

Andrew H -J Wang

List of Publications by Year in descending order

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305
papers

16,653
citations

17440

63
h-index

22166

113
g-index

311
all docs

311
docs citations

311
times ranked

16898
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular structure of a left-handed double helical DNA fragment at atomic resolution. <i>Nature</i> , 1979, 282, 680-686.	27.8	2,099
2	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, 10798-10803.	7.1	427
3	A Cholesterol Biosynthesis Inhibitor Blocks <i>Staphylococcus aureus</i> Virulence. <i>Science</i> , 2008, 319, 1391-1394.	12.6	422
4	Structure, mechanism and function of prenyltransferases. <i>FEBS Journal</i> , 2002, 269, 3339-3354.	0.2	382
5	The molecular structure of the complex of Hoechst 33258 and the DNA dodecamer d(CGCGAATTCGCG). <i>Nucleic Acids Research</i> , 1988, 16, 2671-2690.	14.5	335
6	Molecular structure of r(GCG)d(TATACGC): a DNA-RNA hybrid helix joined to double helical DNA. <i>Nature</i> , 1982, 299, 601-604.	27.8	223
7	Genomic and Proteomic Analysis of Thirty-Nine Structural Proteins of Shrimp White Spot Syndrome Virus. <i>Journal of Virology</i> , 2004, 78, 11360-11370.	3.4	219
8	Mechanism of the Maturation Process of SARS-CoV 3CL Protease. <i>Journal of Biological Chemistry</i> , 2005, 280, 31257-31266.	3.4	215
9	AT base pairs are less stable than GC base pairs in Z-DNA: The crystal structure of d(m5CGTAm5CG). <i>Cell</i> , 1984, 37, 321-331.	28.9	211
10	The hyperthermophile chromosomal protein Sac7d sharply kinks DNA. <i>Nature</i> , 1998, 392, 202-205.	27.8	208
11	Molecular structure of (m5dC-dG) ₃ : the role of the methyl group on 5-methyl cytosine in stabilizing Z-DNA. <i>Nucleic Acids Research</i> , 1982, 10, 7879-7892.	14.5	203
12	Structural studies of atom-specific anticancer drugs acting on DNA. , 1999, 83, 181-215.		192
13	Discovery of virulence factors of pathogenic bacteria. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 93-101.	6.1	191
14	The cAMP Receptor-Like Protein CLP Is a Novel c-di-GMP Receptor Linking Cell-Cell Signaling to Virulence Gene Expression in <i>Xanthomonas campestris</i> . <i>Journal of Molecular Biology</i> , 2010, 396, 646-662.	4.2	191
15	Identification of the Nucleocapsid, Tegument, and Envelope Proteins of the Shrimp White Spot Syndrome Virus. <i>Journal of Virology</i> , 2006, 80, 3021-3029.	3.4	189
16	White Spot Syndrome Virus Annexes a Shrimp STAT To Enhance Expression of the Immediate-Early Gene ie1. <i>Journal of Virology</i> , 2007, 81, 1461-1471.	3.4	188
17	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, 10022-10027.	7.1	173
18	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic <i>Neisseria</i> . <i>PLoS Pathogens</i> , 2009, 5, e1000400.	4.7	170

