Roland Brosch

List of Publications by Year
in descending order

175 papers	26,572 citations	10986 71 h-index	6471 157 g-index
188 all docs	188 docs citations	188 times ranked	16935 citing authors

#	Article	IF	Citations
1	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.	7.1	19
2	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
3	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, .	3.9	3
4	Pathogenomic analyses of Mycobacterium microti, an ESX-1-deleted member of the Mycobacterium tuberculosis complex causing disease in various hosts. Microbial Genomics, 2021, 7, .	2.0	11
5	Breaching the phagosome, the case of the tuberculosis agent. Cellular Microbiology, 2021, 23, e13344.	2.1	18
6	IL-1R1-Dependent Signals Improve Control of Cytosolic Virulent Mycobacteria In Vivo. MSphere, 2021, 6, .	2.9	4
7	ESX-1-Independent Horizontal Gene Transfer by Mycobacterium tuberculosis Complex Strains. MBio, 2021, 12, .	4.1	14
8	Phenotypic and genomic hallmarks of a novel, potentially pathogenic rapidly growing Mycobacterium species related to the Mycobacterium fortuitum complex. Scientific Reports, 2021, 11, 13011.	3.3	6
9	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.	2.4	6
10	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.	13.3	15
11	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.	7.1	9
12	Phthiocerol Dimycocerosates From Mycobacterium tuberculosis Increase the Membrane Activity of Bacterial Effectors and Host Receptors. Frontiers in Cellular and Infection Microbiology, 2020, 10, 420.	3.9	23
13	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.	6.1	22
14	A systematic approach to simultaneously evaluate safety, immunogenicity, and efficacy of novel tuberculosis vaccination strategies. Science Advances, 2020, 6, eaaz1767.	10.3	10
15	TbD1 deletion as a driver of the evolutionary success of modern epidemic Mycobacterium tuberculosis lineages. Nature Communications, 2020, 11, 684.	12.8	68
16	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.	3.3	11
17	The antibiotic bedaquiline activates host macrophage innate immune resistance to bacterial infection. ELife, 2020, 9, .	6.0	66
18	From environmental bacteria to obligate pathogen: the study of adaptations enhancing the persistence of tuberculosis bacilli. , 2020, , .		0

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19	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.	2.5	29
20	ESX/Type VII Secretion Systemsâ€"An Important Way Out for Mycobacterial Proteins. Microbiology Spectrum, 2019, 7, .	3.0	31
21	Mycobacterium abscessusÂvirulence traits unraveled by transcriptomic profiling in amoeba and macrophages. PLoS Pathogens, 2019, 15, e1008069.	4.7	42
22	Intrinsic Antibacterial Activity of Nanoparticles Made of Î²-Cyclodextrins Potentiates Their Effect as Drug Nanocarriers against Tuberculosis. ACS Nano, 2019, 13, 3992-4007.	14.6	42
23	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	16
24	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.	2.4	30
25	Mycobacterial virulence: impact on immunogenicity and vaccine research. F1000Research, 2019, 8, 2025.	1.6	15
26	From environmental bacteria to obligate pathogen: the study of adaptations enhancing the persistence of tuberculosis bacilli. , 2019, , .		0
27	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.	7.1	98
28	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. Nature Microbiology, 2018, 3, 181-188.	13.3	112
29	Multiplexed Quantitation of Intraphagocyte Mycobacterium tuberculosis Secreted Protein Effectors. Cell Reports, 2018, 23, 1072-1084.	6.4	28
30	Evolution of virulence in the Mycobacterium tuberculosis complex. Current Opinion in Microbiology, 2018, 41, 68-75.	5.1	69
31	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.	2.5	47
32	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.	4.7	36
33	ESX-1 and phthiocerol dimycocerosates ofMycobacterium tuberculosisact in concert to cause phagosomal rupture and host cell apoptosis. Cellular Microbiology, 2017, 19, e12726.	2.1	174
34	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.	7.1	219
35	Colonization with Helicobacter is concomitant with modified gut microbiota and drastic failure of the immune control of Mycobacterium tuberculosis. Mucosal Immunology, 2017, 10, 1178-1189.	6.0	46
36	Resistance to Thiacetazone Derivatives Active against Mycobacterium abscessus Involves Mutations in the MmpL5 Transcriptional Repressor MAB_4384. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	51

