

Yves Bourne

List of Publications by Year in descending order

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121
papers

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41344

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123
times ranked

10150
citing authors

#	ARTICLE	IF	CITATIONS
1	Structures of Aplysia AChBP complexes with nicotinic agonists and antagonists reveal distinctive binding interfaces and conformations. EMBO Journal, 2005, 24, 3635-3646.	7.8	602
2	Glycoside hydrolases and glycosyltransferases: families and functional modules. Current Opinion in Structural Biology, 2001, 11, 593-600.	5.7	393
3	Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism 1 Edited by R. Huber. Journal of Molecular Biology, 2000, 296, 295-309.	4.2	388
4	Structural insights into ligand interactions at the acetylcholinesterase peripheral anionic site. EMBO Journal, 2003, 22, 1-12.	7.8	362
5	Acetylcholinesterase inhibition by fasciculin: Crystal structure of the complex. Cell, 1995, 83, 503-512.	28.9	357
6	Crystal structure of a Cbt α -AChBP complex reveals essential interactions between snake β -neurotoxins and nicotinic receptors. EMBO Journal, 2005, 24, 1512-1522.	7.8	302
7	Freeze-frame inhibitor captures acetylcholinesterase in a unique conformation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1449-1454.	7.1	297
8	Crystal structures of the bovine beta 4galactosyltransferase catalytic domain and its complex with uridine diphosphogalactose. EMBO Journal, 1999, 18, 3546-3557.	7.8	266
9	Bacterial glycosidases for the production of universal red blood cells. Nature Biotechnology, 2007, 25, 454-464.	17.5	259
10	ESTHER, the database of the β -hydrolase fold superfamily of proteins: tools to explore diversity of functions. Nucleic Acids Research, 2012, 41, D423-D429.	14.5	244
11	Crystal Structure and Mutational Analysis of the Human CDK2 Kinase Complex with Cell Cycle α Regulatory Protein CksHs1. Cell, 1996, 84, 863-874.	28.9	237
12	Crosslinking of mammalian lectin (galectin-1) by complex biantennary saccharides. Nature Structural and Molecular Biology, 1994, 1, 863-870.	8.2	218
13	Immunocytochemical Localization and Crystal Structure of Human Frequenin (Neuronal Calcium) Tj ETQq1 1 0.784314 rgBT /Overlock 3.4 176		
14	Crystal structure of the bifunctional N-acetylglucosamine 1-phosphate uridyltransferase from Escherichia coli: a paradigm for the related pyrophosphorylase superfamily. EMBO Journal, 1999, 18, 4096-4107.	7.8	174
15	Structure of human lysosomal acid β -glucosidase α a guide for the treatment of Pompe disease. Nature Communications, 2017, 8, 1111.	12.8	169
16	Structural determinants in phycotoxins and AChBP conferring high affinity binding and nicotinic AChR antagonism. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6076-6081.	7.1	156
17	Conformational Flexibility of the Acetylcholinesterase Tetramer Suggested by X-ray Crystallography. Journal of Biological Chemistry, 1999, 274, 30370-30376.	3.4	154
18	Structural determinants for interaction of partial agonists with acetylcholine binding protein and neuronal β 7 nicotinic acetylcholine receptor. EMBO Journal, 2009, 28, 3040-3051.	7.8	153

