

Carmen Buchrieser

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151
papers

10,635
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53
h-index

101
g-index

171
ext. papers

12,429
ext. citations

7.7
avg, IF

5.99
L-index

#	Paper	IF	Citations
151	Differentiation of the major <i>Listeria monocytogenes</i> serovars by multiplex PCR. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 3819-22	9.7	736
150	<i>Escherichia coli</i> induces DNA double-strand breaks in eukaryotic cells. <i>Science</i> , 2006 , 313, 848-51	33.3	661
149	Evidence in the <i>Legionella pneumophila</i> genome for exploitation of host cell functions and high genome plasticity. <i>Nature Genetics</i> , 2004 , 36, 1165-73	36.3	508
148	The genome sequence of the entomopathogenic bacterium <i>Photobacterium luminescens</i> . <i>Nature Biotechnology</i> , 2003 , 21, 1307-13	44.5	485
147	Genome sequence of <i>Streptococcus agalactiae</i> , a pathogen causing invasive neonatal disease. <i>Molecular Microbiology</i> , 2002 , 45, 1499-513	4.1	386
146	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, 760-71	4.1	305
145	A trans-acting riboswitch controls expression of the virulence regulator PrfA in <i>Listeria monocytogenes</i> . <i>Cell</i> , 2009 , 139, 770-9	56.2	291
144	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, 12879-84	11.5	286
143	<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, 1095-106	4.1	267
142	Transcriptome analysis of <i>Listeria monocytogenes</i> identifies three groups of genes differently regulated by PrfA. <i>Molecular Microbiology</i> , 2003 , 47, 1613-25	4.1	265
141	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, 1072-83	3.7	244
140	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, 1831-40	3.5	218
139	Virulence strategies for infecting phagocytes deduced from the in vivo transcriptional program of <i>Legionella pneumophila</i> . <i>Cellular Microbiology</i> , 2006 , 8, 1228-40	3.9	204
138	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	7.6	164
137	<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	23.4	159
136	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, 207-13		155
135	Genomic diversity and evolution within the species <i>Streptococcus agalactiae</i> . <i>Microbes and Infection</i> , 2006 , 8, 1227-43	9.3	153

134	Streptococcus agalactiae clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014 , 5, 4544	17.4	144
133	The high-pathogenicity island of <i>Yersinia pseudotuberculosis</i> can be inserted into any of the three chromosomal asn tRNA genes. <i>Molecular Microbiology</i> , 1998 , 30, 965-78	4.1	142
132	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	7.9	133
131	Two small ncRNAs jointly govern virulence and transmission in <i>Legionella pneumophila</i> . <i>Molecular Microbiology</i> , 2009 , 72, 741-62	4.1	131
130	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, 431-41	9.7	131
129	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, 2903-20	3.9	128
128	Analysis of the <i>Legionella longbeachae</i> genome and transcriptome uncovers unique strategies to cause Legionnaires' disease. <i>PLoS Genetics</i> , 2010 , 6, e1000851	6	126
127	<i>Listeria rocourtiae</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010 , 60, 2210-2214	2.2	119
126	Comparative and functional genomics of legionella identified eukaryotic like proteins as key players in host-pathogen interactions. <i>Frontiers in Microbiology</i> , 2011 , 2, 208	5.7	114
125	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, 2321-9	3.5	111
124	The 102-kilobase pgm 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, 4851-61	3.7	109
123	<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	23.4	104
122	Extensive recombination events and horizontal gene transfer shaped the <i>Legionella pneumophila</i> genomes. <i>BMC Genomics</i> , 2011 , 12, 536	4.5	104
121	Targeting of host organelles by pathogenic bacteria: a sophisticated subversion strategy. <i>Nature Reviews Microbiology</i> , 2016 , 14, 5-19	22.2	96
120	<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, 1901-6	11.5	91
119	Genome sequence of <i>Vibrio splendidus</i> : an abundant planctonic marine species with a large genotypic diversity. <i>Environmental Microbiology</i> , 2009 , 11, 1959-70	5.2	88
118	The <i>Legionella</i> autoinducer synthase LqsA produces an alpha-hydroxyketone signaling molecule. <i>Journal of Biological Chemistry</i> , 2008 , 283, 18113-23	5.4	87
117	More than 18,000 effectors in the 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	11.5	85

