

Carmen Buchrieser

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

151
papers

10,635
citations

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 | 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 |
| 150 | Microbe Profile: - a copycat eukaryote.. <i>Microbiology (United Kingdom)</i> , 2022 , 168, | 2.9 | 2 |
| 149 | Polarized mitochondria as guardians of NK cell fitness. <i>Blood Advances</i> , 2021 , 5, 26-38 | 7.8 | 14 |
| 148 | Dichotomous metabolic networks govern human ILC2 proliferation and function. <i>Nature Immunology</i> , 2021 , 22, 1367-1374 | 19.1 | 7 |
| 147 | Reverting the mode of action of the mitochondrial FF-ATPase by preserves its replication niche. <i>ELife</i> , 2021 , 10, | 8.9 | 1 |
| 146 | Divergent Evolution of RCC1 Repeat Effectors Defines the Range of Ran GTPase Cycle Targets. <i>MBio</i> , 2020 , 11, | 7.8 | 5 |
| 145 | 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 |
| 144 | Celebrating the career and legacy of Professor Pascale Cossart. <i>Molecular Microbiology</i> , 2020 , 113, 535-537 | 11.7 | 1 |
| 143 | Danger-associated metabolic modifications during bacterial infection of macrophages. <i>International Immunology</i> , 2020 , 32, 475-483 | 4.9 | 4 |
| 142 | Metagenomic approaches in microbial ecology: an update on whole-genome and marker gene sequencing analyses. <i>Microbial Genomics</i> , 2020 , 6, | 4.4 | 25 |
| 141 | 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 |
| 140 | Molecular Mimicry: a Paradigm of Host-Microbe Coevolution Illustrated by. <i>MBio</i> , 2020 , 11, | 7.8 | 17 |
| 139 | Evolution and function of bacterial RCC1 repeat effectors. <i>Cellular Microbiology</i> , 2020 , 22, e13246 | 3.9 | 3 |
| 138 | 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 |
| 137 | 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 |
| 136 | Analysis of the Pulmonary Microbiome Composition of <i>Legionella pneumophila</i> -Infected Patients. <i>Methods in Molecular Biology</i> , 2019 , 1921, 429-443 | 1.4 | 4 |
| 135 | Mitochondrial Dynamics and Activity in <i>Legionella</i> -Infected Cells. <i>Methods in Molecular Biology</i> , 2019 , 1921, 205-220 | 1.4 | 1 |

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|-----|---|------|-----|
| 134 | 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 |
| 133 | Symbiont-Mediated Defense against <i>Legionella pneumophila</i> in Amoebae. <i>MBio</i> , 2019 , 10, | 7.8 | 20 |
| 132 | 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 | 4.4 | 14 |
| 131 | A Ca-regulated deAMPylation switch in human and bacterial FIC proteins. <i>Nature Communications</i> , 2019 , 10, 1142 | 17.4 | 14 |
| 130 | Metabolic reprogramming: an innate cellular defence mechanism against intracellular bacteria?. <i>Current Opinion in Immunology</i> , 2019 , 60, 117-123 | 7.8 | 17 |
| 129 | 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 | 9.3 | 4 |
| 128 | Sorting of Phagocytic Cells Infected with <i>Legionella pneumophila</i> . <i>Methods in Molecular Biology</i> , 2019 , 1921, 179-189 | 1.4 | 0 |
| 127 | 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 | 5.2 | 10 |
| 126 | Targeting of RNA Polymerase II by a nuclear <i>Legionella pneumophila</i> Dot/Icm effector SnpL. <i>Cellular Microbiology</i> , 2018 , 20, e12852 | 3.9 | 11 |
| 125 | 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 |
| 124 | <i>Legionella</i> Effectors Explored with INSeq: New Functional Insights. <i>Trends in Microbiology</i> , 2018 , 26, 169-174 | 17.0 | 2 |
| 123 | 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 |
| 122 | The <i>Legionella pneumophila</i> Methyltransferase RomA Methylates Also Non-histone Proteins during Infection. <i>Journal of Molecular Biology</i> , 2018 , 430, 1912-1925 | 6.5 | 9 |
| 121 | Manipulation of Autophagy by Bacterial Pathogens Impacts Host Immunity. <i>Current Issues in Molecular Biology</i> , 2018 , 25, 81-98 | 2.9 | 5 |
| 120 | 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, | 7.8 | 10 |
| 119 | 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 |
| 118 | <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 |
| 117 | CsrA regulates a metabolic switch from amino acid to glycerolipid metabolism. <i>Open Biology</i> , 2017 , 7, | 7 | 23 |

