

Murray Cox

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	<i>Epichloa</i> scottii sp. nov., a new endophyte isolated from <i>Melica uniflora</i> is the missing ancestor of <i>Epichloa</i> disjuncta. <i>IMA Fungus</i> , 2022, 13, 2.	3.8	5
3	Deep ancestry of collapsing networks of nomadic hunter-gatherers in Borneo. <i>Evolutionary Human Sciences</i> , 2022, 4, .	1.7	3
4	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
5	Cross-species transcriptomics identifies core regulatory changes differentiating the asymptomatic asexual and virulent sexual life cycles of grass-symbiotic <i>Epichloa</i> fungi. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	4
6	Reconstruction of gene innovation associated with major evolutionary transitions in the kingdom Fungi. <i>BMC Biology</i> , 2022, 20, .	3.8	6
7	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> , 2022, 9, 1075. doi:10.3390/jof9111075	0.784314	10
8	Cross-kingdom transcriptomic trends in the evolution of hybrid gene expression. <i>Journal of Evolutionary Biology</i> , 2022, 35, 1126-1137.	1.7	2
9	Chronology of natural selection in Oceanian genomes. <i>IScience</i> , 2022, 25, 104583.	4.1	3
10	Characterization of Bicistronic Transcription in Budding Yeast. <i>MSystems</i> , 2021, 6, .	3.8	1
11	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
12	Comparative genomics reveals a core gene toolbox for lifestyle transitions in Hypocreales fungi. <i>Environmental Microbiology</i> , 2021, 23, 3251-3264.	3.8	8
13	Evolution of virulence in a novel family of transmissible megaplasmids. <i>Environmental Microbiology</i> , 2021, 23, 5289-5304.	3.8	5
14	Papua New Guinean Genomes Reveal the Complex Settlement of North Sahul. <i>Molecular Biology and Evolution</i> , 2021, 38, 5107-5121.	8.9	11
15	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
16	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
17	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
18	Chromosome-level genomes provide insights into genome evolution, organization and size in <i>Epichloa</i> fungi. <i>Genomics</i> , 2021, 113, 4267-4275.	2.9	6

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19	Phylogenetic determinants of toxin gene distribution in genomes of <i>Brevibacillus laterosporus</i> . <i>Genomics</i> , 2020, 112, 1042-1053.	2.9	19
20	Chromosome-Level Reference Genome of <i>Venturia effusa</i> , Causative Agent of Pecan Scab. <i>Molecular Plant-Microbe Interactions</i> , 2020, 33, 149-152.	2.6	14
21	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
22	Comparative genetic diversity of <i>Cryptosporidium</i> species causing human infections. <i>Parasitology</i> , 2020, 147, 1532-1537.	1.5	8
23	Mitochondrial evolution in the entomopathogenic fungal genus <i>Beauveria</i> . <i>Archives of Insect Biochemistry and Physiology</i> , 2020, 105, e21754.	1.5	5
24	A different paradigm for the colonisation of Sahul. <i>Archaeology in Oceania</i> , 2020, 55, 182-191.	0.7	1
25	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
26	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
27	Papuan mitochondrial genomes and the settlement of Sahul. <i>Journal of Human Genetics</i> , 2020, 65, 875-887.	2.3	24
28	The importance and prevalence of allopolyploidy in Aotearoa New Zealand. <i>Journal of the Royal Society of New Zealand</i> , 2020, 50, 189-210.	1.9	5
29	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
30	Opportunities for modern genetic technologies to maintain and enhance Aotearoa New Zealand's bioheritage. <i>New Zealand Journal of Ecology</i> , 2020, 44, .	1.1	4
31	Genetics, adaptation to environmental changes and archaic admixture in the pathogenesis of diabetes mellitus in Indigenous Australians. <i>Reviews in Endocrine and Metabolic Disorders</i> , 2019, 20, 321-332.	5.7	2
32	Reduced Virulence of an Introduced Forest Pathogen over 50 Years. <i>Microorganisms</i> , 2019, 7, 420.	3.6	6
33	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
34	Sex-linked genetic diversity originates from persistent sociocultural processes at microgeographic scales. <i>Royal Society Open Science</i> , 2019, 6, 190733.	2.4	0
35	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
36	Breaking Free: The Genomics of Allopolyploidy-Facilitated Niche Expansion in White Clover. <i>Plant Cell</i> , 2019, 31, 1466-1487.	6.6	89

