

# Daan van Aalten

## List of Publications by Year in descending order

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167  
papers

15,513  
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27035

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21239

119  
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173  
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173  
docs citations

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times ranked

21475  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic validation of <i>Aspergillus fumigatus</i> phosphoglucomutase as a viable therapeutic target in invasive aspergillosis. <i>Journal of Biological Chemistry</i> , 2022, 298, 102003.	1.6	3
2	Intellectual disability-associated disruption of O-GlcNAc cycling impairs habituation learning in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2022, 18, e1010159.	1.5	7
3	Bioinformatic prediction of putative conveyers of O-GlcNAc transferase intellectual disability. <i>Journal of Biological Chemistry</i> , 2022, 298, 102276.	1.6	4
4	A missense mutation in a patient with developmental delay affects the activity and structure of the hexosamine biosynthetic pathway enzyme AGX1. <i>FEBS Letters</i> , 2021, 595, 110-122.	1.3	3
5	Genetic and structural validation of phosphomannomutase as a cell wall target in <i>Aspergillus fumigatus</i> . <i>Molecular Microbiology</i> , 2021, 116, 245-259.	1.2	7
6	The citron homology domain as a scaffold for Rho1 signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
7	Loss of O-GlcNAcase catalytic activity leads to defects in mouse embryogenesis. <i>Journal of Biological Chemistry</i> , 2021, 296, 100439.	1.6	28
8	A missense mutation in the catalytic domain of O-GlcNAc transferase links perturbations in protein O-GlcNAcylation to X-linked intellectual disability. <i>FEBS Letters</i> , 2020, 594, 717-727.	1.3	40
9	Native detection of protein O-GlcNAcylation by gel electrophoresis. <i>Analyst</i> , 2020, 145, 6826-6830.	1.7	4
10	Targeting a critical step in fungal hexosamine biosynthesis. <i>Journal of Biological Chemistry</i> , 2020, 295, 8678-8691.	1.6	16
11	A mechanism-inspired UDP-N-acetylglucosamine pyrophosphorylase inhibitor. <i>RSC Chemical Biology</i> , 2020, 1, 13-25.	2.0	20
12	Tools for functional dissection of site-specific O-GlcNAcylation. <i>RSC Chemical Biology</i> , 2020, 1, 98-109.	2.0	22
13	O-GlcNAcase contributes to cognitive function in <i>Drosophila</i> . <i>Journal of Biological Chemistry</i> , 2020, 295, 8636-8646.	1.6	16
14	An intellectual disability syndrome with single-nucleotide variants in O-GlcNAc transferase. <i>European Journal of Human Genetics</i> , 2020, 28, 706-714.	1.4	38
15	Catalytic deficiency of O-GlcNAc transferase leads to X-linked intellectual disability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14961-14970.	3.3	58
16	Genetic recoding to dissect the roles of site-specific protein O-GlcNAcylation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1071-1077.	3.6	50
17	Mechanisms of redundancy and specificity of the <i>Aspergillus fumigatus</i> Crh transglycosylases. <i>Nature Communications</i> , 2019, 10, 1669.	5.8	18
18	Loss of CRMP2 O-GlcNAcylation leads to reduced novel object recognition performance in mice. <i>Open Biology</i> , 2019, 9, 190192.	1.5	17

