

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
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266
all docs

266
docs citations

266
times ranked

14169
citing authors

#	ARTICLE	IF	CITATIONS
1	The α -hydrolase fold. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 197-211.	2.1	1,887
2	Bacterial Biocatalysts: Molecular Biology, Three-Dimensional Structures, and Biotechnological Applications of Lipases. <i>Annual Review of Microbiology</i> , 1999, 53, 315-351.	7.3	927
3	Bacterial lipases. <i>FEMS Microbiology Reviews</i> , 1994, 15, 29-63.	8.6	867
4	α -Hydrolase fold enzymes: the family keeps growing. <i>Current Opinion in Structural Biology</i> , 1999, 9, 732-737.	5.7	752
5	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
6	Crystallographic analysis of the catalytic mechanism of haloalkane dehalogenase. <i>Nature</i> , 1993, 363, 693-698.	27.8	496
7	Structure of bovine pancreatic phospholipase A2 at 1.7 Å resolution. <i>Journal of Molecular Biology</i> , 1981, 147, 97-123.	4.2	466
8	Stereochemistry of chitin hydrolysis by a plant chitinase/lysozyme and x-ray structure of a complex with allosamidin evidence for substrate assisted catalysis. <i>Biochemistry</i> , 1995, 34, 15619-15623.	2.5	349
9	X-ray structures along the reaction pathway of cyclodextrin glycosyltransferase elucidate catalysis in the alpha-amylase family. <i>Nature Structural Biology</i> , 1999, 6, 432-436.	9.7	348
10	Homology modelling and protein engineering strategy of subtilases, the family of subtilisin-like serine proteinases. <i>Protein Engineering, Design and Selection</i> , 1991, 4, 719-737.	2.1	331
11	Substrate-Assisted Catalysis Unifies Two Families of Chitinolytic Enzymes. <i>Journal of the American Chemical Society</i> , 1997, 119, 7954-7959.	13.7	296
12	X-ray structure of phospholipase A2 complexed with a substrate-derived inhibitor. <i>Nature</i> , 1990, 347, 689-691.	27.8	271
13	Active site and catalytic mechanism of phospholipase A2. <i>Nature</i> , 1981, 289, 604-606.	27.8	265
14	Structure of porcine pancreatic phospholipase A2 at 2 Å resolution and comparison with bovine phospholipase A2. <i>Journal of Molecular Biology</i> , 1983, 168, 163-179.	4.2	258
15	Glucansucrases: Three-dimensional structures, reactions, mechanism, α -glucan analysis and their implications in biotechnology and food applications. <i>Journal of Biotechnology</i> , 2013, 163, 250-272.	3.8	250
16	Crystal Structure of <i>Pseudomonas aeruginosa</i> Lipase in the Open Conformation. <i>Journal of Biological Chemistry</i> , 2000, 275, 31219-31225.	3.4	248
17	The crystal structure of <i>Bacillus subtilis</i> lipase: a minimal α -hydrolase fold enzyme. <i>Journal of Molecular Biology</i> , 2001, 309, 215-226.	4.2	242
18	Crystal structures of hevamine, a plant defence protein with chitinase and lysozyme activity, and its complex with an inhibitor. <i>Structure</i> , 1994, 2, 1181-1189.	3.3	234

