

Tzu-Ping Ko

List of Publications by Year in descending order

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123
papers

3,909
citations

147786

31
h-index

138468

58
g-index

136
all docs

136
docs citations

136
times ranked

5011
citing authors

#	ARTICLE	IF	CITATIONS
1	The opportunistic marine pathogen <i>Vibrio parahaemolyticus</i> becomes virulent by acquiring a plasmid that expresses a deadly toxin. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10798-10803.	7.1	427
2	Structure, mechanism and function of prenyltransferases. FEBS Journal, 2002, 269, 3339-3354.	0.2	382
3	Structural insight into catalytic mechanism of PET hydrolase. Nature Communications, 2017, 8, 2106.	12.8	309
4	Bisphosphonates target multiple sites in both cis- and trans-prenyltransferases. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10022-10027.	7.1	173
5	Crystal Structures of Undecaprenyl Pyrophosphate Synthase in Complex with Magnesium, Isopentenyl Pyrophosphate, and Farnesyl Thiopyrophosphate. Journal of Biological Chemistry, 2005, 280, 20762-20774.	3.4	115
6	Crystal Structure of Yeast Cytosine Deaminase. Journal of Biological Chemistry, 2003, 278, 19111-19117.	3.4	113
7	Structure and Mechanism of Helicobacter pylori Fucosyltransferase. Journal of Biological Chemistry, 2007, 282, 9973-9982.	3.4	113
8	Structural studies reveal the molecular mechanism of PETase. FEBS Journal, 2018, 285, 3717-3723.	4.7	112
9	Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1438-1446.	7.1	94
10	Mechanism of Product Chain Length Determination and the Role of a Flexible Loop in Escherichia coli Undecaprenyl-pyrophosphate Synthase Catalysis. Journal of Biological Chemistry, 2001, 276, 47474-47482.	3.4	90
11	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. Biophysical Journal, 2003, 84, 1228-1237.	0.5	76
12	Squalene Synthase As a Target for Chagas Disease Therapeutics. PLoS Pathogens, 2014, 10, e1004114.	4.7	64
13	Structural Analysis of a Glycoside Hydrolase Family 11 Xylanase from Neocallimastix patriciarum. Journal of Biological Chemistry, 2014, 289, 11020-11028.	3.4	64
14	Catalytic Mechanism Revealed by the Crystal Structure of Undecaprenyl Pyrophosphate Synthase in Complex with Sulfate, Magnesium, and Triton. Journal of Biological Chemistry, 2003, 278, 29298-29307.	3.4	57
15	Structure of human erythrocyte catalase. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 241-245.	2.5	55
16	Dietary Flavonoids Luteolin and Quercetin Inhibit Migration and Invasion of Squamous Carcinoma through Reduction of Src/Stat3/S100A7 Signaling. Antioxidants, 2019, 8, 557.	5.1	55
17	Substrate binding mode and reaction mechanism of undecaprenyl pyrophosphate synthase deduced from crystallographic studies. Protein Science, 2004, 13, 971-978.	7.6	54
18	Structural basis for fragmenting the exopolysaccharide of Acinetobacter baumannii by bacteriophage ϕ AB6 tailspike protein. Scientific Reports, 2017, 7, 42711.	3.3	49

