Daan van Aalten

List of Publications by Year
in descending order

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167 papers	15,513 citations	23500 58 h-index	18606 119 g-index
173 all docs	173 docs citations	173 times ranked	19267 citing authors

#	Article	IF	Citations
1	Genetic validation of Aspergillus fumigatus phosphoglucomutase as a viable therapeutic target in invasive aspergillosis. Journal of Biological Chemistry, 2022, 298, 102003.	1.6	3
2	Intellectual disability-associated disruption of O-GlcNAc cycling impairs habituation learning in Drosophila. PLoS Genetics, 2022, 18, e1010159.	1.5	7
3	Bioinformatic prediction of putative conveyers of O-GlcNAc transferase intellectual disability. Journal of Biological Chemistry, 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. FEBS Letters, 2021, 595, 110-122.	1.3	3
5	Genetic and structural validation of phosphomannomutase as a cell wall target in Aspergillus fumigatus. Molecular Microbiology, 2021, 116, 245-259.	1.2	7
6	The citron homology domain as a scaffold for Rho1 signaling. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	9
7	Loss of O-GlcNAcase catalytic activity leads to defects in mouse embryogenesis. Journal of Biological Chemistry, 2021, 296, 100439.	1.6	28
8	A missense mutation in the catalytic domain of Oâ€GlcNAc transferase links perturbations in protein Oâ€GlcNAcylation to Xâ€linked intellectual disability. FEBS Letters, 2020, 594, 717-727.	1.3	40
9	Native detection of protein O-GlcNAcylation by gel electrophoresis. Analyst, The, 2020, 145, 6826-6830.	1.7	4
10	Targeting a critical step in fungal hexosamine biosynthesis. Journal of Biological Chemistry, 2020, 295, 8678-8691.	1.6	16
11	A mechanism-inspired UDP-N-acetylglucosamine pyrophosphorylase inhibitor. RSC Chemical Biology, 2020, 1, 13-25.	2.0	20
12	Tools for functional dissection of site-specific O-GlcNAcylation. RSC Chemical Biology, 2020, 1, 98-109.	2.0	22
13	O-GlcNAcase contributes to cognitive function in Drosophila. Journal of Biological Chemistry, 2020, 295, 8636-8646.	1.6	16
14	An intellectual disability syndrome with single-nucleotide variants in O-GlcNAc transferase. European Journal of Human Genetics, 2020, 28, 706-714.	1.4	38
15	Catalytic deficiency of O-GlcNAc transferase leads to X-linked intellectual disability. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14961-14970.	3.3	58
16	Genetic recoding to dissect the roles of site-specific protein O-GlcNAcylation. Nature Structural and Molecular Biology, 2019, 26, 1071-1077.	3.6	50
17	Mechanisms of redundancy and specificity of the Aspergillus fumigatus Crh transglycosylases. Nature Communications, 2019, 10, 1669.	5.8	18
18	Loss of CRMP2 O-GlcNAcylation leads to reduced novel object recognition performance in mice. Open Biology, 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	UDPâ€GlcNAc Analogues as Inhibitors of Oâ€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 UDPâ€“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. Biochemical Journal, 2016, 473, 1693-1702.	1.7	47
38	<scp>GacA</scp> is essential for <scp>G</scp>roup <scp>A S</scp>treptococcus and defines a new class of monomeric d<scp>TDP</scp>â€4â€dehydrorhamnose reductases (<scp>RmlD</scp>). Molecular Microbiology, 2015, 98, 946-962.	1.2	46
39	Evidence for a Functional O-Linked N-Acetylglucosamine (O-GlcNAc) System in the Thermophilic Bacterium Thermobaculum terrenum. Journal of Biological Chemistry, 2015, 290, 30291-30305.	1.6	29
40	Dual functionality of O -GlcNAc transferase is required for Drosophila development. Open Biology, 2015, 5, 150234.	1.5	32
41	Binding to serine 65â€phosphorylated ubiquitin primes Parkin for optimal <scp>PINK</scp> 1â€dependent phosphorylation and activation. EMBO Reports, 2015, 16, 939-954.	2.0	183
42	N-Myristoyltransferase Is a Cell Wall Target in Aspergillus fumigatus. ACS Chemical Biology, 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. Journal of Neuroscience, 2015, 35, 2492-2507.	1.7	70
44	The active site of O-GlcNAc transferase imposes constraints on substrate sequence. Nature Structural and Molecular Biology, 2015, 22, 744-750.	3.6	114
45	The Early Metazoan Trichoplax adhaerens Possesses a Functional O-GlcNAc System. Journal of Biological Chemistry, 2015, 290, 11969-11982.	1.6	15
46	Tyrosine glycosylation of Rho by Yersinia toxin impairs blastomere cell behaviour in zebrafish embryos. Nature Communications, 2015, 6, 7807.	5.8	37
47	Bisubstrate UDPâ€“peptide conjugates as human O-GlcNAc transferase inhibitors. Biochemical Journal, 2014, 457, 497-502.	1.7	57
48	Elevated O-GlcNAc Levels Activate Epigenetically Repressed Genes and Delay Mouse ESC Differentiation Without Affecting NaÃ¯ve to Primed Cell Transition. Stem Cells, 2014, 32, 2605-2615.	1.4	50
49	O-GlcNAcase: Promiscuous Hexosaminidase or Key Regulator of O-GlcNAc Signaling?. Journal of Biological Chemistry, 2014, 289, 34433-34439.	1.6	50
50	A Structural and Biochemical Model of Processive Chitin Synthesis. Journal of Biological Chemistry, 2014, 289, 23020-23028.	1.6	46
51	Lead Optimization of a Pyrazole Sulfonamide Series of Trypanosoma brucei N-Myristoyltransferase Inhibitors: Identification and Evaluation of CNS Penetrant Compounds as Potential Treatments for Stage 2 Human African Trypanosomiasis. Journal of Medicinal Chemistry, 2014, 57, 9855-9869.	2.9	57
52	Screening-based discovery of Aspergillus fumigatus plant-type chitinase inhibitors. FEBS Letters, 2014, 588, 3282-3290.	1.3	15
53	Genetic and structural validation of <scp>A</scp>spergillus fumigatusâ€¦<scp>UDP</scp>â€<scp>N</scp>â€acetylglucosamine pyrophosphorylase as an antifungal target. Molecular Microbiology, 2013, 89, 479-493.	1.2	29
54	Proteome Wide Purification and Identification of O-GlcNAc-Modified Proteins Using Click Chemistry and Mass Spectrometry. Journal of Proteome Research, 2013, 12, 927-936.	1.8	151