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37	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.	6.4	98
38	Mycobacterium tuberculosis Controls Phagosomal Acidification by Targeting CISH-Mediated Signaling. Cell Reports, 2017, 20, 3188-3198.	6.4	60
39	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. Scientific Reports, 2017, 7, 5702.	3.3	8
40	The Biology and Epidemiology of Mycobacterium canettii. Advances in Experimental Medicine and Biology, 2017, 1019, 27-41.	1.6	25
41	<scp>D</scp>iscovery of the type VII ESXâ€1 secretion needle?. Molecular Microbiology, 2017, 103, 7-12.	2.5	30
42	The Macrophage: A Disputed Fortress in the Battle against Mycobacterium tuberculosis. Frontiers in Microbiology, 2017, 8, 2284.	3.5	195
43	PknG senses amino acid availability to control metabolism and virulence of Mycobacterium tuberculosis. PLoS Pathogens, 2017, 13, e1006399.	4.7	81
44	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to Mycobacterium tuberculosis pathoadaptation. PLoS Pathogens, 2017, 13, e1006752.	4.7	32
45	Genomic characterization of Mycobacterium tuberculosis lineage 7 and a proposed name: â€˜Aethiops vetusâ€™. Microbial Genomics, 2016, 2, e000063.	2.0	22
46	CD4+ T Cells Recognizing PE/PPE Antigens Directly or via Cross Reactivity Are Protective against Pulmonary Mycobacterium tuberculosis Infection. PLoS Pathogens, 2016, 12, e1005770.	4.7	50
47	A new piperidinol derivative targeting mycolic acid transport in Mycobacterium abscessus. Molecular Microbiology, 2016, 101, 515-529.	2.5	100
48	Perspectives on mycobacterial vacuole-to-cytosol translocation: the importance of cytosolic access. Cellular Microbiology, 2016, 18, 1070-1077.	2.1	26
49	A unique PE_PGRS protein inhibiting host cell cytosolic defenses and sustaining full virulence ofMycobacterium marinumin multiple hosts. Cellular Microbiology, 2016, 18, 1489-1507.	2.1	25
50	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
51	The distinct fate of smooth and roughMycobacterium abscessusvariants inside macrophages. Open Biology, 2016, 6, 160185.	3.6	132
52	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	82
53	ESX secretion systems: mycobacterial evolution to counter host immunity. Nature Reviews Microbiology, 2016, 14, 677-691.	28.6	306
54	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.	7.1	103

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55	Evolution of Mycobacterium tuberculosis : New Insights into Pathogenicity and Drug Resistance. Microbiology Spectrum, 2016, 4, .	3.0	17
56	Leprosy in red squirrels. Science, 2016, 354, 702-703.	12.6	5
57	pks5-recombination-mediated surface remodelling in Mycobacterium tuberculosis emergence. Nature Microbiology, 2016, 1, 15019.	13.3	81
58	Genome-wide mosaicism within Mycobacterium abscessus: evolutionary and epidemiological implications. BMC Genomics, 2016, 17, 118.	2.8	56
59	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.	2.5	81
60	The BCG Strain Pool: Diversity Matters. Molecular Therapy, 2016, 24, 201-203.	8.2	14
61	ESAT-6â€"dependent cytosolic pattern recognition drives noncognate tuberculosis control in vivo. Journal of Clinical Investigation, 2016, 126, 2109-2122.	8.2	52
62	Revisiting the role of phospholipases C in virulence and the lifecycle of Mycobacterium tuberculosis. Scientific Reports, 2015, 5, 16918.	3.3	39
63	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.	3.3	78
64	Impact of Mycobacterium tuberculosis RD1-locus on human primary dendritic cell immune functions. Scientific Reports, 2015, 5, 17078.	3.3	18
65	Mycobacterium tuberculosis Meets the Cytosol: The Role of cGAS in Anti-mycobacterial Immunity. Cell Host and Microbe, 2015, 17, 733-735.	11.0	36
66	Type VII Secretion Systems in Gram-Positive Bacteria. Current Topics in Microbiology and Immunology, 2015, 404, 235-265.	1.1	33
67	ESX/type VII secretion systems of mycobacteria: Insights into evolution, pathogenicity and protection. Tuberculosis, 2015, 95, S150-S154.	1.9	56
68	Release of mycobacterial antigens. Immunological Reviews, 2015, 264, 25-45.	6.0	77
69	Cytosolic Access of Mycobacterium tuberculosis: Critical Impact of Phagosomal Acidification Control and Demonstration of Occurrence In Vivo. PLoS Pathogens, 2015, 11, e1004650.	4.7	177
70	Insights on the Emergence of Mycobacterium tuberculosis from the Analysis of Mycobacterium kansasii. Genome Biology and Evolution, 2015, 7, 856-870.	2.5	79
71	Increased protective efficacy of recombinant BCG strains expressing virulence-neutral proteins of the ESX-1 secretion system. Vaccine, 2015, 33, 2710-2718.	3.8	51
72	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.	2.2	54

