

Gavin A Huttley

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

56,016
citations

125106

35
h-index

111975

67
g-index

90
all docs

90
docs citations

90
times ranked

68664
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
3	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	4.9	3,159
4	Genetic Restriction of HIV-1 Infection and Progression to AIDS by a Deletion Allele of the <i>CCR5</i> Structural Gene. <i>Science</i> , 1996, 273, 1856-1862.	6.0	2,365
5	Contrasting Genetic Influence of <i>CCR2</i> and <i>CCR5</i> Variants on HIV-1 Infection and Disease Progression. <i>Science</i> , 1997, 277, 959-965.	6.0	860
6	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
7	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
8	Expansion of circulating T cells resembling follicular helper T cells is a fixed phenotype that identifies a subset of severe systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2010, 62, 234-244.	6.7	593
9	Dating the Origin of the <i>CCR5-Δ32</i> AIDS-Resistance Allele by the Coalescence of Haplotypes. <i>American Journal of Human Genetics</i> , 1998, 62, 1507-1515.	2.6	507
10	PyEvolve: a toolkit for statistical modelling of molecular evolution. <i>BMC Bioinformatics</i> , 2004, 5, 1.	1.2	424
11	Loss of <i>ACTN3</i> gene function alters mouse muscle metabolism and shows evidence of positive selection in humans. <i>Nature Genetics</i> , 2007, 39, 1261-1265.	9.4	278
12	Mitochondrial DNA sequences in ancient Australians: Implications for modern human origins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 537-542.	3.3	204
13	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.	13.9	170
14	A Scan for Linkage Disequilibrium Across the Human Genome. <i>Genetics</i> , 1999, 152, 1711-1722.	1.2	158
15	Adaptive evolution of the tumour suppressor <i>BRCA1</i> in humans and chimpanzees. <i>Nature Genetics</i> , 2000, 25, 410-413.	9.4	153
16	<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.	1.8	126
17	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018, 3, 934.	2.0	116
18	Evolution of the chalcone synthase gene family in the genus <i>Ipomoea</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 3338-3342.	3.3	103

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19	Histone H2A.Z inheritance during the cell cycle and its impact on promoter organization and dynamics. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1076-1083.	3.6	97
20	CCR2 chemokine receptor and AIDS progression. <i>Nature Medicine</i> , 1997, 3, 1052-1053.	15.2	96
21	A unique H2A histone variant occupies the transcriptional start site of active genes. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 25-30.	3.6	91
22	Modelling and bioinformatics studies of the human Kappa-class glutathione transferase predict a novel third glutathione transferase family with similarity to prokaryotic 2-hydroxychromene-2-carboxylate isomerases. <i>Biochemical Journal</i> , 2004, 379, 541-552.	1.7	89
23	Dynamic evolution of venom proteins in squamate reptiles. <i>Nature Communications</i> , 2012, 3, 1066.	5.8	86
24	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019, 10, 4643.	5.8	86
25	Infection with a Virulent Strain of <i>Wolbachia</i> Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito <i>Aedes aegypti</i> . <i>PLoS ONE</i> , 2013, 8, e66482.	1.1	57
26	Comparative genomics reveals the distinct evolutionary trajectories of the robust and complex coral lineages. <i>Genome Biology</i> , 2018, 19, 175.	3.8	57
27	The PHF21B gene is associated with major depression and modulates the stress response. <i>Molecular Psychiatry</i> , 2017, 22, 1015-1025.	4.1	56
28	The "Naked Coral" Hypothesis Revisited " Evidence for and Against Scleractinian Monophyly. <i>PLoS ONE</i> , 2014, 9, e94774.	1.1	50
29	Rates of Genome Evolution and Branching Order from Whole Genome Analysis. <i>Molecular Biology and Evolution</i> , 2007, 24, 1722-1730.	3.5	45
30	How Important Is DNA Replication for Mutagenesis?. <i>Molecular Biology and Evolution</i> , 2000, 17, 929-937.	3.5	44
31	Estimates of the Effect of Natural Selection on Protein-Coding Content. <i>Molecular Biology and Evolution</i> , 2010, 27, 726-734.	3.5	40
32	The human melanocortin-1 receptor locus: analysis of transcription unit, locus polymorphism and haplotype evolution. <i>Gene</i> , 2001, 281, 81-94.	1.0	38
33	Association of polymorphisms of the estrogen receptor gene with anxiety-related traits in children and adolescents: A longitudinal study. <i>American Journal of Medical Genetics Part A</i> , 2002, 114, 169-176.	2.4	38
34	Modeling the Impact of DNA Methylation on the Evolution of BRCA1 in Mammals. <i>Molecular Biology and Evolution</i> , 2004, 21, 1760-1768.	3.5	36
35	RCPdb: An evolutionary classification and codon usage database for repeat-containing proteins. <i>Genome Research</i> , 2007, 17, 1118-1127.	2.4	36
36	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	1.7	35

