

# Roland Brosch

## List of Publications by Year in descending order

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165  
papers

17,580  
citations

11675

70  
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16102

125  
g-index

180  
all docs

180  
docs citations

180  
times ranked

14175  
citing authors

#	ARTICLE	IF	CITATIONS
1	Loss of RD1 contributed to the attenuation of the live tuberculosis vaccines <i>Mycobacterium bovis</i> BCG and <i>Mycobacterium microti</i> . <i>Molecular Microbiology</i> , 2002, 46, 709-717.	2.5	657
2	Recombinant BCG exporting ESAT-6 confers enhanced protection against tuberculosis. <i>Nature Medicine</i> , 2003, 9, 533-539.	30.1	576
3	Phagosomal Rupture by <i>Mycobacterium tuberculosis</i> Results in Toxicity and Host Cell Death. <i>PLoS Pathogens</i> , 2012, 8, e1002507.	4.1	499
4	Genome plasticity of BCG and impact on vaccine efficacy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5596-5601.	7.6	493
5	Identification of variable regions in the genomes of tubercle bacilli using bacterial artificial chromosome arrays. <i>Molecular Microbiology</i> , 1999, 32, 643-655.	2.5	484
6	Insights from the complete genome sequence of <i>Mycobacterium marinum</i> on the evolution of <i>Mycobacterium tuberculosis</i> . <i>Genome Research</i> , 2008, 18, 729-741.	5.6	483
7	Ancient Origin and Gene Mosaicism of the Progenitor of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2005, 1, e5.	4.1	478
8	ESX-1 mediated translocation to the cytosol controls virulence of mycobacteria. <i>Cellular Microbiology</i> , 2012, 14, 1287-1298.	2.3	388
9	Giant plasmid-encoded polyketide synthases produce the macrolide toxin of <i>Mycobacterium ulcerans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1345-1349.	7.6	350
10	ESX secretion systems: mycobacterial evolution to counter host immunity. <i>Nature Reviews Microbiology</i> , 2016, 14, 677-691.	29.2	322
11	Non Mycobacterial Virulence Genes in the Genome of the Emerging Pathogen <i>Mycobacterium abscessus</i> . <i>PLoS ONE</i> , 2009, 4, e5660.	2.5	316
12	High Content Screening Identifies Decaprenyl-Phosphoribose 2-Epimerase as a Target for Intracellular Antimycobacterial Inhibitors. <i>PLoS Pathogens</i> , 2009, 5, e1000645.	4.1	288
13	Dissection of ESAT-6 System 1 of <i>Mycobacterium tuberculosis</i> and Impact on Immunogenicity and Virulence. <i>Infection and Immunity</i> , 2006, 74, 88-98.	2.4	286
14	ESAT-6 from <i>Mycobacterium tuberculosis</i> Dissociates from Its Putative Chaperone CFP-10 under Acidic Conditions and Exhibits Membrane-Lysing Activity. <i>Journal of Bacteriology</i> , 2007, 189, 6028-6034.	2.4	285
15	ESAT-6 proteins: protective antigens and virulence factors?. <i>Trends in Microbiology</i> , 2004, 12, 500-508.	7.7	279
16	Genomic analysis of smooth tubercle bacilli provides insights into ancestry and pathoadaptation of <i>Mycobacterium tuberculosis</i> . <i>Nature Genetics</i> , 2013, 45, 172-179.	20.4	270
17	p62 and NDP52 Proteins Target Intracytosolic <i>Shigella</i> and <i>Listeria</i> to Different Autophagy Pathways. <i>Journal of Biological Chemistry</i> , 2011, 286, 26987-26995.	3.5	262
18	ESX-1 dependent impairment of autophagic flux by <i>Mycobacterium tuberculosis</i> in human dendritic cells. <i>Autophagy</i> , 2012, 8, 1357-1370.	11.0	246

