

Carmen Buchrieser

List of Publications by Year in descending order

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156
papers

13,481
citations

23500

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111
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171
docs citations

171
times ranked

11713
citing authors

#	ARTICLE	IF	CITATIONS
1	Differentiation of the Major <i>Listeria monocytogenes</i> Serovars by Multiplex PCR. <i>Journal of Clinical Microbiology</i> , 2004, 42, 3819-3822.	1.8	915
2	<i>Escherichia coli</i> Induces DNA Double-Strand Breaks in Eukaryotic Cells. <i>Science</i> , 2006, 313, 848-851.	6.0	886
3	Evidence in the <i>Legionella pneumophila</i> genome for exploitation of host cell functions and high genome plasticity. <i>Nature Genetics</i> , 2004, 36, 1165-1173.	9.4	573
4	The genome sequence of the entomopathogenic bacterium <i>Photobacterium luminescens</i> . <i>Nature Biotechnology</i> , 2003, 21, 1307-1313.	9.4	538
5	Genome sequence of <i>Streptococcus agalactiae</i> , a pathogen causing invasive neonatal disease. <i>Molecular Microbiology</i> , 2002, 45, 1499-1513.	1.2	439
6	The virulence plasmid pWR100 and the repertoire of proteins secreted by the type III secretion apparatus of <i>Shigella flexneri</i> . <i>Molecular Microbiology</i> , 2000, 38, 760-771.	1.2	357
7	A trans-Acting Riboswitch Controls Expression of the Virulence Regulator PrfA in <i>Listeria monocytogenes</i> . <i>Cell</i> , 2009, 139, 770-779.	13.5	347
8	How to become a uropathogen: Comparative genomic analysis of extraintestinal pathogenic <i>Escherichia coli</i> strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 12879-12884.	3.3	320
9	<i>Listeria monocytogenes</i> bile salt hydrolase is a PrfA-regulated virulence factor involved in the intestinal and hepatic phases of listeriosis. <i>Molecular Microbiology</i> , 2002, 45, 1095-1106.	1.2	307
10	New Aspects Regarding Evolution and Virulence of <i>Listeria monocytogenes</i> Revealed by Comparative Genomics and DNA Arrays. <i>Infection and Immunity</i> , 2004, 72, 1072-1083.	1.0	307
11	Transcriptome analysis of <i>Listeria monocytogenes</i> identifies three groups of genes differently regulated by PrfA. <i>Molecular Microbiology</i> , 2003, 47, 1613-1625.	1.2	290
12	Analysis of Genome Plasticity in Pathogenic and Commensal <i>Escherichia coli</i> Isolates by Use of DNA Arrays. <i>Journal of Bacteriology</i> , 2003, 185, 1831-1840.	1.0	246
13	Virulence strategies for infecting phagocytes deduced from the in vivo transcriptional program of <i>Legionella pneumophila</i> . <i>Cellular Microbiology</i> , 2006, 8, 1228-1240.	1.1	241
14	<i>Legionella pneumophila</i> Effector RomA Uniquely Modifies Host Chromatin to Repress Gene Expression and Promote Intracellular Bacterial Replication. <i>Cell Host and Microbe</i> , 2013, 13, 395-405.	5.1	211
15	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014, 5, 4544.	5.8	208
16	In Vivo Transcriptional Profiling of <i>Listeria monocytogenes</i> and Mutagenesis Identify New Virulence Factors Involved in Infection. <i>PLoS Pathogens</i> , 2009, 5, e1000449.	2.1	189
17	Genomic diversity and evolution within the species <i>Streptococcus agalactiae</i> . <i>Microbes and Infection</i> , 2006, 8, 1227-1243.	1.0	188
18	Comparison of the genome sequences of <i>Listeria monocytogenes</i> and <i>Listeria innocua</i> : clues for evolution and pathogenicity. <i>FEMS Immunology and Medical Microbiology</i> , 2003, 35, 207-213.	2.7	187