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37	Evidence that Localized Variation in Primate Sequence Divergence Arises from an Influence of Nucleosome Placement on DNA Repair. <i>Molecular Biology and Evolution</i> , 2010, 27, 637-649.	3.5	31
38	Novel and rare functional genomic variants in multiple autoimmune syndrome and Sjögren's syndrome. <i>Journal of Translational Medicine</i> , 2015, 13, 173.	1.8	30
39	CCR5-Δ32 gene deletion in HIV-1 infected patients. <i>Lancet, The</i> , 1997, 350, 741.	6.3	28
40	Statistical Methods for Identifying Sequence Motifs Affecting Point Mutations. <i>Genetics</i> , 2017, 205, 843-856.	1.2	27
41	Nucleotide polymorphism in the chalcone synthase gene locus and evolution of the chalcone synthase multigene family of common morning glory <i>Ipomoea purpurea</i> . <i>Molecular Ecology</i> , 1997, 6, 549-558.	2.0	25
42	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. <i>BMC Evolutionary Biology</i> , 2008, 8, 327.	3.2	25
43	Exploiting CpG Hypermethylability to Identify Phenotypically Significant Variation Within Human Protein-Coding Genes. <i>Genome Biology and Evolution</i> , 2011, 3, 938-949.	1.1	21
44	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen <i>Scedosporium aurantiacum</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	21
45	Whole Exome Sequencing of Extreme Morbid Obesity Patients: Translational Implications for Obesity and Related Disorders. <i>Genes</i> , 2014, 5, 709-725.	1.0	19
46	Pitfalls of the most commonly used models of context dependent substitution. <i>Biology Direct</i> , 2008, 3, 52.	1.9	18
47	Transcriptome Sequencing of Two Phenotypic Mosaic Eucalyptus Trees Reveals Large Scale Transcriptome Re-Modelling. <i>PLoS ONE</i> , 2015, 10, e0123226.	1.1	18
48	Genetic Distance for a General Non-Stationary Markov Substitution Process. <i>Systematic Biology</i> , 2015, 64, 281-293.	2.7	16
49	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	1.7	16
50	Genetic Diversity in the Common Morning Glory. <i>Plant Species Biology</i> , 1996, 11, 41-50.	0.6	15
51	Statistical methods for detecting periodic fragments in DNA sequence data. <i>Biology Direct</i> , 2011, 6, 21.	1.9	12
52	The Embedding Problem for Markov Models of Nucleotide Substitution. <i>PLoS ONE</i> , 2013, 8, e69187.	1.1	12
53	Molecular evolutionary characterization of an Activator (Ac)-like transposable element sequence from pearl millet (<i>Pennisetum glaucum</i>) (Poaceae). <i>Genetica</i> , 1994, 92, 77-89.	0.5	10
54	The Role of DNA Methylation in Genome Defense in Cnidaria and Other Invertebrates. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10

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55	Standard Codon Substitution Models Overestimate Purifying Selection for Non-Stationary Data. <i>Genome Biology and Evolution</i> , 2017, 9, evw308.	1.1	9
56	Vestige: maximum likelihood phylogenetic footprinting. <i>BMC Bioinformatics</i> , 2005, 6, 130.	1.2	8
57	Comparison of methods for estimating the nucleotide substitution matrix. <i>BMC Bioinformatics</i> , 2008, 9, 511.	1.2	8
58	Folding behavior of four silks of giant honey bee reflects the evolutionary conservation of aculeate silk proteins. <i>Insect Biochemistry and Molecular Biology</i> , 2015, 59, 72-79.	1.2	8
59	Quantifying Influences on Intragenomic Mutation Rate. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2641-2652.	0.8	7
60	Machine Learning Techniques for Classifying the Mutagenic Origins of Point Mutations. <i>Genetics</i> , 2020, 215, 25-40.	1.2	7
61	Lake Mungo 3: A response to recent critiques. <i>Archaeology in Oceania</i> , 2001, 36, 170-174.	0.3	6
62	Pathological rate matrices: from primates to pathogens. <i>BMC Bioinformatics</i> , 2008, 9, 550.	1.2	6
63	A comparison of periodicity profile methods for sequence analysis. , 2012, , .		6
64	Regional Context in the Alignment of Biological Sequence Pairs. <i>Journal of Molecular Evolution</i> , 2011, 72, 147-159.	0.8	5
65	Do genomic datasets resolve the correct relationship among the placental, marsupial and monotreme lineages?. <i>Australian Journal of Zoology</i> , 2009, 57, 167.	0.6	5
66	Did aculeate silk evolve as an antifouling material?. <i>PLoS ONE</i> , 2018, 13, e0203948.	1.1	3
67	A PROBABILISTIC METHOD TO IDENTIFY COMPENSATORY SUBSTITUTIONS FOR PATHOGENIC MUTATIONS. , 2007, , .		1
68	NON-REPLICABILITY OF DISEASE GENE RESULTS: A MODELLING PERSPECTIVE. , 2002, , .		0
69	Robust estimation of natural selection using parametric codon models. , 2012, , 111-125.		0