Roland Brosch

List of Publications by Year
in descending order

165	17,580	11675	16102
papers	citations	h-index	g-index

180	180	180	14175
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evolution and emergence of Mycobacterium tuberculosis. FEMS Microbiology Reviews, 2024, 48, .	8.9	6
2	Genomic and phenotypic characterization of Mycobacterium tuberculosisâ€™ closest-related non-tuberculous mycobacteria. Microbiology Spectrum, 2024, 12, .	3.0	0
3	Natural mutations in the sensor kinase of the PhoPR two-component regulatory system modulate virulence of ancestor-like tuberculosis bacilli. PLoS Pathogens, 2023, 19, e1011437.	4.1	4
4	The C terminus of the mycobacterium ESX-1 secretion system substrate ESAT-6 is required for phagosomal membrane damage and virulence. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2122161119.	7.6	33
5	The Mycobacterium tuberculosis PhoPR virulence system regulates expression of the universal second messenger c-di-AMP and impacts vaccine safety and efficacy. Molecular Therapy - Nucleic Acids, 2022, 27, 1235-1248.	5.1	10
6	The MtZ Strain: Molecular Characteristics and Outbreak Investigation of the Most Successful Mycobacterium tuberculosis Strain in Aragon Using Whole-Genome Sequencing. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	4.0	4
7	A lentiviral vector encoding fusion of light invariant chain and mycobacterial antigens induces protective CD4+ TÂcell immunity. Cell Reports, 2022, 40, 111142.	6.3	9
8	A comprehensive update to the Mycobacterium tuberculosis H37Rv reference genome. Nature Communications, 2022, 13, .	13.2	16
9	Pathogenomic analyses of Mycobacterium microti, an ESX-1-deleted member of the Mycobacterium tuberculosis complex causing disease in various hosts. Microbial Genomics, 2021, 7, .	2.1	12
10	Breaching the phagosome, the case of the tuberculosis agent. Cellular Microbiology, 2021, 23, e13344.	2.3	21
11	IL-1R1-Dependent Signals Improve Control of Cytosolic Virulent Mycobacteria In Vivo. MSphere, 2021, 6, .	3.1	4
12	ESX-1-Independent Horizontal Gene Transfer by Mycobacterium tuberculosis Complex Strains. MBio, 2021, 12, .	4.4	17
13	Phenotypic and genomic hallmarks of a novel, potentially pathogenic rapidly growing Mycobacterium species related to the Mycobacterium fortuitum complex. Scientific Reports, 2021, 11, 13011.	3.4	7
14	Proteome remodeling in the Mycobacterium tuberculosis PknG knockout: Molecular evidence for the role of this kinase in cell envelope biogenesis and hypoxia response. Journal of Proteomics, 2021, 244, 104276.	2.5	6
15	Parallel in vivo experimental evolution reveals that increased stress resistance was key for the emergence of persistent tuberculosis bacilli. Nature Microbiology, 2021, 6, 1082-1093.	13.1	16
16	Mucosal delivery of ESX-1â€“expressing BCG strains provides superior immunity against tuberculosis in murine type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20848-20859.	7.6	9
17	Phthiocerol Dimycocerosates From Mycobacterium tuberculosis Increase the Membrane Activity of Bacterial Effectors and Host Receptors. Frontiers in Cellular and Infection Microbiology, 2020, 10, 420.	4.0	27
18	Live attenuated TB vaccines representing the three modern Mycobacterium tuberculosis lineages reveal that the Euroâ€“American genetic background confers optimal vaccine potential. EBioMedicine, 2020, 55, 102761.	6.0	29

#	Article	IF	Citations
19	A systematic approach to simultaneously evaluate safety, immunogenicity, and efficacy of novel tuberculosis vaccination strategies. Science Advances, 2020, 6, eaaz1767.	10.9	11
20	TbD1 deletion as a driver of the evolutionary success of modern epidemic Mycobacterium tuberculosis lineages. Nature Communications, 2020, 11, 684.	13.2	78
