

David M Engelthaler

List of Publications by Year in descending order

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114
papers

7,109
citations

66343

42
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64796

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120
docs citations

120
times ranked

9549
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Performance of Genomic Methods for the Detection of Pyrazinamide Resistance and Heteroresistance in <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0190721.	3.9	6
2	Phylogeography and transmission of <i>M. tuberculosis</i> in Moldova: A prospective genomic analysis. <i>PLoS Medicine</i> , 2022, 19, e1003933.	8.4	16
3	Molecular type distribution and fluconazole susceptibility of clinical <i>Cryptococcus gattii</i> isolates from South African laboratory-based surveillance, 2005–2013. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010448.	3.0	1
4	Applying Genomic Epidemiology to Characterize a COVID-19 Outbreak in a Developmentally Disabled Adult Group Home Setting, Arizona. <i>Frontiers in Public Health</i> , 2021, 9, 668214.	2.7	3
5	St. Louis Encephalitis Virus in the Southwestern United States: A Phylogeographic Case for a Multi-Variant Introduction Event. <i>Frontiers in Genetics</i> , 2021, 12, 667895.	2.3	5
6	Genomic investigation of a household SARS-CoV-2 disease cluster in Arizona involving a cat, dog, and pet owner. <i>One Health</i> , 2021, 13, 100333.	3.4	15
7	Sequencing the pandemic: rapid and high-throughput processing and analysis of COVID-19 clinical samples for 21st century public health. <i>F1000Research</i> , 2021, 10, 48.	1.6	6
8	Normalization of SARS-CoV-2 viral load via RT-qPCR provides higher-resolution data for comparison across time and between patients. <i>Virus Research</i> , 2021, 306, 198604.	2.2	7
9	The detection of <i>Coccidioides</i> from ambient air in Phoenix, Arizona: Evidence of uneven distribution and seasonality. <i>Medical Mycology</i> , 2020, 58, 552-559.	0.7	23
10	Genomic epidemiology and forensics of fungal pathogens. , 2020, , 141-154.		1
11	Molecular Evaluation of Fluoroquinolone Resistance in Serial <i>Mycobacterium tuberculosis</i> Isolates from Individuals Diagnosed with Multidrug-Resistant Tuberculosis. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 65, .	3.2	0
12	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in <i>Acinetobacter baumannii</i> . <i>Frontiers in Public Health</i> , 2020, 8, 451.	2.7	9
13	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	4.1	29
14	Suspected Locally Acquired <i>Coccidioidomycosis</i> in Human, Spokane, Washington, USA. <i>Emerging Infectious Diseases</i> , 2020, 26, 606-609.	4.3	10
15	<i>Rhizopus microsporus</i> Infections Associated with Surgical Procedures, Argentina, 2006–2014. <i>Emerging Infectious Diseases</i> , 2020, 26, 937-944.	4.3	11
16	Genomic analyses of <i>Staphylococcus aureus</i> clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
17	Genomic variant-identification methods may alter <i>Mycobacterium tuberculosis</i> transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	2.0	24
18	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	1.6	14

