Ronald A Harris

List of Publications by Year in descending order

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		61857	64668
101	13,535	43	79
papers	citations	h-index	g-index
112 all docs	112 docs citations	112 times ranked	28001 citing authors

#	Article	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
3	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105.	9.4	647
4	Functional annotation of the human brain methylome identifies tissue-specific epigenetic variation across brain and blood. Genome Biology, 2012, 13, R43.	13.9	585
5	Season of Conception in Rural Gambia Affects DNA Methylation at Putative Human Metastable Epialleles. PLoS Genetics, 2010, 6, e1001252.	1.5	393
6	High-fat maternal diet during pregnancy persistently alters the offspring microbiome in a primate model. Nature Communications, 2014, 5, 3889.	5.8	361
7	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
8	The placental membrane microbiome is altered among subjects with spontaneous preterm birth with and without chorioamnionitis. American Journal of Obstetrics and Gynecology, 2016, 214, 627.e16.	0.7	235
9	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	9.4	225
10	Proinflammatory Role for let-7 MicroRNAS in Experimental Asthma. Journal of Biological Chemistry, 2010, 285, 30139-30149.	1.6	222
11	Transcriptome Profiling of microRNA by Next-Gen Deep Sequencing Reveals Known and Novel miRNA Species in the Lipid Fraction of Human Breast Milk. PLoS ONE, 2013, 8, e50564.	1.1	155
12	A maternal highâ€fat diet modulates fetal SIRT1 histone and protein deacetylase activity in nonhuman primates. FASEB Journal, 2012, 26, 5106-5114.	0.2	154
13	GASZ Is Essential for Male Meiosis and Suppression of Retrotransposon Expression in the Male Germline. PLoS Genetics, 2009, 5, e1000635.	1.5	151
14	Maternal methyl-donor supplementation induces prolonged murine offspring colitis susceptibility in association with mucosal epigenetic and microbiomic changes. Human Molecular Genetics, 2011, 20, 1687-1696.	1.4	135
15	Colonic mucosal DNA methylation, immune response, and microbiome patterns in Tollâ€like receptor 2â€knockout mice. FASEB Journal, 2011, 25, 1449-1460.	0.2	123
16	MicroRNA transcriptome in the newborn mouse ovaries determined by massive parallel sequencing. Molecular Human Reproduction, 2010, 16, 463-471.	1.3	122
17	DNA Methylation Profiling in Inflammatory Bowel Disease Provides New Insights into Disease Pathogenesis. Journal of Crohn's and Colitis, 2016, 10, 77-86.	0.6	115
18	The comparative genomics and complex population history of <i>Papio</i> baboons. Science Advances, 2019, 5, eaau6947.	4.7	115

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19	Primary Human Placental Trophoblasts are Permissive for Zika Virus (ZIKV) Replication. Scientific Reports, 2017, 7, 41389.	1.6	114
20	A sequence-level map of chromosomal breakpoints in the MCF-7 breast cancer cell line yields insights into the evolution of a cancer genome. Genome Research, 2009, 19, 167-177.	2.4	111
21	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	6.0	105
22	The population genomics of rhesus macaques (<i>Macaca mulatta</i>) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	2.4	101
23	Reproductive Longevity Predicts Mutation Rates in Primates. Current Biology, 2018, 28, 3193-3197.e5.	1.8	94
24	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	5.8	91
25	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. American Journal of Human Genetics, 2016, 98, 898-908.	2.6	89
26	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	6.0	87
27	Evolutionary Breakpoints in the Gibbon Suggest Association between Cytosine Methylation and Karyotype Evolution. PLoS Genetics, 2009, 5, e1000538.	1.5	81
28	Sooty mangabey genome sequence provides insight into AIDS resistance in a natural SIV host. Nature, 2018, 553, 77-81.	13.7	81
29	Genomic Hypomethylation in the Human Germline Associates with Selective Structural Mutability in the Human Genome. PLoS Genetics, 2012, 8, e1002692.	1.5	80
30	Genome-wide peripheral blood leukocyte DNA methylation microarrays identified a single association with inflammatory bowel diseases. Inflammatory Bowel Diseases, 2012, 18, 2334-2341.	0.9	80
31	A nonhuman primate model of inherited retinal disease. Journal of Clinical Investigation, 2019, 129, 863-874.	3.9	78
32	Epigenomic footprints across 111 reference epigenomes reveal tissue-specific epigenetic regulation of lincRNAs. Nature Communications, 2015, 6, 6370.	5.8	77
33	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. PLoS Biology, 2020, 18, e3000954.	2.6	73
34	Comparison and quantitative verification of mapping algorithms for whole-genome bisulfite sequencing. Nucleic Acids Research, 2014, 42, e43-e43.	6.5	68
35	Evolutionary genetics and implications of small size and twinning in callitrichine primates. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1467-1472.	3.3	66
36	Serial Fecal Microbiota Transplantation Alters Mucosal Gene Expression in Pediatric Ulcerative Colitis. American Journal of Gastroenterology, 2015, 110, 604-606.	0.2	61

