Yoshinori Akiyama

List of Publications by Year
in descending order

18	648	759233 12	839539 18
papers	citations	h-index	g-index

18	18	18	581
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	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
3	The intramembrane active site of GlpG, an E.â€ƒcoli rhomboid protease, is accessible to water and hydrolyses an extramembrane peptide bond of substrates. Molecular Microbiology, 2007, 64, 435-447.	2.5	55
4	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
5	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
6	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
7	Roles of multimerization and membrane association in the proteolytic functions of FtsH (HflB). EMBO Journal, 2000, 19, 3888-3895.	7.8	38
8	Polypeptide binding of Escherichia coli FtsH (HflB). Molecular Microbiology, 2002, 28, 803-812.	2.5	36
9	Reconstitution of Membrane Proteolysis by FtsH. Journal of Biological Chemistry, 2003, 278, 18146-18153.	3.4	35
10	The TPR domain of BepA is required for productive interaction with substrate proteins and the Î²â€barrel assembly machinery complex. Molecular Microbiology, 2017, 106, 760-776.	2.5	26
11	Involvement of a conserved <scp>GFG</scp> motif region in substrate binding by <scp>R</scp>se<scp>P</scp>, an <scp>E</scp>scherichia coli<scp>S2P</scp> protease. Molecular Microbiology, 2017, 104, 737-751.	2.5	18
12	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
13	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
14	An inÂvivo protease activity assay for investigating the functions of the EscherichiaÂcoli membrane protease HtpX. FEBS Letters, 2019, 593, 842-851.	2.8	13
15	Structural Basis for the Function of the Î²-Barrel Assembly-Enhancing Protease BepA. Journal of Molecular Biology, 2019, 431, 625-635.	4.2	12
16	Fine interaction profiling of VemP and mechanisms responsible for its translocation-coupled arrest-cancelation. ELife, 2020, 9, .	6.0	9
17	Reversible autoinhibitory regulation ofEscherichia colimetallopeptidase BepA for selective Î²-barrel protein degradation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27989-27996.	7.1	4
18	Edge-strand of BepA interacts with immature LptD on the Î²-barrel assembly machine to direct it to on- and off-pathways. ELife, 2021, 10, .	6.0	4