Michael W Parker

List of Publications by Year
in descending order

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340 papers	19,609 citations	9756 73 h-index	16605 123 g-index
354 all docs	354 docs citations	354 times ranked	19900 citing authors

#	Article	IF	Citations
1	Structure and function of glutathione S-transferases. BBA - Proteins and Proteomics, 1994, 1205, 1-18.	2.1	524
2	Structure of a Cholesterol-Binding, Thiol-Activated Cytolysin and a Model of Its Membrane Form. Cell, 1997, 89, 685-692.	13.5	457
3	Structure of the Aeromonas toxin proaerolysin in its water-soluble and membrane-channel states. Nature, 1994, 367, 292-295.	13.7	418
4	Pore-forming protein toxins: from structure to function. Progress in Biophysics and Molecular Biology, 2005, 88, 91-142.	1.4	394
5	AMPK Î² Subunit Targets Metabolic Stress Sensing to Glycogen. Current Biology, 2003, 13, 867-871.	1.8	377
6	The Mechanism of Membrane Insertion for a Cholesterol-Dependent Cytolysin. Cell, 1999, 99, 293-299.	13.5	347
7	Model for growth hormone receptor activation based on subunit rotation within a receptor dimer. Nature Structural and Molecular Biology, 2005, 12, 814-821.	3.6	345
8	Mechanism of Activation of Protein Kinase JAK2 by the Growth Hormone Receptor. Science, 2014, 344, 1249783.	6.0	340
9	Identification of a Membrane-Spanning Domain of the Thiol-Activated Pore-Forming ToxinClostridium perfringensPerfringolysin O:Â An Î±-Helical to Î²-Sheet Transition Identified by Fluorescence Spectroscopyâ€. Biochemistry, 1998, 37, 14563-14574.	1.2	309
10	Three-dimensional structure of class Ï€ glutathione S-transferase from human placenta in complex with S-hexylglutathione at 2.8 Ã... resolution. Journal of Molecular Biology, 1992, 227, 214-226.	2.0	273
11	The Structure of the GM-CSF Receptor Complex Reveals a Distinct Mode of Cytokine Receptor Activation. Cell, 2008, 134, 496-507.	13.5	268
12	The granulocyte-macrophage colony-stimulating factor receptor: linking its structure to cell signaling and its role in disease. Blood, 2009, 114, 1289-1298.	0.6	261
13	A Systematic and Functional Classification of Streptococcus pyogenes That Serves as a New Tool for Molecular Typing and Vaccine Development. Journal of Infectious Diseases, 2014, 210, 1325-1338.	1.9	257
14	Structure of the Alzheimer's Disease Amyloid Precursor Protein Copper Binding Domain. Journal of Biological Chemistry, 2003, 278, 17401-17407.	1.6	248
15	Oncogenic protein interfaces: small molecules, big challenges. Nature Reviews Cancer, 2014, 14, 248-262.	12.8	246
16	Iron- and manganese-containing superoxide dismutases can be distinguished by analysis of their primary structures. FEBS Letters, 1988, 229, 377-382.	1.3	238
17	Crystal structure of the N-terminal, growth factor-like domain of Alzheimer amyloid precursor protein. Nature Structural Biology, 1999, 6, 327-331.	9.7	229
18	Refined structure of the pore-forming domain of colicin A at 2.4 Ã... resolution. Journal of Molecular Biology, 1992, 224, 639-657.	2.0	227

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19	Zanamivir-Resistant Influenza Viruses with a Novel Neuraminidase Mutation. Journal of Virology, 2009, 83, 10366-10373.	1.5	224
20	Insights into autoregulation from the crystal structure of twitchin kinase. Nature, 1994, 369, 581-584.	13.7	217
21	The <scp>GM</scp>â€“<scp>CSF</scp>/<scp>ILâ€3</scp>/<scp>ILâ€5</scp> cytokine receptor family: from ligand recognition to initiation of signaling. Immunological Reviews, 2012, 250, 277-302.	2.8	192
22	Inhibitors of histone acetyltransferases KAT6A/B induce senescence and arrest tumour growth. Nature, 2018, 560, 253-257.	13.7	182
23	Structural Basis for Glycogen Recognition by AMP-Activated Protein Kinase. Structure, 2005, 13, 1453-1462.	1.6	175
24	Two Structural Transitions in Membrane Pore Formation by Pneumolysin, the Pore-Forming Toxin of Streptococcus pneumoniae. Cell, 1999, 97, 647-655.	13.5	174
25	The structures of human glutathione transferase P1-1 in complex with glutathione and various inhibitors at high resolution. Journal of Molecular Biology, 1997, 274, 84-100.	2.0	172
26	Anxiety over GABAA receptor structure relieved by AChBP. Trends in Biochemical Sciences, 2002, 27, 280-287.	3.7	169
27	Rational Design of an Organometallic Glutathione Transferase Inhibitor. Angewandte Chemie - International Edition, 2009, 48, 3854-3857.	7.2	169
28	A mixed disulfide bond in bacterial glutathione transferase: functional and evolutionary implications. Structure, 1998, 6, 721-734.	1.6	163
29	Molecular Dissection of the Interaction between Amyloid Precursor Protein and Its Neuronal Trafficking Receptor SorLA/LR11. Biochemistry, 2006, 45, 2618-2628.	1.2	161
30	Crystal structure of manganese superoxide dismutase from Bacillus stearothermophilus at 2.4 Ã... resolution. Journal of Molecular Biology, 1988, 199, 649-661.	2.0	160
31	Transitional changes in the CRP structure lead to the exposure of proinflammatory binding sites. Nature Communications, 2017, 8, 14188.	5.8	158
32	Human theta class glutathione transferase: the crystal structure reveals a sulfate-binding pocket within a buried active site. Structure, 1998, 6, 309-322.	1.6	147
33	Substrate and pseudosubstrate interactions with protein kinases: determinants of specificity. Trends in Biochemical Sciences, 1994, 19, 440-444.	3.7	146
34	Intrasteric control of AMPK via the Â1 subunit AMP allosteric regulatory site. Protein Science, 2004, 13, 155-165.	3.1	141
35	Ca2+ /S100 regulation of giant protein kinases. Nature, 1996, 380, 636-639.	13.7	138
36	Critical Role for the Second Extracellular Loop in the Binding of Both Orthosteric and Allosteric G Protein-coupled Receptor Ligands. Journal of Biological Chemistry, 2007, 282, 25677-25686.	1.6	137

