

Ronald A Harris

List of Publications by Year in descending order

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Version: 2024-02-01

101
papers

13,535
citations

61984

43
h-index

64796

79
g-index

112
all docs

112
docs citations

112
times ranked

28001
citing authors

#	ARTICLE	IF	CITATIONS
1	Heritability of social behavioral phenotypes and preliminary associations with autism spectrum disorder risk genes in rhesus macaques: A whole exome sequencing study. <i>Autism Research</i> , 2022, 15, 447-463.	3.8	14
2	Clinical presentation, treatment, and genetic and histopathological analysis of juvenile cataracts and secondary glaucoma in a rhesus macaque (<i>Macaca mulatta</i>). <i>Journal of Medical Primatology</i> , 2022, 51, 119-123.	0.6	1
3	Comparative molecular genomic analyses of a spontaneous rhesus macaque model of mismatch repair-deficient colorectal cancer. <i>PLoS Genetics</i> , 2022, 18, e1010163.	3.5	8
4	De novo Mutations in Domestic Cat are Consistent with an Effect of Reproductive Longevity on Both the Rate and Spectrum of Mutations. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	22
5	Origins and Long-Term Patterns of Copy-Number Variation in Rhesus Macaques. <i>Molecular Biology and Evolution</i> , 2021, 38, 1460-1471.	8.9	11
6	Variation in predicted COVID-19 risk among lemurs and lorises. <i>American Journal of Primatology</i> , 2021, 83, e23255.	1.7	7
7	Comparative genomic analysis of sifakas (<i>Propithecus</i>) reveals selection for folivory and high heterozygosity despite endangered status. <i>Science Advances</i> , 2021, 7, .	10.3	14
8	Infant inhibited temperament in primates predicts adult behavior, is heritable, and is associated with anxiety-relevant genetic variation. <i>Molecular Psychiatry</i> , 2021, 26, 6609-6618.	7.9	13
9	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. <i>Science Translational Medicine</i> , 2021, 13, .	12.4	23
10	Pedigree reconstruction and distant pairwise relatedness estimation from genome sequence data: A demonstration in a population of rhesus macaques (<i>Macaca mulatta</i>). <i>Molecular Ecology Resources</i> , 2021, 21, 1333-1346.	4.8	3
11	and Associated Extensive Prolapse-Type Inflammatory Polyposis in Crohn's Colitis.. <i>Annals of Clinical and Laboratory Science</i> , 2021, 51, 868-874.	0.2	1
12	Reduced meiotic recombination in rhesus macaques and the origin of the human recombination landscape. <i>PLoS ONE</i> , 2020, 15, e0236285.	2.5	7
13	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. <i>Science</i> , 2020, 370, .	12.6	105
14	Copy number variants and fixed duplications among 198 rhesus macaques (<i>Macaca mulatta</i>). <i>PLoS Genetics</i> , 2020, 16, e1008742.	3.5	10
15	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. <i>Genome Research</i> , 2020, 30, 826-834.	5.5	48
16	Population-Based Estimation of the Preterm Birth Rate in Lilongwe, Malawi: Making Every Birth Count. <i>AJP Reports</i> , 2020, 10, e78-e86.	0.7	7
17	Unusual sequence characteristics of human chromosome 19 are conserved across 11 nonhuman primates. <i>BMC Evolutionary Biology</i> , 2020, 20, 33.	3.2	18
18	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. <i>PLoS Biology</i> , 2020, 18, e3000954.	5.6	73