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19	A mouse model for functional dissection of TAB1 O-GlcNAcylation. Wellcome Open Research, 2019, 4, 128.	0.9	3
20	A mouse model for functional dissection of TAB1 O-GlcNAcylation. Wellcome Open Research, 2019, 4, 128.	0.9	2
21	UDP-GlcNAc Analogues as Inhibitors of O-GlcNAc Transferase (OGT): Spectroscopic, Computational, and Biological Studies. Chemistry - A European Journal, 2018, 24, 7264-7272.	1.7	8
22	The O-GlcNAc Transferase Intellectual Disability Mutation L254F Distorts the TPR Helix. Cell Chemical Biology, 2018, 25, 513-518.e4.	2.5	30
23	Activity-based E3 ligase profiling uncovers an E3 ligase with esterification activity. Nature, 2018, 556, 381-385.	13.7	178
24	O-GlcNAcase Fragment Discovery with Fluorescence Polarimetry. ACS Chemical Biology, 2018, 13, 1353-1360.	1.6	8
25	Thio-Linked UDP-GlcNAc Peptide Conjugates as O-GlcNAc Transferase Inhibitors. Bioconjugate Chemistry, 2018, 29, 1834-1840.	1.8	34
26	Effects of hypo-O-GlcNAcylation on Drosophila development. Journal of Biological Chemistry, 2018, 293, 7209-7221.	1.6	23
27	Inhibitors against Fungal Cell Wall Remodeling Enzymes. ChemMedChem, 2018, 13, 128-132.	1.6	7
28	The conserved threonine-rich region of the HCF-1PRO repeat activates promiscuous OGT:UDP-GlcNAc glycosylation and proteolysis activities. Journal of Biological Chemistry, 2018, 293, 17754-17768.	1.6	7
29	Mutations in N-acetylglucosamine (O-GlcNAc) transferase in patients with X-linked intellectual disability. Journal of Biological Chemistry, 2017, 292, 12621-12631.	1.6	72
30	A mutant O-GlcNAcase enriches Drosophila developmental regulators. Nature Chemical Biology, 2017, 13, 882-887.	3.9	51
31	Direct Monitoring of Protein O-GlcNAcylation by High-Resolution Native Mass Spectrometry. ACS Chemical Biology, 2017, 12, 2078-2084.	1.6	21
32	Recognition of a glycosylation substrate by the O-GlcNAc transferase TPR repeats. Open Biology, 2017, 7, 170078.	1.5	48
33	Structure of PINK1 and mechanisms of Parkinson's disease-associated mutations. ELife, 2017, 6, .	2.8	71
34	Proteolysis of HCF-1 by Ser/Thr glycosylation-incompetent O-GlcNAc transferase:UDP-GlcNAc complexes. Genes and Development, 2016, 30, 960-972.	2.7	21
35	Glucose and glutamine fuel protein O-GlcNAcylation to control T cell self-renewal and malignancy. Nature Immunology, 2016, 17, 712-720.	7.0	265
36	O-GlcNAc transferase inhibitors: current tools and future challenges. Biochemical Society Transactions, 2016, 44, 88-93.	1.6	65