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37	DNA methylation-associated colonic mucosal immune and defense responses in treatment-naÃ ⁻ ve pediatric ulcerative colitis. Epigenetics, 2014, 9, 1131-1137.	1.3	59
38	In utero exposure to a maternal high-fat diet alters the epigenetic histone code in a murine model. American Journal of Obstetrics and Gynecology, 2014, 210, 463.e1-463.e11.	0.7	58
39	Early Origins of Adult Disease: Approaches for Investigating the Programmable Epigenome in Humans, Nonhuman Primates, and Rodents. ILAR Journal, 2012, 53, 306-321.	1.8	57
40	Centromere Remodeling in Hoolock leuconedys (Hylobatidae) by a New Transposable Element Unique to the Gibbons. Genome Biology and Evolution, 2012, 4, 648-658.	1.1	57
41	Human metastable epiallele candidates link to common disorders. Epigenetics, 2013, 8, 157-163.	1.3	56
42	Hybrid de novo genome assembly and centromere characterization of the gray mouse lemur (Microcebus murinus). BMC Biology, 2017, 15, 110.	1.7	53
43	Maternal High-Fat Diet Modulates the Fetal Thyroid Axis and Thyroid Gene Expression in a Nonhuman Primate Model. Molecular Endocrinology, 2012, 26, 2071-2080.	3.7	49
44	A High-Resolution Map of Synteny Disruptions in Gibbon and Human Genomes. PLoS Genetics, 2006, 2, e223.	1.5	48
45	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. BMC Bioinformatics, 2010, 11, 572.	1.2	48
46	Paternal age in rhesus macaques is positively associated with germline mutation accumulation but not with measures of offspring sociability. Genome Research, 2020, 30, 826-834.	2.4	48
47	Colonic Mucosal Epigenome and Microbiome Development in Children and Adolescents. Journal of Immunology Research, 2016, 2016, 1-7.	0.9	36
48	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (Macaca mulatta). BMC Genomics, 2011, 12, 311.	1.2	30
49	Human-Specific Changes of Genome Structure Detected by Genomic Triangulation. Science, 2007, 316, 235-237.	6.0	25
50	Improved full-length killer cell immunoglobulin-like receptor transcript discovery in Mauritian cynomolgus macaques. Immunogenetics, 2017, 69, 325-339.	1.2	25
51	Genomeâ€wide arrayâ€based copy number profiling in human placentas from unexplained stillbirths. Prenatal Diagnosis, 2011, 31, 932-944.	1.1	23
52	Genomic Variants Associated with Resistance to High Fat Diet Induced Obesity in a Primate Model. Scientific Reports, 2016, 6, 36123.	1.6	23
53	Neuropeptide S receptor 1 is a nonhormonal treatment target in endometriosis. Science Translational Medicine, 2021, 13, .	5.8	23
54	De novo Mutations in Domestic Cat are Consistent with an Effect of Reproductive Longevity on Both the Rate and Spectrum of Mutations. Molecular Biology and Evolution, 2022, 39, .	3.5	22

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55	Comparative Genomic Analyses of the Human NPHP1 Locus Reveal Complex Genomic Architecture and Its Regional Evolution in Primates. PLoS Genetics, 2015, 11, e1005686.	1.5	21
56	Loss of n-6 fatty acid induced pediatric obesity protects against acute murine colitis. FASEB Journal, 2015, 29, 3151-3159.	0.2	19
57	Unusual sequence characteristics of human chromosome 19 are conserved across 11 nonhuman primates. BMC Evolutionary Biology, 2020, 20, 33.	3.2	18
58	Mismatch repair gene mutations lead to lynch syndrome colorectal cancer in rhesus macaques. Genes and Cancer, 2018, 9, 142-152.	0.6	18
59	Designing new microsatellite markers for linkage and population genetic analyses in rhesus macaques and other nonhuman primates. Genomics, 2006, 88, 706-710.	1.3	16
60	MHC genotyping from rhesus macaque exome sequences. Immunogenetics, 2019, 71, 531-544.	1.2	16
61	Pooled genomic indexing of rhesus macaque. Genome Research, 2005, 15, 292-301.	2.4	14
62	Comparative genomic analysis of sifakas (<i>Propithecus</i>) reveals selection for folivory and high heterozygosity despite endangered status. Science Advances, 2021, 7, .	4.7	14
63	Heritability of social behavioral phenotypes and preliminary associations with autism spectrum disorder risk genes in rhesus macaques: A whole exome sequencing study. Autism Research, 2022, 15, 447-463.	2.1	14
64	Infant inhibited temperament in primates predicts adult behavior, is heritable, and is associated with anxiety-relevant genetic variation. Molecular Psychiatry, 2021, 26, 6609-6618.	4.1	13
65	Origins and Long-Term Patterns of Copy-Number Variation in Rhesus Macaques. Molecular Biology and Evolution, 2021, 38, 1460-1471.	3.5	11
66	Copy number variantsÂand fixed duplications among 198 rhesus macaques (Macaca mulatta). PLoS Genetics, 2020, 16, e1008742.	1.5	10
67	Polymorphic microsatellite loci for the common marmoset (<i>Callithrix jacchus</i>) designed using a cost―and timeâ€efficient method. American Journal of Primatology, 2008, 70, 906-910.	0.8	8
68	Comparative molecular genomic analyses of a spontaneous rhesus macaque model of mismatch repair-deficient colorectal cancer. PLoS Genetics, 2022, 18, e1010163.	1.5	8
69	Structural and transcriptomic response to antenatal corticosteroids in an Erk3-null mouse model of respiratoryÂdistress. American Journal of Obstetrics and Gynecology, 2016, 215, 384.e1-384.e89.	0.7	7
70	Reduced meiotic recombination in rhesus macaques and the origin of the human recombination landscape. PLoS ONE, 2020, 15, e0236285.	1.1	7
71	Population-Based Estimation of the Preterm Birth Rate in Lilongwe, Malawi: Making Every Birth Count. AJP Reports, 2020, 10, e78-e86.	0.4	7
72	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	0.8	7