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37	Warfare induces post-marital residence change. <i>Journal of Theoretical Biology</i> , 2019, 474, 52-62.	1.7	3
38	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <i>Cell</i> , 2019, 177, 1010-1021.e32.	28.9	181
39	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
40	CHAPTER 4. Language and Kinship in Deep Time. , 2019, , 68-96.		0
41	Archaic mitochondrial DNA inserts in modern day nuclear genomes. <i>BMC Genomics</i> , 2019, 20, 1017.	2.8	8
42	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. <i>Nature Immunology</i> , 2019, 20, 1299-1310.	14.5	53
43	Evidence of Austronesian Genetic Lineages in East Africa and South Arabia: Complex Dispersal from Madagascar and Southeast Asia. <i>Genome Biology and Evolution</i> , 2019, 11, 748-758.	2.5	15
44	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
45	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
46	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
47	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
48	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
49	Human Perceptions of Megafaunal Extinction Events Revealed by Linguistic Analysis of Indigenous Oral Traditions. <i>Human Ecology</i> , 2018, 46, 461-470.	1.4	17
50	Post-marital residence patterns show lineage-specific evolution. <i>Evolution and Human Behavior</i> , 2018, 39, 594-601.	2.2	24
51	Genomic medicine must reduce, not compound, health inequities: the case for hauora-enhancing genomic resources for New Zealand. <i>New Zealand Medical Journal</i> , 2018, 131, 81-89.	0.5	13
52	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
53	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
54	Complex Patterns of Admixture across the Indonesian Archipelago. <i>Molecular Biology and Evolution</i> , 2017, 34, 2439-2452.	8.9	65

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55	Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network. <i>Scientific Reports</i> , 2017, 7, 2919.	3.3	13
56	Kinship structures create persistent channels for language transmission. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12910-12915.	7.1	18
57	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
58	Insights into the <i>Geobacillus stearothermophilus</i> species based on phylogenomic principles. <i>BMC Microbiology</i> , 2017, 17, 140.	3.3	41
59	<i>Epichloa hybrida</i> , sp. nov., an emerging model system for investigating fungal allopolyploidy. <i>Mycologia</i> , 2017, 109, 1-15.	1.9	43
60	Genome-scale investigation of phenotypically distinct but nearly clonal <i>Trichoderma</i> strains. <i>PeerJ</i> , 2016, 4, e2023.	2.0	3
61	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
62	Bandwidth selection for kernel log-density estimation. <i>Computational Statistics and Data Analysis</i> , 2016, 103, 56-67.	1.2	8
63	Genomic insights into the peopling of the Southwest Pacific. <i>Nature</i> , 2016, 538, 510-513.	27.8	262
64	Genome-wide gene expression dynamics of the fungal pathogen <i>Dothistroma septosporum</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
65	Genomic analyses inform on migration events during the peopling of Eurasia. <i>Nature</i> , 2016, 538, 238-242.	27.8	360
66	Contrasting Linguistic and Genetic Origins of the Asian Source Populations of Malagasy. <i>Scientific Reports</i> , 2016, 6, 26066.	3.3	48
67	The Case of the Missing Ancient Fungal Polyploids. <i>American Naturalist</i> , 2016, 188, 602-614.	2.1	38
68	Reconstructing Demography and Social Behavior During the Neolithic Expansion from Genomic Diversity Across Island Southeast Asia. <i>Genetics</i> , 2016, 204, 1495-1506.	2.9	12
69	Small Traditional Human Communities Sustain Genomic Diversity over Microgeographic Scales despite Linguistic Isolation. <i>Molecular Biology and Evolution</i> , 2016, 33, 2273-2284.	8.9	12
70	Western Eurasian genetic influences in the Indonesian archipelago. <i>Quaternary International</i> , 2016, 416, 243-248.	1.5	8
71	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
72	Fungal endophyte infection of ryegrass reprograms host metabolism and alters development. <i>New Phytologist</i> , 2015, 208, 1227-1240.	7.3	165

