

# Tzu-Ping Ko

## List of Publications by Citations

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126  
papers

2,749  
citations

27  
h-index

49  
g-index

136  
ext. papers

3,375  
ext. citations

6.4  
avg, IF

4.79  
L-index

#	Paper	IF	Citations
126	Structure, mechanism and function of prenyltransferases. <i>FEBS Journal</i> , <b>2002</b> , 269, 3339-54		315
125	The opportunistic marine pathogen <i>Vibrio parahaemolyticus</i> becomes virulent by acquiring a plasmid that expresses a deadly toxin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 10798-803	11.5	284
124	Structural insight into catalytic mechanism of PET hydrolase. <i>Nature Communications</i> , <b>2017</b> , 8, 2106	17.4	160
123	Bisphosphonates target multiple sites in both cis- and trans-prenyltransferases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 10022-7	11.5	150
122	Crystal structure of yeast cytosine deaminase. Insights into enzyme mechanism and evolution. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 19111-7	5.4	93
121	Crystal structures of undecaprenyl pyrophosphate synthase in complex with magnesium, isopentenyl pyrophosphate, and farnesyl thiopyrophosphate: roles of the metal ion and conserved residues in catalysis. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 20762-74	5.4	92
120	Structure and mechanism of <i>Helicobacter pylori</i> fucosyltransferase. A basis for lipopolysaccharide variation and inhibitor design. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 9973-9982	5.4	89
119	Mechanism of product chain length determination and the role of a flexible loop in <i>Escherichia coli</i> undecaprenyl-pyrophosphate synthase catalysis. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 47474-82	5.4	70
118	The refined crystal structure of an eel pout type III antifreeze protein RD1 at 0.62-Å resolution reveals structural microheterogeneity of protein and solvation. <i>Biophysical Journal</i> , <b>2003</b> , 84, 1228-37	2.9	68
117	Structural studies reveal the molecular mechanism of PETase. <i>FEBS Journal</i> , <b>2018</b> , 285, 3717-3723	5.7	62
116	Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 14381-46	11.5	58
115	Squalene synthase as a target for Chagas disease therapeutics. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1004114	7.6	54
114	Structural analysis of a glycoside hydrolase family 11 xylanase from <i>Neocallimastix patriciarum</i> : insights into the molecular basis of a thermophilic enzyme. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 11020-11028	5.4	49
113	Substrate binding mode and reaction mechanism of undecaprenyl pyrophosphate synthase deduced from crystallographic studies. <i>Protein Science</i> , <b>2004</b> , 13, 971-8	6.3	47
112	Catalytic mechanism revealed by the crystal structure of undecaprenyl pyrophosphate synthase in complex with sulfate, magnesium, and triton. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 29298-307	5.4	42
111	Structure of human erythrocyte catalase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2000</b> , 56, 241-5		41
110	Improving specific activity and thermostability of <i>Escherichia coli</i> phytase by structure-based rational design. <i>Journal of Biotechnology</i> , <b>2014</b> , 175, 1-6	3.7	38