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19	<i>Legionella pneumophila</i> Modulates Mitochondrial Dynamics to Trigger Metabolic Repurposing of Infected Macrophages. <i>Cell Host and Microbe</i> , 2017, 22, 302-316.e7.	5.1	187
20	The <i>Legionella pneumophila</i> response regulator LqsR promotes host cell interactions as an element of the virulence regulatory network controlled by RpoS and LetA. <i>Cellular Microbiology</i> , 2007, 9, 2903-2920.	1.1	169
21	Two small ncRNAs jointly govern virulence and transmission in <i>Legionella pneumophila</i> . <i>Molecular Microbiology</i> , 2009, 72, 741-762.	1.2	166
22	More than 18,000 effectors in the <i>Legionella</i> genus genome provide multiple, independent combinations for replication in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2265-2273.	3.3	164
23	Legionnaires' Disease: State of the Art Knowledge of Pathogenesis Mechanisms of <i>Legionella</i> . <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2020, 15, 439-466.	9.6	158
24	The high-pathogenicity island of <i>Yersinia pseudotuberculosis</i> can be inserted into any of the three chromosomal <i>asn</i> tRNA genes. <i>Molecular Microbiology</i> , 1998, 30, 965-978.	1.2	155
25	Multigenome analysis identifies a worldwide distributed epidemic <i>Legionella pneumophila</i> clone that emerged within a highly diverse species. <i>Genome Research</i> , 2008, 18, 431-441.	2.4	155
26	<i>Listeria rocourtiae</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010, 60, 2210-2214.	0.8	145
27	Analysis of the <i>Legionella longbeachae</i> Genome and Transcriptome Uncovers Unique Strategies to Cause Legionnaires' Disease. <i>PLoS Genetics</i> , 2010, 6, e1000851.	1.5	143
28	Adaptation of <i>Legionella pneumophila</i> to the host environment: role of protein secretion, effectors and eukaryotic-like proteins. <i>Current Opinion in Microbiology</i> , 2006, 9, 86-94.	2.3	142
29	Comparative and Functional Genomics of <i>Legionella</i> Identified Eukaryotic Like Proteins as Key Players in Host-Pathogen Interactions. <i>Frontiers in Microbiology</i> , 2011, 2, 208.	1.5	140
30	The 102-Kilobase Unstable Region of <i>Yersinia pestis</i> Comprises a High-Pathogenicity Island Linked to a Pigmentation Segment Which Undergoes Internal Rearrangement. <i>Journal of Bacteriology</i> , 1998, 180, 2321-2329.	1.0	133
31	Extensive recombination events and horizontal gene transfer shaped the <i>Legionella pneumophila</i> genomes. <i>BMC Genomics</i> , 2011, 12, 536.	1.2	130
32	The 102-Kilobase <i>pgm</i> Locus of <i>Yersinia pestis</i> : Sequence Analysis and Comparison of Selected Regions among Different <i>Yersinia pestis</i> and <i>Yersinia pseudotuberculosis</i> Strains. <i>Infection and Immunity</i> , 1999, 67, 4851-4861.	1.0	128
33	Targeting of host organelles by pathogenic bacteria: a sophisticated subversion strategy. <i>Nature Reviews Microbiology</i> , 2016, 14, 5-19.	13.6	124
34	<i>Legionella pneumophila</i> S1P-lyase targets host sphingolipid metabolism and restrains autophagy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1901-1906.	3.3	115
35	Metabolic reprogramming of host cells upon bacterial infection: Why shift to a Warburg-like metabolism?. <i>FEBS Journal</i> , 2018, 285, 2146-2160.	2.2	110
36	Small RNAs, 5' UTR elements and RNA-binding proteins in intracellular bacteria: impact on metabolism and virulence. <i>FEMS Microbiology Reviews</i> , 2015, 39, 331-349.	3.9	102

