List of Publications by Year in descending order

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HIROKI NACAL

| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Structural Basis of Ubiquitin Recognition by a Bacterial Ovarian Tumor Deubiquitinase LotA. Journal of Bacteriology, 2022, 204, JB0037621. | 2.2 | 11 |
| 2 | Recent advances in structural studies of the <i>Legionella pneumophila</i> Dot/Icm type IV secretion system. Microbiology and Immunology, 2022, 66, 67-74. | 1.4 | 9 |
| 3 | Requirement of phosphatidic acid binding for distribution of the bacterial protein Lpg1137 targeting syntaxin 17. Journal of Cell Science, 2022, 135, . | 2.0 | 3 |
| 4 | Reversible modification of mitochondrial ADP/ATP translocases by paired <i>Legionella</i> effector proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 6 |
| 5 | Isolation and Characterization of a Novel Phage SaGU1 that Infects Staphylococcus aureus Clinical Isolates from Patients with Atopic Dermatitis. Current Microbiology, 2021, 78, 1267-1276. | 2.2 | 17 |
| 6 | Legionella hijacks the host Golgi-to-ER retrograde pathway for the association of Legionella-containing vacuole with the ER. PLoS Pathogens, 2021, 17, e1009437. | 4.7 | 22 |
| 7 | Protocol for imaging proteins associated with Legionella-containing vacuoles in host cells. STAR Protocols, 2021, 2, 100410. | 1.2 | 0 |
| 8 | MicroRNA 142-5p promotes tumor growth in oral squamous cell carcinoma via the PI3K/AKT pathway by regulating PTEN. Heliyon, 2021, 7, e08086. | 3.2 | 10 |
| 9 | Staphylococcal Phage in Combination with Staphylococcus epidermidis as a Potential Treatment for Staphylococcus aureus-Associated Atopic Dermatitis and Suppressor of Phage-Resistant Mutants. Viruses, 2021, 13, 7. | 3.3 | 29 |
| 10 | Complete genome and bimodal genomic structure of the amoebal symbiont Neochlamydia strain S13 revealed by ultra-long reads obtained from MinION. Journal of Human Genetics, 2020, 65, 41-48. | 2.3 | 1 |
| 11 | Legionella Manipulates Non-canonical SNARE Pairing Using a Bacterial Deubiquitinase. Cell Reports, 2020, 32, 108107. | 6.4 | 19 |
| 12 | Divergence of Legionella Effectors Reversing Conventional and Unconventional Ubiquitination. Frontiers in Cellular and Infection Microbiology, 2020, 10, 448. | 3.9 | 31 |
| 13 | Structural basis for effector protein recognition by the Dot/Icm Type IVB coupling protein complex. Nature Communications, 2020, 11, 2623. | 12.8 | 29 |
| 14 | Emerging insights into bacterial deubiquitinases. Current Opinion in Microbiology, 2019, 47, 14-19. | 5.1 | 20 |
| 15 | Isolation of the Dot/Icm Type IV Secretion System Core Complex from Legionella pneumophila. Methods in Molecular Biology, 2019, 1921, 241-247. | 0.9 | 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. Environmental Microbiology Reports, 2018, 10, 344-354. | 2.4 | 9 |
| 17 | Amoebal endosymbiont Neochlamydia protects host amoebae against Legionella pneumophila infection by preventing Legionella entry. Microbes and Infection, 2018, 20, 236-244. | 1.9 | 25 |
| 18 | LotA, a <i>Legionella</i> deubiquitinase, has dual catalytic activity and contributes to intracellular growth. Cellular Microbiology, 2018, 20, e12840. | 2.1 | 53 |

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|----|--|------|-----------|
| 19 | Bacterial secretion system skews the fate of Legionella-containing vacuoles towards LC3-associated phagocytosis. Scientific Reports, 2017, 7, 44795. | 3.3 | 36 |
| 20 | Subversion of Host Membrane Dynamics by the Legionella Dot/Icm Type IV Secretion System. Current Topics in Microbiology and Immunology, 2017, 413, 221-242. | 1.1 | 13 |