109	Improving the catalytic performance of a GH11 xylanase by rational protein engineering. <i>Applied Microbiology and Biotechnology</i> , <b>2015</b> , 99, 9503-10	5.7	35
108	Structure, function and inhibition of ent-kaurene synthase from <i>Bradyrhizobium japonicum</i> . <i>Scientific Reports</i> , <b>2014</b> , 4, 6214	4.9	34
107	Phospholipases A2 from <i>Callosellasma rhodostoma</i> venom gland cloning and sequencing of 10 of the cDNAs, three-dimensional modelling and chemical modification of the major isozyme. <i>FEBS Journal</i> , <b>2000</b> , 267, 6684-91		34
106	Improving the specific activity of $\beta$ -mannanase from <i>Aspergillus niger</i> BK01 by structure-based rational design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 663-9	4	32
105	Structure and inhibition of tuberculosinol synthase and decaprenyl diphosphate synthase from <i>Mycobacterium tuberculosis</i> . <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 2892-6	16.4	32
104	Structural and functional analysis of <i>Bacillus subtilis</i> YisP reveals a role of its product in biofilm production. <i>Chemistry and Biology</i> , <b>2014</b> , 21, 1557-63		32
103	Diverse substrate recognition mechanism revealed by <i>Thermotoga maritima</i> Cel5A structures in complex with cellotetraose, cellobiose and mannotriose. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2011</b> , 1814, 1832-40	4	32
102	Structural perspectives of an engineered $\beta$ -1,4-xylanase with enhanced thermostability. <i>Journal of Biotechnology</i> , <b>2014</b> , 189, 175-82	3.7	29
101	<i>Staphylococcus aureus</i> protein SAUG1 acts as a uracil-DNA glycosylase inhibitor. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 1354-64	20.1	29
100	Dietary Flavonoids Luteolin and Quercetin Inhibit Migration and Invasion of Squamous Carcinoma through Reduction of Src/Stat3/S100A7 Signaling. <i>Antioxidants</i> , <b>2019</b> , 8,	7.1	29
99	Structural basis for fragmenting the exopolysaccharide of <i>Acinetobacter baumannii</i> by bacteriophage $\Delta$ B6 tailspike protein. <i>Scientific Reports</i> , <b>2017</b> , 7, 42711	4.9	26
98	Mechanism and inhibition of human UDP-GlcNAc 2-epimerase, the key enzyme in sialic acid biosynthesis. <i>Scientific Reports</i> , <b>2016</b> , 6, 23274	4.9	25
97	Structural insights into the catalytic mechanism of human squalene synthase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 231-41		25
96	Structure and Function of a "Head-to-Middle" Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , <b>2016</b> , 55, 4721-4	16.4	24
95	Structural insight into potential cold adaptation mechanism through a psychrophilic glycoside hydrolase family 10 endo- $\beta$ -1,4-xylanase. <i>Journal of Structural Biology</i> , <b>2016</b> , 193, 206-211	3.4	23
94	Crystal Structure Analysis of the Repair of Iron Centers Protein YtFE and Its Interaction with NO. <i>Chemistry - A European Journal</i> , <b>2016</b> , 22, 9768-76	4.8	23
93	Characterization and crystal structure of a thermostable glycoside hydrolase family 45 1,4- $\beta$ -D-glucanase from <i>Thielavia terrestris</i> . <i>Enzyme and Microbial Technology</i> , <b>2017</b> , 99, 32-37	3.8	22
92	The T4 phage DNA mimic protein Arn inhibits the DNA binding activity of the bacterial histone-like protein H-NS. <i>Journal of Biological Chemistry</i> , <b>2014</b> , 289, 27046-27054	5.4	21

