Suwipa Saen-Oon

List of Publications by Year
in descending order

23 papers	605 citations	687363 13 h-index	713466 21 g-index
24 all docs	24 docs citations	24 times ranked	789 citing authors

#	Article	IF	Citations
1	Î”⁹â€Tetrahydrocannabinolic acid alleviates collagenâ€induced arthritis: Role of PPARÎ³ and CB₁ receptors. British Journal of Pharmacology, 2020, 177, 4034-4054.	5.4	16
2	Monte Carlo simulations using PELE to identify a proteinâ€“protein inhibitor binding site and pose. RSC Advances, 2020, 10, 7058-7064.	3.6	7
3	Atomistic simulations shed new light on the activation mechanisms of RORÎ³ and classify it as Type III nuclear hormone receptor regarding ligand-binding paths. Scientific Reports, 2019, 9, 17249.	3.3	9
4	Computational structureâ€based drug design: Predicting target flexibility. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2018, 8, e1367.	14.6	13
5	A theoretical multiscale treatment of proteinâ€“protein electron transfer: The ferredoxin/ferredoxin-NADP+ reductase and flavodoxin/ferredoxin-NADP+ reductase systems. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 1530-1538.	1.0	10
6	An Alternative Mechanism for the Methylation of Phosphoethanolamine Catalyzed by Plasmodium falciparum Phosphoethanolamine Methyltransferase*. Journal of Biological Chemistry, 2014, 289, 33815-33825.	3.4	12
7	Electron transfer in proteins: theory, applications and future perspectives. Physical Chemistry Chemical Physics, 2013, 15, 15271.	2.8	28
8	Using QM/MM Methods for the Exploration of Electron Transfer Pathways. Current Inorganic Chemistry, 2012, 2, 263-272.	0.2	0
9	Petrosamine, a potent anticholinesterase pyridoacridine alkaloid from a Thai marine sponge Petrosia n. sp. Bioorganic and Medicinal Chemistry, 2008, 16, 6560-6567.	3.0	50
10	Remote Mutations and Active Site Dynamics Correlate with Catalytic Properties of Purine Nucleoside Phosphorylase. Biophysical Journal, 2008, 94, 4078-4088.	0.5	61
11	Insight into why pyrrolidinyl peptide nucleic acid binding to DNA is more stable than the DNAÂ·DNA duplex. Biochemical and Biophysical Research Communications, 2008, 372, 765-771.	2.1	24
12	Tryptophan-Free Human PNP Reveals Catalytic Site Interactions. Biochemistry, 2008, 47, 3202-3215.	2.5	26
13	Atomic detail of chemical transformation at the transition state of an enzymatic reaction. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16543-16548.	7.1	85
14	Transition Path Sampling Study of the Reaction Catalyzed by Purine Nucleoside Phosphorylase. Zeitschrift Fur Physikalische Chemie, 2008, 222, 1359-1374.	2.8	16
15	Vinyldeoxyadenosine in a Sarcinâ^'Ricin RNA Loop and Its Binding to Ricin Toxin A-Chain. Biochemistry, 2007, 46, 6169-6182.	2.5	6
16	Insight into analysis of interactions of saquinavir with HIV-1 protease in comparison between the wild-type and G48V and G48V/L90M mutants based on QM and QM/MM calculations. Journal of Molecular Graphics and Modelling, 2007, 26, 720-727.	2.4	24
17	Particular interaction between efavirenz and the HIV-1 reverse transcriptase binding site as explained by the ONIOM2 method. Chemical Physics Letters, 2005, 405, 198-202.	2.6	26
18	Binding energy analysis for wild-type and Y181C mutant HIV-1 RT/8-Cl TIBO complex structures: Quantum chemical calculations based on the ONIOM method. Proteins: Structure, Function and Bioinformatics, 2005, 61, 859-869.	2.6	45

#	Article	IF	Citations
19	Inhibition of Naja kaouthia venom activities by plant polyphenols. Journal of Ethnopharmacology, 2005, 97, 527-533.	4.1	74
20	Insights into Saquinavir Resistance in the G48V HIV-1 Protease: Quantum Calculations and Molecular Dynamic Simulations. Biophysical Journal, 2005, 88, 867-879.	0.5	55
21	Structural Flexibility of Non-Nucleoside HIV-1 Reverse Transcriptase Inhibitor: 9-Cl TIBO as Explained by Potential Energy Surface and13C and1H NMR Calculations, Based on ab initio and Density Functional Study.. ChemInform, 2003, 34, no.	0.0	0
22	Structural Flexibility of Non-Nucleoside HIV-1 Reverse Transcriptase Inhibitor:â€‰ 9-ClTIBOas Explained by Potential Energy Surface and13C and1H NMR Calculations, Based onab initioand Density Functional Study. Journal of Chemical Information and Computer Sciences, 2003, 43, 1412-1422.	2.8	12
23	Molecular Calculations on the Conformation of the HIV-1 Reverse Transcriptase Inhibitor (+)-() Tj ETQq1 1 0.784314 rgBT /Overlock 1	1.8	6