

# Tomoko Kubori

## List of Publications by Year in descending order

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55  
papers

4,129  
citations

201385

27  
h-index

197535

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docs citations

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times ranked

2781  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural Basis of Ubiquitin Recognition by a Bacterial Ovarian Tumor Deubiquitinase LotA. <i>Journal of Bacteriology</i> , 2022, 204, JB0037621.	1.0	11
2	Recent advances in structural studies of the <i>Legionella pneumophila</i> Dot/Icm type IV secretion system. <i>Microbiology and Immunology</i> , 2022, 66, 67-74.	0.7	9
3	Requirement of phosphatidic acid binding for distribution of the bacterial protein Lpg1137 targeting syntaxin 17. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	3
4	Reversible modification of mitochondrial ADP/ATP translocases by paired <i>Legionella</i> effector proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	6
5	Isolation and Characterization of a Novel Phage SaGU1 that Infects <i>Staphylococcus aureus</i> Clinical Isolates from Patients with Atopic Dermatitis. <i>Current Microbiology</i> , 2021, 78, 1267-1276.	1.0	17
6	<i>Legionella</i> hijacks the host Golgi-to-ER retrograde pathway for the association of <i>Legionella</i> -containing vacuole with the ER. <i>PLoS Pathogens</i> , 2021, 17, e1009437.	2.1	22
7	Protocol for imaging proteins associated with <i>Legionella</i> -containing vacuoles in host cells. <i>STAR Protocols</i> , 2021, 2, 100410.	0.5	0
8	<i>Staphylococcal</i> Phage in Combination with <i>Staphylococcus epidermidis</i> as a Potential Treatment for <i>Staphylococcus aureus</i> -Associated Atopic Dermatitis and Suppressor of Phage-Resistant Mutants. <i>Viruses</i> , 2021, 13, 7.	1.5	29
9	<i>Legionella</i> Manipulates Non-canonical SNARE Pairing Using a Bacterial Deubiquitinase. <i>Cell Reports</i> , 2020, 32, 108107.	2.9	19
10	Divergence of <i>Legionella</i> Effectors Reversing Conventional and Unconventional Ubiquitination. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 448.	1.8	31
11	Structural basis for effector protein recognition by the Dot/Icm Type IVB coupling protein complex. <i>Nature Communications</i> , 2020, 11, 2623.	5.8	29
12	Emerging insights into bacterial deubiquitinases. <i>Current Opinion in Microbiology</i> , 2019, 47, 14-19.	2.3	20
13	Isolation of the Dot/Icm Type IV Secretion System Core Complex from <i>Legionella pneumophila</i> . <i>Methods in Molecular Biology</i> , 2019, 1921, 241-247.	0.4	7
14	LotA, a <i>Legionella</i> deubiquitinase, has dual catalytic activity and contributes to intracellular growth. <i>Cellular Microbiology</i> , 2018, 20, e12840.	1.1	53
15	Bacterial secretion system skews the fate of <i>Legionella</i> -containing vacuoles towards LC3-associated phagocytosis. <i>Scientific Reports</i> , 2017, 7, 44795.	1.6	36
16	Subversion of Host Membrane Dynamics by the <i>Legionella</i> Dot/Icm Type IV Secretion System. <i>Current Topics in Microbiology and Immunology</i> , 2017, 413, 221-242.	0.7	13
17	<i>Legionella</i> RavZ Plays a Role in Preventing Ubiquitin Recruitment to Bacteria-Containing Vacuoles. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 384.	1.8	29
18	Isolation of the Dot/Icm Type IV Secretion System Core Complex from <i>Legionella pneumophila</i> for Negative Stain Electron Microscopy Studies. <i>Bio-protocol</i> , 2017, 7, e2229.	0.2	0