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19	Mitigating a COVID-19 Outbreak Among Major League Baseball Players â€” United States, 2020. Morbidity and Mortality Weekly Report, 2020, 69, 1542-1546.	15.1	27
20	Coyotes as Reservoirs for <i>Onchocerca lupi</i> , United States, 2015â€“2018. Emerging Infectious Diseases, 2020, 26, 2989-2993.	4.3	17
21	Utility of Targeted, Amplicon-Based Deep Sequencing To Detect Resistance to First-Line Tuberculosis Drugs in Botswana. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	2
22	A unique multidrug-resistant clonal Trichophyton population distinct from Trichophyton mentagrophytes/Trichophyton interdigitale complex causing an ongoing alarming dermatophytosis outbreak in India: Genomic insights and resistance profile. Fungal Genetics and Biology, 2019, 133, 103266.	2.1	93
23	Genomic Analyses of Acute Flaccid Myelitis Cases among a Cluster in Arizona Provide Further Evidence of Enterovirus D68 Role. MBio, 2019, 10, .	4.1	15
24	Jet-Setting Koalas Spread Cryptococcus gattii VGII in Australia. MSphere, 2019, 4, .	2.9	8
25	Bedaquiline Microheteroresistance after Cessation of Tuberculosis Treatment. New England Journal of Medicine, 2019, 380, 2178-2180.	27.0	52
26	Phylogenetic Analysis of Francisella tularensis Group A.II Isolates from 5 Patients with Tularemia, Arizona, USA, 2015â€“2017. Emerging Infectious Diseases, 2019, 25, 944-946.	4.3	3
27	Whole-genome and targeted sequencing of drug-resistant Mycobacterium tuberculosis on the iSeq100 and MiSeq: A performance, ease-of-use, and cost evaluation. PLoS Medicine, 2019, 16, e1002794.	8.4	49
28	Utility of Whole-Genome Sequencing to Ascertain Locally Acquired Cases of Coccidioidomycosis, Washington, USA. Emerging Infectious Diseases, 2019, 25, 501-506.	4.3	24
29	Update on the Epidemiology of coccidioidomycosis in the United States. Medical Mycology, 2019, 57, S30-S40.	0.7	104
30	Coccidioidal Meningitis in New York Traced to Texas by Fungal Genomic Analysis. Clinical Infectious Diseases, 2019, 69, 1060-1062.	5.8	11
31	Minority Mycobacterium tuberculosis Genotypic Populations as an Indicator of Subsequent Phenotypic Resistance. American Journal of Respiratory Cell and Molecular Biology, 2019, 61, 789-791.	2.9	11
32	Zoonotic Source Attribution of <i>Salmonella enterica</i> Serotype Typhimurium Using Genomic Surveillance Data, United States. Emerging Infectious Diseases, 2019, 25, 82-91.	4.3	75
33	On the Emergence of Cryptococcus gattii in the Pacific Northwest: Ballast Tanks, Tsunamis, and Black Swans. MBio, 2019, 10, .	4.1	22
34	Dating the Cryptococcus gattii Dispersal to the North American Pacific Northwest. MSphere, 2018, 3, .	2.9	20
35	Improved Subtyping of Staphylococcus aureus Clonal Complex 8 Strains Based on Whole-Genome Phylogenetic Analysis. MSphere, 2018, 3, .	2.9	32
36	Phylogenetic analysis of West Nile Virus in Maricopa County, Arizona: Evidence for dynamic behavior of strains in two major lineages in the American Southwest. PLoS ONE, 2018, 13, e0205801.	2.5	13

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37	Timing the Origin of <i>Cryptococcus gattii</i> sensu stricto, Southeastern United States. <i>Emerging Infectious Diseases</i> , 2018, 24, 2095-2097.	4.3	4
38	Integrating standardized whole genome sequence analysis with a global <i>Mycobacterium tuberculosis</i> antibiotic resistance knowledgebase. <i>Scientific Reports</i> , 2018, 8, 15382.	3.3	75
39	Flucytosine resistance in <i>Cryptococcus gattii</i> is indirectly mediated by the FCY2-FCY1-FUR1 pathway. <i>Medical Mycology</i> , 2018, 56, 857-867.	0.7	18
40	Microbial Ecology and Water Chemistry Impact Regrowth of Opportunistic Pathogens in Full-Scale Reclaimed Water Distribution Systems. <i>Environmental Science & Technology</i> , 2018, 52, 9056-9068.	10.0	59
41	Mixed <i>Mycobacterium tuberculosis</i> "Strain Infections Are Associated With Poor Treatment Outcomes Among Patients With Newly Diagnosed Tuberculosis, Independent of Pretreatment Heteroresistance. <i>Journal of Infectious Diseases</i> , 2018, 218, 1974-1982.	4.0	32
42	Metagenomic Characterization of Antibiotic Resistance Genes in Full-Scale Reclaimed Water Distribution Systems and Corresponding Potable Systems. <i>Environmental Science & Technology</i> , 2018, 52, 6113-6125.	10.0	135
43	Cryptic Microheteroresistance Explains <i>Mycobacterium tuberculosis</i> Phenotypic Resistance. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 1191-1201.	5.6	37
44	<i>Mycobacterium tuberculosis</i> Subculture Results in Loss of Potentially Clinically Relevant Heteroresistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	38
45	Tracing Genetic Exchange and Biogeography of <i>Cryptococcus neoformans</i> var. <i>grubii</i> at the Global Population Level. <i>Genetics</i> , 2017, 207, 327-346.	2.9	105
46	A standardised method for interpreting the association between mutations and phenotypic drug resistance in <i>Mycobacterium tuberculosis</i> . <i>European Respiratory Journal</i> , 2017, 50, 1701354.	6.7	273
47	MLST-Based Population Genetic Analysis in a Global Context Reveals Clonality amongst <i>Cryptococcus neoformans</i> var. <i>grubii</i> VNI Isolates from HIV Patients in Southeastern Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005223.	3.0	59
48	Notes from the Field: Cluster of Acute Flaccid Myelitis in Five Pediatric Patients – Maricopa County, Arizona, 2016. <i>Morbidity and Mortality Weekly Report</i> , 2017, 66, 758-760.	15.1	23
49	Hypervirulent <i>emm</i> 59 Clone in Invasive Group A <i>Streptococcus</i> Outbreak, Southwestern United States. <i>Emerging Infectious Diseases</i> , 2016, 22, 734-738.	4.3	25
50	Whole-Genome Analysis of <i>Cryptococcus gattii</i> , Southeastern United States. <i>Emerging Infectious Diseases</i> , 2016, 22, 1098-1101.	4.3	12
51	Worldwide Phylogenetic Distributions and Population Dynamics of the Genus <i>Histoplasma</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004732.	3.0	95
52	Whole-Genome Sequencing to Determine Origin of Multinational Outbreak of <i>Sarocladium kiliense</i> Bloodstream Infections. <i>Emerging Infectious Diseases</i> , 2016, 22, 476-481.	4.3	44
53	Local Population Structure and Patterns of Western Hemisphere Dispersal for <i>Coccidioides</i> spp., the Fungal Cause of Valley Fever. <i>MBio</i> , 2016, 7, e00550-16.	4.1	71
54	Whole genome SNP typing to investigate methicillin-resistant <i>Staphylococcus aureus</i> carriage in a health-care provider as the source of multiple surgical site infections. <i>Hereditas</i> , 2016, 153, 11.	1.4	10