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37	The Legionella Autoinducer Synthase LqsA Produces an $\hat{\pm}$ -Hydroxyketone Signaling Molecule. Journal of Biological Chemistry, 2008, 283, 18113-18123.	1.6	101
38	The Life Cycle of <i>L. pneumophila</i> : Cellular Differentiation Is Linked to Virulence and Metabolism. Frontiers in Cellular and Infection Microbiology, 2018, 8, 3.	1.8	100
39	Genome sequence of <i>Vibrio splendidus</i> : an abundant planctonic marine species with a large genotypic diversity. Environmental Microbiology, 2009, 11, 1959-1970.	1.8	98
40	Deep sequencing defines the transcriptional map of <i>L. pneumophila</i> and identifies growth phase-dependent regulated ncRNAs implicated in virulence. RNA Biology, 2012, 9, 503-519.	1.5	96
41	Isotopologue Profiling of <i>Legionella pneumophila</i> . Journal of Biological Chemistry, 2010, 285, 22232-22243.	1.6	95
42	Transcriptional profiling of <i>Legionella pneumophila</i> biofilm cells and the influence of iron on biofilm formation. Microbiology (United Kingdom), 2008, 154, 30-41.	0.7	92
43	<i>Legionella</i> pathogenicity: Genome structure, regulatory networks and the host cell response. International Journal of Medical Microbiology, 2007, 297, 577-587.	1.5	88
44	Comparative genomics and transcriptomics of lineages I, II, and III strains of <i>Listeria monocytogenes</i> . BMC Genomics, 2012, 13, 144.	1.2	88
45	From Amoeba to Macrophages: Exploring the Molecular Mechanisms of <i>Legionella pneumophila</i> Infection in Both Hosts. Current Topics in Microbiology and Immunology, 2013, 376, 1-34.	0.7	88
46	NeMeSys: a biological resource for narrowing the gap between sequence and function in the human pathogen <i>Neisseria meningitidis</i> . Genome Biology, 2009, 10, R110.	13.9	86
47	The origins of eukaryotic-like proteins in <i>Legionella pneumophila</i> . International Journal of Medical Microbiology, 2010, 300, 470-481.	1.5	86
48	Pathogenomics of <i>Listeria</i> spp.. International Journal of Medical Microbiology, 2007, 297, 541-557.	1.5	84
49	Global analysis of gene expression in an <i>rpoN</i> mutant of <i>Listeria monocytogenes</i> . Microbiology (United Kingdom), 2004, 150, 1581-1590.	0.7	83
50	The <i>Legionella pneumophila</i> genome evolved to accommodate multiple regulatory mechanisms controlled by the CsrA-system. PLoS Genetics, 2017, 13, e1006629.	1.5	83
51	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnairesâ€™ disease. Genome Biology, 2014, 15, 505.	3.8	82
52	Control of Flagellar Gene Regulation in <i>Legionella pneumophila</i> and Its Relation to Growth Phase. Journal of Bacteriology, 2010, 192, 446-455.	1.0	80
53	Distinct roles of ppGpp and DksA in <i>Legionella pneumophila</i> differentiation. Molecular Microbiology, 2010, 76, 200-219.	1.2	77
54	Multiple major disease-associated clones of <i>Legionella pneumophila</i> have emerged recently and independently. Genome Research, 2016, 26, 1555-1564.	2.4	72

