

Wen Hwa Lee

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43
papers

2,261
citations

24
h-index

45
g-index

45
ext. papers

2,544
ext. citations

8.3
avg, IF

4.11
L-index

#	Paper	IF	Citations
43	Large-scale structural analysis of the classical human protein tyrosine phosphatome. <i>Cell</i> , 2009 , 136, 352-63	56.2	344
42	Structural basis for protein-protein interactions in the 14-3-3 protein family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 17237-42	11.5	240
41	Structural and biochemical characterization of the human cyclophilin family of peptidyl-prolyl isomerases. <i>PLoS Biology</i> , 2010 , 8, e1000439	9.7	170
40	Structure of the CaMKII δ /calmodulin complex reveals the molecular mechanism of CaMKII kinase activation. <i>PLoS Biology</i> , 2010 , 8, e1000426	9.7	167
39	Fast structure-based virtual ligand screening combining FRED, DOCK, and Surflex. <i>Journal of Medicinal Chemistry</i> , 2005 , 48, 6012-22	8.3	96
38	Crystal Structures of the p21-activated kinases PAK4, PAK5, and PAK6 reveal catalytic domain plasticity of active group II PAKs. <i>Structure</i> , 2007 , 15, 201-13	5.2	95
37	Comparative structural analysis of lipid binding START domains. <i>PLoS ONE</i> , 2011 , 6, e19521	3.7	94
36	Reduced phosphatase activity of SHP-2 in LEOPARD syndrome: consequences for PI3K binding on Gab1. <i>FEBS Letters</i> , 2006 , 580, 2477-82	3.8	78
35	Structural basis for low catalytic activity in Lys49 phospholipases A2--a hypothesis: the crystal structure of piratoxin II complexed to fatty acid. <i>Biochemistry</i> , 2001 , 40, 28-36	3.2	73
34	Structural and biochemical characterization of human orphan DHRS10 reveals a novel cytosolic enzyme with steroid dehydrogenase activity. <i>Biochemical Journal</i> , 2007 , 402, 419-27	3.8	69
33	Crystal structure of the PIM2 kinase in complex with an organoruthenium inhibitor. <i>PLoS ONE</i> , 2009 , 4, e7112	3.7	66
32	Novel mutations in ACVR1 result in atypical features in two fibrodysplasia ossificans progressiva patients. <i>PLoS ONE</i> , 2009 , 4, e5005	3.7	62
31	The scientific impact of the Structural Genomics Consortium: a protein family and ligand-centered approach to medically-relevant human proteins. <i>Journal of Structural and Functional Genomics</i> , 2007 , 8, 107-19		55
30	Structural basis of fumarate hydratase deficiency. <i>Journal of Inherited Metabolic Disease</i> , 2011 , 34, 671-65.4		52
29	Characterization of human DHRS6, an orphan short chain dehydrogenase/reductase enzyme: a novel, cytosolic type 2 R-beta-hydroxybutyrate dehydrogenase. <i>Journal of Biological Chemistry</i> , 2006 , 281, 10291-7	5.4	51
28	Crystal structures and inhibitor identification for PTPN5, PTPRR and PTPN7: a family of human MAPK-specific protein tyrosine phosphatases. <i>Biochemical Journal</i> , 2006 , 395, 483-91	3.8	48
27	Structural basis for substrate specificity in human monomeric carbonyl reductases. <i>PLoS ONE</i> , 2009 , 4, e7113	3.7	43