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19	A modified protein precipitation procedure for efficient removal of albumin from serum. <i>Electrophoresis</i> , 2005, 26, 2117-2127.	2.4	161
20	Structural and functional analysis of three β -glucosidases from bacterium <i>Clostridium cellulovorans</i> , fungus <i>Trichoderma reesei</i> and termite <i>Neotermes koshunensis</i> . <i>Journal of Structural Biology</i> , 2011, 173, 46-56.	2.8	161
21	Lipophilic Bisphosphonates as Dual Farnesyl/Geranylgeranyl Diphosphate Synthase Inhibitors: An X-ray and NMR Investigation. <i>Journal of the American Chemical Society</i> , 2009, 131, 5153-5162.	13.7	159
22	The many blades of the β -propeller proteins: conserved but versatile. <i>Trends in Biochemical Sciences</i> , 2011, 36, 553-561.	7.5	158
23	High-throughput screening of soluble recombinant proteins. <i>Protein Science</i> , 2009, 11, 1714-1719.	7.6	145
24	Synthesis, Crystal Structure, Structure-Activity Relationships, and Antiviral Activity of a Potent SARS Coronavirus 3CL Protease Inhibitor. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 4971-4980.	6.4	142
25	Protein expression profiling of the shrimp cellular response to white spot syndrome virus infection. <i>Developmental and Comparative Immunology</i> , 2007, 31, 672-686.	2.3	142
26	Crystallographic studies of metal ion - DNA interactions: different binding modes of cobalt(II), copper(II) and barium(II) to N7 of guanines in Z-DNA and a drug-DNA complex. <i>Nucleic Acids Research</i> , 1993, 21, 4093-4101.	14.5	137
27	The crystal structure of the hyperthermophile chromosomal protein Sso7d bound to DNA. <i>Nature Structural Biology</i> , 1998, 5, 782-786.	9.7	136
28	Cysteine S-Nitrosylation Protects Protein-tyrosine Phosphatase 1B against Oxidation-induced Permanent Inactivation. <i>Journal of Biological Chemistry</i> , 2008, 283, 35265-35272.	3.4	135
29	A one- and two-dimensional NMR study of the B to Z transition of (m5dC-dC) ₃ in methanolic solution. <i>Nucleic Acids Research</i> , 1984, 12, 1243-1263.	14.5	130
30	Structural Basis of Inhibition Specificities of 3C and 3C-like Proteases by Zinc-coordinating and Peptidomimetic Compounds. <i>Journal of Biological Chemistry</i> , 2009, 284, 7646-7655.	3.4	125
31	Crystal Structures of Undecaprenyl Pyrophosphate Synthase in Complex with Magnesium, Isopentenyl Pyrophosphate, and Farnesyl Thiopyrophosphate. <i>Journal of Biological Chemistry</i> , 2005, 280, 20762-20774.	3.4	115
32	Crystal Structure of Yeast Cytosine Deaminase. <i>Journal of Biological Chemistry</i> , 2003, 278, 19111-19117.	3.4	113
33	Structure and Mechanism of <i>Helicobacter pylori</i> Fucosyltransferase. <i>Journal of Biological Chemistry</i> , 2007, 282, 9973-9982.	3.4	113
34	Heterodimeric complexes of Hop2 and Mnd1 function with Dmc1 to promote meiotic homolog juxtaposition and strand assimilation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10572-10577.	7.1	110
35	Terpyridine-platinum(II) complexes are effective inhibitors of mammalian topoisomerases and human thioredoxin reductase 1. <i>Journal of Inorganic Biochemistry</i> , 2009, 103, 1082-1092.	3.5	107
36	Inhibition of Staphyloxanthin Virulence Factor Biosynthesis in <i>Staphylococcus aureus</i> : In Vitro, in Vivo, and Crystallographic Results. <i>Journal of Medicinal Chemistry</i> , 2009, 52, 3869-3880.	6.4	106