21	Discovery of a novel dehydratase of the fatty acid synthase type II critical for ketomycolic acid biosynthesis and virulence of Mycobacterium tuberculosis. Scientific Reports, 2020, 10, 2112.	3.4	11
22	The antibiotic bedaquiline activates host macrophage innate immune resistance to bacterial infection. ELife, 2020, 9, .	5.9	72
23	From environmental bacteria to obligate pathogen: the study of adaptations enhancing the persistence of tuberculosis bacilli. European Respiratory Journal, 2020, , .	7.5	0
24	Shared Pathogenomic Patterns Characterize a New Phylotype, Revealing Transition toward Host-Adaptation Long before Speciation of Mycobacterium tuberculosis. Genome Biology and Evolution, 2019, 11, 2420-2438.	2.6	31
25	ESX/Type VII Secretion Systemsâ€"An Important Way Out for Mycobacterial Proteins. Microbiology Spectrum, 2019, 7, .	3.0	34
26	Mycobacterium abscessusÂvirulence traits unraveled by transcriptomic profiling in amoeba and macrophages. PLoS Pathogens, 2019, 15, e1008069.	4.1	47
27	Intrinsic Antibacterial Activity of Nanoparticles Made of Î²-Cyclodextrins Potentiates Their Effect as Drug Nanocarriers against Tuberculosis. ACS Nano, 2019, 13, 3992-4007.	15.3	46
28	Update on the virulence factors of the obligate pathogen Mycobacterium tuberculosis and related tuberculosis-causing mycobacteria. Infection, Genetics and Evolution, 2019, 72, 67-77.	2.3	18
29	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. Journal of Proteomics, 2019, 192, 321-333.	2.5	31
30	Mycobacterial virulence: impact on immunogenicity and vaccine research. F1000Research, 2019, 8, 2025.	1.6	16
31	From environmental bacteria to obligate pathogen: the study of adaptations enhancing the persistence of tuberculosis bacilli. European Respiratory Journal, 2019, , .	7.5	0
32	Identification of genes required for Mycobacterium abscessus growth in vivo with a prominent role of the ESX-4 locus. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1002-E1011.	7.6	101
33	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. Nature Microbiology, 2018, 3, 181-188.	13.1	117
34	Multiplexed Quantitation of Intraphagocyte Mycobacterium tuberculosis Secreted Protein Effectors. Cell Reports, 2018, 23, 1072-1084.	6.3	30
35	Evolution of virulence in the Mycobacterium tuberculosis complex. Current Opinion in Microbiology, 2018, 41, 68-75.	5.2	72
36	ESX-4, un systÃ¨me de sÃ©crÃ©tion mycobactÃ©rien ancestral, essentiel pour la croissance de Mycobacterium abscessus dans les phagocytes environnementaux et humains. Medecine/Sciences, 2018, 34, 795-797.	0.2	0

#	Article	IF	Citations
37	Unexpected Genomic and Phenotypic Diversity of Mycobacterium africanum Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. Genome Biology and Evolution, 2018, 10, 1858-1874.	2.6	51
38	RD5-mediated lack of PE_PGRS and PPE-MPTR export in BCG vaccine strains results in strong reduction of antigenic repertoire but little impact on protection. PLoS Pathogens, 2018, 14, e1007139.	4.1	39
39	ESX-1 and phthiocerol dimycocerosates ofMycobacterium tuberculosisact in concert to cause phagosomal rupture and host cell apoptosis. Cellular Microbiology, 2017, 19, e12726.	2.3	187
40	Mycobacterial ESX-1 secretion system mediates host cell lysis through bacterium contact-dependent gross membrane disruptions. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1371-1376.	7.6	234
41	Resistance to Thiacetazone Derivatives Active against Mycobacterium abscessus Involves Mutations in the MmpL5 Transcriptional Repressor MAB_4384. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.4	55
42	Recombinant BCG Expressing ESX-1 of Mycobacterium marinum Combines Low Virulence with Cytosolic Immune Signaling and Improved TB Protection. Cell Reports, 2017, 18, 2752-2765.	6.3	102
