

Michael Hiller

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

9,218
citations

196777

29
h-index

100535

70
g-index

94
all docs

94
docs citations

94
times ranked

20256
citing authors

#	ARTICLE	IF	CITATIONS
1	Interspecies transcriptomics identify genes that underlie disproportionate foot growth in jerboas. <i>Current Biology</i> , 2022, 32, 289-303.e6.	1.8	13
2	Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. <i>Cell Reports</i> , 2022, 38, 110280.	2.9	18
3	Reconstruction of evolutionary changes in fat and toxin consumption reveals associations with gene losses in mammals: A case study for the lipase inhibitor <i>PNLIPRP1</i> and the xenobiotic receptor <i>NR1I3</i> . <i>Journal of Evolutionary Biology</i> , 2022, 35, 225-239.	0.8	5
4	Phenotyping in the era of genomics: MaTrics—a digital character matrix to document mammalian phenotypic traits. <i>Mammalian Biology</i> , 2022, 102, 235-249.	0.8	2
5	Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. <i>Science Advances</i> , 2022, 8, eabm6494.	4.7	24
6	DENTIST—using long reads for closing assembly gaps at high accuracy. <i>GigaScience</i> , 2022, 11, .	3.3	13
7	Chromosome-length genome assembly and linkage map of a critically endangered Australian bird: the helmeted honeyeater. <i>GigaScience</i> , 2022, 11, .	3.3	8
8	Contradictory Phylogenetic Signals in the Laurasiatheria Anomaly Zone. <i>Genes</i> , 2022, 13, 766.	1.0	7
9	Recapitulating Evolutionary Divergence in a Single <i>Cis</i> -Regulatory Element Is Sufficient to Cause Expression Changes of the Lens Gene <i>Tdrd7</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 380-392.	3.5	4
10	Decoding bat immunity: the need for a coordinated research approach. <i>Nature Reviews Immunology</i> , 2021, 21, 269-271.	10.6	29
11	Low Threshold for Cutaneous Allergen Sensitization but No Spontaneous Dermatitis or Atopy in <i>FLG</i> -Deficient Mice. <i>Journal of Investigative Dermatology</i> , 2021, 141, 2611-2619.e2.	0.3	8
12	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
13	Two high-quality <i>de novo</i> genomes from single ethanol-preserved specimens of tiny metazoans (<i>Collembola</i>). <i>GigaScience</i> , 2021, 10, .	3.3	17
14	Genomic and anatomical comparisons of skin support independent adaptation to life in water by cetaceans and hippos. <i>Current Biology</i> , 2021, 31, 2124-2139.e3.	1.8	30
15	Comparative <i>de novo</i> assembly and annotation of mantle tissue transcriptomes from the <i>Mytilus edulis</i> species complex (<i>M. edulis</i> , <i>M. galloprovincialis</i> , <i>M. trossulus</i>). <i>Marine Genomics</i> , 2020, 51, 100700.	0.4	11
16	Losses of human disease-associated genes in placental mammals. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz012.	1.5	16
17	The mole genome reveals regulatory rearrangements associated with adaptive intersexuality. <i>Science</i> , 2020, 370, 208-214.	6.0	41
18	Six reference-quality genomes reveal evolution of bat adaptations. <i>Nature</i> , 2020, 583, 578-584.	13.7	210

