

# Harris A Lewin

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2894825/publications.pdf>

Version: 2024-02-01

117  
papers

14,354  
citations

34016

52  
h-index

24179

110  
g-index

125  
all docs

125  
docs citations

125  
times ranked

15642  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ethical, legal, and social issues in the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115859119.	3.3	8
2	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	124
3	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
4	Why sequence all eukaryotes?. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	51
5	Conservation of chromatin conformation in carnivores. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
6	Africa: sequence 100,000 species to safeguard biodiversity. Nature, 2022, 603, 388-392.	13.7	19
7	Augmin-dependent microtubule self-organization drives kinetochore fiber maturation in mammals. Cell Reports, 2022, 39, 110610.	2.9	14
8	Vertebrate Chromosome Evolution. Annual Review of Animal Biosciences, 2021, 9, 1-27.	3.6	34
9	The CALeDNA program: Citizen scientists and researchers inventory California's biodiversity. California Agriculture, 2021, 75, 20-32.	0.5	20
10	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
11	Population genomics of the critically endangered kākāpō. Cell Genomics, 2021, 1, 100002.	3.0	106
12	Platypus and echidna genomes reveal mammalian biology and evolution. Nature, 2021, 592, 756-762.	13.7	85
13	Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22311-22322.	3.3	517
14	An integrated chromosome-scale genome assembly of the Masai giraffe ( <i>Giraffa camelopardalis</i> ) Tj ETQq0 0 0 rgBT /Qverlock 10 Tf 50 2	3.3	13
15	Precision nomenclature for the new genomics. GigaScience, 2019, 8, .	3.3	23
16	Large-scale ruminant genome sequencing provides insights into their evolution and distinct traits. Science, 2019, 364, .	6.0	266
17	Fine-tuned adaptation of embryoâ€‘endometrium pairs at implantation revealed by transcriptome analyses in <i>Bos taurus</i> . PLoS Biology, 2019, 17, e3000046.	2.6	14
18	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. Genome Research, 2019, 29, 576-589.	2.4	39

#	ARTICLE	IF	CITATIONS
19	The National Academy of Sciences Prize in Food and Agriculture Science. <i>Advances in Agronomy</i> , 2019, 158, 311-319.	2.4	0
20	A near-chromosome-scale genome assembly of the gemsbok ( <i>Oryx gazella</i> ): an iconic antelope of the Kalahari desert. <i>GigaScience</i> , 2019, 8, .	3.3	138
21	Earth BioGenome Project: Sequencing life for the future of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4325-4333.	3.3	652
22	Chromosome Segregation Is Biased by Kinetochore Size. <i>Current Biology</i> , 2018, 28, 1344-1356.e5.	1.8	94
23	Reconstruction and evolutionary history of eutherian chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5379-E5388.	3.3	94
24	Synteny Explorer: An Interactive Visualization Application for Teaching Genome Evolution. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2017, 23, 711-720.	2.9	7
25	Diversity and population-genetic properties of copy number variations and multicopy genes in cattle. <i>DNA Research</i> , 2016, 23, 253-262.	1.5	59
26	Systems Analysis of Early Host Gene Expression Provides Clues for Transient <i>Mycobacterium avium</i> ssp <i>avium</i> vs. Persistent <i>Mycobacterium avium</i> ssp <i>paratuberculosis</i> Intestinal Infections. <i>PLoS ONE</i> , 2016, 11, e0161946.	1.1	12
27	Massive dysregulation of genes involved in cell signaling and placental development in cloned cattle conceptus and maternal endometrium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14492-14501.	3.3	44
28	Systematic profiling of short tandem repeats in the cattle genome. <i>Genome Biology and Evolution</i> , 2016, 9, evw256.	1.1	20
29	Identification of a nonsense mutation in APAF1 that is likely causal for a decrease in reproductive efficiency in Holstein dairy cattle. <i>Journal of Dairy Science</i> , 2016, 99, 6693-6701.	1.4	66
30	Memories of Carl from an improbable friend. <i>RNA Biology</i> , 2014, 11, 273-278.	1.5	0
31	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	5.8	124
32	Messenger RNAs in metaphase II oocytes correlate with successful embryo development to the blastocyst stage. <i>Zygote</i> , 2014, 22, 69-79.	0.5	21
33	The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation. <i>Trends in Genetics</i> , 2013, 29, 206-214.	2.9	527
34	Inferring Demography from Runs of Homozygosity in Whole-Genome Sequence, with Correction for Sequence Errors. <i>Molecular Biology and Evolution</i> , 2013, 30, 2209-2223.	3.5	91
35	Draft genome sequence of the Tibetan antelope. <i>Nature Communications</i> , 2013, 4, 1858.	5.8	229
36	Changes in WNT signaling-related gene expression associated with development and cloning in bovine extraembryonic and endometrial tissues during the periimplantation period. <i>Molecular Reproduction and Development</i> , 2013, 80, 977-987.	1.0	15

