

Tzu-Ping Ko

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | Crystal structure and functional implication of bacterial STING.. <i>Nature Communications</i> , 2022 , 13, 26 | 17.4 | 1 |
| 125 | Structural and biological insights into Klebsiella pneumoniae surface polysaccharide degradation by a bacteriophage K1 lyase: implications for clinical use.. <i>Journal of Biomedical Science</i> , 2022 , 29, 9 | 13.3 | 0 |
| 124 | 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 | 5.5 | 0 |
| 123 | Integrated omics approach to unveil antifungal bacterial polyynes as acetyl-CoA acetyltransferase inhibitors.. <i>Communications Biology</i> , 2022 , 5, 454 | 6.7 | 1 |
| 122 | Evidence for an Enzyme-Catalyzed Rauhut-Currier Reaction during the Biosynthesis of Spinosyn A. <i>Journal of the American Chemical Society</i> , 2021 , 143, 20291-20295 | 16.4 | 2 |
| 121 | Structural insights into the substrate selectivity of Exoamine synthases from marine Vibrio sp. QWI-06. <i>Colloids and Surfaces B: Biointerfaces</i> , 2021 , 210, 112224 | 6 | 0 |
| 120 | Crystal structure and functional implication of a bacterial cyclic AMP-AMP-GMP synthetase. <i>Nucleic Acids Research</i> , 2021 , 49, 4725-4737 | 20.1 | 3 |
| 119 | A Unique Carboxylic-Acid Hydrogen-Bond Network (CAHBN) Confers Glutaminy Cyclase Activity on M28 Family Enzymes. <i>Journal of Molecular Biology</i> , 2021 , 433, 166960 | 6.5 | 1 |
| 118 | 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 | 3.4 | |
| 117 | Structural insight into the electron transfer pathway of a self-sufficient P450 monooxygenase. <i>Nature Communications</i> , 2020 , 11, 2676 | 17.4 | 17 |
| 116 | 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> , 2020 , 160, 903-914 | 7.9 | 1 |
| 115 | Versatile cis-isoprenyl Diphosphate Synthase Superfamily Members in Catalyzing Carbon-Carbon Bond Formation. <i>ACS Catalysis</i> , 2020 , 10, 4717-4725 | 13.1 | 7 |
| 114 | Structural insights into thebaine synthase 2 catalysis. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 529, 156-161 | 3.4 | 3 |
| 113 | Structural characterization of borneol dehydrogenase from Pseudomonas sp. TCU-HL1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020 , 76, 309-313 | 1.1 | 3 |
| 112 | Structure of a gut microbial diltiazem-metabolizing enzyme suggests possible substrate binding mode. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 527, 799-804 | 3.4 | 2 |
| 111 | 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 | 3.4 | 6 |
| 110 | Structural basis of polyethylene glycol recognition by antibody. <i>Journal of Biomedical Science</i> , 2020 , 27, 12 | 13.3 | 11 |