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37	Insights into the action of the superfamily of cholesterol-dependent cytolysins from studies of intermedilysin. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 600-605.	3.3	135
38	Human Factor H-Related Protein 5 Has Cofactor Activity, Inhibits C3 Convertase Activity, Binds Heparin and C-Reactive Protein, and Associates with Lipoprotein. Journal of Immunology, 2005, 174, 6250-6256.	0.4	135
39	Crystal structure of a colicin N fragment suggests a model for toxicity. Structure, 1998, 6, 863-874.	1.6	134
40	Siah ubiquitin ligase is structurally related to TRAF and modulates TNF-Î± signaling. Nature Structural Biology, 2002, 9, 68-75.	9.7	129
41	Rendering a membrane protein soluble in water: a common packing motif in bacterial protein toxins. Trends in Biochemical Sciences, 1993, 18, 391-395.	3.7	126
42	Insights into membrane insertion based on studies of colicins. Trends in Biochemical Sciences, 1990, 15, 126-129.	3.7	125
43	The Three-Dimensional Structure of the Human Pi Class Glutathione Transferase P1-1 in Complex with the Inhibitor Ethacrynic Acid and Its Glutathione Conjugate,. Biochemistry, 1997, 36, 576-585.	1.2	125
44	The ligandin (non-substrate) binding site of human pi class glutathione transferase is located in the electrophile binding site (H-site). Journal of Molecular Biology, 1999, 291, 913-926.	2.0	121
45	Crystal Structure of Maleylacetoacetate Isomerase/Glutathione Transferase Zeta Reveals the Molecular Basis for Its Remarkable Catalytic Promiscuityâ€,â€¡. Biochemistry, 2001, 40, 1567-1576.	1.2	119
46	Arresting Pore Formation of a Cholesterol-dependent Cytolysin by Disulfide Trapping Synchronizes the Insertion of the Transmembrane Î²-Sheet from a Prepore Intermediate. Journal of Biological Chemistry, 2001, 276, 8261-8268.	1.6	118
47	A RIPK2 inhibitor delays NOD signalling events yet prevents inflammatory cytokine production. Nature Communications, 2015, 6, 6442.	5.8	112
48	Nitrosylation of Human Glutathione Transferase P1-1 with Dinitrosyl Diglutathionyl Iron Complex in Vitro and in Vivo. Journal of Biological Chemistry, 2005, 280, 42172-42180.	1.6	109
49	Oseltamivir Resistance and the H274Y Neuraminidase Mutation in Seasonal, Pandemic and Highly Pathogenic Influenza Viruses. Drugs, 2009, 69, 2523-2531.	4.9	109
50	Cytoplasmic ATP-sensing Domains Regulate Gating of Skeletal Muscle ClC-1 Chloride Channels. Journal of Biological Chemistry, 2005, 280, 32452-32458.	1.6	106
51	Aerolysin - the ins and outs of a model channel-forming toxin. Molecular Microbiology, 1996, 19, 205-212.	1.2	104
52	Altered kinetics and benzodiazepine sensitivity of a GABAA receptor subunit mutation [Â2(R43Q)] found in human epilepsy. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15170-15175.	3.3	104
53	Potent hepatitis C inhibitors bind directly to NS5A and reduce its affinity for RNA. Scientific Reports, 2014, 4, 4765.	1.6	101
54	The molecular mechanism of pneumolysin, a virulence factor from Streptococcus pneumoniae 1 1Edited by J. Thornton. Journal of Molecular Biology, 1998, 284, 449-461.	2.0	100

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55	A rivet model for channel formation by aerolysin-like pore-forming toxins. EMBO Journal, 2006, 25, 457-466.	3.5	95
56	Identification and characterization of a new cognitive enhancer based on inhibition of insulinâ€regulated aminopeptidase. FASEB Journal, 2008, 22, 4209-4217.	0.2	95
57	Structural Studies of the Alzheimerâ€™s Amyloid Precursor Protein Copper-binding Domain Reveal How it Binds Copper Ions. Journal of Molecular Biology, 2007, 367, 148-161.	2.0	93
58	Molecular Evolution of Glutathione S-Transferases in the Genus Drosophila. Genetics, 2007, 177, 1363-1375.	1.2	92
59	Kinetics of HIV-1 capsid uncoating revealed by single-molecule analysis. ELife, 2018, 7, .	2.8	91
60	Human Glutathione Transferase P1-1 and Nitric Oxide Carriers. Journal of Biological Chemistry, 2001, 276, 42138-42145.	1.6	90
61	TRIM16 Acts as an E3 Ubiquitin Ligase and Can Heterodimerize with Other TRIM Family Members. PLoS ONE, 2012, 7, e37470.	1.1	90
62	Bapineuzumab captures the N-terminus of the Alzheimer's disease amyloid-beta peptide in a helical conformation. Scientific Reports, 2013, 3, 1302.	1.6	89
63	Site-directed Mutagenesis of Human Glutathione Transferase P1-1. Journal of Biological Chemistry, 1995, 270, 1243-1248.	1.6	87
64	The Identification and Structure of the Membrane-spanning Domain of the Clostridium septicum Alpha Toxin. Journal of Biological Chemistry, 2004, 279, 14315-14322.	1.6	87
65	Structures of Perfringolysin O Suggest a Pathway for Activation of Cholesterol-dependent Cytolysins. Journal of Molecular Biology, 2007, 367, 1227-1236.	2.0	87
66	Phosphorothioate backbone modifications of nucleotide-based drugs are potent platelet activators. Journal of Experimental Medicine, 2015, 212, 129-137.	4.2	87
67	From glutathione transferase to pore in a CLIC. European Biophysics Journal, 2002, 31, 356-364.	1.2	85
68	Structure and Evolution of a Novel Dimeric Enzyme from a Clinically Important Bacterial Pathogen. Journal of Biological Chemistry, 2008, 283, 27598-27603.	1.6	85
69	Membrane insertion of the pore-forming domain of colicin A. A spectroscopic study. FEBS Journal, 1991, 196, 599-607.	0.2	84
70	Contrasting, Species-Dependent Modulation of Copper-Mediated Neurotoxicity by the Alzheimer's Disease Amyloid Precursor Protein. Journal of Neuroscience, 2002, 22, 365-376.	1.7	83
71	Tetraspanins as regulators of the tumour microenvironment: implications for metastasis and therapeutic strategies. British Journal of Pharmacology, 2014, 171, 5462-5490.	2.7	81
72	Signalling by the Î²c family of cytokines. Cytokine and Growth Factor Reviews, 2013, 24, 189-201.	3.2	80

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73	Crystallization of glutathione S-transferase from human placenta. Journal of Molecular Biology, 1990, 213, 221-222.	2.0	78
74	Vibrio spp. secrete proaerolysin as a folded dimer without the need for disulphide bond formation. Molecular Microbiology, 1995, 17, 1035-1044.	1.2	78
75	A structure-based mechanism of cisplatin resistance mediated by glutathione transferase P1-1. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13943-13951.	3.3	76
76	Long-chain fatty acyl-CoA esters regulate metabolism via allosteric control of AMPK Î²1 isoforms. Nature Metabolism, 2020, 2, 873-881.	5.1	76
77	Cleaved antitrypsin polymers at atomic resolution. Protein Science, 2000, 9, 417-420.	3.1	73
78	Studies of Glutathione Transferase P1â€1 Bound to a Platinum(IV)â€Based Anticancer Compound Reveal the Molecular Basis of Its Activation. Chemistry - A European Journal, 2011, 17, 7806-7816.	1.7	73
79	Molecular basis for mid-region amyloid-Î² capture by leading Alzheimer's disease immunotherapies. Scientific Reports, 2015, 5, 9649.	1.6	73
80	Identification and development of specific inhibitors for insulin-regulated aminopeptidase as a new class of cognitive enhancers. British Journal of Pharmacology, 2011, 164, 37-47.	2.7	72
81	Molecular basis of cytokine receptor activation. IUBMB Life, 2010, 62, 509-518.	1.5	70
82	Elucidation of the Substrate Binding Site of Siah Ubiquitin Ligase. Structure, 2006, 14, 695-701.	1.6	69
83	Structural basis of allosteric and synergistic activation of AMPK by furan-2-phosphonic derivative C2 binding. Nature Communications, 2016, 7, 10912.	5.8	69
84	Mutagenesis of the active site of the human Theta-class glutathione transferase GSTT2-2: catalysis with different substrates involves different residues. Biochemical Journal, 1996, 319, 315-321.	1.7	68
85	Catalytic Mechanism and Role of Hydroxyl Residues in the Active Site of Theta Class Glutathione S-Transferases. Journal of Biological Chemistry, 1997, 272, 29681-29686.	1.6	68
86	Self-interaction of pneumolysin, the pore-forming protein toxin of Streptococcus pneumoniae. Journal of Molecular Biology, 1998, 284, 1223-1237.	2.0	68
87	Multifunctional Role of Tyr 108 in the Catalytic Mechanism of Human Glutathione Transferase P1-1. Crystallographic and Kinetic Studies on the Y108F Mutant Enzymeâ€,â€¡. Biochemistry, 1997, 36, 6207-6217.	1.2	65
88	The Î²c receptor family â€“ Structural insights and their functional implications. Cytokine, 2015, 74, 247-258.	1.4	65
89	Structure of the Janus Protein Human CLIC2. Journal of Molecular Biology, 2007, 374, 719-731.	2.0	64
90	The GM-CSF receptor family: Mechanism of activation and implications for disease. Growth Factors, 2012, 30, 63-75.	0.5	64

