Peter Man-Un Ung

List of Publications by Year
in descending order

34 papers	1,704 citations	331670 21 h-index	377865 34 g-index
35 all docs	35 docs citations	35 times ranked	2879 citing authors

#	Article	IF	Citations
1	Automated genome mining for natural products. BMC Bioinformatics, 2009, 10, 185.	2.6	219
2	SLC transporters: structure, function, and drug discovery. MedChemComm, 2016, 7, 1069-1081.	3.4	152
3	Binding of a Small Molecule at a Proteinâ€“Protein Interface Regulates the Chaperone Activity of Hsp70â€“Hsp40. ACS Chemical Biology, 2010, 5, 611-622.	3.4	149
4	CSAR Benchmark Exercise of 2010: Selection of the Proteinâ€“Ligand Complexes. Journal of Chemical Information and Modeling, 2011, 51, 2036-2046.	5.4	133
5	CSAR Benchmark Exercise of 2010: Combined Evaluation Across All Submitted Scoring Functions. Journal of Chemical Information and Modeling, 2011, 51, 2115-2131.	5.4	133
6	Molecular Basis for Redox Activation of Epidermal Growth Factor Receptor Kinase. Cell Chemical Biology, 2016, 23, 837-848.	5.2	100
7	Chemical Screens against a Reconstituted Multiprotein Complex: Myricetin Blocks DnaJ Regulation of DnaK through an Allosteric Mechanism. Chemistry and Biology, 2011, 18, 210-221.	6.0	94
8	Redefining the Protein Kinase Conformational Space with Machine Learning. Cell Chemical Biology, 2018, 25, 916-924.e2.	5.2	65
9	Mutagenesis Reveals the Complex Relationships between ATPase Rate and the Chaperone Activities of Escherichia coli Heat Shock Protein 70 (Hsp70/DnaK). Journal of Biological Chemistry, 2010, 285, 21282-21291.	3.4	62
10	A whole-animal platform to advance a clinical kinase inhibitor into new disease space. Nature Chemical Biology, 2018, 14, 291-298.	8.0	56
11	Inhibitor Discovery for the Human GLUT1 from Homology Modeling and Virtual Screening. ACS Chemical Biology, 2016, 11, 1908-1916.	3.4	49
12	Identifying binding hot spots on protein surfaces by mixedâ€solvent molecular dynamics: HIVâ€1 protease as a test case. Biopolymers, 2016, 105, 21-34.	2.4	40
13	A poke in the eye: Inhibiting HIVâ€1 protease through its flapâ€recognition pocket. Biopolymers, 2008, 89, 643-652.	2.4	39
14	An IRAK1â€“PIN1 signalling axis drives intrinsic tumour resistance to radiation therapy. Nature Cell Biology, 2019, 21, 203-213.	10.3	38
15	DFGmodel: Predicting Protein Kinase Structures in Inactive States for Structure-Based Discovery of Type-II Inhibitors. ACS Chemical Biology, 2015, 10, 269-278.	3.4	37
16	Novel selective thiadiazine DYRK1A inhibitor lead scaffold with human pancreatic Î²-cell proliferation activity. European Journal of Medicinal Chemistry, 2018, 157, 1005-1016.	5.5	36
17	Chemical Probes That Selectively Recognize the Earliest AÎ² Oligomers in Complex Mixtures. Journal of the American Chemical Society, 2010, 132, 17655-17657.	13.7	33
18	Exploiting Allosteric Properties of RAF and MEK Inhibitors to Target Therapy-Resistant Tumors Driven by Oncogenic BRAF Signaling. Cancer Discovery, 2021, 11, 1716-1735.	9.4	30

#	Article	IF	Citations
19	KinaMetrix: a web resource to investigate kinase conformations and inhibitor space. Nucleic Acids Research, 2019, 47, D361-D366.	14.5	28
20	Structures of ligand-occupied Î²-Klotho complexes reveal a molecular mechanism underlying endocrine FGF specificity and activity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7819-7824.	7.1	27
21	High-Resolution Structure and Inhibition of the Schizophrenia-Linked Pseudokinase ULK4. Journal of the American Chemical Society, 2020, 142, 33-37.	13.7	24
22	An Allosteric Modulator of HIV-1 Protease Shows Equipotent Inhibition of Wild-Type and Drug-Resistant Proteases. Journal of Medicinal Chemistry, 2014, 57, 6468-6478.	6.4	23
23	Identification of Key Hinge Residues Important for Nucleotide-Dependent Allostery in E. coli Hsp70/DnaK. PLoS Computational Biology, 2013, 9, e1003279.	3.2	20
24	Identification of a G-Protein-Independent Activator of GIRK Channels. Cell Reports, 2020, 31, 107770.	6.4	20
25	GEN3VA: aggregation and analysis of gene expression signatures from related studies. BMC Bioinformatics, 2016, 17, 461.	2.6	17
26	E230Q mutation of the catalytic subunit of cAMP-dependent protein kinase affects local structure and the binding of peptide inhibitor. Biopolymers, 2006, 81, 428-439.	2.4	15
27	Encounter and React: Computer-Guided Design of Covalent Inhibitors. Cell Chemical Biology, 2019, 26, 6-8.	5.2	14
28	Functional and structural analysis of rare SLC2A2 variants associated with Fanconiâ€Bickel syndrome and metabolic traits. Human Mutation, 2019, 40, 983-995.	2.5	13
29	Role of the CCAAT/Enhancer-binding Protein NFATc2 Transcription Factor Cascade in the Induction of Secretory Phospholipase A2. Journal of Biological Chemistry, 2006, 281, 11541-11552.	3.4	10
30	Integrated computational and Drosophila cancer model platform captures previously unappreciated chemicals perturbing a kinase network. PLoS Computational Biology, 2019, 15, e1006878.	3.2	10
31	Systems Pharmacology: An Overview. AAPS Advances in the Pharmaceutical Sciences Series, 2016, , 53-80.	0.6	7
32	Type II Binders Targeting the â€œGLR-Outâ€•Conformation of the Pseudokinase STRADÎ±. Biochemistry, 2021, 60, 289-302.	2.5	6
33	Correction to CSAR Benchmark Exercise of 2010: Selection of the Proteinâ€“Ligand Complexes. Journal of Chemical Information and Modeling, 2011, 51, 2146-2146.	5.4	4
34	DFGmodel: Predicting Protein Kinase Structures in Inactive States for Structure-Based Discovery of Type-II Inhibitors. Biophysical Journal, 2015, 108, 474a.	0.5	1