

# David Couvin

## List of Publications by Year in descending order

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63  
papers

2,501  
citations

361045

20  
h-index

214527

47  
g-index

63  
all docs

63  
docs citations

63  
times ranked

3220  
citing authors

#	ARTICLE	IF	CITATIONS
1	CRISPRCasFinder, an update of CRISPRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins. <i>Nucleic Acids Research</i> , 2018, 46, W246-W251.	6.5	985
2	SITVITWEB – A publicly available international multimarker database for studying <i>Mycobacterium tuberculosis</i> genetic diversity and molecular epidemiology. <i>Infection, Genetics and Evolution</i> , 2012, 12, 755-766.	1.0	380
3	Macro-geographical specificities of the prevailing tuberculosis epidemic as seen through SITVIT2, an updated version of the <i>Mycobacterium tuberculosis</i> genotyping database. <i>Infection, Genetics and Evolution</i> , 2019, 72, 31-43.	1.0	100
4	CRISPRCasdb a successor of CRISPRdb containing CRISPR arrays and cas genes from complete genome sequences, and tools to download and query lists of repeats and spacers. <i>Nucleic Acids Research</i> , 2020, 48, D535-D544.	6.5	88
5	Geospatial distribution of <i>Mycobacterium tuberculosis</i> genotypes in Africa. <i>PLoS ONE</i> , 2018, 13, e0200632.	1.1	54
6	The Guinea-Bissau Family of <i>Mycobacterium tuberculosis</i> Complex Revisited. <i>PLoS ONE</i> , 2011, 6, e18601.	1.1	47
7	Tuberculosis – A global emergency: Tools and methods to monitor, understand, and control the epidemic with specific example of the Beijing lineage. <i>Tuberculosis</i> , 2015, 95, S177-S189.	0.8	47
8	Population Structure among <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Colombia. <i>PLoS ONE</i> , 2014, 9, e93848.	1.1	46
9	Mapping of <i>Mycobacterium tuberculosis</i> Complex Genetic Diversity Profiles in Tanzania and Other African Countries. <i>PLoS ONE</i> , 2016, 11, e0154571.	1.1	41
10	Strain Diversity of <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Afar Pastoral Region of Ethiopia. <i>BioMed Research International</i> , 2014, 2014, 1-12.	0.9	40
11	Genetic diversity and drug susceptibility profile of <i>Mycobacterium tuberculosis</i> isolated from different regions of India. <i>Journal of Infection</i> , 2015, 71, 207-219.	1.7	38
12	Genetic Diversity of <i>Mycobacterium tuberculosis</i> in Peru and Exploration of Phylogenetic Associations with Drug Resistance. <i>PLoS ONE</i> , 2013, 8, e65873.	1.1	38
13	Mixed Infections and Rifampin Heteroresistance among <i>Mycobacterium tuberculosis</i> Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2138-2147.	1.8	37
14	Genetic diversity among multidrug-resistant <i>Mycobacterium tuberculosis</i> strains in Mexico. <i>Infection, Genetics and Evolution</i> , 2013, 14, 434-443.	1.0	30
15	Strain Classification of <i>Mycobacterium tuberculosis</i> Isolates in Brazil Based on Genotypes Obtained by Spoligotyping, <i>Mycobacterial Interspersed Repetitive Unit Typing</i> and the Presence of Large Sequence and Single Nucleotide Polymorphism. <i>PLoS ONE</i> , 2014, 9, e107747.	1.1	30
16	A First Insight on the Population Structure of <i>Mycobacterium tuberculosis</i> Complex as Studied by Spoligotyping and MIRU-VNTRs in Santiago, Chile. <i>PLoS ONE</i> , 2015, 10, e0118007.	1.1	28
17	Two tales: Worldwide distribution of Central Asian (CAS) versus ancestral East-African Indian (EAI) lineages of <i>Mycobacterium tuberculosis</i> underlines a remarkable cleavage for phylogeographical, epidemiological and demographical characteristics. <i>PLoS ONE</i> , 2019, 14, e0219706.	1.1	25
18	Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single bla <sub>CTXA</sub> -1/Incl1/ST3 Plasmid Among Humans and Wild Animals. <i>Frontiers in Microbiology</i> , 2020, 11, 1524.	1.5	25

