

Wen Hwa Lee

List of Publications by Year in descending order

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45
papers

2,792
citations

236912

25
h-index

243610

44
g-index

45
all docs

45
docs citations

45
times ranked

4965
citing authors

#	ARTICLE	IF	CITATIONS
1	Large-Scale Structural Analysis of the Classical Human Protein Tyrosine Phosphatome. <i>Cell</i> , 2009, 136, 352-363.	28.9	421
2	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, 17237-17242.	7.1	340
3	Structural and Biochemical Characterization of the Human Cyclophilin Family of Peptidyl-Prolyl Isomerases. <i>PLoS Biology</i> , 2010, 8, e1000439.	5.6	226
4	Structure of the CaMKII β /Calmodulin Complex Reveals the Molecular Mechanism of CaMKII Kinase Activation. <i>PLoS Biology</i> , 2010, 8, e1000426.	5.6	213
5	Comparative Structural Analysis of Lipid Binding START Domains. <i>PLoS ONE</i> , 2011, 6, e19521.	2.5	117
6	Fast Structure-Based Virtual Ligand Screening Combining FRED, DOCK, and Surflex. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 6012-6022.	6.4	106
7	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, 201-213.	3.3	105
8	Reduced phosphatase activity of SHP2 in LEOPARD syndrome: Consequences for PI3K binding on Gab1. <i>FEBS Letters</i> , 2006, 580, 2477-2482.	2.8	91
9	Structural Basis for Low Catalytic Activity in Lys49 Phospholipases A2A Hypothesis: The Crystal Structure of Piratoxin II Complexed to Fatty Acid. <i>Biochemistry</i> , 2001, 40, 28-36.	2.5	84
10	Structural and biochemical characterization of human orphan DHRS10 reveals a novel cytosolic enzyme with steroid dehydrogenase activity. <i>Biochemical Journal</i> , 2007, 402, 419-427.	3.7	79
11	Crystal Structure of the PIM2 Kinase in Complex with an Organoruthenium Inhibitor. <i>PLoS ONE</i> , 2009, 4, e7112.	2.5	79
12	Novel Mutations in ACVR1 Result in Atypical Features in Two Fibrodysplasia Ossificans Progressiva Patients. <i>PLoS ONE</i> , 2009, 4, e5005.	2.5	78
13	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, 107-119.	1.2	66
14	Structural basis of fumarate hydratase deficiency. <i>Journal of Inherited Metabolic Disease</i> , 2011, 34, 671-676.	3.6	66
15	Characterization of Human DHRS6, an Orphan Short Chain Dehydrogenase/Reductase Enzyme. <i>Journal of Biological Chemistry</i> , 2006, 281, 10291-10297.	3.4	60
16	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, 483-491.	3.7	59
17	Structural Basis for Substrate Specificity in Human Monomeric Carbonyl Reductases. <i>PLoS ONE</i> , 2009, 4, e7113.	2.5	47
18	Preclinical target validation using patient-derived cells. <i>Nature Reviews Drug Discovery</i> , 2015, 14, 149-150.	46.4	46

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19	Structural Comparison of Human Mammalian Ste20-Like Kinases. <i>PLoS ONE</i> , 2010, 5, e11905.	2.5	46
20	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, 1665-1675.	2.2	42
21	Disseminating structural genomics data to the public: from a data dump to an animated story. <i>Trends in Biochemical Sciences</i> , 2006, 31, 76-78.	7.5	42
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, 45093-45101.	3.4	35
23	Molecular models of the procoagulant Factor VIIIa-Factor IXa complex. <i>Journal of Thrombosis and Haemostasis</i> , 2005, 3, 2044-2056.	3.8	31
24	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, 43039-43044.	3.4	31
25	Structural Basis for Different Specificities of Acyltransferases Associated with the Human Cytosolic and Mitochondrial Fatty Acid Synthases. <i>Chemistry and Biology</i> , 2009, 16, 667-675.	6.0	29
26	Open Access Could Transform Drug Discovery: A Case Study of JQ1. <i>Expert Opinion on Drug Discovery</i> , 2016, 11, 321-332.	5.0	28
27	A structural mapping of mutations causing succinyl-CoA:3-ketoacid CoA transferase (SCOT) deficiency. <i>Journal of Inherited Metabolic Disease</i> , 2013, 36, 983-987.	3.6	24
28	Emerging therapies and their delivery for treating age-related macular degeneration. <i>British Journal of Pharmacology</i> , 2022, 179, 1908-1937.	5.4	23
29	Characterization of 14-3-3 Proteins from <i>Cryptosporidium parvum</i> . <i>PLoS ONE</i> , 2011, 6, e14827.	2.5	21
30	Open Access Target Validation Is a More Efficient Way to Accelerate Drug Discovery. <i>PLoS Biology</i> , 2015, 13, e1002164.	5.6	20
31	Crystal Structures of Malonyl-Coenzyme A Decarboxylase Provide Insights into Its Catalytic Mechanism and Disease-Causing Mutations. <i>Structure</i> , 2013, 21, 1182-1192.	3.3	17
32	SGC - Structural Biology and Human Health: A New Approach to Publishing Structural Biology Results. <i>PLoS ONE</i> , 2009, 4, e7675.	2.5	16
33	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.	2.5	15
34	Noonan syndrome type I with <i>PTPN11</i> 3 bp deletion: Structure-function implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 58, 7-13.	2.6	15
35	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.	3.2	15
36	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.	4.7	12

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37	Establishing a reliable framework for harnessing the creative power of the scientific crowd. <i>PLoS Biology</i> , 2017, 15, e2001387.	5.6	10
38	Structural genomics of histone tail recognition. <i>Bioinformatics</i> , 2010, 26, 2629-2630.	4.1	9
39	Accelerating target discovery using pre-competitive open science“ patients need faster innovation more than anyone else. <i>Ecanermedalscience</i> , 2016, 10, ed57.	1.1	7
40	Role of protein structure in variant annotation: structural insight of mutations causing 6-pyruvoyl-tetrahydropterin synthase deficiency. <i>Pathology</i> , 2019, 51, 274-280.	0.6	7
41	Interactive JIMD articles using the iSee concept: turning a new page on structural biology data. <i>Journal of Inherited Metabolic Disease</i> , 2011, 34, 565-567.	3.6	6
42	Analysis of the Structural Determinants for RNA Binding of the Human Protein AUF1/hnRNP D. <i>Biological Chemistry</i> , 2002, 383, 831-837.	2.5	4
43	Crystallization and preliminary diffraction data of neurotoxin Ts-Î³ from the venom of the scorpion <i>Tityus serrulatus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1440-1441.	2.5	2
44	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, 1437-1439.	2.5	1
45	Inhibition of Î±IIbÎ²3 Ligand Binding by an Î±IIb Peptide that Clasps the Hybrid Domain to the Î²I Domain of Î²3. <i>PLoS ONE</i> , 2015, 10, e0134952.	2.5	1