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19	Entrapment of Intracytosolic Bacteria by Septin Cage-like Structures. <i>Cell Host and Microbe</i> , 2010, 8, 433-444.	11.0	241
20	Control of <i>M. tuberculosis</i> ESAT-6 Secretion and Specific T Cell Recognition by PhoP. <i>PLoS Pathogens</i> , 2008, 4, e33.	4.1	238
21	Systematic Genetic Nomenclature for Type VII Secretion Systems. <i>PLoS Pathogens</i> , 2009, 5, e1000507.	4.1	236
22	Mycobacterial ESX-1 secretion system mediates host cell lysis through bacterium contact-dependent gross membrane disruptions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1371-1376.	7.6	234
23	Use of a <i>Mycobacterium tuberculosis</i> H37Rv Bacterial Artificial Chromosome Library for Genome Mapping, Sequencing, and Comparative Genomics. <i>Infection and Immunity</i> , 1998, 66, 2221-2229.	2.4	221
24	ESX/type VII secretion systems and their role in host-pathogen interaction. <i>Current Opinion in Microbiology</i> , 2009, 12, 4-10.	5.2	217
25	Myths and misconceptions: the origin and evolution of <i>Mycobacterium tuberculosis</i> . <i>Nature Reviews Microbiology</i> , 2009, 7, 537-544.	29.2	216
26	Rapid and Simple Approach for Identification of <i>Mycobacterium tuberculosis</i> Complex Isolates by PCR-Based Genomic Deletion Analysis. <i>Journal of Clinical Microbiology</i> , 2002, 40, 2339-2345.	4.4	215
27	Evolutionary history of tuberculosis shaped by conserved mutations in the PhoPR virulence regulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11491-11496.	7.6	208
28	The Macrophage: A Disputed Fortress in the Battle against <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2284.	3.6	201
29	The evolution of mycobacterial pathogenicity: clues from comparative genomics. <i>Trends in Microbiology</i> , 2001, 9, 452-458.	7.7	187
30	ESX-1 and phthiocerol dimycocerosates of <i>Mycobacterium tuberculosis</i> act in concert to cause phagosomal rupture and host cell apoptosis. <i>Cellular Microbiology</i> , 2017, 19, e12726.	2.3	187
31	Disruption of the ESX-5 system of <i>Mycobacterium tuberculosis</i> causes loss of PPE protein secretion, reduction of cell wall integrity and strong attenuation. <i>Molecular Microbiology</i> , 2012, 83, 1195-1209.	2.5	180
32	Cytosolic Access of <i>Mycobacterium tuberculosis</i> : Critical Impact of Phagosomal Acidification Control and Demonstration of Occurrence In Vivo. <i>PLoS Pathogens</i> , 2015, 11, e1004650.	4.1	180
33	Characterization of <i>Mycobacterium orygis</i> as <i>M. tuberculosis</i> Complex Subspecies. <i>Emerging Infectious Diseases</i> , 2012, 18, 653-655.	4.4	177
34	High Content Phenotypic Cell-Based Visual Screen Identifies <i>Mycobacterium tuberculosis</i> Acyltrehalose-Containing Glycolipids Involved in Phagosome Remodeling. <i>PLoS Pathogens</i> , 2010, 6, e1001100.	4.1	166
35	<i>Bacillus Calmette-Guérin</i> Strain Differences Have an Impact on Clinical Outcome in Bladder Cancer Immunotherapy. <i>European Urology</i> , 2014, 66, 677-688.	5.0	166
36	Macro-array and bioinformatic analyses reveal mycobacterial core genes, variation in the ESAT-6 gene family and new phylogenetic markers for the <i>Mycobacterium tuberculosis</i> complex. <i>Microbiology (United Kingdom)</i> , 2004, 150, 483-496.	1.8	163