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73	Role of Maternal Serum Alpha-Fetoprotein and Ultrasonography in Contemporary Detection of Spina Bifida. American Journal of Perinatology, 2015, 32, 1287-1291.	0.6	6
74	Confounding by Repetitive Elements and CpG Islands Does Not Explain the Association between Hypomethylation and Genomic Instability. PLoS Genetics, 2013, 9, e1003333.	1.5	3
75	Pedigree reconstruction and distant pairwise relatedness estimation from genome sequence data: A demonstration in a population of rhesus macaques (<i>Macaca mulatta</i>). Molecular Ecology Resources, 2021, 21, 1333-1346.	2.2	3
76	Spontaneous Spongiform Brainstem Degeneration in a Young Mouse Lemur (Microcebus murinus) with Conspicuous Behavioral, Motor, Growth, and Ocular Pathologies. Comparative Medicine, 2018, 68, 489-495.	0.4	2
77	522: Population-based estimation of the preterm birth rate in Malawi: making every birth count. American Journal of Obstetrics and Gynecology, 2014, 210, S257-S258.	0.7	1
78	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.	0.4	1
79	Clinical presentation, treatment, and genetic and histopathological analysis of juvenile cataracts and secondary glaucoma in a rhesus macaque (<i>Macaca mulatta</i>). Journal of Medical Primatology, 2022, 51, 119-123.	0.3	1
80	and Associated Extensive Prolapse-Type Inflammatory Polyposis in Crohn's Colitis Annals of Clinical and Laboratory Science, 2021, 51, 868-874.	0.2	1
81	DNA Methylation and Microbiota Separation of Ulcerative Colitis in Treatment Naive Children. Inflammatory Bowel Diseases, 2012, 18, S60-S61.	0.9	0
82	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. American Journal of Obstetrics and Gynecology, 2012, 206, S4-S5.	0.7	0
83	169: Novel molecular determinates of newborn health: micro (miRNA) expression profiling in breast milk employing next generation smRNA sequencing. American Journal of Obstetrics and Gynecology, 2012, 206, S88.	0.7	Ο
84	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). American Journal of Obstetrics and Gynecology, 2012, 206, S232-S233.	0.7	0
85	158: Genome wide maternal leukocyte DNA methylation analysis performed longitudinally throughout normal pregnancy. American Journal of Obstetrics and Gynecology, 2014, 210, S92.	0.7	0
86	634: Detection of open neural tube defects (ONTD) as an opportunity for intervention. American Journal of Obstetrics and Gynecology, 2015, 212, S312-S313.	0.7	0
87	345: Novel insights on molecular targets of environmental exposures during pregnancy using placental multiomics integration. American Journal of Obstetrics and Gynecology, 2015, 212, S182.	0.7	Ο
88	293: Transcriptomic analysis reveals potential roles for ERK3 in fetal lung maturation via surfactant protein B and corticotropin releasing hormone. American Journal of Obstetrics and Gynecology, 2015, 212, S157-S158.	0.7	0
89	549: Population-based estimation of the peridontal disease rate in malawi and compliance with preventive/ treatment measures. American Journal of Obstetrics and Gynecology, 2016, 214, S295-S296.	0.7	0
90	23: Antibiotics and betamethasone therapy do not significantly alter the placental microbiome in chorioamnionitis affected pregnancies. American Journal of Obstetrics and Gynecology, 2016, 214, S17.	0.7	0

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91	184: Pre-eclampsia, diabetes, and the placenta: a study in differential gene expression & molecular clues to disease states. American Journal of Obstetrics and Gynecology, 2016, 214, S114-S115.	0.7	0
92	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
93	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
94	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
95	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
96	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
97	Primate phylogenomics uncovers multiple rapid radiations and ancient interspecific introgression. , 2020, 18, e3000954.		0
98	Title is missing!. , 2020, 15, e0236285.		0
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