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73	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.	2.2	74
74	Mycobacterium tuberculosis Exploits Asparagine to Assimilate Nitrogen and Resist Acid Stress during Infection. PLoS Pathogens, 2014, 10, e1003928.	4.7	148
75	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	76
76	Mycobacterium tuberculosis evolutionary pathogenesis and its putative impact on drug development. Future Microbiology, 2014, 9, 969-985.	2.0	27
77	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. Molecular Microbiology, 2014, 94, 742-742.	2.5	0
78	Bacillus Calmette-GuÃ©rin Strain Differences Have an Impact on Clinical Outcome in Bladder Cancer Immunotherapy. European Urology, 2014, 66, 677-688.	1.9	164
79	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.	7.1	204
80	Mycobacterial Pathogenomics and Evolution. Microbiology Spectrum, 2014, 2, MGM2-0025-2013.	3.0	36
81	ESX-1-induced apoptosis is involved in cell-to-cell spread ofMycobacterium tuberculosis. Cellular Microbiology, 2013, 15, 1994-2005.	2.1	116
82	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of Mycobacterium tuberculosis. Nature Genetics, 2013, 45, 172-179.	21.4	264
83	TBCAP; tuberculosis annotation project. Tuberculosis, 2013, 93, 1-5.	1.9	3
84	Characterization ofMycobacterium orygis. Emerging Infectious Diseases, 2013, 19, 521-2.	4.3	5
85	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	142
86	Single Cell Measurements of Vacuolar Rupture Caused by Intracellular Pathogens. Journal of Visualized Experiments, 2013, , e50116.	0.3	21
87	Targeting Type VII/ESX Secretion Systems for Development of Novel Antimycobacterial Drugs. Current Pharmaceutical Design, 2013, 20, 4346-4356.	1.9	17
88	Phagosomal Rupture by Mycobacterium tuberculosis Results in Toxicity and Host Cell Death. PLoS Pathogens, 2012, 8, e1002507.	4.7	479
89	Molecular epidemiology of tuberculosis in rural Matlab, Bangladesh. International Journal of Tuberculosis and Lung Disease, 2012, 16, 319-326.	1.2	16
90	ESX-1 dependent impairment of autophagic flux byMycobacterium tuberculosisin human dendritic cells. Autophagy, 2012, 8, 1357-1370.	9.1	237

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91	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	102
92	Multidrug-Resistant Tuberculosis in Admitted Patients at a Tertiary Referral Hospital of Bangladesh. PLoS ONE, 2012, 7, e40545.	2.5	32
93	The ESX-5 Associated eccB5-eccC5 Locus Is Essential for Mycobacterium tuberculosis Viability. PLoS ONE, 2012, 7, e52059.	2.5	49
94	Characterization ofMycobacterium orygisasM. tuberculosisComplex Subspecies. Emerging Infectious Diseases, 2012, 18, 653-655.	4.3	170
95	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	178
96	Tracking endosomal membrane integrity in single antigen presenting cells. Molecular Immunology, 2012, 51, 9.	2.2	0
97	ESXâ€1â€mediated translocation to the cytosol controls virulence of mycobacteria. Cellular Microbiology, 2012, 14, 1287-1298.	2.1	375
98	Activation of the NLRP3 inflammasome by Mycobacterium tuberculosis is uncoupled from susceptibility to active tuberculosis. European Journal of Immunology, 2012, 42, 374-384.	2.9	150
99	PS1-036. Mycobacterium tuberculosis ESX-1 secretion system is involved in the control of human dendritic cells maturation. Cytokine, 2011, 56, 26.	3.2	0
100	Overexpression of proinflammatory TLR-2-signalling lipoproteins in hypervirulent mycobacterial variants. Cellular Microbiology, 2011, 13, 692-704.	2.1	66
101	Deciphering the role of IS6110 in a highly transmissible Mycobacterium tuberculosis Beijing strain, GC1237. Tuberculosis, 2011, 91, 117-126.	1.9	47
102	p62 and NDP52 Proteins Target Intracytosolic Shigella and Listeria to Different Autophagy Pathways. Journal of Biological Chemistry, 2011, 286, 26987-26995.	3.4	257
103	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.	4.0	66
104	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.	5.5	33
105	High Content Phenotypic Cell-Based Visual Screen Identifies Mycobacterium tuberculosis Acyltrehalose-Containing Glycolipids Involved in Phagosome Remodeling. PLoS Pathogens, 2010, 6, e1001100.	4.7	158
106	Entrapment of Intracytosolic Bacteria by Septin Cage-like Structures. Cell Host and Microbe, 2010, 8, 433-444.	11.0	229
107	Systematic Genetic Nomenclature for Type VII Secretion Systems. PLoS Pathogens, 2009, 5, e1000507.	4.7	233
108	High Content Screening Identifies Decaprenyl-Phosphoribose 2â€² Epimerase as a Target for Intracellular Antimycobacterial Inhibitors. PLoS Pathogens, 2009, 5, e1000645.	4.7	281

