Nushin Bh Aghajari

List of Publications by Year in descending order

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		186265	182427
77	2,775	28	51
papers	citations	h-index	g-index
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80	80	80	2928
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Structures of the psychrophilic Alteromonas haloplanctis α-amylase give insights into cold adaptation at a molecular level. Structure, 1998, 6, 1503-1516.	3.3	212
2	Crystal structures of the psychrophilic αâ€amylase from Alteromonas haloplanctis in its native form and complexed with an inhibitor. Protein Science, 1998, 7, 564-572.	7.6	170
3	The Structure of Barley α-Amylase Isozyme 1 Reveals a Novel Role of Domain C in Substrate Recognition and Binding. Structure, 2003, 11, 973-984.	3.3	142
4	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
5	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
6	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
7	A Flexible Loop at the Dimer Interface is a Part of the Active Site of the Adjacent Monomer of Escherichia coli Orotate Phosphoribosyltransferase,. Biochemistry, 1996, 35, 3803-3809.	2.5	84
8	Structural basis of fibrillar collagen trimerization and related genetic disorders. Nature Structural and Molecular Biology, 2012, 19, 1031-1036.	8.2	79
9	Structural basis of homo- and heterotrimerization of collagen I. Nature Communications, 2017, 8, 14671.	12.8	79
10	Structuring Detergents for Extracting and Stabilizing Functional Membrane Proteins. PLoS ONE, 2011, 6, e18036.	2.5	77
11	Structural basis of α-amylase activation by chloride. Protein Science, 2002, 11, 1435-1441.	7.6	76
12	Trehalulose Synthase Native and Carbohydrate Complexed Structures Provide Insights into Sucrose Isomerization. Journal of Biological Chemistry, 2007, 282, 28126-28136.	3.4	69
13	Enhancement of the thermostability and the catalytic efficiency of Bacillus pumilus CBS protease by site-directed mutagenesis. Biochimie, 2010, 92, 360-369.	2.6	69
14	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
15	Oligosaccharide Binding to Barley α-Amylase 1. Journal of Biological Chemistry, 2005, 280, 32968-32978.	3.4	67
16	Crystallographic Evidence of a Transglycosylation Reaction:  Ternary Complexes of a Psychrophilic α-Amylase,. Biochemistry, 2002, 41, 4273-4280.	2.5	63
17	The â€~pair of sugar tongs' site on the nonâ€catalytic domain C of barley αâ€amylase participates in substrate binding and activity. FEBS Journal, 2007, 274, 5055-5067.	e _{4.7}	61
18	The acid tolerant l-arabinose isomerase from the food grade Lactobacillus sakei 23K is an attractive d-tagatose producer. Bioresource Technology, 2010, 101, 9171-9177.	9.6	60