43	Mycobacterium tuberculosis Controls Phagosomal Acidification by Targeting CISH-Mediated Signaling. Cell Reports, 2017, 20, 3188-3198.	6.3	62
44	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. Scientific Reports, 2017, 7, 5702.	3.4	9
45	The Biology and Epidemiology of Mycobacterium canettii. Advances in Experimental Medicine and Biology, 2017, 1019, 27-41.	0.0	26
46	<scp>D</scp>iscovery of the type VII ESXâ€1 secretion needle?. Molecular Microbiology, 2017, 103, 7-12.	2.5	33
47	The Macrophage: A Disputed Fortress in the Battle against Mycobacterium tuberculosis. Frontiers in Microbiology, 2017, 8, 2284.	3.6	201
48	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2017, 13, e1006399.	4.1	81
49	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to Mycobacterium tuberculosis pathoadaptation. PLoS Pathogens, 2017, 13, e1006752.	4.1	34
50	Genomic characterization of Mycobacterium tuberculosis lineage 7 and a proposed name: â€˜Aethiops vetusâ€™. Microbial Genomics, 2016, 2, e000063.	2.1	22
51	CD4+ T Cells Recognizing PE/PPE Antigens Directly or via Cross Reactivity Are Protective against Pulmonary Mycobacterium tuberculosis Infection. PLoS Pathogens, 2016, 12, e1005770.	4.1	50
52	A new piperidinol derivative targeting mycolic acid transport in Mycobacterium abscessus. Molecular Microbiology, 2016, 101, 515-529.	2.5	102
53	Perspectives on mycobacterial vacuole-to-cytosol translocation: the importance of cytosolic access. Cellular Microbiology, 2016, 18, 1070-1077.	2.3	26
54	A unique PE_PGRS protein inhibiting host cell cytosolic defenses and sustaining full virulence ofMycobacterium marinumin multiple hosts. Cellular Microbiology, 2016, 18, 1489-1507.	2.3	26

#	Article	IF	Citations
55	The changes in mycolic acid structures caused by hadC mutation have a dramatic effect on the virulence of Mycobacterium tuberculosis. Molecular Microbiology, 2016, 99, 794-807.	2.5	32
56	The distinct fate of smooth and roughMycobacterium abscessusvariants inside macrophages. Open Biology, 2016, 6, 160185.	3.7	136
57	Insights into the smoothâ€toâ€rough transitioning in Mycobacterium bolletii unravels a functional Tyr residue conserved in all mycobacterial MmpL family members. Molecular Microbiology, 2016, 99, 866-883.	2.5	87
58	ESX secretion systems: mycobacterial evolution to counter host immunity. Nature Reviews Microbiology, 2016, 14, 677-691.	29.2	322
59	Key experimental evidence of chromosomal DNA transfer among selected tuberculosis-causing mycobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9876-9881.	7.6	110
60	Evolution of Mycobacterium tuberculosis : New Insights into Pathogenicity and Drug Resistance. Microbiology Spectrum, 2016, 4, .	3.0	20
61	Leprosy in red squirrels. Science, 2016, 354, 702-703.	20.9	5
62	pks5-recombination-mediated surface remodelling in Mycobacterium tuberculosis emergence. Nature Microbiology, 2016, 1, 15019.	13.1	87
63	Genome-wide mosaicism within Mycobacterium abscessus: evolutionary and epidemiological implications. BMC Genomics, 2016, 17, 118.	2.9	58
64	Mycobacterial Pan-Genome Analysis Suggests Important Role of Plasmids in the Radiation of Type VII Secretion Systems. Genome Biology and Evolution, 2016, 8, 387-402.	2.6	89
65	The BCG Strain Pool: Diversity Matters. Molecular Therapy, 2016, 24, 201-203.	8.1	15
66	ESAT-6â€“dependent cytosolic pattern recognition drives noncognate tuberculosis control in vivo. Journal of Clinical Investigation, 2016, 126, 2109-2122.	8.2	53
67	Revisiting the role of phospholipases C in virulence and the lifecycle of Mycobacterium tuberculosis. Scientific Reports, 2015, 5, 16918.	3.4	39
68	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. Scientific Reports, 2015, 5, 15443.	3.4	83
69	Impact of Mycobacterium tuberculosis RD1-locus on human primary dendritic cell immune functions. Scientific Reports, 2015, 5, 17078.	3.4	19