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37	The high-pathogenicity island of <i>Yersinia pseudotuberculosis</i> can be inserted into any of the three chromosomal <i>asn</i> tRNA genes. <i>Molecular Microbiology</i> , 1998, 30, 965-978.	2.5	155
38	Activation of the NLRP3 inflammasome by <i>Mycobacterium tuberculosis</i> is uncoupled from susceptibility to active tuberculosis. <i>European Journal of Immunology</i> , 2012, 42, 374-384.	3.3	155
39	Bacterial Artificial Chromosome-Based Comparative Genomic Analysis Identifies <i>Mycobacterium microti</i> as a Natural ESAT-6 Deletion Mutant. <i>Infection and Immunity</i> , 2002, 70, 5568-5578.	2.4	154
40	<i>Mycobacterium tuberculosis</i> Exploits Asparagine to Assimilate Nitrogen and Resist Acid Stress during Infection. <i>PLoS Pathogens</i> , 2014, 10, e1003928.	4.1	152
41	Identification and characterization of the genetic changes responsible for the characteristic smooth-to-rough morphotype alterations of clinically persistent <i>Mycobacterium abscessus</i> . <i>Molecular Microbiology</i> , 2013, 90, 612-629.	2.5	150
42	Genomic Analysis Reveals Variation between <i>Mycobacterium tuberculosis</i> H37Rv and the Attenuated <i>M. tuberculosis</i> H37Ra Strain. <i>Infection and Immunity</i> , 1999, 67, 5768-5774.	2.4	141
43	Functional Analysis of Early Secreted Antigenic Target-6, the Dominant T-cell Antigen of <i>Mycobacterium tuberculosis</i> , Reveals Key Residues Involved in Secretion, Complex Formation, Virulence, and Immunogenicity. <i>Journal of Biological Chemistry</i> , 2005, 280, 33953-33959.	3.5	140
44	Influence of ESAT-6 Secretion System 1 (RD1) of <i>Mycobacterium tuberculosis</i> on the Interaction between Mycobacteria and the Host Immune System. <i>Journal of Immunology</i> , 2005, 174, 3570-3579.	0.8	137
45	The distinct fate of smooth and rough <i>Mycobacterium abscessus</i> variants inside macrophages. <i>Open Biology</i> , 2016, 6, 160185.	3.7	136
46	Modulation of the host immune response by a transient intracellular stage of <i>Mycobacterium ulcerans</i> : the contribution of endogenous mycolactone toxin. <i>Cellular Microbiology</i> , 2005, 7, 1187-1196.	2.3	135
47	ESX-1-induced apoptosis is involved in cell-to-cell spread of <i>Mycobacterium tuberculosis</i> . <i>Cellular Microbiology</i> , 2013, 15, 1994-2005.	2.3	126
48	Mutations in <i>ppe38</i> block PE_PGRS secretion and increase virulence of <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2018, 3, 181-188.	13.1	117
49	Key experimental evidence of chromosomal DNA transfer among selected tuberculosis-causing mycobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9876-9881.	7.6	110
50	Strong Immunogenicity and Cross-Reactivity of <i>Mycobacterium tuberculosis</i> ESX-5 Type VII Secretion-Encoded PE-PPE Proteins Predicts Vaccine Potential. <i>Cell Host and Microbe</i> , 2012, 11, 352-363.	11.0	103
51	Genomic fingerprinting of 80 strains from the WHO multicenter international typing study of <i>Listeria monocytogenes</i> via pulsed-field gel electrophoresis (PFGE). <i>International Journal of Food Microbiology</i> , 1996, 32, 343-355.	4.8	102
52	A new piperidinol derivative targeting mycolic acid transport in <i>Mycobacterium abscessus</i> . <i>Molecular Microbiology</i> , 2016, 101, 515-529.	2.5	102
53	Recombinant BCG Expressing ESX-1 of <i>Mycobacterium marinum</i> Combines Low Virulence with Cytosolic Immune Signaling and Improved TB Protection. <i>Cell Reports</i> , 2017, 18, 2752-2765.	6.3	102
54	Identification of genes required for <i>Mycobacterium abscessus</i> growth in vivo with a prominent role of the ESX-4 locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1002-E1011.	7.6	101