| 21 | Legionella RavZ Plays a Role in Preventing Ubiquitin Recruitment to Bacteria-Containing Vacuoles. Frontiers in Cellular and Infection Microbiology, 2017, 7, 384. | 3.9 | 29 |
| 22 | Isolation of the Dot/Icm Type IV Secretion System Core Complex from Legionella pneumophila for Negative Stain Electron Microscopy Studies. Bio-protocol, 2017, 7, e2229. | 0.4 | 0 |
| 23 | 2S-B1-2Autophagy-related Host System and Legionella. Microscopy (Oxford, England), 2017, 66, i14-i14. | 1.5 | 0 |
| 24 | A Case of Brain Abscess Caused by Medication-Related Osteonecrosis of the Jaw. Case Reports in Dentistry, 2016, 2016, 1-4. | 0.5 | 6 |
| 25 | Draft Genome Sequences of <i>Legionella pneumophila</i> JR32 and Lp01 Laboratory Strains Domesticated in Japan. Genome Announcements, 2016, 4, . | 0.8 | 3 |
| 26 | Microbially cleaved immunoglobulins are sensed by the innate immune receptor LILRA2. Nature Microbiology, 2016, 1, 16054. | 13.3 | 54 |
| 27 | The Type IVB secretion system: an enigmatic chimera. Current Opinion in Microbiology, 2016, 29, 22-29. | 5.1 | 68 |
| 28 | Molecular and structural analysis of Legionella Dotl gives insights into an inner membrane complex essential for type IV secretion. Scientific Reports, 2015, 5, 10912. | 3.3 | 36 |
| 29 | The Machinery at Endoplasmic Reticulum-Plasma Membrane Contact Sites Contributes to Spatial Regulation of Multiple Legionella Effector Proteins. PLoS Pathogens, 2014, 10, e1004222. | 4.7 | 63 |
| 30 | Native structure of a type IV secretion system core complex essential for <i>Legionella</i> pathogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11804-11809. | 7.1 | 62 |
| 31 | Hijacking the Host Proteasome for the Temporal Degradation of Bacterial Effectors. Methods in Molecular Biology, 2014, 1197, 141-152. | 0.9 | 4 |
| 32 | Amoebal Endosymbiont Neochlamydia Genome Sequence Illuminates the Bacterial Role in the Defense of the Host Amoebae against Legionella pneumophila. PLoS ONE, 2014, 9, e95166. | 2.5 | 46 |
| 33 | Identification and functional characterization of K+transporters encoded byLegionella pneumophilaâ€kupgenes. Cellular Microbiology, 2013, 15, 2006-2019. | 2.1 | 4 |
| 34 | Modulation of the Ubiquitination Machinery by Legionella. Current Topics in Microbiology and Immunology, 2013, 376, 227-247. | 1.1 | 34 |
| 35 | Protochlamydia Induces Apoptosis of Human HEp-2 Cells through Mitochondrial Dysfunction Mediated by Chlamydial Protease-Like Activity Factor. PLoS ONE, 2013, 8, e56005. | 2.5 | 13 |
| 36 | Purification and Characterization of Legionella U-Box-Type E3 Ubiquitin Ligase. Methods in Molecular Biology, 2013, 954, 347-354. | 0.9 | 4 |

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|----|--|------|-----------|
| 37 | Type IVB Secretion Systems of Legionella and Other Gram-Negative Bacteria. Frontiers in Microbiology, 2011, 2, 136. | 3.5 | 135 |
| 38 | Bacterial Effector-Involved Temporal and Spatial Regulation by Hijack of the Host Ubiquitin Pathway. Frontiers in Microbiology, 2011, 2, 145. | 3.5 | 17 |
| 39 | Crystal Structure of Legionella DotD: Insights into the Relationship between Type IVB and Type II/III Secretion Systems. PLoS Pathogens, 2010, 6, e1001129. | 4.7 | 50 |
| 40 | Legionella Metaeffector Exploits Host Proteasome to Temporally Regulate Cognate Effector. PLoS Pathogens, 2010, 6, e1001216. | 4.7 | 162 |
| 41 | <i>Legionella</i> translocates an E3 ubiquitin ligase that has multiple Uâ€boxes with distinct functions. Molecular Microbiology, 2008, 67, 1307-1319. | 2.5 | 198 |
| 42 | A C-terminal translocation signal required for Dot/Icm-dependent delivery of the Legionella RalF protein to host cells. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 826-831. | 7.1 | 262 |
