

# Bauke W Dijkstra

## List of Publications by Year in descending order

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265  
papers

22,321  
citations

8181

76  
h-index

9861

141  
g-index

266  
all docs

266  
docs citations

266  
times ranked

14169  
citing authors

#	ARTICLE	IF	CITATIONS
1	Application of microbial 3-ketosteroid $\beta$ -1-dehydrogenases in biotechnology. <i>Biotechnology Advances</i> , 2021, 49, 107751.	11.7	18
2	Xylanases from marine microorganisms: A brief overview on scope, sources, features and potential applications. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2020, 1868, 140312.	2.3	49
3	Relationship of <i>Agaricus bisporus</i> mannose-binding protein to lectins with $\beta$ -trefoil fold. <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 1027-1032.	2.1	4
4	Phenylthiourea Binding to Human Tyrosinase-Related Protein 1. <i>International Journal of Molecular Sciences</i> , 2020, 21, 915.	4.1	13
5	$\beta$ -Xylosidases: Structural Diversity, Catalytic Mechanism, and Inhibition by Monosaccharides. <i>International Journal of Molecular Sciences</i> , 2019, 20, 5524.	4.1	43
6	The role and mechanism of microbial 3-ketosteroid $\beta$ -1-dehydrogenases in steroid breakdown. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2019, 191, 105366.	2.5	29
7	Frontispiece: Structure and Function of Human Tyrosinase and Tyrosinase-Related Proteins. <i>Chemistry - A European Journal</i> , 2018, 24, .	3.3	3
8	Structure and Function of Human Tyrosinase and Tyrosinase-Related Proteins. <i>Chemistry - A European Journal</i> , 2018, 24, 47-55.	3.3	165
9	Structural basis of product inhibition by arabinose and xylose of the thermostable GH43 $\beta$ -1,4-xylosidase from <i>Geobacillus thermoleovorans</i> IT-08. <i>PLoS ONE</i> , 2018, 13, e0196358.	2.5	25
10	Crystal Structure of 4,6- $\beta$ -Glucanotransferase Supports Diet-Driven Evolution of GH70 Enzymes from $\beta$ -Amylases in Oral Bacteria. <i>Structure</i> , 2017, 25, 231-242.	3.3	45
11	The light subunit of mushroom <i>Agaricus bisporus</i> tyrosinase: Its biological characteristics and implications. <i>International Journal of Biological Macromolecules</i> , 2017, 102, 308-314.	7.5	22
12	Study of response of Swiss Webster mice to light subunit of mushroom tyrosinase. <i>Biotechnic and Histochemistry</i> , 2017, 92, 411-416.	1.3	7
13	Structure of Human Tyrosinase Related Protein...1 Reveals a Binuclear Zinc Active Site Important for Melanogenesis. <i>Angewandte Chemie</i> , 2017, 129, 9944-9947.	2.0	12
14	Structure of Human Tyrosinase Related Protein...1 Reveals a Binuclear Zinc Active Site Important for Melanogenesis. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 9812-9815.	13.8	139
15	Large-Scale Recombinant Expression and Purification of Human Tyrosinase Suitable for Structural Studies. <i>PLoS ONE</i> , 2016, 11, e0161697.	2.5	51
16	Crystal structure of recombinant tyrosinase-binding protein MtaL at 1.35 $\text{\AA}$ resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 244-250.	0.8	9
17	Mutation Analysis of the pKa Modulator Residue in $\beta$ -D-xylosidase from <i>Geobacillus Thermoleovorans</i> IT-08: Activity Adaptation to Alkaline and High-Temperature Conditions. <i>Procedia Chemistry</i> , 2016, 18, 39-48.	0.7	4
18	A novel immune-tolerable and permeable lectin-like protein from mushroom <i>Agaricus bisporus</i> . <i>Biochemical and Biophysical Research Communications</i> , 2016, 473, 1090-1093.	2.1	16