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37	Nucleocytoplasmic human O-GlcNAc transferase is sufficient for O-GlcNAcylation of mitochondrial proteins. <i>Biochemical Journal</i> , 2016, 473, 1693-1702.	1.7	47
38	<i>GacA</i> is essential for <i>G</i> roup <i>A</i> <i>S</i> treptococcus and defines a new class of monomeric dTDP-4-dehydrorhamnose reductases ( <i>RmlD</i> ). <i>Molecular Microbiology</i> , 2015, 98, 946-962.	1.2	46
39	Evidence for a Functional O-Linked N-Acetylglucosamine (O-GlcNAc) System in the Thermophilic Bacterium <i>Thermobaculum terrenum</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 30291-30305.	1.6	29
40	Dual functionality of O-GlcNAc transferase is required for <i>Drosophila</i> development. <i>Open Biology</i> , 2015, 5, 150234.	1.5	32
41	Binding to serine 65-phosphorylated ubiquitin primes Parkin for optimal <i>PINK</i> -dependent phosphorylation and activation. <i>EMBO Reports</i> , 2015, 16, 939-954.	2.0	183
42	<i>N</i> -Myristoyltransferase Is a Cell Wall Target in <i>Aspergillus fumigatus</i> . <i>ACS Chemical Biology</i> , 2015, 10, 1425-1434.	1.6	38
43	Phosphorylation of Synaptic Vesicle Protein 2A at Thr84 by Casein Kinase 1 Family Kinases Controls the Specific Retrieval of Synaptotagmin-1. <i>Journal of Neuroscience</i> , 2015, 35, 2492-2507.	1.7	70
44	The active site of O-GlcNAc transferase imposes constraints on substrate sequence. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 744-750.	3.6	114
45	The Early Metazoan <i>Trichoplax adhaerens</i> Possesses a Functional O-GlcNAc System. <i>Journal of Biological Chemistry</i> , 2015, 290, 11969-11982.	1.6	15
46	Tyrosine glycosylation of Rho by <i>Yersinia</i> toxin impairs blastomere cell behaviour in zebrafish embryos. <i>Nature Communications</i> , 2015, 6, 7807.	5.8	37
47	Bisubstrate UDP-peptide conjugates as human O-GlcNAc transferase inhibitors. <i>Biochemical Journal</i> , 2014, 457, 497-502.	1.7	57
48	Elevated <i>O</i> -GlcNAc Levels Activate Epigenetically Repressed Genes and Delay Mouse ESC Differentiation Without Affecting Naïve to Primed Cell Transition. <i>Stem Cells</i> , 2014, 32, 2605-2615.	1.4	50
49	O-GlcNAcase: Promiscuous Hexosaminidase or Key Regulator of O-GlcNAc Signaling?. <i>Journal of Biological Chemistry</i> , 2014, 289, 34433-34439.	1.6	50
50	A Structural and Biochemical Model of Processive Chitin Synthesis. <i>Journal of Biological Chemistry</i> , 2014, 289, 23020-23028.	1.6	46
51	Lead Optimization of a Pyrazole Sulfonamide Series of <i>Trypanosoma brucei</i> <i>N</i> -Myristoyltransferase Inhibitors: Identification and Evaluation of CNS Penetrant Compounds as Potential Treatments for Stage 2 Human African Trypanosomiasis. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 9855-9869.	2.9	57
52	Screening-based discovery of <i>Aspergillus fumigatus</i> plant-type chitinase inhibitors. <i>FEBS Letters</i> , 2014, 588, 3282-3290.	1.3	15
53	Genetic and structural validation of <i>Aspergillus fumigatus</i> ... <i>UDP-N-acetylglucosamine pyrophosphorylase</i> as an antifungal target. <i>Molecular Microbiology</i> , 2013, 89, 479-493.	1.2	29
54	Proteome Wide Purification and Identification of <i>O</i> -GlcNAc-Modified Proteins Using Click Chemistry and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2013, 12, 927-936.	1.8	151