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|-----|--|------|-----|
| 116 | Biological Diversity and Evolution of Type IV Secretion Systems. <i>Current Topics in Microbiology and Immunology</i> , 2017 , 413, 1-30 | 3.3 | 21 |
| 115 | The <i>Legionella pneumophila</i> genome evolved to accommodate multiple regulatory mechanisms controlled by the CsrA-system. <i>PLoS Genetics</i> , 2017 , 13, e1006629 | 6 | 45 |
| 114 | Dynamics and impact of homologous recombination on the evolution of <i>Legionella pneumophila</i> . <i>PLoS Genetics</i> , 2017 , 13, e1006855 | 6 | 21 |
| 113 | <i>Legionella longbeachae</i> Is Immunologically Silent and Highly Virulent In Vivo. <i>Journal of Infectious Diseases</i> , 2017 , 215, 440-451 | 7 | 11 |
| 112 | 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 |
| 111 | <i>Legionella pneumophila</i> restrains autophagy by modulating the host's sphingolipid metabolism. <i>Autophagy</i> , 2016 , 12, 1053-4 | 10.2 | 22 |
| 110 | <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 |
| 109 | Targeting of host organelles by pathogenic bacteria: a sophisticated subversion strategy. <i>Nature Reviews Microbiology</i> , 2016 , 14, 5-19 | 22.2 | 96 |
| 108 | Modulation of Host Autophagy during Bacterial Infection: Sabotaging Host Munitions for Pathogen Nutrition. <i>Frontiers in Immunology</i> , 2016 , 7, 81 | 8.4 | 37 |
| 107 | Multiple major disease-associated clones of <i>Legionella pneumophila</i> have emerged recently and independently. <i>Genome Research</i> , 2016 , 26, 1555-1564 | 9.7 | 48 |
| 106 | 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 |
| 105 | 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 |
| 104 | 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 |
| 103 | <i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014 , 5, 4544 | 17.4 | 144 |
| 102 | <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 |
| 101 | What Genomics Has Taught Us about Intracellular Pathogens: the Example of <i>Listeria monocytogenes</i> 2014 , 361-391 | | |
| 100 | The <i>Legionella pneumophila</i> kai operon is implicated in stress response and confers fitness in competitive environments. <i>Environmental Microbiology</i> , 2014 , 16, 359-81 | 5.2 | 21 |
| 99 | Comparative analyses of <i>Legionella</i> species identifies genetic features of strains causing Legionnaires' disease. <i>Genome Biology</i> , 2014 , 15, 505 | 18.3 | 65 |

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|----|---|------|-----|
| 98 | Comparative analyses of Legionella species identifies genetic features of strains causing Legionnaires' disease 2014 , 15, 505 | | 49 |
| 97 | 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 |
| 96 | 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 |
| 95 | cDNA library construction for next-generation sequencing to determine the transcriptional landscape of Legionella pneumophila. <i>Methods in Molecular Biology</i> , 2013 , 954, 555-66 | 1.4 | 1 |
| 94 | 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 |
| 93 | Legionella pneumophila 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 |
| 92 | Legionnaires Disease 2013 , 147-217 | | 10 |
| 91 | Co-immunoprecipitation: protein-RNA and protein-DNA interaction. <i>Methods in Molecular Biology</i> , 2013 , 954, 583-93 | 1.4 | 6 |
| 90 | Nicotinic acid modulates Legionella pneumophila gene expression and induces virulence traits. <i>Infection and Immunity</i> , 2013 , 81, 945-55 | 3.7 | 16 |
| 89 | 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 |
| 88 | 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 |
| 87 | Interdomain Horizontal Gene Transfer Shaped the Genomes of Legionella pneumophila and Legionella longbeachae 2013 , 199-219 | | 2 |
| 86 | 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 |
| 85 | Legionella pneumophila transcriptional response to chlorine treatment. <i>Water Research</i> , 2012 , 46, 808-16 | 2.5 | 17 |
| 84 | Population variation in NAIP functional copy number confers increased cell death upon Legionella pneumophila infection. <i>Human Immunology</i> , 2012 , 73, 196-200 | 2.3 | 21 |
| 83 | Comparative genomics and transcriptomics of lineages I, II, and III strains of Listeria monocytogenes. <i>BMC Genomics</i> , 2012 , 13, 144 | 4.5 | 60 |
| 82 | Post-translational modifications of host proteins by Legionella pneumophila: a sophisticated survival strategy. <i>Future Microbiology</i> , 2012 , 7, 369-81 | 2.9 | 21 |
| 81 | Characterization of an acetyltransferase that detoxifies aromatic chemicals in Legionella pneumophila. <i>Biochemical Journal</i> , 2012 , 445, 219-28 | 3.8 | 12 |

