

Nushin Bh Aghajari

List of Publications by Year in descending order

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77
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2,775
citations

186265

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182427

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80
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docs citations

80
times ranked

2928
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#	ARTICLE	IF	CITATIONS
1	The <i>Candida glabrata</i> glycogen branching enzyme structure reveals unique features of branching enzymes of the <i>Saccharomycetaceae</i> phylum. <i>Glycobiology</i> , 2022, 32, 343-355.	2.5	2
2	Tertiary and Quaternary Structure Organization in GMP Synthetases: Implications for Catalysis. <i>Biomolecules</i> , 2022, 12, 871.	4.0	2
3	Exploring molecular determinants of <i>polysaccharide lyase family 6A1 enzyme</i> activity. <i>Glycobiology</i> , 2021, 31, 1557-1570.	2.5	9
4	Helices on Interdomain Interface Couple Catalysis in the ATPase Domain with Allostery in <i>Plasmodium falciparum</i> GMP Synthetase. <i>ChemBioChem</i> , 2020, 21, 2805-2817.	2.6	7
5	Structure and catalytic regulation of <i>Plasmodium falciparum</i> IMP specific nucleotidase. <i>Nature Communications</i> , 2020, 11, 3228.	12.8	4
6	Structural determinants increasing flexibility confer cold adaptation in psychrophilic phosphoglycerate kinase. <i>Extremophiles</i> , 2019, 23, 495-506.	2.3	13
7	Lead optimization and biological evaluation of fragment-based cN-II inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2019, 168, 28-44.	5.5	9
8	Structural Basis for the Acceleration of Procollagen Processing by Procollagen C-Proteinase Enhancer-1. <i>Structure</i> , 2018, 26, 1384-1392.e3.	3.3	30
9	Structural basis of homo- and heterotrimerization of collagen I. <i>Nature Communications</i> , 2017, 8, 14671.	12.8	79
10	Expanding the Kinome World: A New Protein Kinase Family Widely Conserved in Bacteria. <i>Journal of Molecular Biology</i> , 2017, 429, 3056-3074.	4.2	24
11	Mechanism of allostery and catalysis in <i>P. falciparum</i> GMP Synthetase. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C248-C248.	0.1	0
12	Diffraction anisotropy falloff in the direction of the detergent belt for two centered monoclinic crystals of OmpF. <i>Data in Brief</i> , 2016, 7, 726-729.	1.0	3
13	Two different centered monoclinic crystals of the <i>E. coli</i> outer-membrane protein OmpF originate from the same building block. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 326-332.	2.6	8
14	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
15	Identification of Noncompetitive Inhibitors of Cytosolic 5'-Nucleotidase II Using a Fragment-Based Approach. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 9680-9696.	6.4	18
16	Probing the Crucial Role of Leu31 and Thr33 of the <i>Bacillus pumilus</i> CBS Alkaline Protease in Substrate Recognition and Enzymatic Depilation of Animal Hide. <i>PLoS ONE</i> , 2014, 9, e108367.	2.5	28
17	The attractive recombinant phytase from <i>Bacillus licheniformis</i> : biochemical and molecular characterization. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5937-5947.	3.6	24
18	Fibrillar Collagen Trimerization: Structural Basis and Related Genetic Disorders. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C1052-C1052.	0.1	0

