

# Murray Cox

## List of Publications by Year in descending order

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135  
papers

7,112  
citations

76326

40  
h-index

69250

77  
g-index

153  
all docs

153  
docs citations

153  
times ranked

10229  
citing authors

#	ARTICLE	IF	CITATIONS
1	SolexaQA: At-a-glance quality assessment of Illumina second-generation sequencing data. BMC Bioinformatics, 2010, 11, 485.	2.6	1,268
2	Genomic analyses inform on migration events during the peopling of Eurasia. Nature, 2016, 538, 238-242.	27.8	360
3	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Research, 2015, 25, 459-466.	5.5	348
4	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the Clavicipitaceae Reveals Dynamics of Alkaloid Loci. PLoS Genetics, 2013, 9, e1003323.	3.5	344
5	Genomic insights into the peopling of the Southwest Pacific. Nature, 2016, 538, 510-513.	27.8	262
6	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	27.8	251
7	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. PLoS Genetics, 2012, 8, e1003088.	3.5	226
8	Recombination-filtered genomic datasets by information maximization. Bioinformatics, 2007, 23, 1851-1853.	4.1	193
9	Multiple Deeply Divergent Denisovan Ancestries in Papuans. Cell, 2019, 177, 1010-1021.e32.	28.9	181
10	Fungal endophyte infection of ryegrass reprograms host metabolism and alters development. New Phytologist, 2015, 208, 1227-1240.	7.3	165
11	Sex-Biased Evolutionary Forces Shape Genomic Patterns of Human Diversity. PLoS Genetics, 2008, 4, e1000202.	3.5	139
12	What triggers grass endophytes to switch from mutualism to pathogenism?. Plant Science, 2011, 180, 190-195.	3.6	135
13	Major East-West Division Underlies Y Chromosome Stratification across Indonesia. Molecular Biology and Evolution, 2010, 27, 1833-1844.	8.9	133
14	Disruption of Signaling in a Fungal-Grass Symbiosis Leads to Pathogenesis. Plant Physiology, 2010, 153, 1780-1794.	4.8	121
15	The Indonesian archipelago: an ancient genetic highway linking Asia and the Pacific. Journal of Human Genetics, 2013, 58, 165-173.	2.3	100
16	The ratio of human X chromosome to autosome diversity is positively correlated with genetic distance from genes. Nature Genetics, 2010, 42, 830-831.	21.4	90
17	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. Plant Cell, 2019, 31, 1466-1487.	6.6	89
18	A small cohort of Island Southeast Asian women founded Madagascar. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2761-2768.	2.6	79

