

Adam C Eyre-Walker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/252368/publications.pdf>

Version: 2024-02-01

146
papers

15,152
citations

18482

62
h-index

22166

113
g-index

166
all docs

166
docs citations

166
times ranked

13053
citing authors

#	ARTICLE	IF	CITATIONS
1	The distribution of fitness effects of new mutations. <i>Nature Reviews Genetics</i> , 2007, 8, 610-618.	16.3	1,234
2	Adaptive protein evolution in <i>Drosophila</i> . <i>Nature</i> , 2002, 415, 1022-1024.	27.8	632
3	Variation in the mutation rate across mammalian genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 756-766.	16.3	438
4	Estimating the Rate of Adaptive Molecular Evolution in the Presence of Slightly Deleterious Mutations and Population Size Change. <i>Molecular Biology and Evolution</i> , 2009, 26, 2097-2108.	8.9	413
5	High genomic deleterious mutation rates in hominids. <i>Nature</i> , 1999, 397, 344-347.	27.8	412
6	The evolution of isochores. <i>Nature Reviews Genetics</i> , 2001, 2, 549-555.	16.3	379
7	The Distribution of Fitness Effects of New Deleterious Amino Acid Mutations in Humans. <i>Genetics</i> , 2006, 173, 891-900.	2.9	360
8	Investigation of the bottleneck leading to the domestication of maize. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 4441-4446.	7.1	359
9	Evidence of Selection upon Genomic GC-Content in Bacteria. <i>PLoS Genetics</i> , 2010, 6, e1001107.	3.5	355
10	Population size and the rate of evolution. <i>Trends in Ecology and Evolution</i> , 2014, 29, 33-41.	8.7	346
11	Joint Inference of the Distribution of Fitness Effects of Deleterious Mutations and Population Demography Based on Nucleotide Polymorphism Frequencies. <i>Genetics</i> , 2007, 177, 2251-2261.	2.9	336
12	Synonymous Codon Usage in <i>Escherichia coli</i> : Selection for Translational Accuracy. <i>Molecular Biology and Evolution</i> , 2006, 24, 374-381.	8.9	290
13	The genomic rate of adaptive evolution. <i>Trends in Ecology and Evolution</i> , 2006, 21, 569-575.	8.7	271
14	Linkage Disequilibrium and Recombination in Hominid Mitochondrial DNA. <i>Science</i> , 1999, 286, 2524-2525.	12.6	270
15	Deleterious Mutations and the Evolution of Sex. <i>Science</i> , 2000, 290, 331-333.	12.6	249
16	Genome Wide Analyses Reveal Little Evidence for Adaptive Evolution in Many Plant Species. <i>Molecular Biology and Evolution</i> , 2010, 27, 1822-1832.	8.9	227
17	Estimation of the Neutrality Index. <i>Molecular Biology and Evolution</i> , 2011, 28, 63-70.	8.9	224
18	Direct Measure of the De Novo Mutation Rate in Autism and Schizophrenia Cohorts. <i>American Journal of Human Genetics</i> , 2010, 87, 316-324.	6.2	222