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19	Identification and characterization of inhibitors of cytoplasmic 5â€²-nucleotidase cN-II issued from virtual screening. <i>Biochemical Pharmacology</i> , 2013, 85, 497-506.	4.4	29
20	Differential properties of native and tagged or untagged recombinant glucose isomerases of <i>Streptomyces</i> sp. SK and possible implication of the glycosylation. <i>Journal of Molecular Catalysis B: Enzymatic</i> , 2013, 94, 82-87.	1.8	4
21	Identification of critical residues for the activity and thermostability of <i>Streptomyces</i> sp. SK glucose isomerase. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9715-9726.	3.6	21
22	The acid tolerant and cold-active Î²-galactosidase from <i>Lactococcus lactis</i> strain is an attractive biocatalyst for lactose hydrolysis. <i>Antonie Van Leeuwenhoek</i> , 2013, 103, 701-712.	1.7	18
23	Mutations inducing an active-site aperture in <i>Rhizobium</i> sp. sucrose isomerase confer hydrolytic activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 298-307.	2.5	11
24	Structural basis of fibrillar collagen trimerization and related genetic disorders. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1031-1036.	8.2	79
25	Production and crystallization of the C-propeptide trimer from human procollagen III. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1209-1213.	0.7	6
26	Engineered glucose isomerase from <i>Streptomyces</i> sp. SK is resistant to Ca ²⁺ inhibition and Co ²⁺ independent. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 537-546.	3.0	16
27	The overexpression of the SAPB of <i>Bacillus pumilus</i> CBS and mutated sapB-L311/T33S/N99Y alkaline proteases in <i>Bacillus subtilis</i> DB430: New attractive properties for the mutant enzyme. <i>Bioresource Technology</i> , 2012, 105, 142-151.	9.6	46
28	Abstract 3835: Identification and characterization of inhibitors of 5â€²-nucleotidase cN-II issued from virtual screening. , 2012, , .		0
29	Supramolecular stabilization of acid tolerant l-arabinose isomerase from <i>Lactobacillus sakei</i> . <i>Chemical Communications</i> , 2011, 47, 12307.	4.1	9
30	Structuring Detergents for Extracting and Stabilizing Functional Membrane Proteins. <i>PLoS ONE</i> , 2011, 6, e18036.	2.5	77
31	Enhancement of the thermostability of the maltogenic amylase MAUS149 by Gly312Ala and Lys436Arg substitutions. <i>Bioresource Technology</i> , 2011, 102, 1740-1746.	9.6	34
32	The acid-tolerant L-arabinose isomerase from the mesophilic <i>Shewanella</i> sp. ANA-3 is highly active at low temperatures. <i>Microbial Cell Factories</i> , 2011, 10, 96.	4.0	28
33	The acid tolerant l-arabinose isomerase from the food grade <i>Lactobacillus sakei</i> 23K is an attractive d-tagatose producer. <i>Bioresource Technology</i> , 2010, 101, 9171-9177.	9.6	60
34	Enhancement of the thermostability and the catalytic efficiency of <i>Bacillus pumilus</i> CBS protease by site-directed mutagenesis. <i>Biochimie</i> , 2010, 92, 360-369.	2.6	69
35	Efficient bioconversion of lactose in milk and whey: immobilization and biochemical characterization of a Î²-galactosidase from the dairy <i>Streptococcus thermophilus</i> LMD9 strain. <i>Research in Microbiology</i> , 2010, 161, 515-525.	2.1	36
36	New Insight into Structure/Function Relationships in Plant .ALPHA.-Amylase Family GH13 Members. <i>Journal of Applied Glycoscience</i> (1999), 2010, 57, 157-162.	0.7	4

