

# Hiroyuki Mori

## List of Publications by Year in descending order

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73  
papers

4,079  
citations

156536

32  
h-index

134545

62  
g-index

76  
all docs

76  
docs citations

76  
times ranked

2904  
citing authors

#	ARTICLE	IF	CITATIONS
1	PiXie Analysis for Monitoring Dynamic Protein Interaction and Folding in a Living Cell. <i>Seibutsu Butsuri</i> , 2021, 61, 036-039.	0.0	0
2	A photo-cross-linking approach to monitor protein dynamics in living cells. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129317.	1.1	20
3	Reversible autoinhibitory regulation of <i>Escherichia coli</i> metallopeptidase BepA for selective $\beta$ -barrel protein degradation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27989-27996.	3.3	4
4	Tree of motility – A proposed history of motility systems in the tree of life. <i>Genes To Cells</i> , 2020, 25, 6-21.	0.5	108
5	Fine interaction profiling of VemP and mechanisms responsible for its translocation-coupled arrest-cancelation. <i>ELife</i> , 2020, 9, .	2.8	9
6	Monitoring substrate enables real-time regulation of a protein localization pathway. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	16
7	Identification and characterization of a translation arrest motif in VemP by systematic mutational analysis. <i>Journal of Biological Chemistry</i> , 2018, 293, 2915-2926.	1.6	18
8	A photo-cross-linking approach to monitor folding and assembly of newly synthesized proteins in a living cell. <i>Journal of Biological Chemistry</i> , 2018, 293, 677-686.	1.6	19
9	Heat shock transcription factor $\sigma^{32}$ defective in membrane transport can be suppressed by transposon insertion into genes encoding a restriction enzyme subunit or a putative autotransporter in <i>Escherichia coli</i> . <i>Genes and Genetic Systems</i> , 2018, 93, 229-235.	0.2	2
10	Tunnel Formation Inferred from the I-Form Structures of the Proton-Driven Protein Secretion Motor SecDF. <i>Cell Reports</i> , 2017, 19, 895-901.	2.9	38
11	The TPR domain of BepA is required for productive interaction with substrate proteins and the $\beta$ -barrel assembly machinery complex. <i>Molecular Microbiology</i> , 2017, 106, 760-776.	1.2	26
12	A Novel SRP Recognition Sequence in the Homeostatic Control Region of Heat Shock Transcription Factor $\sigma^{32}$ . <i>Scientific Reports</i> , 2016, 6, 24147.	1.6	30
13	Nascent chain-monitored remodeling of the Sec machinery for salinity adaptation of marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5513-22.	3.3	57
14	Roles of the membrane-reentrant $\beta$ -hairpin-like loop of RseP protease in selective substrate cleavage. <i>ELife</i> , 2015, 4, .	2.8	41
15	Structural basis of Sec-independent membrane protein insertion by YidC. <i>Nature</i> , 2014, 509, 516-520.	13.7	203
16	Conformational variation of the translocon enhancing chaperone SecDF. <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 107-115.	1.2	10
17	Crystal structure of <i>Escherichia coli</i> YidC, a membrane protein chaperone and insertase. <i>Scientific Reports</i> , 2014, 4, 7299.	1.6	109
18	Structure and function of a membrane component SecDF that enhances protein export. <i>Nature</i> , 2011, 474, 235-238.	13.7	202