#	ARTICLE	IF	CITATIONS
19	Genetic architecture of a complex trait and its implications for fitness and genome-wide association studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1752-1756.	7.1	222
20	Changing Effective Population Size and the McDonald-Kreitman Test. <i>Genetics</i> , 2002, 162, 2017-2024.	2.9	221
21	The Genomic Rate of Adaptive Amino Acid Substitution in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 1350-1360.	8.9	214
22	Recombination and mammalian genome evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1993, 252, 237-243.	2.6	211
23	Synonymous codon bias is related to gene length in <i>Escherichia coli</i> : selection for translational accuracy?. <i>Molecular Biology and Evolution</i> , 1996, 13, 864-872.	8.9	208
24	Translational selection and molecular evolution. <i>Current Opinion in Genetics and Development</i> , 1998, 8, 688-693.	3.3	194
25	Quantifying the Slightly Deleterious Mutation Model of Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2002, 19, 2142-2149.	8.9	191
26	The Assessment of Science: The Relative Merits of Post-Publication Review, the Impact Factor, and the Number of Citations. <i>PLoS Biology</i> , 2013, 11, e1001675.	5.6	191
27	The distribution of bacterial doubling times in the wild. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20180789.	2.6	182
28	A Broad Survey of Recombination in Animal Mitochondria. <i>Molecular Biology and Evolution</i> , 2004, 21, 2319-2325.	8.9	178
29	Evidence for Widespread Degradation of Gene Control Regions in Hominid Genomes. <i>PLoS Biology</i> , 2005, 3, e42.	5.6	178
30	Evidence of Selection on Silent Site Base Composition in Mammals: Potential Implications for the Evolution of Isochores and Junk DNA. <i>Genetics</i> , 1999, 152, 675-683.	2.9	177
31	The McDonald-Kreitman Test and Slightly Deleterious Mutations. <i>Molecular Biology and Evolution</i> , 2008, 25, 1007-1015.	8.9	167
32	Reduced synonymous substitution rate at the start of enterobacterial genes. <i>Nucleic Acids Research</i> , 1993, 21, 4599-4603.	14.5	165
33	The Effect of Variation in the Effective Population Size on the Rate of Adaptive Molecular Evolution in Eukaryotes. <i>Genome Biology and Evolution</i> , 2012, 4, 658-667.	2.5	156
34	Terumi Mukai and the Riddle of Deleterious Mutation Rates. <i>Genetics</i> , 1999, 153, 515-523.	2.9	154
35	Rates of Lateral Gene Transfer in Prokaryotes: High but Why?. <i>Trends in Microbiology</i> , 2015, 23, 598-605.	7.7	153
36	How clonal are human mitochondria?. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 477-483.	2.6	152

#	ARTICLE	IF	CITATIONS
37	The Rate of Adaptive Evolution in Enteric Bacteria. <i>Molecular Biology and Evolution</i> , 2006, 23, 1348-1356.	8.9	146
38	Hundreds of putatively functional small open reading frames in <i>Drosophila</i> . <i>Genome Biology</i> , 2011, 12, R118.	9.6	143
39	Evidence for Pervasive Adaptive Protein Evolution in Wild Mice. <i>PLoS Genetics</i> , 2010, 6, e1000825.	3.5	123
40	A Method for Inferring the Rate of Occurrence and Fitness Effects of Advantageous Mutations. <i>Genetics</i> , 2011, 189, 1427-1437.	2.9	111
41	Problems with Parsimony in Sequences of Biased Base Composition. <i>Journal of Molecular Evolution</i> , 1998, 47, 686-690.	1.8	110
42	The rate of adaptive evolution in animal mitochondria. <i>Molecular Ecology</i> , 2016, 25, 67-78.	3.9	109
43	Evidence for Variation in the Effective Population Size of Animal Mitochondrial DNA. <i>PLoS ONE</i> , 2009, 4, e4396.	2.5	108
44	Correlated rates of synonymous site evolution across plant genomes. <i>Molecular Biology and Evolution</i> , 1997, 14, 455-460.	8.9	106
45	An analysis of codon usage in mammals: Selection or mutation bias?. <i>Journal of Molecular Evolution</i> , 1991, 33, 442-449.	1.8	105
46	Cryptic Variation in the Human Mutation Rate. <i>PLoS Biology</i> , 2009, 7, e1000027.	5.6	101
47	Patterns of Evolutionary Constraints in Intronic and Intergenic DNA of <i>Drosophila</i> . <i>Genome Research</i> , 2004, 14, 273-279.	5.5	99
48	Human disease genes: patterns and predictions. <i>Gene</i> , 2003, 318, 169-175.	2.2	97
49	Quantifying the Variation in the Effective Population Size Within a Genome. <i>Genetics</i> , 2011, 189, 1389-1402.	2.9	91
50	An improved genome of the model marine alga <i>Ostreococcus tauri</i> unfolds by assessing Illumina de novo assemblies. <i>BMC Genomics</i> , 2014, 15, 1103.	2.8	90
51	Questioning Evidence for Recombination in Human Mitochondrial DNA. <i>Science</i> , 2000, 288, 1931-1931.	12.6	88
52	A new perspective on isochore evolution. <i>Gene</i> , 2006, 385, 71-74.	2.2	88
53	What can we learn about the distribution of fitness effects of new mutations from DNA sequence data?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 1187-1193.	4.0	88
54	Estimating the distribution of fitness effects from DNA sequence data: Implications for the molecular clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10335-10340.	7.1	83