91	Structures of Iridoid Synthase from <i>Cantharanthus roseus</i> with Bound NAD(+) , NADPH, or NAD(+) /10-Oxogeraniol: Reaction Mechanisms. <i>Angewandte Chemie - International Edition</i> , <b>2015</b> , 54, 15478-15482	16.4	18
90	Structural and mutagenetic analyses of a 1,3-1,4- $\beta$ -glucanase from <i>Paecilomyces thermophila</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 366-73	4	18
89	Enhanced Zearalenol Hydrolyzing Activity of a Mycoestrogen-Detoxifying Lactonase by Structure-Based Engineering. <i>ACS Catalysis</i> , <b>2016</b> , 6, 7657-7663	13.1	18
88	Structural insight into the electron transfer pathway of a self-sufficient P450 monooxygenase. <i>Nature Communications</i> , <b>2020</b> , 11, 2676	17.4	17
87	Structures of human MST3 kinase in complex with adenine, ADP and Mn <sup>2+</sup> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 145-54		17
86	"Head-to-Middle" and "Head-to-Tail" cis-Prenyl Transferases: Structure of Isosesquilavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 683-687	16.4	17
85	Crystal Structure and Potential Head-to-Middle Condensation Function of a $\gamma$ -Farnesyl Diphosphate Synthase. <i>ACS Omega</i> , <b>2017</b> , 2, 930-936	3.9	15
84	Crystal Structure of a Mycoestrogen-Detoxifying Lactonase from <i>Rhinocladiella mackenziei</i> : Molecular Insight into ZHD Substrate Selectivity. <i>ACS Catalysis</i> , <b>2018</b> , 8, 4294-4298	13.1	15
83	Functional and structural analyses of a 1,4- $\beta$ -endoglucanase from <i>Ganoderma lucidum</i> . <i>Enzyme and Microbial Technology</i> , <b>2016</b> , 86, 67-74	3.8	15
82	Structural Insights to the Heterotetrameric Interaction between the PirA and PirB Toxins and Activation of the Cry-Like Pore-Forming Domain. <i>Toxins</i> , <b>2019</b> , 11,	4.9	14
81	Current Progresses in Phytase Research: Three-Dimensional Structure and Protein Engineering. <i>ChemBioEng Reviews</i> , <b>2015</b> , 2, 76-86	5.2	14
80	Catalytic Role of Conserved Asparagine, Glutamine, Serine, and Tyrosine Residues in Isoprenoid Biosynthesis Enzymes. <i>ACS Catalysis</i> , <b>2018</b> , 8, 4299-4312	13.1	13
79	Crystal structure of vespid phospholipase A(1) reveals insights into the mechanism for cause of membrane dysfunction. <i>Insect Biochemistry and Molecular Biology</i> , <b>2016</b> , 68, 79-88	4.5	13
78	Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , <b>2016</b> , 11, 1362-71	4.9	13
77	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie - International Edition</i> , <b>2016</b> , 55, 4716-20	16.4	12
76	Using structural-based protein engineering to modulate the differential inhibition effects of SAUGI on human and HSV uracil DNA glycosylase. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 4440-9	20.1	11
75	Structural insights into the interaction between phytoplasmal effector causing phyllody 1 and MADS transcription factors. <i>Plant Journal</i> , <b>2019</b> , 100, 706-719	6.9	11
74	Structural basis of polyethylene glycol recognition by antibody. <i>Journal of Biomedical Science</i> , <b>2020</b> , 27, 12	13.3	11

73	Structure, Function, and Inhibition of Staphylococcus aureus Heptaprenyl Diphosphate Synthase. <i>ChemMedChem</i> , <b>2016</b> , 11, 1915-23	3.7	11
72	Structure and mechanism of an antibiotics-synthesizing 3-hydroxykynurenine C-methyltransferase. <i>Scientific Reports</i> , <b>2015</b> , 5, 10100	4.9	10
71	Structural analyses and yeast production of the E1,3-1,4-glucanase catalytic module encoded by the licB gene of Clostridium thermocellum. <i>Enzyme and Microbial Technology</i> , <b>2015</b> , 71, 1-7	3.8	10
70	Structures of the hyperthermophilic chromosomal protein Sac7d in complex with DNA decamers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2004</b> , 60, 1381-7		10
69	Structural insights to heterodimeric cis-prenyltransferases through yeast dehydrodolichyl diphosphate synthase subunit Nus1. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 515, 621-626	3.4	9
68	Use of Cryo-EM To Uncover Structural Bases of pH Effect and Cofactor Bispecificity of Ketol-Acid Reductoisomerase. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 6136-6140	16.4	9
67	NADH/NADPH bi-cofactor-utilizing and thermoactive ketol-acid reductoisomerase from Sulfolobus acidocaldarius. <i>Scientific Reports</i> , <b>2018</b> , 8, 7176	4.9	9
66	Enzymatic characterization and crystal structure analysis of Chlamydomonas reinhardtii dehydroascorbate reductase and their implications for oxidative stress. <i>Plant Physiology and Biochemistry</i> , <b>2017</b> , 120, 144-155	5.4	8
65	Distinct structural features of Rex-family repressors to sense redox levels in anaerobes and aerobes. <i>Journal of Structural Biology</i> , <b>2014</b> , 188, 195-204	3.4	8
64	Structural Basis of Fucosidase Inhibition by Iminocyclitols with Ki Values in the Micro- to Picomolar Range. <i>Angewandte Chemie</i> , <b>2010</b> , 122, 347-350	3.6	8
63	Structure and Function of a Head-to-Middle Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , <b>2016</b> , 128, 4799-4802	3.6	8
62	The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie - International Edition</i> , <b>2018</b> , 57, 15060-15064	16.4	8
61	Reduction in MnSOD promotes the migration and invasion of squamous carcinoma cells. <i>International Journal of Oncology</i> , <b>2019</b> , 54, 1639-1650	4.4	7
60	An Effective Neutralizing Antibody Against Influenza Virus H1N1 from Human B Cells. <i>Scientific Reports</i> , <b>2019</b> , 9, 4546	4.9	7
59	Versatile cis-isoprenyl Diphosphate Synthase Superfamily Members in Catalyzing Carbon-Carbon Bond Formation. <i>ACS Catalysis</i> , <b>2020</b> , 10, 4717-4725	13.1	7
58	Head-to-Head Prenyl Synthases in Pathogenic Bacteria. <i>ChemBioChem</i> , <b>2017</b> , 18, 985-991	3.8	6
57	Crystal structure of LepI, a multifunctional SAM-dependent enzyme which catalyzes pericyclic reactions in leporin biosynthesis. <i>Organic and Biomolecular Chemistry</i> , <b>2019</b> , 17, 2070-2076	3.9	6
56	Crystal structures of S-adenosylhomocysteine hydrolase from the thermophilic bacterium Thermotoga maritima. <i>Journal of Structural Biology</i> , <b>2015</b> , 190, 135-42	3.4	6