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19	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
20	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
21	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
22	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
23	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
24	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
25	Title is missing!. , 2020, 15, e0236285.		0
26	Title is missing!. , 2020, 15, e0236285.		0
27	Title is missing!. , 2020, 15, e0236285.		0
28	Title is missing!. , 2020, 15, e0236285.		0
29	MHC genotyping from rhesus macaque exome sequences. Immunogenetics, 2019, 71, 531-544.	2.4	16
30	Population-Based Estimation of Dental Caries and Periodontal Disease Rates of Gravid and Recently Postpartum Women in Lilongwe, Malawi. AJP Reports, 2019, 09, e268-e274.	0.7	1
31	The comparative genomics and complex population history of <i>Papio</i> baboons. Science Advances, 2019, 5, eaau6947.	10.3	115
32	A nonhuman primate model of inherited retinal disease. Journal of Clinical Investigation, 2019, 129, 863-874.	8.2	78
33	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. Nature, 2018, 553, 77-81.	27.8	81
34	Spontaneous Spongiform Brainstem Degeneration in a Young Mouse Lemur (<i>Microcebus murinus</i>) with Conspicuous Behavioral, Motor, Growth, and Ocular Pathologies. Comparative Medicine, 2018, 68, 489-495.	1.0	2
35	Reproductive Longevity Predicts Mutation Rates in Primates. Current Biology, 2018, 28, 3193-3197.e5.	3.9	94
36	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	12.6	87

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37	Mismatch repair gene mutations lead to lynch syndrome colorectal cancer in rhesus macaques. <i>Genes and Cancer</i> , 2018, 9, 142-152.	1.9	18
38	Primary Human Placental Trophoblasts are Permissive for Zika Virus (ZIKV) Replication. <i>Scientific Reports</i> , 2017, 7, 41389.	3.3	114
39	Improved full-length killer cell immunoglobulin-like receptor transcript discovery in Mauritian cynomolgus macaques. <i>Immunogenetics</i> , 2017, 69, 325-339.	2.4	25
40	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (<i>Microcebus murinus</i>). <i>BMC Biology</i> , 2017, 15, 110.	3.8	53
41	Colonic Mucosal Epigenome and Microbiome Development in Children and Adolescents. <i>Journal of Immunology Research</i> , 2016, 2016, 1-7.	2.2	36
42	549: Population-based estimation of the periodontal disease rate in malawi and compliance with preventive/ treatment measures. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 214, S295-S296.	1.3	0
43	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. <i>American Journal of Human Genetics</i> , 2016, 98, 898-908.	6.2	89
44	Structural and transcriptomic response to antenatal corticosteroids in an Erk3-null mouse model of respiratory distress. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 215, 384.e1-384.e89.	1.3	7
45	The population genomics of rhesus macaques (<i>Macaca mulatta</i>) based on whole-genome sequences. <i>Genome Research</i> , 2016, 26, 1651-1662.	5.5	101
46	Genomic Variants Associated with Resistance to High Fat Diet Induced Obesity in a Primate Model. <i>Scientific Reports</i> , 2016, 6, 36123.	3.3	23
47	DNA Methylation Profiling in Inflammatory Bowel Disease Provides New Insights into Disease Pathogenesis. <i>Journal of Crohn's and Colitis</i> , 2016, 10, 77-86.	1.3	115
48	23: Antibiotics and betamethasone therapy do not significantly alter the placental microbiome in chorioamnionitis affected pregnancies. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 214, S17.	1.3	0
49	184: Pre-eclampsia, diabetes, and the placenta: a study in differential gene expression & molecular clues to disease states. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 214, S114-S115.	1.3	0
50	The placental membrane microbiome is altered among subjects with spontaneous preterm birth with and without chorioamnionitis. <i>American Journal of Obstetrics and Gynecology</i> , 2016, 214, 627.e1-627.e16.	1.3	235
51	Role of Maternal Serum Alpha-Fetoprotein and Ultrasonography in Contemporary Detection of Spina Bifida. <i>American Journal of Perinatology</i> , 2015, 32, 1287-1291.	1.4	6
52	Comparative Genomic Analyses of the Human NPHP1 Locus Reveal Complex Genomic Architecture and Its Regional Evolution in Primates. <i>PLoS Genetics</i> , 2015, 11, e1005686.	3.5	21
53	Loss of n-6 fatty acid induced pediatric obesity protects against acute murine colitis. <i>FASEB Journal</i> , 2015, 29, 3151-3159.	0.5	19
54	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	12.8	91

