

Roland Brosch

List of Publications by Year in descending order

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175
papers

26,572
citations

10986

71
h-index

6471

157
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188
all docs

188
docs citations

188
times ranked

16935
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering the biology of <i>Mycobacterium tuberculosis</i> from the complete genome sequence. <i>Nature</i> , 1998, 393, 537-544.	27.8	7,357
2	A new evolutionary scenario for the <i>Mycobacterium tuberculosis</i> complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 3684-3689.	7.1	1,423
3	Benzothiazinones Kill <i>Mycobacterium tuberculosis</i> by Blocking Arabinan Synthesis. <i>Science</i> , 2009, 324, 801-804.	12.6	660
4	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	645
5	Recombinant BCG exporting ESAT-6 confers enhanced protection against tuberculosis. <i>Nature Medicine</i> , 2003, 9, 533-539.	30.7	571
6	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.	7.1	486
7	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	481
8	Phagosomal Rupture by <i>Mycobacterium tuberculosis</i> Results in Toxicity and Host Cell Death. <i>PLoS Pathogens</i> , 2012, 8, e1002507.	4.7	479
9	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.	5.5	471
10	Ancient Origin and Gene Mosaicism of the Progenitor of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2005, 1, e5.	4.7	469
11	ESX-mediated translocation to the cytosol controls virulence of mycobacteria. <i>Cellular Microbiology</i> , 2012, 14, 1287-1298.	2.1	375
12	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.	7.1	345
13	Non Mycobacterial Virulence Genes in the Genome of the Emerging Pathogen <i>Mycobacterium abscessus</i> . <i>PLoS ONE</i> , 2009, 4, e5660.	2.5	309
14	ESX secretion systems: mycobacterial evolution to counter host immunity. <i>Nature Reviews Microbiology</i> , 2016, 14, 677-691.	28.6	306
15	High Content Screening Identifies Decaprenyl-Phosphoribose 2-Epimerase as a Target for Intracellular Antimycobacterial Inhibitors. <i>PLoS Pathogens</i> , 2009, 5, e1000645.	4.7	281
16	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.	2.2	279
17	Analysis of the proteome of <i>Mycobacterium tuberculosis</i> in silico. <i>Tubercle and Lung Disease</i> , 1999, 79, 329-342.	2.1	277
18	ESAT-6 proteins: protective antigens and virulence factors?. <i>Trends in Microbiology</i> , 2004, 12, 500-508.	7.7	275

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19	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.	2.2	272
20	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.	21.4	264
21	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.	3.4	257
22	ESX-1 dependent impairment of autophagic flux by <i>Mycobacterium tuberculosis</i> in human dendritic cells. <i>Autophagy</i> , 2012, 8, 1357-1370.	9.1	237
23	Control of <i>M. tuberculosis</i> ESAT-6 Secretion and Specific T Cell Recognition by PhoP. <i>PLoS Pathogens</i> , 2008, 4, e33.	4.7	234
24	Systematic Genetic Nomenclature for Type VII Secretion Systems. <i>PLoS Pathogens</i> , 2009, 5, e1000507.	4.7	233
25	Entrapment of Intracytosolic Bacteria by Septin Cage-like Structures. <i>Cell Host and Microbe</i> , 2010, 8, 433-444.	11.0	229
26	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.	2.2	219
27	<i>Mycobacterial</i> 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.	7.1	219
28	ESX/type VII secretion systems and their role in host-pathogen interaction. <i>Current Opinion in Microbiology</i> , 2009, 12, 4-10.	5.1	217
29	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.	3.9	215
30	Myths and misconceptions: the origin and evolution of <i>Mycobacterium tuberculosis</i> . <i>Nature Reviews Microbiology</i> , 2009, 7, 537-544.	28.6	212
31	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.	7.1	204
32	The Macrophage: A Disputed Fortress in the Battle against <i>Mycobacterium tuberculosis</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 2284.	3.5	195
33	The evolution of mycobacterial pathogenicity: clues from comparative genomics. <i>Trends in Microbiology</i> , 2001, 9, 452-458.	7.7	186
34	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	178
35	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.	4.7	177
36	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.	2.1	174