55	The monomeric form of Neisseria DNA mimic protein DMP19 prevents DNA from binding to the histone-like HU protein. <i>PLoS ONE</i> , <b>2017</b> , 12, e0189461	3.7	6
54	Structural insight into a novel indole prenyltransferase in hapalindole-type alkaloid biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , <b>2018</b> , 495, 1782-1788	3.4	6
53	Structure of an antibiotic-synthesizing UDP-glucuronate 4-epimerase MoeE5 in complex with substrate. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 521, 31-36	3.4	6
52	Human DNA Polymerase $\beta$ Can Use a Noncanonical Mechanism for Multiple Mn-Mediated Functions. <i>Journal of the American Chemical Society</i> , <b>2019</b> , 141, 8489-8502	16.4	5
51	Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes. <i>Angewandte Chemie</i> , <b>2012</b> , 124, 4233-4236	3.6	5
50	Structure of fully liganded Hb $\alpha$ s trapped in a tense conformation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2061-71		5
49	Substrate-analogue complex structure of Mycobacterium tuberculosis decaprenyl diphosphate synthase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2019</b> , 75, 212-216	1.1	5
48	Structural insights of the ssDNA binding site in the multifunctional endonuclease AtBFN2 from Arabidopsis thaliana. <i>PLoS ONE</i> , <b>2014</b> , 9, e105821	3.7	5
47	Structure of undecaprenyl pyrophosphate synthase from Acinetobacter baumannii. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2018</b> , 74, 765-769	1.1	5
46	Structures of Iridoid Synthase from Cantharanthus roseus with Bound NAD <sup>+</sup> , NADPH, or NAD <sup>+</sup> /10-Oxogeraniol: Reaction Mechanisms. <i>Angewandte Chemie</i> , <b>2015</b> , 127, 15698-15702	3.6	4
45	Minireview: A Comeback of Hg-Derivatives in Protein Crystallography with Cys-Modification. <i>ChemBioEng Reviews</i> , <b>2015</b> , 2, 133-140	5.2	4
44	Functional and structural investigations of fibronectin-binding protein Apa from Mycobacterium tuberculosis. <i>Biochimica Et Biophysica Acta - General Subjects</i> , <b>2019</b> , 1863, 1351-1359	4	3
43	Structural insights into thebaine synthase 2 catalysis. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 529, 156-161	3.4	3
42	The Arginine Pairs and C-Termini of the Sso7c4 from Sulfolobus solfataricus Participate in Binding and Bending DNA. <i>PLoS ONE</i> , <b>2017</b> , 12, e0169627	3.7	3
41	Head-to-Middle and Head-to-Tail cis-Prenyl Transferases: Structure of Isosesquilavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , <b>2018</b> , 130, 691-695	3.6	3
40	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie</i> , <b>2016</b> , 128, 4794-4798	3.6	3
39	Crystal Structure of PigA: A Prolyl Thioester-Oxidizing Enzyme in Prodigiosin Biosynthesis. <i>ChemBioChem</i> , <b>2019</b> , 20, 193-202	3.8	3
38	Structural characterization of borneol dehydrogenase from Pseudomonas sp. TCU-HL1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2020</b> , 76, 309-313	1.1	3