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19	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> , 2011, 1814, 1832-1840.	2.3	47
20	Structural and Functional Analysis of <i>Bacillus subtilis</i> YisP Reveals a Role of Its Product in Biofilm Production. <i>Chemistry and Biology</i> , 2014, 21, 1557-1563.	6.0	44
21	Structure, function and inhibition of ent-kaurene synthase from <i>Bradyrhizobium japonicum</i> . <i>Scientific Reports</i> , 2014, 4, 6214.	3.3	44
22	Phospholipases A2 from <i>Callosellasma rhodostoma</i> venom gland. <i>FEBS Journal</i> , 2000, 267, 6684-6691.	0.2	43
23	Improving specific activity and thermostability of <i>Escherichia coli</i> phytase by structure-based rational design. <i>Journal of Biotechnology</i> , 2014, 175, 1-6.	3.8	43
24	Structural insights into the catalytic mechanism of human squalene synthase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 231-241.	2.5	40
25	Improving the catalytic performance of a GH11 xylanase by rational protein engineering. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9503-9510.	3.6	40
26	Structure and Inhibition of Tuberculosin Synthase and Decaprenyl Diphosphate Synthase from <i>Mycobacterium tuberculosis</i> . <i>Journal of the American Chemical Society</i> , 2014, 136, 2892-2896.	13.7	37
27	Improving the specific activity of β -mannanase from <i>Aspergillus niger</i> BK01 by structure-based rational design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 663-669.	2.3	36
28	Enhanced β -Zearalenol Hydrolyzing Activity of a Mycoestrogen-Detoxifying Lactonase by Structure-Based Engineering. <i>ACS Catalysis</i> , 2016, 6, 7657-7663.	11.2	36
29	Structural insight into the electron transfer pathway of a self-sufficient P450 monooxygenase. <i>Nature Communications</i> , 2020, 11, 2676.	12.8	35
30	Structural basis of polyethylene glycol recognition by antibody. <i>Journal of Biomedical Science</i> , 2020, 27, 12.	7.0	34
31	Crystal Structure of a Mycoestrogen-Detoxifying Lactonase from <i>Rhinocladiella mackenziei</i> : Molecular Insight into ZHD Substrate Selectivity. <i>ACS Catalysis</i> , 2018, 8, 4294-4298.	11.2	33
32	<i>Staphylococcus aureus</i> protein SAUG1 acts as a uracil-DNA glycosylase inhibitor. <i>Nucleic Acids Research</i> , 2014, 42, 1354-1364.	14.5	32
33	Structural perspectives of an engineered β -1,4-xylanase with enhanced thermostability. <i>Journal of Biotechnology</i> , 2014, 189, 175-182.	3.8	32
34	Structure and Function of a β -Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4721-4724.	13.8	32
35	Mechanism and inhibition of human UDP-GlcNAc 2-epimerase, the key enzyme in sialic acid biosynthesis. <i>Scientific Reports</i> , 2016, 6, 23274.	3.3	32
36	Structural insight into potential cold adaptation mechanism through a psychrophilic glycoside hydrolase family 10 endo- β -1,4-xylanase. <i>Journal of Structural Biology</i> , 2016, 193, 206-211.	2.8	32

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37	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> , 2014, 289, 27046-27054.	3.4	28
38	Crystal Structure Analysis of the Repair of Iron Centers Protein YtfE and Its Interaction with NO. <i>Chemistry - A European Journal</i> , 2016, 22, 9768-9776.	3.3	28
39	Structural Insights to the Heterotetrameric Interaction between the <i>Vibrio parahaemolyticus</i> PirAvp and PirBvp Toxins and Activation of the Cry-Like Pore-Forming Domain. <i>Toxins</i> , 2019, 11, 233.	3.4	26
40	Current Progresses in Phytase Research: Three-dimensional Structure and Protein Engineering. <i>ChemBioEng Reviews</i> , 2015, 2, 76-86.	4.4	24
41	Head-Middle and Head-Tail cis-Prenyl Transferases: Structure of Isosesquilandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 683-687.	13.8	24
42	Structure, Function, and Inhibition of <i>Staphylococcus aureus</i> Heptaprenyl Diphosphate Synthase. <i>ChemMedChem</i> , 2016, 11, 1915-1923.	3.2	23
43	Characterization and crystal structure of a thermostable glycoside hydrolase family 45 1,4- β -endoglucanase from <i>Thielavia terrestris</i> . <i>Enzyme and Microbial Technology</i> , 2017, 99, 32-37.	3.2	23
44	Crystal Structure and Potential Head-to-Middle Condensation Function of a cis-, cis-Farnesyl Diphosphate Synthase. <i>ACS Omega</i> , 2017, 2, 930-936.	3.5	23
45	Structures of Iridoid Synthase from <i>Cantharanthus roseus</i> with Bound NAD ⁺ , NADPH, or NAD ¹⁰ -Oxogeranial: Reaction Mechanisms. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 15478-15482.	13.8	21
46	Structures of human MST3 kinase in complex with adenine, ADP and Mn ²⁺ . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 145-154.	2.5	20
47	Distinct structural features of Rex-family repressors to sense redox levels in anaerobes and aerobes. <i>Journal of Structural Biology</i> , 2014, 188, 195-204.	2.8	20
48	Structural and mutagenetic analyses of a 1,3- α -1,4- β -glucanase from <i>Paecilomyces thermophila</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 366-373.	2.3	20
49	Functional and structural analyses of a 1,4- β -endoglucanase from <i>Ganoderma lucidum</i> . <i>Enzyme and Microbial Technology</i> , 2016, 86, 67-74.	3.2	20
50	Crystal structure and functional implication of bacterial STING. <i>Nature Communications</i> , 2022, 13, 26.	12.8	20
51	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4716-4720.	13.8	19
52	Catalytic Role of Conserved Asparagine, Glutamine, Serine, and Tyrosine Residues in Isoprenoid Biosynthesis Enzymes. <i>ACS Catalysis</i> , 2018, 8, 4299-4312.	11.2	19
53	Structural insights to heterodimeric cis-prenyltransferases through yeast dehydrodolichyl diphosphate synthase subunit Nus1. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 621-626.	2.1	19
54	Structure of an antibiotic-synthesizing UDP-glucuronate 4-epimerase MoeE5 in complex with substrate. <i>Biochemical and Biophysical Research Communications</i> , 2020, 521, 31-36.	2.1	19