116	Transcriptional profiling of Legionella pneumophila biofilm cells and the influence of iron on biofilm formation. <i>Microbiology (United Kingdom)</i> , 2008 , 154, 30-41	2.9	83
115	Small RNAs, 5' UTR elements and RNA-binding proteins in intracellular bacteria: impact on metabolism and virulence. <i>FEMS Microbiology Reviews</i> , 2015 , 39, 331-49	15.1	81
114	Isotopologue profiling of Legionella pneumophila: role of serine and glucose as carbon substrates. <i>Journal of Biological Chemistry</i> , 2010 , 285, 22232-43	5.4	79
113	NeMeSys: a biological resource for narrowing the gap between sequence and function in the human pathogen Neisseria meningitidis. <i>Genome Biology</i> , 2009 , 10, R110	18.3	78
112	Global analysis of gene expression in an rpoN mutant of Listeria monocytogenes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 1581-1590	2.9	77
111	Legionella pathogenicity: genome structure, regulatory networks and the host cell response. <i>International Journal of Medical Microbiology</i> , 2007 , 297, 577-87	3.7	76
110	The origins of eukaryotic-like proteins in Legionella pneumophila. <i>International Journal of Medical Microbiology</i> , 2010 , 300, 470-81	3.7	72
109	Metabolic reprogramming of host cells upon bacterial infection: Why shift to a Warburg-like metabolism?. <i>FEBS Journal</i> , 2018 , 285, 2146-2160	5.7	71
108	From amoeba to macrophages: exploring the molecular mechanisms of Legionella pneumophila infection in both hosts. <i>Current Topics in Microbiology and Immunology</i> , 2013 , 376, 1-34	3.3	70
107	Deep sequencing defines the transcriptional map of L. pneumophila and identifies growth phase-dependent regulated ncRNAs implicated in virulence. <i>RNA Biology</i> , 2012 , 9, 503-19	4.8	69
106	Pathogenomics of Listeria spp. <i>International Journal of Medical Microbiology</i> , 2007 , 297, 541-57	3.7	68
105	Comparative analyses of Legionella species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014 , 15, 505	18.3	65
104	Comparative genomics and transcriptomics of lineages I, II, and III strains of Listeria monocytogenes. <i>BMC Genomics</i> , 2012 , 13, 144	4.5	60
103	Distinct roles of ppGpp and DksA in Legionella pneumophila differentiation. <i>Molecular Microbiology</i> , 2010 , 76, 200-19	4.1	58
102	Synergistic contribution of the Legionella pneumophila lqs genes to pathogen-host interactions. <i>Journal of Bacteriology</i> , 2008 , 190, 7532-47	3.5	57
101	Legionnaires' Disease: State of the Art Knowledge of Pathogenesis Mechanisms of. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2020 , 15, 439-466	34	56
100	The pathogenicity island-associated K15 capsule determinant exhibits a novel genetic structure and correlates with virulence in uropathogenic Escherichia coli strain 536. <i>Infection and Immunity</i> , 2004 , 72, 5993-6001	3.7	54
99	How seryl-phosphorylated HPr inhibits PrfA, a transcription activator of Listeria monocytogenes virulence genes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2005 , 9, 224-34	0.9	53