70	Les bacilles de la tuberculose bovine. Medecine/Sciences, 2015, 31, 123-126.	0.2	2
71	Mycobacterium tuberculosis Meets the Cytosol: The Role of cGAS in Anti-mycobacterial Immunity. Cell Host and Microbe, 2015, 17, 733-735.	11.0	38
72	Type VII Secretion Systems in Gram-Positive Bacteria. Current Topics in Microbiology and Immunology, 2015, 404, 235-265.	0.0	33

#	Article	IF	Citations
73	ESX/type VII secretion systems of mycobacteria: Insights into evolution, pathogenicity and protection. Tuberculosis, 2015, 95, S150-S154.	2.0	58
74	Release of mycobacterial antigens. Immunological Reviews, 2015, 264, 25-45.	6.1	82
75	Cytosolic Access of Mycobacterium tuberculosis: Critical Impact of Phagosomal Acidification Control and Demonstration of Occurrence In Vivo. PLoS Pathogens, 2015, 11, e1004650.	4.1	180
76	Insights on the Emergence of Mycobacterium tuberculosis from the Analysis of Mycobacterium kansasii. Genome Biology and Evolution, 2015, 7, 856-870.	2.6	86
77	Increased protective efficacy of recombinant BCG strains expressing virulence-neutral proteins of the ESX-1 secretion system. Vaccine, 2015, 33, 2710-2718.	4.0	52
78	Mycobacterium abscessus Phospholipase C Expression Is Induced during Coculture within Amoebae and Enhances M. abscessus Virulence in Mice. Infection and Immunity, 2015, 83, 780-791.	2.4	54
79	A Specific Polymorphism in Mycobacterium tuberculosis H37Rv Causes Differential ESAT-6 Expression and Identifies WhiB6 as a Novel ESX-1 Component. Infection and Immunity, 2014, 82, 3446-3456.	2.4	78
80	Mycobacterium tuberculosis Exploits Asparagine to Assimilate Nitrogen and Resist Acid Stress during Infection. PLoS Pathogens, 2014, 10, e1003928.	4.1	152
81	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. Molecular Microbiology, 2014, 93, 835-852.	2.5	79
82	Mycobacterium Tuberculosis Evolutionary Pathogenesis and its Putative Impact on Drug Development. Future Microbiology, 2014, 9, 969-985.	2.0	28
83	Bacillus Calmette-GuÃ©rin Strain Differences Have an Impact on Clinical Outcome in Bladder Cancer Immunotherapy. European Urology, 2014, 66, 677-688.	5.0	166
84	Evolutionary history of tuberculosis shaped by conserved mutations in the PhoPR virulence regulator. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11491-11496.	7.6	208
85	Mycobacterial Pathogenomics and Evolution. Microbiology Spectrum, 2014, 2, MGM2-0025-2013.	3.0	36
86	ESX-1-induced apoptosis is involved in cell-to-cell spread ofMycobacterium tuberculosis. Cellular Microbiology, 2013, 15, 1994-2005.	2.3	126
87	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of Mycobacterium tuberculosis. Nature Genetics, 2013, 45, 172-179.	20.4	270
88	TBCAP; tuberculosis annotation project. Tuberculosis, 2013, 93, 1-5.	2.0	3
89	Characterization ofMycobacterium orygis. Emerging Infectious Diseases, 2013, 19, 521-2.	4.4	5
90	Identification and characterization of the genetic changes responsible for the characteristic smoothâ€toâ€rough morphotype alterations of clinically persistent <scp>M</scp>ycobacterium abscessus. Molecular Microbiology, 2013, 90, 612-629.	2.5	150

#	Article	IF	Citations
91	Single Cell Measurements of Vacuolar Rupture Caused by Intracellular Pathogens. Journal of Visualized Experiments, 2013, , e50116.	0.3	21
92	Targeting Type VII/ESX Secretion Systems for Development of Novel Antimycobacterial Drugs. Current Pharmaceutical Design, 2013, 20, 4346-4356.	1.9	17
93	Phagosomal Rupture by Mycobacterium tuberculosis Results in Toxicity and Host Cell Death. PLoS Pathogens, 2012, 8, e1002507.	4.1	499
94	ESX-1 dependent impairment of autophagic flux byMycobacterium tuberculosisin human dendritic cells. Autophagy, 2012, 8, 1357-1370.	11.0	246
