Andrew H -J Wang

List of Publications by Year
in descending order

305 papers	16,653 citations	20036 63 h-index	25230 113 g-index
311 all docs	311 docs citations	311 times ranked	18709 citing authors

#	Article	IF	Citations
1	Structural basis of an epitope tagging system derived from Haloarcula marismortui bacteriorhodopsin I D94N and its monoclonal antibody GDâ€26. FEBS Journal, 2022, 289, 730-747.	2.2	1
2	Structural and biological insights into Klebsiella pneumoniae surface polysaccharide degradation by a bacteriophage K1 lyase: implications for clinical use. Journal of Biomedical Science, 2022, 29, 9.	2.6	9
3	Biosynthesis of Vitroprocines by Î±-Oxoamine Synthase and Oxidoreductase Identified from Vibrio sp. QWI-06. Organic Letters, 2022, 24, 3281-3285.	2.4	0
4	Structure, catalysis, and inhibition mechanism of prenyltransferase. IUBMB Life, 2021, 73, 40-63.	1.5	34
5	How does <scp>the International Union of Biochemistry and Molecular Biology</scp> support education and training?. Biochemistry and Molecular Biology Education, 2021, 49, 7-8.	0.5	0
6	Crystal structure of the N-terminal domain of TagH reveals a potential drug targeting site. Biochemical and Biophysical Research Communications, 2021, 536, 1-6.	1.0	1
7	Structure-based Development of Human Interleukin-1Î²-Specific Antibody That Simultaneously Inhibits Binding to Both IL-1RI and IL-1RAcP. Journal of Molecular Biology, 2021, 433, 166766.	2.0	10
8	DMTMM-Mediated Intramolecular Cyclization of Acidic Residues in Peptides/Proteins. ACS Omega, 2021, 6, 4708-4718.	1.6	1
9	Concern over use of the term Z-DNA. Nature, 2021, 594, 333-333.	13.7	2
10	A Unique Carboxylic-Acid Hydrogen-Bond Network (CAHBN) Confers Glutaminyl Cyclase Activity on M28 Family Enzymes. Journal of Molecular Biology, 2021, 433, 166960.	2.0	1
11	Synthesis and biological evaluation of phenothiazine derivative-containing hydroxamic acids as potent class II histone deacetylase inhibitors. European Journal of Medicinal Chemistry, 2021, 219, 113419.	2.6	8
12	<scp>IUBMB</scp> Life enters a new era. IUBMB Life, 2021, 73, 9-9.	1.5	0
13	Vibrio cholerae biofilm scaffolding protein RbmA shows an intrinsic, phosphateâ€dependent autoproteolysis activity. IUBMB Life, 2021, 73, 418-431.	1.5	2
14	Structural basis of polyethylene glycol recognition by antibody. Journal of Biomedical Science, 2020, 27, 12.	2.6	34
15	Preparation and characterization of antibody-drug conjugates acting on HER2-positive cancer cells. PLoS ONE, 2020, 15, e0239813.	1.1	9
16	Biochemical and molecular dynamics studies of archaeal polyisoprenyl pyrophosphate phosphatase from Saccharolobus solfataricus. Enzyme and Microbial Technology, 2020, 139, 109585.	1.6	2
17	Development of a Versatile and Modular Linker for Antibodyâ€“Drug Conjugates Based on Oligonucleotide Strand Pairing. Bioconjugate Chemistry, 2020, 31, 1804-1811.	1.8	9
18	Crystal Structure of PigA: A Prolyl Thioesterâ€Oxidizing Enzyme in Prodigiosin Biosynthesis. ChemBioChem, 2019, 20, 193-202.	1.3	7

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19	Enhancement of laccase activity by pre-incubation with organic solvents. Scientific Reports, 2019, 9, 9754.	1.6	35
20	Chaetomella raphigera Î²-glucosidase D2-BGL has intriguing structural features and a high substrate affinity that renders it an efficient cellulase supplement for lignocellulosic biomass hydrolysis. Biotechnology for Biofuels, 2019, 12, 258.	6.2	19
21	Thermococcus sp. 9Â°N DNA polymerase exhibits 3â€²-esterase activity that can be harnessed for DNA sequencing. Communications Biology, 2019, 2, 224.	2.0	6
22	An Effective Neutralizing Antibody Against Influenza Virus H1N1 from Human B Cells. Scientific Reports, 2019, 9, 4546.	1.6	13
23	Crystal Structures of the Câ€Terminally Truncated Endoglucanase Cel9Q from Clostridium thermocellum Complexed with Cellodextrins and Tris. ChemBioChem, 2019, 20, 295-307.	1.3	4