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19	Repeat elements organise 3D genome structure and mediate transcription in the filamentous fungus <i>Epichloa festucae</i> . <i>PLoS Genetics</i> , 2018, 14, e1007467.	3.5	79
20	Complete mitochondrial DNA sequences provide new insights into the Polynesian motif and the peopling of Madagascar. <i>European Journal of Human Genetics</i> , 2010, 18, 575-581.	2.8	75
21	A novel DNA sequence database for analyzing human demographic history. <i>Genome Research</i> , 2008, 18, 1354-1361.	5.5	74
22	Coevolution of languages and genes on the island of Sumba, eastern Indonesia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16022-16026.	7.1	68
23	An Interspecific Fungal Hybrid Reveals Cross-Kingdom Rules for Allopolyploid Gene Expression Patterns. <i>PLoS Genetics</i> , 2014, 10, e1004180.	3.5	68
24	Host Tissue Environment Directs Activities of an <i>Epichloa</i> Endophyte, While It Induces Systemic Hormone and Defense Responses in Its Native Perennial Ryegrass Host. <i>Molecular Plant-Microbe Interactions</i> , 2017, 30, 138-149.	2.6	68
25	Inferring Human Population Sizes, Divergence Times and Rates of Gene Flow From Mitochondrial, X and Y Chromosome Resequencing Data. <i>Genetics</i> , 2007, 177, 2195-2207.	2.9	65
26	Complex Patterns of Admixture across the Indonesian Archipelago. <i>Molecular Biology and Evolution</i> , 2017, 34, 2439-2452.	8.9	65
27	Accuracy of Molecular Dating with the Rho Statistic: Deviations from Coalescent Expectations Under a Range of Demographic Models. <i>Human Biology</i> , 2008, 80, 335-357.	0.2	63
28	Malagasy Genetic Ancestry Comes from an Historical Malay Trading Post in Southeast Borneo. <i>Molecular Biology and Evolution</i> , 2016, 33, 2396-2400.	8.9	62
29	Mitochondrial DNA and the Y chromosome suggest the settlement of Madagascar by Indonesian sea nomad populations. <i>BMC Genomics</i> , 2015, 16, 191.	2.8	61
30	A Core Gene Set Describes the Molecular Basis of Mutualism and Antagonism in <i>Epichloa</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 218-231.	2.6	59
31	Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. <i>New Phytologist</i> , 2013, 198, 525-535.	7.3	55
32	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , 2019, 20, 1299-1310.	14.5	53
33	Autosomal and X-linked single nucleotide polymorphisms reveal a steep Asian-Melanesian ancestry cline in eastern Indonesia and a sex bias in admixture rates. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 1589-1596.	2.6	52
34	An ongoing Austronesian expansion in Island Southeast Asia. <i>Journal of Anthropological Archaeology</i> , 2011, 30, 262-272.	1.6	48
35	Genome-wide gene expression dynamics of the fungal pathogen <i>Dicellaema phaeocephala</i> throughout its infection cycle of the gymnosperm host <i>Pinus radiata</i> . <i>Molecular Plant Pathology</i> , 2016, 17, 210-224.	4.2	48
36	Contrasting Linguistic and Genetic Origins of the Asian Source Populations of Malagasy. <i>Scientific Reports</i> , 2016, 6, 26066.	3.3	48

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37	Contrasting Signatures of Population Growth for Mitochondrial DNA and Y Chromosomes among Human Populations in Africa. <i>Molecular Biology and Evolution</i> , 2008, 25, 517-525.	8.9	45
38	Autosomal Resequencing Data Reveal Late Stone Age Signals of Population Expansion in Sub-Saharan African Foraging and Farming Populations. <i>PLoS ONE</i> , 2009, 4, e6366.	2.5	45
39	A new deep branch of eurasian mtDNA macrohaplogroup M reveals additional complexity regarding the settlement of Madagascar. <i>BMC Genomics</i> , 2009, 10, 605.	2.8	44
40	<i>Epichloa</i> hybrida, sp. nov., an emerging model system for investigating fungal allopolyploidy. <i>Mycologia</i> , 2017, 109, 1-15.	1.9	43
41	Insights into the <i>Geobacillus stearothermophilus</i> species based on phylogenomic principles. <i>BMC Microbiology</i> , 2017, 17, 140.	3.3	41
42	The Case of the Missing Ancient Fungal Polyploids. <i>American Naturalist</i> , 2016, 188, 602-614.	2.1	38
43	Male dominance rarely skews the frequency distribution of Y chromosome haplotypes in human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 11645-11650.	7.1	36
44	Molecular Cloning and Functional Analysis of Gene Clusters for the Biosynthesis of Indole-Diterpenes in <i>Penicillium crustosum</i> and <i>P. janthinellum</i> . <i>Toxins</i> , 2015, 7, 2701-2722.	3.4	33
45	Semi-automatic selection of summary statistics for ABC model choice. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 67-82.	0.6	32
46	The Comoros Show the Earliest Austronesian Gene Flow into the Swahili Corridor. <i>American Journal of Human Genetics</i> , 2018, 102, 58-68.	6.2	32
47	Dothistromin genes at multiple separate loci are regulated by AfIR. <i>Fungal Genetics and Biology</i> , 2013, 51, 12-20.	2.1	30
48	Genome-wide DNA methylation and gene expression patterns reflect genetic ancestry and environmental differences across the Indonesian archipelago. <i>PLoS Genetics</i> , 2020, 16, e1008749.	3.5	30
49	Y-chromosome diversity is inversely associated with language affiliation in paired Austronesian- and Papuan-speaking communities from Solomon Islands. <i>American Journal of Human Biology</i> , 2006, 18, 35-50.	1.6	28
50	ORIGINAL ARTICLE: Coalescent analyses support multiple mainland-to-island dispersals in the evolution of Malagasy <i>Triaenops</i> bats (Chiroptera: Hipposideridae). <i>Journal of Biogeography</i> , 2008, 35, 995-1003.	3.0	28
51	A robust budding model of Balinese water temple networks. <i>World Archaeology</i> , 2009, 41, 112-133.	1.1	28
52	Genomes of Plant-Associated Clavicipitaceae. <i>Advances in Botanical Research</i> , 2014, 70, 291-327.	1.1	28
53	Computational Feature-Sensitive Reconstruction of Language Relationships: Developing the ALINE Distance for Comparative Historical Linguistic Reconstruction. <i>Journal of Quantitative Linguistics</i> , 2008, 15, 340-369.	1.2	27
54	Testing for Archaic Hominin Admixture on the X Chromosome: Model Likelihoods for the Modern Human X Chromosome Region From Summaries of Genealogical Topology Under the Structured Coalescent. <i>Genetics</i> , 2008, 178, 427-437.	2.9	27