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55	Horizontal Transfer of a Virulence Operon to the Ancestor of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2006, 23, 1129-1135.	9.2	96
56	Cell Envelope Protein PPE68 Contributes to <i>Mycobacterium tuberculosis</i> RD1 Immunogenicity Independently of a 10-Kilodalton Culture Filtrate Protein and ESAT-6. <i>Infection and Immunity</i> , 2004, 72, 2170-2176.	2.4	95
57	Comparative genomics of the mycobacteria. <i>International Journal of Medical Microbiology</i> , 2000, 290, 143-152.	3.8	94
58	Structure and Mechanism of the Alkyl Hydroperoxidase AhpC, a Key Element of the <i>Mycobacterium tuberculosis</i> Defense System against Oxidative Stress. <i>Journal of Biological Chemistry</i> , 2005, 280, 25735-25742.	3.5	92
59	<i>Mycobacterial Pan-Genome Analysis Suggests Important Role of Plasmids in the Radiation of Type VII Secretion Systems</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 387-402.	2.6	89
60	Insights into the smooth-to-rough transitioning in <i>Mycobacterium boletii</i> unravels a functional Tyr residue conserved in all mycobacterial MmpL family members. <i>Molecular Microbiology</i> , 2016, 99, 866-883.	2.5	87
61	pks5-recombination-mediated surface remodelling in <i>Mycobacterium tuberculosis</i> emergence. <i>Nature Microbiology</i> , 2016, 1, 15019.	13.1	87
62	Insights on the Emergence of <i>Mycobacterium tuberculosis</i> from the Analysis of <i>Mycobacterium kansasii</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 856-870.	2.6	86
63	<i>Mycobacterial PE, PPE and ESX clusters: novel insights into the secretion of these most unusual protein families</i> . <i>Molecular Microbiology</i> , 2009, 73, 325-328.	2.5	84
64	Genomic expression catalogue of a global collection of BCG vaccine strains show evidence for highly diverged metabolic and cell-wall adaptations. <i>Scientific Reports</i> , 2015, 5, 15443.	3.4	83
65	Release of mycobacterial antigens. <i>Immunological Reviews</i> , 2015, 264, 25-45.	6.1	82
66	PknG senses amino acid availability to control metabolism and virulence of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006399.	4.1	81
67	Genotypic Analysis of <i>Mycobacterium tuberculosis</i> in Bangladesh and Prevalence of the Beijing Strain. <i>Journal of Clinical Microbiology</i> , 2004, 42, 674-682.	4.4	80
68	A glimpse into the past and predictions for the future: the molecular evolution of the tuberculosis agent. <i>Molecular Microbiology</i> , 2014, 93, 835-852.	2.5	79
69	A Specific Polymorphism in <i>Mycobacterium tuberculosis</i> H37Rv Causes Differential ESAT-6 Expression and Identifies WhiB6 as a Novel ESX-1 Component. <i>Infection and Immunity</i> , 2014, 82, 3446-3456.	2.4	78
70	TbD1 deletion as a driver of the evolutionary success of modern epidemic <i>Mycobacterium tuberculosis</i> lineages. <i>Nature Communications</i> , 2020, 11, 684.	13.2	78
71	Common Evolutionary Origin for the Unstable Virulence Plasmid pMUM Found in Geographically Diverse Strains of <i>Mycobacterium ulcerans</i> . <i>Journal of Bacteriology</i> , 2005, 187, 1668-1676.	2.4	74
72	Enhanced Protection against Tuberculosis by Vaccination with Recombinant <i>Mycobacterium microti</i> Vaccine That Induces T Cell Immunity against Region of Difference 1 Antigens. <i>Journal of Infectious Diseases</i> , 2004, 190, 115-122.	3.9	73

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73	Evolution of virulence in the Mycobacterium tuberculosis complex. <i>Current Opinion in Microbiology</i> , 2018, 41, 68-75.	5.2	72
74	The antibiotic bedaquiline activates host macrophage innate immune resistance to bacterial infection. <i>ELife</i> , 2020, 9, .	5.9	72
75	Overexpression of proinflammatory TLR-2-signalling lipoproteins in hypervirulent mycobacterial variants. <i>Cellular Microbiology</i> , 2011, 13, 692-704.	2.3	69
76	ESAT-6 Secretion-Independent Impact of ESX-1 Genes espF and espG1 on Virulence of Mycobacterium tuberculosis. <i>Journal of Infectious Diseases</i> , 2011, 203, 1155-1164.	3.9	68
77	Ability of Biolog and Biotype-100 Systems to Reveal the Taxonomic Diversity of the Pseudomonads. <i>Systematic and Applied Microbiology</i> , 1996, 19, 510-527.	3.0	64
78	Mycobacterium tuberculosis Controls Phagosomal Acidification by Targeting CISH-Mediated Signaling. <i>Cell Reports</i> , 2017, 20, 3188-3198.	6.3	62
79	Taxonomic Diversity of Pseudomonads Revealed by Computer-interpretation of Ribotyping Data. <i>Systematic and Applied Microbiology</i> , 1996, 19, 541-555.	3.0	59
80	ESX/type VII secretion systems of mycobacteria: Insights into evolution, pathogenicity and protection. <i>Tuberculosis</i> , 2015, 95, S150-S154.	2.0	58
81	Genome-wide mosaicism within Mycobacterium abscessus: evolutionary and epidemiological implications. <i>BMC Genomics</i> , 2016, 17, 118.	2.9	58
82	Resistance to Thiacetazone Derivatives Active against Mycobacterium abscessus Involves Mutations in the MmpL5 Transcriptional Repressor MAB_4384. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.4	55
83	Mycobacterium abscessus Phospholipase C Expression Is Induced during Coculture within Amoebae and Enhances M. abscessus Virulence in Mice. <i>Infection and Immunity</i> , 2015, 83, 780-791.	2.4	54
84	ESAT-6-dependent cytosolic pattern recognition drives noncognate tuberculosis control in vivo. <i>Journal of Clinical Investigation</i> , 2016, 126, 2109-2122.	8.2	53
85	The ESX-5 Associated eccB5-eccC5 Locus Is Essential for Mycobacterium tuberculosis Viability. <i>PLoS ONE</i> , 2012, 7, e52059.	2.5	52
86	Increased protective efficacy of recombinant BCG strains expressing virulence-neutral proteins of the ESX-1 secretion system. <i>Vaccine</i> , 2015, 33, 2710-2718.	4.0	52
87	Unexpected Genomic and Phenotypic Diversity of Mycobacterium africanum Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. <i>Genome Biology and Evolution</i> , 2018, 10, 1858-1874.	2.6	51
88	CD4+ T Cells Recognizing PE/PPE Antigens Directly or via Cross Reactivity Are Protective against Pulmonary Mycobacterium tuberculosis Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005770.	4.1	50
89	Deciphering the role of IS6110 in a highly transmissible Mycobacterium tuberculosis Beijing strain, GC1237. <i>Tuberculosis</i> , 2011, 91, 117-126.	2.0	49
90	Mycobacterium abscessus virulence traits unraveled by transcriptomic profiling in amoeba and macrophages. <i>PLoS Pathogens</i> , 2019, 15, e1008069.	4.1	47