24	New paradigm of functional regulation by DNA mimic proteins: Recent updates. IUBMB Life, 2019, 71, 539-548.	1.5	24
25	Antibody-drug conjugates with HER2-targeting antibodies from synthetic antibody libraries are highly potent against HER2-positive human gastric tumor in xenograft models. MAbs, 2019, 11, 153-165.	2.6	10
26	The C-terminal D/E-rich domain of MBD3 is a putative Z-DNA mimic that competes for ZÎ± DNA-binding activity. Nucleic Acids Research, 2018, 46, 11806-11821.	6.5	6
27	Kinetic analysis and structural studies of a highâ€efficiency laccase from Cerrena sp. <scp>RSD</scp>1. FEBS Open Bio, 2018, 8, 1230-1246.	1.0	20
28	Structural Basis for Stabilization of Z-DNA by Cobalt Hexaammine and Magnesium Cations. journal of hand surgery Asian-Pacific volume, The, 2018, , 196-199.	0.2	0
29	Molecular structure of a left-handed double helical DNA fragment at atomic resolution. journal of hand surgery Asian-Pacific volume, The, 2018, , 180-186.	0.2	0
30	Structural basis for fragmenting the exopolysaccharide of Acinetobacter baumannii by bacteriophage Î¦AB6 tailspike protein. Scientific Reports, 2017, 7, 42711.	1.6	49
31	Crystal Structure and Potential Head-to-Middle Condensation Function of a Z,Z-Farnesyl Diphosphate Synthase. ACS Omega, 2017, 2, 930-936.	1.6	23
32	In search of tail-anchored protein machinery in plants: reevaluating the role of arsenite transporters. Scientific Reports, 2017, 7, 46022.	1.6	8
33	Expression, purification and enzymatic characterization of undecaprenyl pyrophosphate phosphatase from Vibrio vulnificus. Protein Expression and Purification, 2017, 133, 121-131.	0.6	4
34	High throughput discovery of influenza virus neutralizing antibodies from phage-displayed synthetic antibody libraries. Scientific Reports, 2017, 7, 14455.	1.6	15
35	The Arginine Pairs and C-Termini of the Sso7c4 from Sulfolobus solfataricus Participate in Binding and Bending DNA. PLoS ONE, 2017, 12, e0169627.	1.1	4
36	Exploring the Mechanism Responsible for Cellulase Thermostability by Structure-Guided Recombination. PLoS ONE, 2016, 11, e0147485.	1.1	32

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37	Moenomycin Biosynthesis: Structure and Mechanism of Action of the Prenyltransferase MoeN5. Angewandte Chemie - International Edition, 2016, 55, 4716-4720.	7.2	19
38	High throughput cytotoxicity screening of anti-HER2 immunotoxins conjugated with antibody fragments from phage-displayed synthetic antibody libraries. Scientific Reports, 2016, 6, 31878.	1.6	19
39	Crystal structure of vespid phospholipase A1 reveals insights into the mechanism for cause of membrane dysfunction. Insect Biochemistry and Molecular Biology, 2016, 68, 79-88.	1.2	18
40	Using structural-based protein engineering to modulate the differential inhibition effects of SAUGI on human and HSV uracil DNA glycosylase. Nucleic Acids Research, 2016, 44, 4440-4449.	6.5	14
41	Determining the N-terminal orientations of recombinant transmembrane proteins in the Escherichia coli plasma membrane. Scientific Reports, 2015, 5, 15086.	1.6	11
42	Chromophore Deprotonation State Alters the Optical Properties of Blue Chromoprotein. PLoS ONE, 2015, 10, e0134108.	1.1	6
43	Structural D/E-rich repeats play multiple roles especially in gene regulation through DNA/RNA mimicry. Molecular BioSystems, 2015, 11, 2144-2151.	2.9	46
44	Predominant structural configuration of natural antibody repertoires enables potent antibody responses against protein antigens. Scientific Reports, 2015, 5, 12411.	1.6	17
45	Specificity of the ModA11, ModA12 and ModD1 epigenetic regulator N6-adenine DNA methyltransferases of Neisseria meningitidis. Nucleic Acids Research, 2015, 43, 4150-4162.	6.5	58
46	Substrate Specificity and Plasticity of FERM-Containing Protein Tyrosine Phosphatases. Structure, 2015, 23, 653-664.	1.6	20