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19	Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22311-22322.	3.3	517
20	Convergent Losses of TLR5 Suggest Altered Extracellular Flagellin Detection in Four Mammalian Lineages. <i>Molecular Biology and Evolution</i> , 2020, 37, 1847-1854.	3.5	35
21	A highly contiguous genome assembly of the bat hawkmoth <i>Hyles vesperilio</i> (Lepidoptera: Sphingidae). <i>GigaScience</i> , 2020, 9, .	3.3	8
22	A genome alignment of 120 mammals highlights ultraconserved element variability and placenta-associated enhancers. <i>GigaScience</i> , 2020, 9, .	3.3	29
23	Clathrinâ€™s adaptor interaction sites are repurposed to stabilize microtubules during mitosis. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	15
24	Interspecies transcriptome analyses identify genes that control the development and evolution of limb skeletal proportion. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	2
25	Convergent vomeronasal system reduction in mammals coincides with convergent losses of calcium signalling and odorantâ€ˆdegrading genes. <i>Molecular Ecology</i> , 2019, 28, 3656-3668.	2.0	18
26	Evolutionary Analysis of Bile Acid-Conjugating Enzymes Reveals a Complex Duplication and Reciprocal Loss History. <i>Genome Biology and Evolution</i> , 2019, 11, 3256-3268.	1.1	11
27	Genes lost during the transition from land to water in cetaceans highlight genomic changes associated with aquatic adaptations. <i>Science Advances</i> , 2019, 5, eaaw6671.	4.7	100
28	Odontogenic ameloblast-associated (ODAM) is inactivated in toothless/enamelless placental mammals and toothed whales. <i>BMC Evolutionary Biology</i> , 2019, 19, 31.	3.2	22
29	Convergent gene losses illuminate metabolic and physiological changes in herbivores and carnivores. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3036-3041.	3.3	78
30	Coding Exon-Structure Aware Realigner (CESAR): Utilizing Genome Alignments for Comparative Gene Annotation. <i>Methods in Molecular Biology</i> , 2019, 1962, 179-191.	0.4	1
31	TFforge utilizes large-scale binding site divergence to identify transcriptional regulators involved in phenotypic differences. <i>Nucleic Acids Research</i> , 2019, 47, e19-e19.	6.5	8
32	RepeatFiller newly identifies megabases of aligning repetitive sequences and improves annotations of conserved non-exonic elements. <i>GigaScience</i> , 2019, 8, .	3.3	22
33	Methods to Detect and Associate Divergence in Cis-Regulatory Elements to Phenotypic Divergence. , 2019, , 113-134.		1
34	The genome of <i>Schmidtea mediterranea</i> and the evolution of core cellular mechanisms. <i>Nature</i> , 2018, 554, 56-61.	13.7	191
35	The axolotl genome and the evolution of key tissue formation regulators. <i>Nature</i> , 2018, 554, 50-55.	13.7	463
36	A genomics approach reveals insights into the importance of gene losses for mammalian adaptations. <i>Nature Communications</i> , 2018, 9, 1215.	5.8	177

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37	Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. <i>Nature Communications</i> , 2018, 9, 4737.	5.8	51
38	The genome of the tegu lizard <i>Salvator merianae</i> : combining Illumina, PacBio, and optical mapping data to generate a highly contiguous assembly. <i>GigaScience</i> , 2018, 7, .	3.3	23
39	REforge associates transcription factor binding site divergence in regulatory elements with phenotypic differences between species. <i>Molecular Biology and Evolution</i> , 2018, 35, 3027-3040.	3.5	12
40	Molecular parallelism in fast-twitch muscle proteins in echolocating mammals. <i>Science Advances</i> , 2018, 4, eaat9660.	4.7	17
41	Loss of Enzymes in the Bile Acid Synthesis Pathway Explains Differences in Bile Composition among Mammals. <i>Genome Biology and Evolution</i> , 2018, 10, 3211-3217.	1.1	23
42	Freiburg RNA tools: a central online resource for RNA-focused research and teaching. <i>Nucleic Acids Research</i> , 2018, 46, W25-W29.	6.5	107
43	Evolution and cell-type specificity of human-specific genes preferentially expressed in progenitors of fetal neocortex. <i>ELife</i> , 2018, 7, .	2.8	160
44	Loss of RXFP2 and INSL3 genes in Afrotheria shows that testicular descent is the ancestral condition in placental mammals. <i>PLoS Biology</i> , 2018, 16, e2005293.	2.6	69
45	Recurrent loss of HMGCS2 shows that ketogenesis is not essential for the evolution of large mammalian brains. <i>ELife</i> , 2018, 7, .	2.8	32
46	Identification of Genetic Mechanisms that Control Limb Bone Proportions During Mammalian Evolution. <i>FASEB Journal</i> , 2018, 32, lb527.	0.2	0
47	Iterative error correction of long sequencing reads maximizes accuracy and improves contig assembly. <i>Briefings in Bioinformatics</i> , 2017, 18, 1-8.	3.2	31
48	chainCleaner improves genome alignment specificity and sensitivity. <i>Bioinformatics</i> , 2017, 33, 1596-1603.	1.8	33
49	CESAR 2.0 substantially improves speed and accuracy of comparative gene annotation. <i>Bioinformatics</i> , 2017, 33, 3985-3987.	1.8	47
50	Increased alignment sensitivity improves the usage of genome alignments for comparative gene annotation. <i>Nucleic Acids Research</i> , 2017, 45, 8369-8377.	6.5	50
51	Genome-Wide Screens for Molecular Convergent Evolution in Mammals. , 2017, , 297-312.		0
52	Transition to an aquatic habitat permitted the repeated loss of the pleiotropic KLK8 gene in mammals. <i>Genome Biology and Evolution</i> , 2017, 9, 3179-3188.	1.1	30
53	A single splice site mutation in human-specific <i>ARHGAP11B</i> causes basal progenitor amplification. <i>Science Advances</i> , 2016, 2, e1601941.	4.7	77
54	Controlling for Phylogenetic Relatedness and Evolutionary Rates Improves the Discovery of Associations Between Speciesâ€™ Phenotypic and Genomic Differences. <i>Molecular Biology and Evolution</i> , 2016, 33, 2135-2150.	3.5	74