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19	Mannose-binding plant lectins: Different structural scaffolds for a common sugar-recognition process. <i>Biochimie</i> , 2001, 83, 645-651.	2.6	149
20	Structural Analysis of the Synaptic Protein Neuroligin and Its β -Neurexin Complex: Determinants for Folding and Cell Adhesion. <i>Neuron</i> , 2007, 56, 979-991.	8.1	142
21	Crystal Structure of <i>Thermotoga maritima</i> α -L-Fucosidase. <i>Journal of Biological Chemistry</i> , 2004, 279, 13119-13128.	3.4	141
22	Crystal structures of two human pyrophosphorylase isoforms in complexes with UDPGlc(Gal)NAc: role of the alternatively spliced insert in the enzyme oligomeric assembly and active site architecture. <i>EMBO Journal</i> , 2001, 20, 6191-6202.	7.8	138
23	Structural basis for the unusual carbohydrate-binding specificity of jacalin towards galactose and mannose. <i>Biochemical Journal</i> , 2002, 364, 173-180.	3.7	138
24	High-throughput automated refolding screening of inclusion bodies. <i>Protein Science</i> , 2009, 13, 2782-2792.	7.6	134
25	Barley α -amylase bound to its endogenous protein inhibitor BASI: crystal structure of the complex at 1.9 Å resolution. <i>Structure</i> , 1998, 6, 649-659.	3.3	129
26	LppX is a lipoprotein required for the translocation of phthiocerol dimycocerosates to the surface of <i>Mycobacterium tuberculosis</i> . <i>EMBO Journal</i> , 2006, 25, 1436-1444.	7.8	126
27	Three-Dimensional structures of complexes of <i>Lathyrus ochrus</i> isolectin I with glucose and mannose: Fine specificity of the monosaccharide-binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 365-376.	2.6	121
28	Crystal Structure of Mouse Acetylcholinesterase. <i>Journal of Biological Chemistry</i> , 1999, 274, 2963-2970.	3.4	117
29	Substrate and Product Trafficking through the Active Center Gorge of Acetylcholinesterase Analyzed by Crystallography and Equilibrium Binding. <i>Journal of Biological Chemistry</i> , 2006, 281, 29256-29267.	3.4	117
30	<i>Helianthus tuberosus</i> lectin reveals a widespread scaffold for mannose-binding lectins. <i>Structure</i> , 1999, 7, 1473-1482.	3.3	107
31	Horse Pancreatic Lipase. <i>Journal of Molecular Biology</i> , 1994, 238, 709-732.	4.2	106
32	Structures of a legume lectin complexed with the human lactotransferrin N2 fragment, and with an isolated biantennary glycopeptide: role of the fucose moiety. <i>Structure</i> , 1994, 2, 209-219.	3.3	105
33	X-ray crystal structure determination and refinement at 1.9 Å... resolution of isolectin I from the seeds of <i>Lathyrus ochrus</i> . <i>Journal of Molecular Biology</i> , 1990, 214, 571-584.	4.2	92
34	Crystal Structure of <i>Streptococcus pneumoniae</i> N-Acetylglucosamine-1-phosphate Uridyltransferase Bound to Acetyl-coenzyme A Reveals a Novel Active Site Architecture. <i>Journal of Biological Chemistry</i> , 2001, 276, 11844-11851.	3.4	92
35	Novel dimeric interface and electrostatic recognition in bacterial Cu,Zn superoxide dismutase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 12774-12779.	7.1	89
36	Crystal Structure of the Human Cell Cycle Protein CksHs1: Single Domain Fold with Similarity to Kinase N-lobe Domain. <i>Journal of Molecular Biology</i> , 1995, 249, 835-842.	4.2	76

