Akira Nakamura

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1077129/publications.pdf

Version: 2024-02-01

87 papers	2,106 citations	27 h-index	276775 41 g-index
88	88	88	2353
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Highlighting the potential utility of MBP crystallization chaperone for Arabidopsis BIL1/BZR1 transcription factor-DNA complex. Scientific Reports, 2021, 11, 3879.	1.6	5
2	Complete Genome Sequence of <i>Kaistia</i> sp. Strain 32K, Isolated from Soil as a Mixed Single Colony with <i>Methylobacterium</i> sp. Strain ME121. Microbiology Resource Announcements, 2021, 10, .	0.3	1
3	Identification of novel interacting regions involving calcineurin and nuclear factor of activated T cells. FASEB Journal, 2020, 34, 3197-3208.	0.2	5
4	Single amino acid mutation altered substrate specificity for <scp>l</scp> -glucose and inositol in <i>scyllo</i> -inositol dehydrogenase isolated from <i>Paracoccus laeviglucosivorans</i> . Bioscience, Biotechnology and Biochemistry, 2020, 84, 734-742.	0.6	1
5	Metabolites Produced by Kaistia sp. 32K Promote Biofilm Formation in Coculture with Methylobacterium sp. ME121. Biology, 2020, 9, 287.	1.3	1
6	A Factor Produced by Kaistia sp. 32K Accelerated the Motility of Methylobacterium sp. ME121. Biomolecules, 2020, 10, 618.	1.8	4
7	Structural basis for the substrate recognition of aminoglycoside 7′′-phosphotransferase-la from <i>Streptomyces hygroscopicus</i> . Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 599-607.	0.4	3
8	Crystal structure of a Ca2+-dependent regulator of flagellar motility reveals the open-closed structural transition. Scientific Reports, 2018, 8, 2014.	1.6	7
9	Structural basis for controlling the enzymatic properties of polymannuronate preferred alginate lyase FlAlyA from the PL-7 family. Chemical Communications, 2018, 54, 555-558.	2.2	49
10	Structural analysis of HTL and D14 proteins reveals the basis for ligand selectivity in Striga. Nature Communications, 2018, 9, 3947.	5 . 8	73
11	Structural basis for brassinosteroid response by BIL1/BZR1. Nature Plants, 2018, 4, 771-776.	4.7	33
12	Structural basis of L-glucose oxidation by scyllo-inositol dehydrogenase: Implications for a novel enzyme subfamily classification. PLoS ONE, 2018, 13, e0198010.	1.1	10
13	Structure and Polymannuronate Specificity of a Eukaryotic Member of Polysaccharide Lyase Family 14. Journal of Biological Chemistry, 2017, 292, 2182-2190.	1.6	24
14	Engineering a short-chain dehydrogenase/reductase for the stereoselective production of (2S,3R,4S)-4-hydroxyisoleucine with three asymmetric centers. Scientific Reports, 2017, 7, 13703.	1.6	11
15	Studies on the regulatory mechanism of isocitrate dehydrogenase 2 using acetylation mimics. Scientific Reports, 2017, 7, 9785.	1.6	26
16	Laminarinase from Flavobacterium sp. reveals the structural basis of thermostability and substrate specificity. Scientific Reports, 2017, 7, 11425.	1.6	22
17	Structural basis of unique ligand specificity of KAI2-like protein from parasitic weed Striga hermonthica. Scientific Reports, 2016, 6, 31386.	1.6	47
18	In-situ and real-time growth observation of high-quality protein crystals under quasi-microgravity on earth. Scientific Reports, 2016, 6, 22127.	1.6	8