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

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

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91	ATP and MO25Î± Regulate the Conformational State of the STRADÎ± 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 Encephalitozoon cuniculi. Protein Science, 2009, 18, 1197-1209.	3.1	27
93	GlcNAcstatins are nanomolar inhibitors of human O-GlcNAcase inducing cellular hyper-O-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 Aspergillus fumigatus <scp>D</scp>-glucosamine-6-phosphate N-acetyltransferase. Biochemical Journal, 2008, 415, 217-223.	1.7	26
105	Glucoseâ€6â€phosphate as a probe for the glucosamineâ€6â€phosphate Nâ€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 BÎ±. ACS Chemical Biology, 2007, 2, 242-246.	1.6	20
107	Efficient synthesis of 1,3,7-substituted xanthines 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. EMBO Reports, 2007, 8, 839-845.	2.0	89
110	Kinetic, inhibition and structural studies on 3-oxoacyl-ACP reductase from Plasmodium falciparum, a key enzyme in fatty acid biosynthesis. Biochemical Journal, 2006, 393, 447-457.	1.7	72
111	Structure and Mechanism of Chitin Deacetylase from the Fungal PathogenColletotrichum lindemuthianumâ€,â€¡. Biochemistry, 2006, 45, 9416-9426.	1.2	149
112	GlcNAcstatin:Â a Picomolar, SelectiveO-GlcNAcase Inhibitor That Modulates IntracellularO-GlcNAcylation Levels. Journal of the American Chemical Society, 2006, 128, 16484-16485.	6.6	136
113	The structure of siglec-7 in complex with sialosides: leads for rational structure-based inhibitor design. Biochemical Journal, 2006, 397, 271-278.	1.7	70
114	TAK1-binding protein 1 is a pseudophosphatase. Biochemical Journal, 2006, 399, 427-434.	1.7	73
115	The ubiquitin-associated domain of AMPK-related kinases regulates conformation and LKB1-mediated phosphorylation and activation. Biochemical Journal, 2006, 394, 545-555.	1.7	95
116	Structural insights into the mechanism and inhibition of eukaryotic O-GlcNAc hydrolysis. EMBO Journal, 2006, 25, 1569-1578.	3.5	181
117	Natural Product Family 18 Chitinase Inhibitors. ChemInform, 2006, 37, no.	0.1	1
118	First Synthesis of Argadin: A Nanomolar Inhibitor of Family-18 Chitinases. European Journal of Organic Chemistry, 2006, 2006, 5002-5006.	1.2	22
119	Siglec-7 Undergoes a Major Conformational Change When Complexed with the Î±(2,8)-Disialylganglioside GT1b. Journal of Biological Chemistry, 2006, 281, 32774-32783.	1.6	82
120	Structural Basis of Reduction-dependent Activation of Human Cystatin F. Journal of Biological Chemistry, 2006, 281, 16570-16575.	1.6	39
121	Screening-based Discovery and Structural Dissection of a Novel Family 18 Chitinase Inhibitor. Journal of Biological Chemistry, 2006, 281, 27278-27285.	1.6	53
122	Specificity and Affinity of Natural Product Cyclopentapeptide Inhibitors against A. fumigatus, Human, and Bacterial Chitinases. Chemistry and Biology, 2005, 12, 65-76.	6.2	109
123	Methylxanthine Drugs Are Chitinase Inhibitors: Investigation of Inhibition and Binding Modes. Chemistry and Biology, 2005, 12, 973-980.	6.2	108