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55	A sweet TET- $\beta$ -glucosyltransferase-synergy of TET proteins and O-GlcNAc transferase in transcription. <i>EMBO Journal</i> , 2013, 32, 612-613.	3.5	11
56	A Novel Allosteric Inhibitor of the Uridine Diphosphate <i>N</i> -Acetylglucosamine Pyrophosphorylase from <i>Trypanosoma brucei</i> . <i>ACS Chemical Biology</i> , 2013, 8, 1981-1987.	1.6	23
57	Chemical tools to probe cellular <i>O</i> -GlcNAc signalling. <i>Biochemical Journal</i> , 2013, 456, 1-12.	1.7	27
58	Structure of a bacterial putative acetyltransferase defines the fold of the human <i>O</i> -GlcNAcase C-terminal domain. <i>Open Biology</i> , 2013, 3, 130021.	1.5	47
59	Genetic and structural validation of <i>Aspergillus fumigatus N</i> -acetylphosphoglucosamine mutase as an antifungal target. <i>Bioscience Reports</i> , 2013, 33, .	1.1	22
60	BslA is a self-assembling bacterial hydrophobin that coats the <i>Bacillus subtilis</i> biofilm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13600-13605.	3.3	244
61	Yeast Mnn9 is both a priming glycosyltransferase and an allosteric activator of mannan biosynthesis. <i>Open Biology</i> , 2013, 3, 130022.	1.5	24
62	The <i>Vibrio cholerae</i> Colonization Factor GbpA Possesses a Modular Structure that Governs Binding to Different Host Surfaces. <i>PLoS Pathogens</i> , 2012, 8, e1002373.	2.1	150
63	IQGAP Proteins Reveal an Atypical Phosphoinositide (aPI) Binding Domain with a Pseudo C2 Domain Fold. <i>Journal of Biological Chemistry</i> , 2012, 287, 22483-22496.	1.6	23
64	Human YKL-39 is a pseudo-chitinase with retained chitooligosaccharide-binding properties. <i>Biochemical Journal</i> , 2012, 446, 149-157.	1.7	55
65	Structural and biochemical characterization of a trapped coenzyme A adduct of <i>Caenorhabditis elegans</i> glucosamine-6-phosphate <i>N</i> -acetyltransferase 1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1019-1029.	2.5	14
66	<i>O</i> -GlcNAcylation of TAB1 modulates TAK1-mediated cytokine release. <i>EMBO Journal</i> , 2012, 31, 1394-1404.	3.5	138
67	<i>O</i> -GlcNAc transferase invokes nucleotide sugar pyrophosphate participation in catalysis. <i>Nature Chemical Biology</i> , 2012, 8, 969-974.	3.9	123
68	Synergy of Peptide and Sugar in <i>O</i> -GlcNAcase Substrate Recognition. <i>Chemistry and Biology</i> , 2012, 19, 173-178.	6.2	48
69	Purification, crystallization and preliminary X-ray diffraction data of UDP-galactopyranose mutase from <i>Aspergillus fumigatus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 705-708.	0.7	3
70	Bisdionin C $\beta$ A Rationally Designed, Submicromolar Inhibitor of Family 18 Chitinases. <i>ACS Medicinal Chemistry Letters</i> , 2011, 2, 428-432.	1.3	20
71	Charge-Surrounded Pockets and Electrostatic Interactions with Small Ions Modulate the Activity of Retroviral Fusion Proteins. <i>PLoS Pathogens</i> , 2011, 7, e1001268.	2.1	17
72	Discovery of catalytically active orthologues of the Parkinson's disease kinase PINK1: analysis of substrate specificity and impact of mutations. <i>Open Biology</i> , 2011, 1, 110012.	1.5	88

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73	O-GlcNAc transfer: size matters. <i>Nature Chemical Biology</i> , 2011, 7, 134-135.	3.9	4
74	Substrate and product analogues as human O-GlcNAc transferase inhibitors. <i>Amino Acids</i> , 2011, 40, 781-792.	1.2	60
75	Comparative structural analysis of retroviral fusion proteins identifies regions that modulate membrane fusion: a potential retroviral achilles heel?. <i>Retrovirology</i> , 2011, 8, .	0.9	0
76	Analyzing Airway Inflammation with Chemical Biology: Dissection of Acidic Mammalian Chitinase Function with a Selective Drug-like Inhibitor. <i>Chemistry and Biology</i> , 2011, 18, 569-579.	6.2	44
77	Protein O-GlcNAcylation Is Required for Fibroblast Growth Factor Signaling in <i>Drosophila</i> . <i>Science Signaling</i> , 2011, 4, ra89.	1.6	24
78	Human OGA binds substrates in a conserved peptide recognition groove. <i>Biochemical Journal</i> , 2010, 432, 1-12.	1.7	58
79	Pseudokinases-remnants of evolution or key allosteric regulators?. <i>Current Opinion in Structural Biology</i> , 2010, 20, 772-781.	2.6	130
80	Screening-based discovery of drug-like O-GlcNAcase inhibitor scaffolds. <i>FEBS Letters</i> , 2010, 584, 694-700.	1.3	29
81	An efficient and versatile synthesis of GlcNAcstatins" potent and selective O-GlcNAcase inhibitors built on the tetrahydroimidazo[1,2-a]pyridine scaffold. <i>Tetrahedron</i> , 2010, 66, 7838-7849.	1.0	9
82	Natural Product-Guided Discovery of a Fungal Chitinase Inhibitor. <i>Chemistry and Biology</i> , 2010, 17, 1275-1281.	6.2	41
83	Cell-Penetrant, Nanomolar O-GlcNAcase Inhibitors Selective against Lysosomal Hexosaminidases. <i>Chemistry and Biology</i> , 2010, 17, 1250-1255.	6.2	52
84	Acetazolamide-based fungal chitinase inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 8334-8340.	1.4	46
85	N-myristoyltransferase inhibitors as new leads to treat sleeping sickness. <i>Nature</i> , 2010, 464, 728-732.	13.7	272
86	Molecular mechanism of elongation factor 1A inhibition by a <i>Legionella pneumophila</i> glycosyltransferase. <i>Biochemical Journal</i> , 2010, 426, 281-292.	1.7	33
87	<i>Streptococcus mutans</i> SMU.623c Codes for a Functional, Metal-Dependent Polysaccharide Deacetylase That Modulates Interactions with Salivary Agglutinin. <i>Journal of Bacteriology</i> , 2009, 191, 394-402.	1.0	22
88	Molecular Mechanisms of Yeast Cell Wall Glucan Remodeling. <i>Journal of Biological Chemistry</i> , 2009, 284, 8461-8469.	1.6	67
89	Synthesis and Structure-based Dissection of Cyclic Peptide Chitinase Inhibitors: New Leads for Antifungal and Anti-Inflammatory Drugs. <i>Advances in Experimental Medicine and Biology</i> , 2009, 611, 525-526.	0.8	2
90	Structure of the LKB1-STRAD-MO25 Complex Reveals an Allosteric Mechanism of Kinase Activation. <i>Science</i> , 2009, 326, 1707-1711.	6.0	287

