Eri Sakata

List of Publications by Year in descending order

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Ερι δλκλτι

 Allosteric control of Ubp6 and the proteasome 2022, 13, 838. Molecular and cellular dynamics of the 26S prop Proteomics, 2021, 1869, 140583. Expanded Coverage of the 26S Proteasome Con Gating. FASEB Journal, 2019, 33, . Expanded Coverage of the 26S Proteasome Con Gating. Cell Reports, 2018, 24, 1301-1315.e5. Structural insights into the functional cycle of the Proceedings of the National Academy of Science 	via a bidirectional switch. Nature Communications, teasome. Biochimica Et Biophysica Acta - Proteins and formational Landscape Reveals Mechanisms of Peptidase formational Landscape Reveals Mechanisms of Peptidase he ATPase module of the 26S proteasome. es of the United States of America, 2017, 114, 1305-1310.	5.8 1.1 0.2 2.9	15 33 0
 Molecular and cellular dynamics of the 26S property Proteomics, 2021, 1869, 140583. Expanded Coverage of the 26S Proteasome Conditional, FASEB Journal, 2019, 33, . Expanded Coverage of the 26S Proteasome Conditional, Cell Reports, 2018, 24, 1301-1315.e5. Structural insights into the functional cycle of the Proceedings of the National Academy of Science 	teasome. Biochimica Et Biophysica Acta - Proteins and Informational Landscape Reveals Mechanisms of Peptidase Informational Landscape Reveals Mechanisms of Peptidase the ATPase module of the 26S proteasome. es of the United States of America, 2017, 114, 1305-1310.	1.1 0.2 2.9	33 0 108
 Expanded Coverage of the 26S Proteasome Cordinating. FASEB Journal, 2019, 33, . Expanded Coverage of the 26S Proteasome Cordinating. Cell Reports, 2018, 24, 1301-1315.e5. Structural insights into the functional cycle of the Proceedings of the National Academy of Science 	nformational Landscape Reveals Mechanisms of Peptidase nformational Landscape Reveals Mechanisms of Peptidase he ATPase module of the 26S proteasome. es of the United States of America, 2017, 114, 1305-1310.	0.2 2.9	0
 Expanded Coverage of the 26S Proteasome Col Gating. Cell Reports, 2018, 24, 1301-1315.e5. Structural insights into the functional cycle of t Proceedings of the National Academy of Science 	nformational Landscape Reveals Mechanisms of Peptidase he ATPase module of the 26S proteasome. es of the United States of America, 2017, 114, 1305-1310.	2.9	108
5 Structural insights into the functional cycle of t	he ATPase module of the 26S proteasome. es of the United States of America, 2017, 114, 1305-1310.		_00
		3.3	151
6 Molecular Details Underlying Dynamic Structur Molecular and Cellular Proteomics, 2017, 16, 8	es and Regulation of the Human 26S Proteasome. 40-854.	2.5	93
7 Cryo-FIB Sample Preparation for Cryo-ET With t 2016, 22, 72-73.	he Volta Phase Plate. Microscopy and Microanalysis,	0.2	0
8 Recent advances in the structural biology of the Biochemistry and Cell Biology, 2016, 79, 437-4	26S proteasome. International Journal of 42.	1.2	34
9 Structure of the human 26S proteasome at a re of Sciences of the United States of America, 20	solution of 3.9 Ã Proceedings of the National Academy 16, 113, 7816-7821.	3.3	174
In Situ Tomography of Membrane Proteins Enal Plate Imaging. Microscopy and Microanalysis, 2	oled by Advanced Cryo-FIB Sample Preparation and Phase 015, 21, 1119-1120.	0.2	2
11 Structural characterization of the interaction of National Academy of Sciences of the United Sta	Ubp6 with the 26S proteasome. Proceedings of the tess of America, 2015, 112, 8626-8631.	3.3	98
Quantitative live-cell imaging reveals spatio-ten proteasome. Nature Communications, 2014, 5,	poral dynamics and cytoplasmic assembly of the 26S 3396.	5.8	111
Localization of the regulatory particle subunit S Biophysical Research Communications, 2013, 4	em1 in the 26S proteasome. Biochemical and 35, 250-254.	1.0	28
14 Cryo–electron tomography reveals a critical r Cell Biology, 2013, 201, 725-740.	ole of RIM1α in synaptic vesicle tethering. Journal of	2.3	110
Localization of the proteasomal ubiquitin recep Proceedings of the National Academy of Scienc	tors Rpn10 and Rpn13 by electron cryomicroscopy. es of the United States of America, 2012, 109, 1479-1484.	3.3	114
16 Near-atomic resolution structural model of the Academy of Sciences of the United States of Ar	yeast 26S proteasome. Proceedings of the National nerica, 2012, 109, 14870-14875.	3.3	242
The Catalytic Activity of Ubp6 Enhances Matura Molecular Cell, 2011, 42, 637-649.	ition of the Proteasomal Regulatory Particle.	4.5	64
18 Crystal Structure of UbcH5bâ^¼Ubiquitin Inter E2â^¼Ub Conjugates. Structure, 2010, 18, 138		16	

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#	Article	IF	CITATIONS
19	Structure of the 26S proteasome from <i>Schizosaccharomyces pombe</i> at subnanometer resolution. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20992-20997.	3.3	130
20	Crystal structure of a chaperone complex that contributes to the assembly of yeast 20S proteasomes. Nature Structural and Molecular Biology, 2008, 15, 228-236.	3.6	101
21	Ultra-high field NMR studies of antibody binding and site-specific phosphorylation of α-synuclein. Biochemical and Biophysical Research Communications, 2007, 363, 795-799.	1.0	36
22	Direct interactions between NEDD8 and ubiquitin E2 conjugating enzymes upregulate cullin-based E3 ligase activity. Nature Structural and Molecular Biology, 2007, 14, 167-168.	3.6	105
23	Solution structure and dynamics of Ufm1, a ubiquitin-fold modifier 1. Biochemical and Biophysical Research Communications, 2006, 343, 21-26.	1.0	55
24	14-3-3η is a novel regulator of parkin ubiquitin ligase. EMBO Journal, 2006, 25, 211-221.	3.5	107
25	Parkin binds the Rpn10 subunit of 26S proteasomes through its ubiquitinâ€like domain. EMBO Reports, 2003, 4, 301-306.	2.0	233