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91	Structural characterization of respiratory syncytial virus fusion inhibitor escape mutants: homology model of the F protein and a syncytium formation assay. Virology, 2003, 311, 275-288.	1.1	63
92	Solution Conformation and Heparin-induced Dimerization of the Full-length Extracellular Domain of the Human Amyloid Precursor Protein. Journal of Molecular Biology, 2006, 357, 493-508.	2.0	63
93	Inhibition of Skeletal Muscle ClC-1 Chloride Channels by Low Intracellular pH and ATP. Journal of Biological Chemistry, 2007, 282, 32780-32791.	1.6	63
94	Copper binding to the Alzheimerâ€™s disease amyloid precursor protein. European Biophysics Journal, 2008, 37, 269-279.	1.2	62
95	Recognition and Detoxification of the Insecticide DDT by Drosophila melanogaster Glutathione S-Transferase D1. Journal of Molecular Biology, 2010, 399, 358-366.	2.0	62
96	Crystal structure of Streptococcus pneumoniae pneumolysin provides key insights into early steps of pore formation. Scientific Reports, 2015, 5, 14352.	1.6	62
97	Drug repurposing: Misconceptions, challenges, and opportunities for academic researchers. Science Translational Medicine, 2021, 13, eabd5524.	5.8	62
98	Parallel Screening of Low Molecular Weight Fragment Libraries: Do Differences in Methodology Affect Hit Identification?. Journal of Biomolecular Screening, 2013, 18, 147-159.	2.6	61
99	Structural Studies of Streptococcus pyogenes Streptolysin O Provide Insights into the Early Steps of Membrane Penetration. Journal of Molecular Biology, 2014, 426, 785-792.	2.0	61
100	Conversion of a transmembrane to a water-soluble protein complex by a single point mutation. Nature Structural Biology, 2002, 9, 729-733.	9.7	59
101	A proposed structural basis for picrotoxinin and picrotin binding in the glycine receptor pore. Journal of Neurochemistry, 2007, 103, 580-589.	2.1	59
102	Small Molecule Binding to Alzheimer Risk Factor CD33 Promotes AÎ² Phagocytosis. IScience, 2019, 19, 110-118.	1.9	59
103	Homology Model of the GABAA Receptor Examined Using Brownian Dynamics. Biophysical Journal, 2005, 88, 3286-3299.	0.2	58
104	Aerolysinâ€”A Paradigm for Membrane Insertion of Beta-Sheet Protein Toxins?. Journal of Structural Biology, 1998, 121, 92-100.	1.3	57
105	LymphotoxinÂÎ± induces apoptosis, necroptosis and inflammatory signals with the same potency as tumour necrosis factor. FEBS Journal, 2013, 280, 5283-5297.	2.2	57
106	Evidence for an Induced-Fit Mechanism Operating in Pi Class Glutathione Transferases,. Biochemistry, 1998, 37, 9912-9917.	1.2	56
107	Development of cognitive enhancers based on inhibition of insulin-regulated aminopeptidase. BMC Neuroscience, 2008, 9, S14.	0.8	56
108	Mapping the Intermedilysin-Human CD59 Receptor Interface Reveals a Deep Correspondence with the Binding Site on CD59 for Complement Binding Proteins C8Î± and C9. Journal of Biological Chemistry, 2011, 286, 20952-20962.	1.6	56

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109	A common channel-forming motif in evolutionarily distant porins. Journal of Structural Biology, 1991, 107, 136-145.	1.3	55
110	Inhibition of ATP-citrate lyase improves NASH, liver fibrosis, and dyslipidemia. Cell Metabolism, 2022, 34, 919-936.e8.	7.2	55
111	Proton release on binding of glutathione to Alpha, Mu and Delta class glutathione transferases. Biochemical Journal, 1999, 344, 419-425.	1.7	54
112	Targeting acute myeloid leukemia by dual inhibition of PI3K signaling and Cdk9-mediated Mcl-1 transcription. Blood, 2013, 122, 738-748.	0.6	53
113	Abeta targets of the biosimilar antibodies of Bapineuzumab, Crenezumab, Solanezumab in comparison to an antibody against N-truncated Abeta in sporadic Alzheimer disease cases and mouse models. Acta Neuropathologica, 2015, 130, 713-729.	3.9	53
114	Structure of the activation domain of the GM-CSF/IL-3/IL-5 receptor common Î²-chain bound to an antagonist. Blood, 2000, 95, 2491-2498.	0.6	52
115	Do current therapeutic anti-AÎ² antibodies for Alzheimerâ€™s disease engage the target?. Acta Neuropathologica, 2014, 127, 803-810.	3.9	52
116	Repurposing of drugs as STAT3 inhibitors for cancer therapy. Seminars in Cancer Biology, 2021, 68, 31-46.	4.3	52
117	Monoubiquitination by the human Fanconi anemia core complex clamps FANCI:FANCD2 on DNA in filamentous arrays. ELife, 2020, 9, .	2.8	52
118	Crystal structure of human insulinâ€regulated aminopeptidase with specificity for cyclic peptides. Protein Science, 2015, 24, 190-199.	3.1	51
119	Protonation of Histidine-132 Promotes Oligomerization of the Channel-Forming Toxin Aerolysin. Biochemistry, 1995, 34, 16450-16455.	1.2	50
120	Monomer-Monomer Interactions Propagate Structural Transitions Necessary for Pore Formation by the Cholesterol-dependent Cytolysins. Journal of Biological Chemistry, 2012, 287, 24534-24543.	1.6	50
121	Structural Flexibility Modulates the Activity of Human Glutathione Transferase P1-1. Journal of Biological Chemistry, 1996, 271, 16193-16198.	1.6	49
122	Crystallization, structural determination and analysis of a novel parasite vaccine candidate: Fasciola hepatica glutathione S-transferase 1 1Edited by R. Huber. Journal of Molecular Biology, 1997, 273, 857-872.	2.0	49
123	The glutathione conjugate of ethacrynic acid can bind to human pi class glutathione transferase P1-1 in two different modes. FEBS Letters, 1997, 419, 32-36.	1.3	49
124	GSTZ1d: a new allele of glutathione transferase zeta and maleylacetoacetate isomerase. Pharmacogenetics and Genomics, 2001, 11, 671-678.	5.7	49
125	Insights into the Structural Basis for Zinc Inhibition of the Glycine Receptor. Journal of Biological Chemistry, 2003, 278, 28985-28992.	1.6	49
126	Amyloid-Î²â€“Anti-Amyloid-Î² Complex Structure Reveals an Extended Conformation in the Immunodominant B-Cell Epitope. Journal of Molecular Biology, 2008, 377, 181-192.	2.0	49

