

Yves Bourne

List of Publications by Year in descending order

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121
papers

9,096
citations

47409

49
h-index

46524

93
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123
all docs

123
docs citations

123
times ranked

11208
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	1.6	1
2	Insights into the atypical autokinase activity of the <i>Pseudomonas aeruginosa</i> GacS histidine kinase and its interaction with RetS. <i>Structure</i> , 2022, , .	1.6	3
3	Comparative mapping of selected structural determinants on the extracellular domains of cholinesterase-like cell-adhesion molecules. <i>Neuropharmacology</i> , 2021, 184, 108381.	2.0	4
4	The Ig-like domain of Punctin/MADD-4 is the primary determinant for interaction with the ectodomain of neuropilin NLG-1. <i>Journal of Biological Chemistry</i> , 2020, 295, 16267-16279.	1.6	11
5	The neuroligins and the synaptic pathway in Autism Spectrum Disorder. <i>Neuroscience and Biobehavioral Reviews</i> , 2020, 119, 37-51.	2.9	40
6	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.	1.7	3
7	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.	3.3	23
8	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.	1.8	48
9	Genetic and enzymatic characterization of 3-O-sulfotransferase SNPs associated with <i>Plasmodium falciparum</i> parasitaemia. <i>Glycobiology</i> , 2018, 28, 534-541.	1.3	5
10	Glycosylate and move! The glycosyltransferase Maf is involved in bacterial flagella formation. <i>Environmental Microbiology</i> , 2018, 20, 228-240.	1.8	20
11	Hot Spots for Protein Partnerships at the Surface of Cholinesterases and Related α/β Hydrolase Fold Proteins or Domains: A Structural Perspective. <i>Molecules</i> , 2018, 23, 35.	1.7	5
12	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.	1.3	9
13	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.	2.1	59
14	Structure of human lysosomal acid α -glucosidase: a guide for the treatment of Pompe disease. <i>Nature Communications</i> , 2017, 8, 1111.	5.8	169
15	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.	1.6	15
16	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.	0.4	1
17	Relationships of human α/β hydrolase fold proteins and other organophosphate-interacting proteins. <i>Chemico-Biological Interactions</i> , 2016, 259, 343-351.	1.7	9
18	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.	6.6	30

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19	Marine Macrocyclic Imines, Pinnatoxins A and G: Structural Determinants and Functional Properties to Distinguish Neuronal AChRs from Muscle nAChRs . <i>Structure</i> , 2015, 23, 1106-1115.	1.6	42
20	Structural and biochemical characterization of the $\text{N-acetylglucosaminidase}$ from <i>Thermotoga maritima</i> : Toward rationalization of mechanistic knowledge in the GH73 family. <i>Glycobiology</i> , 2015, 25, 319-330.	1.3	25
21	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.	1.3	10
22	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.	1.6	20
23	Tracking the Origin and Divergence of Cholinesterases and Neuroligins: The Evolution of Synaptic Proteins. <i>Journal of Molecular Neuroscience</i> , 2014, 53, 362-369.	1.1	11
24	The Neuroligins and Their Ligands: from Structure to Function at the Synapse. <i>Journal of Molecular Neuroscience</i> , 2014, 53, 387-396.	1.1	10
25	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.	1.6	15
26	Proteins with an alpha/beta hydrolase fold: Relationships between subfamilies in an ever-growing superfamily. <i>Chemico-Biological Interactions</i> , 2013, 203, 266-268.	1.7	39
27	Molecular Characterization of Monoclonal Antibodies that Inhibit Acetylcholinesterase by Targeting the Peripheral Site and Backdoor Region. <i>PLoS ONE</i> , 2013, 8, e77226.	1.1	10
28	ESTHER, the database of the α/β -hydrolase fold superfamily of proteins: tools to explore diversity of functions. <i>Nucleic Acids Research</i> , 2012, 41, D423-D429.	6.5	244
29	Structural Insights into Antibody Sequestering and Neutralizing of Na^+ Channel β -Type Modulator from Old World Scorpion Venom. <i>Journal of Biological Chemistry</i> , 2012, 287, 14136-14148.	1.6	20
30	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.	1.2	43
31	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.	1.8	39
32	Structure-function relationships of the α/β -hydrolase fold domain of neuroligin: A comparison with acetylcholinesterase. <i>Chemico-Biological Interactions</i> , 2010, 187, 49-55.	1.7	10
33	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.	1.3	20
34	Structural insights into the exquisite selectivity of neurexin/neuroligin synaptic interactions. <i>EMBO Journal</i> , 2010, 29, 2461-2471.	3.5	38
35	Structural determinants in phycotoxins and AChBP conferring high affinity binding and nicotinic AChR antagonism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6076-6081.	3.3	156
36	A novel $\text{N-acetylgalactosaminidase}$ 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.	1.1	3