47	Structural and Functional Studies of a Newly Grouped Haloquadratum walsbyi Bacteriorhodopsin Reveal the Acid-resistant Light-driven Proton Pumping Activity. Journal of Biological Chemistry, 2015, 290, 29567-29577.	1.6	13
48	In situ proteolysis of the Vibrio cholerae matrix protein RbmA promotes biofilm recruitment. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10491-10496.	3.3	48
49	The opportunistic marine pathogen Vibrio parahaemolyticus 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.	3.3	427
50	Crystal structures of ligandâ€bound octaprenyl pyrophosphate synthase from Escherichia coli reveal the catalytic and chainâ€length determining mechanisms. Proteins: Structure, Function and Bioinformatics, 2015, 83, 37-45.	1.5	22
51	Structural and Functional Roles of Glycosylation in Fungal Laccase from Lentinus sp.. PLoS ONE, 2015, 10, e0120601.	1.1	67
52	Linked Production of Pyroglutamate-Modified Proteins via Self-Cleavage of Fusion Tags with TEV Protease and Autonomous N-Terminal Cyclization with Glutaminyl Cyclase In Vivo. PLoS ONE, 2014, 9, e94812.	1.1	21
53	Crowning Proteins: Modulating the Protein Surface Properties using Crown Ethers. Angewandte Chemie - International Edition, 2014, 53, 13054-13058.	7.2	49
54	Pin1-mediated Sp1 phosphorylation by CDK1 increases Sp1 stability and decreases its DNA-binding activity during mitosis. Nucleic Acids Research, 2014, 42, 13573-13587.	6.5	19

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55	Distinct structural features of Rex-family repressors to sense redox levels in anaerobes and aerobes. Journal of Structural Biology, 2014, 188, 195-204.	1.3	20
56	Squalene Synthase As a Target for Chagas Disease Therapeutics. PLoS Pathogens, 2014, 10, e1004114.	2.1	64
57	Proposed Carrier Lipid-binding Site of Undecaprenyl Pyrophosphate Phosphatase from Escherichia coli. Journal of Biological Chemistry, 2014, 289, 18719-18735.	1.6	36
58	Structural insights into the catalytic mechanism of human squalene synthase. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 231-241.	2.5	40
59	Staphylococcus aureus protein SAUGI acts as a uracil-DNA glycosylase inhibitor. Nucleic Acids Research, 2014, 42, 1354-1364.	6.5	32
60	TcaRâ€“ssDNA complex crystal structure reveals new DNA binding mechanism of the MarR family proteins. Nucleic Acids Research, 2014, 42, 5314-5321.	6.5	9
61	Structure and Inhibition of Tuberculosinol Synthase and Decaprenyl Diphosphate Synthase from Mycobacterium tuberculosis. Journal of the American Chemical Society, 2014, 136, 2892-2896.	6.6	37
62	Coreâ€shell structure microcapsules with dual pHâ€responsive drug release function. Electrophoresis, 2014, 35, 2673-2680.	1.3	23
63	Crystal structure and substrate-binding mode of the mycoestrogen-detoxifying lactonase ZHD from Clonostachys rosea. RSC Advances, 2014, 4, 62321-62325.	1.7	37
64	Structural Insights into Enzymatic Degradation of Oxidized Polyvinyl Alcohol. ChemBioChem, 2014, 15, 1882-1886.	1.3	18
65	The T4 Phage DNA Mimic Protein Arn Inhibits the DNA Binding Activity of the Bacterial Histone-like Protein H-NS. Journal of Biological Chemistry, 2014, 289, 27046-27054.	1.6	28
66	DNA Mimic Proteins: Functions, Structures, and Bioinformatic Analysis. Biochemistry, 2014, 53, 2865-2874.	1.2	46
67	Structural and functional analyses of a glutaminyl cyclase from Ixodes scapularis reveal metal-independent catalysis and inhibitor binding. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 789-801.	2.5	10
68	Reciprocal allosteric regulation of p38Î³ and PTPN3 involves a PDZ domainâ€“modulated complex formation. Science Signaling, 2014, 7, ra98.	1.6	25
69	Structural Insights of the ssDNA Binding Site in the Multifunctional Endonuclease AtBFN2 from Arabidopsis thaliana. PLoS ONE, 2014, 9, e105821.	1.1	7