#	Article	IF	CITATIONS
19	Draft Genome Sequence of Methylobacterium sp. ME121, Isolated from Soil as a Mixed Single Colony with Kaistia sp. 32K. Genome Announcements, 2015, 3, .	0.8	3
20	Yam Tuber Storage Protein Reduces Plant Oxidants Using the Coupled Reactions as Carbonic Anhydrase and Dehydroascorbate Reductase. Molecular Plant, 2015, 8, 1115-1118.	3.9	16
21	Paracoccus laeviglucosivorans sp. nov., an l-glucose-utilizing bacterium isolated from soil. International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 3878-3884.	0.8	21
22	Brevibacillus fulvus sp. nov., isolated from a compost pile. International Journal of Systematic and Evolutionary Microbiology, 2014, 64, 506-512.	0.8	15
23	Structural optimization of SadA, an Fe(II)- and \hat{l}_{\pm} -ketoglutarate-dependent dioxygenase targeting biocatalytic synthesis of N-succinyl-l-threo-3,4-dimethoxyphenylserine. Biochemical and Biophysical Research Communications, 2014, 450, 1458-1461.	1.0	15
24	Nitrite formation from organic nitrogen by <i>Streptomyces antibioticus</i> supporting bacterial cell growth and possible involvement of nitric oxide as an intermediate. Bioscience, Biotechnology and Biochemistry, 2014, 78, 1592-1602.	0.6	5
25	Characterization of LgnR, an IclR family transcriptional regulator involved in the regulation of l-gluconate catabolic genes in Paracoccus sp. 43P. Microbiology (United Kingdom), 2014, 160, 623-634.	0.7	8
26	Crystal structures of the ternary complex of APH(4)-la/Hph with hygromycin B and an ATP analog using a thermostable mutant. Journal of Structural Biology, 2013, 183, 76-85.	1.3	13
27	Structure Analysis of Archaeal AMP Phosphorylase Reveals Two Unique Modes of Dimerization. Journal of Molecular Biology, 2013, 425, 2709-2721.	2.0	9
28	Directed Evolution for Thermostabilization of a Hygromycin B Phosphotransferase from <i>Streptomyces hygroscopicus </i> . Bioscience, Biotechnology and Biochemistry, 2013, 77, 2234-2241.	0.6	10
29	Crystal Structure of a Novel N-Substituted L-Amino Acid Dioxygenase from Burkholderia ambifaria AMMD. PLoS ONE, 2013, 8, e63996.	1.1	19
30	Dynamic, Ligand-dependent Conformational Change Triggers Reaction of Ribose-1,5-bisphosphate Isomerase from Thermococcus kodakarensis KOD1. Journal of Biological Chemistry, 2012, 287, 20784-20796.	1.6	22
31	An l-glucose Catabolic Pathway in Paracoccus Species 43P. Journal of Biological Chemistry, 2012, 287, 40448-40456.	1.6	37
32	Expression, purification, crystallization and preliminary X-ray analysis of a novel N-substituted branched-chainL-amino-acid dioxygenase fromBurkholderia ambifariaAMMD. Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 1067-1069.	0.7	2
33	Improvement in Quality of Protein Crystals Grown in a High Magnetic Field Gradient. Crystal Growth and Design, 2012, 12, 1141-1150.	1.4	33
34	Crystal Structure of a Thermophilic GrpE Protein: Insight into Thermosensing Function for the DnaK Chaperone System. Journal of Molecular Biology, 2010, 396, 1000-1011.	2.0	21
35	Characterization of three putative Lon proteases of Thermus thermophilus HB27 and use of their defective mutants as hosts for production of heterologous proteins. Extremophiles, 2008, 12, 285-296.	0.9	14
36	Enzymatic Analysis of a Thermostabilized Mutant of an <i>Escherichia coli</i> Hygromycin B Phosphotransferase. Bioscience, Biotechnology and Biochemistry, 2008, 72, 2467-2471.	0.6	10