95	Strong Immunogenicity and Cross-Reactivity of Mycobacterium tuberculosis ESX-5 Type VII Secretion -Encoded PE-PPE Proteins Predicts Vaccine Potential. Cell Host and Microbe, 2012, 11, 352-363.	11.0	103
96	Multidrug-Resistant Tuberculosis in Admitted Patients at a Tertiary Referral Hospital of Bangladesh. PLoS ONE, 2012, 7, e40545.	2.5	32
97	The ESX-5 Associated eccB5-eccC5 Locus Is Essential for Mycobacterium tuberculosis Viability. PLoS ONE, 2012, 7, e52059.	2.5	52
98	Characterization ofMycobacterium orygisasM. tuberculosisComplex Subspecies. Emerging Infectious Diseases, 2012, 18, 653-655.	4.4	177
99	Disruption of the ESXâ€5 system of Mycobacterium tuberculosis causes loss of PPE protein secretion, reduction of cell wall integrity and strong attenuation. Molecular Microbiology, 2012, 83, 1195-1209.	2.5	180
100	ESXâ€1â€mediated translocation to the cytosol controls virulence of mycobacteria. Cellular Microbiology, 2012, 14, 1287-1298.	2.3	388
101	Activation of the NLRP3 inflammasome by Mycobacterium tuberculosis is uncoupled from susceptibility to active tuberculosis. European Journal of Immunology, 2012, 42, 374-384.	3.3	155
102	Overexpression of proinflammatory TLR-2-signalling lipoproteins in hypervirulent mycobacterial variants. Cellular Microbiology, 2011, 13, 692-704.	2.3	69
103	Deciphering the role of IS6110 in a highly transmissible Mycobacterium tuberculosis Beijing strain, GC1237. Tuberculosis, 2011, 91, 117-126.	2.0	49
104	p62 and NDP52 Proteins Target Intracytosolic Shigella and Listeria to Different Autophagy Pathways. Journal of Biological Chemistry, 2011, 286, 26987-26995.	3.5	262
105	ESAT-6 Secretion-Independent Impact of ESX-1 Genes espF and espG1 on Virulence of Mycobacterium tuberculosis. Journal of Infectious Diseases, 2011, 203, 1155-1164.	3.9	68
106	Synthesis, biological activity, and evaluation of the mode of action of novel antitubercular benzofurobenzopyrans substituted on A ring. European Journal of Medicinal Chemistry, 2010, 45, 5833-5847.	5.7	35
107	High Content Phenotypic Cell-Based Visual Screen Identifies Mycobacterium tuberculosis Acyltrehalose-Containing Glycolipids Involved in Phagosome Remodeling. PLoS Pathogens, 2010, 6, e1001100.	4.1	166
108	Entrapment of Intracytosolic Bacteria by Septin Cage-like Structures. Cell Host and Microbe, 2010, 8, 433-444.	11.0	241

#	Article	IF	Citations
109	DÃ©couverte dâ€™une nouvelle classe dâ€™antituberculeuxÂ: les benzothiazinones (BTZ). Medecine/Sciences, 2009, 25, 663-665.	0.2	1
110	Systematic Genetic Nomenclature for Type VII Secretion Systems. PLoS Pathogens, 2009, 5, e1000507.	4.1	236
111	High Content Screening Identifies Decaprenyl-Phosphoribose 2â€² Epimerase as a Target for Intracellular Antimycobacterial Inhibitors. PLoS Pathogens, 2009, 5, e1000645.	4.1	288
112	Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. BioEssays, 2009, 31, 378-388.	2.6	44
113	Mycobacterial PE, PPE and ESX clusters: novel insights into the secretion of these most unusual protein families. Molecular Microbiology, 2009, 73, 325-328.	2.5	84
114	Myths and misconceptions: the origin and evolution of Mycobacterium tuberculosis. Nature Reviews Microbiology, 2009, 7, 537-544.	29.2	216
115	ESX/type VII secretion systems and their role in hostâ€“pathogen interaction. Current Opinion in Microbiology, 2009, 12, 4-10.	5.2	217
116	Non Mycobacterial Virulence Genes in the Genome of the Emerging Pathogen Mycobacterium abscessus. PLoS ONE, 2009, 4, e5660.	2.5	316
117	Insights from the complete genome sequence of Mycobacterium marinum on the evolution of Mycobacterium tuberculosis. Genome Research, 2008, 18, 729-741.	5.6	483
118	Functional analysis of a clonal deletion in an epidemic strain of Mycobacterium bovis reveals a role in lipid metabolism. Microbiology (United Kingdom), 2008, 154, 3731-3742.	1.8	13