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55	Widespread Denisovan ancestry in Island Southeast Asia but no evidence of substantial super-archaic hominin admixture. <i>Nature Ecology and Evolution</i> , 2021, 5, 616-624.	7.8	27
56	Indonesian Mitochondrial DNA and Its Opposition to a Pleistocene Era Origin of Proto-Polynesians in Island Southeast Asia. <i>Human Biology</i> , 2005, 77, 179-188.	0.2	26
57	HyLiTE: accurate and flexible analysis of gene expression in hybrid and allopolyploid species. <i>BMC Bioinformatics</i> , 2015, 16, 8.	2.6	25
58	Complex epigenetic regulation of alkaloid biosynthesis and host interaction by heterochromatin protein I in a fungal endophyte-plant symbiosis. <i>Fungal Genetics and Biology</i> , 2019, 125, 71-83.	2.1	25
59	Reconstructing Past Admixture Processes from Local Genomic Ancestry Using Wavelet Transformation. <i>Genetics</i> , 2015, 200, 469-481.	2.9	24
60	Post-marital residence patterns show lineage-specific evolution. <i>Evolution and Human Behavior</i> , 2018, 39, 594-601.	2.2	24
61	Papuan mitochondrial genomes and the settlement of Sahul. <i>Journal of Human Genetics</i> , 2020, 65, 875-887.	2.3	24
62	Conservation and expansion of a necrosis-inducing small secreted protein family from host-variable phytopathogens of the Sclerotiniaceae. <i>Molecular Plant Pathology</i> , 2020, 21, 512-526.	4.2	23
63	Investigating the origins of eastern Polynesians using genome-wide data from the Leeward Society Isles. <i>Scientific Reports</i> , 2018, 8, 1823.	3.3	22
64	Māori oral traditions record and convey indigenous knowledge of marine and freshwater resources. <i>New Zealand Journal of Marine and Freshwater Research</i> , 2018, 52, 487-496.	2.0	22
65	The last sea nomads of the Indonesian archipelago: genomic origins and dispersal. <i>European Journal of Human Genetics</i> , 2017, 25, 1004-1010.	2.8	21
66	A Polynesian Motif on the Y Chromosome: Population Structure in Remote Oceania. <i>Human Biology</i> , 2007, 79, 525-535.	0.2	20
67	Genomic Data Quality Impacts Automated Detection of Lateral Gene Transfer in Fungi. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1301-1314.	1.8	20
68	The Guanine Nucleotide Exchange Factor RIC8 Regulates Conidial Germination through G $\alpha$ Proteins in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2012, 7, e48026.	2.5	20
69	Population growth of Mexican free-tailed bats ( <i>Tadarida brasiliensis mexicana</i> ) predates human agricultural activity. <i>BMC Evolutionary Biology</i> , 2011, 11, 88.	3.2	19
70	Global population genomics of the forest pathogen <i>Dothistroma septosporum</i> reveal chromosome duplications in high dothistromin-producing strains. <i>Molecular Plant Pathology</i> , 2019, 20, 784-799.	4.2	19
71	Phylogenetic determinants of toxin gene distribution in genomes of <i>Brevibacillus laterosporus</i> . <i>Genomics</i> , 2020, 112, 1042-1053.	2.9	19
72	Climate Change Influenced Female Population Sizes Through Time Across the Indonesian Archipelago. <i>Human Biology</i> , 2013, 85, 135-152.	0.2	18