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37	Synthesis, Structure and Thermodynamic Properties of 8-Methylguanine-Containing Oligonucleotides: Z-DNA under Physiological Salt Conditions. <i>Nucleic Acids Research</i> , 1996, 24, 1272-1278.	14.5	101
38	Crystal Structure of Type-III Geranylgeranyl Pyrophosphate Synthase from <i>Saccharomyces cerevisiae</i> and the Mechanism of Product Chain Length Determination. <i>Journal of Biological Chemistry</i> , 2006, 281, 14991-15000.	3.4	99
39	Crystal structures of human glutamyl cyclase, an enzyme responsible for protein N-terminal pyroglutamate formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13117-13122.	7.1	94
40	Proteomics and genomics: perspectives on drug and target discovery. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 1-3.	6.1	92
41	Structural Basis of Electron Transfer Modulation in the Purple CuA Center. <i>Biochemistry</i> , 1999, 38, 5677-5683.	2.5	90
42	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, 47474-47482.	3.4	90
43	Structures of <i>Selenomonas ruminantium</i> Phytase in Complex with Persulfated Phytate. <i>Structure</i> , 2004, 12, 2015-2024.	3.3	90
44	Strategic shotgun proteomics approach for efficient construction of an expression map of targeted protein families in hepatoma cell lines. <i>Proteomics</i> , 2003, 3, 2472-2486.	2.2	89
45	Unusual DNA duplex and hairpin motifs. <i>Nucleic Acids Research</i> , 2003, 31, 2461-2474.	14.5	87
46	Identification of a Novel Prostaglandin Reductase Reveals the Involvement of Prostaglandin E2 Catabolism in Regulation of Peroxisome Proliferator-activated Receptor β Activation. <i>Journal of Biological Chemistry</i> , 2007, 282, 18162-18172.	3.4	86
47	Structure of a Heterotetrameric Geranyl Pyrophosphate Synthase from Mint (<i>Mentha piperita</i>) Reveals Intersubunit Regulation. <i>Plant Cell</i> , 2010, 22, 454-467.	6.6	85
48	Mutations in the substrate entrance region of α -glucosidase from <i>Trichoderma reesei</i> improve enzyme activity and thermostability. <i>Protein Engineering, Design and Selection</i> , 2012, 25, 733-740.	2.1	81
49	White spot syndrome virus protein ICP11: A histone-binding DNA mimic that disrupts nucleosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20758-20763.	7.1	79
50	Structural study of TcaR and its complexes with multiple antibiotics from <i>Staphylococcus epidermidis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8617-8622.	7.1	79
51	Crystal structure of the $[Mg^{2+}-(chromomycin\ A3)_2]-d(TTGGCCAA)_2$ complex reveals GGCC binding specificity of the drug dimer chelated by a metal ion. <i>Nucleic Acids Research</i> , 2004, 32, 2214-2222.	14.5	78
52	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, 1228-1237.	0.5	76
53	Solution Structure of a DNA Duplex Containing acis-Diammineplatinum(II) 1,3-d(GTG) Intrastrand Cross-Link, a Major Adduct in Cells Treated with the Anticancer Drug Carboplatin. <i>Biochemistry</i> , 1999, 38, 12305-12312.	2.5	75
54	The Interactions of Ruthenium Hexaammine with Z-DNA: Crystal Structure of a $RU(NH_3)_6^{3+}$ Salt of d(CGCGCG) at 1.2 Å Resolution. <i>Journal of Biomolecular Structure and Dynamics</i> , 1987, 4, 521-534.	3.5	73

