

Daniel G Bradley

List of Publications by Year in descending order

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Version: 2024-02-01

88
papers

12,191
citations

29994

54
h-index

54797

84
g-index

99
all docs

99
docs citations

99
times ranked

12489
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	12
2	Bronze Age genomes reveal migration to Britain. <i>Nature</i> , 2022, 601, 512-513.	13.7	1
3	Ancient Maltese genomes and the genetic geography of Neolithic Europe. <i>Current Biology</i> , 2022, 32, 2668-2680.e6.	1.8	9
4	Genome-wide local ancestry and evidence for mitonuclear coadaptation in African hybrid cattle populations. <i>IScience</i> , 2022, 25, 104672.	1.9	8
5	Geographical contrasts of Y-chromosomal haplogroups from wild and domestic goats reveal ancient migrations and recent introgressions. <i>Molecular Ecology</i> , 2022, 31, 4364-4380.	2.0	5
6	EVOSHEEP: the makeup of sheep breeds in the ancient Near East. <i>Antiquity</i> , 2021, 95, .	0.5	4
7	Exploring the phylogeography and population dynamics of the giant deer (<i>Megaloceros</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 <i>Proceedings of the National Academy of Sciences</i> , 2021, 288, 20201864.	1.2	6
8	Herded and hunted goat genomes from the dawn of domestication in the Zagros Mountains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	32
9	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
10	Ancient genomics reveals tripartite origins of Japanese populations. <i>Science Advances</i> , 2021, 7, eabh2419.	4.7	24
11	Kouprey (<i>Bos sauveli</i>) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	1.9	8
12	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
13	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	4.7	86
14	Genomic analysis of Irish bog butter. <i>Journal of Archaeological Science: Reports</i> , 2020, 31, 102368.	0.2	2
15	A dynastic elite in monumental Neolithic society. <i>Nature</i> , 2020, 582, 384-388.	13.7	94
16	Animal domestication in the era of ancient genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 449-460.	7.7	119
17	Screening archaeological bone for palaeogenetic and palaeoproteomic studies. <i>PLoS ONE</i> , 2020, 15, e0235146.	1.1	34
18	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17231-17238.	3.3	101

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19	Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. <i>Science</i> , 2019, 365, 173-176.	6.0	138
20	Documenting Domestication. , 2019, , .		78
21	Genomic Evidence of Widespread Admixture from Polar Bears into Brown Bears during the Last Ice Age. <i>Molecular Biology and Evolution</i> , 2018, 35, 1120-1129.	3.5	91
22	Origins and genetic legacies of the Caribbean Taino. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2341-2346.	3.3	64
23	Ancient goat genomes reveal mosaic domestication in the Fertile Crescent. <i>Science</i> , 2018, 361, 85-88.	6.0	149
24	The Icemanâ€™s Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	1.8	39
25	Whole-genome resequencing reveals world-wide ancestry and adaptive introgression events of domesticated cattle in East Asia. <i>Nature Communications</i> , 2018, 9, 2337.	5.8	253
26	Insular Celtic population structure and genomic footprints of migration. <i>PLoS Genetics</i> , 2018, 14, e1007152.	1.5	30
27	The Neolithic Transition in the Baltic Was Not Driven by Admixture with Early European Farmers. <i>Current Biology</i> , 2017, 27, 576-582.	1.8	147
28	Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago. <i>Science Advances</i> , 2017, 3, e1601877.	4.7	100
29	Capturing goats: documenting two hundred years of mitochondrial DNA diversity among goat populations from Britain and Ireland. <i>Biology Letters</i> , 2017, 13, 20160876.	1.0	15
30	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , 2017, 8, 14774.	5.8	114
31	The York Gospels: a 1000-year biological palimpsest. <i>Royal Society Open Science</i> , 2017, 4, 170988.	1.1	66
32	The population genomics of archaeological transition in west Iberia: Investigation of ancient substructure using imputation and haplotype-based methods. <i>PLoS Genetics</i> , 2017, 13, e1006852.	1.5	122
33	Comparing the performance of three ancient <sc>DNA</sc> extraction methods for high-throughput sequencing. <i>Molecular Ecology Resources</i> , 2016, 16, 459-469.	2.2	127
34	A whole mitochondria analysis of the Tyrolean Icemanâ€™s leather provides insights into the animal sources of Copper Age clothing. <i>Scientific Reports</i> , 2016, 6, 31279.	1.6	95
35	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	6.0	230
36	Early farmers from across Europe directly descended from Neolithic Aegeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6886-6891.	3.3	376