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19	Structural Basis of the Substrate Range and Enantioselectivity of Two ( <i>S</i> )-Selective $\alpha$ -Transaminases. <i>Biochemistry</i> , 2016, 55, 4422-4431.	2.5	28
20	Structure and Catalytic Mechanism of 3-Ketosteroid Dehydrogenases. <i>Procedia Chemistry</i> , 2016, 18, 3-11.	0.7	9
21	Active site coupling in <i>Plasmodium falciparum</i> GMP synthetase is triggered by domain rotation. <i>Nature Communications</i> , 2015, 6, 8930.	12.8	24
22	Crystal structure of quinone-dependent alcohol dehydrogenase from <i>Pseudogluconobacter saccharoketogenes</i> . A versatile dehydrogenase oxidizing alcohols and carbohydrates. <i>Protein Science</i> , 2015, 24, 2044-2054.	7.6	17
23	Ironing out Their Differences: Dissecting the Structural Determinants of a Phenylalanine Aminomutase and Ammonia Lyase. <i>ACS Chemical Biology</i> , 2015, 10, 989-997.	3.4	23
24	X-ray crystallographic validation of structure predictions used in computational design for protein stabilization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 940-951.	2.6	17
25	Effect of introducing a disulphide bond between the A and C domains on the activity and stability of <i>Saccharomycopsis fibuligera</i> R64 $\alpha$ -amylase. <i>Journal of Biotechnology</i> , 2015, 195, 8-14.	3.8	10
26	Flexibility of truncated and full-length glucansucrase <i>GTF</i> 180 enzymes from <i>Lactobacillus reuteri</i> 180. <i>FEBS Journal</i> , 2014, 281, 2159-2171.	4.7	21
27	Crystal structures of two <i>Bacillus</i> carboxylesterases with different enantioselectivities. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 567-575.	2.3	20
28	Reducing virulence of the human pathogen <i>Burkholderia</i> by altering the substrate specificity of the quorum-quenching acylase PvdQ. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1568-1573.	7.1	65
29	Structural Investigations into the Stereochemistry and Activity of a Phenylalanine-2,3-aminomutase from <i>Taxus chinensis</i> . <i>Biochemistry</i> , 2014, 53, 3187-3198.	2.5	21
30	Redesign of a Phenylalanine Aminomutase into a Phenylalanine Ammonia Lyase. <i>ChemCatChem</i> , 2013, 5, 1797-1802.	3.7	27
31	Crystal structure of endo-xylogalacturonan hydrolase from <i>Aspergillus tubingensis</i> . <i>FEBS Journal</i> , 2013, 280, 6061-6069.	4.7	14
32	Glucansucrases: Three-dimensional structures, reactions, mechanism, $\alpha$ -glucan analysis and their implications in biotechnology and food applications. <i>Journal of Biotechnology</i> , 2013, 163, 250-272.	3.8	250
33	Biocatalytic and Structural Properties of a Highly Engineered Halohydrin Dehalogenase. <i>ChemBioChem</i> , 2013, 14, 870-881.	2.6	44
34	Crystal Structure and Site-directed Mutagenesis of 3-Ketosteroid $\beta$ -1-Dehydrogenase from <i>Rhodococcus erythropolis</i> SQ1 Explain Its Catalytic Mechanism. <i>Journal of Biological Chemistry</i> , 2013, 288, 35559-35568.	3.4	48
35	Crystal Structure of $\alpha$ -1,4-Glucan Lyase, a Unique Glycoside Hydrolase Family Member with a Novel Catalytic Mechanism. <i>Journal of Biological Chemistry</i> , 2013, 288, 26764-26774.	3.4	22
36	Biochemical Properties and Crystal Structure of a $\beta$ -Phenylalanine Aminotransferase from <i>Variovorax paradoxus</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 185-195.	3.1	29