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55	Crystal structure of vespid phospholipase A1 reveals insights into the mechanism for cause of membrane dysfunction. <i>Insect Biochemistry and Molecular Biology</i> , 2016, 68, 79-88.	2.7	18
56	Structural insights into the interaction between phytoplasmal effector causing phyllody 1 and <sc>MADS</sc> transcription factors. <i>Plant Journal</i> , 2019, 100, 706-719.	5.7	16
57	Structure and mechanism of an antibiotics-synthesizing 3-hydroxykynurenine C-methyltransferase. <i>Scientific Reports</i> , 2015, 5, 10100.	3.3	15
58	Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , 2016, 11, 1362-1371.	3.4	15
59	Enzymatic characterization and crystal structure analysis of <i>Chlamydomonas reinhardtii</i> dehydroascorbate reductase and their implications for oxidative stress. <i>Plant Physiology and Biochemistry</i> , 2017, 120, 144-155.	5.8	15
60	Crystal structure of LepI, a multifunctional SAM-dependent enzyme which catalyzes pericyclic reactions in leporin biosynthesis. <i>Organic and Biomolecular Chemistry</i> , 2019, 17, 2070-2076.	2.8	15
61	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> , 2016, 44, 4440-4449.	14.5	14
62	Versatile <i>cis</i> -isoprenyl Diphosphate Synthase Superfamily Members in Catalyzing Carbon-Carbon Bond Formation. <i>ACS Catalysis</i> , 2020, 10, 4717-4725.	11.2	14
63	Structures of the hyperthermophilic chromosomal protein Sac7d in complex with DNA decamers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1381-1387.	2.5	13
64	Structural analyses and yeast production of the β -1,3-1,4-glucanase catalytic module encoded by the licB gene of <i>Clostridium thermocellum</i> . <i>Enzyme and Microbial Technology</i> , 2015, 71, 1-7.	3.2	13
65	An Effective Neutralizing Antibody Against Influenza Virus H1N1 from Human B Cells. <i>Scientific Reports</i> , 2019, 9, 4546.	3.3	13
66	NADH/NADPH bi-cofactor-utilizing and thermoactive ketol-acid reductoisomerase from <i>Sulfolobus acidocaldarius</i> . <i>Scientific Reports</i> , 2018, 8, 7176.	3.3	12
67	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> , 2019, 141, 6136-6140.	13.7	11
68	The tetrameric structure of sialic acid-synthesizing UDP-GlcNAc 2-epimerase from <i>Acinetobacter baumannii</i> : A comparative study with human GNE. <i>Journal of Biological Chemistry</i> , 2018, 293, 10119-10127.	3.4	10
69	Structure and Function of a α -Head-Middle-Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , 2016, 128, 4799-4802.	2.0	9
70	The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 15060-15064.	13.8	9
71	Reduction in MnSOD promotes the migration and invasion of squamous carcinoma cells. <i>International Journal of Oncology</i> , 2019, 54, 1639-1650.	3.3	9
72	Crystal structure and functional implication of a bacterial cyclic AMP-GMP synthetase. <i>Nucleic Acids Research</i> , 2021, 49, 4725-4737.	14.5	9