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|----|--|-----|-----|
| 80 | 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, 1146-53 | 3.8 | 17 |
| 79 | 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 |
| 78 | 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 |
| 77 | <i>Legionella</i> : from protozoa to humans. <i>Frontiers in Microbiology</i> , 2011 , 2, 182 | 5.7 | 6 |
| 76 | Extensive recombination events and horizontal gene transfer shaped the <i>Legionella pneumophila</i> genomes. <i>BMC Genomics</i> , 2011 , 12, 536 | 4.5 | 104 |
| 75 | Distinct roles of ppGpp and DksA in <i>Legionella pneumophila</i> differentiation. <i>Molecular Microbiology</i> , 2010 , 76, 200-19 | 4.1 | 58 |
| 74 | 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, 1243-59 | 5.2 | 49 |
| 73 | Circadian clock proteins in prokaryotes: hidden rhythms?. <i>Frontiers in Microbiology</i> , 2010 , 1, 130 | 5.7 | 28 |
| 72 | Control of flagellar gene regulation in <i>Legionella pneumophila</i> and its relation to growth phase. <i>Journal of Bacteriology</i> , 2010 , 192, 446-55 | 3.5 | 47 |
| 71 | Isotopologue profiling of <i>Legionella pneumophila</i> : role of serine and glucose as carbon substrates. <i>Journal of Biological Chemistry</i> , 2010 , 285, 22232-43 | 5.4 | 79 |
| 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 | 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 |
| 68 | <i>Listeria rocourtiae</i> sp. nov. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2010 , 60, 2210-2214 | 2.2 | 119 |
| 67 | The origins of eukaryotic-like proteins in <i>Legionella pneumophila</i> . <i>International Journal of Medical Microbiology</i> , 2010 , 300, 470-81 | 3.7 | 72 |
| 66 | Molecular mimicry: an important virulence strategy employed by <i>Legionella pneumophila</i> to subvert host functions. <i>Future Microbiology</i> , 2009 , 4, 691-701 | 2.9 | 40 |
| 65 | 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 |
| 64 | Two small ncRNAs jointly govern virulence and transmission in <i>Legionella pneumophila</i> . <i>Molecular Microbiology</i> , 2009 , 72, 741-62 | 4.1 | 131 |
| 63 | <i>Listeria monocytogenes</i> 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 |

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|----|--|------|-----|
| 62 | Frank Kunst, 1943-2009. <i>Molecular Microbiology</i> , 2009 , 74, 253-6 | 4.1 | |
| 61 | 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 |
| 60 | 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 |
| 59 | NeMeSys: a biological resource for narrowing the gap between sequence and function in the human pathogen <i>Neisseria meningitidis</i> . <i>Genome Biology</i> , 2009 , 10, R110 | 18.3 | 78 |
| 58 | 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 |
| 57 | Synergistic contribution of the <i>Legionella pneumophila</i> <i>lqs</i> genes to pathogen-host interactions. <i>Journal of Bacteriology</i> , 2008 , 190, 7532-47 | 3.5 | 57 |
| 56 | The <i>Legionella</i> autoinducer synthase <i>LqsA</i> produces an alpha-hydroxyketone signaling molecule. <i>Journal of Biological Chemistry</i> , 2008 , 283, 18113-23 | 5.4 | 87 |
| 55 | 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 |
| 54 | Transcriptional profiling of <i>Legionella pneumophila</i> biofilm cells and the influence of iron on biofilm formation. <i>Microbiology (United Kingdom)</i> , 2008 , 154, 30-41 | 2.9 | 83 |
| 53 | Pathogenomics: an updated European Research Agenda. <i>Infection, Genetics and Evolution</i> , 2008 , 8, 386-92 | 5 | 6 |
| 52 | <i>Legionella pneumophila</i> Pathogenesis: Lessons Learned from Genomics 2008 , 1-31 | | 1 |
| 51 | Biodiversity of the species <i>Listeria monocytogenes</i> and the genus <i>Listeria</i> . <i>Microbes and Infection</i> , 2007 , 9, 1147-55 | 9.3 | 41 |
| 50 | The <i>Legionella pneumophila</i> response regulator <i>LqsR</i> promotes host cell interactions as an element of the virulence regulatory network controlled by <i>RpoS</i> and <i>LetA</i> . <i>Cellular Microbiology</i> , 2007 , 9, 2903-20 | 3.9 | 128 |
| 49 | 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 |
| 48 | 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, 1928-39 | 4.8 | 44 |
| 47 | 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, 6078-88 | 4.8 | 49 |
| 46 | <i>Legionella</i> pathogenicity: genome structure, regulatory networks and the host cell response. <i>International Journal of Medical Microbiology</i> , 2007 , 297, 577-87 | 3.7 | 76 |
| 45 | Pathogenomics of <i>Listeria</i> spp. <i>International Journal of Medical Microbiology</i> , 2007 , 297, 541-57 | 3.7 | 68 |