#	ARTICLE	IF	CITATIONS
37	Reference-assisted chromosome assembly. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1785-1790.	3.3	124
38	Systems Biology Analysis of Brucella Infected Peyer's Patch Reveals Rapid Invasion with Modest Transient Perturbations of the Host Transcriptome. PLoS ONE, 2013, 8, e81719.	1.1	24
39	Whole-genome resequencing of two elite sires for the detection of haplotypes under selection in dairy cattle. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7693-7698.	3.3	67
40	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190
41	Comparative Epigenomic Annotation of Regulatory DNA. Cell, 2012, 149, 1381-1392.	13.5	188
42	Old and New Stories: Revelations from Functional Analysis of the Bovine Mammary Transcriptome during the Lactation Cycle. PLoS ONE, 2012, 7, e33268.	1.1	136
43	The yak genome and adaptation to life at high altitude. Nature Genetics, 2012, 44, 946-949.	9.4	708
44	Uncoupled Embryonic and Extra-Embryonic Tissues Compromise Blastocyst Development after Somatic Cell Nuclear Transfer. PLoS ONE, 2012, 7, e38309.	1.1	29
45	Multisite haplotype on cattle chromosome 3 is associated with quantitative trait locus effects on lactation traits. Physiological Genomics, 2011, 43, 1185-1197.	1.0	12
46	Role of SPI-1 Secreted Effectors in Acute Bovine Response to Salmonella enterica Serovar Typhimurium: A Systems Biology Analysis Approach. PLoS ONE, 2011, 6, e26869.	1.1	41
47	Predisposition of cows to mastitis in non-infected mammary glands: effects of dietary-induced negative energy balance during mid-lactation on immune-related genes. Functional and Integrative Genomics, 2011, 11, 151-156.	1.4	10
48	Transferase activity function and system development process are critical in cattle embryo development. Functional and Integrative Genomics, 2011, 11, 139-150.	1.4	9
49	A small set of extra-embryonic genes defines a new landmark for bovine embryo staging. Reproduction, 2011, 141, 79-89.	1.1	33
50	Mammary gene expression profiles during an intramammary challenge reveal potential mechanisms linking negative energy balance with impaired immune response. Physiological Genomics, 2010, 41, 161-170.	1.0	56
51	Rewirable gene regulatory networks in the preimplantation embryonic development of three mammalian species. Genome Research, 2010, 20, 804-815.	2.4	204
52	Endometrium as an early sensor of in vitro embryo manipulation technologies. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5687-5692.	3.3	191
53	It's a Bull's Market. Science, 2009, 324, 478-479.	6.0	28
54	Every genome sequence needs a good map. Genome Research, 2009, 19, 1925-1928.	2.4	148