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127	The Anti-cancer Drug Chlorambucil as a Substrate for the Human Polymorphic Enzyme Glutathione Transferase P1-1: Kinetic Properties and Crystallographic Characterisation of Allelic Variants. Journal of Molecular Biology, 2008, 380, 131-144.	2.0	49
128	Structure of the Lectin Regulatory Domain of the Cholesterol-Dependent Cytolysin Lectinolysin Reveals the Basis for Its Lewis Antigen Specificity. Structure, 2012, 20, 248-258.	1.6	49
129	Direct involvement of the TEN domain at the active site of human telomerase. Nucleic Acids Research, 2011, 39, 1774-1788.	6.5	47
130	Hsp90 increases LIM kinase activity by promoting its homoâ€dimerization. FASEB Journal, 2006, 20, 1218-1220.	0.2	46
131	Synthesis, Structureâ€“Activity Relationships and Brain Uptake of a Novel Series of Benzopyran Inhibitors of Insulin-Regulated Aminopeptidase. Journal of Medicinal Chemistry, 2014, 57, 1368-1377.	2.9	46
132	Dual Mechanism of Interleukin-3 Receptor Blockade by an Anti-Cancer Antibody. Cell Reports, 2014, 8, 410-419.	2.9	46
133	Conformational Changes in the GM-CSF Receptor Suggest a Molecular Mechanism for Affinity Conversion and Receptor Signaling. Structure, 2016, 24, 1271-1281.	1.6	46
134	Substrate-mediated Stabilization of a Tetrameric Drug Target Reveals Achilles Heel in Anthrax. Journal of Biological Chemistry, 2010, 285, 5188-5195.	1.6	44
135	Synthetic dityrosine-linked Î²-amyloid dimers form stable, soluble, neurotoxic oligomers. Chemical Science, 2013, 4, 4449.	3.7	44
136	An intermolecular electrostatic interaction controls the prepore-to-pore transition in a cholesterol-dependent cytolysin. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2204-2209.	3.3	44
137	Conformational Changes in Aerolysin during the Transition from the Water-Soluble Protoxin to the Membrane Channelâ€. Biochemistry, 1997, 36, 15224-15232.	1.2	43
138	Role of nicotinic acetylcholine receptor subunits in the mode of action of neonicotinoid, sulfoximine and spinosyn insecticides in Drosophila melanogaster. Insect Biochemistry and Molecular Biology, 2021, 131, 103547.	1.2	43
139	GSTB1-1 from Proteus mirabilis. Journal of Biological Chemistry, 2002, 277, 18777-18784.	1.6	42
140	Federated repositories of X-ray diffraction images. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 810-814.	2.5	42
141	Studies on the structure and mechanism of a bacterial protein toxin by analytical ultracentrifugation and small-angle neutron scattering 1 1Edited by M. F. Moody. Journal of Molecular Biology, 1999, 293, 1145-1160.	2.0	41
142	Clarification of the role of key active site residues of glutathione transferase Zeta/maleylacetoacetate isomerase by a new spectrophotometric technique. Biochemical Journal, 2003, 374, 731-737.	1.7	41
143	Optimised expression and purification of recombinant human indoleamine 2,3-dioxygenase. Protein Expression and Purification, 2004, 37, 392-398.	0.6	40
144	Structural Determinants for Small-Molecule Activation of Skeletal Muscle AMPK Î±2Î²2Î³1 by the Glucose Importagog SC4. Cell Chemical Biology, 2018, 25, 728-737.e9.	2.5	40

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145	Functional analysis of the evolutionarily conserved proline 53 residue inProteus mirabilisglutathione transferase B1-1. FEBS Letters, 1999, 445, 347-350.	1.3	39
146	Solid-phase synthesis of homodimeric peptides: preparation of covalently-linked dimers of amyloid Î² peptide. Chemical Communications, 2009, , 6228.	2.2	39
147	Characterization of pathogenic human monoclonal autoantibodies against GM-CSF. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7832-7837.	3.3	39
148	Accumulation of JAK activation loop phosphorylation is linked to type I JAK inhibitor withdrawal syndrome in myelofibrosis. Science Advances, 2018, 4, eaat3834.	4.7	39
149	Crystal structure of the HIVâ€1 integrase core domain in complex with sucrose reveals details of an allosteric inhibitory binding site. FEBS Letters, 2010, 584, 1455-1462.	1.3	38
150	An Orally Available 3-Ethoxybenzisoxazole Capsid Binder with Clinical Activity against Human Rhinovirus. ACS Medicinal Chemistry Letters, 2012, 3, 303-307.	1.3	38
151	Cytokine receptor activation at the cell surface. Current Opinion in Structural Biology, 2012, 22, 350-359.	2.6	38
152	CSL311, a novel, potent, therapeutic monoclonal antibody for the treatment of diseases mediated by the common Î² chain of the IL-3, GM-CSF and IL-5 receptors. MAbs, 2016, 8, 436-453.	2.6	38
153	Site-directed mutagenesis of theProteus mirabilisglutathione transferase B1-1 G-site. FEBS Letters, 1998, 423, 122-124.	1.3	37
154	Movement of a Loop in Domain 3 of Aerolysin Is Required for Channel Formationâ€. Biochemistry, 1998, 37, 741-746.	1.2	37
155	Molecular determinants of ginkgolide binding in the glycine receptor pore. Journal of Neurochemistry, 2006, 98, 395-407.	2.1	37
156	Glutathione transferase P1-1: self-preservation of an anti-cancer enzyme. Biochemical Journal, 2003, 376, 71-76.	1.7	35
157	Cholesterol-Dependent Cytolysins: Membrane and Protein Structural Requirements for Pore Formation. Chemical Reviews, 2019, 119, 7721-7736.	23.0	35
158	Tropisetron modulation of the glycine receptor: femtomolar potentiation and a molecular determinant of inhibition. Journal of Neurochemistry, 2007, 100, 758-769.	2.1	34
159	Molecular determinants of common gating of a ClC chloride channel. Nature Communications, 2013, 4, 2507.	5.8	34
160	Discovery and SAR of novel pyrazolo[1,5-a]pyrimidines as inhibitors of CDK9. Bioorganic and Medicinal Chemistry, 2015, 23, 6280-6296.	1.4	34
161	Structural Basis for Receptor Recognition by the Human CD59-Responsive Cholesterol-Dependent Cytolysins. Structure, 2016, 24, 1488-1498.	1.6	34
162	Structural Determinants Defining the Allosteric Inhibition of an Essential Antibiotic Target. Structure, 2016, 24, 1282-1291.	1.6	34

