

Hiroki Nagai

List of Publications by Year in descending order

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63
papers

3,859
citations

201385

27
h-index

128067

60
g-index

65
all docs

65
docs citations

65
times ranked

2514
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	MicroRNA 142-5p promotes tumor growth in oral squamous cell carcinoma via the PI3K/AKT pathway by regulating PTEN. <i>Heliyon</i> , 2021, 7, e08086.	1.4	10
9	<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
10	Complete genome and bimodal genomic structure of the amoebal symbiont <i>Neochlamydia</i> strain S13 revealed by ultra-long reads obtained from MiniON. <i>Journal of Human Genetics</i> , 2020, 65, 41-48.	1.1	1
11	<i>Legionella</i> Manipulates Non-canonical SNARE Pairing Using a Bacterial Deubiquitinase. <i>Cell Reports</i> , 2020, 32, 108107.	2.9	19
12	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
13	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
14	Emerging insights into bacterial deubiquitinases. <i>Current Opinion in Microbiology</i> , 2019, 47, 14-19.	2.3	20
15	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
16	<i>Acanthamoeba</i> S13WT relies on its bacterial endosymbiont to backpack human pathogenic bacteria and resist <i>Legionella</i> infection on solid media. <i>Environmental Microbiology Reports</i> , 2018, 10, 344-354.	1.0	9
17	Amoebal endosymbiont <i>Neochlamydia</i> protects host amoebae against <i>Legionella pneumophila</i> infection by preventing <i>Legionella</i> entry. <i>Microbes and Infection</i> , 2018, 20, 236-244.	1.0	25
18	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

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19	Bacterial secretion system skews the fate of Legionella-containing vacuoles towards LC3-associated phagocytosis. <i>Scientific Reports</i> , 2017, 7, 44795.	1.6	36
20	Subversion of Host Membrane Dynamics by the Legionella Dot/Icm Type IV Secretion System. <i>Current Topics in Microbiology and Immunology</i> , 2017, 413, 221-242.	0.7	13
21	Legionella 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
22	Isolation of the Dot/Icm Type IV Secretion System Core Complex from Legionella pneumophila for Negative Stain Electron Microscopy Studies. <i>Bio-protocol</i> , 2017, 7, e2229.	0.2	0
23	2S-B1-2Autophagy-related Host System and Legionella. <i>Microscopy (Oxford, England)</i> , 2017, 66, i14-i14.	0.7	0
24	A Case of Brain Abscess Caused by Medication-Related Osteonecrosis of the Jaw. <i>Case Reports in Dentistry</i> , 2016, 2016, 1-4.	0.2	6
25	Draft Genome Sequences of Legionella pneumophila JR32 and Lp01 Laboratory Strains Domesticated in Japan. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
26	Microbially cleaved immunoglobulins are sensed by the innate immune receptor LILRA2. <i>Nature Microbiology</i> , 2016, 1, 16054.	5.9	54
27	The Type IVB secretion system: an enigmatic chimera. <i>Current Opinion in Microbiology</i> , 2016, 29, 22-29.	2.3	68
28	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
29	The Machinery at Endoplasmic Reticulum-Plasma Membrane Contact Sites Contributes to Spatial Regulation of Multiple Legionella Effector Proteins. <i>PLoS Pathogens</i> , 2014, 10, e1004222.	2.1	63
30	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
31	Hijacking the Host Proteasome for the Temporal Degradation of Bacterial Effectors. <i>Methods in Molecular Biology</i> , 2014, 1197, 141-152.	0.4	4
32	Amoebal Endosymbiont Neochlamydia Genome Sequence Illuminates the Bacterial Role in the Defense of the Host Amoebae against Legionella pneumophila. <i>PLoS ONE</i> , 2014, 9, e95166.	1.1	46
33	Identification and functional characterization of K ⁺ transporters encoded by Legionella pneumophila kup genes. <i>Cellular Microbiology</i> , 2013, 15, 2006-2019.	1.1	4
34	Modulation of the Ubiquitination Machinery by Legionella. <i>Current Topics in Microbiology and Immunology</i> , 2013, 376, 227-247.	0.7	34
35	Protochlamydia Induces Apoptosis of Human HEp-2 Cells through Mitochondrial Dysfunction Mediated by Chlamydial Protease-Like Activity Factor. <i>PLoS ONE</i> , 2013, 8, e56005.	1.1	13
36	Purification and Characterization of Legionella U-Box-Type E3 Ubiquitin Ligase. <i>Methods in Molecular Biology</i> , 2013, 954, 347-354.	0.4	4