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55	Epigenomic footprints across 111 reference epigenomes reveal tissue-specific epigenetic regulation of lincRNAs. <i>Nature Communications</i> , 2015, 6, 6370.	12.8	77
56	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
57	Serial Fecal Microbiota Transplantation Alters Mucosal Gene Expression in Pediatric Ulcerative Colitis. <i>American Journal of Gastroenterology</i> , 2015, 110, 604-606.	0.4	61
58	634: Detection of open neural tube defects (ONTD) as an opportunity for intervention. <i>American Journal of Obstetrics and Gynecology</i> , 2015, 212, S312-S313.	1.3	0
59	345: Novel insights on molecular targets of environmental exposures during pregnancy using placental multiomics integration. <i>American Journal of Obstetrics and Gynecology</i> , 2015, 212, S182.	1.3	0
60	293: Transcriptomic analysis reveals potential roles for ERK3 in fetal lung maturation via surfactant protein B and corticotropin releasing hormone. <i>American Journal of Obstetrics and Gynecology</i> , 2015, 212, S157-S158.	1.3	0
61	DNA methylation-associated colonic mucosal immune and defense responses in treatment-naïve pediatric ulcerative colitis. <i>Epigenetics</i> , 2014, 9, 1131-1137.	2.7	59
62	Evolutionary genetics and implications of small size and twinning in callitrichine primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1467-1472.	7.1	66
63	Comparison and quantitative verification of mapping algorithms for whole-genome bisulfite sequencing. <i>Nucleic Acids Research</i> , 2014, 42, e43-e43.	14.5	68
64	522: Population-based estimation of the preterm birth rate in Malawi: making every birth count. <i>American Journal of Obstetrics and Gynecology</i> , 2014, 210, S257-S258.	1.3	1
65	In utero exposure to a maternal high-fat diet alters the epigenetic histone code in a murine model. <i>American Journal of Obstetrics and Gynecology</i> , 2014, 210, 463.e1-463.e11.	1.3	58
66	High-fat maternal diet during pregnancy persistently alters the offspring microbiome in a primate model. <i>Nature Communications</i> , 2014, 5, 3889.	12.8	361
67	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
68	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	27.8	320
69	158: Genome wide maternal leukocyte DNA methylation analysis performed longitudinally throughout normal pregnancy. <i>American Journal of Obstetrics and Gynecology</i> , 2014, 210, S92.	1.3	0
70	Confounding by Repetitive Elements and CpG Islands Does Not Explain the Association between Hypomethylation and Genomic Instability. <i>PLoS Genetics</i> , 2013, 9, e1003333.	3.5	3
71	Human metastable epiallele candidates link to common disorders. <i>Epigenetics</i> , 2013, 8, 157-163.	2.7	56
72	Transcriptome Profiling of microRNA by Next-Gen Deep Sequencing Reveals Known and Novel miRNA Species in the Lipid Fraction of Human Breast Milk. <i>PLoS ONE</i> , 2013, 8, e50564.	2.5	155

