Teruki Honma

List of Publications by Year
in descending order

17	400	840776 11	888059 17
papers	citations	h-index	g-index

17	17	17	591
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural Insights into the Molecular Design of Flutolanil Derivatives Targeted for Fumarate Respiration of Parasite Mitochondria. International Journal of Molecular Sciences, 2015, 16, 15287-15308.	4.1	67
2	Construction of an integrated database for hERG blocking small molecules. PLoS ONE, 2018, 13, e0199348.	2.5	44
3	Discovery of Novel Spiroindoline Derivatives as Selective Tankyrase Inhibitors. Journal of Medicinal Chemistry, 2019, 62, 3407-3427.	6.4	43
4	Theoretical Analysis of Activity Cliffs among Benzofuranone-Class Pim1 Inhibitors Using the Fragment Molecular Orbital Method with Molecular Mechanics Poissonâ€“Boltzmann Surface Area (FMO+MM-PBSA) Approach. Journal of Chemical Information and Modeling, 2017, 57, 2996-3010.	5.4	41
5	Design and Discovery of an Orally Efficacious Spiroindolinone-Based Tankyrase Inhibitor for the Treatment of Colon Cancer. Journal of Medicinal Chemistry, 2020, 63, 4183-4204.	6.4	25
6	FMODB: The Worldâ€™s First Database of Quantum Mechanical Calculations for Biomacromolecules Based on the Fragment Molecular Orbital Method. Journal of Chemical Information and Modeling, 2021, 61, 777-794.	5.4	24
7	Structural basis of protein arginine rhamnosylation by glycosyltransferase EarP. Nature Chemical Biology, 2018, 14, 368-374.	8.0	22
8	Intermolecular interaction among Remdesivir, RNA and RNA-dependent RNA polymerase of SARS-CoV-2 analyzed by fragment molecular orbital calculation. Journal of Molecular Graphics and Modelling, 2020, 100, 107695.	2.4	22
9	High-Precision Atomic Charge Prediction for Protein Systems Using Fragment Molecular Orbital Calculation and Machine Learning. Journal of Chemical Information and Modeling, 2020, 60, 3361-3368.	5.4	22
10	Intermolecular Interaction Analyses on SARS-CoV-2 Spike Protein Receptor Binding Domain and Human Angiotensin-Converting Enzyme 2 Receptor-Blocking Antibody/Peptide Using Fragment Molecular Orbital Calculation. Journal of Physical Chemistry Letters, 2021, 12, 4059-4066.	4.6	22
11	Protein ligand interaction analysis against new CaMKK2 inhibitors by use of X-ray crystallography and the fragment molecular orbital (FMO) method. Journal of Molecular Graphics and Modelling, 2020, 99, 107599.	2.4	19
12	Structural Basis of Activin Receptor-Like Kinase 2 (R206H) Inhibition by Bis-heteroaryl Pyrazole-Based Inhibitors for the Treatment of Fibrodysplasia Ossificans Progressiva Identified by the Integration of Ligand-Based and Structure-Based Drug Design Approaches. ACS Omega, 2020, 5, 11411-11423.	3.5	11
13	Special Features of COVID-19 in the FMODB: Fragment Molecular Orbital Calculations and Interaction Energy Analysis of SARS-CoV-2-Related Proteins. Journal of Chemical Information and Modeling, 2021, 61, 4594-4612.	5.4	10
14	Activity cliff for 7-substituted pyrrolo-pyrimidine inhibitors of HCK explained in terms of predicted basicity of the amine nitrogen. Bioorganic and Medicinal Chemistry, 2017, 25, 4259-4264.	3.0	9
15	Design and Synthesis of Tranylcypromine-Derived LSD1 Inhibitors with Improved hERG and Microsomal Stability Profiles. ACS Medicinal Chemistry Letters, 2022, 13, 848-854.	2.8	9
16	A publicâ€“private partnership to enrich the development of in silico predictive models for pharmacokinetic and cardiotoxic properties. Drug Discovery Today, 2021, 26, 1275-1283.	6.4	7
17	Bioisostere Identification by Determining the Amino Acid Binding Preferences of Common Chemical Fragments. Journal of Chemical Information and Modeling, 2017, 57, 2938-2947.	5.4	3