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91	Intrinsic Antibacterial Activity of Nanoparticles Made of $\beta$ -Cyclodextrins Potentiates Their Effect as Drug Nanocarriers against Tuberculosis. ACS Nano, 2019, 13, 3992-4007.	15.3	46
92	Comparative genomics of the leprosy and tubercle bacilli. Research in Microbiology, 2000, 151, 135-142.	2.2	45
93	Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. BioEssays, 2009, 31, 378-388.	2.6	44
94	Revisiting the role of phospholipases C in virulence and the lifecycle of Mycobacterium tuberculosis. Scientific Reports, 2015, 5, 16918.	3.4	39
95	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
96	Mycobacterium tuberculosis Meets the Cytosol: The Role of cGAS in Anti-mycobacterial Immunity. Cell Host and Microbe, 2015, 17, 733-735.	11.0	38
97	Mycobacterial Pathogenomics and Evolution. Microbiology Spectrum, 2014, 2, MGM2-0025-2013.	3.0	36
98	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
99	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to Mycobacterium tuberculosis pathoadaptation. PLoS Pathogens, 2017, 13, e1006752.	4.1	34
100	ESX/Type VII Secretion Systems – An Important Way Out for Mycobacterial Proteins. Microbiology Spectrum, 2019, 7, .	3.0	34
101	Genomic analysis using pulsed-field gel electrophoresis of Escherichia coli O157:H7 isolated from dairy calves during the United States national dairy heifer evaluation project (1991–1992). Veterinary Microbiology, 1996, 48, 223-230.	1.9	33
102	Type VII Secretion Systems in Gram-Positive Bacteria. Current Topics in Microbiology and Immunology, 2015, 404, 235-265.	0.0	33
103	Discovery of the type VII ESX-1 secretion needle?. Molecular Microbiology, 2017, 103, 7-12.	2.5	33
104	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
105	Multidrug-Resistant Tuberculosis in Admitted Patients at a Tertiary Referral Hospital of Bangladesh. PLoS ONE, 2012, 7, e40545.	2.5	32
106	The changes in mycolic acid structures caused by <i>hadC</i> mutation have a dramatic effect on the virulence of <i>Mycobacterium tuberculosis</i> . Molecular Microbiology, 2016, 99, 794-807.	2.5	32
107	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
108	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

