

# Benjamin D Rosen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2105559/publications.pdf>

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	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
2	De novo assembly of the cattle reference genome with single-molecule sequencing. <i>GigaScience</i> , 2020, 9, .	6.4	380
3	An improved pig reference genome sequence to enable pig genetics and genomics research. <i>GigaScience</i> , 2020, 9, .	6.4	187
4	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
5	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018, 50, 57.	3.0	114
6	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
7	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
8	AdaptMap: exploring goat diversity and adaptation. <i>Genetics Selection Evolution</i> , 2018, 50, 61.	3.0	70
9	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
10	Canfam_GSD: De novo chromosome-length genome assembly of the German Shepherd Dog ( <i>Canis lupus</i> ) Tj ETQq00,0 rgBT /Overlock I	6.4	47
11	Continuous chromosome-scale haplotypes assembled from a single interspecies F1 hybrid of yak and cattle. <i>GigaScience</i> , 2020, 9, .	6.4	46
12	Diversity of copy number variation in the worldwide goat population. <i>Heredity</i> , 2019, 122, 636-646.	2.6	42
13	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
14	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
15	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. <i>Small Ruminant Research</i> , 2020, 187, 106095.	1.2	27
16	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
17	A Reference Genome Assembly of Simmental Cattle, <i>&lt;i&gt;Bos taurus taurus&lt;/i&gt;</i> . <i>Journal of Heredity</i> , 2021, 112, 184-191.	2.4	25
18	An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. <i>GigaScience</i> , 2022, 11, .	6.4	24

#	ARTICLE	IF	CITATIONS
19	Chromosome-length genome assembly and structural variations of the primal Basenji dog ( <i>Canis lupus</i> ) Tj ETQq1 1,0784314,rgBT /Ome	2.8	22
20	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
21	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
22	Structural variant-based pangenome construction has low sensitivity to variability of haplotype-resolved bovine assemblies. <i>Nature Communications</i> , 2022, 13, .	12.8	19
23	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
24	Timing and Extent of Inbreeding in African Goats. <i>Frontiers in Genetics</i> , 2019, 10, 537.	2.3	15
25	Genome-wide CNV analysis revealed variants associated with growth traits in African indigenous goats. <i>Genomics</i> , 2020, 112, 1477-1480.	2.9	14
26	A Reference Genome Assembly of American Bison, <i>Bison bison bison</i> . <i>Journal of Heredity</i> , 2021, 112, 174-183.	2.4	14
27	The Australian dingo is an early offshoot of modern breed dogs. <i>Science Advances</i> , 2022, 8, eabm5944.	10.3	14
28	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
29	Copy number variation analysis reveals variants associated with milk production traits in dairy goats. <i>Genomics</i> , 2020, 112, 4934-4937.	2.9	11
30	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
31	Investigation of ancestral alleles in the Bovinae subfamily. <i>BMC Genomics</i> , 2021, 22, 108.	2.8	4
32	Detection of copy number variants in African goats using whole genome sequence data. <i>BMC Genomics</i> , 2021, 22, 398.	2.8	4
33	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
34	Gaur genome reveals expansion of sperm odorant receptors in domesticated cattle. <i>BMC Genomics</i> , 2022, 23, 344.	2.8	3