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55	Inhibition of Geranylgeranyl Diphosphate Synthase by Bisphosphonates: A Crystallographic and Computational Investigation. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 5594-5607.	6.4	73
56	DNA Interactions of Two Clinical Camptothecin Drugs Stabilize Their Active Lactone Forms. <i>Journal of the American Chemical Society</i> , 1998, 120, 2979-2980.	13.7	72
57	The Unique Stacked Rings in the Nucleocapsid of the White Spot Syndrome Virus Virion Are Formed by the Major Structural Protein VP664, the Largest Viral Structural Protein Ever Found. <i>Journal of Virology</i> , 2005, 79, 140-149.	3.4	72
58	A 3D Model of the Membrane Protein Complex Formed by the White Spot Syndrome Virus Structural Proteins. <i>PLoS ONE</i> , 2010, 5, e10718.	2.5	71
59	DNA aptamers as potential anti-HIV agents. <i>Trends in Biochemical Sciences</i> , 2005, 30, 231-234.	7.5	70
60	Structure and Mechanism of an Arabidopsis Medium/Long-Chain-Length Prenyl Pyrophosphate Synthase. <i>Plant Physiology</i> , 2011, 155, 1079-1090.	4.8	68
61	The propeller DNA conformation of poly(dA).poly(dT). <i>Nucleic Acids Research</i> , 1989, 17, 3229-3245.	14.5	67
62	Chicken Heat Shock Protein 90 Is a Component of the Putative Cellular Receptor Complex of Infectious Bursal Disease Virus. <i>Journal of Virology</i> , 2007, 81, 8730-8741.	3.4	67
63	Structural and Functional Roles of Glycosylation in Fungal Laccase from <i>Lentinus sp.</i> . <i>PLoS ONE</i> , 2015, 10, e0120601.	2.5	67
64	Atomic resolution analysis of a 2:1 complex of CpG and acridine orange. <i>Nucleic Acids Research</i> , 1979, 6, 3879-3890.	14.5	66
65	Mechanism of action and inhibition of dehydrosqualene synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21337-21342.	7.1	66
66	Interactions of Quinoxaline Antibiotic and DNA: The Molecular Structure of a Triostin d(CGCTACGC) Complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 319-342.	3.5	65
67	Crystal structure of IcaR, a repressor of the TetR family implicated in biofilm formation in <i>Staphylococcus epidermidis</i> . <i>Nucleic Acids Research</i> , 2008, 36, 1567-1577.	14.5	64
68	Squalene Synthase As a Target for Chagas Disease Therapeutics. <i>PLoS Pathogens</i> , 2014, 10, e1004114.	4.7	64
69	Crystal Structure of Octaprenyl Pyrophosphate Synthase from Hyperthermophilic <i>Thermotoga maritima</i> and Mechanism of Product Chain Length Determination. <i>Journal of Biological Chemistry</i> , 2004, 279, 4903-4912.	3.4	63
70	Crystal structures of the human SUMO-2 protein at 1.6 Å and 1.2 Å resolution. <i>FEBS Journal</i> , 2004, 271, 4114-4122.	0.2	62
71	Crystal Structures of the Blal Repressor from <i>Staphylococcus aureus</i> and Its Complex with DNA: Insights into Transcriptional Regulation of the bla and mec Operons. <i>Journal of Bacteriology</i> , 2005, 187, 1833-1844.	2.2	62
72	The octamers d(CGCGCGCG) and d(CGCATGCG) both crystallize as Z-DNA in the same hexagonal lattice. <i>Biopolymers</i> , 1985, 24, 243-250.	2.4	61