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19	The Association between Mycobacterium Tuberculosis Genotype and Drug Resistance in Peru. PLoS ONE, 2015, 10, e0126271.	1.1	24
20	Molecular Epidemiology of Tuberculosis in Finland, 2008-2011. PLoS ONE, 2013, 8, e85027.	1.1	23
21	Study of Mycobacterium tuberculosis Complex Genotypic Diversity in Malaysia Reveals a Predominance of Ancestral East-African-Indian Lineage with a Malaysia-Specific Signature. PLoS ONE, 2014, 9, e114832.	1.1	21
22	Characterization of the Genetic Diversity of Extensively-Drug Resistant Mycobacterium tuberculosis Clinical Isolates from Pulmonary Tuberculosis Patients in Peru. PLoS ONE, 2014, 9, e112789.	1.1	20
23	SpolSimilaritySearch – A web tool to compare and search similarities between spoligotypes of Mycobacterium tuberculosis complex. Tuberculosis, 2017, 105, 49-52.	0.8	20
24	The population structure of drug-resistant Mycobacterium tuberculosis clinical isolates from Sichuan in China. Infection, Genetics and Evolution, 2012, 12, 718-724.	1.0	19
25	Combined Genotypic, Phylogenetic, and Epidemiologic Analyses of Mycobacterium tuberculosis Genetic Diversity in the Rhône Alpes Region, France. PLoS ONE, 2016, 11, e0153580.	1.1	19
26	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing Mycobacterium tuberculosis genetic diversity in Portuguese-speaking countries. Infection, Genetics and Evolution, 2019, 72, 44-58.	1.0	18
27	Human multidrug-resistant Mycobacterium bovis infection in Mexico. Tuberculosis, 2015, 95, 802-809.	0.8	17
28	Snapshot of the genetic diversity of Mycobacterium tuberculosis isolates in Iraq. International Journal of Mycobacteriology, 2014, 3, 184-196.	0.3	15
29	Four year longitudinal study of Mycobacterium tuberculosis complex isolates in a region of North-Eastern Italy. Infection, Genetics and Evolution, 2014, 26, 58-64.	1.0	15
30	Mycobacterial biomaterials and resources for researchers. Pathogens and Disease, 2018, 76, .	0.8	14
31	Wide Distribution and Specific Resistance Pattern to Third-Generation Cephalosporins of Enterobacter cloacae Complex Members in Humans and in the Environment in Guadeloupe (French) Tj ETQq1 1 0.784314 rgB3 /Overl		
32	Molecular Epidemiology and Genotyping of Mycobacterium tuberculosis Isolated in Baghdad. BioMed Research International, 2014, 2014, 1-15.	0.9	12
33	First insight into the molecular epidemiology of Mycobacterium tuberculosis in Santa Catarina, southern Brazil. Tuberculosis, 2016, 97, 57-64.	0.8	12
34	Comparative study of genotypes of Mycobacterium tuberculosis from a Northern Indian setting with strains reported from other parts of India and neighboring countries. Tuberculosis, 2017, 105, 60-72.	0.8	12
35	Analysis of Mycobacterium tuberculosis Genotypic Lineage Distribution in Chile and Neighboring Countries. PLoS ONE, 2016, 11, e0160434.	1.1	12
36	Mycobacterium tuberculosis Strains Potentially Involved in the TB Epidemic in Sweden a Century Ago. PLoS ONE, 2012, 7, e46848.	1.1	11