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19	Directed evolution of an enantioselective lipase. <i>Chemistry and Biology</i> , 2000, 7, 709-718.	6.0	231
20	Nucleotide Sequence and X-ray Structure of Cyclodextrin Glycosyltransferase from <i>Bacillus circulans</i> Strain 251 in a Maltose-dependent Crystal Form. <i>Journal of Molecular Biology</i> , 1994, 236, 590-600.	4.2	228
21	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
22	1.68-Å... Crystal Structure of Endopolygalacturonase II from <i>Aspergillus niger</i> and Identification of Active Site Residues by Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 1999, 274, 30474-30480.	3.4	203
23	Structure of Human Chitotriosidase. <i>Journal of Biological Chemistry</i> , 2002, 277, 25537-25544.	3.4	185
24	The 1.8 Å... Resolution Structure of Hevamine, a Plant Chitinase/Lysozyme, and Analysis of the Conserved Sequence and Structure Motifs of Glycosyl Hydrolase Family 18. <i>Journal of Molecular Biology</i> , 1996, 262, 243-257.	4.2	183
25	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
26	Crystal structure of haloalkane dehalogenase: an enzyme to detoxify halogenated alkanes.. <i>EMBO Journal</i> , 1991, 10, 1297-1302.	7.8	176
27	Three-dimensional structure and disulfide bond connections in bovine pancreatic phospholipase A2. <i>Journal of Molecular Biology</i> , 1978, 124, 53-60.	4.2	175
28	The Raw Starch Binding Domain of Cyclodextrin Glycosyltransferase from <i>Bacillus circulans</i> Strain 251. <i>Journal of Biological Chemistry</i> , 1996, 271, 32777-32784.	3.4	172
29	Three-dimensional Structure of Endo-1,4-β-xylanase I from <i>Aspergillus niger</i> : Molecular Basis for its Low pH Optimum. <i>Journal of Molecular Biology</i> , 1996, 263, 70-78.	4.2	170
30	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
31	Structure and Function of Human Tyrosinase and Tyrosinase-Related Proteins. <i>Chemistry - A European Journal</i> , 2018, 24, 47-55.	3.3	165
32	Doughnut-shaped structure of a bacterial muramidase revealed by X-ray crystallography. <i>Nature</i> , 1994, 367, 750-753.	27.8	164
33	Extreme Stabilization of a Thermolysin-like Protease by an Engineered Disulfide Bond. <i>Journal of Biological Chemistry</i> , 1997, 272, 11152-11156.	3.4	164
34	Structural evidence for dimerization-regulated activation of an integral membrane phospholipase. <i>Nature</i> , 1999, 401, 717-721.	27.8	162
35	The X-ray Structure of Epoxide Hydrolase from <i>Agrobacterium radiobacter</i> AD1. <i>Journal of Biological Chemistry</i> , 1999, 274, 14579-14586.	3.4	160
36	Engineering of cyclodextrin glycosyltransferase reaction and product specificity. <i>BBA - Proteins and Proteomics</i> , 2000, 1543, 336-360.	2.1	159

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37	Model building of disulfide bonds in proteins with known three-dimensional structure. <i>Protein Engineering, Design and Selection</i> , 1988, 2, 119-125.	2.1	150
38	Structure of Cyclodextrin Glycosyltransferase Complexed with a Maltononaoase Inhibitor at 2.6 Å.. Resolution. Implications for Product Specificity. <i>Biochemistry</i> , 1996, 35, 4241-4249.	2.5	149
39	Structure and mechanism of soluble quinoprotein glucose dehydrogenase. <i>EMBO Journal</i> , 1999, 18, 5187-5194.	7.8	148
40	The three transglycosylation reactions catalyzed by cyclodextrin glycosyltransferase from <i>Bacillus circulans</i> (strain 251) proceed via different kinetic mechanisms. <i>FEBS Journal</i> , 2000, 267, 658-665.	0.2	148
41	Site-Directed Mutations in Tyrosine 195 of Cyclodextrin Glycosyltransferase from <i>Bacillus circulans</i> Strain 251 Affect Activity and Product Specificity. <i>Biochemistry</i> , 1995, 34, 3368-3376.	2.5	146
42	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
43	Refined X-ray Structures of Haloalkane Dehalogenase at pH 6.2 and pH 8.2 and Implications for the Reaction Mechanism. <i>Journal of Molecular Biology</i> , 1993, 232, 856-872.	4.2	143
44	X-ray Structure of Cyclodextrin Glycosyltransferase Complexed with Acarbose. Implications for the Catalytic Mechanism of Glycosidases. <i>Biochemistry</i> , 1995, 34, 2234-2240.	2.5	140
45	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
46	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
47	Crystallographic Studies of the Interaction of Cyclodextrin Glycosyltransferase from <i>Bacillus circulans</i> Strain 251 with Natural Substrates and Products. <i>Journal of Biological Chemistry</i> , 1995, 270, 29256-29264.	3.4	131
48	Structural basis of the chiral selectivity of <i>Pseudomonas cepacia</i> lipase. <i>FEBS Journal</i> , 1998, 254, 333-340.	0.2	128
49	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
50	Topological characterization and modeling of the 3D structure of lipase from <i>Pseudomonas aeruginosa</i> . <i>FEBS Letters</i> , 1993, 332, 143-149.	2.8	112
51	Enhanced activity and altered specificity of phospholipase A2 by deletion of a surface loop. <i>Science</i> , 1989, 244, 82-85.	12.6	111
52	The Cyclization Mechanism of Cyclodextrin Glycosyltransferase (CGTase) as Revealed by a β -Cyclodextrin-CGTase Complex at 1.8-Å Resolution. <i>Journal of Biological Chemistry</i> , 1999, 274, 34868-34876.	3.4	111
53	Structure of the 70-kDa Soluble Lytic Transglycosylase Complexed with Bulgecin A. Implications for the Enzymic Mechanism. <i>Biochemistry</i> , 1995, 34, 12729-12737.	2.5	110
54	High resolution crystal structures of the <i>Escherichia coli</i> lytic transglycosylase slt70 and its complex with a peptidoglycan fragment. <i>Journal of Molecular Biology</i> , 1999, 291, 877-898.	4.2	102

