

David M Engelthaler

List of Publications by Year in descending order

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114
papers

7,109
citations

66343

42
h-index

64796

79
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120
all docs

120
docs citations

120
times ranked

9549
citing authors

#	ARTICLE	IF	CITATIONS
1	Translating RNA sequencing into clinical diagnostics: opportunities and challenges. <i>Nature Reviews Genetics</i> , 2016, 17, 257-271.	16.3	558
2	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
3	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
4	Mapping the Evolution of Hypervirulent <i>Klebsiella pneumoniae</i> . <i>MBio</i> , 2015, 6, e00630.	4.1	270
5	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
6	Multidrug-Resistant <i>Staphylococcus aureus</i> in US Meat and Poultry. <i>Clinical Infectious Diseases</i> , 2011, 52, 1227-1230.	5.8	238
7	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
8	Climatic and Environmental Patterns Associated with Hantavirus Pulmonary Syndrome, Four Corners Region, United States. <i>Emerging Infectious Diseases</i> , 1999, 5, 87-94.	4.3	213
9	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
10	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
11	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. <i>American Journal of Tropical Medicine and Hygiene</i> , 1997, 56, 273-284.	1.4	192
12	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
13	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
14	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
15	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
16	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
17	<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
18	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

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19	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
20	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
21	Update on the Epidemiology of coccidioidomycosis in the United States. <i>Medical Mycology</i> , 2019, 57, S30-S40.	0.7	104
22	Worldwide Phylogenetic Distributions and Population Dynamics of the Genus <i>Histoplasma</i> . <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004732.	3.0	95
23	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
24	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. <i>Fungal Genetics and Biology</i> , 2019, 133, 103266.	2.1	93
25	Testing for Coccidioidomycosis among Patients with Community-Acquired Pneumonia. <i>Emerging Infectious Diseases</i> , 2008, 14, 1053-1059.	4.3	89
26	Rapid Drug Susceptibility Testing of Drug-Resistant <i>Mycobacterium tuberculosis</i> 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
27	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
28	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
29	Zoonotic Source Attribution of <i>Salmonella enterica</i> Serotype Typhimurium Using Genomic Surveillance Data, United States. <i>Emerging Infectious Diseases</i> , 2019, 25, 82-91.	4.3	75
30	Public Health Surveillance for Coccidioidomycosis in Arizona. <i>Annals of the New York Academy of Sciences</i> , 2007, 1111, 96-102.	3.8	73
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	Bedaquiline Microheteroresistance after Cessation of Tuberculosis Treatment. <i>New England Journal of Medicine</i> , 2019, 380, 2178-2180.	27.0	52
39	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
40	Macroscale spatial variation in chronic wound microbiota: A cross-sectional study. <i>Wound Repair and Regeneration</i> , 2011, 19, 80-88.	3.0	49
41	Whole-genome and targeted sequencing of drug-resistant <i>Mycobacterium tuberculosis</i> on the iSeq100 and MiSeq: A performance, ease-of-use, and cost evaluation. <i>PLoS Medicine</i> , 2019, 16, e1002794.	8.4	49
42	PCR Detection of <i>Yersinia pestis</i> in Fleas: Comparison with Mouse Inoculation. <i>Journal of Clinical Microbiology</i> , 1999, 37, 1980-1984.	3.9	49
43	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
44	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
45	Next-Generation Sequencing of <i>Coccidioides immitis</i> Isolated during Cluster Investigation. <i>Emerging Infectious Diseases</i> , 2011, 17, 227-232.	4.3	48
46	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
47	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
48	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
49	Genome Sequence of <i>Staphylococcus aureus</i> Strain CA-347, a USA600 Methicillin-Resistant Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	40
50	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
51	Cyclopropavir Inhibits the Normal Function of the Human Cytomegalovirus UL97 Kinase. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 4682-4691.	3.2	39
52	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
53	<i>Mycobacterium tuberculosis</i> Subculture Results in Loss of Potentially Clinically Relevant Heteroresistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	3.2	38
54	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