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37	Genomic and archaeological evidence suggest a dual origin of domestic dogs. <i>Science</i> , 2016, 352, 1228-1231.	6.0	366
38	A genome-wide association study for genetic susceptibility to <i>Mycobacterium bovis</i> infection in dairy cattle identifies a susceptibility QTL on chromosome 23. <i>Genetics Selection Evolution</i> , 2016, 48, 19.	1.2	53
39	Genomic signals of migration and continuity in Britain before the Anglo-Saxons. <i>Nature Communications</i> , 2016, 7, 10326.	5.8	100
40	Neolithic and Bronze Age migration to Ireland and establishment of the insular Atlantic genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 368-373.	3.3	199
41	Animal origin of 13th-century uterine vellum revealed using noninvasive peptide fingerprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15066-15071.	3.3	140
42	Genome-wide association study for calving performance using high-density genotypes in dairy and beef cattle. <i>Genetics Selection Evolution</i> , 2015, 47, 47.	1.2	63
43	Detection of novel germline mutations for breast cancer in non- <i>BRCA1/2</i> families. <i>FEBS Journal</i> , 2015, 282, 3424-3437.	2.2	50
44	Admixture mapping of tuberculosis and pigmentation-related traits in an African- <i>European</i> hybrid cattle population. <i>Frontiers in Genetics</i> , 2015, 6, 210.	1.1	9
45	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. <i>Nature Communications</i> , 2015, 6, 8912.	5.8	334
46	A second-generation Irish genome-wide association study for amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2015, 36, 1221.e7-1221.e13.	1.5	10
47	Homozygosity mapping in an Irish ALS case-control cohort describes local demographic phenomena and points towards potential recessive risk loci. <i>Genomics</i> , 2015, 105, 237-241.	1.3	15
48	Genome sequencing of the extinct Eurasian wild aurochs, <i>Bos primigenius</i> , illuminates the phylogeography and evolution of cattle. <i>Genome Biology</i> , 2015, 16, 234.	3.8	178
49	How Much Is That in Dog Years? The Advent of Canine Population Genomics. <i>PLoS Genetics</i> , 2014, 10, e1004093.	1.5	46
50	Meta-Analysis of Mitochondrial DNA Reveals Several Population Bottlenecks during Worldwide Migrations of Cattle. <i>Diversity</i> , 2014, 6, 178-187.	0.7	51
51	Genome flux and stasis in a five millennium transect of European prehistory. <i>Nature Communications</i> , 2014, 5, 5257.	5.8	542
52	Analysis of the hexanucleotide repeat expansion and founder haplotype at C9ORF72 in an Irish psychosis case-control sample. <i>Neurobiology of Aging</i> , 2014, 35, 1510.e1-1510.e5.	1.5	20
53	UBQLN2 mutations are not a frequent cause of amyotrophic lateral sclerosis in Ireland. <i>Neurobiology of Aging</i> , 2014, 35, 267.e9-267.e11.	1.5	8
54	Genetic Evidence of African Slavery at the Beginning of the Trans-Atlantic Slave Trade. <i>Scientific Reports</i> , 2014, 4, 5994.	1.6	24