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55	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
56	Engineering of Cyclodextrin Product Specificity and pH Optima of the Thermostable Cyclodextrin Glycosyltransferase from <i>Thermoanaerobacterium thermosulfurigenes</i> EM1. <i>Journal of Biological Chemistry</i> , 1998, 273, 5771-5779.	3.4	100
57	Identification of the Mg ²⁺ -binding site in the P-type ATPase and phosphatase members of the HAD (haloacid dehalogenase) superfamily by structural similarity to the response regulator protein CheY. <i>Biochemical Journal</i> , 1999, 339, 223-226.	3.7	100
58	Protein stabilization by hydrophobic interactions at the surface. <i>FEBS Journal</i> , 1994, 220, 981-985.	0.2	98
59	Three-dimensional Structure of I-2-Haloacid Dehalogenase from <i>Xanthobacter autotrophicus</i> GJ10 Complexed with the Substrate-analogue Formate. <i>Journal of Biological Chemistry</i> , 1997, 272, 33015-33022.	3.4	97
60	X-ray structure of lipoamide dehydrogenase from <i>Azotobacter vinelandii</i> determined by a combination of molecular and isomorphous replacement techniques. <i>Journal of Molecular Biology</i> , 1989, 206, 365-379.	4.2	95
61	Role of the N-terminus in the interaction of pancreatic phospholipase A2 with aggregated substrates. Properties and crystal structure of transaminated phospholipase A2. <i>Biochemistry</i> , 1984, 23, 2759-2766.	2.5	94
62	Hydrophobic Amino Acid Residues in the Acceptor Binding Site Are Main Determinants for Reaction Mechanism and Specificity of Cyclodextrin-glycosyltransferase. <i>Journal of Biological Chemistry</i> , 2001, 276, 44557-44562.	3.4	93
63	Crystallographic and fluorescence studies of the interaction of haloalkane dehalogenase with halide ions. Studies with halide compounds reveal a halide binding site in the active site. <i>Biochemistry</i> , 1993, 32, 9031-9037.	2.5	92
64	Rational design of cyclodextrin glycosyltransferase from <i>Bacillus circulans</i> strain 251 to increase \pm -cyclodextrin production 1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 2000, 296, 1027-1038.	4.2	89
65	The Active Site Topology of <i>Aspergillus niger</i> Endopolygalacturonase II as Studied by Site-directed Mutagenesis. <i>Journal of Biological Chemistry</i> , 2000, 275, 691-696.	3.4	88
66	<i>Thermus thermophilus</i> Glycoside Hydrolase Family 57 Branching Enzyme. <i>Journal of Biological Chemistry</i> , 2011, 286, 3520-3530.	3.4	88
67	EPR characterization of the mononuclear Cu-containing <i>Aspergillus japonicus</i> quercetin 2,3-dioxygenase reveals dramatic changes upon anaerobic binding of substrates. <i>FEBS Journal</i> , 2002, 269, 2971-2979.	0.2	87
68	Crystal Structure at 2.3 Å... Resolution and Revised Nucleotide Sequence of the Thermostable Cyclodextrin Glycosyltransferase from <i>Thermoanaerobacterium thermosulfurigenes</i> EM1. <i>Journal of Molecular Biology</i> , 1996, 256, 611-622.	4.2	84
69	Formation of the Productive ATP-Mg ²⁺ -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
70	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
71	Structural insights into the processivity of endopolygalacturonase I from <i>Aspergillus niger</i> . <i>FEBS Letters</i> , 2003, 554, 462-466.	2.8	82
72	Crystal Structure of Concanavalin B at 1.65 Å... Resolution. An "Inactivated" Chitinase from Seeds of <i>Canavalia ensiformis</i> . <i>Journal of Molecular Biology</i> , 1995, 254, 237-246.	4.2	81