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37	Structure/Function Relationships of Sucrose Isomerases with Different Product Specificity. <i>Journal of Applied Glycoscience</i> (1999), 2010, 57, 219-228.	0.7	2
38	C-terminal Residues Regulate Localization and Function of the Antiapoptotic Protein Bfl-1. <i>Journal of Biological Chemistry</i> , 2009, 284, 30257-30263.	3.4	22
39	Structural determinants of product specificity of sucrose isomerases. <i>FEBS Letters</i> , 2009, 583, 1964-1968.	2.8	22
40	Engineering of the α -amylase from <i>Geobacillus stearothermophilus</i> US100 for detergent incorporation. <i>Biotechnology and Bioengineering</i> , 2009, 102, 380-389.	3.3	51
41	Involvement of cysteine 306 and alanine 63 in the thermostability and oligomeric organization of glucose isomerase from <i>Streptomyces</i> sp. SK. <i>Biologia (Poland)</i> , 2009, 64, 845-851.	1.5	6
42	Rational design of <i>Bacillus stearothermophilus</i> US100 l-arabinose isomerase: Potential applications for d-tagatose production. <i>Biochimie</i> , 2009, 91, 650-653.	2.6	44
43	The importance of an extra loop in the B-domain of an α -amylase from <i>B. stearothermophilus</i> US100. <i>Biochemical and Biophysical Research Communications</i> , 2009, 385, 78-83.	2.1	22
44	Exploring the acidotolerance of β -galactosidase from <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> : an attractive enzyme for lactose bioconversion. <i>Research in Microbiology</i> , 2009, 160, 775-784.	2.1	23
45	An enzyme family reunion – similarities, differences and eccentricities in actions on α -glucans. <i>Biologia (Poland)</i> , 2008, 63, 967-979.	1.5	8
46	Bacterial sucrose isomerases: properties and structural studies. <i>Biologia (Poland)</i> , 2008, 63, 1020-1027.	1.5	11
47	Multi-site substrate binding and interplay in barley α -amylase 1. <i>FEBS Letters</i> , 2008, 582, 2567-2571.	2.8	18
48	Insights into sucrose isomerization from crystal structures of the <i>Pseudomonas mesoacidophila</i> MX-45 sucrose isomerase, MutB. <i>Biocatalysis and Biotransformation</i> , 2008, 26, 111-119.	2.0	5
49	Roles of multiple surface sites, long substrate binding clefts, and carbohydrate binding modules in the action of amylolytic enzymes on polysaccharide substrates. <i>Biocatalysis and Biotransformation</i> , 2008, 26, 59-67.	2.0	4
50	The linker region plays a key role in the adaptation to cold of the cellulase from an Antarctic bacterium. <i>Biochemical Journal</i> , 2007, 407, 293-302.	3.7	57
51	Probing the Essential Catalytic Residues and Substrate Affinity in the Thermoactive <i>Bacillus stearothermophilus</i> US100 l-Arabinose Isomerase by Site-Directed Mutagenesis. <i>Journal of Bacteriology</i> , 2007, 189, 3556-3563.	2.2	27
52	Trehalulose Synthase Native and Carbohydrate Complexed Structures Provide Insights into Sucrose Isomerization. <i>Journal of Biological Chemistry</i> , 2007, 282, 28126-28136.	3.4	69
53	The β -pair of sugar tongs site on the non-catalytic domain C of barley α -amylase participates in substrate binding and activity. <i>FEBS Journal</i> , 2007, 274, 5055-5067.	4.7	61
54	The ABC transporter BmrA from <i>Bacillus subtilis</i> is a functional dimer when in a detergent-solubilized state. <i>Biochemical Journal</i> , 2006, 395, 345-353.	3.7	57