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|-----|---|------|----|
| 109 | 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> , 2020 , 117, 1438-1446 | 11.5 | 58 |
| 108 | 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 | 2 | 1 |
| 107 | Structural insights into the calcium dependence of Stig cyclases.. <i>RSC Advances</i> , 2019 , 9, 13182-13185 | 3.7 | 2 |
| 106 | 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 | 3.9 | 6 |
| 105 | Structural Insights to the Heterotetrameric Interaction between the PirA and PirB Toxins and Activation of the Cry-Like Pore-Forming Domain. <i>Toxins</i> , 2019 , 11, | 4.9 | 14 |
| 104 | Structural insights to heterodimeric cis-prenyltransferases through yeast dehydrodolichyl diphosphate synthase subunit Nus1. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 515, 621-626 | 3.4 | 9 |
| 103 | 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 | 4 | 3 |
| 102 | Human DNA Polymerase β Can Use a Noncanonical Mechanism for Multiple Mn-Mediated Functions. <i>Journal of the American Chemical Society</i> , 2019 , 141, 8489-8502 | 16.4 | 5 |
| 101 | Reduction in MnSOD promotes the migration and invasion of squamous carcinoma cells. <i>International Journal of Oncology</i> , 2019 , 54, 1639-1650 | 4.4 | 7 |
| 100 | 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 | 7.9 | 2 |
| 99 | Complex structures of MoeN5 with substrate analogues suggest sequential catalytic mechanism. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 511, 800-805 | 3.4 | 2 |
| 98 | 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 | 16.4 | 9 |
| 97 | An Effective Neutralizing Antibody Against Influenza Virus H1N1 from Human B Cells. <i>Scientific Reports</i> , 2019 , 9, 4546 | 4.9 | 7 |
| 96 | Crystal Structure of PigA: A Prolyl Thioester-Oxidizing Enzyme in Prodigiosin Biosynthesis. <i>ChemBioChem</i> , 2019 , 20, 193-202 | 3.8 | 3 |
| 95 | Structural insights into the interaction between phytoplasmal effector causing phyllody 1 and MADS transcription factors. <i>Plant Journal</i> , 2019 , 100, 706-719 | 6.9 | 11 |
| 94 | 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 | 1.1 | 5 |
| 93 | Dietary Flavonoids Luteolin and Quercetin Inhibit Migration and Invasion of Squamous Carcinoma through Reduction of Src/Stat3/S100A7 Signaling. <i>Antioxidants</i> , 2019 , 8, | 7.1 | 29 |
| 92 | Crystal Structure of a Mycoestrogen-Detoxifying Lactonase from <i>Rhinochadiella mackenziei</i> : Molecular Insight into ZHD Substrate Selectivity. <i>ACS Catalysis</i> , 2018 , 8, 4294-4298 | 13.1 | 15 |

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|----|---|------|----|
| 91 | Catalytic Role of Conserved Asparagine, Glutamine, Serine, and Tyrosine Residues in Isoprenoid Biosynthesis Enzymes. <i>ACS Catalysis</i> , 2018 , 8, 4299-4312 | 13.1 | 13 |
| 90 | Structural insight into a novel indole prenyltransferase in hapalindole-type alkaloid biosynthesis. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 495, 1782-1788 | 3.4 | 6 |
| 89 | Head-to-Middle and Head-to-Tail cis-Prenyl Transferases: Structure of Isosesquilavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , 2018 , 130, 691-695 | 3.6 | 3 |
| 88 | Innenstruktur: Head-to-Middle and Head-to-Tail cis-Prenyl Transferases: Structure of Isosesquilavandulyl Diphosphate Synthase (Angew. Chem. 3/2018). <i>Angewandte Chemie</i> , 2018 , 130, 861-861 | 3.6 | 3 |
| 87 | Structural studies reveal the molecular mechanism of PETase. <i>FEBS Journal</i> , 2018 , 285, 3717-3723 | 5.7 | 62 |
| 86 | NADH/NADPH bi-cofactor-utilizing and thermoactive ketol-acid reductoisomerase from <i>Sulfolobus acidocaldarius</i> . <i>Scientific Reports</i> , 2018 , 8, 7176 | 4.9 | 9 |
| 85 | "Head-to-Middle" and "Head-to-Tail" cis-Prenyl Transferases: Structure of Isosesquilavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 683-687 | 16.4 | 17 |
| 84 | Struktur: The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement (Angew. Chem. 46/2018). <i>Angewandte Chemie</i> , 2018 , 130, 15506-15506 | 3.6 | |
| 83 | The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie</i> , 2018 , 130, 15280-15284 | 3.6 | 2 |
| 82 | Structure of undecaprenyl pyrophosphate synthase from <i>Acinetobacter baumannii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018 , 74, 765-769 | 1.1 | 5 |
| 81 | The Crystal Structure of a Class of Cyclases that Catalyze the Cope Rearrangement. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 15060-15064 | 16.4 | 8 |
| 80 | The tetrameric structure of sialic acid-synthesizing UDP-GlcNAc 2-epimerase from : A comparative study with human GNE. <i>Journal of Biological Chemistry</i> , 2018 , 293, 10119-10127 | 5.4 | 1 |
| 79 | Characterization and crystal structure of a thermostable glycoside hydrolase family 45 1,4-Endoglucanase from <i>Thielavia terrestris</i> . <i>Enzyme and Microbial Technology</i> , 2017 , 99, 32-37 | 3.8 | 22 |
| 78 | Structural basis for fragmenting the exopolysaccharide of <i>Acinetobacter baumannii</i> by bacteriophage Φ B6 tailspike protein. <i>Scientific Reports</i> , 2017 , 7, 42711 | 4.9 | 26 |
| 77 | Crystal Structure and Potential Head-to-Middle Condensation Function of a γ -Farnesyl Diphosphate Synthase. <i>ACS Omega</i> , 2017 , 2, 930-936 | 3.9 | 15 |
| 76 | Head-to-Head Prenyl Synthases in Pathogenic Bacteria. <i>ChemBioChem</i> , 2017 , 18, 985-991 | 3.8 | 6 |
| 75 | 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 | 5.4 | 8 |
| 74 | 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 | 3.7 | 3 |