#	ARTICLE	IF	CITATIONS
55	Synonymous Codon Bias Is Not Caused by Mutation Bias in G+C-Rich Genes in Humans. <i>Molecular Biology and Evolution</i> , 2001, 18, 982-986.	8.9	79
56	Synonymous substitution rates in enterobacteria.. <i>Genetics</i> , 1995, 140, 1407-1412.	2.9	79
57	The other side of the nearly neutral theory, evidence of slightly advantageous back-mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16992-16997.	7.1	77
58	The large-scale distribution of somatic mutations in cancer genomes. <i>Human Mutation</i> , 2012, 33, 136-143.	2.5	77
59	Adaptive Evolution Is Substantially Impeded by Hillâ€™Robertson Interference in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 442-455.	8.9	77
60	The evolution of courtship behaviors through the origination of a new gene in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7478-7483.	7.1	76
61	Human Triallelic Sites: Evidence for a New Mutational Mechanism?. <i>Genetics</i> , 2010, 184, 233-241.	2.9	76
62	The Problem of Counting Sites in the Estimation of the Synonymous and Nonsynonymous Substitution Rates: Implications for the Correlation Between the Synonymous Substitution Rate and Codon Usage Bias. <i>Genetics</i> , 2003, 165, 1587-1597.	2.9	75
63	Divergence and Polymorphism Under the Nearly Neutral Theory of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2008, 67, 418-426.	1.8	74
64	Population genomics of picophytoplankton unveils novel chromosome hypervariability. <i>Science Advances</i> , 2017, 3, e1700239.	10.3	73
65	Large scale variation in the rate of germ-line de novo mutation, base composition, divergence and diversity in humans. <i>PLoS Genetics</i> , 2018, 14, e1007254.	3.5	73
66	Does Human mtDNA Recombine?. <i>Journal of Molecular Evolution</i> , 2001, 53, 430-435.	1.8	67
67	Mutation pressure, natural selection, and the evolution of base composition in <i>Drosophila</i> . <i>Genetica</i> , 1998, 102/103, 49-60.	1.1	65
68	Mitochondrial Replacement Therapy: Are Mito-nuclear Interactions Likely To Be a Problem?. <i>Genetics</i> , 2017, 205, 1365-1372.	2.9	65
69	Spontaneous Mutation Rate in the Smallest Photosynthetic Eukaryotes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1770-1779.	8.9	65
70	The Decline of Isochores in Mammals: An Assessment of the GC Content Variation Along the Mammalian Phylogeny. <i>Journal of Molecular Evolution</i> , 2004, 58, 653-660.	1.8	63
71	Mitochondrial Steve: paternal inheritance of mitochondria in humans. <i>Trends in Ecology and Evolution</i> , 2003, 18, 2-4.	8.7	62
72	How and Why DNA Barcodes Underestimate the Diversity of Microbial Eukaryotes. <i>PLoS ONE</i> , 2011, 6, e16342.	2.5	62