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163	Crystallization of a proform of aerolysin, a hole-forming toxin from Aeromonas hydrophila. Journal of Molecular Biology, 1990, 212, 561-562.	2.0	33
164	Promiscuous DNA-binding of a mutant zinc finger protein corrupts the transcriptome and diminishes cell viability. Nucleic Acids Research, 2017, 45, 1130-1143.	6.5	33
165	A Family of Dual-Activity Glycosyltransferase-Phosphorylases Mediates Mannogen Turnover and Virulence in Leishmania Parasites. Cell Host and Microbe, 2019, 26, 385-399.e9.	5.1	33
166	The structure of the extracellular domains of human interleukin 11Î± receptor reveals mechanisms of cytokine engagement. Journal of Biological Chemistry, 2020, 295, 8285-8301.	1.6	33
167	The role of electrostatic charge in the membrane insertion of colicin A. Calculation and mutation. FEBS Journal, 1994, 220, 155-163.	0.2	32
168	A structurally derived consensus pattern for theta class glutathione transferases. Protein Engineering, Design and Selection, 1996, 9, 327-332.	1.0	32
169	Cholesterol-dependent cytolysins: from water-soluble state to membrane pore. Biophysical Reviews, 2018, 10, 1337-1348.	1.5	32
170	Repurposing the selective estrogen receptor modulator bazedoxifene to suppress gastrointestinal cancer growth. EMBO Molecular Medicine, 2019, 11, .	3.3	32
171	The Impact of Nitric Oxide Toxicity on the Evolution of the Glutathione Transferase Superfamily. Journal of Biological Chemistry, 2013, 288, 24936-24947.	1.6	31
172	The structure of the PA28â€“20S proteasome complex from Plasmodium falciparum and implications for proteostasis. Nature Microbiology, 2019, 4, 1990-2000.	5.9	31
173	An ALYREF-MYCN coactivator complex drives neuroblastoma tumorigenesis through effects on USP3 and MYCN stability. Nature Communications, 2021, 12, 1881.	5.8	31
174	Regulation of Insulin-Regulated Membrane Aminopeptidase Activity by Its C-Terminal Domain. Biochemistry, 2011, 50, 2611-2622.	1.2	30
175	The role of Rdl in resistance to phenylpyrazoles in Drosophila melanogaster. Insect Biochemistry and Molecular Biology, 2014, 54, 11-21.	1.2	30
176	Mutations of gly to ala in human glutathione transferase P1-1 affect helix 2 (G-site) and induce positive cooperativity in the binding of glutathione 1 1Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 1717-1725.	2.0	29
177	Crystal Structure of a Putative Methyltransferase from Mycobacterium tuberculosis : Misannotation of a Genome Clarified by Protein Structural Analysis. Journal of Bacteriology, 2003, 185, 4057-4065.	1.0	29
178	Solution Structure of Glutathione Bound to Human Glutathione Transferase P1-1:Â Comparison of NMR Measurements with the Crystal Structureâ€. Biochemistry, 1998, 37, 3020-3027.	1.2	28
179	Structure of Alzheimer's disease amyloid precursor protein copper-binding domain at atomic resolution. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 819-824.	0.7	28
180	Phosphorylation of syndapin I F-BAR domain at two helix-capping motifs regulates membrane tubulation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3760-3765.	3.3	28

#	Article	IF	Citations
181	A dual role for the N-terminal domain of the IL-3 receptor in cell signalling. Nature Communications, 2018, 9, 386.	5.8	28
182	Role of the Î² Common (Î²c) Family of Cytokines in Health and Disease. Cold Spring Harbor Perspectives in Biology, 2018, 10, a028514.	2.3	28
183	Mechanistic Scrutiny Identifies a Kinetic Role for Cytochrome b5 Regulation of Human Cytochrome P450c17 (CYP17A1, P450 17A1). PLoS ONE, 2015, 10, e0141252.	1.1	28
184	Insights into Interactions between the Î±-Helical Region of the Salmon Calcitonin Antagonists and the Human Calcitonin Receptor using Photoaffinity Labeling. Journal of Biological Chemistry, 2005, 280, 28610-28622.	1.6	27
185	Determinants of oligosaccharide specificity of the carbohydrate-binding modules of AMP-activated protein kinase. Biochemical Journal, 2015, 468, 245-257.	1.7	26
186	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. Angewandte Chemie - International Edition, 2019, 58, 16780-16784.	7.2	26
187	Membrane Topology of the Colicin A Pore-forming Domain Analyzed by Disulfide Bond Engineering. Journal of Biological Chemistry, 1996, 271, 15401-15406.	1.6	25
188	Structure of native HIV-1 cores and their interactions with IP6 and CypA. Science Advances, 2021, 7, eabj5715.	4.7	25
189	Reaction hijacking of tyrosine tRNA synthetase as a new whole-of-life-cycle antimalarial strategy. Science, 2022, 376, 1074-1079.	6.0	25
190	Calorimetric and structural studies of the nitric oxide carrier S-nitrosoglutathione bound to human glutathione transferase P1-1. Protein Science, 2006, 15, 1093-1105.	3.1	24
191	Fragmentâ€Based Design of Ligands Targeting a Novel Site on the Integrase Enzyme of Human Immunodeficiency Virusâ€...1. ChemMedChem, 2011, 6, 258-261.	1.6	24
192	Protein structure and computational drug discovery. Biochemical Society Transactions, 2018, 46, 1367-1379.	1.6	24
193	Drugging MYCN Oncogenic Signaling through the MYCN-PA2G4 Binding Interface. Cancer Research, 2019, 79, 5652-5667.	0.4	24
194	CaMKK2 is inactivated by cAMP-PKA signaling and 14-3-3 adaptor proteins. Journal of Biological Chemistry, 2020, 295, 16239-16250.	1.6	24
195	Human Glutathione Transferase T2-2 Discloses Some Evolutionary Strategies for Optimization of Substrate Binding to the Active Site of Glutathione Transferases. Journal of Biological Chemistry, 2001, 276, 5427-5431.	1.6	23
196	Cryptic clues as to how water-soluble protein toxins form pores in membranes. Toxicon, 2003, 42, 1-6.	0.8	23
197	Preventing serpin aggregation: The molecular mechanism of citrate action upon antitrypsin unfolding. Protein Science, 2008, 17, 2127-2133.	3.1	23
198	Disarming Bacterial Virulence through Chemical Inhibition of the DNA Binding Domain of an AraC-like Transcriptional Activator Protein. Journal of Biological Chemistry, 2013, 288, 31115-31126.	1.6	23

#	Article	IF	Citations
199	Shifting Substrate Specificity of Human Glutathione Transferase (from Class Pi to Class Alpha) by a Single Point Mutation. Biochemical and Biophysical Research Communications, 1998, 252, 184-189.	1.0	22
200	Identification of Essential Residues in the Erm(B) rRNA Methyltransferase of Clostridium perfringens. Antimicrobial Agents and Chemotherapy, 2002, 46, 1253-1261.	1.4	22
201	Identification and characterization of GSTT3, a third murine Theta class glutathione transferase. Biochemical Journal, 2002, 366, 323-332.	1.7	22
202	Identification of modulating residues defining the catalytic cleft of insulin-regulated aminopeptidase. Biochemistry and Cell Biology, 2008, 86, 251-261.	0.9	22
203	Intracellular Î²-Nicotinamide Adenine Dinucleotide Inhibits the Skeletal Muscle ClC-1 Chloride Channel. Journal of Biological Chemistry, 2012, 287, 25808-25820.	1.6	22
204	The genetics, structure and function of the M1 aminopeptidase oxytocinase subfamily and their therapeutic potential in immune-mediated disease. Human Immunology, 2019, 80, 281-289.	1.2	22
205	From Knock-Out Phenotype to Three-Dimensional Structure of a Promising Antibiotic Target from Streptococcus pneumoniae. PLoS ONE, 2013, 8, e83419.	1.1	22
206	A single amino acid substitution can restore the solubility of aggregated colicin A mutants in Escherichia coli. Protein Engineering, Design and Selection, 1994, 7, 1495-1500.	1.0	21
207	Kinetic properties of missense mutations in patients with glutathione synthetase deficiency. Biochemical Journal, 2000, 349, 275.	1.7	21
208	Contribution of Glycine 146 to a Conserved Folding Module Affecting Stability and Refolding of Human Glutathione Transferase P1-1. Journal of Biological Chemistry, 2003, 278, 1291-1302.	1.6	21
209	Phenylalanine-544 Plays a Key Role in Substrate and Inhibitor Binding by Providing a Hydrophobic Packing Point at the Active Site of Insulin-Regulated Aminopeptidase. Molecular Pharmacology, 2010, 78, 600-607.	1.0	21
210	EPO does not promote interaction between the erythropoietin and beta-common receptors. Scientific Reports, 2018, 8, 12457.	1.6	21
211	Discovery of Benzoylsulfonohydrazides as Potent Inhibitors of the Histone Acetyltransferase KAT6A. Journal of Medicinal Chemistry, 2019, 62, 7146-7159.	2.9	21
212	Regulation and crystallization of phosphorylated and dephosphorylated forms of truncated dimeric phenylalanine hydroxylase. Protein Science, 1997, 6, 1352-1357.	3.1	20
213	Evaluation of the role of two conserved active-site residues in Beta class glutathione S-transferases. Biochemical Journal, 2000, 351, 341-346.	1.7	20
214	Thermodynamic Description of the Effect of the Mutation Y49F on Human Glutathione Transferase P1-1 in Binding with Glutathione and the Inhibitor S-Hexylglutathione. Journal of Biological Chemistry, 2003, 278, 46938-46948.	1.6	20
215	Purification, crystallization and preliminary X-ray diffraction studies to near-atomic resolution of dihydrodipicolinate synthase from methicillin-resistantStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 659-661.	0.7	20
216	The Binding of Syndapin SH3 Domain to Dynamin Proline-rich Domain Involves Short and Long Distance Elements. Journal of Biological Chemistry, 2016, 291, 9411-9424.	1.6	20

