

Benjamin D Rosen

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

2,262
citations

430874

18
h-index

377865

34
g-index

49
all docs

49
docs citations

49
times ranked

3157
citing authors

#	ARTICLE	IF	CITATIONS
1	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	6.4	24
2	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	10.3	14
3	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	2.8	3
4	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	12.8	19
5	A Reference Genome Assembly of Simmental Cattle, <i>Bos taurus taurus</i>. <i>Journal of Heredity</i> , 2021, 112, 184-191.	2.4	25
6	Experiences from the Implementation of Community-Based Goat Breeding Programs in Malawi and Uganda: A Potential Approach for Conservation and Improvement of Indigenous Small Ruminants in Smallholder Farms. <i>Sustainability</i> , 2021, 13, 1494.	3.2	6
7	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i>. <i>Journal of Heredity</i> , 2021, 112, 174-183.	2.4	14
8	Investigation of ancestral alleles in the Bovinae subfamily. <i>BMC Genomics</i> , 2021, 22, 108.	2.8	4
9	Chromosome-length genome assembly and structural variations of the primal Basenji dog (<i>Canis lupus</i>) Tj ETQq1 1,0784314,rgBT/O	2.8	22
10	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	2.8	4
11	VarGoats project: a dataset of 1159 whole-genome sequences to dissect <i>Capra hircus</i> global diversity. <i>Genetics Selection Evolution</i> , 2021, 53, 86.	3.0	16
12	Assessing <i>Bos taurus</i> introgression in the UOA <i>Bos indicus</i> assembly. <i>Genetics Selection Evolution</i> , 2021, 53, 96.	3.0	3
13	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020, 112, 1477-1480.	2.9	14
14	Reprogramming of Root Cells during Nitrogen-Fixing Symbiosis Involves Dynamic Polysome Association of Coding and Noncoding RNAs. <i>Plant Cell</i> , 2020, 32, 352-373.	6.6	20
15	Copy number variation analysis reveals variants associated with milk production traits in dairy goats. <i>Genomics</i> , 2020, 112, 4934-4937.	2.9	11
16	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
17	Comparative whole genome DNA methylation profiling across cattle tissues reveals global and tissue-specific methylation patterns. <i>BMC Biology</i> , 2020, 18, 85.	3.8	34
18	Haplotype-resolved genomes provide insights into structural variation and gene content in Angus and Brahman cattle. <i>Nature Communications</i> , 2020, 11, 2071.	12.8	84

#	ARTICLE	IF	CITATIONS
19	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
20	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. <i>Small Ruminant Research</i> , 2020, 187, 106095.	1.2	27
21	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
22	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog (<i>Canis lupus</i>) Tj ETQq0,0,0 rgBT /Overlock 1	6.4	47
23	Integrating Signals from Sperm Methylome Analysis and Genome-Wide Association Study for a Better Understanding of Male Fertility in Cattle. <i>Epigenomes</i> , 2019, 3, 10.	1.8	12
24	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019, 10, 537.	2.3	15
25	Comparative analyses of sperm DNA methylomes among human, mouse and cattle provide insights into epigenomic evolution and complex traits. <i>Epigenetics</i> , 2019, 14, 260-276.	2.7	25
26	New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. <i>BMC Genomics</i> , 2019, 20, 1000.	2.8	21
27	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019, 122, 636-646.	2.6	42
28	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , 2019, 10, 260.	12.8	161
29	Comparative whole genome DNA methylation profiling of cattle sperm and somatic tissues reveals striking hypomethylated patterns in sperm. <i>GigaScience</i> , 2018, 7, .	6.4	60
30	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <i>Genetics Selection Evolution</i> , 2018, 50, 58.	3.0	87
31	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018, 50, 57.	3.0	114
32	AdaptMap: exploring goat diversity and adaptation. <i>Genetics Selection Evolution</i> , 2018, 50, 61.	3.0	70
33	Single-molecule sequencing and chromatin conformation capture enable de novo reference assembly of the domestic goat genome. <i>Nature Genetics</i> , 2017, 49, 643-650.	21.4	600
34	Whole genome structural analysis of Caribbean hair sheep reveals quantitative link to West African ancestry. <i>PLoS ONE</i> , 2017, 12, e0179021.	2.5	29