

Yoshiaki Yasutake

List of Publications by Year in descending order

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48
papers

909
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471509

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h-index

477307

29
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48
all docs

48
docs citations

48
times ranked

1300
citing authors

#	ARTICLE	IF	CITATIONS
1	How Oligomerization Contributes to the Thermostability of an Archaeon Protein. <i>Journal of Biological Chemistry</i> , 2004, 279, 32957-32967.	3.4	78
2	Structure of the type II-asparaginase from the hyperthermophilic archaeon <i>Pyrococcus horikoshii</i> at 2.16 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 294-301.	2.5	63
3	Crystal Structure of the <i>Pyrococcus horikoshii</i> Isopropylmalate Isomerase Small Subunit Provides Insight into the Dual Substrate Specificity of the Enzyme. <i>Journal of Molecular Biology</i> , 2004, 344, 325-333.	4.2	52
4	Structure of the Monomeric Isocitrate Dehydrogenase. <i>Structure</i> , 2002, 10, 1637-1648.	3.3	48
5	Structural characterization of the <i>Acetobacter xylinum</i> endo-1,4-glucanase CMCax required for cellulose biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 1069-1077.	2.6	47
6	Elucidation of stability determinants of cold-adapted monomeric isocitrate dehydrogenase from a psychrophilic bacterium, <i>Colwellia maris</i> , by construction of chimeric enzymes. <i>Microbiology (United Kingdom)</i> , 2008, 152, 1087-1094.	1.8	10
7	Structural implications for heavy metal-induced reversible assembly and aggregation of a protein: the case of <i>Pyrococcus horikoshii</i> CutA1. <i>FEBS Letters</i> , 2004, 556, 167-174.	2.8	43
8	Crystal Structure of the Monomeric Isocitrate Dehydrogenase in the Presence of NADP ⁺ . <i>Journal of Biological Chemistry</i> , 2003, 278, 36897-36904.	3.4	41
9	Structural Evidence for Enhancement of Sequential Vitamin D3 Hydroxylation Activities by Directed Evolution of Cytochrome P450 Vitamin D3 Hydroxylase. <i>Journal of Biological Chemistry</i> , 2010, 285, 31193-31201.	3.4	40
10	A Single Mutation at the Ferredoxin Binding Site of P450 Vdh Enables Efficient Biocatalytic Production of 25-Hydroxyvitamin D ₃ . <i>ChemBioChem</i> , 2013, 14, 2284-2291.	2.6	40
11	Structure-guided mutagenesis for the improvement of substrate specificity of <i>Bacillus megaterium</i> glucose dehydrogenase IV. <i>FEBS Journal</i> , 2012, 279, 3264-3275.	4.7	36
12	Mutational robustness of 16S ribosomal RNA, shown by experimental horizontal gene transfer in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19220-19225.	7.1	35
13	Crystal structure of cytochrome P450 MoxA from <i>Nonomuraea recticatena</i> (CYP105). <i>Biochemical and Biophysical Research Communications</i> , 2007, 361, 876-882.	2.1	33
14	Cloning and Heterologous Expression of the Aurachin RE Biosynthesis Gene Cluster Afford a New Cytochrome P450 for Quinoline Hydroxylation. <i>ChemBioChem</i> , 2013, 14, 1085-1093.	2.6	28
15	Anodized gold surface enables mediator-free and low-overpotential electrochemical oxidation of NADH: A facile method for the development of an NAD ⁺ -dependent enzyme biosensor. <i>Sensors and Actuators B: Chemical</i> , 2019, 288, 512-518.	7.8	22
16	Crystal structure analysis reveals a novel forkhead-associated domain of ESAT6 secretion system C protein in <i>Staphylococcus aureus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 659-664.	2.6	19
17	Structural evidence for guanidine-protein side chain interactions: crystal structure of CutA from <i>Pyrococcus horikoshii</i> in 3M guanidine hydrochloride. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 185-191.	2.1	18
18	Structural Insights into Unique Substrate Selectivity of <i>Thermoplasma acidophilum</i> d-Aldohexose Dehydrogenase. <i>Journal of Molecular Biology</i> , 2007, 367, 1034-1046.	4.2	18