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19	The ABC transporter BmrA from Bacillus subtilis is a functional dimer when in a detergent-solubilized state. Biochemical Journal, 2006, 395, 345-353.	3.7	57
20	The linker region plays a key role in the adaptation to cold of the cellulase from an Antarctic bacterium. Biochemical Journal, 2007, 407, 293-302.	3.7	57
21	Crystallization and preliminary Xâ€ray diffraction studies of αâ€amylase from the antarctic psychrophile <i>Alteromonas haloplanctis</i> A23. Protein Science, 1996, 5, 2128-2129.	7.6	54
22	Engineering of the αâ€amylase from <i>Geobacillus stearothermophilus</i> US100 for detergent incorporation. Biotechnology and Bioengineering, 2009, 102, 380-389.	3.3	51
23	The overexpression of the SAPB of Bacillus pumilus CBS and mutated sapB-L31I/T33S/N99Y alkaline proteases in Bacillus subtilis DB430: New attractive properties for the mutant enzyme. Bioresource Technology, 2012, 105, 142-151.	9.6	46
24	Rational design of Bacillus stearothermophilus US100 l-arabinose isomerase: Potential applications for d-tagatose production. Biochimie, 2009, 91, 650-653.	2.6	44
25	Specific inhibition of barley \hat{l} ±-amylase \hat{s} 62 by barley \hat{l} ±-amylase/subtilisin inhibitor depends on charge interactions and can be conferred to isozyme \hat{s} 61 by mutation. FEBS Journal, 2000, 267, 1019-1029.	0.2	37
26	Efficient bioconversion of lactose in milk and whey: immobilization and biochemical characterization of a \hat{I}^2 -galactosidase from the dairy Streptococcus thermophilus LMD9 strain. Research in Microbiology, 2010, 161, 515-525.	2.1	36
27	Enhancement of the thermostability of the maltogenic amylase MAUS149 by Gly312Ala and Lys436Arg substitutions. Bioresource Technology, 2011, 102, 1740-1746.	9.6	34
28	Structural Basis for the Acceleration of Procollagen Processing by Procollagen C-Proteinase Enhancer-1. Structure, 2018, 26, 1384-1392.e3.	3.3	30
29	Identification and characterization of inhibitors of cytoplasmic 5′-nucleotidase cN-II issued from virtual screening. Biochemical Pharmacology, 2013, 85, 497-506.	4.4	29
30	The acid-tolerant L-arabinose isomerase from the mesophilic Shewanella sp. ANA-3 is highly active at low temperatures. Microbial Cell Factories, 2011, 10, 96.	4.0	28
31	Probing the Crucial Role of Leu31 and Thr33 of the Bacillus pumilus CBS Alkaline Protease in Substrate Recognition and Enzymatic Depilation of Animal Hide. PLoS ONE, 2014, 9, e108367.	2.5	28
32	Probing the Essential Catalytic Residues and Substrate Affinity in the Thermoactive Bacillus stearothermophilus US100 l -Arabinose Isomerase by Site-Directed Mutagenesis. Journal of Bacteriology, 2007, 189, 3556-3563.	2.2	27
33	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
34	The attractive recombinant phytase from Bacillus licheniformis: biochemical and molecular characterization. Applied Microbiology and Biotechnology, 2014, 98, 5937-5947.	3.6	24
35	Active site coupling in Plasmodium falciparum GMP synthetase is triggered by domain rotation. Nature Communications, 2015, 6, 8930.	12.8	24
36	Expanding the Kinome World: A New Protein Kinase Family Widely Conserved in Bacteria. Journal of Molecular Biology, 2017, 429, 3056-3074.	4.2	24

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37	Exploring the acidotolerance of \hat{l}^2 -galactosidase from Lactobacillus delbrueckii subsp. bulgaricus: an attractive enzyme for lactose bioconversion. Research in Microbiology, 2009, 160, 775-784.	2.1	23
38	C-terminal Residues Regulate Localization and Function of the Antiapoptotic Protein Bfl-1. Journal of Biological Chemistry, 2009, 284, 30257-30263.	3 . 4	22
39	Structural determinants of product specificity of sucrose isomerases. FEBS Letters, 2009, 583, 1964-1968.	2.8	22
40	The importance of an extra loop in the B-domain of an α-amylase from B. stearothermophilus US100. Biochemical and Biophysical Research Communications, 2009, 385, 78-83.	2.1	22
41	Specificity Modulation of Barley α-Amylase through Biased Random Mutagenesis Involving a Conserved Tripeptide in β → α Loop 7 of the Catalytic (β/α)8-Barrel Domainâ€. Biochemistry, 2001, 40, 12844-12854.	2.5	21
42	Expression, purification, crystallization and preliminary X-ray crystallographic studies of a psychrophilic cellulase fromPseudoalteromonas haloplanktis. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1256-1258.	2.5	21
43	Identification of critical residues for the activity and thermostability of Streptomyces sp. SK glucose isomerase. Applied Microbiology and Biotechnology, 2013, 97, 9715-9726.	3.6	21
44	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
45	Multiâ€site substrate binding and interplay in barley αâ€amylase 1. FEBS Letters, 2008, 582, 2567-2571.	2.8	18
46	The acid tolerant and cold-active \hat{l}^2 -galactosidase from Lactococcus lactis strain is an attractive biocatalyst for lactose hydrolysis. Antonie Van Leeuwenhoek, 2013, 103, 701-712.	1.7	18
47	Identification of Noncompetitive Inhibitors of Cytosolic 5′-Nucleotidase II Using a Fragment-Based Approach. Journal of Medicinal Chemistry, 2015, 58, 9680-9696.	6.4	18
48	Engineered glucose isomerase from Streptomyces sp. SK is resistant to Ca2+ inhibition and Co2+ independent. Journal of Industrial Microbiology and Biotechnology, 2012, 39, 537-546.	3.0	16
49	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
50	Biased mutagenesis in the N-terminal region by degenerate oligonucleotide gene shuffling enhances secretory expression of barley α-amylase 2 in yeast. Protein Engineering, Design and Selection, 2005, 18, 515-526.	2.1	13
51	Structural determinants increasing flexibility confer cold adaptation in psychrophilic phosphoglycerate kinase. Extremophiles, 2019, 23, 495-506.	2.3	13
52	Expression, purification, crystallization and preliminary X-ray crystallographic studies of the trehalulose synthase MutB fromPseudomonas mesoacidophilaMX-45. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 100-103.	0.7	11
53	Bacterial sucrose isomerases: properties and structural studies. Biologia (Poland), 2008, 63, 1020-1027.	1.5	11
54	Mutations inducing an active-site aperture inRhizobiumsp. sucrose isomerase confer hydrolytic activity. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 298-307.	2.5	11