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37	Type IVB Secretion Systems of Legionella and Other Gram-Negative Bacteria. <i>Frontiers in Microbiology</i> , 2011, 2, 136.	1.5	135
38	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
39	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
40	Legionella Metaeffector Exploits Host Proteasome to Temporally Regulate Cognate Effector. <i>PLoS Pathogens</i> , 2010, 6, e1001216.	2.1	162
41	<i>Legionella</i> translocates an E3 ubiquitin ligase that has multiple Uboxes with distinct functions. <i>Molecular Microbiology</i> , 2008, 67, 1307-1319.	1.2	198
42	A C-terminal translocation signal required for Dot/Icm-dependent delivery of the Legionella RalF protein to host cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 826-831.	3.3	262
43	The Structure of RalF, an ADP-ribosylation Factor Guanine Nucleotide Exchange Factor from <i>Legionella pneumophila</i> , Reveals the Presence of a Cap over the Active Site. <i>Journal of Biological Chemistry</i> , 2005, 280, 1392-1400.	1.6	92
44	Show me the substrates: modulation of host cell function by type IV secretion systems. <i>Cellular Microbiology</i> , 2003, 5, 373-383.	1.1	103
45	A Bacterial Guanine Nucleotide Exchange Factor Activates ARF on Legionella Phagosomes. <i>Science</i> , 2002, 295, 679-682.	6.0	530
46	Conformational switching of <i>Escherichia coli</i> RNA polymerase-promoter binary complex is facilitated by elongation factor GreA and GreB. <i>Genes To Cells</i> , 2001, 6, 389-401.	0.5	20
47	The DotA protein from <i>Legionella pneumophila</i> is secreted by a novel process that requires the Dot/Icm transporter. <i>EMBO Journal</i> , 2001, 20, 5962-5970.	3.5	95
48	Identification of Icm protein complexes that play distinct roles in the biogenesis of an organelle permissive for <i>Legionella pneumophila</i> intracellular growth. <i>Molecular Microbiology</i> , 2000, 38, 719-736.	1.2	166
49	Polymerase Arrest at the σ^P Promoter during Transcription Initiation. <i>Journal of Biological Chemistry</i> , 2000, 275, 10899-10904.	1.6	26
50	GroEL is involved in activation of <i>Escherichia coli</i> RNA polymerase devoid of the omega subunit in vivo. <i>FEBS Journal</i> , 1999, 266, 228-235.	0.2	49
51	Efficient solubilization of proteins overproduced as inclusion bodies by use of an extreme concentration of glycerol. <i>Technical Tips Online</i> , 1998, 3, 141-143.	0.2	2
52	Reduction in Abortive Transcription from the σ^P Promoter by Mutations in Region 3 of the β '70 Subunit of <i>Escherichia coli</i> RNA Polymerase. <i>Journal of Biological Chemistry</i> , 1998, 273, 9872-9877.	1.6	28
53	Protein footprinting technique.. <i>Seibutsu Butsuri</i> , 1998, 38, 116-118.	0.0	1
54	Functional Domains of <i>Escherichia coli</i> Single-Stranded DNA Binding Protein As Assessed by Analyses of the Deletion Mutants. <i>Biochemistry</i> , 1997, 36, 6732-6738.	1.2	20

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55	Regions of the Escherichia coli primary sigma factor σ^{70} that are involved in interaction with RNA polymerase core enzyme. <i>Genes To Cells</i> , 1997, 2, 725-734.	0.5	50
56	A distinct segment of the sigma 32 polypeptide is involved in DnaK-mediated negative control of the heat shock response in Escherichia coli.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 10280-10284.	3.3	73
57	Regulation of the Heat-Shock Response in Bacteria. <i>Annual Review of Microbiology</i> , 1993, 47, 321-350.	2.9	500
58	Heat induction of σ^{32} synthesis mediated by mRNA secondary structure: a primary step of the heat shock response in Escherichia coli. <i>Nucleic Acids Research</i> , 1993, 21, 5449-5455.	6.5	68
59	Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region. <i>Nucleic Acids Research</i> , 1992, 20, 3305-3308.	6.5	173
60	Regulation of the heat shock response in E coli: involvement of positive and negative cis-acting elements in translational control of σ^{32} synthesis. <i>Biochimie</i> , 1991, 73, 1473-1479.	1.3	17
61	Interplay of two cis-acting mRNA regions in translational control of sigma 32 synthesis during the heat shock response of Escherichia coli.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 10515-10519.	3.3	155
62	Roles and regulation of the heat shock σ factor σ^{32} in Escherichia coli. <i>Antonie Van Leeuwenhoek</i> , 1990, 58, 187-190.	0.7	12
63	Transcriptional regulation of the heat shock regulatory gene rpoH in Escherichia coli: involvement of a novel catabolite-sensitive promoter. <i>Journal of Bacteriology</i> , 1990, 172, 2710-2715.	1.0	77