

Tomonao Inobe

List of Publications by Year in descending order

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33
papers

1,085
citations

471061

17
h-index

454577

30
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34
all docs

34
docs citations

34
times ranked

1288
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteasome-mediated protein degradation is enhanced by fusion ubiquitin with unstructured degron. <i>Biochemical and Biophysical Research Communications</i> , 2018, 501, 948-954.	1.0	2
2	N-Acyl dopamine induces aggresome formation without proteasome inhibition and enhances protein aggregation via p62/SQSTM1 expression. <i>Scientific Reports</i> , 2018, 8, 9585.	1.6	20
3	Conserved Sequence Preferences Contribute to Substrate Recognition by the Proteasome. <i>Journal of Biological Chemistry</i> , 2016, 291, 14526-14539.	1.6	56
4	Novel method for the high-throughput production of phosphorylation site-specific monoclonal antibodies. <i>Scientific Reports</i> , 2016, 6, 25174.	1.6	13
5	Rapamycin-induced oligomer formation system of FRB-FKBP fusion proteins. <i>Journal of Bioscience and Bioengineering</i> , 2016, 122, 40-46.	1.1	40
6	Proteasomal degradation of damaged polyubiquitin. <i>Biochemical and Biophysical Research Communications</i> , 2016, 471, 34-40.	1.0	2
7	N-Terminal Coiled-Coil Structure of ATPase Subunits of 26S Proteasome Is Crucial for Proteasome Function. <i>PLoS ONE</i> , 2015, 10, e0134056.	1.1	9
8	Inhibition of the 26S proteasome by peptide mimics of the coiled-coil region of its ATPase subunits. <i>Biochemical and Biophysical Research Communications</i> , 2015, 468, 143-150.	1.0	7
9	Sequence composition of disordered regions fine-tunes protein half-life. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 214-221.	3.6	109
10	Regulation of Proteasomal Degradation by Modulating Proteasomal Initiation Regions. <i>ACS Chemical Biology</i> , 2015, 10, 2537-2543.	1.6	13
11	Artificial regulation of p53 function by modulating its assembly. <i>Biochemical and Biophysical Research Communications</i> , 2015, 467, 322-327.	1.0	6
12	Paradigms of protein degradation by the proteasome. <i>Current Opinion in Structural Biology</i> , 2014, 24, 156-164.	2.6	102
13	Sequence- and Species-Dependence of Proteasomal Processivity. <i>ACS Chemical Biology</i> , 2012, 7, 1444-1453.	1.6	50
14	Dissecting a Bimolecular Process of MgATP ²⁺ Binding to the Chaperonin GroEL. <i>Journal of Molecular Biology</i> , 2011, 410, 343-356.	2.0	10
15	Defining the geometry of the two-component proteasome degron. <i>Nature Chemical Biology</i> , 2011, 7, 161-167.	3.9	149
16	Unstructured Region-mediated Substrate Recognition by the Proteasome. <i>Seibutsu Butsuri</i> , 2011, 51, 276-277.	0.0	0
17	1P034 1YA0915 Defining the geometry of the two-component proteasome degron (Protein:Structure & Tj ETQq1	1.0	0
18	Substrate selection by the proteasome during degradation of protein complexes. <i>Nature Chemical Biology</i> , 2009, 5, 29-36.	3.9	108

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19	How to pick a protein and pull at it. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1135-1136.	3.6	7
20	Asymmetry of the GroEL-GroES Complex under Physiological Conditions as Revealed by Small-Angle X-Ray Scattering. <i>Biophysical Journal</i> , 2008, 94, 1392-1402.	0.2	18
21	1P041 SELECTING PROTEINS FOR DEGRADATION: THE INITIATION STEP(Proteins-functions, methodology,) Tj ETQq1 1 0.784314 rgBT 0.0	0.0	0
22	The Equilibrium Unfolding Intermediate Observed at pH 4 and its Relationship with the Kinetic Folding Intermediates in Green Fluorescent Protein. <i>Journal of Molecular Biology</i> , 2006, 361, 969-982.	2.0	41
23	The allosteric transition of the chaperonin groel fromescherichia coli as studied by solution X-ray scattering. <i>Macromolecular Research</i> , 2006, 14, 166-172.	1.0	1
24	Characterization of Archaeal Group II Chaperonin-ADP-Metal Fluoride Complexes. <i>Journal of Biological Chemistry</i> , 2005, 280, 40375-40383.	1.6	29
25	Role of the Helical Protrusion in the Conformational Change and Molecular Chaperone Activity of the Archaeal Group II Chaperonin. <i>Journal of Biological Chemistry</i> , 2004, 279, 18834-18839.	1.6	41
26	Oligomeric Hsp33 with Enhanced Chaperone Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 55760-55769.	1.6	27
27	Ï Value Analysis of an Allosteric Transition of GroEL based on a Single-pathway Model. <i>Journal of Molecular Biology</i> , 2004, 339, 199-205.	2.0	8
28	Denaturation and reassembly of chaperonin GroEL studied by solution X-ray scattering. <i>Protein Science</i> , 2003, 12, 672-680.	3.1	20
29	Equilibrium and Kinetics of the Allosteric Transition of GroEL Studied by Solution X-ray Scattering and Fluorescence Spectroscopy. <i>Journal of Molecular Biology</i> , 2003, 327, 183-191.	2.0	28
30	The Allosteric Transition of GroEL Induced by Metal Fluoride-ADP Complexes. <i>Journal of Molecular Biology</i> , 2003, 329, 121-134.	2.0	19
31	Fast Compaction of Ï-Lactalbumin During Folding Studied by Stopped-flow X-ray Scattering. <i>Journal of Molecular Biology</i> , 2002, 321, 121-132.	2.0	100
32	The Use of the Time-Resolved X-Ray Solution Scattering for Studies of Globular Proteins. <i>Spectroscopy</i> , 2002, 16, 127-138.	0.8	3
33	Nucleotide binding to the chaperonin GroEL: non-cooperative binding of ATP analogs and ADP, and cooperative effect of ATP. <i>BBA - Proteins and Proteomics</i> , 2001, 1545, 160-173.	2.1	47