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37	Mechanism of Acetylcholinesterase Inhibition by Fasciculin: A 5-ns Molecular Dynamics Simulation. <i>Journal of the American Chemical Society</i> , 2002, 124, 6153-6161.	13.7	75
38	The Crystal Structures of Apo and Complexed <i>Saccharomyces cerevisiae</i> GNA1 Shed Light on the Catalytic Mechanism of an Amino-sugar N-Acetyltransferase. <i>Journal of Biological Chemistry</i> , 2001, 276, 16328-16334.	3.4	74
39	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73
40	Primary and Three-Dimensional Structure of Lactotransferrin (Lactoferrin) Glycans. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 21-32.	1.6	71
41	Crystal structure of the cell cycle-regulatory protein <i>suc1</i> reveals a beta-hinge conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 10232-10236.	7.1	70
42	Identification of the Catalytic Nucleophile of the Family 29 α -L-Fucosidase from <i>Thermotoga maritima</i> through Trapping of a Covalent Glycosyl-Enzyme Intermediate and Mutagenesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 47394-47399.	3.4	70
43	Data bank of three-dimensional structures of disaccharides: Part II, N-acetyllactosaminic type N-glycans. Comparison with the crystal structure of a biantennary octasaccharide. <i>Glycoconjugate Journal</i> , 1991, 8, 456-483.	2.7	64
44	Expression and characterization of the protein Rv1399c from <i>Mycobacterium tuberculosis</i> . <i>FEBS Journal</i> , 2004, 271, 3953-3961.	0.2	61
45	Glycosyltransferases, glycoside hydrolases: surprise, surprise!. <i>Current Opinion in Structural Biology</i> , 2008, 18, 527-533.	5.7	59
46	Cyclic imine toxins from dinoflagellates: a growing family of potent antagonists of the nicotinic acetylcholine receptors. <i>Journal of Neurochemistry</i> , 2017, 142, 41-51.	3.9	59
47	Soluble monomeric acetylcholinesterase from mouse: Expression, purification, and crystallization in complex with fasciculin. <i>Protein Science</i> , 1996, 5, 672-679.	7.6	56
48	The Crystal Structure of the <i>Calystegia sepium</i> Agglutinin Reveals a Novel Quaternary Arrangement of Lectin Subunits with a β^2 -Prism Fold. <i>Journal of Biological Chemistry</i> , 2004, 279, 527-533.	3.4	54
49	Protein-carbohydrate interactions. <i>Current Opinion in Structural Biology</i> , 1993, 3, 681-686.	5.7	52
50	Interaction between the SifA Virulence Factor and Its Host Target SKIP Is Essential for <i>Salmonella</i> Pathogenesis. <i>Journal of Biological Chemistry</i> , 2009, 284, 33151-33160.	3.4	52
51	Overview of the Structure-Function Relationships of Mannose-Specific Lectins from Plants, Algae and Fungi. <i>International Journal of Molecular Sciences</i> , 2019, 20, 254.	4.1	48
52	The Structure of Human DNase I Bound to Magnesium and Phosphate Ions Points to a Catalytic Mechanism Common to Members of the DNase I-like Superfamily. <i>Biochemistry</i> , 2012, 51, 10250-10258.	2.5	43
53	Marine Macrocyclic Imines, Pinnatoxins A and C: Structural Determinants and Functional Properties to Distinguish Neuronal $\alpha 7$ from Muscle $\alpha 2\beta 3$ nAChRs. <i>Structure</i> , 2015, 23, 1106-1115.	3.3	42
54	The size, shape and specificity of the sugar-binding site of the jacalin-related lectins is profoundly affected by the proteolytic cleavage of the subunits. <i>Biochemical Journal</i> , 2002, 367, 817-824.	3.7	41