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19	2S-B1-2Autophagy-related Host System and Legionella. <i>Microscopy</i> (Oxford, England), 2017, 66, i14-i14.	0.7	0
20	Microbially cleaved immunoglobulins are sensed by the innate immune receptor LILRA2. <i>Nature Microbiology</i> , 2016, 1, 16054.	5.9	54
21	The Type IVB secretion system: an enigmatic chimera. <i>Current Opinion in Microbiology</i> , 2016, 29, 22-29.	2.3	68
22	Life with Bacterial Secretion Systems. <i>PLoS Pathogens</i> , 2016, 12, e1005562.	2.1	2
23	Molecular and structural analysis of Legionella DotI gives insights into an inner membrane complex essential for type IV secretion. <i>Scientific Reports</i> , 2015, 5, 10912.	1.6	36
24	Native structure of a type IV secretion system core complex essential for Legionella pathogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11804-11809.	3.3	62
25	Hijacking the Host Proteasome for the Temporal Degradation of Bacterial Effectors. <i>Methods in Molecular Biology</i> , 2014, 1197, 141-152.	0.4	4
26	Modulation of the Ubiquitination Machinery by Legionella. <i>Current Topics in Microbiology and Immunology</i> , 2013, 376, 227-247.	0.7	34
27	Purification and Characterization of Legionella U-Box-Type E3 Ubiquitin Ligase. <i>Methods in Molecular Biology</i> , 2013, 954, 347-354.	0.4	4
28	2PT124 Legionella DotI and DotJ form a multimeric subcomplex associated with the core complex of the Dot/Icm type IVB secretion system(The 50th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2012, 52, S125-S126.	0.0	0
29	Type IVB Secretion Systems of Legionella and Other Gram-Negative Bacteria. <i>Frontiers in Microbiology</i> , 2011, 2, 136.	1.5	135
30	Bacterial Effector-Involved Temporal and Spatial Regulation by Hijack of the Host Ubiquitin Pathway. <i>Frontiers in Microbiology</i> , 2011, 2, 145.	1.5	17
31	Crystal Structure of Legionella DotD: Insights into the Relationship between Type IVB and Type II/III Secretion Systems. <i>PLoS Pathogens</i> , 2010, 6, e1001129.	2.1	50
32	Legionella Metaeffector Exploits Host Proteasome to Temporally Regulate Cognate Effector. <i>PLoS Pathogens</i> , 2010, 6, e1001216.	2.1	162
33	Legionella translocates an E3 ubiquitin ligase that has multiple U-boxes with distinct functions. <i>Molecular Microbiology</i> , 2008, 67, 1307-1319.	1.2	198
34	A pathway branching in transcription initiation in Escherichia coli. <i>Molecular Microbiology</i> , 2006, 59, 1807-1817.	1.2	56
35	Assembly of the inner rod determines needle length in the type III secretion injectisome. <i>Nature</i> , 2006, 441, 637-640.	13.7	176
36	Structural Insights into the Assembly of the Type III Secretion Needle Complex. <i>Science</i> , 2004, 306, 1040-1042.	6.0	330

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37	Disruption of type III secretion in <i>Salmonella enterica</i> serovar Typhimurium by external guide sequences. <i>Nucleic Acids Research</i> , 2004, 32, 848-854.	6.5	25
38	Temporal Regulation of <i>Salmonella</i> Virulence Effector Function by Proteasome-Dependent Protein Degradation. <i>Cell</i> , 2003, 115, 333-342.	13.5	262
39	Synthesis and Localization of the <i>Salmonella</i> SPI-1 Type III Secretion Needle Complex Proteins PrgI and PrgJ. <i>Journal of Bacteriology</i> , 2003, 185, 3480-3483.	1.0	54
40	<i>Salmonella</i> Type III Secretion-Associated Protein InvE Controls Translocation of Effector Proteins into Host Cells. <i>Journal of Bacteriology</i> , 2002, 184, 4699-4708.	1.0	107
41	Molecular and functional analysis of the type III secretion signal of the <i>Salmonella enterica</i> InvJ protein. <i>Molecular Microbiology</i> , 2002, 46, 769-779.	1.2	71
42	Genetic Analysis of Assembly of the <i>Salmonella enterica</i> Serovar Typhimurium Type III Secretion-Associated Needle Complex. <i>Journal of Bacteriology</i> , 2001, 183, 1159-1167.	1.0	157
43	Molecular Characterization and Assembly of the Type III Protein Secretion System. <i>Seibutsu Butsuri</i> , 2001, 41, 306-308.	0.0	0
44	Molecular characterization and assembly of the needle complex of the <i>Salmonella typhimurium</i> type III protein secretion system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 10225-10230.	3.3	315
45	Supramolecular Structure on the <i>Salmonella typhimurium</i> Cell Envelope.. <i>Seibutsu Butsuri</i> , 1999, 39, 116-118.	0.0	0
46	Bacterial flagellation and cell division. <i>Genes To Cells</i> , 1998, 3, 625-634.	0.5	59
47	Flagellar filament elongation can be impaired by mutations in the hook protein FlgE of <i>Salmonella typhimurium</i> : a possible role of the hook as a passage for the anti-sigma factor FlgM. <i>Molecular Microbiology</i> , 1998, 27, 1129-1139.	1.2	16
48	Supramolecular Structure of the <i>Salmonella typhimurium</i> Type III Protein Secretion System. <i>Science</i> , 1998, 280, 602-605.	6.0	852
49	Physical interference between <i>Escherichia coli</i> RNA polymerase molecules transcribing in tandem enhances abortive synthesis and misincorporation. <i>Nucleic Acids Research</i> , 1997, 25, 2640-2647.	6.5	20
50	Assembly of the switch complex onto the MS ring complex of <i>Salmonella typhimurium</i> does not require any other flagellar proteins. <i>Journal of Bacteriology</i> , 1997, 179, 813-817.	1.0	76
51	Purification and characterization of the flagellar hookâ€œbasal body complex of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 1997, 24, 399-410.	1.2	37
52	A new model for transcription initiation and its regulation.. <i>Seibutsu Butsuri</i> , 1997, 37, 249-253.	0.0	0
53	A Branched Pathway in the Early Stage of Transcription by <i>Escherichia coli</i> RNA Polymerase. <i>Journal of Molecular Biology</i> , 1996, 256, 449-457.	2.0	93
54	Kinetics of Transcription in a Minute Column. <i>Nucleic Acids Research</i> , 1996, 24, 1380-1381.	6.5	3

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55	Morphological pathway of flagellar assembly in <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 1992, 226, 433-446.	2.0	250