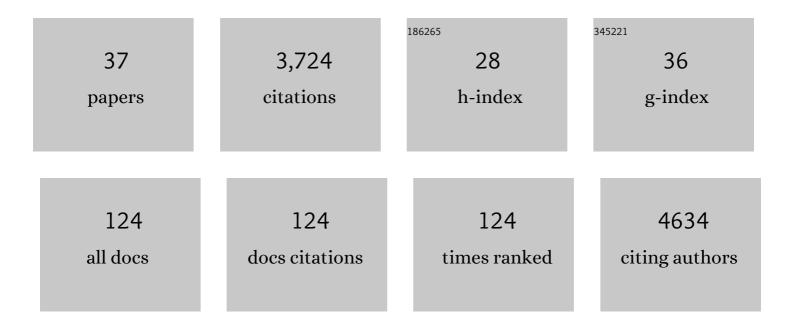
Xiayang Qiu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Lysosomal integral membrane protein-2 as a phospholipid receptor revealed by biophysical and cellular studies. Nature Communications, 2017, 8, 1908.	12.8	43
2	HDL surface lipids mediate CETP binding as revealed by electron microscopy and molecular dynamics simulation. Scientific Reports, 2015, 5, 8741.	3.3	48
3	Structural basis for allosteric, substrate-dependent stimulation of SIRT1 activity by resveratrol. Genes and Development, 2015, 29, 1316-1325.	5.9	179
4	Optimizing glucokinase activator binding kinetics to lower in vivo hypoglycemia risk. MedChemComm, 2014, 5, 802-807.	3.4	9
5	Structural Basis for AMPK Activation: Natural and Synthetic Ligands Regulate Kinase Activity from Opposite Poles by Different Molecular Mechanisms. Structure, 2014, 22, 1161-1172.	3.3	159
6	Insights into Mechanism of Glucokinase Activation. Journal of Biological Chemistry, 2012, 287, 13598-13610.	3.4	53
7	Crystal Structures of Cholesteryl Ester Transfer Protein in Complex with Inhibitors. Journal of Biological Chemistry, 2012, 287, 37321-37329.	3.4	63
8	Structural basis of transfer between lipoproteins by cholesteryl ester transfer protein. Nature Chemical Biology, 2012, 8, 342-349.	8.0	123
9	Designing glucokinase activators with reduced hypoglycemia risk: discovery of N,N-dimethyl-5-(2-methyl-6-((5-methylpyrazin-2-yl)-carbamoyl)benzofuran-4-yloxy)pyrimidine-2-carboxamide as a clinical candidate for the treatment of type 2 diabetes mellitus. MedChemComm, 2011, 2, 828.	3.4	62
10	Structural and biophysical insight into cholesteryl ester-transfer protein. Biochemical Society Transactions, 2011, 39, 1000-1005.	3.4	11
11	Assessment of cholesteryl ester transfer protein inhibitors for interaction with proteins involved in the immune response to infection. Journal of Lipid Research, 2010, 51, 967-974.	4.2	26
12	SRT1720, SRT2183, SRT1460, and Resveratrol Are Not Direct Activators of SIRT1. Journal of Biological Chemistry, 2010, 285, 8340-8351.	3.4	794
13	Escherichia coli expression, purification and characterization of functional full-length recombinant α2β2γ3 heterotrimeric complex of human AMP-activated protein kinase. Protein Expression and Purification, 2010, 73, 189-197.	1.3	21

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#	Article	IF	CITATIONS
19	Structure of apo acyl carrier protein and a proposal to engineer protein crystallization through metal ions. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1545-1554.	2.5	43
20	Indole Naphthyridinones as Inhibitors of Bacterial Enoyl-ACP Reductases FabI and FabK. Journal of Medicinal Chemistry, 2003, 46, 1627-1635.	6.4	152
21	Discovery of a Novel and Potent Class of Fabl-Directed Antibacterial Agents. Antimicrobial Agents and Chemotherapy, 2002, 46, 3118-3124.	3.2	162
22	Discovery of Aminopyridine-Based Inhibitors of Bacterial Enoyl-ACP Reductase (FabI). Journal of Medicinal Chemistry, 2002, 45, 3246-3256.	6.4	111
23	Refined structures of β-ketoacyl-acyl carrier protein synthase III. Journal of Molecular Biology, 2001, 307, 341-356.	4.2	154
24	1,4-Disubstituted imidazoles are potential antibacterial agents functioning as inhibitors of enoyl acyl carrier protein reductase (Fabl). Bioorganic and Medicinal Chemistry Letters, 2001, 11, 2061-2065.	2.2	120
25	Inhibitors of bacterial enoyl acyl carrier protein reductase (FabI): 2,9-disubstituted 1,2,3,4-tetrahydropyrido[3,4-b]indoles as potential antibacterial agents. Bioorganic and Medicinal Chemistry Letters, 2001, 11, 2241-2244.	2.2	65
26	Crystallization ofEscherichia coliβ-ketoacyl-ACP synthase III and the use of a dry flash-cooling technique for data collection. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 747-748.	2.5	5
27	Expression, Purification, and Crystallization of the Escherichia coli Selenomethionyl β-Ketoacyl–Acyl Carrier Protein Synthase III. Biochemical and Biophysical Research Communications, 2000, 270, 100-107.	2.1	21
28	Crystal Structure of β-Ketoacyl-Acyl Carrier Protein Synthase III. Journal of Biological Chemistry, 1999, 274, 36465-36471.	3.4	133
29	Cooperative Structural Dynamics and a Novel Fidelity Mechanism in Histidyl-tRNA Synthetases‡. Biochemistry, 1999, 38, 12296-12304.	2.5	31
30	Molecular basis for triclosan activity involves a flipping loop in the active site. Protein Science, 1999, 8, 2529-2532.	7.6	99
31	Human Herpesvirus Proteases. , 1999, , 93-115.		3
32	Active Site Cavity of Herpesvirus Proteases Revealed by the Crystal Structure of Herpes Simplex Virus Protease/Inhibitor Complex‡. Biochemistry, 1997, 36, 14023-14029.	2.5	72
33	Crystal structure of human osteoclast cathepsin K complex with E-64. Nature Structural Biology, 1997, 4, 109-111.	9.7	109
34	Comparison of highâ€resolution structures of the diphtheria toxin repressor in complex with cobalt and zinc at the cationâ€anion binding site. Protein Science, 1997, 6, 1114-1118.	7.6	40
35	High-Resolution Structure of the Diphtheria Toxin Repressor Complexed with Cobalt and Manganese Reveals an SH3-like Third Domain and Suggests a Possible Role of Phosphate as Co-corepressorâ€,‡. Biochemistry, 1996, 35, 12292-12302.	2.5	94
36	Unique fold and active site in cytomegalovirus protease. Nature, 1996, 383, 275-279.	27.8	168

#	Article	IF	CITATIONS
37	Three-dimensional structure of the diphtheria toxin repressor in complex with divalent cation co-repressors. Structure, 1995, 3, 87-100.	3.3	133