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37	Characterization of <i>Mycobacterium orygis</i> as <i>M. tuberculosis</i> Complex Subspecies. Emerging Infectious Diseases, 2012, 18, 653-655.	4.3	170
38	Bacillus Calmette-Guérin Strain Differences Have an Impact on Clinical Outcome in Bladder Cancer Immunotherapy. European Urology, 2014, 66, 677-688.	1.9	164
39	Macro-array and bioinformatic analyses reveal mycobacterial "core" 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
40	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
41	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
42	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
43	Activation of the NLRP3 inflammasome by <i>Mycobacterium tuberculosis</i> is uncoupled from susceptibility to active tuberculosis. European Journal of Immunology, 2012, 42, 374-384.	2.9	150
44	Mycobacterium tuberculosis Exploits Asparagine to Assimilate Nitrogen and Resist Acid Stress during Infection. PLoS Pathogens, 2014, 10, e1003928.	4.7	148
45	Identification and characterization of the genetic changes responsible for the characteristic smooth-to-rough morphotype alterations of clinically persistent <i>Mycobacterium abscessus</i> . Molecular Microbiology, 2013, 90, 612-629.	2.5	142
46	Genomic Analysis Reveals Variation between <i>Mycobacterium tuberculosis</i> H37Rv and the Attenuated <i>M. tuberculosis</i> H37Ra Strain. Infection and Immunity, 1999, 67, 5768-5774.	2.2	141
47	Influence of ESAT-6 Secretion System 1 (RD1) of <i>Mycobacterium tuberculosis</i> on the Interaction between Mycobacteria and the Host Immune System. Journal of Immunology, 2005, 174, 3570-3579.	0.8	137
48	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
49	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
50	The distinct fate of smooth and rough <i>Mycobacterium abscessus</i> variants inside macrophages. Open Biology, 2016, 6, 160185.	3.6	132
51	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
52	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. Nature, 1998, 396, 190-190.	27.8	119
53	ESX-1-induced apoptosis is involved in cell-to-cell spread of <i>Mycobacterium tuberculosis</i> . Cellular Microbiology, 2013, 15, 1994-2005.	2.1	116
54	Mutations in ppe38 block PE_PGRS secretion and increase virulence of Mycobacterium tuberculosis. Nature Microbiology, 2018, 3, 181-188.	13.3	112

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55	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
56	Genomic fingerprinting of 80 strains from the WHO multicenter international typing study of <i>Listeria monocytogenes</i> via pulsed-field gel electrophoresis (PFGE). International Journal of Food Microbiology, 1996, 32, 343-355.	4.7	102
57	Strong Immunogenicity and Cross-Reactivity of <i>Mycobacterium tuberculosis</i> ESX-5 Type VII Secretion-Encoded PE-PPE Proteins Predicts Vaccine Potential. Cell Host and Microbe, 2012, 11, 352-363.	11.0	102
58	Comparative Genomics Uncovers Large Tandem Chromosomal Duplications in <i>Mycobacterium bovis</i> /BCG Pasteur. Yeast, 2000, 1, 111-123.	1.7	101
59	A new piperidinol derivative targeting mycolic acid transport in <i>Mycobacterium abscessus</i> . Molecular Microbiology, 2016, 101, 515-529.	2.5	100
60	Recombinant BCG Expressing ESX-1 of <i>Mycobacterium marinum</i> Combines Low Virulence with Cytosolic Immune Signaling and Improved TB Protection. Cell Reports, 2017, 18, 2752-2765.	6.4	98
61	Identification of genes required for <i>Mycobacterium abscessus</i> 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
62	Horizontal Transfer of a Virulence Operon to the Ancestor of <i>Mycobacterium tuberculosis</i> . Molecular Biology and Evolution, 2006, 23, 1129-1135.	8.9	95
63	Cell Envelope Protein PPE68 Contributes to <i>Mycobacterium tuberculosis</i> RD1 Immunogenicity Independently of a 10-Kilodalton Culture Filtrate Protein and ESAT-6. Infection and Immunity, 2004, 72, 2170-2176.	2.2	94
64	Comparative genomics of the mycobacteria. International Journal of Medical Microbiology, 2000, 290, 143-152.	3.6	93
65	Structure and Mechanism of the Alkyl Hydroperoxidase AhpC, a Key Element of the <i>Mycobacterium tuberculosis</i> Defense System against Oxidative Stress. Journal of Biological Chemistry, 2005, 280, 25735-25742.	3.4	92
66	<i>Mycobacterium</i> 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
67	Insights into the smooth-to-rough transitioning in <i>Mycobacterium boletii</i> unravels a functional Tyr residue conserved in all mycobacterial MmpL family members. Molecular Microbiology, 2016, 99, 866-883.	2.5	82
68	pks5-recombination-mediated surface remodelling in <i>Mycobacterium tuberculosis</i> emergence. Nature Microbiology, 2016, 1, 15019.	13.3	81
69	<i>Mycobacterium</i> 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
70	PknG senses amino acid availability to control metabolism and virulence of <i>Mycobacterium tuberculosis</i> . PLoS Pathogens, 2017, 13, e1006399.	4.7	81
71	Genotypic Analysis of <i>Mycobacterium tuberculosis</i> in Bangladesh and Prevalence of the Beijing Strain. Journal of Clinical Microbiology, 2004, 42, 674-682.	3.9	80
72	Genomics of <i>Mycobacterium bovis</i> . Tuberculosis, 2001, 81, 157-163.	1.9	79