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55	The neuroligins and the synaptic pathway in Autism Spectrum Disorder. <i>Neuroscience and Biobehavioral Reviews</i> , 2020, 119, 37-51.	6.1	40
56	Distinct oligomeric forms of the <i>Pseudomonas aeruginosa</i> RetS sensor domain modulate accessibility to the ligand binding site. <i>Environmental Microbiology</i> , 2010, 12, 1775-1786.	3.8	39
57	Proteins with an alpha/beta hydrolase fold: Relationships between subfamilies in an ever-growing superfamily. <i>Chemico-Biological Interactions</i> , 2013, 203, 266-268.	4.0	39
58	Crystal structure and mutational analysis of the <i>Saccharomyces cerevisiae</i> cell cycle regulatory protein Cks1: implications for domain swapping, anion binding and protein interactions. <i>Structure</i> , 2000, 8, 841-850.	3.3	38
59	Structural insights into the exquisite selectivity of neurexin/neuroligin synaptic interactions. <i>EMBO Journal</i> , 2010, 29, 2461-2471.	7.8	38
60	Structural Insights into the Catalytic Mechanism of Bacterial Guanosine-diphospho-d-mannose Pyrophosphorylase and Its Regulation by Divalent Ions. <i>Journal of Biological Chemistry</i> , 2010, 285, 27468-27476.	3.4	33
61	Crystal Structure of the GalNAc/Gal-Specific Agglutinin from the Phytopathogenic Ascomycete <i>Sclerotinia sclerotiorum</i> Reveals Novel Adaptation of a β^2 -Trefoil Domain. <i>Journal of Molecular Biology</i> , 2010, 400, 715-723.	4.2	33
62	Dissection of the Bifunctional <i>Escherichia coli</i> N-Acetylglucosamine-1-phosphate Uridyltransferase Enzyme into Autonomously Functional Domains and Evidence That Trimerization Is Absolutely Required for Glucosamine-1-phosphate Acetyltransferase Activity and Cell Growth. <i>Journal of Biological Chemistry</i> , 2001, 276, 3833-3839.	3.4	32
63	Gene Overexpression and Biochemical Characterization of the Biotechnologically Relevant Chlorogenic Acid Hydrolase from <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 5624-5632.	3.1	32
64	Interactions of plant lectins with the components of the bacterial cell wall peptidoglycan. <i>Biochemical Systematics and Ecology</i> , 1994, 22, 153-159.	1.3	30
65	The Mtr2-Mex67 NTF2-like Domain Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 48395-48403.	3.4	30
66	Structural insights into conformational flexibility at the peripheral site and within the active center gorge of AChE. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 159-165.	4.0	30
67	Steric and Dynamic Parameters Influencing In Situ Cycloadditions to Form Triazole Inhibitors with Crystalline Acetylcholinesterase. <i>Journal of the American Chemical Society</i> , 2016, 138, 1611-1621.	13.7	30
68	<i>Aspergillus niger</i> Protein EstA Defines a New Class of Fungal Esterases within the β^1/β^2 Hydrolase Fold Superfamily of Proteins. <i>Structure</i> , 2004, 12, 677-687.	3.3	29
69	Conformational Remodeling of Femtomolar Inhibitor ⁺ Acetylcholinesterase Complexes in the Crystalline State. <i>Journal of the American Chemical Society</i> , 2010, 132, 18292-18300.	13.7	29
70	Crystallization and preliminary X-ray study of horse pancreatic lipase. <i>Journal of Molecular Biology</i> , 1989, 205, 259-261.	4.2	27
71	Inhibition of mouse acetylcholinesterase by fasciculin: Crystal structure of the complex and mutagenesis of fasciculin. <i>Toxicon</i> , 1998, 36, 1613-1622.	1.6	25
72	Crystal structure of the conserved hypothetical protein Rv1155 from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2005, 579, 215-221.	2.8	25