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55	Coding exon-structure aware realigner (CESAR) utilizes genome alignments for accurate comparative gene annotation. <i>Nucleic Acids Research</i> , 2016, 44, e103-e103.	6.5	47
56	Identification and expression patterns of novel long non-coding RNAs in neural progenitors of the developing mammalian cortex. <i>Neurogenesis (Austin, Tex)</i> , 2015, 2, e995524.	1.5	15
57	Insights into Sex Chromosome Evolution and Aging from the Genome of a Short-Lived Fish. <i>Cell</i> , 2015, 163, 1527-1538.	13.5	251
58	Computational methods to detect conserved non-genic elements in phylogenetically isolated genomes: application to zebrafish. <i>Nucleic Acids Research</i> , 2013, 41, e151-e151.	6.5	84
59	Hundreds of conserved non-coding genomic regions are independently lost in mammals. <i>Nucleic Acids Research</i> , 2012, 40, 11463-11476.	6.5	48
60	A "Forward Genomics" Approach Links Genotype to Phenotype using Independent Phenotypic Losses among Related Species. <i>Cell Reports</i> , 2012, 2, 817-823.	2.9	133
61	GREAT improves functional interpretation of cis-regulatory regions. <i>Nature Biotechnology</i> , 2010, 28, 495-501.	9.4	3,789
62	Conserved introns reveal novel transcripts in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2009, 19, 1289-1300.	2.4	38
63	Widespread and subtle: alternative splicing at short-distance tandem sites. <i>Trends in Genetics</i> , 2008, 24, 246-255.	2.9	60
64	TassDB: a database of alternative tandem splice sites. <i>Nucleic Acids Research</i> , 2007, 35, D188-D192.	6.5	27
65	Phylogenetically widespread alternative splicing at unusual GYNGYN donors. <i>Genome Biology</i> , 2006, 7, R65.	13.9	33
66	Single-Nucleotide Polymorphisms in NAGNAG Acceptors Are Highly Predictive for Variations of Alternative Splicing. <i>American Journal of Human Genetics</i> , 2006, 78, 291-302.	2.6	58
67	Using RNA secondary structures to guide sequence motif finding towards single-stranded regions. <i>Nucleic Acids Research</i> , 2006, 34, e117-e117.	6.5	147
68	Non-EST based prediction of exon skipping and intron retention events using Pfam information. <i>Nucleic Acids Research</i> , 2005, 33, 5611-5621.	6.5	25
69	Creation and disruption of protein features by alternative splicing – a novel mechanism to modulate function. <i>Genome Biology</i> , 2005, 6, R58.	13.9	28
70	Widespread occurrence of alternative splicing at NAGNAG acceptors contributes to proteome plasticity. <i>Nature Genetics</i> , 2004, 36, 1255-1257.	9.4	201
71	Efficient prediction of alternative splice forms using protein domain homology. <i>In Silico Biology</i> , 2004, 4, 195-208.	0.4	5
72	Vision-related convergent gene losses reveal SERPINE3's unknown role in the eye. <i>ELife</i> , 0, 11, .	2.8	9