

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	SITVITBovisâ€”a publicly available database and mapping tool to get an improved overview of animal and human cases caused by <i>Mycobacterium bovis</i>. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	3
2	KaruBioNet: a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies). Bioinformatics Advances, 2022, 2, .	0.9	7
3	High Prevalence of blaCTXMâ€”1/Incl1-Î³3/ST3 Plasmids in Extended-Spectrum Î²-Lactamase-Producing Escherichia coli Isolates Collected From Domestic Animals in Guadeloupe (French West Indies). Frontiers in Microbiology, 2022, 13, .	1.5	3
4	getSequenceInfo: a suite of tools allowing to get genome sequence information from public repositories. BMC Bioinformatics, 2022, 23, .	1.2	1
5	MTBCtools: a non-exhaustive list of software tools/resources for bioinformatics analyses of Mycobacterium tuberculosis complex, the causative agent of tuberculosis. International Journal of Mycobacteriology, 2021, 9, 18.	0.3	2
6	First approach to the population structure of Mycobacterium tuberculosis complex in the indigenous population in Puerto NariÃ±o-Amazonas, Colombia. PLoS ONE, 2021, 16, e0245084.	1.1	5
7	Dissemination of Extended-Spectrum-Î²-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 InclH2/ST1 Plasmid. Antimicrobial Agents and Chemotherapy, 2021, 65, .	1.4	9
8	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 ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.5	1
9	Draft Genome Sequence of Enterobacter oligotrophicus, Isolated from the Microbiome of a Lizard in the Caribbean. Microbiology Resource Announcements, 2021, 10, e0060221.	0.3	1
10	Title is missing!. , 2021, 16, e0245084.		0
11	Title is missing!. , 2021, 16, e0245084.		0
12	Title is missing!. , 2021, 16, e0245084.		0
13	Title is missing!. , 2021, 16, e0245084.		0
14	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. Nucleic Acids Research, 2020, 48, D535-D544.	6.5	88
15	Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single blaCTXâ€”Mâ€”1/Incl1/ST3 Plasmid Among Humans and Wild Animals. Frontiers in Microbiology, 2020, 11, 1524.	1.5	25
16	Local adaptive evolution of two distinct clades of Beijing and T families of Mycobacterium tuberculosis in Chongqing: a Bayesian population structure and phylogenetic study. Infectious Diseases of Poverty, 2020, 9, 59.	1.5	1
17	Population structure of multidrug-resistant Mycobacterium tuberculosis clinical isolates in Colombia. Tuberculosis, 2020, 125, 102011.	0.8	4
18	Novel methods included in SpolLineages tool for fast and precise prediction of Mycobacterium tuberculosis complex spoligotype families. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	7

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19	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
20	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
21	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
22	Clonal expansion across the seas as seen through CPLP-TB database: A joint effort in cataloguing <i>Mycobacterium tuberculosis</i> genetic diversity in Portuguese-speaking countries. <i>Infection, Genetics and Evolution</i> , 2019, 72, 44-58.	1.0	18
23	<i>Mycobacterial biomaterials and resources for researchers</i> . <i>Pathogens and Disease</i> , 2018, 76, .	0.8	14
24	Genotypic diversity of <i>Mycobacterium tuberculosis</i> in Buenos Aires, Argentina. <i>Infection, Genetics and Evolution</i> , 2018, 62, 1-7.	1.0	8
25	CRISPRCasFinder, an update of CRISRFinder, includes a portable version, enhanced performance and integrates search for Cas proteins. <i>Nucleic Acids Research</i> , 2018, 46, W246-W251.	6.5	985
26	Geospatial distribution of <i>Mycobacterium tuberculosis</i> genotypes in Africa. <i>PLoS ONE</i> , 2018, 13, e0200632.	1.1	54
27	Comparative study of genotypes of <i>Mycobacterium tuberculosis</i> from a Northern Indian setting with strains reported from other parts of India and neighboring countries. <i>Tuberculosis</i> , 2017, 105, 60-72.	0.8	12
28	SpolSimilaritySearch – A web tool to compare and search similarities between spoligotypes of <i>Mycobacterium tuberculosis</i> complex. <i>Tuberculosis</i> , 2017, 105, 49-52.	0.8	20
29	Genetic diversity of <i>Mycobacterium tuberculosis</i> from Par��, 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
30	<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
31	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
32	First insight into the molecular epidemiology of <i>Mycobacterium tuberculosis</i> in Santa Catarina, southern Brazil. <i>Tuberculosis</i> , 2016, 97, 57-64.	0.8	12
33	Combined Genotypic, Phylogenetic, and Epidemiologic Analyses of <i>Mycobacterium tuberculosis</i> Genetic Diversity in the Rh��ne Alpes Region, France. <i>PLoS ONE</i> , 2016, 11, e0153580.	1.1	19
34	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
35	Analysis of <i>Mycobacterium tuberculosis</i> Genotypic Lineage Distribution in Chile and Neighboring Countries. <i>PLoS ONE</i> , 2016, 11, e0160434.	1.1	12
36	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

