

# Daniel G Bradley

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1118028/publications.pdf>

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	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
2	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	6.0	746
3	Genetic evidence for Near-Eastern origins of European cattle. <i>Nature</i> , 2001, 410, 1088-1091.	13.7	547
4	Genome flux and stasis in a five millennium transect of European prehistory. <i>Nature Communications</i> , 2014, 5, 5257.	5.8	542
5	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
6	African Pastoralism: Genetic Imprints of Origins and Migrations. <i>Science</i> , 2002, 296, 336-339.	6.0	488
7	Microsatellite DNA Variation and the Evolution, Domestication and Phylogeography of Taurine and Zebu Cattle ( <i>Bos taurus</i> and <i>Bos indicus</i> ). <i>Genetics</i> , 1997, 146, 1071-1086.	1.2	430
8	DNA markers reveal the complexity of livestock domestication. <i>Nature Reviews Genetics</i> , 2003, 4, 900-910.	7.7	428
9	Ancient DNA, pig domestication, and the spread of the Neolithic into Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15276-15281.	3.3	414
10	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
11	Genomic and archaeological evidence suggest a dual origin of domestic dogs. <i>Science</i> , 2016, 352, 1228-1231.	6.0	366
12	Genetic Evidence for the Convergent Evolution of Light Skin in Europeans and East Asians. <i>Molecular Biology and Evolution</i> , 2006, 24, 710-722.	3.5	344
13	Upper Palaeolithic genomes reveal deep roots of modern Eurasians. <i>Nature Communications</i> , 2015, 6, 8912.	5.8	334
14	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
15	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	6.0	230
16	Zebu Cattle Are an Exclusive Legacy of the South Asia Neolithic. <i>Molecular Biology and Evolution</i> , 2010, 27, 1-6.	3.5	217
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Delineating the genetic heterogeneity of ALS using targeted high-throughput sequencing. <i>Journal of Medical Genetics</i> , 2013, 50, 776-783.	1.5	151
22	Ancient goat genomes reveal mosaic domestication in the Fertile Crescent. <i>Science</i> , 2018, 361, 85-88.	6.0	149
23	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
24	Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.	13.7	143
25	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
26	Ancient cattle genomics, origins, and rapid turnover in the Fertile Crescent. <i>Science</i> , 2019, 365, 173-176.	6.0	138
27	Genetics and domestic cattle origins. <i>Evolutionary Anthropology</i> , 1998, 6, 79-86.	1.7	127
28	Comparing the performance of three ancient <i>scp</i> >DNA</scp> extraction methods for high-throughput sequencing. <i>Molecular Ecology Resources</i> , 2016, 16, 459-469.	2.2	127
29	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
30	A Y-Chromosome Signature of Hegemony in Gaelic Ireland. <i>American Journal of Human Genetics</i> , 2006, 78, 334-338.	2.6	119
31	Animal domestication in the era of ancient genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 449-460.	7.7	119
32	Genetic correlation between amyotrophic lateral sclerosis and schizophrenia. <i>Nature Communications</i> , 2017, 8, 14774.	5.8	114
33	Y-chromosome variation and Irish origins. <i>Nature</i> , 2000, 404, 351-352.	13.7	113
34	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
35	Mitochondrial sequence variation suggests an African influence in Portuguese cattle. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 597-603.	1.2	100
36	Genomic signals of migration and continuity in Britain before the Anglo-Saxons. <i>Nature Communications</i> , 2016, 7, 10326.	5.8	100

#	ARTICLE	IF	CITATIONS
37	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
38	A whole mitochondria analysis of the Tyrolean Iceman's leather provides insights into the animal sources of Copper Age clothing. <i>Scientific Reports</i> , 2016, 6, 31279.	1.6	95
39	Genetic Signatures of a Mediterranean Influence in Iberian Peninsula Sheep Husbandry. <i>Molecular Biology and Evolution</i> , 2006, 23, 1420-1426.	3.5	94
40	A dynastic elite in monumental Neolithic society. <i>Nature</i> , 2020, 582, 384-388.	13.7	94
41	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
42	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	4.7	86
43	Morphological and genetic evidence for early Holocene cattle management in northeastern China. <i>Nature Communications</i> , 2013, 4, 2755.	5.8	82
44	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
45	Documenting Domestication. , 2019, , .		78
46	Ancient DNA analysis of 101 cattle remains: limits and prospects. <i>Journal of Archaeological Science</i> , 2004, 31, 695-710.	1.2	76
47	A Complete Mitochondrial Genome Sequence from a Mesolithic Wild Aurochs ( <i>Bos primigenius</i> ). <i>PLoS ONE</i> , 2010, 5, e9255.	1.1	73
48	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
49	A Genome Wide Association Scan of Bovine Tuberculosis Susceptibility in Holstein-Friesian Dairy Cattle. <i>PLoS ONE</i> , 2012, 7, e30545.	1.1	66
50	The York Gospels: a 1000-year biological palimpsest. <i>Royal Society Open Science</i> , 2017, 4, 170988.	1.1	66
51	The scale and nature of Viking settlement in Ireland from Y-chromosome admixture analysis. <i>European Journal of Human Genetics</i> , 2006, 14, 1288-1294.	1.4	64
52	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
53	The Differential Evolutionary Dynamics of Avian Cytokine and TLR Gene Classes. <i>Journal of Immunology</i> , 2010, 184, 6993-7000.	0.4	63
54	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

