

Chun-Chi Chen

List of Publications by Year in descending order

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91
papers

2,545
citations

185998

28
h-index

233125

45
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98
all docs

98
docs citations

98
times ranked

2951
citing authors

#	ARTICLE	IF	CITATIONS
1	KRAS(G12D) can be targeted by potent inhibitors via formation of salt bridge. <i>Cell Discovery</i> , 2022, 8, 5.	3.1	52
2	Crystal structure and biochemical analysis of the specialized deoxynivalenolâ€“detoxifying glyoxalase SPG from <i>Gossypium hirsutum</i> . <i>International Journal of Biological Macromolecules</i> , 2022, 200, 388-396.	3.6	9
3	Molecular Basis for a Toluene Monooxygenase to Govern Substrate Selectivity. <i>ACS Catalysis</i> , 2022, 12, 2831-2839.	5.5	11
4	Substrate-Binding Mode of a Thermophilic PET Hydrolase and Engineering the Enzyme to Enhance the Hydrolytic Efficacy. <i>ACS Catalysis</i> , 2022, 12, 3033-3040.	5.5	50
5	Structural and Functional Insights into a Nonheme Iron- and Î±-Ketoglutarate-Dependent Halogenase That Catalyzes Chlorination of Nucleotide Substrates. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0249721.	1.4	8
6	Structural insights into the cyclization of unusual brasilane-type sesquiterpenes. <i>International Journal of Biological Macromolecules</i> , 2022, 209, 1784-1791.	3.6	2
7	A Structural and Bioinformatics Investigation of a Fungal Squalene Synthase and Comparisons with Other Membrane Proteins. <i>ACS Omega</i> , 2022, 7, 22601-22612.	1.6	2
8	Structural insights to a bi-functional isoprenyl diphosphate synthase that can catalyze head-to-tail and head-to-middle condensation. <i>International Journal of Biological Macromolecules</i> , 2022, 214, 492-499.	3.6	0
9	Advanced Understanding of the Electron Transfer Pathway of Cytochrome P450s. <i>ChemBioChem</i> , 2021, 22, 1317-1328.	1.3	23
10	Terpene Cyclases and Prenyltransferases: Structures and Mechanisms of Action. <i>ACS Catalysis</i> , 2021, 11, 290-303.	5.5	13
11	Overview of antiviral drug candidates targeting coronaviral 3Câ€“like main proteases. <i>FEBS Journal</i> , 2021, 288, 5089-5121.	2.2	28
12	General features to enhance enzymatic activity of poly(ethylene terephthalate) hydrolysis. <i>Nature Catalysis</i> , 2021, 4, 425-430.	16.1	92
13	Enhancing PET hydrolytic enzyme activity by fusion of the celluloseâ€“binding domain of cellobiohydrolase I from <i>Trichoderma reesei</i> . <i>Journal of Biotechnology</i> , 2021, 334, 47-50.	1.9	40
14	Functional and structural investigation of a novel Î²-mannanase BaMan113A from <i>Bacillus</i> sp. N16-5. <i>International Journal of Biological Macromolecules</i> , 2021, 182, 899-909.	3.6	19
15	Dendronized Arm Snowflake Polymer as a Highly Branched Scaffold for Cellular Imaging and Delivery. <i>Biomacromolecules</i> , 2021, 22, 3791-3799.	2.6	3
16	Catalytically inactive lytic polysaccharide monooxygenase PcAA14A enhances the enzyme-mediated hydrolysis of polyethylene terephthalate. <i>International Journal of Biological Macromolecules</i> , 2021, 190, 456-462.	3.6	13
17	Structural investigation of a thermostable 1,2-Î²-mannobiose phosphorylase from <i>Thermoanaerobacter</i> sp. X-514. <i>Biochemical and Biophysical Research Communications</i> , 2021, 579, 54-61.	1.0	6
18	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.	1.0	19