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73	Structures of Maltohexaose and Maltoheptaose Bound at the Donor Sites of Cyclodextrin Glycosyltransferase Give Insight into the Mechanisms of Transglycosylation Activity and Cyclodextrin Size Specificity. <i>Biochemistry</i> , 2000, 39, 7772-7780.	2.5	81
74	The 1.7 Å... crystal structure of the apo form of the soluble quinoprotein glucose dehydrogenase from <i>Acinetobacter calcoaceticus</i> reveals a novel internal conserved sequence repeat. <i>Journal of Molecular Biology</i> , 1999, 289, 319-333.	4.2	80
75	Crystal structure of <i>Escherichia coli</i> lytic transglycosylase Slt35 reveals a lysozyme-like catalytic domain with an EF-hand. <i>Structure</i> , 1999, 7, 1167-1180.	3.3	79
76	Crystal Structure of Quinohemoprotein Alcohol Dehydrogenase from <i>Comamonas testosteroni</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 3727-3732.	3.4	78
77	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
78	Bacterial phospholipase A: structure and function of an integral membrane phospholipase. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2000, 1488, 91-101.	2.4	77
79	Crystal structure of bovine pancreatic phospholipase A2 covalently inhibited by p-bromo-phenacyl-bromide. <i>Journal of Molecular Biology</i> , 1988, 200, 181-188.	4.2	76
80	Characterization of the Î²-lactam binding site of penicillin acylase of <i>Escherichia coli</i> by structural and site-directed mutagenesis studies. <i>Protein Engineering, Design and Selection</i> , 2000, 13, 857-863.	2.1	76
81	Trapping and Characterization of the Reaction Intermediate in Cyclodextrin Glycosyltransferase by Use of Activated Substrates and a Mutant Enzyme. <i>Biochemistry</i> , 1997, 36, 9927-9934.	2.5	75
82	Functional Analysis of the Copper-Dependent Quercetin 2,3-Dioxygenase. 1. Ligand-Induced Coordination Changes Probed by X-ray Crystallography: Inhibition, Ordering Effect, and Mechanistic Insights. <i>Biochemistry</i> , 2002, 41, 7955-7962.	2.5	73
83	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
84	Crystal Structures of Intermediates in the Dehalogenation of Haloalkanoates by I-2-Haloacid Dehalogenase. <i>Journal of Biological Chemistry</i> , 1999, 274, 30672-30678.	3.4	71
85	Kinetic Characterization and X-ray Structure of a Mutant of Haloalkane Dehalogenase with Higher Catalytic Activity and Modified Substrate Range. <i>Biochemistry</i> , 1996, 35, 13186-13195.	2.5	70
86	Bacterial lipases for biotechnological applications. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 1997, 3, 3-12.	1.8	70
87	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
88	Identification of the Mg ²⁺ -binding site in the P-type ATPase and phosphatase members of the HAD (haloacid dehalogenase) superfamily by structural similarity to the response regulator protein CheY. <i>Biochemical Journal</i> , 1999, 339, 223.	3.7	67
89	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
90	Mutation of Tyrosine Residues Involved in the Alkylation Half Reaction of Epoxide Hydrolase from <i>Agrobacterium radiobacter</i> AD1 Results in Improved Enantioselectivity. <i>Journal of the American Chemical Society</i> , 1999, 121, 7417-7418.	13.7	65