#	ARTICLE	IF	CITATIONS
55	SyntenyTracker: a tool for defining homologous synteny blocks using radiation hybrid maps and whole-genome sequence. BMC Research Notes, 2009, 2, 148.	0.6	28
56	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
57	Breakpoint regions and homologous synteny blocks in chromosomes have different evolutionary histories. Genome Research, 2009, 19, 770-777.	2.4	163
58	Gene expression profiles of bovine caruncular and intercaruncular endometrium at implantation. Physiological Genomics, 2009, 39, 14-27.	1.0	145
59	Modulation of the Bovine Trophoblastic Innate Immune Response by <i>Brucella abortus</i> . Infection and Immunity, 2008, 76, 1897-1907.	1.0	55
60	Aberrant gene expression patterns in placentomes are associated with phenotypically normal and abnormal cattle cloned by somatic cell nuclear transfer. Physiological Genomics, 2008, 33, 65-77.	1.0	73
61	Nutrition-induced ketosis alters metabolic and signaling gene networks in liver of periparturient dairy cows. Physiological Genomics, 2007, 32, 105-116.	1.0	292
62	Nuclear reprogramming of cloned embryos and its implications for therapeutic cloning. Nature Genetics, 2007, 39, 295-302.	9.4	533
63	Plane of nutrition prepartum alters hepatic gene expression and function in dairy cows as assessed by longitudinal transcript and metabolic profiling. Physiological Genomics, 2006, 27, 29-41.	1.0	173
64	Accelerated expansion of group IID-like phospholipase A2 genes in <i>Bos taurus</i> . Genomics, 2006, 87, 527-533.	1.3	11
65	Discovery of eight novel divergent homologs expressed in cattle placenta. Physiological Genomics, 2006, 25, 405-413.	1.0	30
66	Identification of a missense mutation in the bovine ABCG2 gene with a major effect on the QTL on chromosome 6 affecting milk yield and composition in Holstein cattle. Genome Research, 2005, 15, 936-944.	2.4	335
67	A high-resolution whole-genome cattle-human comparative map reveals details of mammalian chromosome evolution. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18526-18531.	3.3	115
68	Global gene expression profiles reveal significant nuclear reprogramming by the blastocyst stage after cloning. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17582-17587.	3.3	184
69	Temporal gene expression profiling of liver from periparturient dairy cows reveals complex adaptive mechanisms in hepatic function. Physiological Genomics, 2005, 23, 217-226.	1.0	198
70	A 7872 cDNA microarray and its use in bovine functional genomics. Veterinary Immunology and Immunopathology, 2005, 105, 235-245.	0.5	52
71	Dynamics of Mammalian Chromosome Evolution Inferred from Multispecies Comparative Maps. Science, 2005, 309, 613-617.	6.0	542
72	A 1463 Gene Cattle-Human Comparative Map With Anchor Points Defined by Human Genome Sequence Coordinates. Genome Research, 2004, 14, 1424-1437.	2.4	133