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55	Overexpression, purification, crystallization and preliminary diffraction studies of the Protaminobacter rubrum sucrose isomerase SmuA. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 74-76.	0.7	20
56	Insights into Early Extracellular Matrix Evolution: Spongin Short Chain Collagen-Related Proteins Are Homologous to Basement Membrane Type IV Collagens and Form a Novel Family Widely Distributed in Invertebrates. Molecular Biology and Evolution, 2006, 23, 2288-2302.	8.9	106
57	Interactions of barley Î±-amylase isozymes with Ca ²⁺ , substrates and proteinaceous inhibitors. Biocatalysis and Biotransformation, 2006, 24, 83-93.	2.0	1
58	Expression, purification, crystallization and preliminary X-ray crystallographic studies of the trehalulose synthase MutB from Pseudomonas mesoacidophila MX-45. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 100-103.	0.7	11
59	Biased mutagenesis in the N-terminal region by degenerate oligonucleotide gene shuffling enhances secretory expression of barley Î±-amylase 2 in yeast. Protein Engineering, Design and Selection, 2005, 18, 515-526.	2.1	13
60	Oligosaccharide Binding to Barley Î±-Amylase 1. Journal of Biological Chemistry, 2005, 280, 32968-32978.	3.4	67
61	Cooperative Effect of Two Surface Amino Acid Mutations (Q252L and E170K) in Glucose Dehydrogenase from Bacillus megaterium IWG3 on Stabilization of Its Oligomeric State. Applied and Environmental Microbiology, 2005, 71, 3285-3293.	3.1	26
62	Structure of a Full Length Psychrophilic Cellulase from Pseudoalteromonas haloplanktis revealed by X-ray Diffraction and Small Angle X-ray Scattering. Journal of Molecular Biology, 2005, 348, 1211-1224.	4.2	97
63	The Structure of Barley Î±-Amylase Isozyme 1 Reveals a Novel Role of Domain C in Substrate Recognition and Binding. Structure, 2003, 11, 973-984.	3.3	142
64	Expression, purification, crystallization and preliminary X-ray crystallographic studies of a psychrophilic cellulase from Pseudoalteromonas haloplanktis. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1256-1258.	2.5	21
65	Crystal structures of a psychrophilic metalloprotease reveal new insights into catalysis by cold-adapted proteases. Proteins: Structure, Function and Bioinformatics, 2003, 50, 636-647.	2.6	106
66	X-Ray Crystal Structure of the Multidomain Endoglucanase Cel9G from Clostridium cellulolyticum Complexed with Natural and Synthetic Cello-Oligosaccharides. Journal of Bacteriology, 2003, 185, 4127-4135.	2.2	68
67	Probing the Role of Divalent Metal Ions in a Bacterial Psychrophilic Metalloprotease: Binding Studies of an Enzyme in the Crystalline State by X-Ray Crystallography. Journal of Bacteriology, 2003, 185, 4195-4203.	2.2	15
68	Crystallographic Evidence of a Transglycosylation Reaction: Ternary Complexes of a Psychrophilic Î±-Amylase. Biochemistry, 2002, 41, 4273-4280.	2.5	63
69	Expression, purification and preliminary crystallographic studies of Î±-amylase isozyme 1 from barley seeds. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 683-686.	2.5	10
70	Structural basis of Î±-amylase activation by chloride. Protein Science, 2002, 11, 1435-1441.	7.6	76
71	Specificity Modulation of Barley Î±-Amylase through Biased Random Mutagenesis Involving a Conserved Tripeptide in Î²' Loop 7 of the Catalytic (Î²/Î±)8-Barrel Domain. Biochemistry, 2001, 40, 12844-12854.	2.5	21
72	Specific inhibition of barley Î±-amylase f2 by barley Î±-amylase/subtilisin inhibitor depends on charge interactions and can be conferred to isozyme f1 by mutation. FEBS Journal, 2000, 267, 1019-1029.	0.2	37

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73	Structures of the psychrophilic <i>Alteromonas haloplanctis</i> α -amylase give insights into cold adaptation at a molecular level. <i>Structure</i> , 1998, 6, 1503-1516.	3.3	212
74	Crystal structures of the psychrophilic α -amylase from <i>Alteromonas haloplanctis</i> in its native form and complexed with an inhibitor. <i>Protein Science</i> , 1998, 7, 564-572.	7.6	170
75	A Flexible Loop at the Dimer Interface is a Part of the Active Site of the Adjacent Monomer of <i>Escherichia coli</i> Orotate Phosphoribosyltransferase. <i>Biochemistry</i> , 1996, 35, 3803-3809.	2.5	84
76	Crystallization and preliminary X-ray diffraction studies of α -amylase from the antarctic psychrophile <i>Alteromonas haloplanctis</i> A23. <i>Protein Science</i> , 1996, 5, 2128-2129.	7.6	54
77	Crystallization and Preliminary X-ray Diffraction Studies on the Apo form of Orotate Phosphoribosyltransferase from <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1994, 241, 292-294.	4.2	9