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91	ATP and MO251± Regulate the Conformational State of the STRAD1± Pseudokinase and Activation of the LKB1 Tumour Suppressor. PLoS Biology, 2009, 7, e1000126.	2.6	118
92	Structural and functional characterization of a putative polysaccharide deacetylase of the human parasite <i>Encephalitozoon cuniculi</i>. Protein Science, 2009, 18, 1197-1209.	3.1	27
93	GlcNAcstatins are nanomolar inhibitors of human <i>O</i>-GlcNAcase inducing cellular hyper-<i>O</i>-GlcNAcylation. Biochemical Journal, 2009, 420, 221-227.	1.7	83
94	Solid-phase synthesis of cyclic peptide chitinase inhibitors: SAR of the argifin scaffold. Organic and Biomolecular Chemistry, 2009, 7, 259-268.	1.5	35
95	SPPS of the Natural Product Chitinase Inhibitor Argifin: Library Generation and Biological Evaluation. Advances in Experimental Medicine and Biology, 2009, 611, 143-144.	0.8	0
96	Structure of the OSR1 kinase, a hypertension drug target. Proteins: Structure, Function and Bioinformatics, 2008, 73, 1082-1087.	1.5	39
97	Structure-Based Dissection of the Natural Product Cyclopentapeptide Chitinase Inhibitor Argifin. Chemistry and Biology, 2008, 15, 295-301.	6.2	59
98	Chemical Dissection of the Link between Streptozotocin, O-GlcNAc, and Pancreatic Cell Death. Chemistry and Biology, 2008, 15, 799-807.	6.2	48
99	Structural insights into mechanism and specificity of O-GlcNAc transferase. EMBO Journal, 2008, 27, 2780-2788.	3.5	102
100	Putting glycobiology on a structural footing. Current Opinion in Structural Biology, 2008, 18, 525-526.	2.6	0
101	Molecular mechanisms of O-GlcNAcylation. Current Opinion in Structural Biology, 2008, 18, 551-557.	2.6	53
102	Highly specific inhibition of leukaemia virus membrane fusion by interaction of peptide antagonists with a conserved region of the coiled coil of envelope. Retrovirology, 2008, 5, 70.	0.9	11
103	Mutation of the PDK1 PH Domain Inhibits Protein Kinase B/Akt, Leading to Small Size and Insulin Resistance. Molecular and Cellular Biology, 2008, 28, 3258-3272.	1.1	115
104	Structural and kinetic differences between human and <i>Aspergillus fumigatus</i> <scp>D</scp>-glucosamine-6-phosphate <i>N</i>-acetyltransferase. Biochemical Journal, 2008, 415, 217-223.	1.7	26
105	Glucose-6-phosphate as a probe for the glucosamine-6-phosphate <i>N</i>-acetyltransferase Michaelis complex. FEBS Letters, 2007, 581, 5597-5600.	1.3	15
106	Novel Inositol Phospholipid Headgroup Surrogate Crystallized in the Pleckstrin Homology Domain of Protein Kinase B±. ACS Chemical Biology, 2007, 2, 242-246.	1.6	20
107	Efficient synthesis of 1,3,7-substituted xanthenes by a safety-catch protection strategy. Tetrahedron, 2007, 63, 12294-12302.	1.0	23
108	Structure of Saccharomyces cerevisiae Chitinase 1 and Screening-Based Discovery of Potent Inhibitors. Chemistry and Biology, 2007, 14, 589-599.	6.2	72