3

#	Article	IF	CITATIONS
37	ãf—ãf ©ã,¹ãfŸãf‰DNAã®è‡è£½é−‹å§‹åå¿æã,'制御ã™ã,‹ãf¡ã,«ãf‹ã,ºãf. Kagaku To Seibutsu, 2008, 46, 38	30-3 85 0	O
38	Anaerobic Elemental Sulfur Reduction by Fungus (i>Fusarium oxysporum (i>. Bioscience, Biotechnology and Biochemistry, 2007, 71, 2402-2407.	0.6	26
39	Structural basis for regulation of bifunctional roles in replication initiator protein. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18484-18489.	3.3	34
40	Correlation between cellulose binding and activity of celluloseâ€binding domain mutants of ⟨i⟩Humicola grisea⟨ i⟩ cellobiohydrolase 1. FEBS Letters, 2007, 581, 5891-5896.	1.3	42
41	Expression and purification of F-plasmid RepE and preliminary X-ray crystallographic study of its complex with operator DNA. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 346-349.	0.7	9
42	Crystallization and preliminary crystallographic analysis of hygromycin B phosphotransferase from Escherichia coli. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 685-688.	0.7	2
43	Crystal structure of TTHA1657 (AT-rich DNA-binding protein; p25) from Thermus thermophilus HB8 at 2.16 Ã resolution. Proteins: Structure, Function and Bioinformatics, 2006, 66, 755-759.	1.5	16
44	Regulation of cyclodextrin glucanotransferase synthesis in Bacillus ohbensis. FEMS Microbiology Letters, 2006, 149, 221-226.	0.7	11
45	Tuberibacillus calidus gen. nov., sp. nov., isolated from a compost pile and reclassification of Bacillus naganoensis Tomimura et al. 1990 as Pullulanibacillus naganoensis gen. nov., comb. nov. and Bacillus laevolacticus Andersch et al. 1994 as Sporolactobacillus laevolacticus comb. nov International lournal of Systematic and Evolutionary Microbiology. 2006. 56. 2545-2551.	0.8	76
46	Isolation of a low-molecular-weight, multicopy plasmid, pNHK101, from Thermus sp. TK10 and its use as an expression vector for T. thermophilus HB27. Plasmid, 2005, 54, 70-79.	0.4	12
47	In vivo directed evolution for thermostabilization of Escherichia coli hygromycin B phosphotransferase and the use of the gene as a selection marker in the host-vector system of Thermus thermophilus. Journal of Bioscience and Bioengineering, 2005, 100, 158-163.	1.1	61
48	Pseudomonas azotifigens sp. nov., a novel nitrogen-fixing bacterium isolated from a compost pile. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 1539-1544.	0.8	61
49	Planifilum fimeticola gen. nov., sp. nov. and Planifilum fulgidum sp. nov., novel members of the family â€Thermoactinomycetaceae' isolated from compost. International Journal of Systematic and Evolutionary Microbiology, 2005, 55, 2101-2104.	0.8	68
50	Isolation of Flavohemoglobin from the ActinomyceteStreptomyces antibioticusGrown without External Nitric Oxide Stress. Bioscience, Biotechnology and Biochemistry, 2004, 68, 1106-1112.	0.6	9
51	Functional analysis of the small subunit of the putative homoaconitase fromPyrococcus horikoshiiin theThermuslysine biosynthetic pathway. FEMS Microbiology Letters, 2004, 233, 315-324.	0.7	19
52	Nucleotide sequence of the cryptic plasmid pTT8 from Thermus thermophilus HB8 and isolation and characterization of its high-copy-number mutant. Plasmid, 2004, 51, 227-237.	0.4	18
53	Unusual Transcription Regulation of theniaDGene under Anaerobic Conditions Supporting Fungal Ammonia Fermentation. Bioscience, Biotechnology and Biochemistry, 2004, 68, 978-980.	0.6	16
54	Fungal Ammonia Fermentation, a Novel Metabolic Mechanism That Couples the Dissimilatory and Assimilatory Pathways of Both Nitrate and Ethanol. Journal of Biological Chemistry, 2004, 279, 12414-12420.	1.6	84

#	Article	IF	Citations
55	The N-terminal domain of the replication initiator protein RepE is a dimerization domain forming a stable dimer. Biochemical and Biophysical Research Communications, 2004, 315, 10-15.	1.0	6
56	Functional analysis of the small subunit of the putative homoaconitase from Pyrococcus horikoshii in the Thermus lysine biosynthetic pathway. FEMS Microbiology Letters, 2004, 233, 315-324.	0.7	13
57	A Possible Role of NADPH-Dependent Cytochrome P450nor Isozyme in Glycolysis under Denitrifying Conditions. Bioscience, Biotechnology and Biochemistry, 2003, 67, 1109-1114.	0.6	10
58	Formate-forming Fungal Catabolic Pathway to Supply Electrons to Nitrate Respiration. Bioscience, Biotechnology and Biochemistry, 2003, 67, 937-939.	0.6	12
59	Denitrification of Nitrate by the FungusCylindrocarpon tonkinense. Bioscience, Biotechnology and Biochemistry, 2003, 67, 1115-1120.	0.6	34
60	Ammonia Fermentation, a Novel Anoxic Metabolism of Nitrate by Fungi. Journal of Biological Chemistry, 2002, 277, 1892-1896.	1.6	132
61	Comparison of gene structures and enzymatic properties between two endoglucanases from Humicola grisea. Journal of Biotechnology, 1999, 67, 85-97.	1.9	37
62	Overproduction of recombinant Trichoderma reesei cellulases by Aspergillus oryzae and their enzymatic properties. Journal of Biotechnology, 1998, 65, 163-171.	1.9	54
63	Isolation of the Gene and Characterization of the Enzymatic Properties of a Major Exoglucanase of Humicola grisea without a Cellulose-Binding Domain. Journal of Biochemistry, 1998, 124, 717-725.	0.9	25
64	Overproduction of .ALPHAglucosidase in Aspergillus niger transformed with the cloned gene aglA Journal of General and Applied Microbiology, 1998, 44, 177-181.	0.4	11
65	Cloning, Sequencing, and Expression of a Thermostable Cellulase Gene of <i>Humicola grisea </i> Bioscience, Biotechnology and Biochemistry, 1997, 61, 245-250.	0.6	19
66	Cloning of a Gene Encoding a Putative Xylanase with a Cellulose-Binding Domain from <i>Humicola grisea < /i>. Bioscience, Biotechnology and Biochemistry, 1997, 61, 1593-1595.</i>	0.6	6
67	Cloning and sequencing of an \hat{I}_{\pm} -glucosidase gene from Aspergillus niger and its expression in A. nidulans. Journal of Biotechnology, 1997, 53, 75-84.	1.9	54
68	Cloning, sequencing, and expression of the cellulase genes of Humicola grisea var. thermoidea. Journal of Biotechnology, 1996, 50, 137-147.	1.9	43
69	Enhanced expression of crylA(a) gene of Bacillus thuringiensis in Escherichia coli. Journal of Bioscience and Bioengineering, 1996, 82, 306-308.	0.9	1
70	Isolation and characterization of the nuclease O gene (nucO) from Aspergillus oryzae. Current Genetics, 1996, 30, 312-317.	0.8	4
71	Analysis of Cre1 binding sites in theTrichoderma reesei cbh1upstream region. FEMS Microbiology Letters, 1996, 145, 361-366.	0.7	70
72	Cloning of a Gene Encoding a Putative Carbon Catabolite Repressor from Trichoderma reesei. Bioscience, Biotechnology and Biochemistry, 1996, 60, 173-176.	0.6	32