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19	Bifunctional quorum-quenching and antibiotic-acylase MacQ forms a 170-kDa capsule-shaped molecule containing spacer polypeptides. <i>Scientific Reports</i> , 2017, 7, 8946.	3.3	16
20	Developing a codon optimization method for improved expression of recombinant proteins in actinobacteria. <i>Scientific Reports</i> , 2019, 9, 8338.	3.3	16
21	HIV-1 with HBV-associated Q151M substitution in RT becomes highly susceptible to entecavir: structural insights into HBV-RT inhibition by entecavir. <i>Scientific Reports</i> , 2018, 8, 1624.	3.3	15
22	Structural features in common of HBV and HIV-1 resistance against chirally-distinct nucleoside analogues entecavir and lamivudine. <i>Scientific Reports</i> , 2020, 10, 3021.	3.3	15
23	Structure of the quinoline N-hydroxylating cytochrome P450 RauA, an essential enzyme that confers antibiotic activity on aurachin alkaloids. <i>FEBS Letters</i> , 2014, 588, 105-110.	2.8	14
24	Structural insights into the mechanism of the drastic changes in enzymatic activity of the cytochrome P450 vitamin D ₃ hydroxylase (CYP107BR1) caused by a mutation distant from the active site. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 266-275.	0.8	12
25	Crystallization and preliminary X-ray diffraction studies of vitamin D ₃ hydroxylase, a novel cytochrome P450 isolated from <i>Pseudonocardia autotrophica</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 372-375.	0.7	11
26	Molecular properties of two proteins homologous to PduO-type ATP:cob(I)alamin adenosyltransferase from <i>Sulfolobus tokodaii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 446-457.	2.6	10
27	Total synthesis of aurachins C, D, and L, and a structurally simplified analog of aurachin C. <i>Bioscience, Biotechnology and Biochemistry</i> , 2014, 78, 1324-1327.	1.3	10
28	Flash-cooling of macromolecular crystals in a capillary to overcome increased mosaicity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 39-45.	2.5	8
29	Structure of the HIV-1 reverse transcriptase Q151M mutant: insights into the inhibitor resistance of HIV-1 reverse transcriptase and the structure of the nucleotide-binding pocket of <i>Hepatitis B virus</i> polymerase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1384-1390.	0.8	8
30	Active-site deformation in the structure of HIV-1 RT with HBV-associated septuple amino acid substitutions rationalizes the differential susceptibility of HIV-1 and HBV against 4 ^E -modified nucleoside RT inhibitors. <i>Biochemical and Biophysical Research Communications</i> , 2019, 509, 943-948.	2.1	8
31	Bacterial triacylglycerol lipase is a potential cholesterol esterase: Identification of a key determinant for sterol-binding specificity. <i>International Journal of Biological Macromolecules</i> , 2021, 167, 578-586.	7.5	8
32	Structural insights into the substrate stereospecificity of d-threo-3-hydroxyaspartate dehydratase from <i>Delftia</i> sp. HT23: a useful enzyme for the synthesis of optically pure l-threo- and d-erythro-3-hydroxyaspartate. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 7137-7150.	3.6	7
33	Crystallization and preliminary X-ray diffraction studies of monomeric isocitrate dehydrogenase by the MAD method using Mn atoms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1682-1685.	2.5	5
34	Crystallization and preliminary crystallographic analysis of the cellulose biosynthesis-related protein CMCax from <i>Acetobacter xylinum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 252-254.	0.7	5
35	Structures of <i>Burkholderia thailandensis</i> nucleoside kinase: implications for the catalytic mechanism and nucleoside selectivity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 945-956.	2.5	5
36	Production of recombinant extracellular cholesterol esterase using consistently active promoters in <i>Burkholderia stabilis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1974-1984.	1.3	5

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37	Câ€œterminal tail derived from the neighboring subunit is critical for the activity of <i>Thermoplasma acidophilum</i>â€™aldohexose dehydrogenase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 74, 801-807.	2.6	4
38	Electrochemically boosted cytochrome P450 reaction that efficiently produces 25-hydroxyvitamin D3. <i>Journal of Catalysis</i> , 2020, 384, 30-36.	6.2	4
39	Scaffold size-dependent effect on the enhanced uptake of antibiotics and other compounds by <i>Escherichia coli</i> and <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2022, 12, 5609.	3.3	4
40	Biochemical and Structural Properties of Entecavir-Resistant Hepatitis B Virus Polymerase with L180M/M204V Mutations. <i>Journal of Virology</i> , 2021, 95, e0240120.	3.4	3
41	Crystal structure of the hypothetical protein ST2072 from <i>Sulfolobus tokodaii</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 1127-1131.	2.6	2
42	Complete Genome Sequence of an Efficient Vitamin D 3 -Hydroxylating Bacterium, <i>Pseudonocardia autotrophica</i> NBRC 12743. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	2
43	Nrp1 is Activated by Konjac Ceramide Binding-Induced Structural Rigidification of the a1a2 Domain. <i>Cells</i> , 2020, 9, 517.	4.1	2
44	Crystallization and preliminary crystallographic analysis of NAD ⁺ -preferring aldohexose dehydrogenase from the thermoacidophilic archaeon <i>Thermoplasma acidophilum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 586-589.	0.7	1
45	Properties of emu (<i>Dromaius novaehollandiae</i>) albumen proteins. <i>Food Research International</i> , 2012, 49, 567-571.	6.2	1
46	Efficient production of active form of vitamin D3 by microbial conversion. <i>Synthesiology</i> , 2012, 4, 227-235.	0.2	1
47	Crystallization and preliminary X-ray diffraction studies of D-threo-3-hydroxyaspartate dehydratase isolated from <i>Delftia</i> sp. HT23. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1131-1134.	0.7	1
48	Efficient production of active form of vitamin D3 by microbial conversion. <i>Synthesiology</i> , 2011, 4, 222-229.	0.2	1