37	Crystal structure and functional implication of a bacterial cyclic AMP-AMP-GMP synthetase. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 4725-4737	20.1	3
36	SH3-like motif-containing C-terminal domain of staphylococcal teichoic acid transporter suggests possible function. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2016</b> , 84, 1328-32	4.2	3
35	Structural insights into the calcium dependence of Stig cyclases.. <i>RSC Advances</i> , <b>2019</b> , 9, 13182-13185	3.7	2
34	Crystal structure of the blue fluorescent protein with a Leu-Leu-Gly tri-peptide chromophore derived from the purple chromoprotein of <i>Stichodactyla haddoni</i> . <i>International Journal of Biological Macromolecules</i> , <b>2019</b> , 130, 675-684	7.9	2
33	Complex structures of MoeN5 with substrate analogues suggest sequential catalytic mechanism. <i>Biochemical and Biophysical Research Communications</i> , <b>2019</b> , 511, 800-805	3.4	2
32	Structural basis for the antipolymer activity of Hb $\alpha$ trapped in a tense conformation. <i>Journal of Molecular Structure</i> , <b>2015</b> , 1099, 99-107	3.4	2
31	Roles of tryptophan residue and disulfide bond in the variable lid region of oxidized polyvinyl alcohol hydrolase. <i>Biochemical and Biophysical Research Communications</i> , <b>2014</b> , 452, 509-14	3.4	2
30	Expression, Purification, Crystallization, and X-ray Structural Analysis of CRISPR-Associated Protein Cas6 from <i>Methanocaldococcus jannaschii</i> . <i>Crystals</i> , <b>2017</b> , 7, 344	2.3	2
29	Crystallization and preliminary X-ray diffraction analysis of (R)-carbonyl reductase from <i>Candida parapsilosis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 800-2	1.1	2
28	Evidence for an Enzyme-Catalyzed Rauhut-Currier Reaction during the Biosynthesis of Spinosyn A. <i>Journal of the American Chemical Society</i> , <b>2021</b> , 143, 20291-20295	16.4	2
27	Structure of a gut microbial diltiazem-metabolizing enzyme suggests possible substrate binding mode. <i>Biochemical and Biophysical Research Communications</i> , <b>2020</b> , 527, 799-804	3.4	2
26	Titelbild: Structure and Function of a Head-to-Middle Prenyltransferase: Lavandulyl Diphosphate Synthase (Angew. Chem. 15/2016). <i>Angewandte Chemie</i> , <b>2016</b> , 128, 4689-4689	3.6	2
25	The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie</i> , <b>2018</b> , 130, 15280-15284	3.6	2
24	Structural insight into the differential interactions between the DNA mimic protein SAUG1 and two gamma herpesvirus uracil-DNA glycosylases. <i>International Journal of Biological Macromolecules</i> , <b>2020</b> , 160, 903-914	7.9	1
23	Binding mode of the oxidized dimer of NAD <sup>+</sup> to RSP, a Rex-family repressor. <i>Biochemical and Biophysical Research Communications</i> , <b>2015</b> , 456, 733-6	3.4	1
22	Preliminary X-ray diffraction analysis of thermostable $\beta$ 1,4-xylanase from <i>Streptomyces</i> sp. S9. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 105-7	1.1	1
21	Preliminary X-ray diffraction analysis of a thermophilic $\beta$ 1,3-1,4-glucanase from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 946-8	1.1	1
20	Crystallization and preliminary X-ray diffraction analysis of the S-adenosylhomocysteine hydrolase (SAHH) from <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2014</b> , 70, 1563-5	1.1	1