119	Control of M. tuberculosis ESAT-6 Secretion and Specific T Cell Recognition by PhoP. PLoS Pathogens, 2008, 4, e33.	4.1	238
120	The PE and PPE Protein Families ofMycobacterium tuberculosis. , 2008, , 131-150.		15
121	ESAT-6 from Mycobacterium tuberculosis Dissociates from Its Putative Chaperone CFP-10 under Acidic Conditions and Exhibits Membrane-Lysing Activity. Journal of Bacteriology, 2007, 189, 6028-6034.	2.4	285
122	Genome plasticity of BCG and impact on vaccine efficacy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5596-5601.	7.6	493
123	Pathogenomics: Insights into Tuberculosis and Related Mycobacterial Diseases. , 2006, , 211-230.		1
124	Apports de la gÃ©nomique des mycobactÃ©ries a la dÃ©finition de nouvelles stratÃ©gies thÃ©rapeutiques et vaccinales anti-tuberculeuses. Revue Francophone Des Laboratoires, 2006, 2006, 23-30.	0.0	0
125	â€œA Re-Evaluation of M. prototuberculosisâ€: Continuing the Debate. PLoS Pathogens, 2006, 2, e95.	4.1	21
126	Horizontal Transfer of a Virulence Operon to the Ancestor of Mycobacterium tuberculosis. Molecular Biology and Evolution, 2006, 23, 1129-1135.	9.2	96

#	Article	IF	Citations
127	Dissection of ESAT-6 System 1 of Mycobacterium tuberculosis and Impact on Immunogenicity and Virulence. Infection and Immunity, 2006, 74, 88-98.	2.4	286
128	Genomics of theMycobacterium tuberculosiscomplex andMycobacterium leprae. , 2005, , .		0
129	Modulation of the host immune response by a transient intracellular stage of Mycobacterium ulcerans: the contribution of endogenous mycolactone toxin. Cellular Microbiology, 2005, 7, 1187-1196.	2.3	135
130	Common Evolutionary Origin for the Unstable Virulence Plasmid pMUM Found in Geographically Diverse Strains of Mycobacterium ulcerans. Journal of Bacteriology, 2005, 187, 1668-1676.	2.4	74
131	Ancient Origin and Gene Mosaicism of the Progenitor of Mycobacterium tuberculosis. PLoS Pathogens, 2005, 1, e5.	4.1	478
132	Influence of ESAT-6 Secretion System 1 (RD1) of Mycobacterium tuberculosis on the Interaction between Mycobacteria and the Host Immune System. Journal of Immunology, 2005, 174, 3570-3579.	0.8	137
133	Structure and Mechanism of the Alkyl Hydroperoxidase AhpC, a Key Elementof the Mycobacterium tuberculosis Defense System against OxidativeStress. Journal of Biological Chemistry, 2005, 280, 25735-25742.	3.5	92
134	Functional Analysis of Early Secreted Antigenic Target-6, the Dominant T-cell Antigen of Mycobacterium tuberculosis, Reveals Key Residues Involved in Secretion, Complex Formation, Virulence, and Immunogenicity. Journal of Biological Chemistry, 2005, 280, 33953-33959.	3.5	140
135	Tuberculosis: from genome to vaccine. Expert Review of Vaccines, 2005, 4, 541-551.	4.5	22
136	Cell Envelope Protein PPE68 Contributes toMycobacterium tuberculosisRD1 Immunogenicity Independently of a 10-Kilodalton Culture Filtrate Protein and ESAT-6. Infection and Immunity, 2004, 72, 2170-2176.	2.4	95
137	Enhanced Protection against Tuberculosis by Vaccination with RecombinantMycobacterium microtiVaccine That Induces T Cell Immunity against Region of Difference 1 Antigens. Journal of Infectious Diseases, 2004, 190, 115-122.	3.9	73
138	GenotypicAnalysis of Mycobacterium tuberculosis in Bangladesh andPrevalence of the BeijingStrain. Journal of Clinical Microbiology, 2004, 42, 674-682.	4.4	80
139	Giant plasmid-encoded polyketide synthases produce the macrolide toxin of Mycobacterium ulcerans. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1345-1349.	7.6	350
140	Macro-array and bioinformatic analyses reveal mycobacterial â€˜coreâ€™ genes, variation in the ESAT-6 gene family and new phylogenetic markers for the Mycobacterium tuberculosis complex. Microbiology (United Kingdom), 2004, 150, 483-496.	1.8	163