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55	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. <i>Microbial Genomics</i> , 2020, 6, .	1.0	69
56	The Pathogenicity Island-Associated K15 Capsule Determinant Exhibits a Novel Genetic Structure and Correlates with Virulence in Uropathogenic <i>Escherichia coli</i> Strain 536. <i>Infection and Immunity</i> , 2004, 72, 5993-6001.	1.0	67
57	Comparative Transcriptome Analysis of <i>Listeria monocytogenes</i> Strains of the Two Major Lineages Reveals Differences in Virulence, Cell Wall, and Stress Response. <i>Applied and Environmental Microbiology</i> , 2007, 73, 6078-6088.	1.4	66
58	Synergistic Contribution of the <i>Legionella pneumophila</i> lqs Genes to Pathogen-Host Interactions. <i>Journal of Bacteriology</i> , 2008, 190, 7532-7547.	1.0	66
59	Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014, 15, 505.	13.9	62
60	<i>Listeria monocytogenes</i> forms respond to cell wall deficiency by modifying gene expression and the mode of division. <i>Molecular Microbiology</i> , 2009, 73, 306-322.	1.2	61
61	Genome Dynamics in <i>Legionella</i> : The Basis of Versatility and Adaptation to Intracellular Replication. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2013, 3, a009993-a009993.	2.9	60
62	How Seryl-Phosphorylated HPr Inhibits PrfA, a Transcription Activator of <i>Listeria monocytogenes</i> Virulence Genes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2005, 9, 224-234.	1.0	59
63	The autoinducer synthase LqsA and putative sensor kinase LqsS regulate phagocyte interactions, extracellular filaments and a genomic island of <i>Legionella pneumophila</i> . <i>Environmental Microbiology</i> , 2010, 12, 1243-1259.	1.8	59
64	The <i>Legionella pneumophila</i> orphan sensor kinase LqsT regulates competence and pathogen-host interactions as a component of the LAI circuit. <i>Environmental Microbiology</i> , 2013, 15, 646-662.	1.8	59
65	Cloning and assembly strategies in microbial genome projects. <i>Microbiology (United Kingdom)</i> , 1999, 145, 2625-2634.	0.7	56
66	<i>Legionella pneumophila</i> adaptation to intracellular life and the host response: Clues from genomics and transcriptomics. <i>FEBS Letters</i> , 2007, 581, 2829-2838.	1.3	53
67	Characterization of a Variant of vga (A) Conferring Resistance to Streptogramin A and Related Compounds. <i>Antimicrobial Agents and Chemotherapy</i> , 2000, 44, 2271-2275.	1.4	50
68	The Presence of the Internalin Gene in Natural Atypically Hemolytic <i>Listeria innocua</i> Strains Suggests Descent from <i>L. monocytogenes</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 1928-1939.	1.4	49
69	Molecular mimicry: an important virulence strategy employed by <i>Legionella pneumophila</i> to subvert host functions. <i>Future Microbiology</i> , 2009, 4, 691-701.	1.0	49
70	Biodiversity of the species <i>Listeria monocytogenes</i> and the genus <i>Listeria</i> . <i>Microbes and Infection</i> , 2007, 9, 1147-1155.	1.0	48
71	<i>Legionella pneumophila</i> type IV effectors hijack the transcription and translation machinery of the host cell. <i>Trends in Cell Biology</i> , 2014, 24, 771-778.	3.6	46
72	<i>Legionella pneumophila</i> CsrA regulates a metabolic switch from amino acid to glycerolipid metabolism. <i>Open Biology</i> , 2017, 7, 170149.	1.5	46

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73	Characterization of the flexible genome complement of the commensal <i>Escherichia coli</i> strain AO 34/86 (O83â€š:â€šK24â€š:â€šSH31). <i>Microbiology (United Kingdom)</i> , 2005, 151, 385-398.	0.7	45
74	<sc>IroT/mavN</sc>, a new iron-regulated gene involved in <sc>Legionella pneumophila</sc> virulence against amoebae and macrophages. <i>Environmental Microbiology</i> , 2015, 17, 1338-1350.	1.8	45
75	Molecular Mimicry: a Paradigm of Host-Microbe Coevolution Illustrated by <sc>Legionella</sc>. <i>MBio</i> , 2020, 11, .	1.8	45
76	Modulation of Host Autophagy during Bacterial Infection: Sabotaging Host Munitions for Pathogen Nutrition. <i>Frontiers in Immunology</i> , 2016, 7, 81.	2.2	44
77	The High-Pathogenicity Island of <sc>Yersinia enterocolitica</sc> Ye8081 Undergoes Low-Frequency Deletion but Not Precise Excision, Suggesting Recent Stabilization in the Genome. <i>Infection and Immunity</i> , 1999, 67, 5091-5099.	1.0	42
78	DNA Microarray for Identification and Typing of <i>Staphylococcus aureus</i> Isolates. <i>Journal of Clinical Microbiology</i> , 2004, 42, 2054-2064.	1.8	41
79	Dynamics and impact of homologous recombination on the evolution of <i>Legionella pneumophila</i> . <i>PLoS Genetics</i> , 2017, 13, e1006855.	1.5	41
80	Pathogenomics of mobile genetic elements of toxigenic bacteria. <i>International Journal of Medical Microbiology</i> , 2004, 293, 453-461.	1.5	40
81	Growth-phase-dependent mobility of the <i>lvh</i> -encoding region in <i>Legionella pneumophila</i> strain Paris. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3561-3568.	0.7	38
82	The Î±-hydroxyketone LAI-1 regulates motility, Lqs-dependent phosphorylation signalling and gene expression of <sc>Legionella pneumophila</sc>. <i>Molecular Microbiology</i> , 2016, 99, 778-793.	1.2	38
83	Genetic diversity of <i>Listeria monocytogenes</i> recovered from infected persons and pork, seafood and dairy products on retail sale in France during 2000 and 2001. <i>International Journal of Food Microbiology</i> , 2007, 114, 187-194.	2.1	37
84	Circadian Clock Proteins in Prokaryotes: Hidden Rhythms?. <i>Frontiers in Microbiology</i> , 2010, 1, 130.	1.5	36
85	GamA is a eukaryotic-like glucoamylase responsible for glycogen- and starch-degrading activity of <i>Legionella pneumophila</i> . <i>International Journal of Medical Microbiology</i> , 2011, 301, 133-139.	1.5	36
86	Metabolic reprogramming: an innate cellular defence mechanism against intracellular bacteria?. <i>Current Opinion in Immunology</i> , 2019, 60, 117-123.	2.4	36
87	Dichotomous metabolic networks govern human ILC2 proliferation and function. <i>Nature Immunology</i> , 2021, 22, 1367-1374.	7.0	34
88	Translocated <i>Legionella pneumophila</i> small RNAs mimic eukaryotic microRNAs targeting the host immune response. <i>Nature Communications</i> , 2022, 13, 762.	5.8	34
89	Bacterial remodelling of the host epigenome: functional role and evolution of effectors methylating host histones. <i>Cellular Microbiology</i> , 2015, 17, 1098-1107.	1.1	33
90	Symbiont-Mediated Defense against <i>Legionella pneumophila</i> in Amoebae. <i>MBio</i> , 2019, 10, .	1.8	33