19	Crystal structure and functional implication of bacterial STING.. <i>Nature Communications</i> , <b>2022</b> , 13, 26	17.4	1
18	Cloning, expression, identification and characterization of borneol dehydrogenase isozymes in <i>Pseudomonas</i> sp. TCU-HL1. <i>Protein Expression and Purification</i> , <b>2020</b> , 175, 105715	2	1
17	A Unique Carboxylic-Acid Hydrogen-Bond Network (CAHBN) Confers Glutaminyl Cyclase Activity on M28 Family Enzymes. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 166960	6.5	1
16	Crystal structures of Staphylococcal SaeR reveal possible DNA-binding modes. <i>Biochemical and Biophysical Research Communications</i> , <b>2016</b> , 474, 686-690	3.4	1
15	The tetrameric structure of sialic acid-synthesizing UDP-GlcNAc 2-epimerase from : A comparative study with human GNE. <i>Journal of Biological Chemistry</i> , <b>2018</b> , 293, 10119-10127	5.4	1
14	Integrated omics approach to unveil antifungal bacterial polyynes as acetyl-CoA acetyltransferase inhibitors.. <i>Communications Biology</i> , <b>2022</b> , 5, 454	6.7	1
13	Structural and biological insights into <i>Klebsiella pneumoniae</i> surface polysaccharide degradation by a bacteriophage K1 lyase: implications for clinical use.. <i>Journal of Biomedical Science</i> , <b>2022</b> , 29, 9	13.3	0
12	Structural insights into the substrate selectivity of Hexoamine synthases from marine <i>Vibrio</i> sp. QWI-06. <i>Colloids and Surfaces B: Biointerfaces</i> , <b>2021</b> , 210, 112224	6	0
11	Synergic action of an inserted carbohydrate-binding module in a glycoside hydrolase family 5 endoglucanase.. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2022</b> , 78, 633-646	5.5	0
10	Innenr�ktitelbild: Head-to-Middle and Head-to-Tail Cis-Prenyl Transferases: Structure of Isosqualavandulyl Diphosphate Synthase (Angew. Chem. 3/2018). <i>Angewandte Chemie</i> , <b>2018</b> , 130, 861-861	3.6	0
9	Titelbild: Structures of Iridoid Synthase from <i>Cantharanthus roseus</i> with Bound NAD <sup>+</sup> , NADPH, or NAD <sup>+</sup> /10-Oxogeranial: Reaction Mechanisms (Angew. Chem. 51/2015). <i>Angewandte Chemie</i> , <b>2015</b> , 127, 15517-15517	3.6	0
8	R�ktitelbild: Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes (Angew. Chem. 17/2012). <i>Angewandte Chemie</i> , <b>2012</b> , 124, 4314-4314	3.6	0
7	Back Cover: Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes (Angew. Chem. Int. Ed. 17/2012). <i>Angewandte Chemie - International Edition</i> , <b>2012</b> , 51, 4240-4240	16.4	0
6	2P592 Maturation and Mechanism Based Inhibitor Design of SARS-CoV 3CL Protease : Implication in Antiviral 3C(L) Protease Drug Design(55. Drug design and delivery,Poster Session,Abstract,Meeting Program of EABS &BSJ 2006). <i>Seibutsu Butsuri</i> , <b>2006</b> , 46, S443	0	0
5	1P195 Crystal structure of infectious bursal disease virus VP2 subviral particle : Implications in virion assembly and immunogenicity(6. Macromolecular assembly,Poster Session,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , <b>2006</b> , 46, S195	0	0
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2	Crystal structure of the N-terminal domain of TagH reveals a potential drug targeting site. <i>Biochemical and Biophysical Research Communications</i> , <b>2021</b> , 536, 1-6	3.4	0



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