

Katsuhide Yutani

List of Publications by Year in descending order

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25
papers

870
citations

687363

13
h-index

580821

25
g-index

25
all docs

25
docs citations

25
times ranked

671
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal structure of methionine aminopeptidase from hyperthermophile, <i>Pyrococcus furiosus</i> a1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1998, 284, 101-124.	4.2	143
2	Effect of a single amino acid substitution on stability of conformation of a protein. <i>Nature</i> , 1977, 267, 274-275.	27.8	139
3	Contribution of the Hydrophobic Effect to the Stability of Human Lysozyme: Calorimetric Studies and X-ray Structural Analyses of the Nine Valine to Alanine Mutants. <i>Biochemistry</i> , 1997, 36, 688-698.	2.5	103
4	Thermodynamics of protein denaturation at temperatures over 100°C: CutA1 mutant proteins substituted with hydrophobic and charged residues. <i>Scientific Reports</i> , 2015, 5, 15545.	3.3	65
5	A general rule for the relationship between hydrophobic effect and conformational stability of a protein: stability and structure of a series of hydrophobic mutants of human lysozyme. <i>Journal of Molecular Biology</i> , 1998, 280, 749-761.	4.2	61
6	Hyper-thermostability of CutA1 protein, with a denaturation temperature of nearly 150°C. <i>FEBS Letters</i> , 2006, 580, 4224-4230.	2.8	54
7	The Unusually Slow Relaxation Kinetics of the Folding-unfolding of Pyrrolidone Carboxyl Peptidase from a Hyperthermophile, <i>Pyrococcus furiosus</i> . <i>Journal of Molecular Biology</i> , 2002, 316, 991-1003.	4.2	51
8	Are the parameters of various stabilization factors estimated from mutant human lysozymes compatible with other proteins?. <i>Protein Engineering, Design and Selection</i> , 2001, 14, 127-134.	2.1	48
9	Entropic Stabilization of the Tryptophan Synthase β -Subunit from a Hyperthermophile, <i>Pyrococcus furiosus</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 11062-11071.	3.4	42
10	Electrostatic Stabilization in Methionine Aminopeptidase from Hyperthermophile <i>Pyrococcus furiosus</i> . <i>Biochemistry</i> , 1998, 37, 5939-5946.	2.5	37
11	Thermodynamic Basis for the Stabilities of Three CutA1s from <i>Pyrococcus horikoshii</i> , <i>Thermus thermophilus</i> , and <i>Oryza sativa</i> , with Unusually High Denaturation Temperatures. <i>Biochemistry</i> , 2008, 47, 721-730.	2.5	29
12	Effect of single amino acid substitutions on the protease susceptibility of tryptophan synthase α subunit. <i>FEBS Journal</i> , 1985, 150, 17-21.	0.2	22
13	Role of charged residues in stabilization of <i>Pyrococcus horikoshii</i> CutA1, which has a denaturation temperature of nearly 150°C. <i>FEBS Journal</i> , 2012, 279, 78-90.	4.7	17
14	Unusually Slow Denaturation and Refolding Processes of Pyrrolidone Carboxyl Peptidase from a Hyperthermophile Are Highly Cooperative: A Real-Time NMR Studies. <i>Biochemistry</i> , 2004, 43, 11906-11915.	2.5	13
15	Remarkable improvement in the heat stability of CutA1 from <i>Escherichia coli</i> by rational protein design. <i>Journal of Biochemistry</i> , 2010, 148, 449-58.	1.7	10
16	Strategy for Stabilization of CutA1 Proteins Due to Ion-Ion Interactions at Temperatures of over 100°C. <i>Biochemistry</i> , 2018, 57, 2649-2656.	2.5	7
17	Characterization of the Denatured Structure of Pyrrolidone Carboxyl Peptidase from a Hyperthermophile under Nondenaturing Conditions: A Role of the C-Terminal β -Helix of the Protein in Folding and Stability. <i>Biochemistry</i> , 2007, 46, 3664-3672.	2.5	6
18	Ion-ion interactions in the denatured state contribute to the stabilization of CutA1 proteins. <i>Scientific Reports</i> , 2018, 8, 7613.	3.3	6

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19	Structure of putative CutA1 from <i>Homo sapiens</i> determined at 2.05 Å resolution. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 351-357.	0.7	5
20	Thermodynamic analysis of unusually thermostable CutA1 protein from human brain and its protease susceptibility. Journal of Biochemistry, 2015, 157, 169-176.	1.7	4
21	Structural Characterization of a Trapped Folding Intermediate of Pyrrolidone Carboxyl Peptidase from a Hyperthermophile. Biochemistry, 2012, 51, 6089-6096.	2.5	3
22	What is the Highest Temperature at which the Conformation of a Globular Protein can be Maintained? The Current State and the Prospect for Protein Stability Study. Seibutsu Butsuri, 2009, 49, 226-231.	0.1	2
23	The confirmation of the denatured structure of pyrrolidone carboxyl peptidase under non-denaturing conditions: Difference in helix propensity of two synthetic peptides with single amino acid substitution. Proteins: Structure, Function and Bioinformatics, 2008, 71, 737-742.	2.6	1
24	Evaluating the strengths of salt bridges in the CutA1 protein using molecular dynamic simulations: a comparison of different force fields. FEBS Open Bio, 2019, 9, 1939-1956.	2.3	1
25	Confirmation of the formation of salt bridges in the denatured state of CutA1 protein using molecular dynamics simulations. Biophysics and Physicobiology, 2019, 16, 176-184.	1.0	1