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73	Crystal structure of infectious bursal disease virus VP2 subviral particle at 2.6Å... resolution: Implications in virion assembly and immunogenicity. <i>Journal of Structural Biology</i> , 2006, 155, 74-86.	2.8	61
74	Crystal structure of actinomycin D bound to the CTG triplet repeat sequences linked to neurological diseases. <i>Nucleic Acids Research</i> , 2002, 30, 4910-4917.	14.5	60
75	Glycan Array on Aluminum Oxide-Coated Glass Slides through Phosphonate Chemistry. <i>Journal of the American Chemical Society</i> , 2010, 132, 13371-13380.	13.7	58
76	Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of <i>Neisseria meningitidis</i> . <i>Nucleic Acids Research</i> , 2015, 43, 4150-4162.	14.5	58
77	Molecular structure of an A-DNA decamer d(ACCGCCGGT). <i>FEBS Journal</i> , 1989, 181, 295-307.	0.2	57
78	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, 29298-29307.	3.4	57
79	A novel DNA structure induced by the anticancer bisplatinum compound crosslinked to a GpC site in DNA. <i>Nature Structural Biology</i> , 1995, 2, 577-586.	9.7	56
80	Structural studies of interactions between anticancer platinum drugs and DNA. <i>Progress in Biophysics and Molecular Biology</i> , 1996, 66, 81-111.	2.9	56
81	Structural Studies of a Stable Parallel-Stranded DNA Duplex Incorporating Isoguanine:Cytosine and Isocytosine:Guanine Basepairs by Nuclear Magnetic Resonance Spectroscopy. <i>Biophysical Journal</i> , 1998, 75, 1163-1171.	0.5	55
82	Crystal structures of the chromosomal proteins Sso7d/Sac7d bound to DNA containing T-G mismatched base-pairs. <i>Journal of Molecular Biology</i> , 2000, 303, 395-403.	4.2	55
83	Crystal Structure of the Hyperthermophilic Archaeal DNA-Binding Protein Sso10b2 at a Resolution of 1.85 Angstroms. <i>Journal of Bacteriology</i> , 2003, 185, 4066-4073.	2.2	55
84	Dual binding sites for translocation catalysis by <i>Escherichia coli</i> glutathionylspermidine synthetase. <i>EMBO Journal</i> , 2006, 25, 5970-5982.	7.8	55
85	Crystal Structure of d-Aminoacylase from <i>Alcaligenes faecalis</i> DA1. <i>Journal of Biological Chemistry</i> , 2003, 278, 4957-4962.	3.4	54
86	Substrate binding mode and reaction mechanism of undecaprenyl pyrophosphate synthase deduced from crystallographic studies. <i>Protein Science</i> , 2004, 13, 971-978.	7.6	54
87	Early detection of antibodies against various structural proteins of the SARS-associated coronavirus in SARS patients. <i>Journal of Biomedical Science</i> , 2004, 11, 117-126.	7.0	54
88	Biochemical and immunological studies of nucleocapsid proteins of severe acute respiratory syndrome and 229E human coronaviruses. <i>Proteomics</i> , 2005, 5, 925-937.	2.2	53
89	The Hexameric Structures of Human Heat Shock Protein 90. <i>PLoS ONE</i> , 2011, 6, e19961.	2.5	53
90	Structural basis of mercury- and zinc-conjugated complexes as SARS-CoV 3C-like protease inhibitors. <i>FEBS Letters</i> , 2007, 581, 5454-5458.	2.8	51

