

Yves Bourne

List of Publications by Year in descending order

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121
papers

9,096
citations

41344

49
h-index

40979

93
g-index

123
all docs

123
docs citations

123
times ranked

10150
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. | 3.4 | 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, , . | 3.3 | 3 |
| 3 | 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 |
| 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. | 3.4 | 11 |
| 5 | The neuroligins and the synaptic pathway in Autism Spectrum Disorder. <i>Neuroscience and Biobehavioral Reviews</i> , 2020, 119, 37-51. | 6.1 | 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. | 4.0 | 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. | 7.1 | 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. | 4.1 | 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. | 2.5 | 5 |
| 10 | Glycosylate and move! The glycosyltransferase Maf is involved in bacterial flagella formation. <i>Environmental Microbiology</i> , 2018, 20, 228-240. | 3.8 | 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. | 3.8 | 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. | 2.8 | 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. | 3.9 | 59 |
| 14 | Structure of human lysosomal acid α -glucosidase- a guide for the treatment of Pompe disease. <i>Nature Communications</i> , 2017, 8, 1111. | 12.8 | 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. | 3.3 | 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. | 0.8 | 1 |
| 17 | Relationships of human α/β hydrolase fold proteins and other organophosphate-interacting proteins. <i>Chemico-Biological Interactions</i> , 2016, 259, 343-351. | 4.0 | 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. | 13.7 | 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. | 3.3 | 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. | 2.5 | 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. | 2.8 | 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. | 3.4 | 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. | 2.3 | 11 |
| 24 | 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 |
| 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. | 3.4 | 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. | 4.0 | 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. | 2.5 | 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. | 14.5 | 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. | 3.4 | 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. | 2.5 | 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. | 3.8 | 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. | 4.0 | 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. | 2.8 | 20 |
| 34 | Structural insights into the exquisite selectivity of neurexin/neuroligin synaptic interactions. <i>EMBO Journal</i> , 2010, 29, 2461-2471. | 7.8 | 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. | 7.1 | 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. | 2.0 | 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. | 3.4 | 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. | 4.2 | 33 |
| 39 | Conformational Remodeling of Femtomolar Inhibitorâ€™Acetylcholinesterase Complexes in the Crystalline State. <i>Journal of the American Chemical Society</i> , 2010, 132, 18292-18300. | 13.7 | 29 |
| 40 | 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 |
| 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. | 7.8 | 153 |
| 42 | High-throughput automated refolding screening of inclusion bodies. <i>Protein Science</i> , 2009, 13, 2782-2792. | 7.6 | 134 |
| 43 | Glycosyltransferases, glycoside hydrolases: surprise, surprise!. <i>Current Opinion in Structural Biology</i> , 2008, 18, 527-533. | 5.7 | 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. | 3.1 | 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. | 8.1 | 142 |
| 47 | Bacterial glycosidases for the production of universal red blood cells. <i>Nature Biotechnology</i> , 2007, 25, 454-464. | 17.5 | 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. | 3.4 | 117 |
| 49 | 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 |
| 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. | 7.8 | 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. | 2.3 | 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. | 2.3 | 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. | 2.3 | 3 |
| 54 | Crystal structure of a Cbtxâ€™AChBP complex reveals essential interactions between snake Î±-neurotoxins and nicotinic receptors. <i>EMBO Journal</i> , 2005, 24, 1512-1522. | 7.8 | 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. | 7.8 | 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. | 4.0 | 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. | 4.0 | 0 |
| 58 | (28) Structural insights into AChE inhibition by monoclonal antibodies. <i>Chemico-Biological Interactions</i> , 2005, 157-158, 397-400. | 4.0 | 3 |
| 59 | Crystal structure of the conserved hypothetical protein Rv1155 from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2005, 579, 215-221. | 2.8 | 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. | 3.4 | 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. | 3.3 | 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. | 3.3 | 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. | 2.6 | 7 |
| 65 | Crystal Structure of <i>Thermotoga maritima</i> β -glucosidase. <i>Journal of Biological Chemistry</i> , 2004, 279, 13119-13128. | 3.4 | 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. | 7.1 | 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. | 7.8 | 362 |
| 70 | Identification of the Catalytic Nucleophile of the Family 29 β -glucosidase 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 |
| 71 | The Mtr2-Mex67 NTF2-like Domain Complex. <i>Journal of Biological Chemistry</i> , 2003, 278, 48395-48403. | 3.4 | 30 |
| 72 | 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 |