98	The Legionella pneumophila orphan sensor kinase LqsT regulates competence and pathogen-host interactions as a component of the LAI-1 circuit. <i>Environmental Microbiology</i> , 2013 , 15, 646-62	5.2	50
97	The autoinducer synthase LqsA and putative sensor kinase LqsS regulate phagocyte interactions, extracellular filaments and a genomic island of Legionella pneumophila. <i>Environmental Microbiology</i> , 2010 , 12, 1243-59	5.2	49
96	Comparative transcriptome analysis of Listeria monocytogenes strains of the two major lineages reveals differences in virulence, cell wall, and stress response. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 6078-88	4.8	49
95	Comparative analyses of Legionella species identifies genetic features of strains causing Legionnaires' disease 2014 , 15, 505		49
94	Genome dynamics in Legionella: the basis of versatility and adaptation to intracellular replication. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2013 , 3,	5.4	48
93	Characterization of a variant of vga(A) conferring resistance to streptogramin A and related compounds. <i>Antimicrobial Agents and Chemotherapy</i> , 2000 , 44, 2271-5	5.9	48
92	Cloning and assembly strategies in microbial genome projects. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 10), 2625-34	2.9	48
91	Multiple major disease-associated clones of Legionella pneumophila have emerged recently and independently. <i>Genome Research</i> , 2016 , 26, 1555-1564	9.7	48
90	The Life Cycle of : Cellular Differentiation Is Linked to Virulence and Metabolism. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018 , 8, 3	5.9	47
89	Control of flagellar gene regulation in Legionella pneumophila and its relation to growth phase. <i>Journal of Bacteriology</i> , 2010 , 192, 446-55	3.5	47
88	Legionella pneumophila adaptation to intracellular life and the host response: clues from genomics and transcriptomics. <i>FEBS Letters</i> , 2007 , 581, 2829-38	3.8	47
87	Listeria monocytogenes L-forms respond to cell wall deficiency by modifying gene expression and the mode of division. <i>Molecular Microbiology</i> , 2009 , 73, 306-22	4.1	46
86	The Legionella pneumophila genome evolved to accommodate multiple regulatory mechanisms controlled by the CsrA-system. <i>PLoS Genetics</i> , 2017 , 13, e1006629	6	45
85	The presence of the internalin gene in natural atypically hemolytic Listeria innocua strains suggests descent from L. monocytogenes. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 1928-39	4.8	44
84	Characterization of the flexible genome complement of the commensal Escherichia coli strain A0 34/86 (O83 : K24 : H31). <i>Microbiology (United Kingdom)</i> , 2005 , 151, 385-398	2.9	42
83	Biodiversity of the species Listeria monocytogenes and the genus Listeria. <i>Microbes and Infection</i> , 2007 , 9, 1147-55	9.3	41
82	Molecular mimicry: an important virulence strategy employed by Legionella pneumophila to subvert host functions. <i>Future Microbiology</i> , 2009 , 4, 691-701	2.9	40
81	Pathogenomics of mobile genetic elements of toxigenic bacteria. <i>International Journal of Medical Microbiology</i> , 2004 , 293, 453-61	3.7	40

80	The high-pathogenicity island of <i>Yersinia enterocolitica</i> Ye8081 undergoes low-frequency deletion but not precise excision, suggesting recent stabilization in the genome. <i>Infection and Immunity</i> , 1999 , 67, 5091-9	3.7	38
79	<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, 771-8	18.3	37
78	Modulation of Host Autophagy during Bacterial Infection: Sabotaging Host Munitions for Pathogen Nutrition. <i>Frontiers in Immunology</i> , 2016 , 7, 81	8.4	37
77	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	2.9	35
76	DNA microarray for identification and typing of <i>Staphylococcus aureus</i> isolates. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 2054-64	9.7	35
75	IroT/mavN, a new iron-regulated gene involved in <i>Legionella pneumophila</i> virulence against amoebae and macrophages. <i>Environmental Microbiology</i> , 2015 , 17, 1338-50	5.2	34
74	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, 133-9	3.7	33
73	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, 187-94	5.8	32
72	The β -hydroxyketone LAI-1 regulates motility, Lqs-dependent phosphorylation signalling and gene expression of <i>Legionella pneumophila</i> . <i>Molecular Microbiology</i> , 2016 , 99, 778-93	4.1	29
71	Circadian clock proteins in prokaryotes: hidden rhythms?. <i>Frontiers in Microbiology</i> , 2010 , 1, 130	5.7	28
70	The <i>Legionella pneumophila</i> LetA/LetS two-component system exhibits rheostat-like behavior. <i>Infection and Immunity</i> , 2010 , 78, 2571-83	3.7	25
69	Significant role for <i>ladC</i> in initiation of <i>Legionella pneumophila</i> infection. <i>Infection and Immunity</i> , 2008 , 76, 3075-85	3.7	25
68	Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. <i>Microbial Genomics</i> , 2020 , 6,	4.4	25
67	<i>CsrA</i> regulates a metabolic switch from amino acid to glycerolipid metabolism. <i>Open Biology</i> , 2017 , 7,	7	23
66	<i>Legionella pneumophila</i> restrains autophagy by modulating the host's sphingolipid metabolism. <i>Autophagy</i> , 2016 , 12, 1053-4	10.2	22
65	Biological Diversity and Evolution of Type IV Secretion Systems. <i>Current Topics in Microbiology and Immunology</i> , 2017 , 413, 1-30	3.3	21
64	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, 359-81	5.2	21
63	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	2.3	21

