

# Nicolaas Claudius Gey van Pittius

## List of Publications by Year in descending order

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85  
papers

6,044  
citations

53660

45  
h-index

74018

75  
g-index

86  
all docs

86  
docs citations

86  
times ranked

6048  
citing authors

#	ARTICLE	IF	CITATIONS
1	Type VII secretion " mycobacteria show the way. <i>Nature Reviews Microbiology</i> , 2007, 5, 883-891.	13.6	628
2	Evolution and expansion of the <i>Mycobacterium tuberculosis</i> PE and PPE multigene families and their association with the duplication of the ESAT-6 (esx) gene cluster regions. <i>BMC Evolutionary Biology</i> , 2006, 6, 95.	3.2	388
3	Patients with Active Tuberculosis often Have Different Strains in the Same Sputum Specimen. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2004, 169, 610-614.	2.5	267
4	Systematic Genetic Nomenclature for Type VII Secretion Systems. <i>PLoS Pathogens</i> , 2009, 5, e1000507.	2.1	233
5	PPE and PE_PGRS proteins of <i>Mycobacterium marinum</i> are transported via the type VII secretion system ESX5. <i>Molecular Microbiology</i> , 2009, 73, 329-340.	1.2	233
6	A Balancing Act: Efflux/Influx in Mycobacterial Drug Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 3181-3189.	1.4	212
7	Novel <i>Mycobacterium tuberculosis</i> Complex Pathogen, <i>M. mungi</i> . <i>Emerging Infectious Diseases</i> , 2010, 16, 1296-1299.	2.0	204
8	Effect of household and community interventions on the burden of tuberculosis in southern Africa: the ZAMSTAR community-randomised trial. <i>Lancet, The</i> , 2013, 382, 1183-1194.	6.3	186
9	Emergence and Spread of Extensively and Totally Drug-Resistant Tuberculosis, South Africa. <i>Emerging Infectious Diseases</i> , 2013, 19, 449-455.	2.0	182
10	Reinfection and Mixed Infection Cause Changing <i>Mycobacterium tuberculosis</i> Drug-Resistance Patterns. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2005, 172, 636-642.	2.5	173
11	Rifampicin Reduces Susceptibility to Ofloxacin in Rifampicin-resistant <i>Mycobacterium tuberculosis</i> through Efflux. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2011, 184, 269-276.	2.5	149
12	<i>Mycobacterium tuberculosis</i> Beijing genotype: A template for success. <i>Tuberculosis</i> , 2011, 91, 510-523.	0.8	139
13	Emergence and Spread of Extensively and Totally Drug-Resistant Tuberculosis, South Africa. <i>Emerging Infectious Diseases</i> , 2013, 19, 449-455.	2.0	127
14	Mutation rate and the emergence of drug resistance in <i>Mycobacterium tuberculosis</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 292-302.	1.3	123
15	The role of IS6110 in the evolution of <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2007, 87, 393-404.	0.8	103
16	The Diagnostic Performance of the GenoType MTBDR plus Version 2 Line Probe Assay Is Equivalent to That of the Xpert MTB/RIF Assay. <i>Journal of Clinical Microbiology</i> , 2012, 50, 3712-3716.	1.8	103
17	<i>Mycobacterium tuberculosis</i> strains with the Beijing genotype demonstrate variability in virulence associated with transmission. <i>Tuberculosis</i> , 2010, 90, 319-325.	0.8	101
18	Comparative Analysis of <i>Mycobacterium tuberculosis</i> pe and ppe Genes Reveals High Sequence Variation and an Apparent Absence of Selective Constraints. <i>PLoS ONE</i> , 2012, 7, e30593.	1.1	83