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73	Kinship structures create persistent channels for language transmission. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12910-12915.	7.1	18
74	Intergenic DNA sequences from the human X chromosome reveal high rates of global gene flow. BMC Genetics, 2008, 9, 76.	2.7	17
75	Isolation, contact and social behavior shaped genetic diversity in West Timor. Journal of Human Genetics, 2014, 59, 494-503.	2.3	17
76	Human Perceptions of Megafaunal Extinction Events Revealed by Linguistic Analysis of Indigenous Oral Traditions. Human Ecology, 2018, 46, 461-470.	1.4	17
77	Marine resources in Māori oral tradition: He kai moana, he kai māte hinengaro. Journal of Marine and Island Cultures, 2013, 2, 59-68.	0.2	16
78	Accuracy of Molecular Dating with the Rho Statistic: Deviations from Coalescent Expectations Under a Range of Demographic Models. Human Biology, 2009, 81, 911-933.	0.2	15
79	Evidence of Austronesian Genetic Lineages in East Africa and South Arabia: Complex Dispersal from Madagascar and Southeast Asia. Genome Biology and Evolution, 2019, 11, 748-758.	2.5	15
80	Relaxed Observance of Traditional Marriage Rules Allows Social Connectivity without Loss of Genetic Diversity. Molecular Biology and Evolution, 2015, 32, 2254-2262.	8.9	14
81	Chromosome-Level Reference Genome of <i>Venturia effusa</i> , Causative Agent of Pecan Scab. Molecular Plant-Microbe Interactions, 2020, 33, 149-152.	2.6	14
82	A question of scale: Human migrations writ large and small. BMC Biology, 2010, 8, 98.	3.8	13
83	The Domain of the Replicators. Current Anthropology, 2011, 52, 105-125.	1.6	13
84	Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network. Scientific Reports, 2017, 7, 2919.	3.3	13
85	Genomic medicine must reduce, not compound, health inequities: the case for hauora-enhancing genomic resources for New Zealand. New Zealand Medical Journal, 2018, 131, 81-89.	0.5	13
86	Regime Shifts in Balinese <i>Subaks</i> . Current Anthropology, 2014, 55, 232-239.	1.6	12
87	Reconstructing Demography and Social Behavior During the Neolithic Expansion from Genomic Diversity Across Island Southeast Asia. Genetics, 2016, 204, 1495-1506.	2.9	12
88	Small Traditional Human Communities Sustain Genomic Diversity over Microgeographic Scales despite Linguistic Isolation. Molecular Biology and Evolution, 2016, 33, 2273-2284.	8.9	12
89	Minimal hierarchical analysis of global human Y-chromosome SNP diversity by PCR-RFLP. Anthropological Science, 2006, 114, 69-74.	0.4	11
90	Papua New Guinean Genomes Reveal the Complex Settlement of North Sahul. Molecular Biology and Evolution, 2021, 38, 5107-5121.	8.9	11