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55	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
56	Epidemiology and Investigation of Melioidosis, Southern Arizona. <i>Emerging Infectious Diseases</i> , 2011, 17, 1286-1288.	4.3	35
57	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
58	Improved Subtyping of <i>Staphylococcus aureus</i> Clonal Complex 8 Strains Based on Whole-Genome Phylogenetic Analysis. <i>MSphere</i> , 2018, 3, .	2.9	32
59	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
60	<i>Coccidioidomycosis</i> . <i>Chest</i> , 2013, 143, 776-781.	0.8	31
61	<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
62	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	4.1	29
63	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
64	Mitigating a COVID-19 Outbreak Among Major League Baseball Players in United States, 2020. <i>Morbidity and Mortality Weekly Report</i> , 2020, 69, 1542-1546.	15.1	27
65	The Reemergence of <i>Aedes aegypti</i> in Arizona. <i>Emerging Infectious Diseases</i> , 1997, 3, 241-242.	4.3	27
66	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
67	<i>In Vitro</i> System for Modeling Influenza A Virus Resistance under Drug Pressure. <i>Antimicrobial Agents and Chemotherapy</i> , 2010, 54, 3442-3450.	3.2	25
68	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
69	Utility of Whole-Genome Sequencing to Ascertain Locally Acquired Cases of <i>Coccidioidomycosis</i> , Washington, USA. <i>Emerging Infectious Diseases</i> , 2019, 25, 501-506.	4.3	24
70	Genomic variant-identification methods may alter <i>Mycobacterium tuberculosis</i> transmission inferences. <i>Microbial Genomics</i> , 2020, 6, .	2.0	24
71	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
72	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

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73	<i>Notes from the Field:</i> Cluster of Acute Flaccid Myelitis in Five Pediatric Patients â€” Maricopa County, Arizona, 2016. Morbidity and Mortality Weekly Report, 2017, 66, 758-760.	15.1	23
74	On the Emergence of <i>Cryptococcus gattii</i> in the Pacific Northwest: Ballast Tanks, Tsunamis, and Black Swans. MBio, 2019, 10, .	4.1	22
75	Dating the <i>Cryptococcus gattii</i> Dispersal to the North American Pacific Northwest. MSphere, 2018, 3, .	2.9	20
76	Flucytosine resistance in <i>Cryptococcus gattii</i> is indirectly mediated by the FCY2-FCY1-FUR1 pathway. Medical Mycology, 2018, 56, 857-867.	0.7	18
77	Coyotes as Reservoirs for <i>Onchocerca lupi</i>, United States, 2015â€”2018. Emerging Infectious Diseases, 2020, 26, 2989-2993.	4.3	17
78	Rapid quantification of single-nucleotide mutations in mixed influenza A viral populations using allele-specific mixture analysis. Journal of Virological Methods, 2010, 163, 109-115.	2.1	16
79	Phylogeography and transmission of <i>M. tuberculosis</i> in Moldova: A prospective genomic analysis. PLoS Medicine, 2022, 19, e1003933.	8.4	16
80	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
81	Genomic investigation of a household SARS-CoV-2 disease cluster in Arizona involving a cat, dog, and pet owner. One Health, 2021, 13, 100333.	3.4	15
82	Quantities of <i>Yersinia pestis</i> in Fleas (Siphonaptera: Pulicidae, Ceratophyllidae, and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 387 Td Entomology, 2000, 37, 422-426.	1.8	14
83	Reply to â€œSouth Asia Instead of Nepal May Be the Origin of the Haitian Cholera Outbreak Strainâ€. MBio, 2011, 2, e00245-11.	4.1	14
84	MetaGeniE: Characterizing Human Clinical Samples Using Deep Metagenomic Sequencing. PLoS ONE, 2014, 9, e110915.	2.5	14
85	Next-generation sequencing-based user-friendly platforms for drug-resistant tuberculosis diagnosis: A promise for the near future. International Journal of Mycobacteriology, 2016, 5, S27-S28.	0.6	14
86	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 2020, 9, 657.	1.6	14
87	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
88	Whole-Genome Analysis of <i>Cryptococcus gattii</i>, Southeastern United States. Emerging Infectious Diseases, 2016, 22, 1098-1101.	4.3	12
89	Rapid and robust phylotyping of spa t003, a dominant MRSA clone in Luxembourg and other European countries. BMC Infectious Diseases, 2013, 13, 339.	2.9	11
90	Coccidioidal Meningitis in New York Traced to Texas by Fungal Genomic Analysis. Clinical Infectious Diseases, 2019, 69, 1060-1062.	5.8	11

