Gavin A Huttley

List of Publications by Year
in descending order

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	The Role of DNA Methylation in Genome Defense in Cnidaria and Other Invertebrates. Molecular Biology and Evolution, 2022, 39, .	3.5	10
2	Quantifying Influences on Intragenomic Mutation Rate. G3: Genes, Genomes, Genetics, 2020, 10, 2641-2652.	0.8	7
3	Machine Learning Techniques for Classifying the Mutagenic Origins of Point Mutations. Genetics, 2020, 215, 25-40.	1.2	7
4	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. MSystems, 2020, 5, .	1.7	16
5	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
6	Species abundance information improves sequence taxonomy classification accuracy. Nature Communications, 2019, 10, 4643.	5.8	86
7	redbiom: a Rapid Sample Discovery and Feature Characterization System. MSystems, 2019, 4, .	1.7	35
8	Did aculeate silk evolve as an antifouling material?. PLoS ONE, 2018, 13, e0203948.	1.1	3
9	Comparative genomics reveals the distinct evolutionary trajectories of the robust and complex coral lineages. Genome Biology, 2018, 19, 175.	3.8	57
10	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2â€™s q2-feature-classifier plugin. Microbiome, 2018, 6, 90.	4.9	3,159
11	q2-sample-classifier: machine-learning tools for microbiome classification and regression. Journal of Open Source Software, 2018, 3, 934.	2.0	116
12	Standard Codon Substitution Models Overestimate Purifying Selection for Non-Stationary Data. Genome Biology and Evolution, 2017, 9, evw308.	1.1	9
13	Statistical Methods for Identifying Sequence Motifs Affecting Point Mutations. Genetics, 2017, 205, 843-856.	1.2	27
14	The PHF21B gene is associated with major depression and modulates the stress response. Molecular Psychiatry, 2017, 22, 1015-1025.	4.1	56
15	Novel and rare functional genomic variants in multiple autoimmune syndrome and SjÃ¶grenâ€™s syndrome. Journal of Translational Medicine, 2015, 13, 173.	1.8	30
16	Draft Genome of Australian Environmental Strain WM 09.24 of the Opportunistic Human Pathogen Scedosporium aurantiacum. Genome Announcements, 2015, 3, .	0.8	21
17	Transcriptome Sequencing of Two Phenotypic Mosaic Eucalyptus Trees Reveals Large Scale Transcriptome Re-Modelling. PLoS ONE, 2015, 10, e0123226.	1.1	18
18	Genetic Distance for a General Non-Stationary Markov Substitution Process. Systematic Biology, 2015, 64, 281-293.	2.7	16

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19	Folding behavior of four silks of giant honey bee reflects the evolutionary conservation of aculeate silk proteins. Insect Biochemistry and Molecular Biology, 2015, 59, 72-79.	1.2	8
20	The â€œNaked Coralâ€•Hypothesis Revisited â€“ Evidence for and Against Scleractinian Monophyly. PLoS ONE, 2014, 9, e94774.	1.1	50
21	Whole Exome Sequencing of Extreme Morbid Obesity Patients: Translational Implications for Obesity and Related Disorders. Genes, 2014, 5, 709-725.	1.0	19
22	Cryptococcus gattii in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. MBio, 2014, 5, e01464-14.	1.8	126
23	The Embedding Problem for Markov Models of Nucleotide Substitution. PLoS ONE, 2013, 8, e69187.	1.1	12
24	Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti. PLoS ONE, 2013, 8, e66482.	1.1	57
25	Histone H2A.Z inheritance during the cell cycle and its impact on promoter organization and dynamics. Nature Structural and Molecular Biology, 2012, 19, 1076-1083.	3.6	97
26	A comparison of periodicity profile methods for sequence analysis. , 2012, , .		6
27	A unique H2A histone variant occupies the transcriptional start site of active genes. Nature Structural and Molecular Biology, 2012, 19, 25-30.	3.6	91
28	Dynamic evolution of venom proteins in squamate reptiles. Nature Communications, 2012, 3, 1066.	5.8	86
29	Robust estimation of natural selection using parametric codon models. , 2012, , 111-125.		0
30	Regional Context in the Alignment of Biological Sequence Pairs. Journal of Molecular Evolution, 2011, 72, 147-159.	0.8	5
31	Statistical methods for detecting periodic fragments in DNA sequence data. Biology Direct, 2011, 6, 21.	1.9	12
32	Exploiting CpG Hypermutability to Identify Phenotypically Significant Variation Within Human Protein-Coding Genes. Genome Biology and Evolution, 2011, 3, 938-949.	1.1	21
33	Expansion of circulating T cells resembling follicular helper T cells is a fixed phenotype that identifies a subset of severe systemic lupus erythematosus. Arthritis and Rheumatism, 2010, 62, 234-244.	6.7	593
34	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	9.0	31,818
35	Estimates of the Effect of Natural Selection on Protein-Coding Content. Molecular Biology and Evolution, 2010, 27, 726-734.	3.5	40
36	Evidence that Localized Variation in Primate Sequence Divergence Arises from an Influence of Nucleosome Placement on DNA Repair. Molecular Biology and Evolution, 2010, 27, 637-649.	3.5	31