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73	Structural and biochemical characterization of the \hat{N} -acetylglucosaminidase from <i>Thermotoga maritima</i> : Toward rationalization of mechanistic knowledge in the GH73 family. <i>Glycobiology</i> , 2015, 25, 319-330.	2.5	25
74	Substrate binding mode and catalytic mechanism of human heparan sulfate α -glucuronyl C5 epimerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6760-6765.	7.1	23
75	Structure of a polyisoprenoid binding domain from <i>Saccharophagus degradans</i> implicated in plant cell wall breakdown. <i>FEBS Letters</i> , 2010, 584, 1577-1584.	2.8	20
76	Structural Insights into Antibody Sequestering and Neutralizing of Na ⁺ Channel $\hat{\alpha}$ -Type Modulator from Old World Scorpion Venom. <i>Journal of Biological Chemistry</i> , 2012, 287, 14136-14148.	3.4	20
77	Crystal Structure of Snake Venom Acetylcholinesterase in Complex with Inhibitory Antibody Fragment Fab410 Bound at the Peripheral Site. <i>Journal of Biological Chemistry</i> , 2015, 290, 1522-1535.	3.4	20
78	Glycosylate and move! The glycosyltransferase Maf is involved in bacterial flagella formation. <i>Environmental Microbiology</i> , 2018, 20, 228-240.	3.8	20
79	Crystallization and Preliminary X-ray Diffraction Studies of the Soluble 14 kDa $\hat{\alpha}$ -Galactoside-binding Lectin from Bovine Heart. <i>Journal of Molecular Biology</i> , 1994, 235, 787-789.	4.2	19
80	A Mutation in the Human Cyclin-dependent Kinase Interacting Protein, CksHs2, Interferes With Cyclin-dependent Kinase Binding and Biological Function, but Preserves Protein Structure and Assembly. <i>Journal of Molecular Biology</i> , 1996, 261, 646-657.	4.2	16
81	Structural Characterization of Agonist and Antagonist-Bound Acetylcholine-Binding Protein From <i>Aplysia californica</i> . <i>Journal of Molecular Neuroscience</i> , 2006, 30, 101-102.	2.3	15
82	Structural and Functional Characterization of the <i>Clostridium perfringens</i> N-Acetylmannosamine-6-phosphate 2-Epimerase Essential for the Sialic Acid Salvage Pathway. <i>Journal of Biological Chemistry</i> , 2014, 289, 35215-35224.	3.4	15
83	Structural and functional insights into the periplasmic detector domain of the GacS histidine kinase controlling biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2017, 7, 11262.	3.3	15
84	[5] Pancreatic lipases and their complexes with colipases and inhibitors: Crystallization and crystal packing. <i>Methods in Enzymology</i> , 1997, 284, 107-119.	1.0	14
85	Crystallization and preliminary X-ray diffraction study of <i>Lathyrus ochrus</i> isolectin II complexed to the human lactotransferrin N2 fragment. <i>Journal of Molecular Biology</i> , 1992, 227, 938-941.	4.2	13
86	Characterization, Crystallization and Preliminary X-ray Crystallographic Analysis of the Complex between Barley $\hat{\alpha}$ -Amylase and the Bifunctional $\hat{\alpha}$ -Amylase/Subtilisin Inhibitor from Barley Seeds. <i>Journal of Molecular Biology</i> , 1994, 236, 368-371.	4.2	13
87	Functional characterization of the glycosyltransferase domain of penicillin-binding protein 1a from <i>Thermotoga maritima</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 1036-1042.	2.3	11
88	Tracking the Origin and Divergence of Cholinesterases and Neuroligins: The Evolution of Synaptic Proteins. <i>Journal of Molecular Neuroscience</i> , 2014, 53, 362-369.	2.3	11
89	The Ig-like domain of Punctin/MADD-4 is the primary determinant for interaction with the ectodomain of neuroligin NLG-1. <i>Journal of Biological Chemistry</i> , 2020, 295, 16267-16279.	3.4	11
90	Co-crystallization and preliminary X-ray diffraction studies of <i>Lathyrus ochrus</i> isolectin I with Di- and trisaccharides, and a biantennary octosaccharide. <i>Journal of Molecular Biology</i> , 1990, 213, 211-213.	4.2	10

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91	Structure–function relationships of the $\hat{1}\pm/\hat{1}^2$ -hydrolase fold domain of neuroligin: A comparison with acetylcholinesterase. <i>Chemico-Biological Interactions</i> , 2010, 187, 49-55.	4.0	10
92	Molecular Characterization of Monoclonal Antibodies that Inhibit Acetylcholinesterase by Targeting the Peripheral Site and Backdoor Region. <i>PLoS ONE</i> , 2013, 8, e77226.	2.5	10
93	The Neuroligins and Their Ligands: from Structure to Function at the Synapse. <i>Journal of Molecular Neuroscience</i> , 2014, 53, 387-396.	2.3	10
94	Structural basis for carbohydrate binding properties of a plant chitinase-like agglutinin with conserved catalytic machinery. <i>Journal of Structural Biology</i> , 2015, 190, 115-121.	2.8	10
95	Relationships of human $\hat{1}\pm/\hat{1}^2$ hydrolase fold proteins and other organophosphate-interacting proteins. <i>Chemico-Biological Interactions</i> , 2016, 259, 343-351.	4.0	9
96	Structural insights into a family 39 glycoside hydrolase from the gut symbiont <i>Bacteroides cellulosilyticus</i> WH2. <i>Journal of Structural Biology</i> , 2017, 197, 227-235.	2.8	9
97	Crystallization and preliminary X-ray studies of two isolectins from the seeds of <i>Lathyrus ochrus</i> . <i>Journal of Molecular Biology</i> , 1988, 202, 685-687.	4.2	8
98	Crystallization and preliminary crystallographic study of human CksHs1: A cell cycle regulatory protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 70-73.	2.6	8
99	In vitro cleavage of the <i>Lathyrus nissolia</i> isolectins. <i>Plant Science</i> , 1989, 62, 181-189.	3.6	7
100	Crystal structure of <i>E. coli</i> yddE protein reveals a striking homology with diaminopimelate epimerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 764-767.	2.6	7
101	The Role of Structural Water Molecules in Protein–Saccharide Complexes. , 1993, , 321-337.		7
102	Crystal Structure of Mouse Acetylcholinesterase. , 1998, , 315-322.		7
103	Genetic and enzymatic characterization of 3-O-sulfotransferase SNPs associated with <i>Plasmodium falciparum</i> parasitaemia. <i>Glycobiology</i> , 2018, 28, 534-541.	2.5	5
104	Hot Spots for Protein Partnerships at the Surface of Cholinesterases and Related $\hat{1}\pm/\hat{1}^2$ Hydrolase Fold Proteins or Domains—A Structural Perspective. <i>Molecules</i> , 2018, 23, 35.	3.8	5
105	Comparative mapping of selected structural determinants on the extracellular domains of cholinesterase-like cell-adhesion molecules. <i>Neuropharmacology</i> , 2021, 184, 108381.	4.1	4
106	(28) Structural insights into AChE inhibition by monoclonal antibodies. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 397-400.	4.0	3
107	Structural Comparison of Three Crystalline Complexes of a Peptidic Toxin With a Synaptic Acetylcholine Recognition Protein. <i>Journal of Molecular Neuroscience</i> , 2006, 30, 103-104.	2.3	3
108	A novel $\hat{1}\pm$ -N-acetylgalactosaminidase family with an NAD ⁺ -dependent catalytic mechanism suitable for enzymatic removal of blood group A antigens. <i>Biocatalysis and Biotransformation</i> , 2010, 28, 22-32.	2.0	3