26	The Kaposi's sarcoma-associated herpesvirus complement control protein (KCP) binds to heparin and cell surfaces via positively charged amino acids in CCP1-2. <i>Molecular Immunology</i> , 2006 , 43, 1665-75	4.3	41
25	Preclinical target validation using patient-derived cells. <i>Nature Reviews Drug Discovery</i> , 2015 , 14, 149-50	64.1	40
24	Disseminating structural genomics data to the public: from a data dump to an animated story. <i>Trends in Biochemical Sciences</i> , 2006 , 31, 76-8	10.3	38
23	Structural comparison of human mammalian ste20-like kinases. <i>PLoS ONE</i> , 2010 , 5, e11905	3.7	36
22	The Kaposi's sarcoma-associated herpesvirus complement control protein mimics human molecular mechanisms for inhibition of the complement system. <i>Journal of Biological Chemistry</i> , 2004 , 279, 45093-101	5.4	34
21	Structural basis for different specificities of acyltransferases associated with the human cytosolic and mitochondrial fatty acid synthases. <i>Chemistry and Biology</i> , 2009 , 16, 667-75		25
20	Molecular models of the procoagulant factor VIIIa-factor IXa complex. <i>Journal of Thrombosis and Haemostasis</i> , 2005 , 3, 2044-56	15.4	25
19	A structural mapping of mutations causing succinyl-CoA:3-ketoacid CoA transferase (SCOT) deficiency. <i>Journal of Inherited Metabolic Disease</i> , 2013 , 36, 983-7	5.4	20
18	Inhibitory member of the apoptosis-stimulating proteins of the p53 family (iASPP) interacts with protein phosphatase 1 via a noncanonical binding motif. <i>Journal of Biological Chemistry</i> , 2011 , 286, 43039-44	5.4	20
17	Open Access Could Transform Drug Discovery: A Case Study of JQ1. <i>Expert Opinion on Drug Discovery</i> , 2016 , 11, 321-32	6.2	19
16	Characterization of 14-3-3 proteins from <i>Cryptosporidium parvum</i> . <i>PLoS ONE</i> , 2011 , 6, e14827	3.7	19
15	Crystal structures of malonyl-coenzyme A decarboxylase provide insights into its catalytic mechanism and disease-causing mutations. <i>Structure</i> , 2013 , 21, 1182-92	5.2	16
14	Open access target validation is a more efficient way to accelerate drug discovery. <i>PLoS Biology</i> , 2015 , 13, e1002164	9.7	16
13	SGC--structural biology and human health: a new approach to publishing structural biology results. <i>PLoS ONE</i> , 2009 , 4, e7675	3.7	14
12	Structure-activity relationships of human AKR-type oxidoreductases involved in bile acid synthesis: AKR1D1 and AKR1C4. <i>Molecular and Cellular Endocrinology</i> , 2009 , 301, 199-204	4.4	14
11	Noonan syndrome type I with PTPN11 3 bp deletion: structure-function implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 7-13	4.2	13
10	Comparison of different crystal forms of 3-dehydroquinase from <i>Salmonella typhi</i> and its implication for the enzyme activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 798-804		12
9	Structural genomics of histone tail recognition. <i>Bioinformatics</i> , 2010 , 26, 2629-30	7.2	9

8	Establishing a reliable framework for harnessing the creative power of the scientific crowd. <i>PLoS Biology</i> , 2017 , 15, e2001387	9.7	8
7	The SGC beyond structural genomics: redefining the role of 3D structures by coupling genomic stratification with fragment-based discovery. <i>Essays in Biochemistry</i> , 2017 , 61, 495-503	7.6	8
6	Emerging therapies and their delivery for treating age-related macular degeneration. <i>British Journal of Pharmacology</i> , 2021 ,	8.6	6
5	Role of protein structure in variant annotation: structural insight of mutations causing 6-pyruvoyl-tetrahydropterin synthase deficiency. <i>Pathology</i> , 2019 , 51, 274-280	1.6	4
4	Analysis of the structural determinants for RNA binding of the human protein AUF1/hnRNP D. <i>Biological Chemistry</i> , 2002 , 383, 831-7	4.5	4
3	Crystallization and preliminary diffraction data of neurotoxin Ts-gamma from the venom of the scorpion <i>Tityus serrulatus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1440-1		2
2	Inhibition of $\alpha\beta\beta$ Ligand Binding by an $\alpha\beta$ Peptide that Clasps the Hybrid Domain to the β Domain of β . <i>PLoS ONE</i> , 2015 , 10, e0134952	3.7	1
1	Crystallization and preliminary X-ray diffraction studies of piratoxin II, a phospholipase A2 isolated from the venom of <i>Bothrops pirajai</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1437-9		1