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37	AcmD, a Homolog of the Major Autolysin AcmA of <i>Lactococcus lactis</i> , Binds to the Cell Wall and Contributes to Cell Separation and Autolysis. <i>PLoS ONE</i> , 2013, 8, e72167.	2.5	66
38	Self-Processing Cysteine-Dependent N-terminal Nucleophile Hydrolases. , 2013, , 3653-3657.		0
39	Functional and Structural Characterization of Î±-(1â†’2) Branching Sucrase Derived from DSR-E Glucansucrase. <i>Journal of Biological Chemistry</i> , 2012, 287, 7915-7924.	3.4	78
40	Glycosidic bond specificity of glucansucrases: on the role of acceptor substrate binding residues. <i>Biotransformation</i> , 2012, 30, 366-376.	2.0	53
41	Structural Determinants of the Î²-Selectivity of a Bacterial Aminotransferase. <i>Journal of Biological Chemistry</i> , 2012, 287, 28495-28502.	3.4	30
42	The role of conserved inulosucrase residues in the reaction and product specificity of <i>Lactobacillus reuteri</i> inulosucrase. <i>FEBS Journal</i> , 2012, 279, 3612-3621.	4.7	23
43	Structure and Catalytic Mechanism of 3-Ketosteroid-Î²(5)-dehydrogenase from <i>Rhodococcus jostii</i> RHA1 Genome. <i>Journal of Biological Chemistry</i> , 2012, 287, 30975-30983.	3.4	25
44	Enhancement of the enantioselectivity of carboxylesterase A by structure-based mutagenesis. <i>Journal of Biotechnology</i> , 2012, 158, 36-43.	3.8	23
45	Characterization of Aptamer-Protein Complexes by X-ray Crystallography and Alternative Approaches. <i>International Journal of Molecular Sciences</i> , 2012, 13, 10537-10552.	4.1	39
46	Structural investigation of the transmembrane C domain of the mannitol permease from <i>Escherichia coli</i> using 5-FTrp fluorescence spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 861-868.	2.6	8
47	Structure of the Î±-1,6/Î±-1,4-specific glucansucrase GTFA from <i>Lactobacillus reuteri</i> 121. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1448-1454.	0.7	47
48	A genetically engineered protein domain binding to bacterial murein, archaeal pseudomurein, and fungal chitin cell wall material. <i>Applied Microbiology and Biotechnology</i> , 2012, 96, 729-737.	3.6	9
49	Biophysical characterization of mutants of <i>Bacillus subtilis</i> lipase evolved for thermostability: Factors contributing to increased activity retention. <i>Protein Science</i> , 2012, 21, 487-497.	7.6	49
50	Purification, crystallization and preliminary X-ray crystallographic analysis of 3-ketosteroid Î² <sup>1</sup> -dehydrogenase from <i>Rhodococcus erythropolis</i> SQ1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 551-556.	0.7	16
51	Mechanism-Inspired Engineering of Phenylalanine Aminomutase for Enhanced Î²-Regioselective Asymmetric Amination of Cinnamates. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 482-486.	13.8	48
52	Crystal Structure of <i>Agaricus bisporus</i> Mushroom Tyrosinase: Identity of the Tetramer Subunits and Interaction with Tropolone. <i>Biochemistry</i> , 2011, 50, 5477-5486.	2.5	648
53	Crystal Structure of Inulosucrase from <i>Lactobacillus</i> : Insights into the Substrate Specificity and Product Specificity of GH68 Fructansucrases. <i>Journal of Molecular Biology</i> , 2011, 412, 80-93.	4.2	63
54	A Minimum of Three Motifs Is Essential for Optimal Binding of Pseudomurein Cell Wall-Binding Domain of <i>Methanothermobacter thermautotrophicus</i> . <i>PLoS ONE</i> , 2011, 6, e21582.	2.5	7