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91	Crystallographic Studies of the Interactions of Escherichia coli Lytic Transglycosylase Slt35 with Peptidoglycan. <i>Biochemistry</i> , 2000, 39, 1924-1934.	2.5	65
92	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
93	Directed Evolution of an Enantioselective <i>Bacillus subtilis</i> Lipase. <i>Biocatalysis and Biotransformation</i> , 2003, 21, 67-73.	2.0	64
94	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
95	Active-site structure of the soluble quinoprotein glucose dehydrogenase complexed with methylhydrazine: A covalent cofactor-inhibitor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 11787-11791.	7.1	63
96	Three-way Stabilization of the Covalent Intermediate in Amylomaltase, an α -Amylase-like Transglycosylase. <i>Journal of Biological Chemistry</i> , 2007, 282, 17242-17249.	3.4	63
97	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
98	Structural Basis of Phospholipase Activity of <i>Staphylococcus hyicus</i> lipase. <i>Journal of Molecular Biology</i> , 2007, 371, 447-456.	4.2	60
99	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
100	Kinetic Analysis and X-ray Structure of Haloalkane Dehalogenase with a Modified Halide-Binding Site. <i>Biochemistry</i> , 1998, 37, 15013-15023.	2.5	57
101	Reassessment of Acarbose as a Transition State Analogue Inhibitor of Cyclodextrin Glycosyltransferase. <i>Biochemistry</i> , 1998, 37, 17192-17198.	2.5	57
102	The role of arginine 47 in the cyclization and coupling reactions of cyclodextrin glycosyltransferase from <i>Bacillus circulans</i> strain 251. <i>FEBS Journal</i> , 2000, 267, 3432-3441.	0.2	57
103	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
104	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
105	Lipolytic enzymes LipA and LipB from <i>Bacillus subtilis</i> differ in regulation of gene expression, biochemical properties, and three-dimensional structure. <i>FEBS Letters</i> , 2001, 502, 89-92.	2.8	55
106	Improved Catalytic Properties of Halohydrin Dehalogenase by Modification of the Halide-Binding Site. <i>Biochemistry</i> , 2005, 44, 6609-6618.	2.5	53
107	Glycosidic bond specificity of glucansucrases: on the role of acceptor substrate binding residues. <i>Biocatalysis and Biotransformation</i> , 2012, 30, 366-376.	2.0	53
108	Large-Scale Recombinant Expression and Purification of Human Tyrosinase Suitable for Structural Studies. <i>PLoS ONE</i> , 2016, 11, e0161697.	2.5	51

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109	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
110	The effect of cavity-filling mutations on the thermostability of <i>Bacillus stearothermophilus</i> neutral protease. <i>Protein Engineering, Design and Selection</i> , 1992, 5, 421-426.	2.1	49
111	The structure of the <i>Escherichia coli</i> phosphotransferase II Amannitol reveals a novel fold with two conformations of the active site. <i>Structure</i> , 1998, 6, 377-388.	3.3	49
112	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
113	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
114	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
115	Mechanism-Inspired Engineering of Phenylalanine Aminomutase for Enhanced Regioselective Asymmetric Amination of Cinnamates. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 482-486.	13.8	48
116	Crystal Structure and Site-directed Mutagenesis of 3-Ketosteroid 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
117	Mutations converting cyclodextrin glycosyltransferase from a transglycosylase into a starch hydrolase. <i>FEBS Letters</i> , 2002, 514, 189-192.	2.8	47
118	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
119	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
120	Structure of the 1,6/1,4-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
121	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
122	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
123	Crystal Structure of 4,6-Glucanotransferase Supports Diet-Driven Evolution of GH70 Enzymes from 1-Amylases in Oral Bacteria. <i>Structure</i> , 2017, 25, 231-242.	3.3	45
124	Structural requirements of pyrroloquinoline quinone dependent enzymatic reactions. <i>Protein Science</i> , 2000, 9, 1265-1273.	7.6	44
125	Catalytic mechanism and product specificity of cyclodextrin glycosyltransferase, a prototypical transglycosylase from the 1-amylase family. <i>Enzyme and Microbial Technology</i> , 2002, 30, 295-304.	3.2	44
126	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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127	Biocatalytic and Structural Properties of a Highly Engineered Halohydrin Dehalogenase. <i>ChemBioChem</i> , 2013, 14, 870-881.	2.6	44
128	Crystal structure of the high-alkaline serine protease PB92 from <i>Bacillus alcalophilus</i> . <i>Protein Engineering, Design and Selection</i> , 1992, 5, 405-411.	2.1	43
129	The structure of an energy-coupling protein from bacteria, IIBcellobiose, reveals similarity to eukaryotic protein tyrosine phosphatases. <i>Structure</i> , 1997, 5, 217-225.	3.3	43
130	X-ray structure of antistasin at 1.9Å resolution and its modelled complex with blood coagulation factor Xa. <i>EMBO Journal</i> , 1997, 16, 5151-5161.	7.8	43
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