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73	Reconstructing Past Admixture Processes from Local Genomic Ancestry Using Wavelet Transformation. <i>Genetics</i> , 2015, 200, 469-481.	2.9	24
74	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
75	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
76	HyLiTE: accurate and flexible analysis of gene expression in hybrid and allopolyploid species. <i>BMC Bioinformatics</i> , 2015, 16, 8.	2.6	25
77	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
78	A recent bottleneck of Y chromosome diversity coincides with a global change in culture. <i>Genome Research</i> , 2015, 25, 459-466.	5.5	348
79	Draft Genome Sequences of Three Strains of <i>Geobacillus stearothermophilus</i> Isolated from a Milk Powder Manufacturing Plant. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
80	Draft Genome Sequence of the Filamentous Fungus <i>Penicillium paxilli</i> (ATCC 26601). <i>Genome Announcements</i> , 2015, 3, .	0.8	1
81	Relaxed Observance of Traditional Marriage Rules Allows Social Connectivity without Loss of Genetic Diversity. <i>Molecular Biology and Evolution</i> , 2015, 32, 2254-2262.	8.9	14
82	High Frequency Haplotypes are Expected Events, not Historical Figures. <i>F1000Research</i> , 2015, 4, 666.	1.6	3
83	High Frequency Haplotypes are Expected Events, not Historical Figures. <i>F1000Research</i> , 2015, 4, 666.	1.6	4
84	Isolation, contact and social behavior shaped genetic diversity in West Timor. <i>Journal of Human Genetics</i> , 2014, 59, 494-503.	2.3	17
85	Regime Shifts in Balinese <i>Subaks</i> . <i>Current Anthropology</i> , 2014, 55, 232-239.	1.6	12
86	An Interspecific Fungal Hybrid Reveals Cross-Kingdom Rules for Allopolyploid Gene Expression Patterns. <i>PLoS Genetics</i> , 2014, 10, e1004180.	3.5	68
87	Genomes of Plant-Associated Clavicipitaceae. <i>Advances in Botanical Research</i> , 2014, 70, 291-327.	1.1	28
88	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
89	SMARTPOP: inferring the impact of social dynamics on genetic diversity through high speed simulations. <i>BMC Bioinformatics</i> , 2014, 15, 175.	2.6	5
90	Reconstructing past changes in locus-specific recombination rates. <i>BMC Genetics</i> , 2013, 14, 11.	2.7	4