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109	Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. BioEssays, 2009, 31, 378-388.	2.5	41
110	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	82
111	Myths and misconceptions: the origin and evolution of Mycobacterium tuberculosis. Nature Reviews Microbiology, 2009, 7, 537-544.	28.6	212
112	ESX/type VII secretion systems and their role in hostâ€“pathogen interaction. Current Opinion in Microbiology, 2009, 12, 4-10.	5.1	217
113	Benzothiazinones Kill Mycobacterium tuberculosis by Blocking Arabinan Synthesis. Science, 2009, 324, 801-804.	12.6	660
114	Non Mycobacterial Virulence Genes in the Genome of the Emerging Pathogen Mycobacterium abscessus. PLoS ONE, 2009, 4, e5660.	2.5	309
115	Le BCGÂ: histoire molÃ©culaire et nouvelles perspectives. Revue Des Maladies Respiratoires, 2008, 25, 85-86.	1.7	0
116	Insights from the complete genome sequence of Mycobacterium marinum on the evolution of Mycobacterium tuberculosis. Genome Research, 2008, 18, 729-741.	5.5	471
117	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	12
118	Control of M. tuberculosis ESAT-6 Secretion and Specific T Cell Recognition by PhoP. PLoS Pathogens, 2008, 4, e33.	4.7	234
119	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.	2.2	272
120	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.	7.1	486
121	Cutting-edge science and the future of tuberculosis control. Bulletin of the World Health Organization, 2007, 85, 410-412.	3.3	0
122	Pathogenomics: Insights into Tuberculosis and Related Mycobacterial Diseases. , 2006, , 211-230.		1
123	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
124	â€œA Re-Evaluation of M. prototuberculosisâ€• Continuing the Debate. PLoS Pathogens, 2006, 2, e95.	4.7	18
125	Horizontal Transfer of a Virulence Operon to the Ancestor of Mycobacterium tuberculosis. Molecular Biology and Evolution, 2006, 23, 1129-1135.	8.9	95
126	Dissection of ESAT-6 System 1 of Mycobacterium tuberculosis and Impact on Immunogenicity and Virulence. Infection and Immunity, 2006, 74, 88-98.	2.2	279

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127	Genomics of theMycobacterium tuberculosiscomplex andMycobacterium leprae. , 2005, , .		0
128	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.	2.1	135
129	Common Evolutionary Origin for the Unstable Virulence Plasmid pMUM Found in Geographically Diverse Strains of Mycobacterium ulcerans. Journal of Bacteriology, 2005, 187, 1668-1676.	2.2	74
130	Ancient Origin and Gene Mosaicism of the Progenitor of Mycobacterium tuberculosis. PLoS Pathogens, 2005, 1, e5.	4.7	469
131	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
132	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.	3.4	92
133	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.	3.4	133
134	Tuberculosis: from genome to vaccine. Expert Review of Vaccines, 2005, 4, 541-551.	4.4	22
135	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.	2.2	94
136	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.	4.0	73
137	GenotypicAnalysis of Mycobacterium tuberculosis in Bangladesh andPrevalence of the BeijingStrain. Journal of Clinical Microbiology, 2004, 42, 674-682.	3.9	80
138	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.	7.1	345
139	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	159
140	ESAT-6 proteins: protective antigens and virulence factors?. Trends in Microbiology, 2004, 12, 500-508.	7.7	275
141	Recombinant BCG exporting ESAT-6 confers enhanced protection against tuberculosis. Nature Medicine, 2003, 9, 533-539.	30.7	571
142	La gÃ©nomique et le dÃ©veloppement de nouvelles stratÃ©gies thÃ©rapeutiques et prÃ©ventives dans la lutte contre la tuberculose. MÃ©decine Et Maladies Infectieuses, 2003, 33, 141-146.	5.0	0
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.	3.9	22
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.	2.2	152