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73	Substrate-analogue complex structure of <i>Mycobacterium tuberculosis</i> decaprenyl diphosphate synthase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 212-216.	0.8	9
74	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> , 2022, 29, 9.	7.0	9
75	Crystal structures of S-adenosylhomocysteine hydrolase from the thermophilic bacterium <i>Thermotoga maritima</i> . <i>Journal of Structural Biology</i> , 2015, 190, 135-142.	2.8	8
76	The monomeric form of <i>Neisseria</i> DNA mimic protein DMP19 prevents DNA from binding to the histone-like HU protein. <i>PLoS ONE</i> , 2017, 12, e0189461.	2.5	8
77	Structural insight into a novel indole prenyltransferase in hapalindole-type alkaloid biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1782-1788.	2.1	8
78	Human DNA Polymerase β Can Use a Noncanonical Mechanism for Multiple Mn ²⁺ -Mediated Functions. <i>Journal of the American Chemical Society</i> , 2019, 141, 8489-8502.	13.7	8
79	Evidence for an Enzyme-Catalyzed Carrier Reaction during the Biosynthesis of Spinosyn A. <i>Journal of the American Chemical Society</i> , 2021, 143, 20291-20295.	13.7	8
80	Integrated omics approach to unveil antifungal bacterial polyynes as acetyl-CoA acetyltransferase inhibitors. <i>Communications Biology</i> , 2022, 5, 454.	4.4	8
81	Structure of undecaprenyl pyrophosphate synthase from <i>Acinetobacter baumannii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 765-769.	0.8	7
82	Crystal Structure of PigA: A Prolyl Thioester-Oxidizing Enzyme in Prodigiosin Biosynthesis. <i>ChemBioChem</i> , 2019, 20, 193-202.	2.6	7
83	Functional and structural investigations of fibronectin-binding protein Apa from <i>Mycobacterium tuberculosis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1351-1359.	2.4	7
84	Structural insights into thebaine synthase 2 catalysis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 156-161.	2.1	7
85	Structural Insights of the ssDNA Binding Site in the Multifunctional Endonuclease AtBFN2 from <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2014, 9, e105821.	2.5	7
86	Head-to-Head Prenyl Synthases in Pathogenic Bacteria. <i>ChemBioChem</i> , 2017, 18, 985-991.	2.6	6
87	Structure of a gut microbial diltiazem-metabolizing enzyme suggests possible substrate binding mode. <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 799-804.	2.1	6
88	Structure of fully liganded Hb $\alpha 2\beta 2$ strapped in a tense conformation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2061-2071.	2.5	5
89	Minireview: A Comeback of Hg Derivatives in Protein Crystallography with Cys Modification. <i>ChemBioEng Reviews</i> , 2015, 2, 133-140.	4.4	5
90	SH3-like motif-containing C-terminal domain of staphylococcal teichoic acid transporter suggests possible function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1328-1332.	2.6	5

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91	Head-to-Middle and Head-to-Tail cis Prenyl Transferases: Structure of Isosqualavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , 2018, 130, 691-695.	2.0	5
92	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> , 2019, 130, 675-684.	7.5	5
93	The Arginine Pairs and C-Termini of the Sso7c4 from <i>Sulfolobus solfataricus</i> Participate in Binding and Bending DNA. <i>PLoS ONE</i> , 2017, 12, e0169627.	2.5	4
94	Complex structures of MoeN5 with substrate analogues suggest sequential catalytic mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2019, 511, 800-805.	2.1	4
95	Structural characterization of borneol dehydrogenase from <i>Pseudomonas</i> sp. TCU-HL1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 309-313.	0.8	4
96	Roles of tryptophan residue and disulfide bond in the variable lid region of oxidized polyvinyl alcohol hydrolase. <i>Biochemical and Biophysical Research Communications</i> , 2014, 452, 509-514.	2.1	3
97	Structural basis for the antipolymer activity of Hb1 α 2 β 2 trapped in a tense conformation. <i>Journal of Molecular Structure</i> , 2015, 1099, 99-107.	3.6	3
98	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie</i> , 2016, 128, 4794-4798.	2.0	3
99	Expression, Purification, Crystallization, and X-ray Structural Analysis of CRISPR-Associated Protein Cas6 from <i>Methanocaldococcus jannaschii</i> . <i>Crystals</i> , 2017, 7, 344.	2.2	3
100	Synergic action of an inserted carbohydrate-binding module in a glycoside hydrolase family 5 endoglucanase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2022, 78, 633-646.	2.3	3
101	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> , 2014, 70, 800-802.	0.8	2
102	Titelbild: Structure and Function of a Head-to-Middle Prenyltransferase: Lavandulyl Diphosphate Synthase (<i>Angew. Chem.</i> 15/2016). <i>Angewandte Chemie</i> , 2016, 128, 4689-4689.	2.0	2
103	Crystal structures of Staphylococcal SaeR reveal possible DNA-binding modes. <i>Biochemical and Biophysical Research Communications</i> , 2016, 474, 686-690.	2.1	2
104	The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie</i> , 2018, 130, 15280-15284.	2.0	2
105	Structural insights into the calcium dependence of Stig cyclases. <i>RSC Advances</i> , 2019, 9, 13182-13185.	3.6	2
106	Structural insights into the substrate selectivity of β -oxoamine synthases from marine <i>Vibrio</i> sp. QWI-06. <i>Colloids and Surfaces B: Biointerfaces</i> , 2022, 210, 112224.	5.0	2
107	Preliminary X-ray diffraction analysis of thermostable β -1,4-xylanase from <i>Streptomyces</i> sp. S9. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 105-107.	0.8	1
108	Preliminary X-ray diffraction analysis of a thermophilic β -1,3 α -1,4-glucanase from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 946-948.	0.8	1