#	ARTICLE	IF	CITATIONS
73	Recommendations for improving statistical inference in population genomics. <i>PLoS Biology</i> , 2022, 20, e3001669.	5.6	60
74	Are pangenomes adaptive or not?. <i>Nature Microbiology</i> , 2017, 2, 1576-1576.	13.3	59
75	The Evolution of Isochores: Evidence From SNP Frequency Distributions. <i>Genetics</i> , 2002, 162, 1805-1810.	2.9	56
76	Differentiating Between Selection and Mutation Bias. <i>Genetics</i> , 1997, 147, 1983-1987.	2.9	55
77	An investigation of the variation in the transition bias among various animal mitochondrial DNA. <i>Gene</i> , 2005, 355, 58-66.	2.2	53
78	A Problem With the Correlation Coefficient as a Measure of Gene Expression Divergence. <i>Genetics</i> , 2009, 183, 1597-1600.	2.9	53
79	A Resolution of the Mutation Load Paradox in Humans. <i>Genetics</i> , 2012, 191, 1321-1330.	2.9	50
80	A reanalysis of the indirect evidence for recombination in human mitochondrial DNA. <i>Heredity</i> , 2004, 92, 282-288.	2.6	48
81	Evidence that both G + C rich and G + C poor isochores are replicated early and late in the cell cycle. <i>Nucleic Acids Research</i> , 1992, 20, 1497-1501.	14.5	41
82	The close proximity of <i>Escherichia coli</i> genes: Consequences for stop codon and synonymous codon use. <i>Journal of Molecular Evolution</i> , 1996, 42, 73-78.	1.8	41
83	Research groups: How big should they be?. <i>PeerJ</i> , 2015, 3, e989.	2.0	41
84	The muddle about mutations. <i>Nature</i> , 1997, 387, 135-136.	27.8	39
85	Do mitochondria recombine in humans?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2000, 355, 1573-1580.	4.0	39
86	The Positive Correlation between dN/dS and dS in Mammals Is Due to Runs of Adjacent Substitutions. <i>Molecular Biology and Evolution</i> , 2011, 28, 1371-1380.	8.9	38
87	The Correlation Between Linkage Disequilibrium and Distance: Implications for Recombination in Hominid Mitochondria. <i>Molecular Biology and Evolution</i> , 2001, 18, 2132-2135.	8.9	36
88	Transposable Elements: Insertion Pattern and Impact on Gene Expression Evolution in Hominids. <i>Molecular Biology and Evolution</i> , 2010, 27, 1955-1962.	8.9	36
89	Estimating the Rate of Adaptive Molecular Evolution When the Evolutionary Divergence Between Species is Small. <i>Journal of Molecular Evolution</i> , 2012, 74, 61-68.	1.8	34
90	Analysis of the Phylogenetic Distribution of Isochores in Vertebrates and a Test of the Thermal Stability Hypothesis. <i>Journal of Molecular Evolution</i> , 2002, 55, 356-363.	1.8	33