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37	Population structure and circulating genotypes of drug-sensitive and drug-resistant <i>Mycobacterium tuberculosis</i> clinical isolates in São Paulo state, Brazil. <i>Infection, Genetics and Evolution</i> , 2013, 14, 39-45.	1.0	10
38	<i>Mycobacterium tuberculosis</i> causing tuberculous lymphadenitis in Maputo, Mozambique. <i>BMC Microbiology</i> , 2015, 15, 268.	1.3	10
39	Genetic diversity of <i>Mycobacterium tuberculosis</i> from Pará, Brazil, reveals a higher frequency of ancestral strains than previously reported in South America. <i>Infection, Genetics and Evolution</i> , 2017, 56, 62-72.	1.0	9
40	Dissemination of Extended-Spectrum-β-Lactamase-Producing <i>Enterobacter cloacae</i> Complex from a Hospital to the Nearby Environment in Guadeloupe (French West Indies): ST114 Lineage Coding for a Successful IncHI2/ST1 Plasmid. <i>Antimicrobial Agents and Chemotherapy</i> , 2021, 65, .	1.4	9
41	Predicting <i>Mycobacterium tuberculosis</i> Complex Clades Using Knowledge-Based Bayesian Networks. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	8
42	Heterogeneity among <i>Mycobacterium ulcerans</i> from French Guiana Revealed by Multilocus Variable Number Tandem Repeat Analysis (MLVA). <i>PLoS ONE</i> , 2015, 10, e0118597.	1.1	8
43	Genotypic diversity of <i>Mycobacterium tuberculosis</i> in Buenos Aires, Argentina. <i>Infection, Genetics and Evolution</i> , 2018, 62, 1-7.	1.0	8
44	Genotypic characterization and historical perspective of <i>Mycobacterium tuberculosis</i> among older and younger Finns, 2008–2011. <i>Clinical Microbiology and Infection</i> , 2014, 20, 1134-1139.	2.8	7
45	Novel methods included in SpolLineages tool for fast and precise prediction of <i>Mycobacterium tuberculosis</i> complex spoligotype families. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	7
46	KaruBioNet: a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies). <i>Bioinformatics Advances</i> , 2022, 2, .	0.9	7
47	Phylogenetic associations with drug-resistant <i>Mycobacterium tuberculosis</i> isolates in a paediatric population. <i>International Journal of Tuberculosis and Lung Disease</i> , 2014, 18, 1172-1179.	0.6	6
48	A snapshot of the predominant single nucleotide polymorphism cluster groups of <i>Mycobacterium tuberculosis</i> clinical isolates in Delhi, India. <i>Tuberculosis</i> , 2016, 100, 72-81.	0.8	5
49	First approach to the population structure of <i>Mycobacterium tuberculosis</i> complex in the indigenous population in Puerto Nariño-Amazonas, Colombia. <i>PLoS ONE</i> , 2021, 16, e0245084.	1.1	5
50	Predominance of Uganda genotype of <i>Mycobacterium tuberculosis</i> isolated from Ugandan patients with tuberculous lymphadenitis. <i>BMC Research Notes</i> , 2015, 8, 398.	0.6	4
51	Insights on the <i>Mycobacterium tuberculosis</i> population structure associated with migrants from Portuguese-speaking countries over a three-year period in Greater Lisbon, Portugal: Implications at the public health level. <i>Infection, Genetics and Evolution</i> , 2019, 71, 159-165.	1.0	4
52	Population structure of multidrug-resistant <i>Mycobacterium tuberculosis</i> clinical isolates in Colombia. <i>Tuberculosis</i> , 2020, 125, 102011.	0.8	4
53	<i>Mycobacterium tuberculosis</i> genotypes and predominant clones among the multidrug-resistant isolates in Spain 1998–2005. <i>Infection, Genetics and Evolution</i> , 2017, 55, 117-126.	1.0	3
54	SITVITBovis—a publicly available database and mapping tool to get an improved overview of animal and human cases caused by <i>Mycobacterium bovis</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	3

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55	High Prevalence of blaCTXMâ€“1/IncI1-Î³/ST3 Plasmids in Extended-Spectrum Î²-Lactamase-Producing Escherichia coli Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	3
56	MTBCtools: a non-exhaustive list of software tools/resources for bioinformatics analyses of Mycobacterium tuberculosis complex, the causative agent of tuberculosis. <i>International Journal of Mycobacteriology</i> , 2021, 9, 18.	0.3	2
57	Local adaptive evolution of two distinct clades of Beijing and T families of Mycobacterium tuberculosis in Chongqing: a Bayesian population structure and phylogenetic study. <i>Infectious Diseases of Poverty</i> , 2020, 9, 59.	1.5	1
58	Draft Genome Sequence of Enterobacter oligotrophicus, Isolated from the Microbiome of a Lizard in the Caribbean. <i>Microbiology Resource Announcements</i> , 2021, 10, e0060221.	0.3	1
59	getSequenceInfo: a suite of tools allowing to get genome sequence information from public repositories. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
60	Title is missing!. , 2021, 16, e0245084.		0
61	Title is missing!. , 2021, 16, e0245084.		0
62	Title is missing!. , 2021, 16, e0245084.		0
63	Title is missing!. , 2021, 16, e0245084.		0