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55	Expression, purification and preliminary crystallographic studies of α-amylase isozyme 1 from barley seeds. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 683-686.	2.5	10
56	Crystallization and Preliminary X-ray Diffraction Studies on the Apo form of Orotate Phosphoribosyltransferase from Escherichia coli. Journal of Molecular Biology, 1994, 241, 292-294.	4.2	9
57	Supramolecular stabilization of acid tolerant l-arabinose isomerase from Lactobacillus sakei. Chemical Communications, 2011, 47, 12307.	4.1	9
58	Lead optimization and biological evaluation of fragment-based cN-II inhibitors. European Journal of Medicinal Chemistry, 2019, 168, 28-44.	5.5	9
59	Exploring molecular determinants of <i>polysaccharide lyase family 6–1 enzyme</i> activity. Glycobiology, 2021, 31, 1557-1570.	2.5	9
60	An enzyme family reunion — similarities, differences and eccentricities in actions on α-glucans. Biologia (Poland), 2008, 63, 967-979.	1.5	8
61	Two different centered monoclinic crystals of the E. coli outer-membrane protein OmpF originate from the same building block. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 326-332.	2.6	8
62	Helices on Interdomain Interface Couple Catalysis in the ATPPase Domain with Allostery in <i>Plasmodium falciparum </i> GMP Synthetase. ChemBioChem, 2020, 21, 2805-2817.	2.6	7
63	Involvement of cysteine 306 and alanine 63 in the thermostability and oligomeric organization of glucose isomerase from Streptomyces sp. SK. Biologia (Poland), 2009, 64, 845-851.	1.5	6
64	Production and crystallization of the C-propeptide trimer from human procollagen III. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1209-1213.	0.7	6
65	Insights into sucrose isomerization from crystal structures of thePseudomonas mesoacidophilaMX-45 sucrose isomerase, MutB. Biocatalysis and Biotransformation, 2008, 26, 111-119.	2.0	5
66	Roles of multiple surface sites, long substrate binding clefts, and carbohydrate binding modules in the action of amylolytic enzymes on polysaccharide substrates. Biocatalysis and Biotransformation, 2008, 26, 59-67.	2.0	4
67	Differential properties of native and tagged or untagged recombinant glucose isomerases of Streptomyces sp. SK and possible implication of the glycosylation. Journal of Molecular Catalysis B: Enzymatic, 2013, 94, 82-87.	1.8	4
68	Structure and catalytic regulation of Plasmodium falciparum IMP specific nucleotidase. Nature Communications, 2020, 11, 3228.	12.8	4
69	New Insight into Structure/Function Relationships in Plant .ALPHAAmylase Family GH13 Members. Journal of Applied Glycoscience (1999), 2010, 57, 157-162.	0.7	4
70	Diffraction anisotropy falloff in the direction of the detergent belt for two centered monoclinic crystals of OmpF. Data in Brief, 2016, 7, 726-729.	1.0	3
71	Structure/Function Relationships of Sucrose Isomerases with Different Product Specificity. Journal of Applied Glycoscience (1999), 2010, 57, 219-228.	0.7	2
72	The <i>Candida glabrata </i> glycogen branching enzyme structure reveals unique features of branching enzymes of the <i>Saccharomycetaceae </i> phylum. Glycobiology, 2022, 32, 343-355.	2.5	2

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73	Tertiary and Quaternary Structure Organization in GMP Synthetases: Implications for Catalysis. Biomolecules, 2022, 12, 871.	4.0	2
74	Interactions of barley α-amylase isozymes with Ca2 + , substrates and proteinaceous inhibitors. Biocatalysis and Biotransformation, 2006, 24, 83-93.	2.0	1
75	Mechanism of allostery and catalysis in P. falciparum GMP Synthetase. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C248-C248.	0.1	0
76	Abstract 3835: Identification and characterization of inhibitors of $5\hat{a} \in ^2$ -nucleotidase cN-II issued from virtual screening., 2012, , .		0
77	Fibrillar Collagen Trimerization: Structural Basis and Related Genetic Disorders. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C1052-C1052.	0.1	O