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55	Rapid Drug Susceptibility Testing of Drug-Resistant Mycobacterium tuberculosis Isolates Directly from Clinical Samples by Use of Amplicon Sequencing: a Proof-of-Concept Study. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2058-2067.	3.9	76
56	KlebSeq, a Diagnostic Tool for Surveillance, Detection, and Monitoring of <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 2582-2596.	3.9	50
57	Tick-Borne Relapsing Fever Outbreak Among a High School Football Team at an Outdoor Education Camping Trip, Arizona, 2014. <i>American Journal of Tropical Medicine and Hygiene</i> , 2016, 95, 546-550.	1.4	7
58	Next-generation sequencing-based user-friendly platforms for drug-resistant tuberculosis diagnosis: A promise for the near future. <i>International Journal of Mycobacteriology</i> , 2016, 5, S27-S28.	0.6	14
59	Translating RNA sequencing into clinical diagnostics: opportunities and challenges. <i>Nature Reviews Genetics</i> , 2016, 17, 257-271.	16.3	558
60	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. <i>Microbial Genomics</i> , 2016, 2, e000074.	2.0	237
61	MLST and Whole-Genome-Based Population Analysis of <i>Cryptococcus gattii</i> VGIII Links Clinical, Veterinary and Environmental Strains, and Reveals Divergent Serotype Specific Sub-populations and Distant Ancestors. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004861.	3.0	49
62	Detection of Low-Level Mixed-Population Drug Resistance in <i>Mycobacterium tuberculosis</i> Using High Fidelity Amplicon Sequencing. <i>PLoS ONE</i> , 2015, 10, e0126626.	2.5	93
63	Genomic Analysis of the Emergence and Rapid Global Dissemination of the Clonal Group 258 <i>Klebsiella pneumoniae</i> Pandemic. <i>PLoS ONE</i> , 2015, 10, e0133727.	2.5	195
64	Australia in the global picture of the molecular epidemiology of <i>Cryptococcus gattii</i> molecular type VGII. <i>Microbiology Australia</i> , 2015, 36, 67.	0.4	3
65	Mapping the Evolution of Hypervirulent <i>Klebsiella pneumoniae</i> . <i>MBio</i> , 2015, 6, e00630.	4.1	270
66	Valley Fever: Finding New Places for an Old Disease: <i>Coccidioides immitis</i> Found in Washington State Soil Associated With Recent Human Infection. <i>Clinical Infectious Diseases</i> , 2015, 60, e1-e3.	5.8	153
67	Comparative Analysis of Subtyping Methods against a Whole-Genome-Sequencing Standard for <i>Salmonella enterica</i> Serotype Enteritidis. <i>Journal of Clinical Microbiology</i> , 2015, 53, 212-218.	3.9	112
68	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2015, 10, e0130955.	2.5	40
69	<i>Cryptococcus gattii</i> in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. <i>MBio</i> , 2014, 5, e01464-14.	4.1	126
70	MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. <i>PLoS ONE</i> , 2014, 9, e110915.	2.5	14
71	Whole-Genome Analysis of <i>Exserohilum rostratum</i> from an Outbreak of Fungal Meningitis and Other Infections. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3216-3222.	3.9	52
72	<i>Coccidioides immitis</i> identified in soil outside of its known range - Washington, 2013. <i>Morbidity and Mortality Weekly Report</i> , 2014, 63, 450.	15.1	30