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91	In Vitro Modification of Human Centromere Protein CENP-C Fragments by Small Ubiquitin-like Modifier (SUMO) Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 39653-39662.	3.4	50
92	Self-cleavage of fusion protein in vivo using TEV protease to yield native protein. <i>Protein Science</i> , 2005, 14, 936-941.	7.6	50
93	Structures of Human Golgi-resident Glutamyl Cyclase and Its Complexes with Inhibitors Reveal a Large Loop Movement upon Inhibitor Binding. <i>Journal of Biological Chemistry</i> , 2011, 286, 12439-12449.	3.4	50
94	Crowning Proteins: Modulating the Protein Surface Properties using Crown Ethers. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13054-13058.	13.8	49
95	Structural basis for fragmenting the exopolysaccharide of <i>Acinetobacter baumannii</i> by bacteriophage ϕ AB6 tailspike protein. <i>Scientific Reports</i> , 2017, 7, 42711.	3.3	49
96	In situ proteolysis of the <i>Vibrio cholerae</i> matrix protein RbmA promotes biofilm recruitment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10491-10496.	7.1	48
97	Structure of Actinomycin D bound with (GAAGCTTC) ₂ and (GATGCTTC) ₂ and Its Binding to the (CAG) _n :(CTG) _n Triplet Sequence As Determined by NMR Analysis. <i>Journal of the American Chemical Society</i> , 1996, 118, 8791-8801.	13.7	47
98	Structural Basis for Catalytic and Inhibitory Mechanisms of Human Prostaglandin Reductase PTGR2. <i>Structure</i> , 2008, 16, 1714-1723.	3.3	46
99	DNA Mimic Proteins: Functions, Structures, and Bioinformatic Analysis. <i>Biochemistry</i> , 2014, 53, 2865-2874.	2.5	46
100	Structural D/E-rich repeats play multiple roles especially in gene regulation through DNA/RNA mimicry. <i>Molecular BioSystems</i> , 2015, 11, 2144-2151.	2.9	46
101	Molecular Structure of the Complex Formed Between the Anticancer Drug Cisplatin and d(pGpG): C222 ₁ Crystal Form. <i>Journal of Biomolecular Structure and Dynamics</i> , 1990, 8, 315-330.	3.5	43
102	DNA with 2'-5' Phosphodiester Bonds Forms a Duplex Structure in the A-type Conformation. <i>Journal of the American Chemical Society</i> , 1995, 117, 837-838.	13.7	43
103	XC1028 from <i>Xanthomonas campestris</i> adopts a PilZ domain-like structure without a c-di-GMP switch. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 282-288.	2.6	43
104	Intermolecular Binding between TIFA-FHA and TIFA-pT Mediates Tumor Necrosis Factor Alpha Stimulation and NF- κ B Activation. <i>Molecular and Cellular Biology</i> , 2012, 32, 2664-2673.	2.3	43
105	The Functional Role of the Binuclear Metal Center in d-Aminoacylase. <i>Journal of Biological Chemistry</i> , 2004, 279, 13962-13967.	3.4	42
106	Structures of Cobalt(III)-Pepleomycin and Cobalt(III)-Deglycopepleomycin (green forms) Determined by NMR Studies. <i>FEBS Journal</i> , 1997, 244, 818-828.	0.2	41
107	Crystal structure of the left-handed archaeal RadA helical filament: identification of a functional motif for controlling quaternary structures and enzymatic functions of RecA family proteins. <i>Nucleic Acids Research</i> , 2007, 35, 1787-1801.	14.5	40
108	Structures of a potent phenylalkyl bisphosphonate inhibitor bound to farnesyl and geranylgeranyl diphosphate synthases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 73, 431-439.	2.6	40

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109	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
110	High-resolution A-DNA crystal structures of d(AGGGGCCCT). An A-DNA model of poly(dG).poly(dC). <i>FEBS Journal</i> , 1999, 261, 413-420.	0.2	39
111	Binding Modes of Zaragozic Acid A to Human Squalene Synthase and Staphylococcal Dehydrosqualene Synthase. <i>Journal of Biological Chemistry</i> , 2012, 287, 18750-18757.	3.4	39
112	Barbatusin and cyclobutatusin, two novel diterpenoids from <i>coleus barbatus bentham</i> . <i>Tetrahedron</i> , 1977, 33, 1457-1467.	1.9	38
113	NMR studies on the binding of antitumor drug nogalamycin to DNA hexamer d(CGACG). <i>Nucleic Acids Research</i> , 1990, 18, 4851-4858.	14.5	38
114	Structure of the Alkalohyperthermophilic <i>Archaeoglobus fulgidus</i> Lipase Contains a Unique C-Terminal Domain Essential for Long-Chain Substrate Binding. <i>Journal of Molecular Biology</i> , 2009, 390, 672-685.	4.2	38
115	Structural basis for the antibody neutralization of <i>Herpes simplex virus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1935-1945.	2.5	38
116	Crystal structure and substrate-binding mode of cellulase 12A from <i>Thermotoga maritima</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1193-1204.	2.6	37
117	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
118	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.	3.6	37
119	Structure of 11-deoxydaunomycin bound to DNA containing a phosphorothioate. <i>Journal of Molecular Biology</i> , 1990, 215, 313-320.	4.2	36
120	Probing the DNA kink structure induced by the hyperthermophilic chromosomal protein Sac7d. <i>Nucleic Acids Research</i> , 2005, 33, 430-438.	14.5	36
121	Structural Basis of Fucosidase Inhibition by Iminocyclitols with K_i Values in the Micro-to Picomolar Range. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 337-340.	13.8	36
122	High-resolution structures of <i>Neotermes koshunensis</i> β -glucosidase mutants provide insights into the catalytic mechanism and the synthesis of glucoconjugates. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 829-838.	2.5	36
123	Proposed Carrier Lipid-binding Site of Undecaprenyl Pyrophosphate Phosphatase from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18719-18735.	3.4	36
124	Cyclic diguanylic acid behaves as a host molecule for planar intercalators. <i>FEBS Letters</i> , 1990, 264, 223-227.	2.8	35
125	Monofunctional platinum amine complexes destabilize DNA significantly. <i>FEBS Journal</i> , 1998, 256, 253-260.	0.2	35
126	Probing the Conformational Change of <i>Escherichia coli</i> Undecaprenyl Pyrophosphate Synthase during Catalysis Using an Inhibitor and Tryptophan Mutants. <i>Journal of Biological Chemistry</i> , 2002, 277, 7369-7376.	3.4	35