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109	Multiplexed Quantitation of Intraphagocyte Mycobacterium tuberculosis Secreted Protein Effectors. Cell Reports, 2018, 23, 1072-1084.	6.3	30
110	Live attenuated TB vaccines representing the three modern Mycobacterium tuberculosis lineages reveal that the Euro-American genetic background confers optimal vaccine potential. EBioMedicine, 2020, 55, 102761.	6.0	29
111	<i>Mycobacterium Tuberculosis</i> Evolutionary Pathogenesis and its Putative Impact on Drug Development. Future Microbiology, 2014, 9, 969-985.	2.0	28
112	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
113	Perspectives on mycobacterial vacuole-to-cytosol translocation: the importance of cytosolic access. Cellular Microbiology, 2016, 18, 1070-1077.	2.3	26
114	A unique PE_PGRS protein inhibiting host cell cytosolic defenses and sustaining full virulence of <i>Mycobacterium marinum</i> in multiple hosts. Cellular Microbiology, 2016, 18, 1489-1507.	2.3	26
115	The Biology and Epidemiology of Mycobacterium canettii. Advances in Experimental Medicine and Biology, 2017, 1019, 27-41.	0.0	26
116	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
117	Tuberculosis: from genome to vaccine. Expert Review of Vaccines, 2005, 4, 541-551.	4.5	22
118	Genomic characterization of Mycobacterium tuberculosis lineage 7 and a proposed name: <i>Aethiops vetus</i> <sup>TM</sup> . Microbial Genomics, 2016, 2, e000063.	2.1	22
119	Mycobacterial genomics. Transactions of the Royal Society of Tropical Medicine and Hygiene, 2002, 96, 1-6.	1.8	21
120	<i>IS6110</i> Re-Evaluation of M. prototuberculosis Continuing the Debate. PLoS Pathogens, 2006, 2, e95.	4.1	21
121	Single Cell Measurements of Vacuolar Rupture Caused by Intracellular Pathogens. Journal of Visualized Experiments, 2013, , e50116.	0.3	21
122	Breaching the phagosome, the case of the tuberculosis agent. Cellular Microbiology, 2021, 23, e13344.	2.3	21
123	Evolution of <i>Mycobacterium tuberculosis</i> : New Insights into Pathogenicity and Drug Resistance. Microbiology Spectrum, 2016, 4, .	3.0	20
124	Impact of Mycobacterium tuberculosis RD1-locus on human primary dendritic cell immune functions. Scientific Reports, 2015, 5, 17078.	3.4	19
125	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
126	ESX-1-Independent Horizontal Gene Transfer by Mycobacterium tuberculosis Complex Strains. MBio, 2021, 12, .	4.4	17



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127	Targeting Type VII/ESX Secretion Systems for Development of Novel Antimycobacterial Drugs. <i>Current Pharmaceutical Design</i> , 2013, 20, 4346-4356.	1.9	17
128	Parallel in vivo experimental evolution reveals that increased stress resistance was key for the emergence of persistent tuberculosis bacilli. <i>Nature Microbiology</i> , 2021, 6, 1082-1093.	13.1	16
129	Mycobacterial virulence: impact on immunogenicity and vaccine research. <i>F1000Research</i> , 2019, 8, 2025.	1.6	16
130	A comprehensive update to the <i>Mycobacterium tuberculosis</i> H37Rv reference genome. <i>Nature Communications</i> , 2022, 13, .	13.2	16
131	The BCG Strain Pool: Diversity Matters. <i>Molecular Therapy</i> , 2016, 24, 201-203.	8.1	15
132	The PE and PPE Protein Families of <i>Mycobacterium tuberculosis</i> ., 2008, , 131-150.		15
133	Functional analysis of a clonal deletion in an epidemic strain of <i>Mycobacterium bovis</i> reveals a role in lipid metabolism. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3731-3742.	1.8	13
134	Pathogenomic analyses of <i>Mycobacterium microti</i> , an ESX-1-deleted member of the <i>Mycobacterium tuberculosis</i> complex causing disease in various hosts. <i>Microbial Genomics</i> , 2021, 7, .	2.1	12
135	A systematic approach to simultaneously evaluate safety, immunogenicity, and efficacy of novel tuberculosis vaccination strategies. <i>Science Advances</i> , 2020, 6, eaaz1767.	10.9	11
136	Discovery of a novel dehydratase of the fatty acid synthase type II critical for ketomycolic acid biosynthesis and virulence of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2020, 10, 2112.	3.4	11
137	The <i>Mycobacterium tuberculosis</i> PhoPR virulence system regulates expression of the universal second messenger c-di-AMP and impacts vaccine safety and efficacy. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 1235-1248.	5.1	10
138	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. <i>Scientific Reports</i> , 2017, 7, 5702.	3.4	9
139	Mucosal delivery of ESX-1-expressing BCG strains provides superior immunity against tuberculosis in murine type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20848-20859.	7.6	9
140	A lentiviral vector encoding fusion of light invariant chain and mycobacterial antigens induces protective CD4+ T cell immunity. <i>Cell Reports</i> , 2022, 40, 111142.	6.3	9
141	Phenotypic and genomic hallmarks of a novel, potentially pathogenic rapidly growing <i>Mycobacterium</i> species related to the <i>Mycobacterium fortuitum</i> complex. <i>Scientific Reports</i> , 2021, 11, 13011.	3.4	7
142	Genomics of <i>Mycobacterium Tuberculosis</i> and <i>Mycobacterium Leprae</i> ., 0, , 93-109.		6
143	Tools for the Population Genomics of the Tubercle Bacilli. <i>Genome Research</i> , 2000, 10, 1837-1839.	5.6	6
144	Proteome remodeling in the <i>Mycobacterium tuberculosis</i> PknG knockout: Molecular evidence for the role of this kinase in cell envelope biogenesis and hypoxia response. <i>Journal of Proteomics</i> , 2021, 244, 104276.	2.5	6