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37	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.	1.6	33
38	Crystal Structure of the GalNAc/Gal-Specific Agglutinin from the Phytopathogenic Ascomycete <i>Sclerotinia sclerotiorum</i> Reveals Novel Adaptation of a Î²-Trefoil Domain. <i>Journal of Molecular Biology</i> , 2010, 400, 715-723.	2.0	33
39	Conformational Remodeling of Femtomolar Inhibitor~Acetylcholinesterase Complexes in the Crystalline State. <i>Journal of the American Chemical Society</i> , 2010, 132, 18292-18300.	6.6	29
40	Interaction between the SifA Virulence Factor and Its Host Target SKIP Is Essential for Salmonella Pathogenesis. <i>Journal of Biological Chemistry</i> , 2009, 284, 33151-33160.	1.6	52
41	Structural determinants for interaction of partial agonists with acetylcholine binding protein and neuronal Î±7 nicotinic acetylcholine receptor. <i>EMBO Journal</i> , 2009, 28, 3040-3051.	3.5	153
42	High-throughput automated refolding screening of inclusion bodies. <i>Protein Science</i> , 2009, 13, 2782-2792.	3.1	134
43	Glycosyltransferases, glycoside hydrolases: surprise, surprise!. <i>Current Opinion in Structural Biology</i> , 2008, 18, 527-533.	2.6	59
44	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.	1.4	32
45	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
46	Structural Analysis of the Synaptic Protein Neuroligin and Its Î²-Neurexin Complex: Determinants for Folding and Cell Adhesion. <i>Neuron</i> , 2007, 56, 979-991.	3.8	142
47	Bacterial glycosidases for the production of universal red blood cells. <i>Nature Biotechnology</i> , 2007, 25, 454-464.	9.4	259
48	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.	1.6	117
49	Crystal structure of a Cbtx~AChBP complex reveals essential interactions between snake Î±-neurotoxins and nicotinic receptors. <i>EMBO Journal</i> , 2006, 25, 266-266.	3.5	1
50	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.	3.5	126
51	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.	1.1	11
52	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.	1.1	15
53	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.	1.1	3
54	Crystal structure of a Cbtx~AChBP complex reveals essential interactions between snake Î±-neurotoxins and nicotinic receptors. <i>EMBO Journal</i> , 2005, 24, 1512-1522.	3.5	302

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55	Structures of Aplysia AChBP complexes with nicotinic agonists and antagonists reveal distinctive binding interfaces and conformations. <i>EMBO Journal</i> , 2005, 24, 3635-3646.	3.5	602
56	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.	1.7	30
57	(27) <i>A. niger</i> protein EstA, perhaps a new electrotactin, defines a new class of fungal esterases within the β -glucosidase fold superfamily. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 395-396.	1.7	0
58	(28) Structural insights into AChE inhibition by monoclonal antibodies. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 397-400.	1.7	3
59	Crystal structure of the conserved hypothetical protein Rv1155 from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2005, 579, 215-221.	1.3	25
60	The Crystal Structure of the <i>Calystegia sepium</i> Agglutinin Reveals a Novel Quaternary Arrangement of Lectin Subunits with a β -Prism Fold. <i>Journal of Biological Chemistry</i> , 2004, 279, 527-533.	1.6	54
61	Expression and characterization of the protein Rv1399c from <i>Mycobacterium tuberculosis</i> . <i>FEBS Journal</i> , 2004, 271, 3953-3961.	0.2	61
62	<i>Aspergillus niger</i> Protein EstA Defines a New Class of Fungal Esterases within the β -Glucosidase Fold Superfamily of Proteins. <i>Structure</i> , 2004, 12, 677-687.	1.6	29
63	<i>Aspergillus niger</i> Protein EstA Defines a New Class of Fungal Esterases within the β -Glucosidase Fold Superfamily of Proteins. <i>Structure</i> , 2004, 12, 1545.	1.6	0
64	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.	1.5	7
65	Crystal Structure of <i>Thermotoga maritima</i> β -L-Fucosidase. <i>Journal of Biological Chemistry</i> , 2004, 279, 13119-13128.	1.6	141
66	Freeze-frame inhibitor captures acetylcholinesterase in a unique conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1449-1454.	3.3	297
67	Click chemistry: an original approach for drug discovery. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2004, 60, s23-s23.	0.3	0
68	Mechanism of acetylcholinesterase inhibition by fasciculin. , 2004, , 727-728.		0
69	Structural insights into ligand interactions at the acetylcholinesterase peripheral anionic site. <i>EMBO Journal</i> , 2003, 22, 1-12.	3.5	362
70	Identification of the Catalytic Nucleophile of the Family 29 β -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.	1.6	70
71	The Mtr2-Mex67 NTF2-like Domain Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 48395-48403.	1.6	30
72	Structural basis for the unusual carbohydrate-binding specificity of jacalin towards galactose and mannose. <i>Biochemical Journal</i> , 2002, 364, 173-180.	1.7	138