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91	Polarized mitochondria as guardians of NK cell fitness. <i>Blood Advances</i> , 2021, 5, 26-38.	2.5	32
92	Significant Role for <i>ladC</i> in Initiation of <i>Legionella pneumophila</i> Infection. <i>Infection and Immunity</i> , 2008, 76, 3075-3085.	1.0	31
93	The <i>Legionella pneumophila</i> LetA/LetS Two-Component System Exhibits Rheostat-Like Behavior. <i>Infection and Immunity</i> , 2010, 78, 2571-2583.	1.0	30
94	Biological Diversity and Evolution of Type IV Secretion Systems. <i>Current Topics in Microbiology and Immunology</i> , 2017, 413, 1-30.	0.7	29
95	Post-translational modifications of host proteins by <i>Legionella pneumophila</i> : a sophisticated survival strategy. <i>Future Microbiology</i> , 2012, 7, 369-381.	1.0	28
96	<i>Legionella pneumophila</i> restrains autophagy by modulating the host's sphingolipid metabolism. <i>Autophagy</i> , 2016, 12, 1053-1054.	4.3	28
97	Fatty acid composition modulates sensitivity of <i>Legionella pneumophila</i> to warnericin RK, an antimicrobial peptide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 1146-1153.	1.4	27
98	A Ca ²⁺ -regulated deAMPylation switch in human and bacterial FIC proteins. <i>Nature Communications</i> , 2019, 10, 1142.	5.8	27
99	The <i>Legionella pneumophila</i> <i>kai</i> operon is implicated in stress response and confers fitness in competitive environments. <i>Environmental Microbiology</i> , 2014, 16, 359-381.	1.8	26
100	Intracellular parasitism, the driving force of evolution of <i>Legionella pneumophila</i> and the genus <i>Legionella</i> . <i>Genes and Immunity</i> , 2019, 20, 394-402.	2.2	25
101	An improved direct viable count for the enumeration of bacteria in milk. <i>International Journal of Food Microbiology</i> , 1993, 20, 227-237.	2.1	24
102	<i>Listeria monocytogenes</i> and the Genus <i>Listeria</i> . , 2006, , 404-476.		23
103	<i>Legionella pneumophila</i> transcriptional response to chlorine treatment. <i>Water Research</i> , 2012, 46, 808-816.	5.3	22
104	A Comprehensive Review on the Manipulation of the Sphingolipid Pathway by Pathogenic Bacteria. <i>Frontiers in Cell and Developmental Biology</i> , 2019, 7, 168.	1.8	22
105	Population variation in NAIP functional copy number confers increased cell death upon <i>Legionella pneumophila</i> infection. <i>Human Immunology</i> , 2012, 73, 196-200.	1.2	21
106	Targeting of RNA Polymerase II by a nuclear <i>Legionella pneumophila</i> Dot/Icm effector SnpL. <i>Cellular Microbiology</i> , 2018, 20, e12852.	1.1	21
107	Induction of Competence for Natural Transformation in <i>Legionella pneumophila</i> and Exploitation for Mutant Construction. <i>Methods in Molecular Biology</i> , 2013, 954, 183-195.	0.4	19
108	Nicotinic Acid Modulates <i>Legionella pneumophila</i> Gene Expression and Induces Virulence Traits. <i>Infection and Immunity</i> , 2013, 81, 945-955.	1.0	19