#	ARTICLE	IF	CITATIONS
91	Partitioning the Variation in Mammalian Substitution Rates. <i>Molecular Biology and Evolution</i> , 2003, 20, 10-17.	8.9	33
92	Variation in synonymous codon use and DNA polymorphism within the <i>Drosophila</i> genome. <i>Journal of Evolutionary Biology</i> , 2006, 19, 1-11.	1.7	33
93	Molecular Evolutionary Consequences of Island Colonization. <i>Genome Biology and Evolution</i> , 2016, 8, 1876-1888.	2.5	33
94	The Effect of Transposable Element Insertions on Gene Expression Evolution in Rodents. <i>PLoS ONE</i> , 2009, 4, e4321.	2.5	32
95	Nearly Neutral Evolution across the <i>Drosophila melanogaster</i> Genome. <i>Molecular Biology and Evolution</i> , 2018, 35, 2685-2694.	8.9	32
96	Patterns of Base Composition Within the Genes of <i>Drosophila melanogaster</i> . <i>Journal of Molecular Evolution</i> , 1998, 46, 534-541.	1.8	31
97	The Accumulation of Gene Regulation Through Time. <i>Genome Biology and Evolution</i> , 2011, 3, 667-673.	2.5	31
98	Investigating Evolutionary Rate Variation in Bacteria. <i>Journal of Molecular Evolution</i> , 2019, 87, 317-326.	1.8	31
99	DNA mismatch repair and synonymous codon evolution in mammals.. <i>Molecular Biology and Evolution</i> , 1994, 11, 88-98.	8.9	29
100	DNA sequence diversity and the efficiency of natural selection in animal mitochondrial DNA. <i>Heredity</i> , 2017, 118, 88-95.	2.6	28
101	On the prospect of achieving accurate joint estimation of selection with population history. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	28
102	Why Are Translationally Sub-Optimal Synonymous Codons Used in <i>Escherichia coli</i> ?. <i>Journal of Molecular Evolution</i> , 2001, 53, 225-236.	1.8	25
103	The Genomic Distribution and Local Context of Coincident SNPs in Human and Chimpanzee. <i>Genome Biology and Evolution</i> , 2010, 2, 547-557.	2.5	25
104	Reply to Macaulay et al. (1999): mitochondrial DNA recombination-reasons to panic. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 2041-2042.	2.6	20
105	The Compositional Evolution of the Murid Genome. <i>Journal of Molecular Evolution</i> , 2002, 55, 197-201.	1.8	20
106	Evolutionary genetics: Direct evidence of recombination in human mitochondrial DNA. <i>Heredity</i> , 2004, 93, 321-321.	2.6	20
107	Organellar Inheritance in the Green Lineage: Insights from <i>Ostreococcus tauri</i> . <i>Genome Biology and Evolution</i> , 2013, 5, 1503-1511.	2.5	20
108	The comparative population genetics of <i>Neisseria meningitidis</i> and <i>Neisseria gonorrhoeae</i> . <i>PeerJ</i> , 2019, 7, e7216.	2.0	20

#	ARTICLE	IF	CITATIONS
109	The distance between <i>Escherichia coli</i> genes is related to gene expression levels. <i>Journal of Bacteriology</i> , 1995, 177, 5368-5369.	2.2	18
110	Fluctuating Selection Models and McDonald-Kreitman Type Analyses. <i>PLoS ONE</i> , 2014, 9, e84540.	2.5	18
111	How Much of the Variation in the Mutation Rate Along the Human Genome Can Be Explained?. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1667-1670.	1.8	18
112	Impact of Mutation Rate and Selection at Linked Sites on DNA Variation across the Genomes of Humans and Other Homininae. <i>Genome Biology and Evolution</i> , 2020, 12, 3550-3561.	2.5	18
113	Extensive Variation in the Mutation Rate Between and Within Human Genes Associated with Mendelian Disease. <i>Human Mutation</i> , 2016, 37, 488-494.	2.5	17
114	Nucleotide Substitution Rate Estimation in Enterobacteria: Approximate and Maximum-Likelihood Methods Lead to Similar Conclusions. <i>Molecular Biology and Evolution</i> , 2001, 18, 2124-2126.	8.9	15
115	The Excess of Small Inverted Repeats in Prokaryotes. <i>Journal of Molecular Evolution</i> , 2008, 67, 291-300.	1.8	15
116	A Selection Index for Gene Expression Evolution and Its Application to the Divergence between Humans and Chimpanzees. <i>PLoS ONE</i> , 2012, 7, e34935.	2.5	15
117	EVOLUTION: Enhanced: Size Does Not Matter for Mitochondrial DNA. <i>Science</i> , 2006, 312, 537-538.	12.6	14
118	Does Adaptive Protein Evolution Proceed by Large or Small Steps at the Amino Acid Level?. <i>Molecular Biology and Evolution</i> , 2019, 36, 990-998.	8.9	14
119	Fitness Effects of Spontaneous Mutations in Picoeukaryotic Marine Green Algae. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2063-2071.	1.8	13
120	Mitochondrial DNA Sequence Diversity in Mammals: A Correlation between the Effective and Census Population Sizes. <i>Genome Biology and Evolution</i> , 2020, 12, 2441-2449.	2.5	13
121	Response to Kondrashov. <i>Trends in Genetics</i> , 2001, 17, 77-78.	6.7	11
122	A Dissection of Volatility in Yeast. <i>Molecular Biology and Evolution</i> , 2005, 22, 2022-2026.	8.9	10
123	The role of DNA replication and isochores in generating mutation and silent substitution rate variance in mammals. <i>Genetical Research</i> , 1992, 60, 61-67.	0.9	9
124	Why Are Young and Old Repetitive Elements Distributed Differently in the Human Genome?. <i>Journal of Molecular Evolution</i> , 2005, 60, 290-296.	1.8	9
125	ODoSE: A Webserver for Genome-Wide Calculation of Adaptive Divergence in Prokaryotes. <i>PLoS ONE</i> , 2013, 8, e62447.	2.5	9
126	The Role of Mutation Rate Variation and Genetic Diversity in the Architecture of Human Disease. <i>PLoS ONE</i> , 2014, 9, e90166.	2.5	9