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55	Morphological and genetic evidence for early Holocene cattle management in northeastern China. <i>Nature Communications</i> , 2013, 4, 2755.	5.8	82
56	Delineating the genetic heterogeneity of ALS using targeted high-throughput sequencing. <i>Journal of Medical Genetics</i> , 2013, 50, 776-783.	1.5	151
57	The Origins of Cattle. , 2012, , 1-10.		3
58	A Genome Wide Association Scan of Bovine Tuberculosis Susceptibility in Holstein-Friesian Dairy Cattle. <i>PLoS ONE</i> , 2012, 7, e30545.	1.1	66
59	Cognitive and clinical characteristics of patients with amyotrophic lateral sclerosis carrying a C9orf72 repeat expansion: a population-based cohort study. <i>Lancet Neurology</i> , The, 2012, 11, 232-240.	4.9	493
60	Dual Origins of Dairy Cattle Farming – Evidence from a Comprehensive Survey of European Y-Chromosomal Variation. <i>PLoS ONE</i> , 2011, 6, e15922.	1.1	79
61	Zebu Cattle Are an Exclusive Legacy of the South Asia Neolithic. <i>Molecular Biology and Evolution</i> , 2010, 27, 1-6.	3.5	217
62	The Differential Evolutionary Dynamics of Avian Cytokine and TLR Gene Classes. <i>Journal of Immunology</i> , 2010, 184, 6993-7000.	0.4	63
63	Cattle demographic history modelled from autosomal sequence variation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2010, 365, 2531-2539.	1.8	69
64	A Complete Mitochondrial Genome Sequence from a Mesolithic Wild Aurochs (<i>Bos primigenius</i>). <i>PLoS ONE</i> , 2010, 5, e9255.	1.1	73
65	Contrasting evolution of diversity at two disease-associated chicken genes. <i>Immunogenetics</i> , 2009, 61, 303-314.	1.2	13
66	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
67	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	6.0	746
68	Evidence of balanced diversity at the chicken interleukin 4 receptor alpha chain locus. <i>BMC Evolutionary Biology</i> , 2009, 9, 136.	3.2	13
69	Detecting the effects of selection at the population level in six bovine immune genes. <i>BMC Genetics</i> , 2008, 9, 62.	2.7	10
70	Genetic investigation of the patrilineal kinship structure of early medieval Ireland. <i>American Journal of Physical Anthropology</i> , 2008, 136, 415-422.	2.1	18
71	A genome-wide association study of sporadic ALS in a homogenous Irish population. <i>Human Molecular Genetics</i> , 2007, 17, 768-774.	1.4	182
72	Mitochondrial DNA analysis shows a Near Eastern Neolithic origin for domestic cattle and no indication of domestication of European aurochs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1377-1385.	1.2	209

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73	Ancient DNA, pig domestication, and the spread of the Neolithic into Europe. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15276-15281.	3.3	414
74	Duality in <i>Bos indicus</i> mtDNA diversity: Support for geographical complexity in zebu domestication. , 2007, , 385-391.		35
75	Genetic Evidence for the Convergent Evolution of Light Skin in Europeans and East Asians. Molecular Biology and Evolution, 2006, 24, 710-722.	3.5	344
76	A Y-Chromosome Signature of Hegemony in Gaelic Ireland. American Journal of Human Genetics, 2006, 78, 334-338.	2.6	119
77	The scale and nature of Viking settlement in Ireland from Y-chromosome admixture analysis. European Journal of Human Genetics, 2006, 14, 1288-1294.	1.4	64
78	Y-chromosomes and the extent of patrilineal ancestry in Irish surnames. Human Genetics, 2006, 119, 212-219.	1.8	61
79	Assessing the Relative Ages of Admixture in the Bovine Hybrid Zones of Africa and the Near East Using X Chromosome Haplotype Mosaicism. Genetics, 2006, 173, 1503-1510.	1.2	57
80	Genetic Signatures of a Mediterranean Influence in Iberian Peninsula Sheep Husbandry. Molecular Biology and Evolution, 2006, 23, 1420-1426.	3.5	94
81	Ancient DNA analysis of 101 cattle remains: limits and prospects. Journal of Archaeological Science, 2004, 31, 695-710.	1.2	76
82	DNA markers reveal the complexity of livestock domestication. Nature Reviews Genetics, 2003, 4, 900-910.	7.7	428
83	African Pastoralism: Genetic Imprints of Origins and Migrations. Science, 2002, 296, 336-339.	6.0	488
84	Genetic evidence for Near-Eastern origins of European cattle. Nature, 2001, 410, 1088-1091.	13.7	547
85	Y-chromosome variation and Irish origins. Nature, 2000, 404, 351-352.	13.7	113
86	Mitochondrial sequence variation suggests an African influence in Portuguese cattle. Proceedings of the Royal Society B: Biological Sciences, 1999, 266, 597-603.	1.2	100
87	Genetics and domestic cattle origins. Evolutionary Anthropology, 1998, 6, 79-86.	1.7	127
88	Microsatellite DNA Variation and the Evolution, Domestication and Phylogeography of Taurine and Zebu Cattle (<i>Bos taurus</i> and <i>Bos indicus</i>). Genetics, 1997, 146, 1071-1086.	1.2	430