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73	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.	2.5	79
74	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.	3.3	78
75	Release of mycobacterial antigens. <i>Immunological Reviews</i> , 2015, 264, 25-45.	6.0	77
76	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	76
77	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.	2.2	74
78	A Specific Polymorphism in <i>Mycobacterium tuberculosis</i> H37Rv Causes Differential ESAT-6 Expression and Identifies <i>WhiB6</i> as a Novel ESX-1 Component. <i>Infection and Immunity</i> , 2014, 82, 3446-3456.	2.2	74
79	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.	4.0	73
80	Evolution of virulence in the <i>Mycobacterium tuberculosis</i> complex. <i>Current Opinion in Microbiology</i> , 2018, 41, 68-75.	5.1	69
81	TbD1 deletion as a driver of the evolutionary success of modern epidemic <i>Mycobacterium tuberculosis</i> lineages. <i>Nature Communications</i> , 2020, 11, 684.	12.8	68
82	Overexpression of proinflammatory TLR-2-signalling lipoproteins in hypervirulent mycobacterial variants. <i>Cellular Microbiology</i> , 2011, 13, 692-704.	2.1	66
83	ESAT-6 Secretion-Independent Impact of ESX-1 Genes <i>espF</i> and <i>espG1</i> on Virulence of <i>Mycobacterium tuberculosis</i> . <i>Journal of Infectious Diseases</i> , 2011, 203, 1155-1164.	4.0	66
84	The antibiotic bedaquiline activates host macrophage innate immune resistance to bacterial infection. <i>ELife</i> , 2020, 9, .	6.0	66
85	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.	2.8	63
86	<i>Mycobacterium tuberculosis</i> Controls Phagosomal Acidification by Targeting CISH-Mediated Signaling. <i>Cell Reports</i> , 2017, 20, 3188-3198.	6.4	60
87	Taxonomic Diversity of Pseudomonads Revealed by Computer-interpretation of Ribotyping Data. <i>Systematic and Applied Microbiology</i> , 1996, 19, 541-555.	2.8	59
88	ESX/type VII secretion systems of mycobacteria: Insights into evolution, pathogenicity and protection. <i>Tuberculosis</i> , 2015, 95, S150-S154.	1.9	56
89	Genome-wide mosaicism within <i>Mycobacterium abscessus</i> : evolutionary and epidemiological implications. <i>BMC Genomics</i> , 2016, 17, 118.	2.8	56
90	<i>Mycobacterium abscessus</i> Phospholipase C Expression Is Induced during Coculture within Amoebae and Enhances <i>M. abscessus</i> Virulence in Mice. <i>Infection and Immunity</i> , 2015, 83, 780-791.	2.2	54