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109	Structural insights into the recognition of substrates and activators by the OSR1 kinase. <i>EMBO Reports</i> , 2007, 8, 839-845.	2.0	89
110	Kinetic, inhibition and structural studies on 3-oxoacyl-ACP reductase from <i>Plasmodium falciparum</i> , a key enzyme in fatty acid biosynthesis. <i>Biochemical Journal</i> , 2006, 393, 447-457.	1.7	72
111	Structure and Mechanism of Chitin Deacetylase from the Fungal Pathogen <i>Colletotrichum lindemuthianum</i> . <i>Biochemistry</i> , 2006, 45, 9416-9426.	1.2	149
112	GlcNAcstatin: A Picomolar, Selective O-GlcNAcase Inhibitor That Modulates Intracellular O-GlcNAcylation Levels. <i>Journal of the American Chemical Society</i> , 2006, 128, 16484-16485.	6.6	136
113	The structure of siglec-7 in complex with sialosides: leads for rational structure-based inhibitor design. <i>Biochemical Journal</i> , 2006, 397, 271-278.	1.7	70
114	TAK1-binding protein 1 is a pseudophosphatase. <i>Biochemical Journal</i> , 2006, 399, 427-434.	1.7	73
115	The ubiquitin-associated domain of AMPK-related kinases regulates conformation and LKB1-mediated phosphorylation and activation. <i>Biochemical Journal</i> , 2006, 394, 545-555.	1.7	95
116	Structural insights into the mechanism and inhibition of eukaryotic O-GlcNAc hydrolysis. <i>EMBO Journal</i> , 2006, 25, 1569-1578.	3.5	181
117	Natural Product Family 18 Chitinase Inhibitors. <i>ChemInform</i> , 2006, 37, no.	0.1	1
118	First Synthesis of Argadin: A Nanomolar Inhibitor of Family-18 Chitinases. <i>European Journal of Organic Chemistry</i> , 2006, 2006, 5002-5006.	1.2	22
119	Siglec-7 Undergoes a Major Conformational Change When Complexed with the $\beta$ -(2,8)-Disialylganglioside GT1b. <i>Journal of Biological Chemistry</i> , 2006, 281, 32774-32783.	1.6	82
120	Structural Basis of Reduction-dependent Activation of Human Cystatin F. <i>Journal of Biological Chemistry</i> , 2006, 281, 16570-16575.	1.6	39
121	Screening-based Discovery and Structural Dissection of a Novel Family 18 Chitinase Inhibitor. <i>Journal of Biological Chemistry</i> , 2006, 281, 27278-27285.	1.6	53
122	Specificity and Affinity of Natural Product Cyclopentapeptide Inhibitors against <i>A. fumigatus</i> , Human, and Bacterial Chitinases. <i>Chemistry and Biology</i> , 2005, 12, 65-76.	6.2	109
123	Methylxanthine Drugs Are Chitinase Inhibitors: Investigation of Inhibition and Binding Modes. <i>Chemistry and Biology</i> , 2005, 12, 973-980.	6.2	108
124	The N-Acetyl-D-glucosaminylphosphatidylinositol De-N-acetylase of Glycosylphosphatidylinositol Biosynthesis Is a Zinc Metalloenzyme. <i>Journal of Biological Chemistry</i> , 2005, 280, 22831-22838.	1.6	38
125	Crystal Structure and Binding Properties of the <i>Serratia marcescens</i> Chitin-binding Protein CBP21. <i>Journal of Biological Chemistry</i> , 2005, 280, 11313-11319.	1.6	257
126	Structure and metal-dependent mechanism of peptidoglycan deacetylase, a streptococcal virulence factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15429-15434.	3.3	196