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55	Biochemical characterization of a glucoamylase from <i>Saccharomycopsis fibuligera</i> R64. <i>Biologia (Poland)</i> , 2011, 66, 27-32.	1.5	5
56	Murein and pseudomurein cell wall binding domains of bacteria and archaea—a comparative view. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 921-928.	3.6	46
57	Crystallization and preliminary X-ray crystallographic analysis of tyrosinase from the mushroom <i>Agaricus bisporus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 575-578.	0.7	26
58	Cloning, overexpression, purification, crystallization and preliminary X-ray analysis of 3-ketosteroid 4 <sup>5</sup> -dehydrogenase from <i>Rhodococcus jostii</i> RHA1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1269-1273.	0.7	4
59	<i>Thermus thermophilus</i> Glycoside Hydrolase Family 57 Branching Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 3520-3530.	3.4	88
60	Structures of an Isopenicillin N Converting Ntn-Hydrolase Reveal Different Catalytic Roles for the Active Site Residues of Precursor and Mature Enzyme. <i>Structure</i> , 2010, 18, 301-308.	3.3	24
61	Two Major Archaeal Pseudomurein Endoisopeptidases: PeiW and PeiP. <i>Archaea</i> , 2010, 2010, 1-4.	2.3	17
62	Crystal structure of a 117 kDa glucansucrase fragment provides insight into evolution and product specificity of GH70 enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 21406-21411.	7.1	140
63	The quorum-quenching <i>N</i> -acyl homoserine lactone acylase PvdQ is an Ntn-hydrolase with an unusual substrate-binding pocket. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 686-691.	7.1	124
64	Crystal Structure of the Leucine Aminopeptidase from <i>Pseudomonas putida</i> Reveals the Molecular Basis for its Enantioselectivity and Broad Substrate Specificity. <i>Journal of Molecular Biology</i> , 2010, 398, 703-714.	4.2	28
65	The crystal structure of a hyperthermoactive exopolygalacturonase from <i>Thermotoga maritima</i> reveals a unique tetramer. <i>FEBS Letters</i> , 2009, 583, 3665-3670.	2.8	27
66	Crystallization and preliminary X-ray analysis of carnein, a serine protease from <i>Pomoea carnea</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 383-385.	0.7	1
67	Crystal Structure and Biochemical Properties of a Novel Thermostable Esterase Containing an Immunoglobulin-Like Domain. <i>Journal of Molecular Biology</i> , 2009, 385, 949-962.	4.2	36
68	A Novel Genetic Selection System for Improved Enantioselectivity of <i>Bacillus subtilis</i> Lipase A. <i>ChemBioChem</i> , 2008, 9, 1110-1115.	2.6	60
69	Loop Grafting of <i>Bacillus subtilis</i> Lipase A: Inversion of Enantioselectivity. <i>Chemistry and Biology</i> , 2008, 15, 782-789.	6.0	35
70	Biochemical and crystallographic characterization of a glucansucrase from <i>Lactobacillus reuteri</i> 180. <i>Biocatalysis and Biotransformation</i> , 2008, 26, 12-17.	2.0	31
71	Elimination of competing hydrolysis and coupling side reactions of a cyclodextrin glucanotransferase by directed evolution. <i>Biochemical Journal</i> , 2008, 413, 517-525.	3.7	47
72	Structural and Mutational Characterization of the Catalytic A-module of the Mannuronan C-5-epimerase AlgE4 from <i>Azotobacter vinelandii</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 23819-23828.	3.4	44

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73	Crystal Structures of Native and Inactivated cis-3-Chloroacrylic Acid Dehalogenase. <i>Journal of Biological Chemistry</i> , 2007, 282, 2440-2449.	3.4	33
74	Structure of <i>Escherichia coli</i> Lytic Transglycosylase MltA with Bound Chitohexaose. <i>Journal of Biological Chemistry</i> , 2007, 282, 21197-21205.	3.4	33
75	Three-way Stabilization of the Covalent Intermediate in Amylomaltase, an $\hat{\alpha}$ -Amylase-like Transglycosylase. <i>Journal of Biological Chemistry</i> , 2007, 282, 17242-17249.	3.4	63
76	Biochemical and structural exploration of the catalytic capacity of <i>Sulfolobus</i> KDG aldolases. <i>Biochemical Journal</i> , 2007, 403, 421-430.	3.7	32
77	Structural Basis of Phospholipase Activity of <i>Staphylococcus hyicus</i> lipase. <i>Journal of Molecular Biology</i> , 2007, 371, 447-456.	4.2	60
78	Identification of Acceptor Substrate Binding Subsites +2 and +3 in the Amylomaltase from <i>Thermus thermophilus</i> HB8. <i>Biochemistry</i> , 2007, 46, 5261-5269.	2.5	46
79	Crystallization and preliminary crystallographic analysis of an esterase with a novel domain from the hyperthermophile <i>Thermotoga maritima</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 777-779.	0.7	7
80	Purification, crystallization and preliminary X-ray analysis of a thermostable glycoside hydrolase family 43 $\hat{\beta}$ -xylosidase from <i>Geobacillus thermoleovorans</i> IT-08. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 932-935.	0.7	5
81	Fortuitous structure determination of 'as-isolated' <i>Escherichia coli</i> bacterioferritin in a novel crystal form. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1061-1066.	0.7	20
82	Structural mimicry for vinculin activation by IpaA, a virulence factor of <i>Shigella flexneri</i> . <i>EMBO Reports</i> , 2006, 7, 794-799.	4.5	26
83	Directed Evolution of <i>Bacillus subtilis</i> Lipase A by Use of Enantiomeric Phosphonate Inhibitors: Crystal Structures and Phage Display Selection. <i>ChemBioChem</i> , 2006, 7, 149-157.	2.6	64
84	The X-Ray Structure of the Haloalcohol Dehalogenase HheA from <i>Arthrobacter</i> sp. Strain AD2: Insight into Enantioselectivity and Halide Binding in the Haloalcohol Dehalogenase Family. <i>Journal of Bacteriology</i> , 2006, 188, 4051-4056.	2.2	33
85	<i>Acetobacter turbidans</i> $\hat{\alpha}$ -Amino Acid Ester Hydrolase. <i>Journal of Biological Chemistry</i> , 2006, 281, 5804-5810.	3.4	27
86	A crystallographic study of Cys69Ala flavodoxin II from <i>Azotobacter vinelandii</i> : Structural determinants of redox potential. <i>Protein Science</i> , 2005, 14, 2284-2295.	7.6	48
87	<i>Escherichia coli</i> MltA: MAD phasing and refinement of a tetartohedrally twinned protein crystal structure. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 613-621.	2.5	11
88	Improved Catalytic Properties of Halohydrin Dehalogenase by Modification of the Halide-Binding Site. <i>Biochemistry</i> , 2005, 44, 6609-6618.	2.5	53
89	Structural Basis for the Enantioselectivity of an Epoxide Ring Opening Reaction Catalyzed by Halo Alcohol Dehalogenase HheC. <i>Journal of the American Chemical Society</i> , 2005, 127, 13338-13343.	13.7	70
90	Crystal Structure of MltA from <i>Escherichia coli</i> Reveals a Unique Lytic Transglycosylase Fold. <i>Journal of Molecular Biology</i> , 2005, 352, 1068-1080.	4.2	56