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37	Mycobacterium tuberculosis causing tuberculous lymphadenitis in Maputo, Mozambique. BMC Microbiology, 2015, 15, 268.	1.3	10
38	Heterogeneity among Mycobacterium ulcerans from French Guiana Revealed by Multilocus Variable Number Tandem Repeat Analysis (MLVA). PLoS ONE, 2015, 10, e0118597.	1.1	8
39	The Association between Mycobacterium Tuberculosis Genotype and Drug Resistance in Peru. PLoS ONE, 2015, 10, e0126271.	1.1	24
40	Mixed Infections and Rifampin Heteroresistance among Mycobacterium tuberculosis Clinical Isolates. Journal of Clinical Microbiology, 2015, 53, 2138-2147.	1.8	37
41	Tuberculosis – A global emergency: Tools and methods to monitor, understand, and control the epidemic with specific example of the Beijing lineage. Tuberculosis, 2015, 95, S177-S189.	0.8	47
42	Genetic diversity and drug susceptibility profile of Mycobacterium tuberculosis isolated from different regions of India. Journal of Infection, 2015, 71, 207-219.	1.7	38
43	Human multidrug-resistant Mycobacterium bovis infection in Mexico. Tuberculosis, 2015, 95, 802-809.	0.8	17
44	A First Insight on the Population Structure of Mycobacterium tuberculosis Complex as Studied by Spoligotyping and MIRU-VNTRs in Santiago, Chile. PLoS ONE, 2015, 10, e0118007.	1.1	28
45	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
46	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
47	Genotypic characterization and historical perspective of Mycobacterium tuberculosis among older and younger Finns, 2008–2011. Clinical Microbiology and Infection, 2014, 20, 1134-1139.	2.8	7
48	Strain Diversity of <i>Mycobacterium tuberculosis</i> Isolates from Pulmonary Tuberculosis Patients in Afar Pastoral Region of Ethiopia. BioMed Research International, 2014, 2014, 1-12.	0.9	40
49	Molecular Epidemiology and Genotyping of <i>Mycobacterium tuberculosis</i> Isolates in Baghdad. BioMed Research International, 2014, 2014, 1-15.	0.9	12
50	Phylogenetic associations with drug-resistant <i>Mycobacterium tuberculosis</i> isolates in a paediatric population. International Journal of Tuberculosis and Lung Disease, 2014, 18, 1172-1179.	0.6	6
51	Population Structure among Mycobacterium tuberculosis Isolates from Pulmonary Tuberculosis Patients in Colombia. PLoS ONE, 2014, 9, e93848.	1.1	46
52	Predicting <i>Mycobacterium tuberculosis</i> Complex Clades Using Knowledge-Based Bayesian Networks. BioMed Research International, 2014, 2014, 1-11.	0.9	8
53	Snapshot of the genetic diversity of Mycobacterium tuberculosis isolates in Iraq. International Journal of Mycobacteriology, 2014, 3, 184-196.	0.3	15
54	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

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55	Strain Classification of Mycobacterium tuberculosis Isolates in Brazil Based on Genotypes Obtained by Spoligotyping, Mycobacterial Interspersed Repetitive Unit Typing and the Presence of Large Sequence and Single Nucleotide Polymorphism. PLoS ONE, 2014, 9, e107747.	1.1	30
56	Population structure and circulating genotypes of drug-sensitive and drug-resistant Mycobacterium tuberculosis clinical isolates in São Paulo state, Brazil. Infection, Genetics and Evolution, 2013, 14, 39-45.	1.0	10
57	Genetic diversity among multidrug-resistant Mycobacterium tuberculosis strains in Mexico. Infection, Genetics and Evolution, 2013, 14, 434-443.	1.0	30
58	Molecular Epidemiology of Tuberculosis in Finland, 2008-2011. PLoS ONE, 2013, 8, e85027.	1.1	23
59	Genetic Diversity of Mycobacterium tuberculosis in Peru and Exploration of Phylogenetic Associations with Drug Resistance. PLoS ONE, 2013, 8, e65873.	1.1	38
60	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
61	SITVITWEB – A publicly available international multimer database for studying Mycobacterium tuberculosis genetic diversity and molecular epidemiology. Infection, Genetics and Evolution, 2012, 12, 755-766.	1.0	380
62	Mycobacterium tuberculosis Strains Potentially Involved in the TB Epidemic in Sweden a Century Ago. PLoS ONE, 2012, 7, e46848.	1.1	11
63	The Guinea-Bissau Family of Mycobacterium tuberculosis Complex Revisited. PLoS ONE, 2011, 6, e18601.	1.1	47