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127	Role of T-loop Phosphorylation in PDK1 Activation, Stability, and Substrate Binding. <i>Journal of Biological Chemistry</i> , 2005, 280, 18797-18802.	1.6	36
128	Crystal Structure of the PTPL1/FAP-1 Human Tyrosine Phosphatase Mutated in Colorectal Cancer. <i>Journal of Biological Chemistry</i> , 2005, 280, 8180-8187.	1.6	34
129	An efficient synthesis of argifin: A natural product chitinase inhibitor with chemotherapeutic potential. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2005, 15, 4717-4721.	1.0	39
130	The Non-catalytic Chitin-binding Protein CBP21 from <i>Serratia marcescens</i> Is Essential for Chitin Degradation. <i>Journal of Biological Chemistry</i> , 2005, 280, 28492-28497.	1.6	321
131	Natural product family 18 chitinase inhibitors. <i>Natural Product Reports</i> , 2005, 22, 563.	5.2	79
132	Interactions of a Family 18 Chitinase with the Designed Inhibitor HM508 and Its Degradation Product, Chitobiono- $\beta$ -lactone. <i>Journal of Biological Chemistry</i> , 2004, 279, 3612-3619.	1.6	47
133	Structural insights into the regulation of PDK1 by phosphoinositides and inositol phosphates. <i>EMBO Journal</i> , 2004, 23, 3918-3928.	3.5	167
134	Crystal structure of MO25 $\beta$ in complex with the C terminus of the pseudo kinase STE20-related adaptor. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 193-200.	3.6	62
135	Purification, crystallization and preliminary X-ray diffraction of a proteolytic fragment of PDK1 containing the pleckstrin homology domain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 314-316.	2.5	4
136	PRODRG: a tool for high-throughput crystallography of protein-ligand complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1355-1363.	2.5	4,230
137	Mutational and computational analysis of the role of conserved residues in the active site of a family 18 chitinase. <i>FEBS Journal</i> , 2004, 271, 253-262.	0.2	164
138	Structure of the D142N mutant of the family 18 chitinase ChiB from <i>Serratia marcescens</i> and its complex with allosamidin. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2004, 1696, 103-111.	1.1	56
139	Analysis of the LKB1-STRAD-MO25 complex. <i>Journal of Cell Science</i> , 2004, 117, 6365-6375.	1.2	130
140	Structure-Based Exploration of Cyclic Dipeptide Chitinase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 5713-5720.	2.9	134
141	Structures of <i>Bacillus subtilis</i> PdaA, a family 4 carbohydrate esterase, and a complex with N-acetyl-glucosamine. <i>FEBS Letters</i> , 2004, 570, 13-19.	1.3	83
142	PDK1, the master regulator of AGC kinase signal transduction. <i>Seminars in Cell and Developmental Biology</i> , 2004, 15, 161-170.	2.3	715
143	Pound-Wise but Penny-Foolish. <i>Structure</i> , 2003, 11, 1051-1059.	1.6	90
144	PAS Domains. <i>Journal of Biological Chemistry</i> , 2003, 278, 18434-18439.	1.6	73