70	Mechanistic insights to catalysis by a zinc-dependent bi-functional nuclease from Arabidopsis thaliana. Biocatalysis and Agricultural Biotechnology, 2013, 2, 191-195.	1.5	5
71	Crystal structure of a Trimeresurus mucrosquamatus venom metalloproteinase providing new insights into the inhibition by endogenous tripeptide inhibitors. Toxicon, 2013, 71, 140-146.	0.8	11
72	Electrostatic droplets assisted in situ synthesis of superparamagnetic chitosan microparticles for magnetic-responsive controlled drug release and copper ion removal. Journal of Materials Chemistry B, 2013, 1, 2205.	2.9	30

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73	Using Haloarcula marismortui Bacteriorhodopsin as a Fusion Tag for Enhancing and Visible Expression of Integral Membrane Proteins in Escherichia coli. PLoS ONE, 2013, 8, e56363.	1.1	33
74	Neisseria conserved hypothetical protein DMP12 is a DNA mimic that binds to histone-like HU protein. Nucleic Acids Research, 2013, 41, 5127-5138.	6.5	16
75	Crystal Structure of Vaccinia Viral A27 Protein Reveals a Novel Structure Critical for Its Function and Complex Formation with A26 Protein. PLoS Pathogens, 2013, 9, e1003563.	2.1	32
76	Structural basis for the antibody neutralization ofHerpes simplex virus. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1935-1945.	2.5	38
77	Structural Insights into RbmA, a Biofilm Scaffolding Protein of V. Cholerae. PLoS ONE, 2013, 8, e82458.	1.1	34
78	The role of protein glycosylation in laccases from Lentinus sp.. FASEB Journal, 2013, 27, 561.9.	0.2	0
79	Mutations in the substrate entrance region of Â-glucosidase from Trichoderma reesei improve enzyme activity and thermostability. Protein Engineering, Design and Selection, 2012, 25, 733-740.	1.0	81
80	Intermolecular Binding between TIFA-FHA and TIFA-pT Mediates Tumor Necrosis Factor Alpha Stimulation and NF-Î°B Activation. Molecular and Cellular Biology, 2012, 32, 2664-2673.	1.1	43
81	Binding Modes of Zaragozic Acid A to Human Squalene Synthase and Staphylococcal Dehydrosqualene Synthase. Journal of Biological Chemistry, 2012, 287, 18750-18757.	1.6	39
82	Facile Synthesis of Radial-Like Macroporous Superparamagnetic Chitosan Spheres with In-Situ Co-Precipitation and Gelation of Ferro-Gels. PLoS ONE, 2012, 7, e49329.	1.1	23
83	Neisseria conserved protein DMP19 is a DNA mimic protein that prevents DNA binding to a hypothetical nitrogen-response transcription factor. Nucleic Acids Research, 2012, 40, 5718-5730.	6.5	26
84	Inhibition of glutaminyl cyclase attenuates cell migration modulated by monocyte chemoattractant proteins. Biochemical Journal, 2012, 442, 403-412.	1.7	20
85	Engineering of dual-functional hybrid glucanases. Protein Engineering, Design and Selection, 2012, 25, 771-780.	1.0	10
86	Back Cover: Insights into the Mechanism of the Antibiotic-Synthesizing Enzyme MoeO5 from Crystal Structures of Different Complexes (Angew. Chem. Int. Ed. 17/2012). Angewandte Chemie - International Edition, 2012, 51, 4240-4240.	7.2	0
87	Enhanced activity of Thermotoga maritima cellulase 12A by mutating a unique surface loop. Applied Microbiology and Biotechnology, 2012, 95, 661-669.	1.7	34
88	Structure-based development of bacterial nitroreductase against nitrobenzodiazepine-induced hypnosis. Biochemical Pharmacology, 2012, 83, 1690-1699.	2.0	13
89	High-resolution structures ofNeotermes koshunensisÎ²-glucosidase mutants provide insights into the catalytic mechanism and the synthesis of glucoconjugates. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 829-838.	2.5	36
90	Functional Studies of ssDNA Binding Ability of MarR Family Protein TcaR from Staphylococcus epidermidis. PLoS ONE, 2012, 7, e45665.	1.1	6

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91	Structural and functional analysis of three Î²-glucosidases from bacterium Clostridium cellulovorans, fungus Trichoderma reesei and termite Neotermes koshunensis. Journal of Structural Biology, 2011, 173, 46-56.	1.3	161