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91	ESAT-6â€“dependent cytosolic pattern recognition drives noncognate tuberculosis control in vivo. <i>Journal of Clinical Investigation</i> , 2016, 126, 2109-2122.	8.2	52
92	Increased protective efficacy of recombinant BCG strains expressing virulence-neutral proteins of the ESX-1 secretion system. <i>Vaccine</i> , 2015, 33, 2710-2718.	3.8	51
93	Resistance to Thiacetazone Derivatives Active against <i>Mycobacterium abscessus</i> Involves Mutations in the MmpL5 Transcriptional Repressor MAB_4384. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	51
94	CD4+ T Cells Recognizing PE/PPE Antigens Directly or via Cross Reactivity Are Protective against Pulmonary <i>Mycobacterium tuberculosis</i> Infection. <i>PLoS Pathogens</i> , 2016, 12, e1005770.	4.7	50
95	The ESX-5 Associated eccB5-eccC5 Locus Is Essential for <i>Mycobacterium tuberculosis</i> Viability. <i>PLoS ONE</i> , 2012, 7, e52059.	2.5	49
96	Deciphering the role of IS6110 in a highly transmissible <i>Mycobacterium tuberculosis</i> Beijing strain, GC1237. <i>Tuberculosis</i> , 2011, 91, 117-126.	1.9	47
97	Unexpected Genomic and Phenotypic Diversity of <i>Mycobacterium africanum</i> Lineage 5 Affects Drug Resistance, Protein Secretion, and Immunogenicity. <i>Genome Biology and Evolution</i> , 2018, 10, 1858-1874.	2.5	47
98	Colonization with <i>Helicobacter</i> is concomitant with modified gut microbiota and drastic failure of the immune control of <i>Mycobacterium tuberculosis</i> . <i>Mucosal Immunology</i> , 2017, 10, 1178-1189.	6.0	46
99	Comparative genomics of the leprosy and tubercle bacilli. <i>Research in Microbiology</i> , 2000, 151, 135-142.	2.1	45
100	Use of pulsed field gel electrophoresis to compare large DNA-restriction fragments of <i>Listeria monocytogenes</i> strains belonging to serogroups 1/2 and 3. <i>International Journal of Food Microbiology</i> , 1991, 14, 297-304.	4.7	44
101	<i>Mycobacterium abscessus</i> virulence traits unraveled by transcriptomic profiling in amoeba and macrophages. <i>PLoS Pathogens</i> , 2019, 15, e1008069.	4.7	42
102	Intrinsic Antibacterial Activity of Nanoparticles Made of β -Cyclodextrins Potentiates Their Effect as Drug Nanocarriers against Tuberculosis. <i>ACS Nano</i> , 2019, 13, 3992-4007.	14.6	42
103	Pathogenicity in the tubercle bacillus: molecular and evolutionary determinants. <i>BioEssays</i> , 2009, 31, 378-388.	2.5	41
104	Revisiting the role of phospholipases C in virulence and the lifecycle of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2015, 5, 16918.	3.3	39
105	<i>Mycobacterial Pathogenomics and Evolution</i> . <i>Microbiology Spectrum</i> , 2014, 2, MGM2-0025-2013.	3.0	36
106	<i>Mycobacterium tuberculosis</i> Meets the Cytosol: The Role of cGAS in Anti-mycobacterial Immunity. <i>Cell Host and Microbe</i> , 2015, 17, 733-735.	11.0	36
107	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. <i>PLoS Pathogens</i> , 2018, 14, e1007139.	4.7	36
108	Genomic analysis using pulsed-field gel electrophoresis of <i>Escherichia coli</i> O157:H7 isolated from dairy calves during the United States national dairy heifer evaluation project (1991â€“1992). <i>Veterinary Microbiology</i> , 1996, 48, 223-230.	1.9	33

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109	Synthesis, biological activity, and evaluation of the mode of action of novel antitubercular benzofurobenzopyrans substituted on A ring. <i>European Journal of Medicinal Chemistry</i> , 2010, 45, 5833-5847.	5.5	33
110	Type VII Secretion Systems in Gram-Positive Bacteria. <i>Current Topics in Microbiology and Immunology</i> , 2015, 404, 235-265.	1.1	33
111	Multidrug-Resistant Tuberculosis in Admitted Patients at a Tertiary Referral Hospital of Bangladesh. <i>PLoS ONE</i> , 2012, 7, e40545.	2.5	32
112	The changes in mycolic acid structures caused by <i>hadC</i> mutation have a dramatic effect on the virulence of <i>Mycobacterium tuberculosis</i> . <i>Molecular Microbiology</i> , 2016, 99, 794-807.	2.5	32
113	Horizontal acquisition of a hypoxia-responsive molybdenum cofactor biosynthesis pathway contributed to <i>Mycobacterium tuberculosis</i> pathoadaptation. <i>PLoS Pathogens</i> , 2017, 13, e1006752.	4.7	32
114	ESX/Type VII Secretion Systems – An Important Way Out for Mycobacterial Proteins. <i>Microbiology Spectrum</i> , 2019, 7, .	3.0	31
115	Discovery of the type VII ESX secretion needle?. <i>Molecular Microbiology</i> , 2017, 103, 7-12.	2.5	30
116	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. <i>Journal of Proteomics</i> , 2019, 192, 321-333.	2.4	30
117	Shared Pathogenomic Patterns Characterize a New Phylotype, Revealing Transition toward Host-Adaptation Long before Speciation of <i>Mycobacterium tuberculosis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2420-2438.	2.5	29
118	Multiplexed Quantitation of Intraphagocyte <i>Mycobacterium tuberculosis</i> Secreted Protein Effectors. <i>Cell Reports</i> , 2018, 23, 1072-1084.	6.4	28
119	<i>Mycobacterium tuberculosis</i> evolutionary pathogenesis and its putative impact on drug development. <i>Future Microbiology</i> , 2014, 9, 969-985.	2.0	27
120	Perspectives on mycobacterial vacuole-to-cytosol translocation: the importance of cytosolic access. <i>Cellular Microbiology</i> , 2016, 18, 1070-1077.	2.1	26
121	A unique PE_PGRS protein inhibiting host cell cytosolic defenses and sustaining full virulence of <i>Mycobacterium marinum</i> in multiple hosts. <i>Cellular Microbiology</i> , 2016, 18, 1489-1507.	2.1	25
122	The Biology and Epidemiology of <i>Mycobacterium canettii</i> . <i>Advances in Experimental Medicine and Biology</i> , 2017, 1019, 27-41.	1.6	25
123	Characterization of <i>Listeria</i> strains isolated from soft cheese. <i>International Journal of Food Microbiology</i> , 1993, 18, 161-166.	4.7	24
124	Phthiocerol Dimycocerosates From <i>Mycobacterium tuberculosis</i> Increase the Membrane Activity of Bacterial Effectors and Host Receptors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 420.	3.9	23
125	Is <i>Mycobacterium africanum</i> Subtype II (Uganda I and Uganda II) a Genetically Well-Defined Subspecies of the <i>Mycobacterium tuberculosis</i> Complex?. <i>Journal of Clinical Microbiology</i> , 2003, 41, 1345-1348.	3.9	22
126	Tuberculosis: from genome to vaccine. <i>Expert Review of Vaccines</i> , 2005, 4, 541-551.	4.4	22