#	ARTICLE	IF	CITATIONS
55	Y-chromosomes and the extent of patrilineal ancestry in Irish surnames. <i>Human Genetics</i> , 2006, 119, 212-219.	1.8	61
56	Assessing the Relative Ages of Admixture in the Bovine Hybrid Zones of Africa and the Near East Using X Chromosome Haplotype Mosaicism. <i>Genetics</i> , 2006, 173, 1503-1510.	1.2	57
57	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
58	Meta-Analysis of Mitochondrial DNA Reveals Several Population Bottlenecks during Worldwide Migrations of Cattle. <i>Diversity</i> , 2014, 6, 178-187.	0.7	51
59	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
60	How Much Is That in Dog Years? The Advent of Canine Population Genomics. <i>PLoS Genetics</i> , 2014, 10, e1004093.	1.5	46
61	The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. <i>Current Biology</i> , 2018, 28, 2348-2355.e9.	1.8	39
62	Duality in <i>Bos indicus</i> mtDNA diversity: Support for geographical complexity in zebu domestication. , 2007, , 385-391.		35
63	Screening archaeological bone for palaeogenetic and palaeoproteomic studies. <i>PLoS ONE</i> , 2020, 15, e0235146.	1.1	34
64	Hered 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
65	Insular Celtic population structure and genomic footprints of migration. <i>PLoS Genetics</i> , 2018, 14, e1007152.	1.5	30
66	Genetic Evidence of African Slavery at the Beginning of the Trans-Atlantic Slave Trade. <i>Scientific Reports</i> , 2014, 4, 5994.	1.6	24
67	Ancient genomics reveals tripartite origins of Japanese populations. <i>Science Advances</i> , 2021, 7, eabh2419.	4.7	24
68	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
69	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
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	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
72	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

#	ARTICLE	IF	CITATIONS
73	Contrasting evolution of diversity at two disease-associated chicken genes. <i>Immunogenetics</i> , 2009, 61, 303-314.	1.2	13
74	Evidence of balanced diversity at the chicken interleukin 4 receptor alpha chain locus. <i>BMC Evolutionary Biology</i> , 2009, 9, 136.	3.2	13
75	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
76	Detecting the effects of selection at the population level in six bovine immune genes. <i>BMC Genetics</i> , 2008, 9, 62.	2.7	10
77	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
78	Admixture mapping of tuberculosis and pigmentation-related traits in an African-â€œEuropean hybrid cattle population. <i>Frontiers in Genetics</i> , 2015, 6, 210.	1.1	9
79	Ancient Maltese genomes and the genetic geography of Neolithic Europe. <i>Current Biology</i> , 2022, 32, 2668-2680.e6.	1.8	9
80	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
81	Kouprey ( <i>Bos sauveli</i> ) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	1.9	8
82	Genome-wide local ancestry and evidence for mitonuclear coadaptation in African hybrid cattle populations. <i>IScience</i> , 2022, 25, 104672.	1.9	8
83	Exploring the phylogeography and population dynamics of the giant deer ( <i>Megaloceros</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj <i>Sciences</i> , 2021, 288, 20201864.	1.2	6
84	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
85	EVOSHEEP: the makeup of sheep breeds in the ancient Near East. <i>Antiquity</i> , 2021, 95, .	0.5	4
86	The Origins of Cattle. , 2012, , 1-10.		3
87	Genomic analysis of Irish bog butter. <i>Journal of Archaeological Science: Reports</i> , 2020, 31, 102368.	0.2	2
88	Bronze Age genomes reveal migration to Britain. <i>Nature</i> , 2022, 601, 512-513.	18.7	1