#	ARTICLE	IF	CITATIONS
73	Conservation of Babesia bovis Small Heat Shock Protein (Hsp20) among Strains and Definition of T Helper Cell Epitopes Recognized by Cattle with Diverse Major Histocompatibility Complex Class II Haplotypes. <i>Infection and Immunity</i> , 2004, 72, 1096-1106.	1.0	31
74	Cytokine mRNA expression in B cells from bovine leukemia virus-infected cattle with persistent lymphocytosis. <i>Cytokine</i> , 2004, 28, 25-28.	1.4	20
75	Cloning and characterization of FAM13A1 gene near a milk protein QTL on BTA6: evidence for population-wide linkage disequilibrium in Israeli Holsteins. <i>Genomics</i> , 2004, 84, 374-383.	1.3	54
76	MHC class II-like genes in cattle, MHCLA, with similarity to genes encoding NK cell stimulatory ligands. <i>Immunogenetics</i> , 2003, 55, 16-22.	1.2	7
77	Neospora caninum -Infected Cattle Develop Parasite-Specific CD4 + Cytotoxic T Lymphocytes. <i>Infection and Immunity</i> , 2003, 71, 3272-3279.	1.0	53
78	A Cattle Human Comparative Map Built with Cattle BAC-Ends and Human Genome Sequence. <i>Genome Research</i> , 2003, 13, 1966-1972.	2.4	126
79	DNA-Encoded Fetal Liver Tyrosine Kinase 3 Ligand and Granulocyte Macrophage-Colony-Stimulating Factor Increase Dendritic Cell Recruitment to the Inoculation Site and Enhance Antigen-Specific CD4+ T Cell Responses Induced by DNA Vaccination of Outbred Animals. <i>Journal of Immunology</i> , 2002, 169, 3837-3846.	0.4	56
80	A 3800 GENE MICROARRAY FOR CATTLE FUNCTIONAL GENOMICS: COMPARISON OF GENE EXPRESSION IN SPLEEN, PLACENTA, AND BRAIN. <i>Animal Biotechnology</i> , 2002, 13, 163-172.	0.7	63
81	Major Histocompatibility Complex Class II DR-Restricted Memory CD4 + T Lymphocytes Recognize Conserved Immunodominant Epitopes of Anaplasma marginale Major Surface Protein 1a. <i>Infection and Immunity</i> , 2002, 70, 5521-5532.	1.0	44
82	Highly Conserved Regions of the Immunodominant Major Surface Protein 2 of the Genogroup II Ehrlichial Pathogen Anaplasma marginale Are Rich in Naturally Derived CD4+ T Lymphocyte Epitopes that Elicit Strong Recall Responses. <i>Journal of Immunology</i> , 2001, 166, 1114-1124.	0.4	58
83	CD4 + T Lymphocytes from Calves Immunized with Anaplasma marginale Major Surface Protein 1 (MSP1), a Heteromeric Complex of MSP1a and MSP1b, Preferentially Recognize the MSP1a Carboxyl Terminus That Is Conserved among Strains. <i>Infection and Immunity</i> , 2001, 69, 6853-6862.	1.0	57
84	Phylogenomic Analysis of the 20S Proteasome Gene Family from Early-Diverging Eukaryotes. <i>Journal of Molecular Evolution</i> , 2000, 51, 532-543.	0.8	40
85	Compass of 47,787 cattle ESTs. <i>Animal Biotechnology</i> , 2000, 11, 75-241.	0.7	33
86	An Ordered Comparative Map of the Cattle and Human Genomes. <i>Genome Research</i> , 2000, 10, 1359-1368.	2.4	271
87	Comparative organization and function of the major histocompatibility complex of domesticated cattle. <i>Immunological Reviews</i> , 1999, 167, 145-158.	2.8	125
88	Fine-Mapping of a Region of Variation in Recombination Rate on BTA23 to the D23S22-D23S23 Interval Using Sperm Typing and Meiotic Breakpoint Analysis. <i>Genomics</i> , 1999, 59, 143-149.	1.3	10
89	Comparative analysis of 82 expressed sequence tags from a cattle ovary cDNA library. <i>Mammalian Genome</i> , 1998, 9, 545-549.	1.0	53
90	Development of a Syngeneic Bovine Fibroblast Cell Line: Implications for the Study of Bovine Cytotoxic T Lymphocytes. <i>Viral Immunology</i> , 1998, 11, 37-48.	0.6	9