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91	Genetic architecture of gene regulation in Indonesian populations identifies QTLs associated with global and local ancestries. <i>American Journal of Human Genetics</i> , 2022, 109, 50-65.	6.2	11
92	Ancient Solomon Islands mtDNA: assessing Holocene settlement and the impact of European contact. <i>Journal of Archaeological Science</i> , 2010, 37, 1161-1170.	2.4	10
93	Ancient DNA and its contribution to understanding the human history of the Pacific Islands. <i>Archaeology in Oceania</i> , 2018, 53, 205-219.	0.7	10
94	Mycelial biomass and concentration of loline alkaloids driven by complex population structure in <i>Epichloa uncinata</i> and meadow fescue ( <i>Schedonorus pratensis</i> ). <i>Mycologia</i> , 2020, 112, 474-490.	1.9	9
95	Regulation of host-infection ability in the grass-symbiotic fungus <i>Epichloa festucae</i> by histone H3K9 and H3K36 methyltransferases. <i>Environmental Microbiology</i> , 2021, 23, 2116-2131.	3.8	9
96	Episodes of Diversification and Isolation in Island Southeast Asian and Near Oceanian Male Lineages. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	9
97	Exploring molecular signaling in plant-fungal symbioses using high throughput RNA sequencing. <i>Plant Signaling and Behavior</i> , 2010, 5, 1353-1358.	2.4	8
98	Bandwidth selection for kernel log-density estimation. <i>Computational Statistics and Data Analysis</i> , 2016, 103, 56-67.	1.2	8
99	Western Eurasian genetic influences in the Indonesian archipelago. <i>Quaternary International</i> , 2016, 416, 243-248.	1.5	8
100	Archaic mitochondrial DNA inserts in modern day nuclear genomes. <i>BMC Genomics</i> , 2019, 20, 1017.	2.8	8
101	Comparative genetic diversity of <i>Cryptosporidium</i> species causing human infections. <i>Parasitology</i> , 2020, 147, 1532-1537.	1.5	8
102	Comparative genomics reveals a core gene toolbox for lifestyle transitions in Hypocreales fungi. <i>Environmental Microbiology</i> , 2021, 23, 3251-3264.	3.8	8
103	An informatics consult approach for generating clinical evidence for treatment decisions. <i>BMC Medical Informatics and Decision Making</i> , 2021, 21, 281.	3.0	8
104	Reduced Virulence of an Introduced Forest Pathogen over 50 Years. <i>Microorganisms</i> , 2019, 7, 420.	3.6	6
105	Greater genetic and regulatory plasticity of retained duplicates in <i>Epichloa</i> endophytic fungi. <i>Molecular Ecology</i> , 2019, 28, 5103-5114.	3.9	6
106	Chromosome-level genomes provide insights into genome evolution, organization and size in <i>Epichloe</i> fungi. <i>Genomics</i> , 2021, 113, 4267-4275.	2.9	6
107	Reconstruction of gene innovation associated with major evolutionary transitions in the kingdom Fungi. <i>BMC Biology</i> , 2022, 20, .	3.8	6
108	Genetic continuity across a deeply divergent linguistic contact zone in North Maluku, Indonesia. <i>BMC Genetics</i> , 2011, 12, 100.	2.7	5

