modeling, 2012, 52, 1854-1864.	5.4	6
14	A computational study of the binding of 3-(arylidene) anabaseines to two major brain nicotinic acetylcholine receptors and to the acetylcholine binding protein. European Journal of Medicinal Chemistry, 2010, 45, 2433-2446.	5.5	9
15	Quantitative structureâ€“activity relationship modeling of bioconcentration factors of polychlorinated biphenyls. Toxicological and Environmental Chemistry, 2010, 92, 1233-1247.	1.2	4
16	Computational Chemistry Approaches for Understanding how Structure Determines Properties. Zeitschrift Fur Naturforschung - Section B Journal of Chemical Sciences, 2009, 64, 773-777.	0.7	2
17	QSAR modeling of the antifungal activity against Candida albicans for a diverse set of organic compounds. Bioorganic and Medicinal Chemistry, 2008, 16, 7055-7069.	3.0	22
18	Quantitative Structureâ€“Property Relationship Studies on Ostwald Solubility and Partition Coefficients of Organic Solutes in Ionic Liquids. Journal of Chemical & Engineering Data, 2008, 53, 1085-1092.	1.9	25

#	Article	IF	Citations
19	Synthesis and bioassay of improved mosquito repellents predicted from chemical structure. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7359-7364.	7.1	89