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19	Structure basis of non-structural protein pA151R from African Swine Fever Virus. <i>Biochemical and Biophysical Research Communications</i> , 2020, 532, 108-113.	1.0	4
20	Functional and Structural Insights into a Novel Promiscuous Ketoreductase of the Lugdunomycin Biosynthetic Pathway. <i>ACS Chemical Biology</i> , 2020, 15, 2529-2538.	1.6	7
21	A Cyclic di-GMP Network Is Present in Gram-Positive <i>Streptococcus</i> and Gram-Negative <i>Proteus</i> Species. <i>ACS Infectious Diseases</i> , 2020, 6, 2672-2687.	1.8	10
22	Structural insight into the electron transfer pathway of a self-sufficient P450 monooxygenase. <i>Nature Communications</i> , 2020, 11, 2676.	5.8	35
23	Versatile <i>cis</i> -isoprenyl Diphosphate Synthase Superfamily Members in Catalyzing Carbon-Carbon Bond Formation. <i>ACS Catalysis</i> , 2020, 10, 4717-4725.	5.5	14
24	Structural insights into thebaine synthase 2 catalysis. <i>Biochemical and Biophysical Research Communications</i> , 2020, 529, 156-161.	1.0	7
25	Enzymatic degradation of plant biomass and synthetic polymers. <i>Nature Reviews Chemistry</i> , 2020, 4, 114-126.	13.8	213
26	Structure of a gut microbial diltiazem-metabolizing enzyme suggests possible substrate binding mode. <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 799-804.	1.0	6
27	Crystal structure and proposed mechanism of an enantioselective hydroalkoxylation enzyme from <i>Penicillium herquei</i> . <i>Biochemical and Biophysical Research Communications</i> , 2019, 516, 801-805.	1.0	2
28	Crystal structure of TchmY from <i>Actinoplanes teichomyceticus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 570-575.	0.4	1
29	Structural insights into the calcium dependence of Stig cyclases. <i>RSC Advances</i> , 2019, 9, 13182-13185.	1.7	2
30	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.	1.5	15
31	Structural insights to heterodimeric <i>cis</i> -prenyltransferases through yeast dehydrololichyl diphosphate synthase subunit Nus1. <i>Biochemical and Biophysical Research Communications</i> , 2019, 515, 621-626.	1.0	19
32	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.	1.1	7
33	A Structural Change in Butyrophilin upon Phosphoantigen Binding Underlies Phosphoantigen-Mediated $\text{V}\beta 9\text{V}\beta 2$ Cell Activation. <i>Immunity</i> , 2019, 50, 1043-1053.e5.	6.6	94
34	Complex structures of MoeN5 with substrate analogues suggest sequential catalytic mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2019, 511, 800-805.	1.0	4
35	Discovery of Lipophilic Bisphosphonates That Target Bacterial Cell Wall and Quinone Biosynthesis. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 2564-2581.	2.9	18
36	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.	0.4	9

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37	Crystal Structure of a Mycoestrogen-Detoxifying Lactonase from <i>Rhinochlaidiella mackenziei</i> : Molecular Insight into ZHD Substrate Selectivity. <i>ACS Catalysis</i> , 2018, 8, 4294-4298.	5.5	33
38	Catalytic Role of Conserved Asparagine, Glutamine, Serine, and Tyrosine Residues in Isoprenoid Biosynthesis Enzymes. <i>ACS Catalysis</i> , 2018, 8, 4299-4312.	5.5	19
39	Structural insight into a novel indole prenyltransferase in hapalindole-type alkaloid biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1782-1788.	1.0	8
40	Head-to-Middle- and Head-to-Tail-cis Prenyl Transferases: Structure of Isosquilavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , 2018, 130, 691-695.	1.6	5
41	Innen- und Außenbild: Head-to-Middle- und Head-to-Tail-cis Prenyl Transferases: Structure of Isosquilavandulyl Diphosphate Synthase (<i>Angew. Chem.</i> 3/2018). <i>Angewandte Chemie</i> , 2018, 130, 861-861.	1.6	0
42	Head-to-Middle- und Head-to-Tail-cis Prenyl Transferases: Structure of Isosquilavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 683-687.	7.2	24
43	Abbildung: 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.	1.6	0
44	The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie</i> , 2018, 130, 15280-15284.	1.6	2
45	The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 15060-15064.	7.2	9
46	Insight into the functional roles of Glu175 in the hyperthermostable xylanase XYL10C-N through structural analysis and site-saturation mutagenesis. <i>Biotechnology for Biofuels</i> , 2018, 11, 159.	6.2	21
47	Structural studies reveal the molecular mechanism of PETase. <i>FEBS Journal</i> , 2018, 285, 3717-3723.	2.2	112
48	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.	1.6	23
49	Structural insight into catalytic mechanism of PET hydrolase. <i>Nature Communications</i> , 2017, 8, 2106.	5.8	309
50	Characterization and crystal structure of a novel zearalenone hydrolase from <i>Cladophialophora bantiana</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 515-519.	0.4	35
51	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4716-4720.	7.2	19
52	Structure and Function of a Head-to-Middle-Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 4721-4724.	7.2	32
53	Functional and structural analysis of <i>Pichia pastoris</i> -expressed <i>Aspergillus niger</i> 1,4-β-endoglucanase. <i>Biochemical and Biophysical Research Communications</i> , 2016, 475, 8-12.	1.0	34
54	Enhanced β-Zearalenol Hydrolyzing Activity of a Mycoestrogen-Detoxifying Lactonase by Structure-Based Engineering. <i>ACS Catalysis</i> , 2016, 6, 7657-7663.	5.5	36