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73	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.	1.7	41
74	Mechanism of Acetylcholinesterase Inhibition by Fasciculin: A 5-ns Molecular Dynamics Simulation. <i>Journal of the American Chemical Society</i> , 2002, 124, 6153-6161.	6.6	75
75	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73
76	Mannose-binding plant lectins: Different structural scaffolds for a common sugar-recognition process. <i>Biochimie</i> , 2001, 83, 645-651.	1.3	149
77	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.	3.5	138
78	Glycoside hydrolases and glycosyltransferases: families and functional modules. <i>Current Opinion in Structural Biology</i> , 2001, 11, 593-600.	2.6	393
79	Crystal Structure of Streptococcus pneumoniae 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.	1.6	92
80	Dissection of the Bifunctional Escherichia coli 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.	1.6	32
81	The Crystal Structures of Apo and Complexed Saccharomyces cerevisiae GNA1 Shed Light on the Catalytic Mechanism of an Amino-sugar N-Acetyltransferase. <i>Journal of Biological Chemistry</i> , 2001, 276, 16328-16334.	1.6	74
82	Immunocytochemical Localization and Crystal Structure of Human Frequenin (Neuronal Calcium) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50 3	1.6	176
83	Crystal structure and mutational analysis of the Saccharomyces cerevisiae cell cycle regulatory protein Cks1: implications for domain swapping, anion binding and protein interactions. <i>Structure</i> , 2000, 8, 841-850.	1.6	38
84	Active and inhibited human catalase structures: ligand and NADPH binding and catalytic mechanism 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2000, 296, 295-309.	2.0	388
85	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
86	Crystal structures of the bovine beta 4galactosyltransferase catalytic domain and its complex with uridine diphosphogalactose. <i>EMBO Journal</i> , 1999, 18, 3546-3557.	3.5	266
87	Crystal structure of the bifunctional N-acetylglucosamine 1-phosphate uridyltransferase from Escherichia coli: a paradigm for the related pyrophosphorylase superfamily. <i>EMBO Journal</i> , 1999, 18, 4096-4107.	3.5	174
88	Helianthus tuberosus lectin reveals a widespread scaffold for mannose-binding lectins. <i>Structure</i> , 1999, 7, 1473-1482.	1.6	107
89	Conformational Flexibility of the Acetylcholinesterase Tetramer Suggested by X-ray Crystallography. <i>Journal of Biological Chemistry</i> , 1999, 274, 30370-30376.	1.6	154
90	Crystal Structure of Mouse Acetylcholinesterase. <i>Journal of Biological Chemistry</i> , 1999, 274, 2963-2970.	1.6	117