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19	Novel Cause of Tuberculosis in Meerkats, South Africa. <i>Emerging Infectious Diseases</i> , 2013, 19, 2004-2007.	2.0	81
20	Application of Sensitive and Specific Molecular Methods To Uncover Global Dissemination of the Major RD <sup>Rio</sup> Sublineage of the Latin American-Mediterranean <i>Mycobacterium tuberculosis</i> Spoligotype Family. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1259-1267.	1.8	80
21	Zoonotic tuberculosis and brucellosis in Africa: neglected zoonoses or minor public-health issues? The outcomes of a multi-disciplinary workshop. <i>Annals of Tropical Medicine and Parasitology</i> , 2009, 103, 401-411.	1.6	69
22	The non-clonality of drug resistance in Beijing-genotype isolates of <i>Mycobacterium tuberculosis</i> from the Western Cape of South Africa. <i>BMC Genomics</i> , 2010, 11, 670.	1.2	69
23	Safe <i>Mycobacterium tuberculosis</i> DNA Extraction Method That Does Not Compromise Integrity. <i>Journal of Clinical Microbiology</i> , 2006, 44, 254-256.	1.8	66
24	Phosphoproteomics analysis of a clinical <i>Mycobacterium tuberculosis</i> Beijing isolate: expanding the mycobacterial phosphoproteome catalog. <i>Frontiers in Microbiology</i> , 2015, 6, 6.	1.5	65
25	Frequent Homologous Recombination Events in <i>Mycobacterium tuberculosis</i> PE/PPE Multigene Families: Potential Role in Antigenic Variability. <i>Journal of Bacteriology</i> , 2008, 190, 7838-7846.	1.0	64
26	Evidence for a rapid rate of molecular evolution at the hypervariable and immunogenic <i>Mycobacterium tuberculosis</i> PPE38 gene region. <i>BMC Evolutionary Biology</i> , 2009, 9, 237.	3.2	64
27	The complex architecture of mycobacterial promoters. <i>Tuberculosis</i> , 2013, 93, 60-74.	0.8	64
28	Discordance between Mycobacterial Interspersed Repetitive-Unit-Variable-Number Tandem-Repeat Typing and IS <sub>6110</sub> Restriction Fragment Length Polymorphism Genotyping for Analysis of <i>Mycobacterium tuberculosis</i> Beijing Strains in a Setting of High Incidence of Tuberculosis. <i>Journal of Clinical Microbiology</i> , 2008, 46, 3338-3345.	1.8	63
29	Emergence and treatment of multidrug resistant (MDR) and extensively drug-resistant (XDR) tuberculosis in South Africa. <i>Infection, Genetics and Evolution</i> , 2012, 12, 686-694.	1.0	62
30	Recombination in <i>pe/ppe</i> genes contributes to genetic variation in <i>Mycobacterium tuberculosis</i> lineages. <i>BMC Genomics</i> , 2016, 17, 151.	1.2	62
31	The plasmid-mediated evolution of the mycobacterial ESX (Type VII) secretion systems. <i>BMC Evolutionary Biology</i> , 2016, 16, 62.	3.2	61
32	Tuberculosis due to Resistant Haarlem Strain, Tunisia. <i>Emerging Infectious Diseases</i> , 2005, 11, 957-961.	2.0	60
33	Mutations in the <i>rrs</i> A1401G Gene and Phenotypic Resistance to Amikacin and Capreomycin in <i>Mycobacterium tuberculosis</i> . <i>Microbial Drug Resistance</i> , 2012, 18, 193-197.	0.9	60
34	GenoType MTBDR <sub>sl</sub> Line Probe Assay Shortens Time to Diagnosis of Extensively Drug-Resistant Tuberculosis in a High-Throughput Diagnostic Laboratory. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 1298-1305.	2.5	58
35	Population Structure of Mixed <i>Mycobacterium tuberculosis</i> Infection Is Strain Genotype and Culture Medium Dependent. <i>PLoS ONE</i> , 2013, 8, e70178.	1.1	57
36	Evidence that the Spread of <i>Mycobacterium tuberculosis</i> Strains with the Beijing Genotype Is Human Population Dependent. <i>Journal of Clinical Microbiology</i> , 2007, 45, 2263-2266.	1.8	54