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55	Crystal structure and genetic modifications of FI-CMCase from <i>Aspergillus aculeatus</i> F-50. <i>Biochemical and Biophysical Research Communications</i> , 2016, 478, 565-572.	1.0	10
56	Functional and structural analyses of a 1,4- β -D-endoglucanase from <i>Ganoderma lucidum</i> . <i>Enzyme and Microbial Technology</i> , 2016, 86, 67-74.	1.6	20
57	Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , 2016, 11, 1362-1371.	1.6	15
58	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.	1.3	32
59	Structural basis of collagen recognition by human osteoclast-associated receptor and design of osteoclastogenesis inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1038-1043.	3.3	25
60	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.	1.6	0
61	Combinatorial RNA Interference Therapy Prevents Selection of Pre-existing HBV Variants in Human Liver Chimeric Mice. <i>Scientific Reports</i> , 2015, 5, 15259.	1.6	16
62	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.	7.2	21
63	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.	1.6	13
64	Antibacterial Drug Leads: DNA and Enzyme Multitargeting. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 1215-1227.	2.9	48
65	Current Progresses in Phytase Research: Three-Dimensional Structure and Protein Engineering. <i>ChemBioEng Reviews</i> , 2015, 2, 76-86.	2.6	24
66	Improving the catalytic performance of a GH11 xylanase by rational protein engineering. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9503-9510.	1.7	40
67	Crystallization and preliminary X-ray diffraction analysis of an endo-1,4- β -D-glucanase from <i>Aspergillus aculeatus</i> F-50. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 397-400.	0.4	2
68	Heat- and Alkali-Stable Xylanases: Application, Protein Structure and Engineering. <i>ChemBioEng Reviews</i> , 2015, 2, 95-106.	2.6	17
69	Crystal structures of S-adenosylhomocysteine hydrolase from the thermophilic bacterium <i>Thermotoga maritima</i> . <i>Journal of Structural Biology</i> , 2015, 190, 135-142.	1.3	8
70	Crystal structures of ligand-bound octaprenyl pyrophosphate synthase from <i>Escherichia coli</i> reveal the catalytic and chain-length determining mechanisms. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 37-45.	1.5	22
71	Squalene Synthase As a Target for Chagas Disease Therapeutics. <i>PLoS Pathogens</i> , 2014, 10, e1004114.	2.1	64
72	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.	0.4	1

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73	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.	0.4	1
74	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.	1.9	43
75	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.	1.1	20
76	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.	1.1	36
77	Structural Analysis of a Glycoside Hydrolase Family 11 Xylanase from <i>Neocallimastix patriciarum</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 11020-11028.	1.6	64
78	Functional and structural studies of pullulanase from <i>Anoxybacillus</i> sp. LM18-11. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1685-1693.	1.5	55
79	Crystal structure and substrate-binding mode of the mycoestrogen-detoxifying lactonase ZHD from <i>Clonostachys rosea</i> . <i>RSC Advances</i> , 2014, 4, 62321-62325.	1.7	37
80	Structural perspectives of an engineered β -1,4-xylanase with enhanced thermostability. <i>Journal of Biotechnology</i> , 2014, 189, 175-182.	1.9	32
81	Structure, function and inhibition of ent-kaurene synthase from <i>Bradyrhizobium japonicum</i> . <i>Scientific Reports</i> , 2014, 4, 6214.	1.6	44
82	Insights into TIM β -Barrel Prenyl Transferase Mechanisms: Crystal Structures of PcrB from <i>Bacillus subtilis</i> and <i>Staphylococcus aureus</i> . <i>ChemBioChem</i> , 2013, 14, 195-199.	1.3	10
83	Preliminary X-ray diffraction analysis of octaprenyl pyrophosphate synthase from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 328-331.	0.7	3
84	Structural and functional analyses of catalytic domain of GH10 xylanase from <i>Thermoanaerobacterium saccharolyticum</i> JW/SL-YS485. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1256-1265.	1.5	13
85	VP2 Dominated CD4+ T Cell Responses against Enterovirus 71 and Cross-Reactivity against Coxsackievirus A16 and Polioviruses in a Healthy Population. <i>Journal of Immunology</i> , 2013, 191, 1637-1647.	0.4	21
86	Preliminary X-ray diffraction analysis of thermostable β -1,4-mannanase from <i>Aspergillus niger</i> BK01. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1100-1102.	0.7	3
87	The substrate/product-binding modes of a novel GH120 β -xylosidase (XylC) from <i>Thermoanaerobacterium saccharolyticum</i> JW/SL-YS485. <i>Biochemical Journal</i> , 2012, 448, 401-407.	1.7	16
88	Crystal structures of d-psicose 3-epimerase from <i>Clostridium cellulolyticum</i> H10 and its complex with ketohexose sugars. <i>Protein and Cell</i> , 2012, 3, 123-131.	4.8	69
89	Rational design to improve thermostability and specific activity of the truncated <i>Fibrobacter succinogenes</i> 1,3-1,4- β -d-glucanase. <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 111-121.	1.7	27
90	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.	1.1	47

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91	Crystal Structures of Bacillus Alkaline Phytase in Complex with Divalent Metal ions and Inositol Hexasulfate. Journal of Molecular Biology, 2011, 409, 214-224.	2.0	34