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73	Molecular genotyping of <i>Acinetobacter</i> spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. <i>Journal of Medical Microbiology</i> , 2013, 62, 1295-1300.	1.8	4
74	Rapid and robust phylotyping of <i>spa</i> t003, a dominant MRSA clone in Luxembourg and other European countries. <i>BMC Infectious Diseases</i> , 2013, 13, 339.	2.9	11
75	Genome Sequence of <i>Staphylococcus aureus</i> Strain CA-347, a USA600 Methicillin-Resistant Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	40
76	Coccidioidomycosis. <i>Chest</i> , 2013, 143, 776-781.	0.8	31
77	Evolution of a Pathogen: A Comparative Genomics Analysis Identifies a Genetic Pathway to Pathogenesis in <i>Acinetobacter</i> . <i>PLoS ONE</i> , 2013, 8, e54287.	2.5	134
78	Comparison of TaqMan PCR Assays for Detection of the Melioidosis Agent <i>Burkholderia pseudomallei</i> in Clinical Specimens. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2059-2062.	3.9	44
79	Genome Sequence of <i>Candidatus Microthrix parvicella</i> -Bio17-1, a Long-Chain-Fatty-Acid-Accumulating Filamentous Actinobacterium from a Biological Wastewater Treatment Plant. <i>Journal of Bacteriology</i> , 2012, 194, 6670-6671.	2.2	27
80	Characterization of Ceftazidime Resistance Mechanisms in Clinical Isolates of <i>Burkholderia pseudomallei</i> from Australia. <i>PLoS ONE</i> , 2012, 7, e30789.	2.5	75
81	Necrotizing Cutaneous Mucormycosis after a Tornado in Joplin, Missouri, in 2011. <i>New England Journal of Medicine</i> , 2012, 367, 2214-2225.	27.0	297
82	Towards a rapid molecular diagnostic for melioidosis: Comparison of DNA extraction methods from clinical specimens. <i>Journal of Microbiological Methods</i> , 2012, 88, 179-181.	1.6	26
83	Whole Genome Sequence Typing to Investigate the <i>Apophysomyces</i> Outbreak following a Tornado in Joplin, Missouri, 2011. <i>PLoS ONE</i> , 2012, 7, e49989.	2.5	66
84	Multidrug-Resistant <i>Staphylococcus aureus</i> in US Meat and Poultry. <i>Clinical Infectious Diseases</i> , 2011, 52, 1227-1230.	5.8	238
85	Epidemiology and Investigation of Melioidosis, Southern Arizona. <i>Emerging Infectious Diseases</i> , 2011, 17, 1286-1288.	4.3	35
86	Diversity of 16S-23S rDNA Internal Transcribed Spacer (ITS) Reveals Phylogenetic Relationships in <i>Burkholderia pseudomallei</i> and Its Near-Neighbors. <i>PLoS ONE</i> , 2011, 6, e29323.	2.5	33
87	Triple Combination Antiviral Drug (TCAD) Composed of Amantadine, Oseltamivir, and Ribavirin Impedes the Selection of Drug-Resistant Influenza A Virus. <i>PLoS ONE</i> , 2011, 6, e29778.	2.5	48
88	Macroscale spatial variation in chronic wound microbiota: A cross-sectional study. <i>Wound Repair and Regeneration</i> , 2011, 19, 80-88.	3.0	49
89	Population Genetics of <i>Vibrio cholerae</i> from Nepal in 2010: Evidence on the Origin of the Haitian Outbreak. <i>MBio</i> , 2011, 2, e00157-11.	4.1	268
90	Next-Generation Sequencing of <i>Coccidioides immitis</i> Isolated during Cluster Investigation. <i>Emerging Infectious Diseases</i> , 2011, 17, 227-232.	4.3	48