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|----|--|------|-----|
| 73 | The monomeric form of Neisseria DNA mimic protein DMP19 prevents DNA from binding to the histone-like HU protein. <i>PLoS ONE</i> , 2017 , 12, e0189461 | 3.7 | 6 |
| 72 | Structural insight into catalytic mechanism of PET hydrolase. <i>Nature Communications</i> , 2017 , 8, 2106 | 17.4 | 160 |
| 71 | Expression, Purification, Crystallization, and X-ray Structural Analysis of CRISPR-Associated Protein Cas6 from <i>Methanocaldococcus jannaschii</i> . <i>Crystals</i> , 2017 , 7, 344 | 2.3 | 2 |
| 70 | Mechanism and inhibition of human UDP-GlcNAc 2-epimerase, the key enzyme in sialic acid biosynthesis. <i>Scientific Reports</i> , 2016 , 6, 23274 | 4.9 | 25 |
| 69 | Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie</i> , 2016 , 128, 4794-4798 | 3.6 | 3 |
| 68 | Crystal structure of vespid phospholipase A(1) reveals insights into the mechanism for cause of membrane dysfunction. <i>Insect Biochemistry and Molecular Biology</i> , 2016 , 68, 79-88 | 4.5 | 13 |
| 67 | 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, 4440-9 | 20.1 | 11 |
| 66 | Functional and structural analyses of a 1,4-β-D-glucanase from <i>Ganoderma lucidum</i> . <i>Enzyme and Microbial Technology</i> , 2016 , 86, 67-74 | 3.8 | 15 |
| 65 | Structures of Trypanosome Vacuolar Soluble Pyrophosphatases: Antiparasitic Drug Targets. <i>ACS Chemical Biology</i> , 2016 , 11, 1362-71 | 4.9 | 13 |
| 64 | 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 | 3.4 | 23 |
| 63 | Structure and Function of a Head-to-Middle Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie</i> , 2016 , 128, 4799-4802 | 3.6 | 8 |
| 62 | Crystal Structure Analysis of the Repair of Iron Centers Protein YtfE and Its Interaction with NO. <i>Chemistry - A European Journal</i> , 2016 , 22, 9768-76 | 4.8 | 23 |
| 61 | SH3-like motif-containing C-terminal domain of staphylococcal teichoic acid transporter suggests possible function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84, 1328-32 | 4.2 | 3 |
| 60 | Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 4716-20 | 16.4 | 12 |
| 59 | Structure and Function of a "Head-to-Middle" Prenyltransferase: Lavandulyl Diphosphate Synthase. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 4721-4 | 16.4 | 24 |
| 58 | Titelbild: Structure and Function of a Head-to-Middle Prenyltransferase: Lavandulyl Diphosphate Synthase (Angew. Chem. 15/2016). <i>Angewandte Chemie</i> , 2016 , 128, 4689-4689 | 3.6 | 2 |
| 57 | Crystal structures of Staphylococcal SaeR reveal possible DNA-binding modes. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 474, 686-690 | 3.4 | 1 |
| 56 | Enhanced Zearalenol Hydrolyzing Activity of a Mycoestrogen-Detoxifying Lactonase by Structure-Based Engineering. <i>ACS Catalysis</i> , 2016 , 6, 7657-7663 | 13.1 | 18 |