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37	Phage-based detection of bacterial pathogens. <i>Analyst, The</i> , 2014, 139, 2617-2626.	1.7	54
38	Geospatial distribution of <i>Mycobacterium tuberculosis</i> genotypes in Africa. <i>PLoS ONE</i> , 2018, 13, e0200632.	1.1	54
39	<i>Mycobacterium tuberculosis</i> Population Structure Determines the Outcome of Genetics-Based Second-Line Drug Resistance Testing. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 2420-2427.	1.4	53
40	Iron acquisition strategies in mycobacteria. <i>Tuberculosis</i> , 2015, 95, 123-130.	0.8	53
41	Whole genome sequence analysis of <i>Mycobacterium suricattae</i> . <i>Tuberculosis</i> , 2015, 95, 682-688.	0.8	52
42	Mycosin-1, a subtilisin-like serine protease of <i>Mycobacterium tuberculosis</i> , is cell wall-associated and expressed during infection of macrophages. <i>BMC Microbiology</i> , 2002, 2, 30.	1.3	50
43	Population Structure of Multi- and Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Strains in South Africa. <i>Journal of Clinical Microbiology</i> , 2012, 50, 995-1002.	1.8	50
44	The mycosins of <i>Mycobacterium tuberculosis</i> H37Rv: a family of subtilisin-like serine proteases. <i>Gene</i> , 2000, 254, 147-155.	1.0	49
45	Bovine tuberculosis in African buffaloes: observations regarding <i>Mycobacterium bovis</i> shedding into water and exposure to environmental mycobacteria. <i>BMC Veterinary Research</i> , 2007, 3, 23.	0.7	49
46	Programmatically Selected Multidrug-Resistant Strains Drive the Emergence of Extensively Drug-Resistant Tuberculosis in South Africa. <i>PLoS ONE</i> , 2013, 8, e70919.	1.1	44
47	Fluorometric Assay for Testing Rifampin Susceptibility of <i>Mycobacterium tuberculosis</i> Complex. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1369-1373.	1.8	43
48	The mechanisms responsible for 2-dimensional pattern formation in bacterial macrofiber populations grown on solid surfaces: fiber joining and the creation of exclusion zones. <i>BMC Microbiology</i> , 2002, 2, 1.	1.3	41
49	Prevalence and Distribution of Non-Tuberculous Mycobacteria (NTM) in Cattle, African Buffaloes ( <i>Syncerus caffer</i> ) and their Environments in South Africa. <i>Transboundary and Emerging Diseases</i> , 2013, 60, 74-84.	1.3	40
50	Insights into the evolutionary history of tubercle bacilli as disclosed by genetic rearrangements within a PE_PGRS duplicated gene pair. <i>BMC Evolutionary Biology</i> , 2006, 6, 107.	3.2	39
51	The clinical relevance of Mycobacterial pharmacogenetics. <i>Tuberculosis</i> , 2009, 89, 199-202.	0.8	37
52	Progenitor strain introduction of <i>Mycobacterium bovis</i> at the wildlife-livestock interface can lead to clonal expansion of the disease in a single ecosystem. <i>Infection, Genetics and Evolution</i> , 2017, 51, 235-238.	1.0	35
53	Modification of the QuantiFERON-TB Gold (In-Tube) assay for the diagnosis of <i>Mycobacterium bovis</i> infection in African buffaloes ( <i>Syncerus caffer</i> ). <i>Veterinary Immunology and Immunopathology</i> , 2011, 142, 113-118.	0.5	34
54	ESAT-6 and CFP-10: What Is the Diagnosis?. <i>Infection and Immunity</i> , 2002, 70, 6509-6511.	1.0	32

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55	INFECTION OF AFRICAN BUFFALO ( <i>SYNCERUS CAFFER</i> ) BY <i>ORYX BACILLUS</i> , A RARE MEMBER OF THE ANTELOPE CLADE OF THE <i>MYCOBACTERIUM TUBERCULOSIS</i> COMPLEX. <i>Journal of Wildlife Diseases</i> , 2012, 48, 849-857.	0.3	31
56	Detection of <i>Mycobacterium tuberculosis</i> infection in dogs in a high-risk setting. <i>Research in Veterinary Science</i> , 2012, 92, 414-419.	0.9	31
57	Independent Large Scale Duplications in Multiple <i>M. tuberculosis</i> Lineages Overlapping the Same Genomic Region. <i>PLoS ONE</i> , 2012, 7, e26038.	1.1	30
58	Comparative Genomics and Proteomic Analysis of Four Non-tuberculous <i>Mycobacterium</i> Species and <i>Mycobacterium tuberculosis</i> Complex: Occurrence of Shared Immunogenic Proteins. <i>Frontiers in Microbiology</i> , 2016, 7, 795.	1.5	30
59	Pulmonary Infection due to <i>Mycobacterium bovis</i> in a Black Rhinoceros ( <i>Diceros bicornis minor</i> ) in South Africa. <i>Journal of Wildlife Diseases</i> , 2009, 45, 1187-1193.	0.3	28
60	Evaluation of the Capilia TB Assay for Culture Confirmation of <i>Mycobacterium tuberculosis</i> Infections in Zambia and South Africa. <i>Journal of Clinical Microbiology</i> , 2010, 48, 3773-3775.	1.8	28
61	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. <i>Journal of Proteome Research</i> , 2017, 16, 3841-3851.	1.8	27
62	Pulmonary infection due to the dassie bacillus ( <i>Mycobacterium tuberculosis</i> complex sp.) in a free-living dassie (rock hyrax <i>Procavia capensis</i> ) from South Africa. <i>Tuberculosis</i> , 2008, 88, 80-83.	0.8	25
63	Mixed infections of <i>Corynebacterium pseudotuberculosis</i> and non-tuberculous mycobacteria in South African antelopes presenting with tuberculosis-like lesions. <i>Veterinary Microbiology</i> , 2011, 147, 340-345.	0.8	25
64	<i>Mycobacteria</i> and Disease in Southern Africa. <i>Transboundary and Emerging Diseases</i> , 2013, 60, 147-156.	1.3	18
65	Detection of <i>Mycobacterium kansasii</i> infection in a rhesus macaque ( <i>Macaca mulatta</i> ) using a modified QuantiFERON-TB Gold assay. <i>Veterinary Immunology and Immunopathology</i> , 2010, 136, 330-334.	0.5	16
66	Pulmonary Infection Due to <i>Mycobacterium goodii</i> in a Spotted Hyena ( <i>Crocuta crocuta</i> ) from South Africa. <i>Journal of Wildlife Diseases</i> , 2008, 44, 151-154.	0.3	14
67	Characterization of <i>Mycobacterium orygis</i> . <i>Emerging Infectious Diseases</i> , 2012, 18, 1708-1709.	2.0	14
68	Clinical Relevance of Nontuberculous <i>Mycobacteria</i> Isolated from Sputum in a Gold Mining Workforce in South Africa: An Observational, Clinical Study. <i>BioMed Research International</i> , 2015, 2015, 1-10.	0.9	14
69	A metabolomics investigation of the function of the ESX-1 gene cluster in mycobacteria. <i>Microbial Pathogenesis</i> , 2016, 100, 268-275.	1.3	14
70	Assessing the progress of <i>Mycobacterium tuberculosis</i> H37Rv structural genomics. <i>Tuberculosis</i> , 2015, 95, 131-136.	0.8	12
71	Multiple, independent, identical IS6110 insertions in <i>Mycobacterium tuberculosis</i> PPE genes. <i>Tuberculosis</i> , 2009, 89, 439-442.	0.8	11
72	Molecular Epidemiological Interpretation of the Epidemic of Extensively Drug-Resistant Tuberculosis in South Africa. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3650-3653.	1.8	11