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91	An approach to prevent aggregation during the purification and crystallization of wild type acyl coenzyme A: Isopenicillin N acyltransferase from <i>Penicillium chrysogenum</i> . <i>Protein Expression and Purification</i> , 2005, 41, 61-67.	1.3	10
92	Structural and kinetic studies on ligand binding in wild-type and active-site mutants of penicillin acylase. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 473-480.	2.1	27
93	The X-ray Structure of trans-3-Chloroacrylic Acid Dehalogenase Reveals a Novel Hydration Mechanism in the Tautomerase Superfamily. <i>Journal of Biological Chemistry</i> , 2004, 279, 11546-11552.	3.4	42
94	Structure of Spa15, a type III secretion chaperone from <i>Shigella flexneri</i> with broad specificity. <i>EMBO Reports</i> , 2004, 5, 477-483.	4.5	50
95	Purification, crystallization and preliminary X-ray analysis of the lytic transglycosylase MltA from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 758-760.	2.5	4
96	Three-dimensional structures of enzymes useful for $\beta$ -lactam antibiotic production. <i>Current Opinion in Biotechnology</i> , 2004, 15, 356-363.	6.6	18
97	Novel Biocatalysts by Identification and Design. <i>Biocatalysis and Biotransformation</i> , 2004, 22, 141-146.	2.0	22
98	Structure and mechanism of a bacterial haloalcohol dehalogenase: a new variation of the short-chain dehydrogenase/reductase fold without an NAD(P)H binding site. <i>EMBO Journal</i> , 2003, 22, 4933-4944.	7.8	102
99	Structure and mechanism of bacterial dehalogenases: different ways to cleave a carbon-halogen bond. <i>Current Opinion in Structural Biology</i> , 2003, 13, 722-730.	5.7	82
100	Catalysis and regulation from structure to function. <i>Current Opinion in Structural Biology</i> , 2003, 13, 706-708.	5.7	1
101	X-ray analysis of two antibiotic-synthesizing bacterial ester hydrolases: preliminary results. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 158-160.	2.5	4
102	Oils used in microbatch crystallization do not remove a detergent from the drops they cover. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2345-2347.	2.5	4
103	<i>Acetobacter turbidans</i> $\alpha$ -amino acid ester hydrolase: merohedral twinning in P21 obscured by pseudo-translational NCS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2237-2241.	2.5	15
104	Improved thermostability of <i>Bacillus circulans</i> cyclodextrin glycosyltransferase by the introduction of a salt bridge. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 54, 128-134.	2.6	38
105	Directed Evolution of an Enantioselective <i>Bacillus subtilis</i> Lipase. <i>Biocatalysis and Biotransformation</i> , 2003, 21, 67-73.	2.0	64
106	Engineering cyclodextrin glycosyltransferase into a starch hydrolase with a high exo-specificity. <i>Journal of Biotechnology</i> , 2003, 103, 203-212.	3.8	16
107	Conversion of Cyclodextrin Glycosyltransferase into a Starch Hydrolase by Directed Evolution: The Role of Alanine 230 in Acceptor Subsite +1. <i>Biochemistry</i> , 2003, 42, 7518-7526.	2.5	57
108	Formation of the Productive ATP-Mg <sup>2+</sup> -bound Dimer of GlcV, an ABC-ATPase from <i>Sulfolobus solfataricus</i> . <i>Journal of Molecular Biology</i> , 2003, 334, 255-267.	4.2	84