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109	The pleiotropic <i>Legionella</i> transcription factor LvbR links the Lqs and c-di-GMP regulatory networks to control biofilm architecture and virulence. <i>Environmental Microbiology</i> , 2019, 21, 1035-1053.	1.8	19
110	Human single-chain urokinase is activated by the ompTins PgtE of <i>Salmonella enterica</i> and P of <i>Yersinia pestis</i> despite mutations of active site residues. <i>Molecular Microbiology</i> , 2013, 89, 507-517.	1.2	18
111	Evolution and function of bacterial RCC1 repeat effectors. <i>Cellular Microbiology</i> , 2020, 22, e13246.	1.1	18
112	The evolution and role of eukaryotic-like domains in environmental intracellular bacteria: the battle with a eukaryotic cell. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	18
113	<i>Legionella longbeachae</i> is immunologically silent and highly virulent <i>in vivo</i> . <i>Journal of Infectious Diseases</i> , 2017, 215, jiw560.	1.9	16
114	Intracellular parasitism, the driving force of evolution of <i>Legionella pneumophila</i> and the genus <i>Legionella</i> . <i>Microbes and Infection</i> , 2019, 21, 230-236.	1.0	16
115	A Unique cis-Encoded Small Noncoding RNA Is Regulating <i>Legionella pneumophila</i> Hfq Expression in a Life Cycle-Dependent Manner. <i>MBio</i> , 2017, 8, .	1.8	15
116	Microbe Profile: <i>Legionella pneumophila</i> - a copycat eukaryote. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	0.7	14
117	MAMs are attractive targets for bacterial repurposing of the host cell. <i>BioEssays</i> , 2017, 39, 1600171.	1.2	13
118	The <i>Legionella pneumophila</i> Methyltransferase RomA Methylates Also Non-histone Proteins during Infection. <i>Journal of Molecular Biology</i> , 2018, 430, 1912-1925.	2.0	13
119	Characterization of an acetyltransferase that detoxifies aromatic chemicals in <i>Legionella pneumophila</i> . <i>Biochemical Journal</i> , 2012, 445, 219-228.	1.7	12
120	Legionnaires™ Disease. , 2013, , 147-217.		12
121	Evolutionary Dissection of the Dot/Icm System Based on Comparative Genomics of 58 <i>Legionella</i> Species. <i>Genome Biology and Evolution</i> , 2019, 11, 2619-2632.	1.1	12
122	Use of DNA arrays for the analysis of outbreak-related strains of <i>Listeria monocytogenes</i> . <i>International Journal of Medical Microbiology</i> , 2006, 296, 559-562.	1.5	11
123	Divergent Evolution of <i>Legionella</i> RCC1 Repeat Effectors Defines the Range of Ran GTPase Cycle Targets. <i>MBio</i> , 2020, 11, .	1.8	11
124	<i>Legionella</i> : from protozoa to humans. <i>Frontiers in Microbiology</i> , 2011, 2, 182.	1.5	10
125	Patho-epigenetics: histone deacetylases as targets of pathogens and therapeutics. <i>MicroLife</i> , 2021, 2, .	1.0	9
126	Pathogenomics: An updated European Research Agenda. <i>Infection, Genetics and Evolution</i> , 2008, 8, 386-393.	1.0	8

