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	Type II Binders Targeting the "GLR-Out" Conformation of the Pseudokinase STRADα. Biochemistry, 2021, 60, 289-302.	2.5	6
2	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
3	High-Resolution Structure and Inhibition of the Schizophrenia-Linked Pseudokinase ULK4. Journal of the American Chemical Society, 2020, 142, 33-37.	13.7	24
4	Identification of a G-Protein-Independent Activator of GIRK Channels. Cell Reports, 2020, 31, 107770.	6.4	20
5	An IRAK1–PIN1 signalling axis drives intrinsic tumour resistance to radiation therapy. Nature Cell Biology, 2019, 21, 203-213.	10.3	38
6	Integrated computational and Drosophila cancer model platform captures previously unappreciated chemicals perturbing a kinase network. PLoS Computational Biology, 2019, 15, e1006878.	3.2	10
7	Structures of ligand-occupied β-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
8	Functional and structural analysis of rare SLC2A2 variants associated with Fanconi–Bickel syndrome and metabolic traits. Human Mutation, 2019, 40, 983-995.	2.5	13
9	Encounter and React: Computer-Guided Design of Covalent Inhibitors. Cell Chemical Biology, 2019, 26, 6-8.	5.2	14
10	KinaMetrix: a web resource to investigate kinase conformations and inhibitor space. Nucleic Acids Research, 2019, 47, D361-D366.	14.5	28
11	A whole-animal platform to advance a clinical kinase inhibitor into new disease space. Nature Chemical Biology, 2018, 14, 291-298.	8.0	56
12	Redefining the Protein Kinase Conformational Space with Machine Learning. Cell Chemical Biology, 2018, 25, 916-924.e2.	5.2	65
13	Novel selective thiadiazine DYRK1A inhibitor lead scaffold with human pancreatic β-cell proliferation activity. European Journal of Medicinal Chemistry, 2018, 157, 1005-1016.	5.5	36
14	Systems Pharmacology: An Overview. AAPS Advances in the Pharmaceutical Sciences Series, 2016, , 53-80.	0.6	7
15	Inhibitor Discovery for the Human GLUT1 from Homology Modeling and Virtual Screening. ACS Chemical Biology, 2016, 11, 1908-1916.	3.4	49
16	Identifying binding hot spots on protein surfaces by mixed-solvent molecular dynamics: HIV-1 protease as a test case. Biopolymers, 2016, 105, 21-34.	2.4	40
17	Molecular Basis for Redox Activation of Epidermal Growth Factor Receptor Kinase. Cell Chemical Biology, 2016, 23, 837-848.	5.2	100
18	GEN3VA: aggregation and analysis of gene expression signatures from related studies. BMC Bioinformatics, 2016, 17, 461.	2.6	17

#	Article	IF	Citations
19	SLC transporters: structure, function, and drug discovery. MedChemComm, 2016, 7, 1069-1081.	3.4	152
20	DFGmodel: Predicting Protein Kinase Structures in Inactive States for Structure-Based Discovery of Type-II Inhibitors. Biophysical Journal, 2015, 108, 474a.	0.5	1
21	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
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	CSAR Benchmark Exercise of 2010: Selection of the Protein–Ligand Complexes. Journal of Chemical Information and Modeling, 2011, 51, 2036-2046.	5.4	133
25	Correction to CSAR Benchmark Exercise of 2010: Selection of the Protein–Ligand Complexes. Journal of Chemical Information and Modeling, 2011, 51, 2146-2146.	5.4	4
26	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
27	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
28	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
29	Chemical Probes That Selectively Recognize the Earliest $A\beta$ Oligomers in Complex Mixtures. Journal of the American Chemical Society, 2010, 132, 17655-17657.	13.7	33
30	Binding of a Small Molecule at a Protein–Protein Interface Regulates the Chaperone Activity of Hsp70–Hsp40. ACS Chemical Biology, 2010, 5, 611-622.	3.4	149
31	Automated genome mining for natural products. BMC Bioinformatics, 2009, 10, 185.	2.6	219
32	A poke in the eye: Inhibiting HIV-1 protease through its flap-recognition pocket. Biopolymers, 2008, 89, 643-652.	2.4	39
33	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
34	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