124	The N-Acetyl-D-glucosaminylphosphatidylinositol De-N-acetylase of Glycosylphosphatidylinositol Biosynthesis Is a Zinc Metalloenzyme. Journal of Biological Chemistry, 2005, 280, 22831-22838.	1.6	38
125	Crystal Structure and Binding Properties of the Serratia marcescens Chitin-binding Protein CBP21. Journal of Biological Chemistry, 2005, 280, 11313-11319.	1.6	257
126	Structure and metal-dependent mechanism of peptidoglycan deacetylase, a streptococcal virulence factor. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15429-15434.	3.3	196

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127	Role of T-loop Phosphorylation in PDK1 Activation, Stability, and Substrate Binding. Journal of Biological Chemistry, 2005, 280, 18797-18802.	1.6	36
128	Crystal Structure of the PTPL1/FAP-1 Human Tyrosine Phosphatase Mutated in Colorectal Cancer. Journal of Biological Chemistry, 2005, 280, 8180-8187.	1.6	34
129	An efficient synthesis of argifin: A natural product chitinase inhibitor with chemotherapeutic potential. Bioorganic and Medicinal Chemistry Letters, 2005, 15, 4717-4721.	1.0	39
130	The Non-catalytic Chitin-binding Protein CBP21 from Serratia marcescens Is Essential for Chitin Degradation. Journal of Biological Chemistry, 2005, 280, 28492-28497.	1.6	321
131	Natural product family 18 chitinase inhibitors. Natural Product Reports, 2005, 22, 563.	5.2	79
132	Interactions of a Family 18 Chitinase with the Designed Inhibitor HM508 and Its Degradation Product, Chitobiono-Î´-lactone. Journal of Biological Chemistry, 2004, 279, 3612-3619.	1.6	47
133	Structural insights into the regulation of PDK1 by phosphoinositides and inositol phosphates. EMBO Journal, 2004, 23, 3918-3928.	3.5	167
134	Crystal structure of MO25Î± in complex with the C terminus of the pseudo kinase STE20-related adaptor. Nature Structural and Molecular Biology, 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. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 314-316.	2.5	4
136	PRODRG: a tool for high-throughput crystallography of proteinâ€“ligand complexes. Acta Crystallographica Section D: Biological Crystallography, 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. FEBS Journal, 2004, 271, 253-262.	0.2	164
138	Structure of the D142N mutant of the family 18 chitinase ChiB from Serratia marcescens and its complex with allosamidin. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2004, 1696, 103-111.	1.1	56
139	Analysis of the LKB1-STRAD-MO25 complex. Journal of Cell Science, 2004, 117, 6365-6375.	1.2	130
140	Structure-Based Exploration of Cyclic Dipeptide Chitinase Inhibitors. Journal of Medicinal Chemistry, 2004, 47, 5713-5720.	2.9	134
141	Structures ofBacillus subtilisPdaA, a family 4 carbohydrate esterase, and a complex withN-acetyl-glucosamine. FEBS Letters, 2004, 570, 13-19.	1.3	83
142	PDK1, the master regulator of AGC kinase signal transduction. Seminars in Cell and Developmental Biology, 2004, 15, 161-170.	2.3	715
143	Pound-Wise but Penny-Foolish. Structure, 2003, 11, 1051-1059.	1.6	90
144	PAS Domains. Journal of Biological Chemistry, 2003, 278, 18434-18439.	1.6	73