#	ARTICLE	IF	CITATIONS
145	Evolution and emergence of <i>Mycobacterium tuberculosis</i> . FEMS Microbiology Reviews, 2024, 48, .	8.9	6
146	Characterization of <i>Mycobacterium orygis</i> . Emerging Infectious Diseases, 2013, 19, 521-2.	4.4	5
147	Leprosy in red squirrels. Science, 2016, 354, 702-703.	20.9	5
148	Evolution of <i>Mycobacterium tuberculosis</i> : New Insights into Pathogenicity and Drug Resistance. , 0, , 495-515.		5
149	ESX/Type VII Secretion Systems-An Important Way Out for Mycobacterial Proteins. , 0, , 351-362.		5
150	IL-1R1-Dependent Signals Improve Control of Cytosolic Virulent Mycobacteria <i>In Vivo</i> . MSphere, 2021, 6, .	3.1	4
151	The MtZ Strain: Molecular Characteristics and Outbreak Investigation of the Most Successful <i>Mycobacterium tuberculosis</i> Strain in Aragon Using Whole-Genome Sequencing. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	4.0	4
152	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
153	TBCAP; tuberculosis annotation project. Tuberculosis, 2013, 93, 1-5.	2.0	3
154	Mycobacterial Pathogenomics and Evolution. , 0, , 27-47.		3
155	Les bacilles de la tuberculose bovine. Medecine/Sciences, 2015, 31, 123-126.	0.2	2
156	Pathogenomics: Insights into Tuberculosis and Related Mycobacterial Diseases. , 2006, , 211-230.		1
157	DÃ©couverte d'une nouvelle classe d'antituberculeux: les benzothiazinones (BTZ). Medecine/Sciences, 2009, 25, 663-665.	0.2	1
158	Genomics of the <i>Mycobacterium tuberculosis</i> complex and <i>Mycobacterium leprae</i> . , 2005, , .		0
159	Apports de la gÃ©nÃ©tique 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
160	ESX-4, un systÃ©me de sÃ©crÃ©tion mycobactÃ©rien ancestral, essentiel pour la croissance de <i>Mycobacterium abscessus</i> dans les phagocytes environnementaux et humains. Medecine/Sciences, 2018, 34, 795-797.	0.2	0
161	ESAT-6 and the Mycobacterial ESX Secretion Systems. , 0, , 211-222.		0
162	The Mycobacteria: a Postgenomic View. , 0, , 49-89.		0

#	ARTICLE	IF	CITATIONS
163	From environmental bacteria to obligate pathogen: the study of adaptations enhancing the persistence of tuberculosis bacilli. European Respiratory Journal, 2019, , .	7.5	0
164	From environmental bacteria to obligate pathogen: the study of adaptations enhancing the persistence of tuberculosis bacilli. European Respiratory Journal, 2020, , .	7.5	0
165	Genomic and phenotypic characterization of <i>Mycobacterium tuberculosis</i> ™ closest-related non-tuberculous mycobacteria. Microbiology Spectrum, 2024, 12, .	3.0	0