#	ARTICLE	IF	CITATIONS
91	Genetic Evaluation of a Demographic Bottleneck in the Greater Prairie Chicken. <i>Conservation Biology</i> , 1998, 12, 836-843.	2.4	114
92	A New Approach to the Problem of Multiple Comparisons in the Genetic Dissection of Complex Traits. <i>Genetics</i> , 1998, 150, 1699-1706.	1.2	165
93	A phylogenetic analysis of cattle DRB3 alleles with a deletion of codon 65. <i>Immunogenetics</i> , 1997, 47, 23-29.	1.2	15
94	Aberrant expression of immunoglobulin mRNA in bovine leukemia virus-infected cattle. <i>Veterinary Immunology and Immunopathology</i> , 1996, 53, 87-94.	0.5	8
95	Use of Flow Cytometry and RT-PCR for Detecting Gene Expression by Single Cells. <i>BioTechniques</i> , 1996, 21, 286-291.	0.8	26
96	Linkage information content and efficiency of full-sib and half-sib designs for gene mapping. <i>Theoretical and Applied Genetics</i> , 1995, 90, 699-706.	1.8	17
97	Gene-Centromere Mapping of Bovine DYA, DRB3, and PRL Using Secondary Oocytes and First Polar Bodies: Evidence for Four-Strand Double Crossovers between DYA and DRB3. <i>Genomics</i> , 1995, 27, 33-39.	1.3	21
98	Genetic Mapping of F13A to BTA23 by Sperm Typing: Difference in Recombination Rate between Bulls in the DYA-PRL Interval. <i>Genomics</i> , 1995, 27, 113-118.	1.3	33
99	Order of bovine DRB3, DYA, and PRL determined by sperm typing. <i>Mammalian Genome</i> , 1993, 4, 113-118.	1.0	47
100	Close linkage between bovine prolactin and BoLA-DRB3 genes: Genetic mapping in cattle by single sperm typing. <i>Genomics</i> , 1992, 13, 44-48.	1.3	66
101	Development of persistent lymphocytosis in cattle is closely associated with DRB2. <i>Immunogenetics</i> , 1992, 37, 64-68.	1.2	25
102	RFLP analysis of SLA haplotypes in Swiss large white and American Hampshire pigs using SLA class I and class II probes. <i>Animal Biotechnology</i> , 1991, 2, 75-91.	0.7	10
103	Integrated Strategies and Methodologies for the Genetic Improvement of Animals. <i>Journal of Dairy Science</i> , 1990, 73, 2647-2656.	1.4	2
104	Isoelectric focusing of bovine major histocompatibility complex class II molecules. <i>European Journal of Immunology</i> , 1989, 19, 567-570.	1.6	13
105	Disease Resistance and Immune Response Genes in Cattle: Strategies for Their Detection and Evidence of Their Existence. <i>Journal of Dairy Science</i> , 1989, 72, 1334-1348.	1.4	56
106	Phenotypic characterization of bovine lymphoblastoid cell lines. <i>Veterinary Immunology and Immunopathology</i> , 1989, 23, 293-307.	0.5	26
107	Genetic aspects of bovine leukaemia virus infection and disease progression. <i>Animal Genetics</i> , 1989, 20, 337-339.	0.6	6
108	Association between BoLA and subclinical bovine leukemia virus infection in a herd of Holstein-Friesian cows. <i>Immunogenetics</i> , 1988, 27, 338-344.	1.2	76

#	ARTICLE	IF	CITATIONS
109	Peripheral B Lymphocyte Percentage as an Indicator of Subclinical Progression of Bovine Leukemia Virus Infection. <i>Journal of Dairy Science</i> , 1988, 71, 2526-2534.	1.4	24
110	Current and potential applications of DNA probes in the clinical immunology laboratory. <i>Clinical Immunology Newsletter</i> , 1988, 9, 91-93.	0.1	0
111	The development and analysis of species specific and cross reactive monoclonal antibodies to leukocyte differentiation antigens and antigens of the major histocompatibility complex for use in the study of the immune system in cattle and other species. <i>Veterinary Immunology and Immunopathology</i> , 1987, 15, 337-376.	0.5	277
112	Monoclonal Antibodies: Pragmatic Application of Immunology and Cell Biology <sup>2</sup> . <i>Journal of Animal Science</i> , 1986, 63, 288-309.	0.2	12
113	Monoclonal antibodies that distinguish bovine T and B lymphocytes. <i>Veterinary Immunology and Immunopathology</i> , 1985, 9, 87-102.	0.5	40
114	Monosaccharides define two immunodominant structures of chicken fetal antigen. <i>Cell Differentiation</i> , 1983, 12, 245-248.	1.3	4
115	Characterization of a genetically segregating determinant of chicken fetal antigen by a new hapten inhibition of microcytotoxicity (HIM) assay. <i>Biochemical Genetics</i> , 1982, 20, 425-436.	0.8	7
116	Identification of a galactose-like component of a chicken onco-developmental antigen. <i>Journal of Heredity</i> , 1981, 72, 257-260.	1.0	10
117	Ethical, Legal, and Social Issues in the Earth BioGenome Project. <i>SSRN Electronic Journal</i> , 0, , .	0.4	3