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37	Do genomic datasets resolve the correct relationship among the placental, marsupial and monotreme lineages?. Australian Journal of Zoology, 2009, 57, 167.	0.6	5
38	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
39	Comparison of methods for estimating the nucleotide substitution matrix. BMC Bioinformatics, 2008, 9, 511.	1.2	8
40	Pathological rate matrices: from primates to pathogens. BMC Bioinformatics, 2008, 9, 550.	1.2	6
41	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. BMC Evolutionary Biology, 2008, 8, 327.	3.2	25
42	Pitfalls of the most commonly used models of context dependent substitution. Biology Direct, 2008, 3, 52.	1.9	18
43	Rates of Genome Evolution and Branching Order from Whole Genome Analysis. Molecular Biology and Evolution, 2007, 24, 1722-1730.	3.5	45
44	RCPdb: An evolutionary classification and codon usage database for repeat-containing proteins. Genome Research, 2007, 17, 1118-1127.	2.4	36
45	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	13.9	170
46	Loss of ACTN3 gene function alters mouse muscle metabolism and shows evidence of positive selection in humans. Nature Genetics, 2007, 39, 1261-1265.	9.4	278
47	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	13.7	661
48	A PROBABILISTIC METHOD TO IDENTIFY COMPENSATORY SUBSTITUTIONS FOR PATHOGENIC MUTATIONS. , 2007, , .		1
49	Vestige: maximum likelihood phylogenetic footprinting. BMC Bioinformatics, 2005, 6, 130.	1.2	8
50	Modeling the Impact of DNA Methylation on the Evolution of BRCA1 in Mammals. Molecular Biology and Evolution, 2004, 21, 1760-1768.	3.5	36
51	PyEvolve: a toolkit for statistical modelling of molecular evolution. BMC Bioinformatics, 2004, 5, 1.	1.2	424
52	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. Biochemical Journal, 2004, 379, 541-552.	1.7	89
53	Association of polymorphisms of the estrogen receptor gene with anxiety-related traits in children and adolescents: A longitudinal study. American Journal of Medical Genetics Part A, 2002, 114, 169-176.	2.4	38
54	NON-REPLICABILITY OF DISEASE GENE RESULTS: A MODELLING PERSPECTIVE. , 2002, , .		0

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55	The human melanocortin-1 receptor locus: analysis of transcription unit, locus polymorphism and haplotype evolution. Gene, 2001, 281, 81-94.	1.0	38
56	Lake Mungo 3: A response to recent critiques. Archaeology in Oceania, 2001, 36, 170-174.	0.3	6
57	Mitochondrial DNA sequences in ancient Australians: Implications for modern human origins. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 537-542.	3.3	204
58	How Important Is DNA Replication for Mutagenesis?. Molecular Biology and Evolution, 2000, 17, 929-937.	3.5	44
59	Adaptive evolution of the tumour suppressor BRCA1 in humans and chimpanzees. Nature Genetics, 2000, 25, 410-413.	9.4	153
60	A Scan for Linkage Disequilibrium Across the Human Genome. Genetics, 1999, 152, 1711-1722.	1.2	158
61	Dating the Origin of the CCR5-Î”32 AIDS-Resistance Allele by the Coalescence of Haplotypes. American Journal of Human Genetics, 1998, 62, 1507-1515.	2.6	507
62	Contrasting Genetic Influence of CCR2 and CCR5 Variants on HIV-1 Infection and Disease Progression. Science, 1997, 277, 959-965.	6.0	860
63	CCR5-Î”32 gene deletion in HIV-1 infected patients. Lancet, The, 1997, 350, 741.	6.3	28
64	CCR2 chemokine receptor and AIDS progression. Nature Medicine, 1997, 3, 1052-1053.	15.2	96
65	Nucleotide polymorphism in the chalcone synthaseâ€A locus and evolution of the chalcone synthase multigene family of common morning glory Ipomoea purpurea. Molecular Ecology, 1997, 6, 549-558.	2.0	25
66	Genetic Restriction of HIV-1 Infection and Progression to AIDS by a Deletion Allele of the CKR5 Structural Gene. Science, 1996, 273, 1856-1862.	6.0	2,365
67	Genetic Diversity in the Common Morning Glory. Plant Species Biology, 1996, 11, 41-50.	0.6	15
68	Evolution of the chalcone synthase gene family in the genus Ipomoea.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 3338-3342.	3.3	103
69	Molecular evolutionary characterization of an Activator (Ac)-like transposable element sequence from pearl millet (Pennisetum glaucum) (Poaceae). Genetica, 1994, 92, 77-89.	0.5	10