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145	High Resolution Crystal Structures of Siglec-7. Journal of Biological Chemistry, 2003, 278, 3372-3377.	1.6	109
146	Crystal Structures of Allosamidin Derivatives in Complex with Human Macrophage Chitinase. Journal of Biological Chemistry, 2003, 278, 20110-20116.	1.6	71
147	Structure and Ligand-induced Conformational Change of the 39-kDa Glycoprotein from Human Articular Chondrocytes. Journal of Biological Chemistry, 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. Biochemical Journal, 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. Biochemical Journal, 2003, 375, 255-262.	1.7	116
150	Engineering Photocycle Dynamics. Journal of Biological Chemistry, 2002, 277, 6463-6468.	1.6	12
151	Structure of Human Chitotriosidase. Journal of Biological Chemistry, 2002, 277, 25537-25544.	1.6	185
152	High-resolution structures of a chitinase complexed with natural product cyclopentapeptide inhibitors: Mimicry of carbohydrate substrate. Proceedings of the National Academy of Sciences of the United States of America, 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. Biochemical Journal, 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. Biochemical Journal, 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. Current Biology, 2002, 12, 1256-1262.	1.8	273
156	Structure of the photoactive yellow protein reconstituted with caffeic acid at 1.16â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 585-590.	2.5	13
157	High resolution crystal structure of the human PDK1 catalytic domain defines the regulatory phosphopeptide docking site. EMBO Journal, 2002, 21, 4219-4228.	3.5	176
158	The crystal structure of Î”3-Î”2-enoyl-CoA isomerase. Journal of Molecular Biology, 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 Ã… resolution 1 1Edited by R. Huber. Journal of Molecular Biology, 2001, 313, 1127-1138.	2.0	70
160	Crystallization and X-ray diffraction studies of the fatty-acid responsive transcription factor FadR fromEscherichia coli. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 469-471.	2.5	6
161	Crystallization and X-ray diffraction analysis of peroxisomal Î”3-Î”2-enoyl-CoA isomerase fromSaccharomyces cerevisiae. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1020-1023.	2.5	5
162	Crystal Structure of Carboxypeptidase A Complexed with d-Cysteine at 1.75 Ã… â^' Inhibitor-Induced Conformational Changes,. Biochemistry, 2000, 39, 10082-10089.	1.2	27

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163	Conformational substates in different crystal forms of the photoactive yellow proteinâ€"Correlation with theoretical and experimental flexibility. Protein Science, 2000, 9, 64-72.	3.1	31
164	Sequence, chromophore extraction and 3-D model of the photoactive yellow protein from Rhodobacter sphaeroides. BBA - Proteins and Proteomics, 1998, 1385, 1-6.	2.1	39
165	Dynamic Properties of the Guanine Nucleotide Binding Protein Î± Subunit and Comparison of Its Guanosine Triphosphate Hydrolase Domain with That ofrasp21â€. Biochemistry, 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. Methods, 1998, 14, 318-328.	1.9	30
167	Essential dynamics of DNA containing a cis.syn cyclobutane thymine dimer lesion. Nucleic Acids Research, 1998, 26, 1939-1946.	6.5	69