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145	High Resolution Crystal Structures of Siglec-7. <i>Journal of Biological Chemistry</i> , 2003, 278, 3372-3377.	1.6	109
146	Crystal Structures of Allosamidin Derivatives in Complex with Human Macrophage Chitinase. <i>Journal of Biological Chemistry</i> , 2003, 278, 20110-20116.	1.6	71
147	Structure and Ligand-induced Conformational Change of the 39-kDa Glycoprotein from Human Articular Chondrocytes. <i>Journal of Biological Chemistry</i> , 2003, 278, 30206-30212.	1.6	125
148	Binding of phosphatidylinositol 3,4,5-trisphosphate to the pleckstrin homology domain of protein kinase B induces a conformational change. <i>Biochemical Journal</i> , 2003, 375, 531-538.	1.7	243
149	Structural basis for UCN-01 (7-hydroxystaurosporine) specificity and PDK1 (3-phosphoinositide-dependent protein kinase-1) inhibition. <i>Biochemical Journal</i> , 2003, 375, 255-262.	1.7	116
150	Engineering Photocycle Dynamics. <i>Journal of Biological Chemistry</i> , 2002, 277, 6463-6468.	1.6	12
151	Structure of Human Chitotriosidase. <i>Journal of Biological Chemistry</i> , 2002, 277, 25537-25544.	1.6	185
152	High-resolution structures of a chitinase complexed with natural product cyclopentapeptide inhibitors: Mimicry of carbohydrate substrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9127-9132.	3.3	93
153	The transfer of transthyretin and receptor-binding properties from the plasma retinol-binding protein to the epididymal retinoic acid-binding protein. <i>Biochemical Journal</i> , 2002, 362, 265.	1.7	11
154	The cyclic dipeptide CI-4 [cyclo-(l-Arg-d-Pro)] inhibits family 18 chitinases by structural mimicry of a reaction intermediate. <i>Biochemical Journal</i> , 2002, 368, 23-27.	1.7	57
155	High-Resolution Structure of the Pleckstrin Homology Domain of Protein Kinase B/Akt Bound to Phosphatidylinositol (3,4,5)-Trisphosphate. <i>Current Biology</i> , 2002, 12, 1256-1262.	1.8	273
156	Structure of the photoactive yellow protein reconstituted with caffeic acid at 1.16 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 585-590.	2.5	13
157	High resolution crystal structure of the human PDK1 catalytic domain defines the regulatory phosphopeptide docking site. <i>EMBO Journal</i> , 2002, 21, 4219-4228.	3.5	176
158	The crystal structure of $\hat{P}^3\hat{P}^2$ -enoyl-CoA isomerase. <i>Journal of Molecular Biology</i> , 2001, 309, 845-853.	2.0	50
159	Crystal structure of the liganded SCP-2-like domain of human peroxisomal multifunctional enzyme type 2 at 1.75 Å resolution. Edited by R. Huber. <i>Journal of Molecular Biology</i> , 2001, 313, 1127-1138.	2.0	70
160	Crystallization and X-ray diffraction studies of the fatty-acid responsive transcription factor FadR from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 469-471.	2.5	6
161	Crystallization and X-ray diffraction analysis of peroxisomal $\hat{P}^3\hat{P}^2$ -enoyl-CoA isomerase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1020-1023.	2.5	5
162	Crystal Structure of Carboxypeptidase A Complexed with d-Cysteine at 1.75 Å Inhibitor-Induced Conformational Changes. <i>Biochemistry</i> , 2000, 39, 10082-10089.	1.2	27

#	ARTICLE	IF	CITATIONS
163	Conformational substates in different crystal forms of the photoactive yellow proteinâ€”Correlation with theoretical and experimental flexibility. <i>Protein Science</i> , 2000, 9, 64-72.	3.1	31
164	Sequence, chromophore extraction and 3-D model of the photoactive yellow protein from <i>Rhodobacter sphaeroides</i> . <i>BBA - Proteins and Proteomics</i> , 1998, 1385, 1-6.	2.1	39
165	Dynamic Properties of the Guanine Nucleotide Binding Protein $\hat{\pm}$ Subunit and Comparison of Its Guanosine Triphosphate Hydrolase Domain with That of rasp21â€”. <i>Biochemistry</i> , 1998, 37, 3137-3142.	1.2	24
166	Essential Dynamics from NMR Clusters: Dynamic Properties of the Myb DNA-Binding Domain and a Hinge-Bending Enhancing Variant. <i>Methods</i> , 1998, 14, 318-328.	1.9	30
167	Essential dynamics of DNA containing a cis.syn cyclobutane thymine dimer lesion. <i>Nucleic Acids Research</i> , 1998, 26, 1939-1946.	6.5	69