141	ESAT-6 proteins: protective antigens and virulence factors?. Trends in Microbiology, 2004, 12, 500-508.	7.7	279
142	Recombinant BCG exporting ESAT-6 confers enhanced protection against tuberculosis. Nature Medicine, 2003, 9, 533-539.	30.1	576
143	Is Mycobacterium africanum Subtype II (Uganda I and Uganda II) a Genetically Well-Defined Subspecies of the Mycobacterium tuberculosis Complex?. Journal of Clinical Microbiology, 2003, 41, 1345-1348.	4.4	23
144	Bacterial Artificial Chromosome-Based Comparative Genomic Analysis Identifies Mycobacterium microti as a Natural ESAT-6 Deletion Mutant. Infection and Immunity, 2002, 70, 5568-5578.	2.4	154

#	Article	IF	Citations
145	Rapid and Simple Approach for Identification of Mycobacterium tuberculosis Complex Isolates by PCR-Based Genomic Deletion Analysis. Journal of Clinical Microbiology, 2002, 40, 2339-2345.	4.4	215
146	Loss of RD1 contributed to the attenuation of the live tuberculosis vaccines Mycobacterium bovis BCG and Mycobacterium microti. Molecular Microbiology, 2002, 46, 709-717.	2.5	657
147	Mycobacterial genomics. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2002, 96, 1-6.	1.8	21
148	The evolution of mycobacterial pathogenicity: clues from comparative genomics. Trends in Microbiology, 2001, 9, 452-458.	7.7	187
149	Tools for the Population Genomics of the Tubercle Bacilli. Genome Research, 2000, 10, 1837-1839.	5.6	6
150	Comparative genomics of the leprosy and tubercle bacilli. Research in Microbiology, 2000, 151, 135-142.	2.2	45
151	Comparative genomics of the mycobacteria. International Journal of Medical Microbiology, 2000, 290, 143-152.	3.8	94
152	Identification of variable regions in the genomes of tubercle bacilli using bacterial artificial chromosome arrays. Molecular Microbiology, 1999, 32, 643-655.	2.5	484
153	Genomic Analysis Reveals Variation between Mycobacterium tuberculosis H37Rv and the Attenuated M. tuberculosis H37Ra Strain. Infection and Immunity, 1999, 67, 5768-5774.	2.4	141
154	The high-pathogenicity island of Yersinia pseudotuberculosis can be inserted into any of the three chromosomal asn tRNA genes. Molecular Microbiology, 1998, 30, 965-978.	2.5	155
155	Use of a Mycobacterium tuberculosis H37Rv Bacterial Artificial Chromosome Library for Genome Mapping, Sequencing, and Comparative Genomics. Infection and Immunity, 1998, 66, 2221-2229.	2.4	221
156	Genomic analysis using pulsed-field gel electrophoresis of Escherichia coli 0157:H7 isolated from dairy calves during the United States national dairy heifer evaluation project (1991â€“1992). Veterinary Microbiology, 1996, 48, 223-230.	1.9	33
157	Genomic fingerprinting of 80 strains from the WHO multicenter international typing study of Listeria monocytogenes via pulsed-field gel electrophoresis (PFGE). International Journal of Food Microbiology, 1996, 32, 343-355.	4.8	102
158	Ability of Biolog and Biotype-100 Systems to Reveal the Taxonomic Diversity of the Pseudomonads. Systematic and Applied Microbiology, 1996, 19, 510-527.	3.0	64
159	Taxonomic Diversity of Pseudomonads Revealed by Computer-interpretation of Ribotyping Data. Systematic and Applied Microbiology, 1996, 19, 541-555.	3.0	59
160	Genomics ofMycobacterium Tuberculosis and Mycobacterium Leprae. , 0, , 93-109.		6
161	Evolution ofMycobacterium tuberculosis: New Insights into Pathogenicity and Drug Resistance. , 0, , 495-515.		5
162	ESX/Type VII Secretion Systems-An Important Way Out for Mycobacterial Proteins. , 0, , 351-362.		5

#	Article	IF	Citations
163	Mycobacterial Pathogenomics and Evolution. , 0, , 27-47.		3
164	ESAT-6 and the Mycobacterial ESX Secretion Systems. , 0, , 211-222.		0
165	The Mycobacteria: a Postgenomic View. , 0, , 49-89.		0