92	Conformational change upon product binding to Klebsiella pneumoniae UDP-glucose dehydrogenase: A possible inhibition mechanism for the key enzyme in polymyxin resistance. Journal of Structural Biology, 2011, 175, 300-310.	1.3	20
93	The Hexameric Structures of Human Heat Shock Protein 90. PLoS ONE, 2011, 6, e19961.	1.1	53
94	A Novel Tetrameric PilZ Domain Structure from Xanthomonads. PLoS ONE, 2011, 6, e22036.	1.1	20
95	The many blades of the Î²-propeller proteins: conserved but versatile. Trends in Biochemical Sciences, 2011, 36, 553-561.	3.7	158
96	Crystal structure and substrateâ€binding mode of cellulase 12A from Thermotoga maritima. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1193-1204.	1.5	37
97	Structure and mechanism of Escherichia coli glutathionylspermidine amidase belonging to the family of cysteine; histidineâ€dependent amidohydrolases/peptidases. Protein Science, 2011, 20, 557-566.	3.1	9
98	Structure and Mechanism of an Arabidopsis Medium/Long-Chain-Length Prenyl Pyrophosphate Synthase Â Â. Plant Physiology, 2011, 155, 1079-1090.	2.3	68
99	Structures of Human Golgi-resident Glutaminyl Cyclase and Its Complexes with Inhibitors Reveal a Large Loop Movement upon Inhibitor Binding. Journal of Biological Chemistry, 2011, 286, 12439-12449.	1.6	50
100	Terpyridine Platinum(II) Complexes Inhibit Cysteine Proteases by Binding to Active-site Cysteine. Journal of Biomolecular Structure and Dynamics, 2011, 29, 267-282.	2.0	16
101	Modulation of Substrate Specificities of d-Sialic Acid Aldolase through Single Mutations of Val-251. Journal of Biological Chemistry, 2011, 286, 14057-14064.	1.6	10
102	Crystal Structures of the Laminarinase Catalytic Domain from Thermotoga maritima MSB8 in Complex with Inhibitors. Journal of Biological Chemistry, 2011, 286, 45030-45040.	1.6	35
103	The DNA-recognition fold of Sso7c4 suggests a new member of SpoVT-AbrB superfamily from archaea. Nucleic Acids Research, 2011, 39, 6764-6774.	6.5	14
104	Binding and catalysis of Humulus lupulus adenylate isopentenyltransferase for the synthesis of isopentenylated diadenosine polyphosphates. FEBS Letters, 2010, 584, 4083-4088.	1.3	4
105	Structural Basis of Î±â€Fucosidase Inhibition by Iminocyclitols with K_i Values in the Microâ€to Picomolar Range. Angewandte Chemie - International Edition, 2010, 49, 337-340.	7.2	36
106	The dimeric transmembrane domain of prolyl dipeptidase DPPâ€IV contributes to its quaternary structure and enzymatic activities. Protein Science, 2010, 19, 1627-1638.	3.1	29
107	Studying submicrosecond protein folding kinetics using a photolabile caging strategy and timeâ€resolved photoacoustic calorimetry. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2973-2983.	1.5	8
108	A 3D Model of the Membrane Protein Complex Formed by the White Spot Syndrome Virus Structural Proteins. PLoS ONE, 2010, 5, e10718.	1.1	71

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109	Structure of a Heterotetrameric Geranyl Pyrophosphate Synthase from Mint (Mentha piperita) Reveals Intersubunit Regulation Â. Plant Cell, 2010, 22, 454-467.	3.1	85
110	Mechanism of action and inhibition of dehydrosqualene synthase. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 21337-21342.	3.3	66
111	A rationally designed peptide enhances homologous recombination in vitro and resistance to DNA damaging agents in vivo. Nucleic Acids Research, 2010, 38, 4361-4371.	6.5	0
112	Crystal structure and substrate specificity of plant adenylate isopentenyltransferase from Humulus lupulus: distinctive binding affinity for purine and pyrimidine nucleotides. Nucleic Acids Research, 2010, 38, 1738-1748.	6.5	16
113	Protein S-Thiolation by Glutathionylspermidine (Gsp). Journal of Biological Chemistry, 2010, 285, 25345-25353.	1.6	35