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127	Genomic characterization of Mycobacterium tuberculosis lineage 7 and a proposed name: <i>M. tuberculosis</i> <i>vetus</i> ™. <i>Microbial Genomics</i> , 2016, 2, e000063.	2.0	22
128	Live attenuated TB vaccines representing the three modern Mycobacterium tuberculosis lineages reveal that the Euro-American genetic background confers optimal vaccine potential. <i>EBioMedicine</i> , 2020, 55, 102761.	6.1	22
129	Mycobacterial genomics. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 2002, 96, 1-6.	1.8	21
130	Single Cell Measurements of Vacuolar Rupture Caused by Intracellular Pathogens. <i>Journal of Visualized Experiments</i> , 2013, , e50116.	0.3	21
131	The C terminus of the mycobacterium ESX-1 secretion system substrate ESAT-6 is required for phagosomal membrane damage and virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2122161119.	7.1	19
132	Re-Evaluation of <i>M. prototuberculosis</i> : Continuing the Debate. <i>PLoS Pathogens</i> , 2006, 2, e95.	4.7	18
133	Impact of Mycobacterium tuberculosis RD1-locus on human primary dendritic cell immune functions. <i>Scientific Reports</i> , 2015, 5, 17078.	3.3	18
134	Breaching the phagosome, the case of the tuberculosis agent. <i>Cellular Microbiology</i> , 2021, 23, e13344.	2.1	18
135	Evolution of <i>Mycobacterium tuberculosis</i> : New Insights into Pathogenicity and Drug Resistance. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	17
136	Targeting Type VII/ESX Secretion Systems for Development of Novel Antimycobacterial Drugs. <i>Current Pharmaceutical Design</i> , 2013, 20, 4346-4356.	1.9	17
137	Molecular epidemiology of tuberculosis in rural Matlab, Bangladesh. <i>International Journal of Tuberculosis and Lung Disease</i> , 2012, 16, 319-326.	1.2	16
138	Update on the virulence factors of the obligate pathogen Mycobacterium tuberculosis and related tuberculosis-causing mycobacteria. <i>Infection, Genetics and Evolution</i> , 2019, 72, 67-77.	2.3	16
139	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.	13.3	15
140	Mycobacterial virulence: impact on immunogenicity and vaccine research. <i>F1000Research</i> , 2019, 8, 2025.	1.6	15
141	The BCG Strain Pool: Diversity Matters. <i>Molecular Therapy</i> , 2016, 24, 201-203.	8.2	14
142	ESX-1-Independent Horizontal Gene Transfer by Mycobacterium tuberculosis Complex Strains. <i>MBio</i> , 2021, 12, .	4.1	14
143	Functional analysis of a clonal deletion in an epidemic strain of Mycobacterium bovis reveals a role in lipid metabolism. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3731-3742.	1.8	12
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