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109	SMARTPOP: inferring the impact of social dynamics on genetic diversity through high speed simulations. BMC Bioinformatics, 2014, 15, 175.	2.6	5
110	Draft Genome Sequences of Three Strains of <i>Geobacillus stearothermophilus</i> Isolated from a Milk Powder Manufacturing Plant. Genome Announcements, 2015, 3, .	0.8	5
111	Mitochondrial evolution in the entomopathogenic fungal genus <i>Beauveria</i> . Archives of Insect Biochemistry and Physiology, 2020, 105, e21754.	1.5	5
112	The importance and prevalence of allopolyploidy in Aotearoa New Zealand. Journal of the Royal Society of New Zealand, 2020, 50, 189-210.	1.9	5
113	Evolution of virulence in a novel family of transmissible mega-plasmids. Environmental Microbiology, 2021, 23, 5289-5304.	3.8	5
114	<i>Epichloa</i> <i>scottii</i> sp. nov., a new endophyte isolated from <i>Melica uniflora</i> is the missing ancestor of <i>Epichloa</i> <i>disjuncta</i> . IMA Fungus, 2022, 13, 2.	3.8	5
115	Reconstructing past changes in locus-specific recombination rates. BMC Genetics, 2013, 14, 11.	2.7	4
116	Opportunities for modern genetic technologies to maintain and enhance Aotearoa New Zealand's bioheritage. New Zealand Journal of Ecology, 2020, 44, .	1.1	4
117	High Frequency Haplotypes are Expected Events, not Historical Figures. F1000Research, 2015, 4, 666.	1.6	4
118	Cross-species transcriptomics identifies core regulatory changes differentiating the asymptomatic asexual and virulent sexual life cycles of grass-symbiotic <i>Epichloa</i> fungi. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
119	Genome-scale investigation of phenotypically distinct but nearly clonal <i>Trichoderma</i> strains. PeerJ, 2016, 4, e2023.	2.0	3
120	Warfare induces post-marital residence change. Journal of Theoretical Biology, 2019, 474, 52-62.	1.7	3
121	High Frequency Haplotypes are Expected Events, not Historical Figures. F1000Research, 2015, 4, 666.	1.6	3
122	Deep ancestry of collapsing networks of nomadic hunter-gatherers in Borneo. Evolutionary Human Sciences, 2022, 4, .	1.7	3
123	Chronology of natural selection in Oceanian genomes. IScience, 2022, 25, 104583.	4.1	3
124	Genetics, adaptation to environmental changes and archaic admixture in the pathogenesis of diabetes mellitus in Indigenous Australians. Reviews in Endocrine and Metabolic Disorders, 2019, 20, 321-332.	5.7	2
125	Cross-kingdom transcriptomic trends in the evolution of hybrid gene expression. Journal of Evolutionary Biology, 2022, 35, 1126-1137.	1.7	2
126	Climate Change Influenced Female Population Sizes through Time across the Indonesian Archipelago. Human Biology, 2013, 85, 135.	0.2	1



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127	A flexible theoretical representation for the temporal dynamics of structured populations as paths on polytope complexes. <i>Journal of Mathematical Biology</i> , 2015, 71, 735-766.	1.9	1
128	Draft Genome Sequence of the Filamentous Fungus <i>Penicillium paxilli</i> (ATCC 26601). <i>Genome Announcements</i> , 2015, 3, .	0.8	1
129	A different paradigm for the colonisation of Sahul. <i>Archaeology in Oceania</i> , 2020, 55, 182-191.	0.7	1
130	Characterization of Bicistronic Transcription in Budding Yeast. <i>MSystems</i> , 2021, 6, .	3.8	1
131	The secreted proteome of necrotrophic <i>Ciborinia camelliae</i> causes non-host-specific virulence. <i>Plant Pathology</i> , 0, , .	2.4	1
132	Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales. <i>Royal Society Open Science</i> , 2019, 6, 190733.	2.4	0
133	CHAPTER 4. Language and Kinship in Deep Time. , 2019, , 68-96.		0
134	Correlated Transcriptional Responses Provide Insights into the Synergy Mechanisms of the Furazolidone, Vancomycin, and Sodium Deoxycholate Triple Combination in <i>Escherichia coli</i> . <i>MSphere</i> , 2021, 6, e0062721.	2.9	0
135	Telomere-to-Telomere Genome Sequences across a Single Genus Reveal Highly Variable Chromosome Rearrangement Rates but Absolute Stasis of Chromosome Number. <i>Journal of Fungi (Basel)</i> , Tj ETQq1 1 0.784314 ngBT /Overclock 10 T		