114	Structural study of TcaR and its complexes with multiple antibiotics from Staphylococcus epidermidis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8617-8622.	3.3	79
115	Flavin-containing reductase: new perspective on the detoxification of nitrobenzodiazepine. Expert Opinion on Drug Metabolism and Toxicology, 2010, 6, 967-981.	1.5	7
116	Glycan Array on Aluminum Oxide-Coated Glass Slides through Phosphonate Chemistry. Journal of the American Chemical Society, 2010, 132, 13371-13380.	6.6	58
117	Conformational changes associated with cofactor/substrate binding of 6-phosphogluconate dehydrogenase from Escherichia coli and Klebsiella pneumoniae: Implications for enzyme mechanism. Journal of Structural Biology, 2010, 169, 25-35.	1.3	33
118	The cAMP Receptor-Like Protein CLP Is a Novel c-di-GMP Receptor Linking Cellâ€“Cell Signaling to Virulence Gene Expression in Xanthomonas campestris. Journal of Molecular Biology, 2010, 396, 646-662.	2.0	191
119	Crystal Structure and Functional Analysis of the Glutaminyl Cyclase from Xanthomonas campestris. Journal of Molecular Biology, 2010, 401, 374-388.	2.0	23
120	Enhanced Specificity of Mint Geranyl Pyrophosphate Synthase by Modifying the R-Loop Interactions. Journal of Molecular Biology, 2010, 404, 859-873.	2.0	4
121	Three New Structures of Left-Handed RadA Helical Filaments: Structural Flexibility of N-Terminal Domain Is Critical for Recombinase Activity. PLoS ONE, 2009, 4, e4890.	1.1	15
122	Phasevarions Mediate Random Switching of Gene Expression in Pathogenic Neisseria. PLoS Pathogens, 2009, 5, e1000400.	2.1	170
123	Structural Basis of Inhibition Specificities of 3C and 3C-like Proteases by Zinc-coordinating and Peptidomimetic Compounds. Journal of Biological Chemistry, 2009, 284, 7646-7655.	1.6	125
124	Structure, Assembly, and Mechanism of a PLP-Dependent Dodecameric l-Aspartate Î²-Decarboxylase. Structure, 2009, 17, 517-529.	1.6	22
125	Characterization of Escherichia coli nitroreductase NfsB in the metabolism of nitrobenzodiazepines. Biochemical Pharmacology, 2009, 78, 96-103.	2.0	18
126	Structural bioinformatics analysis of free cysteines in protein environments. Journal of the Taiwan Institute of Chemical Engineers, 2009, 40, 123-129.	2.7	6

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127	Crystal structure of RecX: A potent regulatory protein of RecA from Xanthomonas campestris. Proteins: Structure, Function and Bioinformatics, 2009, 74, 530-537.	1.5	6
128	XC1028 from Xanthomonas campestris adopts a PilZ domainâ€like structure without a câ€diâ€GMP switch. Proteins: Structure, Function and Bioinformatics, 2009, 75, 282-288.	1.5	43
129	Terpyridineâ€“platinum(II) complexes are effective inhibitors of mammalian topoisomerases and human thioredoxin reductase 1. Journal of Inorganic Biochemistry, 2009, 103, 1082-1092.	1.5	107
130	High-throughput screening of soluble recombinant proteins. Protein Science, 2009, 11, 1714-1719.	3.1	145
131	Unique GTP-Binding Pocket and Allostery of Uridylate Kinase from a Gram-Negative Phytopathogenic Bacterium. Journal of Molecular Biology, 2009, 385, 1113-1126.	2.0	10
132	Structure of the Alkalohyperthermophilic Archaeoglobus fulgidus Lipase Contains a Unique C-Terminal Domain Essential for Long-Chain Substrate Binding. Journal of Molecular Biology, 2009, 390, 672-685.	2.0	38
133	Insights into the Alkyl Peroxide Reduction Pathway of Xanthomonas campestris Bacterioferritin Comigratory Protein from the Trapped Intermediateâ€“Ligand Complex Structures. Journal of Molecular Biology, 2009, 390, 951-966.	2.0	28
134	Inhibition of Staphyloxanthin Virulence Factor Biosynthesis in Staphylococcus aureus: In Vitro, in Vivo, and Crystallographic Results. Journal of Medicinal Chemistry, 2009, 52, 3869-3880.	2.9	106