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127	Analysis of the Pulmonary Microbiome Composition of Legionella pneumophila-Infected Patients. <i>Methods in Molecular Biology</i> , 2019, 1921, 429-443.	0.4	8
128	Reverting the mode of action of the mitochondrial FOF1-ATPase by Legionella pneumophila preserves its replication niche. <i>ELife</i> , 2021, 10, .	2.8	8
129	Specific regions of genome plasticity and genetic diversity of the commensal Escherichia coli A0 34/86. <i>International Journal of Medical Microbiology</i> , 2006, 296, 541-546.	1.5	7
130	Co-immunoprecipitation: Proteinâ€“RNA and Proteinâ€“DNA Interaction. <i>Methods in Molecular Biology</i> , 2013, 954, 583-593.	0.4	7
131	Persistent Legionnairesâ€™ Disease and Associated Antibiotic Treatment Engender a Highly Disturbed Pulmonary Microbiome Enriched in Opportunistic Microorganisms. <i>MBio</i> , 2020, 11, .	1.8	6
132	Danger-associated metabolic modifications during bacterial infection of macrophages. <i>International Immunology</i> , 2020, 32, 475-483.	1.8	6
133	Manipulation of Autophagy by Bacterial Pathogens Impacts Host Immunity. <i>Current Issues in Molecular Biology</i> , 2018, 25, 81-98.	1.0	5
134	Genomic erosion and horizontal gene transfer shape functional differences of the ExlA toxin in Pseudomonas spp.. <i>IScience</i> , 2022, 25, 104596.	1.9	5
135	A plague o' both your hosts. <i>Nature</i> , 2001, 413, 467-469.	13.7	4
136	Genetic Tools for Use with Listeria monocytogenes. , 0, , 620-633.		4
137	Genomics of Listeria monocytogenes and Other Members of the Genus Listeria. , 0, , 125-145.		3
138	Legionella Effectors Explored with INSeq: New Functional Insights. <i>Trends in Microbiology</i> , 2018, 26, 169-170.	3.5	2
139	Mitochondrial Dynamics and Activity in Legionella-Infected Cells. <i>Methods in Molecular Biology</i> , 2019, 1921, 205-220.	0.4	2
140	Sorting of Phagocytic Cells Infected with Legionella pneumophila. <i>Methods in Molecular Biology</i> , 2019, 1921, 179-189.	0.4	2
141	Listeria Genomics. , 2007, , 33-62.		1
142	From functional genomics to systems (micro)biology. <i>Current Opinion in Microbiology</i> , 2009, 12, 528-530.	2.3	1
143	cDNA Library Construction for Next-Generation Sequencing to Determine the Transcriptional Landscape of Legionella pneumophila. <i>Methods in Molecular Biology</i> , 2013, 954, 555-566.	0.4	1
144	Editorial overview: Hostâ€“pathogen interactions shaped through evolutionary and regulatory processes. <i>Current Opinion in Microbiology</i> , 2018, 41, v-viii.	2.3	1

#	ARTICLE	IF	CITATIONS
145	Celebrating the career and legacy of Professor Pascale Cossart. <i>Molecular Microbiology</i> , 2020, 113, 535-537.	1.2	1
146	Gene Expression and Virulence in <i>Legionella</i> : the Flagellar Regulon. , 0, , 327-332.		1
147	<i>Legionella pneumophila</i> Pathogenesis: Lessons Learned from Genomics. , 2008, , 1-31.		1
148	GÃ©nÃ©mique comparative. <i>Annales De L'Institut Pasteur / ActualitÃ©s</i> , 2002, 11, 33-49.	0.1	0
149	<i>Listeriae</i> . , 2006, , .		0
150	Genomics of the Opportunistic Pathogen <i>Legionella pneumophila</i> . , 2006, , 315-337.		0
151	Frank Kunst, 1943â€”2009. <i>Molecular Microbiology</i> , 2009, 74, 253-256.	1.2	0
152	What Genomics Has Taught Us about Intracellular Pathogens: the Example of <i>Listeria monocytogenes</i> . , 2014, , 361-391.		0
153	Editorial: Pathogens and disease special issue ETOX18. <i>Pathogens and Disease</i> , 2019, 77, .	0.8	0
154	Evolution of <i>Listeria monocytogenes</i> . , 0, , 489-499.		0
155	Genome Sequencing and Genomics. , 0, , 377-380.		0
156	Manipulation of Autophagy by Bacterial Pathogens Impacts Host Immunity. , 2017, , .		0