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91	Barley α -amylase bound to its endogenous protein inhibitor BAI: crystal structure of the complex at 1.9 Å resolution. <i>Structure</i> , 1998, 6, 649-659.	1.6	129
92	Inhibition of mouse acetylcholinesterase by fasciculin: Crystal structure of the complex and mutagenesis of fasciculin. <i>Toxicon</i> , 1998, 36, 1613-1622.	0.8	25
93	Crystal Structure of Mouse Acetylcholinesterase. , 1998, , 315-322.		7
94	Fasciculin Inhibition of Mouse Acetylcholinesterase. , 1998, , 331-338.		0
95	[5] Pancreatic lipases and their complexes with colipases and inhibitors: Crystallization and crystal packing. <i>Methods in Enzymology</i> , 1997, 284, 107-119.	0.4	14
96	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.	2.0	16
97	Crystal Structure and Mutational Analysis of the Human CDK2 Kinase Complex with Cell Cycle-Regulatory Protein CksHs1. <i>Cell</i> , 1996, 84, 863-874.	13.5	237
98	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.	3.3	89
99	Soluble monomeric acetylcholinesterase from mouse: Expression, purification, and crystallization in complex with fasciculin. <i>Protein Science</i> , 1996, 5, 672-679.	3.1	56
100	Crystal structure of the cell cycle-regulatory protein suc1 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.	3.3	70
101	Crystallization and preliminary crystallographic study of human CksHs1: A cell cycle regulatory protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 21, 70-73.	1.5	8
102	Acetylcholinesterase inhibition by fasciculin: Crystal structure of the complex. <i>Cell</i> , 1995, 83, 503-512.	13.5	357
103	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.	2.0	76
104	Interactions of plant lectins with the components of the bacterial cell wall peptidoglycan. <i>Biochemical Systematics and Ecology</i> , 1994, 22, 153-159.	0.6	30
105	Crosslinking of mammalian lectin (galactin-1) by complex biantennary saccharides. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 863-870.	3.6	218
106	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.	1.6	105
107	Crystallization and Preliminary X-ray Diffraction Studies of the Soluble 14 kDa β -Galactoside-binding Lectin from Bovine Heart. <i>Journal of Molecular Biology</i> , 1994, 235, 787-789.	2.0	19
108	Characterization, Crystallization and Preliminary X-ray Crystallographic Analysis of the Complex between Barley α -Amylase and the Bifunctional α -Amylase/Subtilisin Inhibitor from Barley Seeds. <i>Journal of Molecular Biology</i> , 1994, 236, 368-371.	2.0	13

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109	Horse Pancreatic Lipase. <i>Journal of Molecular Biology</i> , 1994, 238, 709-732.	2.0	106
110	Primary and Three-Dimensional Structure of Lactotransferrin (Lactoferrin) Glycans. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 21-32.	0.8	71
111	Protein-carbohydrate interactions. <i>Current Opinion in Structural Biology</i> , 1993, 3, 681-686.	2.6	52
112	The Role of Structural Water Molecules in Protein-Saccharide Complexes. , 1993, , 321-337.		7
113	Crystallization and preliminary X-ray diffraction study of Lathyrus ochrus isolectin II complexed to the human lactotransferrin N2 fragment. <i>Journal of Molecular Biology</i> , 1992, 227, 938-941.	2.0	13
114	Monoclonal antibody 117,C-11 recognizes three exposed regions on the surface of the Lathyrus ochrus isolectin I. <i>Immunology Letters</i> , 1991, 30, 47-51.	1.1	2
115	Data bank of three-dimensional structures of disaccharides: Part II, N-acetyllactosaminic type N-glycans. Comparison with the crystal structure of a biantennary octosaccharide. <i>Glycoconjugate Journal</i> , 1991, 8, 456-483.	1.4	64
116	Three-Dimensionnal structures of complexes of Lathyrus ochrus isolectin I with glucose and mannose: Fine specificity of the monosaccharide-binding site. <i>Proteins: Structure, Function and Bioinformatics</i> , 1990, 8, 365-376.	1.5	121
117	Co-crystallization and preliminary X-ray diffraction studies of Lathyrus ochrus isolectin I with Di- and trisaccharides, and a biantennary octosaccharide. <i>Journal of Molecular Biology</i> , 1990, 213, 211-213.	2.0	10
118	X-ray crystal structure determination and refinement at 1.9 Å... resolution of isolectin I from the seeds of Lathyrus ochrus. <i>Journal of Molecular Biology</i> , 1990, 214, 571-584.	2.0	92
119	In vitro cleavage of the Lathyrus nissolia isolectins. <i>Plant Science</i> , 1989, 62, 181-189.	1.7	7
120	Crystallization and preliminary X-ray study of horse pancreatic lipase. <i>Journal of Molecular Biology</i> , 1989, 205, 259-261.	2.0	27
121	Crystallization and preliminary X-ray studies of two isolectins from the seeds of Lathyrus ochrus. <i>Journal of Molecular Biology</i> , 1988, 202, 685-687.	2.0	8