62	Post-translational modifications of host proteins by Legionella pneumophila: a sophisticated survival strategy. <i>Future Microbiology</i> , 2012 , 7, 369-81	2.9	21
61	Dynamics and impact of homologous recombination on the evolution of Legionella pneumophila. <i>PLoS Genetics</i> , 2017 , 13, e1006855	6	21
60	Symbiont-Mediated Defense against Legionella pneumophila in Amoebae. <i>MBio</i> , 2019 , 10,	7.8	20
59	Bacterial remodelling of the host epigenome: functional role and evolution of effectors methylating host histones. <i>Cellular Microbiology</i> , 2015 , 17, 1098-107	3.9	19
58	Listeria monocytogenes and the Genus Listeria 2006 , 404-476		18
57	Metabolic reprogramming: an innate cellular defence mechanism against intracellular bacteria?. <i>Current Opinion in Immunology</i> , 2019 , 60, 117-123	7.8	17
56	Legionella pneumophila transcriptional response to chlorine treatment. <i>Water Research</i> , 2012 , 46, 808-162.5	12.5	17
55	Fatty acid composition modulates sensitivity of Legionella pneumophila to warnericin RK, an antimicrobial peptide. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 1146-53	3.8	17
54	An improved direct viable count for the enumeration of bacteria in milk. <i>International Journal of Food Microbiology</i> , 1993 , 20, 227-37	5.8	17
53	Molecular Mimicry: a Paradigm of Host-Microbe Coevolution Illustrated by. <i>MBio</i> , 2020 , 11,	7.8	17
52	Human single-chain urokinase is activated by the ompTins PgtE of Salmonella enterica and Pla of Yersinia pestis despite mutations of active site residues. <i>Molecular Microbiology</i> , 2013 , 89, 507-17	4.1	16
51	Induction of competence for natural transformation in Legionella pneumophila and exploitation for mutant construction. <i>Methods in Molecular Biology</i> , 2013 , 954, 183-95	1.4	16
50	Nicotinic acid modulates Legionella pneumophila gene expression and induces virulence traits. <i>Infection and Immunity</i> , 2013 , 81, 945-55	3.7	16
49	Intracellular parasitism, the driving force of evolution of Legionella pneumophila and the genus Legionella. <i>Genes and Immunity</i> , 2019 , 20, 394-402	4.4	14
48	A Ca-regulated deAMPylation switch in human and bacterial FIC proteins. <i>Nature Communications</i> , 2019 , 10, 1142	17.4	14
47	Polarized mitochondria as guardians of NK cell fitness. <i>Blood Advances</i> , 2021 , 5, 26-38	7.8	14
46	Characterization of an acetyltransferase that detoxifies aromatic chemicals in Legionella pneumophila. <i>Biochemical Journal</i> , 2012 , 445, 219-28	3.8	12
45	A Comprehensive Review on the Manipulation of the Sphingolipid Pathway by Pathogenic Bacteria. <i>Frontiers in Cell and Developmental Biology</i> , 2019 , 7, 168	5.7	11

44	Targeting of RNA Polymerase II by a nuclear Legionella pneumophila Dot/Icm effector SnpL. <i>Cellular Microbiology</i> , 2018 , 20, e12852	3.9	11
43	Legionella longbeachae Is Immunologically Silent and Highly Virulent In Vivo. <i>Journal of Infectious Diseases</i> , 2017 , 215, 440-451	7	11
42	A Unique cis-Encoded Small Noncoding RNA Is Regulating Legionella pneumophila Hfq Expression in a Life Cycle-Dependent Manner. <i>MBio</i> , 2017 , 8,	7.8	10
41	Legionnaires Disease 2013 , 147-217		10
40	The pleiotropic Legionella 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	5.2	10
39	The Legionella pneumophila Methyltransferase RomA Methylates Also Non-histone Proteins during Infection. <i>Journal of Molecular Biology</i> , 2018 , 430, 1912-1925	6.5	9
38	Use of DNA arrays for the analysis of outbreak-related strains of Listeria monocytogenes. <i>International Journal of Medical Microbiology</i> , 2006 , 296, 559-62	3.7	9
37	MAMs are attractive targets for bacterial repurposing of the host cell: MAM-functions might be key for undermining an infected cell. <i>BioEssays</i> , 2017 , 39, 1600171	4.1	8
36	Specific regions of genome plasticity and genetic diversity of the commensal Escherichia coli A034/86. <i>International Journal of Medical Microbiology</i> , 2006 , 296, 541-6	3.7	7
35	Dichotomous metabolic networks govern human ILC2 proliferation and function. <i>Nature Immunology</i> , 2021 , 22, 1367-1374	19.1	7
34	Co-immunoprecipitation: protein-RNA and protein-DNA interaction. <i>Methods in Molecular Biology</i> , 2013 , 954, 583-93	1.4	6
33	Legionella: from protozoa to humans. <i>Frontiers in Microbiology</i> , 2011 , 2, 182	5.7	6
32	Pathogenomics: an updated European Research Agenda. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 386-93	3.5	6
31	The Genus Listeria and Listeria monocytogenes. <i>Food Additives</i> , 2007 , 1-20		6
30	Divergent Evolution of RCC1 Repeat Effectors Defines the Range of Ran GTPase Cycle Targets. <i>MBio</i> , 2020 , 11,	7.8	5
29	Manipulation of Autophagy by Bacterial Pathogens Impacts Host Immunity. <i>Current Issues in Molecular Biology</i> , 2018 , 25, 81-98	2.9	5
28	Analysis of the Pulmonary Microbiome Composition of Legionella pneumophila-Infected Patients. <i>Methods in Molecular Biology</i> , 2019 , 1921, 429-443	1.4	4
27	Intracellular parasitism, the driving force of evolution of Legionella pneumophila and the genus Legionella. <i>Microbes and Infection</i> , 2019 , 21, 230-236	9.3	4