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19	Post-liberation cleavage of signal peptides is catalyzed by the site-2 protease (S2P) in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 13740-13745.	3.3	67
20	Conformational Transition of Sec Machinery Inferred from Bacterial SecYE Structures. <i>Seibutsu Butsuri</i> , 2009, 49, 288-289.	0.0	0
21	Conformational transition of Sec machinery inferred from bacterial SecYE structures. <i>Nature</i> , 2008, 455, 988-991.	13.7	206
22	Crystal Structure of the Translocation ATPase SecA from <i>Thermus thermophilus</i> Reveals a Parallel, Head-to-Head Dimer. <i>Journal of Molecular Biology</i> , 2006, 364, 248-258.	2.0	84
23	Purification, crystallization and preliminary X-ray diffraction of SecDF, a translocon-associated membrane protein, from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 376-380.	0.7	22
24	Cloning, expression, purification, crystallization and initial crystallographic analysis of the preprotein translocation ATPase SecA from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 909-912.	0.7	2
25	The Long $\alpha$ -Helix of SecA Is Important for the ATPase Coupling of Translocation. <i>Journal of Biological Chemistry</i> , 2006, 281, 36249-36256.	1.6	36
26	Different modes of SecY-SecA interactions revealed by site-directed in vivo photo-cross-linking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 16159-16164.	3.3	106
27	SecM facilitates translocase function of SecA by localizing its biosynthesis. <i>Genes and Development</i> , 2005, 19, 436-444.	2.7	32
28	Mutational Analysis of Transmembrane Regions 3 and 4 of SecY, a Central Component of Protein Translocase. <i>Journal of Bacteriology</i> , 2004, 186, 3960-3969.	1.0	10
29	Interfering mutations provide in vivo evidence that <i>Escherichia coli</i> SecE functions in multimeric states. <i>Molecular Genetics and Genomics</i> , 2003, 268, 808-815.	1.0	7
30	Importance of transmembrane segments in <i>Escherichia coli</i> SecY. <i>Molecular Genetics and Genomics</i> , 2003, 269, 180-187.	1.0	5
31	Nearest Neighbor Analysis of the SecYEG Complex. 2. Identification of a SecY <sup>+</sup> SecE Cytosolic Interface. <i>Biochemistry</i> , 2003, 42, 7442-7447.	1.2	10
32	Nearest Neighbor Analysis of the SecYEG Complex. 1. Identification of a SecY <sup>+</sup> SecG Interface. <i>Biochemistry</i> , 2003, 42, 7434-7441.	1.2	16
33	A SecE Mutation That Modulates SecY-SecE Translocase Assembly, Identified as a Specific Suppressor of SecY Defects. <i>Journal of Bacteriology</i> , 2003, 185, 948-956.	1.0	13
34	Biochemical Characterization of a Mutationally Altered Protein Translocase: Proton Motive Force Stimulation of the Initiation Phase of Translocation. <i>Journal of Bacteriology</i> , 2003, 185, 405-412.	1.0	25
35	Fluorescence Resonance Energy Transfer Analysis of Protein Translocase. <i>Journal of Biological Chemistry</i> , 2003, 278, 14257-14264.	1.6	50
36	Superactive SecY Variants That Fulfill the Essential Translocation Function with a Reduced Cellular Quantity. <i>Journal of Biological Chemistry</i> , 2002, 277, 48550-48557.	1.6	10

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37	Isolation of a diterpenoid substance with potent neuroprotective activity from fetal calf serum. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3288-3293.	3.3	53
38	Roles of the C-Terminal End of SecY in Protein Translocation and Viability of Escherichia coli. Journal of Bacteriology, 2002, 184, 2243-2250.	1.0	19
39	The Sec protein-translocation pathway. Trends in Microbiology, 2001, 9, 494-500.	3.5	259
40	An essential amino acid residue in the protein translocation channel revealed by targeted random mutagenesis of SecY. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 5128-5133.	3.3	65
41	Genetic dissection of SecA: suppressor mutations against thesecY205translocase defect. Genes To Cells, 2000, 5, 991-999.	0.5	26
42	Length recognition at the N-terminal tail for the initiation of FtsH-mediated proteolysis. EMBO Reports, 2000, 1, 47-52.	2.0	49
43	Characterization of a Mutant Form of SecA That Alleviates a SecY Defect at Low Temperature and Shows a Synthetic Defect with SecY Alteration at High Temperature. Journal of Biochemistry, 2000, 127, 1071-1079.	0.9	11
44	A Mutation in secY That Causes Enhanced SecA Insertion and Impaired Late Functions in Protein Translocation. Journal of Bacteriology, 2000, 182, 3377-3382.	1.0	9
45	Two Independent Mechanisms Down-regulate the Intrinsic SecA ATPase Activity. Journal of Biological Chemistry, 2000, 275, 33209-33212.	1.6	23
46	Second transmembrane segment of FtsH plays a role in its proteolytic activity and homo-oligomerization. FEBS Letters, 1999, 460, 554-558.	1.3	16
47	Roles of SecG in ATP- and SecA-dependent protein translocation. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 13567-13572.	3.3	39
48	Roles of the Periplasmic Domain of Escherichia coli FtsH (HflB) in Protein Interactions and Activity Modulation. Journal of Biological Chemistry, 1998, 273, 22326-22333.	1.6	44
49	Syd, a SecY-interacting Protein, Excludes SecA from the SecYE Complex with an Altered SecY24 Subunit. Journal of Biological Chemistry, 1998, 273, 18835-18840.	1.6	26
50	Amino-Terminal Region of SecA Is Involved in the Function of SecG for Protein Translocation into Escherichia coli Membrane Vesicles. Journal of Biochemistry, 1998, 124, 122-129.	0.9	32
51	Short Hydrophobic Segments in the Mature Domain of ProOmpA Determine Its Stepwise Movement during Translocation across the Cytoplasmic Membrane of Escherichia coli. Journal of Biological Chemistry, 1997, 272, 5880-5886.	1.6	34
52	In Vitro Analysis of the Stop-transfer Process during Translocation across the Cytoplasmic Membrane of Escherichia coli. Journal of Biological Chemistry, 1997, 272, 20082-20087.	1.6	21
53	The hydrophobic region of signal peptides is involved in the interaction with membrane-bound SecA. Biochimica Et Biophysica Acta - Biomembranes, 1997, 1326, 23-36.	1.4	29
54	Characterization of a Potential Catalytic Residue, Asp-133, in the High Affinity ATP-binding Site of SecA, Translocation ATPase. Journal of Biological Chemistry, 1996, 271, 17439-17444.	1.6	22