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91	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
92	<i>Rhizopus microsporus</i> Infections Associated with Surgical Procedures, Argentina, 2006–2014. Emerging Infectious Diseases, 2020, 26, 937-944.	4.3	11
93	No Resistance Plasmid in <i>Yersinia pestis</i> , North America. Emerging Infectious Diseases, 2010, 16, 885-887.	4.3	10
94	Whole genome SNP typing to investigate methicillin-resistant Staphylococcus aureus carriage in a health-care provider as the source of multiple surgical site infections. Hereditas, 2016, 153, 11.	1.4	10
95	Suspected Locally Acquired Coccidioidomycosis in Human, Spokane, Washington, USA. Emerging Infectious Diseases, 2020, 26, 606-609.	4.3	10
96	Bacterial Genome Wide Association Studies (bGWAS) and Transcriptomics Identifies Cryptic Antimicrobial Resistance Mechanisms in Acinetobacter baumannii. Frontiers in Public Health, 2020, 8, 451.	2.7	9
97	Jet-Setting Koalas Spread Cryptococcus gattii VGII in Australia. MSphere, 2019, 4, .	2.9	8
98	Tick-Borne Relapsing Fever Outbreak Among a High School Football Team at an Outdoor Education Camping Trip, Arizona, 2014. American Journal of Tropical Medicine and Hygiene, 2016, 95, 546-550.	1.4	7
99	Normalization of SARS-CoV-2 viral load via RT-qPCR provides higher-resolution data for comparison across time and between patients. Virus Research, 2021, 306, 198604.	2.2	7
100	Sequencing the pandemic: rapid and high-throughput processing and analysis of COVID-19 clinical samples for 21st century public health. F1000Research, 2021, 10, 48.	1.6	6
101	Genomic analyses of Staphylococcus aureus clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. Microbial Genomics, 2020, 6, .	2.0	6
102	Comparative Performance of Genomic Methods for the Detection of Pyrazinamide Resistance and Heteroresistance in Mycobacterium tuberculosis. Journal of Clinical Microbiology, 2022, 60, JCM0190721.	3.9	6
103	St. Louis Encephalitis Virus in the Southwestern United States: A Phylogeographic Case for a Multi-Variant Introduction Event. Frontiers in Genetics, 2021, 12, 667895.	2.3	5
104	Methods for sequencing the pandemic: benefits of rapid or high-throughput processing. F1000Research, 0, 10, 48.	1.6	5
105	Molecular genotyping of Acinetobacter spp. isolated in Arizona, USA, using multilocus PCR and mass spectrometry. Journal of Medical Microbiology, 2013, 62, 1295-1300.	1.8	4
106	Timing the Origin of Cryptococcus gattii sensu stricto, Southeastern United States. Emerging Infectious Diseases, 2018, 24, 2095-2097.	4.3	4
107	Australia in the global picture of the molecular epidemiology of Cryptococcus gattii molecular type VGII. Microbiology Australia, 2015, 36, 67.	0.4	3
108	Phylogenetic Analysis of Francisella tularensis Group A.II Isolates from 5 Patients with Tularemia, Arizona, USA, 2015–2017. Emerging Infectious Diseases, 2019, 25, 944-946.	4.3	3

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109	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
110	Utility of Targeted, Amplicon-Based Deep Sequencing To Detect Resistance to First-Line Tuberculosis Drugs in Botswana. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	2
111	Genomic epidemiology and forensics of fungal pathogens. , 2020, , 141-154.		1
112	Molecular type distribution and fluconazole susceptibility of clinical <i>Cryptococcus gattii</i> isolates from South African laboratory-based surveillance, 2005â€“2013. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010448.	3.0	1
113	Reply to Dr Wiwanitkit. <i>Medical Mycology</i> , 2010, 48, 680-680.	0.7	0
114	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