26	Danger-associated metabolic modifications during bacterial infection of macrophages. <i>International Immunology</i> , 2020 , 32, 475-483	4.9	4
25	Genetic Tools for Use with <i>Listeria monocytogenes</i> 620-633		4
24	Persistent Legionnaires' Disease and Associated Antibiotic Treatment Engender a Highly Disturbed Pulmonary Microbiome Enriched in Opportunistic Microorganisms. <i>MBio</i> , 2020 , 11,	7.8	3
23	Translocated <i>Legionella pneumophila</i> small RNAs mimic eukaryotic microRNAs targeting the host immune response.. <i>Nature Communications</i> , 2022 , 13, 762	17.4	3
22	Genomics of <i>Listeria monocytogenes</i> and Other Members of the Genus <i>Listeria</i> 125-145		3
21	Evolution and function of bacterial RCC1 repeat effectors. <i>Cellular Microbiology</i> , 2020 , 22, e13246	3.9	3
20	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	3.9	2
19	<i>Legionella</i> Effectors Explored with INSeq: New Functional Insights. <i>Trends in Microbiology</i> , 2018 , 26, 169-174	17.4	2
18	Patho-epigenetics: histone deacetylases as targets of pathogens and therapeutics. <i>MicroLife</i> ,	5	2
17	Interdomain Horizontal Gene Transfer Shaped the Genomes of <i>Legionella pneumophila</i> and <i>Legionella longbeachae</i> 2013 , 199-219		2
16	Microbe Profile: - a copycat eukaryote.. <i>Microbiology (United Kingdom)</i> , 2022 , 168,	2.9	2
15	Mitochondrial Dynamics and Activity in <i>Legionella</i> -Infected Cells. <i>Methods in Molecular Biology</i> , 2019 , 1921, 205-220	1.4	1
14	cDNA library construction for next-generation sequencing to determine the transcriptional landscape of <i>Legionella pneumophila</i> . <i>Methods in Molecular Biology</i> , 2013 , 954, 555-66	1.4	1
13	<i>Listeria</i> Genomics 2007 , 33-62		1
12	Gene Expression and Virulence in <i>Legionella</i> : the Flagellar Regulon 327-332		1
11	<i>Legionella pneumophila</i> Pathogenesis: Lessons Learned from Genomics 2008 , 1-31		1
10	Reverting the mode of action of the mitochondrial FF-ATPase by preserves its replication niche. <i>ELife</i> , 2021 , 10,	8.9	1
9	Sorting of Phagocytic Cells Infected with <i>Legionella pneumophila</i> . <i>Methods in Molecular Biology</i> , 2019 , 1921, 179-189	1.4	0

- 8 Celebrating the career and legacy of Professor Pascale Cossart. *Molecular Microbiology*, **2020**, 113, 535-537
- 7 What Genomics Has Taught Us about Intracellular Pathogens: the Example of *Listeria monocytogenes* **2014**, 361-391
- 6 Frank Kunst, 1943-2009. *Molecular Microbiology*, **2009**, 74, 253-6 4.1
- 5 Two Important Bacterial Pathogens Causing Community Acquired Pneumonia: *Streptococcus pneumoniae* and *Legionella pneumophila* 103-138
- 4 Genomics of the Opportunistic Pathogen *Legionella pneumophila* **2006**, 315-337
- 3 Génomique comparative. *Annales De L'Institut Pasteur / Actualités*, **2002**, 11, 33-49
- 2 Evolution of *Listeria monocytogenes* 489-499
- 1 Genome Sequencing and Genomics 377-380