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73	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. <i>PLoS Genetics</i> , 2012, 8, e1002692.	3.5	80
74	Early Origins of Adult Disease: Approaches for Investigating the Programmable Epigenome in Humans, Nonhuman Primates, and Rodents. <i>ILAR Journal</i> , 2012, 53, 306-321.	1.8	57
75	Maternal High-Fat Diet Modulates the Fetal Thyroid Axis and Thyroid Gene Expression in a Nonhuman Primate Model. <i>Molecular Endocrinology</i> , 2012, 26, 2071-2080.	3.7	49
76	Centromere Remodeling in Hoolock leuconedys (Hylobatidae) by a New Transposable Element Unique to the Gibbons. <i>Genome Biology and Evolution</i> , 2012, 4, 648-658.	2.5	57
77	DNA Methylation and Microbiota Separation of Ulcerative Colitis in Treatment Naive Children. <i>Inflammatory Bowel Diseases</i> , 2012, 18, S60-S61.	1.9	0
78	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. <i>Genome Biology</i> , 2012, 13, R43.	9.6	585
79	A maternal high-fat diet modulates fetal SIRT1 histone and protein deacetylase activity in nonhuman primates. <i>FASEB Journal</i> , 2012, 26, 5106-5114.	0.5	154
80	Genome-wide peripheral blood leukocyte DNA methylation microarrays identified a single association with inflammatory bowel diseases. <i>Inflammatory Bowel Diseases</i> , 2012, 18, 2334-2341.	1.9	80
81	8: A primate epigenome-wide custom array of 244K reveals that a maternal high fat (HF) diet discriminately alters the fetal liver methylome in a primate model of maternal obesity. <i>American Journal of Obstetrics and Gynecology</i> , 2012, 206, S4-S5.	1.3	0
82	169: Novel molecular determinates of newborn health: micro (miRNA) expression profiling in breast milk employing next generation smRNA sequencing. <i>American Journal of Obstetrics and Gynecology</i> , 2012, 206, S88.	1.3	0
83	513: Antenatal glucocorticoids and postnatal surfactant treatment partially rescues neonatal lethality and pulmonary immaturity in an ERK3-/- knockout (ko) murine model of intrauterine growth restriction (IUGR). <i>American Journal of Obstetrics and Gynecology</i> , 2012, 206, S232-S233.	1.3	0
84	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (<i>Macaca mulatta</i>). <i>BMC Genomics</i> , 2011, 12, 311.	2.8	30
85	Genome-wide array-based copy number profiling in human placentas from unexplained stillbirths. <i>Prenatal Diagnosis</i> , 2011, 31, 932-944.	2.3	23
86	Maternal methyl-donor supplementation induces prolonged murine offspring colitis susceptibility in association with mucosal epigenetic and microbiomic changes. <i>Human Molecular Genetics</i> , 2011, 20, 1687-1696.	2.9	135
87	Colonic mucosal DNA methylation, immune response, and microbiome patterns in Toll-like receptor 2-knockout mice. <i>FASEB Journal</i> , 2011, 25, 1449-1460.	0.5	123
88	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. <i>BMC Bioinformatics</i> , 2010, 11, 572.	2.6	48
89	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , 2010, 28, 1097-1105.	17.5	647
90	Proinflammatory Role for let-7 MicroRNAs in Experimental Asthma. <i>Journal of Biological Chemistry</i> , 2010, 285, 30139-30149.	3.4	222

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91	Season of Conception in Rural Gambia Affects DNA Methylation at Putative Human Metastable Epialleles. <i>PLoS Genetics</i> , 2010, 6, e1001252.	3.5	393
92	MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. <i>Molecular Human Reproduction</i> , 2010, 16, 463-471.	2.8	122
93	A sequence-level map of chromosomal breakpoints in the MCF-7 breast cancer cell line yields insights into the evolution of a cancer genome. <i>Genome Research</i> , 2009, 19, 167-177.	5.5	111
94	Evolutionary Breakpoints in the Gibbon Suggest Association between Cytosine Methylation and Karyotype Evolution. <i>PLoS Genetics</i> , 2009, 5, e1000538.	3.5	81
95	GASZ Is Essential for Male Meiosis and Suppression of Retrotransposon Expression in the Male Germline. <i>PLoS Genetics</i> , 2009, 5, e1000635.	3.5	151
96	Polymorphic microsatellite loci for the common marmoset (<i>Callithrix jacchus</i>) designed using a cost-effective and time-efficient method. <i>American Journal of Primatology</i> , 2008, 70, 906-910.	1.7	8
97	Human-Specific Changes of Genome Structure Detected by Genomic Triangulation. <i>Science</i> , 2007, 316, 235-237.	12.6	25
98	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
99	Designing new microsatellite markers for linkage and population genetic analyses in rhesus macaques and other nonhuman primates. <i>Genomics</i> , 2006, 88, 706-710.	2.9	16
100	A High-Resolution Map of Synteny Disruptions in Gibbon and Human Genomes. <i>PLoS Genetics</i> , 2006, 2, e223.	3.5	48
101	Pooled genomic indexing of rhesus macaque. <i>Genome Research</i> , 2005, 15, 292-301.	5.5	14