Yoshinori Akiyama

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Escherichia coli S2P intramembrane protease RseP regulates ferric citrate uptake by cleaving the sigma factor regulator FecR. Journal of Biological Chemistry, 2021, 296, 100673.	3.4	14
2	Moving toward generalizable NZ-1 labeling for 3D structure determination with optimized epitope-tag insertion. Acta Crystallographica Section D: Structural Biology, 2021, 77, 645-662.	2.3	18
3	Edge-strand of BepA interacts with immature LptD on the β-barrel assembly machine to direct it to on- and off-pathways. ELife, 2021, 10, .	6.0	4
4	Reversible autoinhibitory regulation ofEscherichia colimetallopeptidase BepA for selective β-barrel protein degradation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27989-27996.	7.1	4
5	Fine interaction profiling of VemP and mechanisms responsible for its translocation-coupled arrest-cancelation. ELife, 2020, 9, .	6.0	9
6	An <i>inÂvivo</i> protease activity assay for investigating the functions of the <i>EscherichiaÂcoli</i> membrane protease HtpX. FEBS Letters, 2019, 593, 842-851.	2.8	13
7	Structural Basis for the Function of the β-Barrel Assembly-Enhancing Protease BepA. Journal of Molecular Biology, 2019, 431, 625-635.	4.2	12
8	Involvement of a conserved <scp>GFG</scp> motif region in substrate binding by <scp>R</scp> se <scp>P</scp> , an <scp><i>E</i></scp> <i>scherichia coli</i> S2P protease. Molecular Microbiology, 2017, 104, 737-751.	2.5	18
9	The TPR domain of BepA is required for productive interaction with substrate proteins and the βâ€barrel assembly machinery complex. Molecular Microbiology, 2017, 106, 760-776.	2.5	26
10	Environment of the Active Site Region of RseP, an Escherichia coli Regulated Intramembrane Proteolysis Protease, Assessed by Site-directed Cysteine Alkylation. Journal of Biological Chemistry, 2007, 282, 4553-4560.	3.4	39
11	The intramembrane active site of GlpG, an E. coli rhomboid protease, is accessible to water and hydrolyses an extramembrane peptide bond of substrates. Molecular Microbiology, 2007, 64, 435-447.	2.5	55
12	The Escherichia coli plasma membrane contains two PHB (prohibitin homology) domain protein complexes of opposite orientations. Molecular Microbiology, 2006, 60, 448-457.	2.5	47
13	Reconstitution of Membrane Proteolysis by FtsH. Journal of Biological Chemistry, 2003, 278, 18146-18153.	3.4	35
14	The Cpx stress response system ofEscherichia colisenses plasma membrane proteins and controls HtpX, a membrane protease with a cytosolic active site. Genes To Cells, 2002, 7, 653-662.	1.2	102
15	Polypeptide binding of Escherichia coli FtsH (HflB). Molecular Microbiology, 2002, 28, 803-812.	2.5	36
16	Roles of multimerization and membrane association in the proteolytic functions of FtsH (HflB). EMBO Journal, 2000, 19, 3888-3895.	7.8	38
17	Roles of the Periplasmic Domain of Escherichia coliFtsH (HflB) in Protein Interactions and Activity Modulation. Journal of Biological Chemistry, 1998, 273, 22326-22333.	3.4	44
18	FtsH (HflB) Is an ATP-dependent Protease Selectively Acting on SecY and Some Other Membrane Proteins. Journal of Biological Chemistry, 1996, 271, 31196-31201.	3.4	134