#	Article	IF	Citations
217	Glutathione transferase P1â€1 as an arsenic drugâ€sequestering enzyme. Protein Science, 2017, 26, 317-326.	3.1	20
218	Functional and structural analysis of cytokine-selective IL6ST defects that cause recessive hyper-IgE syndrome. Journal of Allergy and Clinical Immunology, 2021, 148, 585-598.	1.5	20
219	Proton release on binding of glutathione to Alpha, Mu and Delta class glutathione transferases. Biochemical Journal, 1999, 344, 419.	1.7	19
220	Engineering a New C-terminal Tail in the H-site of Human Glutathione Transferase P1-1: Structural and Functional Consequences. Journal of Molecular Biology, 2003, 325, 111-122.	2.0	19
221	Amiloride Is a Competitive Inhibitor of Coxsackievirus B3 RNA Polymerase. Journal of Virology, 2011, 85, 10364-10374.	1.5	19
222	Molecular and structural insight into lysine selection on substrate and ubiquitin lysine 48 by the ubiquitin-conjugating enzyme Cdc34. Cell Cycle, 2013, 12, 1732-1744.	1.3	19
223	Design of proteasome inhibitors with oral efficacy in vivo against Plasmodium falciparum and selectivity over the human proteasome. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
224	Crystallization and preliminary X-ray analysis of a thiol-activated cytolysin. FEBS Letters, 1996, 397, 290-292.	1.3	18
225	Thiophene inhibitors of PDE4: Crystal structures show a second binding mode at the catalytic domain of PDE4D2. Bioorganic and Medicinal Chemistry Letters, 2011, 21, 7089-7093.	1.0	18
226	Structure of the lysine specific protease <scp>K</scp>gp from <scp>P</scp>orphyromonas gingivalis, a target for improved oral health. Protein Science, 2015, 24, 162-166.	3.1	18
227	Two-step mechanism involving active-site conformational changes regulates human telomerase DNA binding. Biochemical Journal, 2015, 465, 347-357.	1.7	18
228	Structures of thermolabile mutants of human glutathione transferase P1-1 1 1Edited by R. Huber. Journal of Molecular Biology, 2000, 302, 295-302.	2.0	17
229	Expression, purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase fromBacillus anthracisin the presence of pyruvate. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 188-191.	0.7	17
230	Purification, crystallization, small-angle X-ray scattering and preliminary X-ray diffraction analysis of the SH2 domain of the Csk-homologous kinase. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 336-339.	0.7	17
231	Ex vivo 18O-labeling mass spectrometry identifies a peripheral amyloid Î² clearance pathway. Molecular Neurodegeneration, 2017, 12, 18.	4.4	17
232	Crystallographic phases through genetic engineering: experiences with colicin A. Protein Engineering, Design and Selection, 1989, 2, 399-405.	1.0	16
233	Binding and Kinetic Mechanisms of the Zeta Class Glutathione Transferase. Journal of Biological Chemistry, 2004, 279, 33336-33342.	1.6	16
234	A structural view of PA2G4 isoforms with opposing functions in cancer. Journal of Biological Chemistry, 2020, 295, 16100-16112.	1.6	16

#	Article	IF	Citations
235	Influence of the Hâ€site residue 108 on human glutathione transferase P1â€1 ligand binding: Structureâ€thermodynamic relationships and thermal stability. Protein Science, 2009, 18, 2454-2470.	3.1	15
236	A Key Motif in the Cholesterol-Dependent Cytolysins Reveals a Large Family of Related Proteins. MBio, 2020, 11, .	1.8	15
237	Purification, crystallisation and preliminary X-ray diffraction characterisation of methanol dehydrogenase from Methylosinus trichosporium OB3b. FEBS Journal, 1987, 164, 223-227.	0.2	14
238	Crystallization and preliminary X-ray diffraction studies of a glutathione S-Transferase from the Australian sheep blowfly, Lucilia cuprina. Journal of Molecular Biology, 1994, 236, 1407-1409.	2.0	14
239	The purification, crystallization and preliminary X-ray diffraction analysis of dihydrodipicolinate synthase fromClostridium botulinum. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 206-208.	0.7	14
240	Crystallization and preliminary X-ray analysis of dihydrodipicolinate synthase fromClostridium botulinumin the presence of its substrate pyruvate. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 253-255.	0.7	14
241	Structural approaches to probing metal interaction with proteins. Journal of Inorganic Biochemistry, 2012, 115, 138-147.	1.5	14
242	Properties and Utility of the Peculiar Mixed Disulfide in the Bacterial Glutathione Transferase B1-1. Biochemistry, 2002, 41, 4686-4693.	1.2	13
243	Naturally occurring Phe151Leu substitution near a conserved folding module lowers stability of glutathione transferase P1â€“1. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1649, 16-23.	1.1	13
244	Diuretic drug binding to human glutathione transferase P1â€1: potential role of Cysâ€101 revealed in the double mutant C47S/Y108V. Journal of Molecular Recognition, 2011, 24, 220-234.	1.1	13
245	An Activation-Specific Platelet Inhibitor That Can Be Turned On/Off by Medically Used Hypothermia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 2015-2023.	1.1	13
246	Phosphorylation of Serine 779 in Fibroblast Growth Factor Receptor 1 and 2 by Protein Kinase Cïµ Regulates Ras/Mitogen-activated Protein Kinase Signaling and Neuronal Differentiation. Journal of Biological Chemistry, 2013, 288, 14874-14885.	1.6	13
247	Activity-Modulating Monoclonal Antibodies to the Human Serine Protease HtrA3 Provide Novel Insights into Regulating HtrA Proteolytic Activities. PLoS ONE, 2014, 9, e108235.	1.1	13
248	A novel combination therapy targeting ubiquitin-specific protease 5 in MYCN-driven neuroblastoma. Oncogene, 2021, 40, 2367-2381.	2.6	13
249	Crystallization and preliminary X-ray analysis of the human-specific toxin intermedilysin. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 347-349.	2.5	12
250	Crystallization of the glycogen-binding domain of the AMP-activated protein kinase Î² subunit and preliminary X-ray analysis. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 39-42.	0.7	12
251	Structural Basis for Antibody Discrimination between Two Hormones That Recognize the Parathyroid Hormone Receptor. Journal of Biological Chemistry, 2009, 284, 15557-15563.	1.6	12
252	Dihydropyridine inhibition of the glycine receptor: Subunit selectivity and a molecular determinant of inhibition. Neuropharmacology, 2009, 56, 318-327.	2.0	12