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127	Protein S-Thiolation by Glutathionylspermidine (Gsp). <i>Journal of Biological Chemistry</i> , 2010, 285, 25345-25353.	3.4	35
128	Crystal Structures of the Laminarinase Catalytic Domain from <i>Thermotoga maritima</i> MSB8 in Complex with Inhibitors. <i>Journal of Biological Chemistry</i> , 2011, 286, 45030-45040.	3.4	35
129	Enhancement of laccase activity by pre-incubation with organic solvents. <i>Scientific Reports</i> , 2019, 9, 9754.	3.3	35
130	Crystal Structure of A Z-DNA Fragment Containing Thymine/2-Amino adenine Base Pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1986, 4, 157-172.	3.5	34
131	Deoxyadenosine and Thymidine Bases Held Proximal and Distal by Means of a Covalently-Linked Dimensional Analogue of dA·dT: Intramolecular vs Intermolecular Hydrogen Bonding1. <i>Journal of the American Chemical Society</i> , 1996, 118, 10744-10751.	13.7	34
132	Determinants of the inhibition of a Taiwan habu venom metalloproteinase by its endogenous inhibitors revealed by X-ray crystallography and synthetic inhibitor analogues. <i>FEBS Journal</i> , 2002, 269, 3047-3056.	0.2	34
133	Enhanced activity of <i>Thermotoga maritima</i> cellulase 12A by mutating a unique surface loop. <i>Applied Microbiology and Biotechnology</i> , 2012, 95, 661-669.	3.6	34
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273	Binding and catalysis of <i>Humulus lupulus</i> adenylyl isopentenyltransferase for the synthesis of isopentenylated diadenosine polyphosphates. <i>FEBS Letters</i> , 2010, 584, 4083-4088.	2.8	4
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288	Conformation of Nucleic Acids and Their Interactions with Drugs. <i>ACS Symposium Series</i> , 1984, , 105-136.	0.5	0

#	ARTICLE	IF	CITATIONS
289	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	0.784314	0
290	PL-5 Structural and functional analysis of enzyme targets for drug design(Plenary) Tj ETQq0 0 0 rgBT /Overlock 10	0.1	0
291	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 ETQq1 1 0.784314 rgBT /Overlock 10	0.784314	0
292	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 ETQq0 0 0 rgBT /Overlock 10	0.1	0
293	1P220 The DNA-recognition fold of Sso7c4 suggests an ancestral role in the evolution of \hat{I}^2 -barrel protein family(7. Nucleic acid binding protein,Poster Session,Abstract,Meeting Program of EABS & BS) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.784314	0
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300	The role of protein glycosylation in laccases from <i>Lentinus</i> sp.. FASEB Journal, 2013, 27, 561.9.	0.5	0
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305	Biosynthesis of Vitroprocines by \hat{I}^{\pm} -Oxoamine Synthase and Oxidoreductase Identified from <i>Vibrio</i> sp. QWI-06. Organic Letters, 2022, 24, 3281-3285.	4.6	0