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55	Escherichia coli FtsH is a membrane-bound, ATP-dependent protease which degrades the heat-shock transcription factor sigma 32.. EMBO Journal, 1995, 14, 2551-2560.	3.5	399
56	Stepwise Movement of Preproteins in the Process of Translocation across the Cytoplasmic Membrane of Escherichia coli. Journal of Biological Chemistry, 1995, 270, 30862-30868.	1.6	111
57	Escherichia coli FtsH is a membrane-bound, ATP-dependent protease which degrades the heat-shock transcription factor sigma 32. EMBO Journal, 1995, 14, 2551-60.	3.5	171
58	Induction of heat shock proteins by abnormal proteins results from stabilization and not increased synthesis of sigma 32 in Escherichia coli. Journal of Bacteriology, 1994, 176, 5648-5653.	1.0	85
59	Association of N-ethylmaleimide-sensitive factor with synaptic vesicles. FEBS Letters, 1994, 350, 253-257.	1.3	61
60	Binding mode of glucans to alpha-glucan phosphorylase isozymes and their chimeric enzymes. , 1994, , 167-171.		0
61	Engineered plant phosphorylase showing extraordinarily high affinity for various alpha-glucan molecules. Protein Science, 1993, 2, 1621-1629.	3.1	13
62	Heat induction of alpha-32 synthesis mediated by mRNA secondary structure: a primary step of the heat shock response in Escherichia coli. Nucleic Acids Research, 1993, 21, 5449-5455.	6.5	68
63	The Escherichia coli FtsH protein is a prokaryotic member of a protein family of putative ATPases involved in membrane functions, cell cycle control, and gene expression. Journal of Bacteriology, 1993, 175, 1344-1351.	1.0	241
64	A chimeric alpha-glucan phosphorylase of plant type L and H isozymes. Functional role of 78-residue insertion in type L isozyme.. Journal of Biological Chemistry, 1993, 268, 5574-5581.	1.6	31
65	A chimeric alpha-glucan phosphorylase of plant type L and H isozymes. Functional role of 78-residue insertion in type L isozyme. Journal of Biological Chemistry, 1993, 268, 5574-81.	1.6	31
66	Structure and function of the ftsH gene in Escherichia coli. Research in Microbiology, 1991, 142, 279-282.	1.0	100
67	Potato tuber type H phosphorylase isozyme. Molecular cloning, nucleotide sequence, and expression of a full-length cDNA in Escherichia coli.. Journal of Biological Chemistry, 1991, 266, 18446-18453.	1.6	38
68	Structural Relationships in Higher Plant alpha-Glucan Phosphorylase Isozymes Differently Localized within Cells. , 1991, , 401-403.		0
69	Potato tuber type H phosphorylase isozyme. Molecular cloning, nucleotide sequence, and expression of a full-length cDNA in Escherichia coli. Journal of Biological Chemistry, 1991, 266, 18446-53.	1.6	32
70	Increased expression of genes for basic fibroblast growth factor and transforming growth factor type beta 2 in human benign prostatic hyperplasia. Prostate, 1990, 16, 71-80.	1.2	193
71	UDP-Glucose Pyrophosphorylase from Potato Tuber: cDNA Cloning and Sequencing1. Journal of Biochemistry, 1990, 108, 321-326.	0.9	62
72	Interrelationship between Ca2+-dependent phospholipid base-exchange reaction and phospholipase D-like activity in bovine retina. Lipids and Lipid Metabolism, 1989, 1003, 98-107.	2.6	10

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73	Molecular Cloning of cDNA Encoding Potato Amyloplast $\alpha$ -Glucan Phosphorylase and the Structure of Its Transit Peptide <sup>1</sup> . Journal of Biochemistry, 1989, 106, 691-695.	0.9	41