#	Article	IF	Citations
253	Crystallization of dihydrodipicolinate synthase from a clinical isolate ofStreptococcus pneumoniae. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 32-36.	0.7	12
254	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin. PLoS ONE, 2020, 15, e0229000.	1.1	12
255	A DARPin targeting activated Mac-1 is a novel diagnostic tool and potential anti-inflammatory agent in myocarditis, sepsis and myocardial infarction. Basic Research in Cardiology, 2021, 116, 17.	2.5	12
256	Mechanism of Bloom syndrome complex assembly required for double Holliday junction dissolution and genome stability. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	12
257	Human Glutathione Transferase T2-2 Discloses Some Evolutionary Strategies for Optimization of the Catalytic Activity of Glutathione Transferases. Journal of Biological Chemistry, 2001, 276, 5432-5437.	1.6	11
258	Crystallization and preliminary X-ray diffraction analysis of the Fab fragment of WO2, an antibody specific for the AÎ² peptides associated with Alzheimer's disease. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 438-441.	0.7	11
259	Cloning, expression and crystallization of dihydrodipicolinate reductase from methicillin-resistantStaphylococcus aureus. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 57-60.	0.7	11
260	Propargyloxyproline Regio- and Stereoisomers for Click-Conjugation of Peptides: Synthesis and Application in Linear and Cyclic Peptides. Australian Journal of Chemistry, 2015, 68, 1365.	0.5	11
261	PROTEIN SECONDARY STRUCTURE PREDICTION USING SUPPORT VECTOR MACHINES AND A NEW FEATURE REPRESENTATION. International Journal of Computational Intelligence and Applications, 2006, 06, 551-567.	0.6	10
262	Cloning, expression, purification and crystallization of dihydrodipicolinate synthase from the psychrophileShewanella benthica. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1511-1516.	0.7	10
263	Crystallization and preliminary X-ray diffraction analysis of the Fab portion of the Alzheimer's disease immunotherapy candidate bapineuzumab complexed with amyloid-Î². Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 374-377.	0.4	10
264	An Intermolecular Ï€-Stacking Interaction Drives Conformational Changes Necessary to Î²-Barrel Formation in a Pore-Forming Toxin. MBio, 2019, 10, .	1.8	10
265	The Structural Basis for a Transition State That Regulates Pore Formation in a Bacterial Toxin. MBio, 2019, 10, .	1.8	10
266	Fluorescence Microscopy Assay to Measure HIV-1 Capsid Uncoating Kinetics in vitro. Bio-protocol, 2019, 9, e3297.	0.2	10
267	Crystallization and preliminary x-ray analysis of the auto-inhibited twitchin kinase. Journal of Molecular Biology, 1994, 236, 1259-1261.	2.0	9
268	Crystallization and preliminary crystallographic studies of the copper-binding domain of the amyloid precursor protein of Alzheimer's disease. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 93-95.	0.7	9
269	Crystallization and preliminary X-ray diffraction analysis of the ternary human GM-CSF receptor complex. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 711-714.	0.7	9
270	The extended catalysis of glutathione transferase. FEBS Letters, 2011, 585, 341-345.	1.3	9

#	Article	IF	Citations
271	Evolutionary comparisons predict that dimerization of human cytochrome P450 aromatase increases its enzymatic activity and efficiency. Journal of Steroid Biochemistry and Molecular Biology, 2015, 154, 294-301.	1.2	9
272	The C-terminal extension of human telomerase reverse transcriptase is necessary for high affinity binding to telomeric DNA. Biochimie, 2016, 128-129, 114-121.	1.3	9
273	AMP and adenosine are both ligands for adenosine 2B receptor signaling. Bioorganic and Medicinal Chemistry Letters, 2018, 28, 202-206.	1.0	9
274	Reaction mechanism of the bioluminescent protein mnemiopsin1 revealed by X-ray crystallography and QM/MM simulations. Journal of Biological Chemistry, 2019, 294, 20-27.	1.6	9
275	Discovery of Acylsulfonohydrazide-Derived Inhibitors of the Lysine Acetyltransferase, KAT6A, as Potent Senescence-Inducing Anti-Cancer Agents. Journal of Medicinal Chemistry, 2020, 63, 4655-4684.	2.9	9
276	Evaluation of the role of two conserved active-site residues in Beta class glutathione S-transferases. Biochemical Journal, 2000, 351, 341.	1.7	8
277	Expression, purification, crystallization and preliminary X-ray diffraction analysis of chloride intracellular channel 2 (CLIC2). Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 961-963.	0.7	8
278	Manipulating the Lewis antigen specificity of the cholesterol-dependent cytolysin lectinolysin. Frontiers in Immunology, 2012, 3, 330.	2.2	8
279	Crystallization and preliminary X-ray diffraction analysis of the interleukin-3 alpha receptor bound to the Fab fragment of antibody CSL362. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 358-361.	0.4	8
280	Bridging Crystal Engineering and Drug Discovery by Utilizing Intermolecular Interactions and Molecular Shapes in Crystals. Angewandte Chemie, 2019, 131, 16936-16940.	1.6	8
281	X-ray crystallography shines a light on pore-forming toxins. Methods in Enzymology, 2021, 649, 1-46.	0.4	8
282	Cholesterolâ€dependent cytolysins: The outstanding questions. IUBMB Life, 2022, 74, 1169-1179.	1.5	8
283	Crystallization and preliminary X-ray analysis of phosphoporin from the outer membrane of Escherichia coli. Journal of Molecular Biology, 1991, 222, 881-884.	2.0	7
284	Glutamic acid-65 is an essential residue for catalysis in Proteus mirabilis glutathione S-transferase B1-1. Biochemical Journal, 2002, 363, 189.	1.7	7
285	Control of Virulence Gene Expression by the Master Regulator, CfaD, in the Prototypical Enterotoxigenic Escherichia coli Strain, H10407. Frontiers in Microbiology, 2017, 8, 1525.	1.5	7
286	QM/MM simulations provide insight into the mechanism of bioluminescence triggering in ctenophore photoproteins. PLoS ONE, 2017, 12, e0182317.	1.1	7
287	Crystallization and preliminary X-ray diffraction analysis of human endoplasmic reticulum aminopeptidase 2. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 468-471.	0.7	6
288	A Homodimer Model Can Resolve the Conundrum as to How Cytochrome P450 Oxidoreductase and Cytochrome b5 Compete for the Same Binding Site on Cytochrome P450c17. Current Protein and Peptide Science, 2017, 18, 515-521.	0.7	6