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109	An evolutionary perspective on the first disulfide bond in members of the cholinesterase-carboxylesterase (COesterase) family: Possible outcomes for cholinesterase expression in prokaryotes. <i>Chemico-Biological Interactions</i> , 2019, 308, 179-184.	4.0	3
110	Insights into the atypical autokinase activity of the <i>Pseudomonas aeruginosa</i> GacS histidine kinase and its interaction with RetS. <i>Structure</i> , 2022, , .	3.3	3
111	Monoclonal antibody 117,C-11 recognizes three exposed regions on the surface of the <i>Lathyrus ochrus</i> isolectin I. <i>Immunology Letters</i> , 1991, 30, 47-51.	2.5	2
112	Crystal structure of a Cbtxâ€“AChBP complex reveals essential interactions between snake Î±-neurotoxins and nicotinic receptors. <i>EMBO Journal</i> , 2006, 25, 266-266.	7.8	1
113	NMR assignments of the GacS histidine-kinase periplasmic detection domain from <i>Pseudomonas aeruginosa</i> PAO1. <i>Biomolecular NMR Assignments</i> , 2017, 11, 25-28.	0.8	1
114	Molecular basis for substrate recognition and septum cleavage by AtIA, the major N-acetylglucosaminidase of <i>Enterococcus faecalis</i> . <i>Journal of Biological Chemistry</i> , 2022, , 101915.	3.4	1
115	<i>Aspergillus niger</i> Protein EstA Defines a New Class of Fungal Esterases within the Î±/Î² Hydrolase Fold Superfamily of Proteins. <i>Structure</i> , 2004, 12, 1545.	3.3	0
116	(27) <i>A. niger</i> protein â€œEstAâ€“, perhaps a new electrotactin, defines a new class of fungal esterases within the Î±/Î² hydrolase fold superfamily. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 395-396.	4.0	0
117	A novel Î±-N-acetylgalactosaminidase family with a NAD ⁺ -dependent catalytic mechanism suitable for enzymatic removal of blood group A antigens. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2007, 63, s15-s15.	0.3	0
118	Crystal structure of glucosamine-6 phosphate N-acetyltransferase 1: a novel member of the GNAT superfamily. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2000, 56, s245-s245.	0.3	0
119	Click chemistry: an original approach for drug discovery. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, s23-s23.	0.3	0
120	Mechanism of acetylcholinesterase inhibition by fasciculin. , 2004, , 727-728.		0
121	Fasciculin Inhibition of Mouse Acetylcholinesterase. , 1998, , 331-338.		0