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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.	3.9	215
146	A new evolutionary scenario for the Mycobacterium tuberculosis complex. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3684-3689.	7.1	1,423
147	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	645
148	Mycobacterial genomics. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2002, 96, 1-6.	1.8	21
149	The evolution of mycobacterial pathogenicity: clues from comparative genomics. Trends in Microbiology, 2001, 9, 452-458.	7.7	186
150	Genomics of Mycobacterium bovis. Tuberculosis, 2001, 81, 157-163.	1.9	79
151	Comparative Genomics Uncovers Large Tandem Chromosomal Duplications inMycobacterium bovisBCG Pasteur. Yeast, 2000, 1, 111-123.	1.7	101
152	Tools for the Population Genomics of the Tubercle Bacilli. Genome Research, 2000, 10, 1837-1839.	5.5	6
153	Comparative genomics of the leprosy and tubercle bacilli. Research in Microbiology, 2000, 151, 135-142.	2.1	45
154	Comparative genomics of the mycobacteria. International Journal of Medical Microbiology, 2000, 290, 143-152.	3.6	93
155	Identification of variable regions in the genomes of tubercle bacilli using bacterial artificial chromosome arrays. Molecular Microbiology, 1999, 32, 643-655.	2.5	481
156	Analysis of the proteome of Mycobacterium tuberculosis in silico. Tubercle and Lung Disease, 1999, 79, 329-342.	2.1	277
157	Genomic Analysis Reveals Variation between Mycobacterium tuberculosis H37Rv and the Attenuated M. tuberculosis H37Ra Strain. Infection and Immunity, 1999, 67, 5768-5774.	2.2	141
158	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. Nature, 1998, 393, 537-544.	27.8	7,357
159	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. Nature, 1998, 396, 190-190.	27.8	119
160	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
161	Use of a Mycobacterium tuberculosis H37Rv Bacterial Artificial Chromosome Library for Genome Mapping, Sequencing, and Comparative Genomics. Infection and Immunity, 1998, 66, 2221-2229.	2.2	219
162	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

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163	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.	4.7	102
164	Ability of Biolog and Biotype-100 Systems to Reveal the Taxonomic Diversity of the Pseudomonads. Systematic and Applied Microbiology, 1996, 19, 510-527.	2.8	63
165	Taxonomic Diversity of Pseudomonads Revealed by Computer-interpretation of Ribotyping Data. Systematic and Applied Microbiology, 1996, 19, 541-555.	2.8	59
166	Characterization of Listeria strains isolated from soft cheese. International Journal of Food Microbiology, 1993, 18, 161-166.	4.7	24
167	EpidÃ©mie de listÃ©riose en France en 1992 aspects microbiologiques. MÃ©decine Et Maladies Infectieuses, 1992, 22, 35-40.	5.0	6
168	Subtyping of Listeria monocytogenes serovar 4b by use of low-frequency-cleavage restriction endonucleases and pulsed-field gel electrophoresis. Research in Microbiology, 1991, 142, 667-675.	2.1	131
169	Use of pulsed field gel electrophoresis to compare large DNA-restriction fragments of Listeria monocytogenes strains belonging to serogroups 1/2 and 3. International Journal of Food Microbiology, 1991, 14, 297-304.	4.7	44
170	Genomics ofMycobacterium Tuberculosis and Mycobacterium Leprae. , 0, , 93-109.		6
171	Evolution ofMycobacterium tuberculosis: New Insights into Pathogenicity and Drug Resistance. , 0, , 495-515.		3
172	ESX/Type VII Secretion Systems-An Important Way Out for Mycobacterial Proteins. , 0, , 351-362.		5
173	Mycobacterial Pathogenomics and Evolution. , 0, , 27-47.		3
174	ESAT-6 and the Mycobacterial ESX Secretion Systems. , 0, , 211-222.		0
175	The Mycobacteria: a Postgenomic View. , 0, , 49-89.		0