135	Lipophilic Bisphosphonates as Dual Farnesyl/Geranylgeranyl Diphosphate Synthase Inhibitors: An X-ray and NMR Investigation. Journal of the American Chemical Society, 2009, 131, 5153-5162.	6.6	159
136	Anti-sense morpholino oligonucleotide assay shows critical involvement for NF-ÎºB activation in the production of Wnt-1 protein by HepG2 cells: oncology implications. Journal of Biomedical Science, 2008, 15, 633-43.	2.6	4
137	Structures of a potent phenylalkyl bisphosphonate inhibitor bound to farnesyl and geranylgeranyl diphosphate synthases. Proteins: Structure, Function and Bioinformatics, 2008, 73, 431-439.	1.5	40
138	Crystal structure of DFA0005 complexed with Î±â€ketoglutarate: A novel member of the ICL/PEPM superfamily from alkaliâ€tolerant Deinococcus ficus. Proteins: Structure, Function and Bioinformatics, 2008, 73, 362-371.	1.5	0
139	Right or left turn? RecA family protein filaments promote homologous recombination through clockwise axial rotation. BioEssays, 2008, 30, 48-56.	1.2	18
140	Discovery of virulence factors of pathogenic bacteria. Current Opinion in Chemical Biology, 2008, 12, 93-101.	2.8	191
141	Proteomics and genomics: perspectives on drug and target discovery. Current Opinion in Chemical Biology, 2008, 12, 1-3.	2.8	92
142	A Cholesterol Biosynthesis Inhibitor Blocks Staphylococcus aureus Virulence. Science, 2008, 319, 1391-1394.	6.0	422
143	Cysteine S-Nitrosylation Protects Protein-tyrosine Phosphatase 1B against Oxidation-induced Permanent Inactivation. Journal of Biological Chemistry, 2008, 283, 35265-35272.	1.6	135
144	Structural Basis for Catalytic and Inhibitory Mechanisms of Human Prostaglandin Reductase PTGR2. Structure, 2008, 16, 1714-1723.	1.6	46

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145	Crystal Structure of the C-Terminal Domain of a Flagellar Hook-Capping Protein from Xanthomonas campestris. Journal of Molecular Biology, 2008, 381, 189-199.	2.0	22
146	The First Crystal Structure of Gluconolactonase Important in the Glucose Secondary Metabolic Pathways. Journal of Molecular Biology, 2008, 384, 604-614.	2.0	31
147	Inhibition of Geranylgeranyl Diphosphate Synthase by Bisphosphonates: A Crystallographic and Computational Investigation. Journal of Medicinal Chemistry, 2008, 51, 5594-5607.	2.9	73
148	Precise Mapping of Increased Sialylation Pattern and the Expression of Acute Phase Proteins Accompanying Murine Tumor Progression in BALB/c Mouse by Integrated Sera Proteomics and Glycomics. Journal of Proteome Research, 2008, 7, 3293-3303.	1.8	27
149	Crystal structure of IcaR, a repressor of the TetR family implicated in biofilm formation in Staphylococcus epidermidis. Nucleic Acids Research, 2008, 36, 1567-1577.	6.5	64
150	White spot syndrome virus protein ICP11: A histone-binding DNA mimic that disrupts nucleosome assembly. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20758-20763.	3.3	79
151	A conserved hydrogen-bond network in the catalytic centre of animal glutaminyl cyclases is critical for catalysis. Biochemical Journal, 2008, 411, 181-190.	1.7	26
152	Structure-Based Inhibitors Exhibit Differential Activities againstHelicobacter pyloriandEscherichia coliUndecaprenyl Pyrophosphate Synthases. Journal of Biomedicine and Biotechnology, 2008, 2008, 1-6.	3.0	31
153	Taiwan proteomics society: an organization affiliated with HUPO. Molecular and Cellular Proteomics, 2008, 7, 1584-5.	2.5	0
154	White Spot Syndrome Virus Annexes a Shrimp STAT To Enhance Expression of the Immediate-Early Gene ie1. Journal of Virology, 2007, 81, 1461-1471.	1.5	188
155	Structure and Mechanism of Helicobacter pylori Fucosyltransferase. Journal of Biological Chemistry, 2007, 282, 9973-9982.	1.6	113
156	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. Nucleic Acids Research, 2007, 35, 1787-1801.	6.5	40
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