#	Article	IF	CITATIONS
73	Purification and Characterization of Cellulases from <i>Humicola grisea </i> Bioscience, Biotechnology and Biochemistry, 1996, 60, 77-82.	0.6	29
74	Analysis of Cre1 binding sites in the Trichoderma reesei cbh1 upstream region. FEMS Microbiology Letters, 1996, 145, 361-366.	0.7	3
75	Composition and location of crylA genes in Bacillus thuringiensis strain FU-2-7 Journal of General and Applied Microbiology, 1996, 42, 337-341.	0.4	0
76	Cloning of a New <i>crylA</i> (<i>a</i>) Gene from <i>Bacillus thuringiensis</i> Strain FU-2-7 and Analysis of Chimaeric CrylA(a) Proteins for Toxicity. Bioscience, Biotechnology and Biochemistry, 1994, 58, 830-835.	0.6	25
77	Hall effect of metallic Langmuir–Blodgett films based on bisethylenedioxytetrathiafulvalene complex of decyltetracyanoquinodimethane. Applied Physics Letters, 1994, 64, 2602-2604.	1.5	7
78	Replacement of an amino acid residue of cyclodextrin glucanotransferase of Bacillus ohbensis doubles the production of \hat{l}^3 -cyclodextrin. Journal of Biotechnology, 1994, 32, 283-288.	1.9	46
79	Four Aromatic Residues in the Active Center of Cyclodextrin Glucanotransferase from Alkalophilic Bacillus sp. 1011: Effects of Replacements on Substrate Binding and Cyclization Characteristics. Biochemistry, 1994, 33, 9929-9936.	1.2	78
80	Extracellular Production of <i>Bacillus ohbensis </i> Cyclodextrin Glucanotransferase by <ib. <="" i="" subtilis=""> Bioscience, Biotechnology and Biochemistry, 1993, 57, 346-347.</ib.>	0.6	10
81	Identification of the Cellulose-Binding Domain of aBacillus subtilisEndoglucanase Distinct from Its Catalytic Domain. Bioscience, Biotechnology and Biochemistry, 1993, 57, 260-264.	0.6	8
82	Gene cloning and characterization of a novel extracellular ribonuclease of Bacillus subtilis. FEBS Journal, 1992, 209, 121-127.	0.2	24
83	Use of a Triple Protease-deficient Mutant ofBacillus subtilisas a Host for Secretion of aB. subtilisCellulase and TEMβ-Laetamase. Agricultural and Biological Chemistry, 1991, 55, 2367-2374.	0.3	0
84	Cloning and sequencing of a cyclodextrin glucanotransferase gene from Bacillus ohbensis and its expression in Escherichia coli. Applied Microbiology and Biotechnology, 1991, 35, 600-5.	1.7	47
85	Construction and characterization of multicopy expression-vectors in Streptomyces spp. Molecular Genetics and Genomics, 1987, 210, 468-475.	2.4	18
86	Nucleotide sequence of a cellulase gene of Bacillus subtilis. FEBS Journal, 1987, 164, 317-320.	0.2	53
87	Molecular cloning of a cellulase gene from Bacillus subtilis and its expression in Escherichia coli Agricultural and Biological Chemistry, 1986, 50, 233-237.	0.3	28