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73	Detection of natural infection with <i>Mycobacterium intracellulare</i> in healthy wild-caught Chacma baboons ( <i>Papio ursinus</i> ) by ESAT-6 and CFP-10 IFN- $\gamma$ ELISPOT tests following a tuberculosis outbreak. <i>BMC Microbiology</i> , 2008, 8, 27.	1.3	10
74	A metabolomics approach exploring the function of the ESX-3 type VII secretion system of <i>M. smegmatis</i> . <i>Metabolomics</i> , 2013, 9, 631-641.	1.4	10
75	Moxifloxacin Retains Antimycobacterial Activity in the Presence of <i>gyrA</i> Mutations. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2912-2915.	1.4	10
76	Genetic profile of <i>Mycobacterium tuberculosis</i> and treatment outcomes in human pulmonary tuberculosis in Tanzania. <i>Tanzania Journal of Health Research</i> , 2014, 16, 58-69.	0.1	7
77	A regulatory variant in the C1Q gene cluster is associated with tuberculosis susceptibility and C1qA plasma levels in a South African population. <i>Immunogenetics</i> , 2020, 72, 305-314.	1.2	7
78	Insertion Element IS6110-Based Restriction Fragment Length Polymorphism Genotyping of <i>Mycobacterium tuberculosis</i> . <i>Methods in Molecular Biology</i> , 2009, 465, 353-370.	0.4	7
79	Spectrum of non-tuberculous mycobacteria identified using standard biochemical testing vs. 16S sequencing [Short communication]. <i>International Journal of Tuberculosis and Lung Disease</i> , 2013, 17, 267-269.	0.6	4
80	Two promoters in the <i>esx-3</i> gene cluster of <i>Mycobacterium smegmatis</i> respond inversely to different iron concentrations in vitro. <i>BMC Research Notes</i> , 2017, 10, 426.	0.6	3
81	Expression and production of soluble <i>Mycobacterium tuberculosis</i> H37Rv mycosin-3. <i>Biochemistry and Biophysics Reports</i> , 2016, 5, 448-452.	0.7	2
82	Chapter 9: Tuberculosis Recurrence: Exogenous or Endogenous?. <i>Progress in Respiratory Research</i> , 2011, , 73-80.	0.1	1
83	Chapter 11: Acquisition, Transmission and Amplification of Drug-Resistant Tuberculosis. <i>Progress in Respiratory Research</i> , 2011, , 96-104.	0.1	1
84	Designation of Major Mycobacterial Interspersed Repetitive-Unit Types within <i>Mycobacterium tuberculosis</i> Beijing Genotype, an Important Point. <i>Journal of Clinical Microbiology</i> , 2007, 45, 4092-4093.	1.8	0
85	Mycobacterial Interspersed Repetitive-Unit "Variable-Number Tandem-Repeat Analysis and Beijing/W Family of <i>Mycobacterium tuberculosis</i> Authors' Reply: Table 1.. <i>Journal of Clinical Microbiology</i> , 2011, 49, 2780-2781.	1.8	0