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109	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> , 2014, 70, 1563-1565.	0.8	1
110	Binding mode of the oxidized β -anomer of NAD ⁺ to RSP, a Rex-family repressor. <i>Biochemical and Biophysical Research Communications</i> , 2015, 456, 733-736.	2.1	1
111	Cloning, expression, identification and characterization of borneol dehydrogenase isozymes in <i>Pseudomonas</i> sp. TCU-HL1. <i>Protein Expression and Purification</i> , 2020, 175, 105715.	1.3	1
112	Structural insight into the differential interactions between the DNA mimic protein SAUGI and two gamma herpesvirus uracil-DNA glycosylases. <i>International Journal of Biological Macromolecules</i> , 2020, 160, 903-914.	7.5	1
113	Crystal structure of the N-terminal domain of TagH reveals a potential drug targeting site. <i>Biochemical and Biophysical Research Communications</i> , 2021, 536, 1-6.	2.1	1
114	A Unique Carboxylic-Acid Hydrogen-Bond Network (CAHBN) Confers Glutaminyl Cyclase Activity on M28 Family Enzymes. <i>Journal of Molecular Biology</i> , 2021, 433, 166960.	4.2	1
115	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) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 650 417	0.784314	0
116	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) Tj ETQq0 0 0.784314 rgBT /Overlock 10 T 650 417	0.784314	0
117	1P219 Structure of the left-handed archaeal RadA filament : a subunit rotation motif controls homologous DNA strand exchange reaction(7. Nucleic acid binding protein,Poster) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 650 417	0.784314	0
118	2P058 Dual Binding Sites for Translocation Catalysis by <i>E. coli</i> Glutathionylspermidine Synthetase(29.) Tj ETQq0 0 0.1 rgBT /Overlock 10 T 650 417 Seibutsu Butsuri, 2006, 46, S310.	0.1	0
119	Crystal Structures and Computer Screened Inhibitors of <i>Helicobacter pylori</i> Undecaprenyl Pyrophosphate Synthase. , 2007, , .		0
120	Back Cover: Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes (<i>Angew. Chem. Int. Ed.</i> 17/2012). <i>Angewandte Chemie - International Edition</i> , 2012, 51, 4240-4240.	13.8	0
121	Titelbild: Structures of Iridoid Synthase from <i>Cantharanthus roseus</i> with Bound NAD ⁺ , NADPH, or NAD ⁺ /10-Oxogeranial: Reaction Mechanisms (<i>Angew. Chem.</i> 51/2015). <i>Angewandte Chemie</i> , 2015, 127, 15517-15517.	2.0	0
122	InnenrÃ¼cktitelbild: α -Head- β -Middle- and α -Head- β -Tail- γ -Prenyl Transferases: Structure of Isosqualandulyl Diphosphate Synthase (<i>Angew. Chem.</i> 3/2018). <i>Angewandte Chemie</i> , 2018, 130, 861-861.	2.0	0
123	RÃ¼cktitelbild: The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement (<i>Angew. Chem.</i> 46/2018). <i>Angewandte Chemie</i> , 2018, 130, 15506-15506.	2.0	0