| 43 | The Structure of RalF, an ADP-ribosylation Factor Guanine Nucleotide Exchange Factor from Legionella pneumophila, Reveals the Presence of a Cap over the Active Site. Journal of Biological Chemistry, 2005, 280, 1392-1400. | 3.4 | 92 |
| 44 | Show me the substrates: modulation of host cell function by type IV secretion systems. Cellular Microbiology, 2003, 5, 373-383. | 2.1 | 103 |
| 45 | A Bacterial Guanine Nucleotide Exchange Factor Activates ARF on <i>Legionella</i> Phagosomes. Science, 2002, 295, 679-682. | 12.6 | 530 |
| 46 | Conformational switching ofEscherichia coliRNA polymerase-promoter binary complex is facilitated by elongation factor GreA and GreB. Genes To Cells, 2001, 6, 389-401. | 1.2 | 20 |
| 47 | The DotA protein from Legionella pneumophila is secreted by a novel process that requires the Dot/Icm transporter. EMBO Journal, 2001, 20, 5962-5970. | 7.8 | 95 |
| 48 | Identification of Icm protein complexes that play distinct roles in the biogenesis of an organelle permissive for Legionella pneumophila intracellular growth. Molecular Microbiology, 2000, 38, 719-736. | 2.5 | 166 |
| 49 | Polymerase Arrest at the λP R Promoter during Transcription Initiation. Journal of Biological Chemistry, 2000, 275, 10899-10904. | 3.4 | 26 |
| 50 | GroEL is involved in activation of Escherichia coli RNA polymerase devoid of the omega subunit in vivo. FEBS Journal, 1999, 266, 228-235. | 0.2 | 49 |
| 51 | Efficient solubilization of proteins overproduced as inclusion bodies by use of an extreme concentration of glycerol. Technical Tips Online, 1998, 3, 141-143. | 0.2 | 2 |
| 52 | Reduction in Abortive Transcription from the λPR Promoter by Mutations in Region 3 of the Ï,70 Subunit of Escherichia coli RNA Polymerase. Journal of Biological Chemistry, 1998, 273, 9872-9877. | 3.4 | 28 |
| 53 | Protein footprinting technique Seibutsu Butsuri, 1998, 38, 116-118. | 0.1 | 1 |
| 54 | Functional Domains of Escherichia coli Single-Stranded DNA Binding Protein As Assessed by Analyses of the Deletion Mutants. Biochemistry, 1997, 36, 6732-6738. | 2.5 | 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. Genes To Cells, 1997, 2, 725-734. | 1.2 | 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 Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 10280-10284. | 7.1 | 73 |
| 57 | Regulation of the Heat-Shock Response in Bacteria. Annual Review of Microbiology, 1993, 47, 321-350. | 7.3 | 500 |
| 58 | Heat induction of Î,32synthesis mediated by mRNA secondary structure: a primary step of the heat shock response inEscherichia coli. Nucleic Acids Research, 1993, 21, 5449-5455. | 14.5 | 68 |
| 59 | Systematic sequencing of theEscherichia coligenome: analysis of the 0 – 2.4 min region. Nucleic Acids Research, 1992, 20, 3305-3308. | 14.5 | 173 |
| 60 | Regulation of the heat shock response in E coli: involvement of positive and negative cis-acting elements in translational control of $lf32$ synthesis. Biochimie, 1991, 73, 1473-1479. | 2.6 | 17 |
| 61 | Interplay of two cis-acting mRNA regions in translational control of sigma 32 synthesis during the heat shock response of Escherichia coli Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 10515-10519. | 7.1 | 155 |
| 62 | Roles and regulation of the heat shock ? factor ?32 in Escherichia coli. Antonie Van Leeuwenhoek, 1990, 58, 187-190. | 1.7 | 12 |
| 63 | Transcriptional regulation of the heat shock regulatory gene rpoH in Escherichia coli: involvement of a novel catabolite-sensitive promoter, lournal of Bacteriology, 1990, 172, 2710-2715. | 2.2 | 77 |