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|----|--|------|-----|
| 44 | 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 |
| 43 | Listeria Genomics 2007 , 33-62 | | 1 |
| 42 | The Genus Listeria and Listeria monocytogenes. <i>Food Additives</i> , 2007 , 1-20 | | 6 |
| 41 | Growth-phase-dependent mobility of the lvh-encoding region in Legionella pneumophila strain Paris. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 3561-3568 | 2.9 | 35 |
| 40 | How to become a uropathogen: comparative genomic analysis of extraintestinal pathogenic Escherichia coli strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 12879-84 | 11.5 | 286 |
| 39 | Escherichia coli induces DNA double-strand breaks in eukaryotic cells. <i>Science</i> , 2006 , 313, 848-51 | 33.3 | 661 |
| 38 | Adaptation of Legionella pneumophila 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 |
| 37 | 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 |
| 36 | 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, 541-6 | 3.7 | 7 |
| 35 | Genomics of the Opportunistic Pathogen Legionella pneumophila 2006 , 315-337 | | |
| 34 | Virulence strategies for infecting phagocytes deduced from the in vivo transcriptional program of Legionella pneumophila. <i>Cellular Microbiology</i> , 2006 , 8, 1228-40 | 3.9 | 204 |
| 33 | Genomic diversity and evolution within the species Streptococcus agalactiae. <i>Microbes and Infection</i> , 2006 , 8, 1227-43 | 9.3 | 153 |
| 32 | Listeria monocytogenes and the Genus Listeria 2006 , 404-476 | | 18 |
| 31 | 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 |
| 30 | 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 |
| 29 | Global analysis of gene expression in an rpoN mutant of Listeria monocytogenes. <i>Microbiology (United Kingdom)</i> , 2004 , 150, 1581-1590 | 2.9 | 77 |
| 28 | DNA macroarray for identification and typing of Staphylococcus aureus isolates. <i>Journal of Clinical Microbiology</i> , 2004 , 42, 2054-64 | 9.7 | 35 |
| 27 | New aspects regarding evolution and virulence of Listeria monocytogenes revealed by comparative genomics and DNA arrays. <i>Infection and Immunity</i> , 2004 , 72, 1072-83 | 3.7 | 244 |

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|----|--|------|-----|
| 26 | 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 | 3.7 | 54 |
| 25 | 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 |
| 24 | 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 |
| 23 | Pathogenomics of mobile genetic elements of toxigenic bacteria. <i>International Journal of Medical Microbiology</i> , 2004 , 293, 453-61 | 3.7 | 40 |
| 22 | 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 |
| 21 | 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 |
| 20 | 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 |
| 19 | The genome sequence of the entomopathogenic bacterium <i>Photorhabdus luminescens</i> . <i>Nature Biotechnology</i> , 2003 , 21, 1307-13 | 44.5 | 485 |
| 18 | <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 |
| 17 | Genome sequence of <i>Streptococcus agalactiae</i> , a pathogen causing invasive neonatal disease. <i>Molecular Microbiology</i> , 2002 , 45, 1499-513 | 4.1 | 386 |
| 16 | Génomique comparative. <i>Annales De L'Institut Pasteur / Actualités</i> , 2002 , 11, 33-49 | | |
| 15 | 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 |
| 14 | 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 |
| 13 | Cloning and assembly strategies in microbial genome projects. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 10), 2625-34 | 2.9 | 48 |
| 12 | 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 |
| 11 | 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 |
| 10 | 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, 965-78 | 4.1 | 142 |
| 9 | 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 |

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|---|---|-----|----|
| 8 | 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 |
| 7 | Two Important Bacterial Pathogens Causing Community Acquired Pneumonia: Streptococcus pneumoniae and Legionella pneumophila103-138 | | |
| 6 | Gene Expression and Virulence in Legionella: the Flagellar Regulon327-332 | | 1 |
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