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|----|---|------|-----|
| 55 | Structure, Function, and Inhibition of Staphylococcus aureus Heptaprenyl Diphosphate Synthase. <i>ChemMedChem</i> , 2016 , 11, 1915-23 | 3-7 | 11 |
| 54 | Improving the catalytic performance of a GH11 xylanase by rational protein engineering. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 9503-10 | 5-7 | 35 |
| 53 | Crystal structures of S-adenosylhomocysteine hydrolase from the thermophilic bacterium <i>Thermotoga maritima</i> . <i>Journal of Structural Biology</i> , 2015 , 190, 135-42 | 3-4 | 6 |
| 52 | Structural basis for the antipolymer activity of Hb α trapped in a tense conformation. <i>Journal of Molecular Structure</i> , 2015 , 1099, 99-107 | 3-4 | 2 |
| 51 | 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> , 2015 , 112, 10798-803 | 11.5 | 284 |
| 50 | Titelbild: Structures of Iridoid Synthase from <i>Cantharanthus roseus</i> with Bound NAD ⁺ , NADPH, or NAD ⁺ /10-Oxogeranial: Reaction Mechanisms (Angew. Chem. 51/2015). <i>Angewandte Chemie</i> , 2015 , 127, 15517-15517 | 3.6 | |
| 49 | Structure and mechanism of an antibiotics-synthesizing 3-hydroxykynurenine C-methyltransferase. <i>Scientific Reports</i> , 2015 , 5, 10100 | 4-9 | 10 |
| 48 | 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 | 16.4 | 18 |
| 47 | Structures of Iridoid Synthase from <i>Cantharanthus roseus</i> with Bound NAD ⁺ , NADPH, or NAD ⁺ /10-Oxogeranial: Reaction Mechanisms. <i>Angewandte Chemie</i> , 2015 , 127, 15698-15702 | 3.6 | 4 |
| 46 | Minireview: A Comeback of Hg-Derivatives in Protein Crystallography with Cys-Modification. <i>ChemBioEng Reviews</i> , 2015 , 2, 133-140 | 5-2 | 4 |
| 45 | Binding mode of the oxidized β anomer of NAD ⁺ to RSP, a Rex-family repressor. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 456, 733-6 | 3-4 | 1 |
| 44 | 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 | 3.8 | 10 |
| 43 | Current Progresses in Phytase Research: Three-Dimensional Structure and Protein Engineering. <i>ChemBioEng Reviews</i> , 2015 , 2, 76-86 | 5-2 | 14 |
| 42 | Structure, function and inhibition of ent-kaurene synthase from <i>Bradyrhizobium japonicum</i> . <i>Scientific Reports</i> , 2014 , 4, 6214 | 4-9 | 34 |
| 41 | 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, 663-9 | 4 | 32 |
| 40 | Structure and inhibition of tuberculosinol synthase and decaprenyl diphosphate synthase from <i>Mycobacterium tuberculosis</i> . <i>Journal of the American Chemical Society</i> , 2014 , 136, 2892-6 | 16.4 | 32 |
| 39 | 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> , 2014 , 289, 11020-11028 | 5-4 | 49 |
| 38 | Structural perspectives of an engineered β 1,4-xylanase with enhanced thermostability. <i>Journal of Biotechnology</i> , 2014 , 189, 175-82 | 3-7 | 29 |