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91	Cyclopropavir Inhibits the Normal Function of the Human Cytomegalovirus UL97 Kinase. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4682-4691.	3.2	39
92	Reply to "South Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strain". <i>MBio</i> , 2011, 2, e00245-11.	4.1	14
93	Molecular Investigations of a Locally Acquired Case of Melioidosis in Southern AZ, USA. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1347.	3.0	23
94	Whole Genome Sequence Analysis of <i>Cryptococcus gattii</i> from the Pacific Northwest Reveals Unexpected Diversity. <i>PLoS ONE</i> , 2011, 6, e28550.	2.5	63
95	Rapid quantification of single-nucleotide mutations in mixed influenza A viral populations using allele-specific mixture analysis. <i>Journal of Virological Methods</i> , 2010, 163, 109-115.	2.1	16
96	BurkDiff: A Real-Time PCR Allelic Discrimination Assay for <i>Burkholderia Pseudomallei</i> and <i>B. mallei</i> . <i>PLoS ONE</i> , 2010, 5, e15413.	2.5	38
97	"In Vitro" System for Modeling Influenza A Virus Resistance under Drug Pressure. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 3442-3450.	3.2	25
98	Reply to Dr Wiwanitkit. <i>Medical Mycology</i> , 2010, 48, 680-680.	0.7	0
99	Development of a rapid, cost-effective TaqMan Real-Time PCR Assay for identification and differentiation of <i>Coccidioides immitis</i> and <i>Coccidioides posadasii</i> . <i>Medical Mycology</i> , 2010, 48, 466-469.	0.7	36
100	No Resistance Plasmid in <i>Yersinia pestis</i> , North America. <i>Emerging Infectious Diseases</i> , 2010, 16, 885-887.	4.3	10
101	Community Analysis of Chronic Wound Bacteria Using 16S rRNA Gene-Based Pyrosequencing: Impact of Diabetes and Antibiotics on Chronic Wound Microbiota. <i>PLoS ONE</i> , 2009, 4, e6462.	2.5	199
102	Triple Combination of Oseltamivir, Amantadine, and Ribavirin Displays Synergistic Activity against Multiple Influenza Virus Strains In Vitro. <i>Antimicrobial Agents and Chemotherapy</i> , 2009, 53, 4115-4126.	3.2	105
103	Phylogeography of <i>Francisella tularensis</i> : Global Expansion of a Highly Fit Clone. <i>Journal of Bacteriology</i> , 2009, 191, 2474-2484.	2.2	176
104	The impact of excess heat events in Maricopa County, Arizona: 2000-2005. <i>International Journal of Biometeorology</i> , 2008, 52, 765-772.	3.0	62
105	Testing for Coccidioidomycosis among Patients with Community-Acquired Pneumonia. <i>Emerging Infectious Diseases</i> , 2008, 14, 1053-1059.	4.3	89
106	Human Plague in the Southwestern United States, 1957-2004: Spatial Models of Elevated Risk of Human Exposure to <i>Yersinia pestis</i> . <i>Journal of Medical Entomology</i> , 2007, 44, 530-537.	1.8	44
107	Public Health Surveillance for Coccidioidomycosis in Arizona. <i>Annals of the New York Academy of Sciences</i> , 2007, 1111, 96-102.	3.8	73
108	Modeling relationships between climate and the frequency of human plague cases in the southwestern United States, 1960-1997.. <i>American Journal of Tropical Medicine and Hygiene</i> , 2002, 66, 186-196.	1.4	147

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109	Quantities of <i>Yersinia pestis</i> in Fleas (Siphonaptera: Pulicidae, Ceratophyllidae, and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Entomology, 2000, 37, 422-426.	1.8	14
110	Climatic and Environmental Patterns Associated with Hantavirus Pulmonary Syndrome, Four Corners Region, United States. Emerging Infectious Diseases, 1999, 5, 87-94.	4.3	213
111	PCR Detection of <i>Yersinia pestis</i> in Fleas: Comparison with Mouse Inoculation. Journal of Clinical Microbiology, 1999, 37, 1980-1984.	3.9	49
112	The Reemergence of <i>Aedes aegypti</i> in Arizona. Emerging Infectious Diseases, 1997, 3, 241-242.	4.3	27
113	Patterns of Association with Host and Habitat: Antibody Reactive with Sin Nombre Virus in Small Mammals in the Major Biotic Communities of the Southwestern United States. American Journal of Tropical Medicine and Hygiene, 1997, 56, 273-284.	1.4	192
114	Methods for sequencing the pandemic: benefits of rapid or high-throughput processing. F1000Research, 0, 10, 48.	1.6	5