

Katsuhide Yutani

List of Publications by Year in descending order

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25
papers

870
citations

687363

13
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580821

25
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all docs

25
docs citations

25
times ranked

671
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluating the strengths of salt bridges in the CutA1 protein using molecular dynamic simulations: a comparison of different force fields. <i>FEBS Open Bio</i> , 2019, 9, 1939-1956.	2.3	1
2	Confirmation of the formation of salt bridges in the denatured state of CutA1 protein using molecular dynamics simulations. <i>Biophysics and Physicobiology</i> , 2019, 16, 176-184.	1.0	1
3	Strategy for Stabilization of CutA1 Proteins Due to Ion-Ion Interactions at Temperatures of over 100 Å°C. <i>Biochemistry</i> , 2018, 57, 2649-2656.	2.5	7
4	Ion-Ion interactions in the denatured state contribute to the stabilization of CutA1 proteins. <i>Scientific Reports</i> , 2018, 8, 7613.	3.3	6
5	Thermodynamics of protein denaturation at temperatures over 100 Å°C: CutA1 mutant proteins substituted with hydrophobic and charged residues. <i>Scientific Reports</i> , 2015, 5, 15545.	3.3	65
6	Thermodynamic analysis of unusually thermostable CutA1 protein from human brain and its protease susceptibility. <i>Journal of Biochemistry</i> , 2015, 157, 169-176.	1.7	4
7	Structural Characterization of a Trapped Folding Intermediate of Pyrrolidone Carboxyl Peptidase from a Hyperthermophile. <i>Biochemistry</i> , 2012, 51, 6089-6096.	2.5	3
8	Role of charged residues in stabilization of <i>Pyrococcus horikoshii</i> CutA1, which has a denaturation temperature of nearly 150 Å°C. <i>FEBS Journal</i> , 2012, 279, 78-90.	4.7	17
9	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
10	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. <i>Seibutsu Butsuri</i> , 2009, 49, 226-231.	0.1	2
11	Structure of putative CutA1 from <i>Homo sapiens</i> determined at 2.05 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 351-357.	0.7	5
12	The confirmation of the denatured structure of pyrrolidone carboxyl peptidase under nondenaturing conditions: Difference in helix propensity of two synthetic peptides with single amino acid substitution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 737-742.	2.6	1
13	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
14	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
15	Hyper-thermostability of CutA1 protein, with a denaturation temperature of nearly 150 Å°C. <i>FEBS Letters</i> , 2006, 580, 4224-4230.	2.8	54
16	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
17	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
18	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

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19	Are the parameters of various stabilization factors estimated from mutant human lysozymes compatible with other proteins?. Protein Engineering, Design and Selection, 2001, 14, 127-134.	2.1	48
20	Electrostatic Stabilization in Methionine Aminopeptidase from Hyperthermophile Pyrococcus furiosus. Biochemistry, 1998, 37, 5939-5946.	2.5	37
21	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. Journal of Molecular Biology, 1998, 280, 749-761.	4.2	61
22	Crystal structure of methionine aminopeptidase from hyperthermophile, Pyrococcus furiosus a1 Edited by R. Huber. Journal of Molecular Biology, 1998, 284, 101-124.	4.2	143
23	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,. Biochemistry, 1997, 36, 688-698.	2.5	103
24	Effect of single amino acid substitutions on the protease susceptibility of tryptophan synthase a subunit. FEBS Journal, 1985, 150, 17-21.	0.2	22
25	Effect of a single amino acid substitution on stability of conformation of a protein. Nature, 1977, 267, 274-275.	27.8	139