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109	Crystal Structures of the ATPase Subunit of the Glucose ABC Transporter from <i>Sulfolobus solfataricus</i> : Nucleotide-free and Nucleotide-bound Conformations. <i>Journal of Molecular Biology</i> , 2003, 330, 343-358.	4.2	145
110	The fully conserved Asp residue in conserved sequence region I of the $\alpha$ -amylase family is crucial for the catalytic site architecture and activity. <i>FEBS Letters</i> , 2003, 541, 47-51.	2.8	25
111	Structural insights into the processivity of endopolygalacturonase I from <i>Aspergillus niger</i> . <i>FEBS Letters</i> , 2003, 554, 462-466.	2.8	82
112	Single-Crystal EPR Study at 95GHz of the Type 2 Copper Site of the Inhibitor-Bound Quercetin 2,3-Dioxygenase. <i>Biophysical Journal</i> , 2003, 85, 4047-4054.	0.5	8
113	Detergent organisation in crystals of monomeric outer membrane phospholipase A. <i>Journal of Structural Biology</i> , 2003, 141, 122-131.	2.8	20
114	The Sequence and Crystal Structure of the $\alpha$ -Amino Acid Ester Hydrolase from <i>Xanthomonas citri</i> Define a New Family of $\beta$ -Lactam Antibiotic Acylases. <i>Journal of Biological Chemistry</i> , 2003, 278, 23076-23084.	3.4	37
115	Crystal Structure and Carbohydrate-binding Properties of the Human Cartilage Glycoprotein-39. <i>Journal of Biological Chemistry</i> , 2003, 278, 37753-37760.	3.4	183
116	Crystal Structure of Quinohemoprotein Alcohol Dehydrogenase from <i>Comamonas testosteroni</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 3727-3732.	3.4	78
117	Structure of Human Chitotriosidase. <i>Journal of Biological Chemistry</i> , 2002, 277, 25537-25544.	3.4	185
118	The Remote Substrate Binding Subsite $\alpha$ 6 in Cyclodextrin-glycosyltransferase Controls the Transferase Activity of the Enzyme via an Induced-fit Mechanism. <i>Journal of Biological Chemistry</i> , 2002, 277, 11113-11119.	3.4	43
119	Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: A Inhibition, Ordering Effect, and Mechanistic Insights. <i>Biochemistry</i> , 2002, 41, 7955-7962.	2.5	73
120	Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 2. X-ray Absorption Studies of Native Enzyme and Anaerobic Complexes with the Substrates Quercetin and Myricetin. <i>Biochemistry</i> , 2002, 41, 7963-7968.	2.5	37
121	Anaerobic enzyme*substrate structures provide insight into the reaction mechanism of the copper-dependent quercetin 2,3-dioxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16625-16630.	7.1	170
122	Functional importance of calcium binding sites in outer membrane phospholipase A. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002, 1561, 230-237.	2.6	3
123	Mutations converting cyclodextrin glycosyltransferase from a transglycosylase into a starch hydrolase. <i>FEBS Letters</i> , 2002, 514, 189-192.	2.8	47
124	Crystal Structure of the Copper-Containing Quercetin 2,3-Dioxygenase from <i>Aspergillus japonicus</i> . <i>Structure</i> , 2002, 10, 259-268.	3.3	216
125	Expression and characterization of active site mutants of hevamine, a chitinase from the rubber tree <i>Hevea brasiliensis</i> . <i>FEBS Journal</i> , 2002, 269, 893-901.	0.2	72
126	Biochemical properties and three-dimensional structures of two extracellular lipolytic enzymes from <i>Bacillus subtilis</i> . <i>Colloids and Surfaces B: Biointerfaces</i> , 2002, 26, 37-46.	5.0	47



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