#	ARTICLE	IF	CITATIONS
127	The effect of constraint on the rate of evolution in neutral models with biased mutation.. <i>Genetics</i> , 1992, 131, 233-234.	2.9	8
128	Mutation pressure, natural selection, and the evolution of base composition in <i>Drosophila</i> . <i>Contemporary Issues in Genetics and Evolution</i> , 1998, , 49-60.	0.9	7
129	Synonymous substitutions are clustered in enterobacterial genes. <i>Journal of Molecular Evolution</i> , 1994, 39, 448-51.	1.8	6
130	Evolutionary genomics: reading the bands. <i>BioEssays</i> , 2000, 22, 105-107.	2.5	6
131	Understanding the Degradation of Hominid Gene Control. <i>PLoS Computational Biology</i> , 2006, 2, e19.	3.2	6
132	The outstanding scientist, R.A. Fisher: his views on eugenics and race. <i>Heredity</i> , 2021, 126, 565-576.	2.6	6
133	Are sites with multiple single nucleotide variants in cancer genomes a consequence of drivers, hypermutable sites or sequencing errors?. <i>PeerJ</i> , 2016, 4, e2391.	2.0	6
134	A Test of Whether Selection Maintains Isochores Using Sites Polymorphic for Alu and L1 Element Insertions. <i>Genetics</i> , 2002, 160, 815-817.	2.9	6
135	Searching for Sequence Directed Mutagenesis in Eukaryotes. <i>Journal of Molecular Evolution</i> , 2007, 64, 1-3.	1.8	5
136	A new test suggests hundreds of amino acid polymorphisms in humans are subject to balancing selection. <i>PLoS Biology</i> , 2022, 20, e3001645.	5.6	5
137	Does very short patch (VSP) repair efficiency vary in relation to gene expression levels?. <i>Journal of Molecular Evolution</i> , 1995, 40, 705-706.	1.8	4
138	A Test of Amino Acid Reversibility. <i>Journal of Molecular Evolution</i> , 2001, 52, 467-469.	1.8	3
139	Mitochondrial replacement and its effects on human health. <i>Human Reproduction Update</i> , 2019, 25, 392-394.	10.8	3
140	Changing Population Size in McDonaldâ€™Kreitman Style Analyses: Artifactual Correlations and Adaptive Evolution between Humans and Chimpanzees. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
141	Patterns of selection in the evolution of a transposable element. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	3
142	Evolutionary genomics. <i>Trends in Ecology and Evolution</i> , 1999, 14, 176.	8.7	2
143	Signatures of selection on mitonuclear integrated genes uncover hidden mitogenomic variation in fur seals. <i>Genome Biology and Evolution</i> , 0, , .	2.5	2
144	Editorial. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	1

#	ARTICLE	IF	CITATIONS
145	Editorial. <i>Genome Biology and Evolution</i> , 2019, 11, 1958-1958.	2.5	0
146	Factors That Affect the Rates of Adaptive and Nonadaptive Evolution at the Gene Level in Humans and Chimpanzees. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	0