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|----|--|------|----|
| 37 | 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, 509-14 | 3-4 | 2 |
| 36 | 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 | 5-4 | 21 |
| 35 | 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 | 3-4 | 8 |
| 34 | Squalene synthase as a target for Chagas disease therapeutics. <i>PLoS Pathogens</i> , 2014 , 10, e1004114 | 7-6 | 54 |
| 33 | 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, 105-7 | 1-1 | 1 |
| 32 | Structural insights into the catalytic mechanism of human squalene synthase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 231-41 | | 25 |
| 31 | 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, 1557-63 | | 32 |
| 30 | <i>Staphylococcus aureus</i> protein SAUGI acts as a uracil-DNA glycosylase inhibitor. <i>Nucleic Acids Research</i> , 2014 , 42, 1354-64 | 20-1 | 29 |
| 29 | Preliminary X-ray diffraction analysis of a thermophilic β 1,3-1,4-glucanase from <i>Clostridium thermocellum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014 , 70, 946-8 | 1-1 | 1 |
| 28 | 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, 1563-5 | 1-1 | 1 |
| 27 | 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, 800-2 | 1-1 | 2 |
| 26 | 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 | 3-7 | 38 |
| 25 | Structural and mutagenetic analyses of a 1,3-1,4- β -glucanase from <i>Paecilomyces thermophila</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 366-73 | 4 | 18 |
| 24 | Structural insights of the ssDNA binding site in the multifunctional endonuclease AtBFN2 from <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2014 , 9, e105821 | 3-7 | 5 |
| 23 | Structure of fully liganded Hb α 2s trapped in a tense conformation. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 2061-71 | | 5 |
| 22 | Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes. <i>Angewandte Chemie</i> , 2012 , 124, 4233-4236 | 3-6 | 5 |
| 21 | Röntgenbild: Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes (Angew. Chem. 17/2012). <i>Angewandte Chemie</i> , 2012 , 124, 4314-4314 | 3-6 | |
| 20 | 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> , 2012 , 51, 4240-4240 | 16-4 | |

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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, 1832-40 | 4 | 32 |
| 18 | Structural Basis of β -Fucosidase Inhibition by Iminocyclitols with Ki Values in the Micro- to Picomolar Range. <i>Angewandte Chemie</i> , 2010 , 122, 347-350 | 3.6 | 8 |
| 17 | Structures of human MST3 kinase in complex with adenine, ADP and Mn ²⁺ . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 145-54 | | 17 |
| 16 | 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> , 2007 , 104, 10022-7 | 11.5 | 150 |
| 15 | Structure and mechanism of <i>Helicobacter pylori</i> fucosyltransferase. A basis for lipopolysaccharide variation and inhibitor design. <i>Journal of Biological Chemistry</i> , 2007 , 282, 9973-9982 | 5.4 | 89 |
| 14 | 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> , 2006 , 46, S443 | 0 | |
| 13 | 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> , 2006 , 46, S195 | 0 | |
| 12 | 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 Session,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S201 | 0 | |
| 11 | 2P058 Dual Binding Sites for Translocation Catalysis by E. coli Glutathionylspermidine Synthetase(29. Protein structure and dynamics (II),Poster Session,Abstract,Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S310 | 0 | |
| 10 | 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> , 2005 , 280, 20762-74 | 5.4 | 92 |
| 9 | Substrate binding mode and reaction mechanism of undecaprenyl pyrophosphate synthase deduced from crystallographic studies. <i>Protein Science</i> , 2004 , 13, 971-8 | 6.3 | 47 |
| 8 | Structures of the hyperthermophilic chromosomal protein Sac7d in complex with DNA decamers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1381-7 | | 10 |
| 7 | Crystal structure of yeast cytosine deaminase. Insights into enzyme mechanism and evolution. <i>Journal of Biological Chemistry</i> , 2003 , 278, 19111-7 | 5.4 | 93 |
| 6 | 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> , 2003 , 84, 1228-37 | 2.9 | 68 |
| 5 | Catalytic mechanism revealed by the crystal structure of undecaprenyl pyrophosphate synthase in complex with sulfate, magnesium, and triton. <i>Journal of Biological Chemistry</i> , 2003 , 278, 29298-307 | 5.4 | 42 |
| 4 | Structure, mechanism and function of prenyltransferases. <i>FEBS Journal</i> , 2002 , 269, 3339-54 | | 315 |
| 3 | 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> , 2001 , 276, 47474-82 | 5.4 | 70 |
| 2 | Structure of human erythrocyte catalase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000 , 56, 241-5 | | 41 |

- 1 Phospholipases A2 from *Callosellasma rhodostoma* venom gland cloning and sequencing of 10 of the cDNAs, three-dimensional modelling and chemical modification of the major isozyme. *FEBS Journal*, **2000**, 267, 6684-91