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91	Climate Change Influenced Female Population Sizes Through Time Across the Indonesian Archipelago. <i>Human Biology</i> , 2013, 85, 135-152.	0.2	18
92	Dothistromin genes at multiple separate loci are regulated by AflR. <i>Fungal Genetics and Biology</i> , 2013, 51, 12-20.	2.1	30
93	Marine resources in Māori oral tradition: He kai moana, he kai māte hinengaro. <i>Journal of Marine and Island Cultures</i> , 2013, 2, 59-68.	0.2	16
94	The Indonesian archipelago: an ancient genetic highway linking Asia and the Pacific. <i>Journal of Human Genetics</i> , 2013, 58, 165-173.	2.3	100
95	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the Clavicipitaceae Reveals Dynamics of Alkaloid Loci. <i>PLoS Genetics</i> , 2013, 9, e1003323.	3.5	344
96	Fragmentation of an aflatoxin-like gene cluster in a forest pathogen. <i>New Phytologist</i> , 2013, 198, 525-535.	7.3	55
97	Climate Change Influenced Female Population Sizes through Time across the Indonesian Archipelago. <i>Human Biology</i> , 2013, 85, 135.	0.2	1
98	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. <i>PLoS Genetics</i> , 2012, 8, e1003088.	3.5	226
99	A small cohort of Island Southeast Asian women founded Madagascar. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2761-2768.	2.6	79
100	The Guanine Nucleotide Exchange Factor RIC8 Regulates Conidial Germination through G β Proteins in <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2012, 7, e48026.	2.5	20
101	The Domain of the Replicators. <i>Current Anthropology</i> , 2011, 52, 105-125.	1.6	13
102	Genetic continuity across a deeply divergent linguistic contact zone in North Maluku, Indonesia. <i>BMC Genetics</i> , 2011, 12, 100.	2.7	5
103	An ongoing Austronesian expansion in Island Southeast Asia. <i>Journal of Anthropological Archaeology</i> , 2011, 30, 262-272.	1.6	48
104	What triggers grass endophytes to switch from mutualism to pathogenism?. <i>Plant Science</i> , 2011, 180, 190-195.	3.6	135
105	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
106	SolexaQA: At-a-glance quality assessment of Illumina second-generation sequencing data. <i>BMC Bioinformatics</i> , 2010, 11, 485.	2.6	1,268
107	A question of scale: Human migrations writ large and small. <i>BMC Biology</i> , 2010, 8, 98.	3.8	13
108	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

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109	The ratio of human X chromosome to autosome diversity is positively correlated with genetic distance from genes. <i>Nature Genetics</i> , 2010, 42, 830-831.	21.4	90
110	Major East-West Division Underlies Y Chromosome Stratification across Indonesia. <i>Molecular Biology and Evolution</i> , 2010, 27, 1833-1844.	8.9	133
111	Autosomal and X-linked single nucleotide polymorphisms reveal a steep Asianâ€“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
112	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
113	Disruption of Signaling in a Fungal-Grass Symbiosis Leads to Pathogenesis. <i>Plant Physiology</i> , 2010, 153, 1780-1794.	4.8	121
114	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
115	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
116	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
117	A robust budding model of Balinese water temple networks. <i>World Archaeology</i> , 2009, 41, 112-133.	1.1	28
118	Accuracy of Molecular Dating with the Rho Statistic: Deviations from Coalescent Expectations Under a Range of Demographic Models. <i>Human Biology</i> , 2009, 81, 911-933.	0.2	15
119	ORIGINAL ARTICLE: Coalescent analyses support multiple mainlandâ€“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
120	Intergenic DNA sequences from the human X chromosome reveal high rates of global gene flow. <i>BMC Genetics</i> , 2008, 9, 76.	2.7	17
121	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
122	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
123	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
124	Testing for Archaic Hominin Admixture on the X Chromosome: Model Likelihoods for the Modern Human <i>RRM2P4</i> Region From Summaries of Genealogical Topology Under the Structured Coalescent. <i>Genetics</i> , 2008, 178, 427-437.	2.9	27
125	A novel DNA sequence database for analyzing human demographic history. <i>Genome Research</i> , 2008, 18, 1354-1361.	5.5	74
126	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

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127	Sex-Biased Evolutionary Forces Shape Genomic Patterns of Human Diversity. <i>PLoS Genetics</i> , 2008, 4, e1000202.	3.5	139
128	Recombination-filtered genomic datasets by information maximization. <i>Bioinformatics</i> , 2007, 23, 1851-1853.	4.1	193
129	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
130	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
131	A Polynesian Motif on the Y Chromosome: Population Structure in Remote Oceania. <i>Human Biology</i> , 2007, 79, 525-535.	0.2	20
132	Minimal hierarchical analysis of global human Y-chromosome SNP diversity by PCR-RFLP. <i>Anthropological Science</i> , 2006, 114, 69-74.	0.4	11
133	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
134	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
135	The secreted proteome of necrotrophic <i>Ciborinia camelliae</i> causes non-host-specific virulence. <i>Plant Pathology</i> , 0, , .	2.4	1