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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. | 3.7 | 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. | 13.7 | 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. | 2.6 | 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. | 7.8 | 138 |
| 78 | Glycoside hydrolases and glycosyltransferases: families and functional modules. <i>Current Opinion in Structural Biology</i> , 2001, 11, 593-600. | 5.7 | 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. | 3.4 | 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. | 3.4 | 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. | 3.4 | 74 |
| 82 | Immunocytochemical Localization and Crystal Structure of Human Frequenin (Neuronal Calcium) Tj ETQq0 0 0 rgBTJ /Overlock_10 Tf 50 3 | 3.4 | 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. | 3.3 | 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. | 4.2 | 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. | 7.8 | 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. | 7.8 | 174 |
| 88 | Helianthus tuberosus lectin reveals a widespread scaffold for mannose-binding lectins. <i>Structure</i> , 1999, 7, 1473-1482. | 3.3 | 107 |
| 89 | Conformational Flexibility of the Acetylcholinesterase Tetramer Suggested by X-ray Crystallography. <i>Journal of Biological Chemistry</i> , 1999, 274, 30370-30376. | 3.4 | 154 |
| 90 | Crystal Structure of Mouse Acetylcholinesterase. <i>Journal of Biological Chemistry</i> , 1999, 274, 2963-2970. | 3.4 | 117 |

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| 91 | 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 |
| 92 | 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 |
| 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. | 1.0 | 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. | 4.2 | 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. | 28.9 | 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. | 7.1 | 89 |
| 99 | Soluble monomeric acetylcholinesterase from mouse: Expression, purification, and crystallization in complex with fasciculin. <i>Protein Science</i> , 1996, 5, 672-679. | 7.6 | 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. | 7.1 | 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. | 2.6 | 8 |
| 102 | Acetylcholinesterase inhibition by fasciculin: Crystal structure of the complex. <i>Cell</i> , 1995, 83, 503-512. | 28.9 | 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. | 4.2 | 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. | 1.3 | 30 |
| 105 | Crosslinking of mammalian lectin (galactin-1) by complex biantennary saccharides. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 863-870. | 8.2 | 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. | 3.3 | 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. | 4.2 | 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. | 4.2 | 13 |

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|-----|--|-----|-----------|
| 109 | Horse Pancreatic Lipase. <i>Journal of Molecular Biology</i> , 1994, 238, 709-732. | 4.2 | 106 |
| 110 | Primary and Three-Dimensional Structure of Lactotransferrin (Lactoferrin) Glycans. <i>Advances in Experimental Medicine and Biology</i> , 1994, 357, 21-32. | 1.6 | 71 |
| 111 | Protein-carbohydrate interactions. <i>Current Opinion in Structural Biology</i> , 1993, 3, 681-686. | 5.7 | 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. | 4.2 | 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. | 2.5 | 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. | 2.7 | 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. | 2.6 | 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. | 4.2 | 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. | 4.2 | 92 |
| 119 | In vitro cleavage of the Lathyrus nissolia isolectins. <i>Plant Science</i> , 1989, 62, 181-189. | 3.6 | 7 |
| 120 | Crystallization and preliminary X-ray study of horse pancreatic lipase. <i>Journal of Molecular Biology</i> , 1989, 205, 259-261. | 4.2 | 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. | 4.2 | 8 |