#	Article	IF	Citations
289	Structure-function analysis of the AMPK activator SC4 and identification of a potent pan AMPK activator. Biochemical Journal, 2022, 479, 1181-1204.	1.7	6
290	More than one way to make a hole. Nature Structural Biology, 1997, 4, 250-253.	9.7	5
291	PEGylation of a proprotein convertase peptide inhibitor for vaginal route of drug delivery: In vitro bioactivity, stability and in vivo pharmacokinetics. Peptides, 2012, 38, 266-274.	1.2	5
292	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. Structure, 2018, 26, 948-959.e5.	1.6	5
293	The mechanism of GM-CSF inhibition by human GM-CSF auto-antibodies suggests novel therapeutic opportunities. MAbs, 2018, 10, 1-12.	2.6	5
294	Cyclic Hexapeptide Mimics of the LEDGF Integrase Recognition Loop in Complex with HIVâ€1 Integrase. ChemMedChem, 2018, 13, 1555-1565.	1.6	5
295	Development of [18F]MIPS15692, a radiotracer with inÂvitro proof-of-concept for the imaging of MER tyrosine kinase (MERTK) in neuroinflammatory disease. European Journal of Medicinal Chemistry, 2021, 226, 113822.	2.6	5
296	Insights into Membrane Insertion Based on Studies of Colicins. Molecular Biology Intelligence Unit, 1996, , 5-23.	0.2	5
297	Structural biology of cell surface receptors implicated in Alzheimerâ€™s disease. Biophysical Reviews, 2022, 14, 233-255.	1.5	5
298	Protein topology classification using two-stage support vector machines. Genome Informatics, 2006, 17, 259-69.	0.4	5
299	Preliminary X-ray crystallographic studies of a newly defined human theta-class glutathione transferase. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 148-150.	2.5	4
300	Dichloromethane mediatedin vivoselection and functional characterization of rat glutathioneS-transferase theta 1-1 variants. FEBS Journal, 2001, 268, 4001-4010.	0.2	4
301	Crystallization of the receptor-binding domain of parathyroid hormone-related protein in complex with a neutralizing monoclonal antibody Fab fragment. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 336-338.	0.7	4
302	Preparation, crystallization and preliminary X-ray diffraction analysis of two intestinal fatty-acid binding proteins in the presence of 11-(dansylamino)undecanoic acid. Acta Crystallographica Section F: Structural Biology Communications, 2011, 67, 291-295.	0.7	4
303	Crystal structure of the Leishmania major MIX protein: A scaffold protein that mediates proteinâ€“protein interactions. Protein Science, 2011, 20, 1060-1068.	3.1	4
304	Anti-AÎ² antibody target engagement: a response to Siemers et al.. Acta Neuropathologica, 2014, 128, 611-614.	3.9	4
305	Comparative three-dimensional structure of cholesterol-dependent cytolysins. , 2006, , 659-670.		4
306	Abstract 5371: PRMT5 inhibitors as novel treatment for cancers. Cancer Research, 2015, 75, 5371-5371.	0.4	4

#	Article	IF	Citations
307	Histidine H-2 n.m.r. resonances of sperm whale oxy-, carbonyl-, and met-myoglobin. Journal of the Chemical Society Chemical Communications, 1981, , 208.	2.0	3
308	Valine 10 May Act as a Driver for Product Release from the Active Site of Human Glutathione Transferase P1-1â€,â€¡. Biochemistry, 2000, 39, 15961-15970.	1.2	3
309	Small Molecule Proprotein Convertase Inhibitors for Inhibition of Embryo Implantation. PLoS ONE, 2013, 8, e81380.	1.1	3
310	Crystallization and preliminary X-ray analysis of glutathione transferases from cyanobacteria. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 475-477.	0.7	2
311	Computational Analysis of Amiloride Analogue Inhibitors of Coxsackie Virus B3 RNA Polymerase. Journal of Proteomics and Bioinformatics, 2014, s9, 004.	0.4	2
312	Discovery of Phosphodiesterase-4 Inhibitors: Serendipity and Rational Drug Design. Australian Journal of Chemistry, 2014, 67, 1780.	0.5	2
313	Targeting of Câ€type lectinâ€like receptorÂ2 or P2Y12 for the prevention of platelet activation by immunotherapeutic CpG oligodeoxynucleotides: comment. Journal of Thrombosis and Haemostasis, 2018, 16, 181-185.	1.9	2
314	Sequence comparisons of cytochrome P450 aromatases from Australian animals predict differences in enzymatic activity and/or efficiencyâ€. Biology of Reproduction, 2020, 102, 1261-1269.	1.2	2
315	A STUDY ON THE EFFECT OF USING PHYSICO-CHEMICAL FEATURES IN PROTEIN SECONDARY STRUCTURE PREDICTION. , 2006, , .		2
316	Messing with Î²c: A unique receptor with many goals. Seminars in Immunology, 2021, 54, 101513.	2.7	2
317	Protein crystallography in Australia. Australian and New Zealand Journal of Medicine, 1995, 25, 876-882.	0.5	1
318	Crystallization and preliminary X-ray diffraction analysis of the unliganded human growth hormone receptor. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2380-2382.	2.5	1
319	Real Value Solvent Accessibility Prediction using Adaptive Support Vector Regression. , 2007, , .		1
320	Unexpected mechanisms of action for a cytokine receptor-blocking antibody. Molecular and Cellular Oncology, 2014, 1, e969129.	0.3	1
321	An Escherichia coli Cell-Free System for Recombinant Protein Synthesis on a Milligram Scale. Methods in Molecular Biology, 2011, 752, 17-28.	0.4	1
322	Structure and Assembly of the Channel-Forming Aeromonas Toxin Aerolysin. Molecular Biology Intelligence Unit, 1996, , 79-95.	0.2	1
323	The Crystal Structure of the Manganese Superoxide Dismutase from Geobacillus stearothermophilus: Parker and Blake (1988) Revisited. Australian Journal of Chemistry, 2020, 73, 145.	0.5	1
324	Selective Inhibitors of Arginine Methyl Transferase 5 (PRMT5) As a Novel Treatment for Î²-Thalassemia and Sickle Cell Disease.. Blood, 2012, 120, 2129-2129.	0.6	1

#	Article	IF	Citations
325	Cytokine Receptors and their Ligands. , 2022, , .		1
326	78. Cytokine, 2014, 70, 46.	1.4	0
327	Mechanism of JAK2 Activation by the Archetype Class I Cytokine Receptor, the Growth Hormone Receptor. Biophysical Journal, 2016, 110, 31a.	0.2	0
328	Nitric Oxide Interacting with Glutathione Transferases. , 2017, , 191-195.		0
329	Structure and Function of the Proteasome Activator PA28 of the Malaria Parasite Plasmodium falciparum. Microscopy and Microanalysis, 2019, 25, 1324-1325.	0.2	0
330	Strategies for Crystallizing the N-Terminal Growth Factor Domain of Amyloid Precursor Protein. , 2004, , .		0
331	Abstract 469: CD151 and cell motility in prostate cancer. , 2012, , .		0
332	Abstract A19: The selective targeting of cell survival pathways in leukemia. , 2013, , .		0
333	The GM-CSF receptor â€“ mechanisms for affinity conversion and signalling. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C1279-C1279.	0.0	0
334	Accumulation of JAK Activation-Loop Phosphorylation Promotes Type I JAK Inhibitor Withdrawal Syndrome in Myelofibrosis. Blood, 2018, 132, 1787-1787.	0.6	0
335	The structure of the Plasmodium falciparum 20S proteasome in complex with the PA28 activator. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a118-a118.	0.0	0
336	Abstract 4962: Repurposingbazedoxifeneto suppress gastrointestinal cancer growth. , 2019, , .		0
337	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin. , 2020, 15, e0229000.		0
338	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin. , 2020, 15, e0229000.		0
339	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin. , 2020, 15, e0229000.		0
340	Preparation and purification of mono-ubiquitinated proteins using Avi-tagged ubiquitin. , 2020, 15, e0229000.		0