

# Luca Ermini

## List of Publications by Year in descending order

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Version: 2024-02-01

38  
papers

3,179  
citations

279798

23  
h-index

330143

37  
g-index

39  
all docs

39  
docs citations

39  
times ranked

5800  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. <i>Molecular Ecology</i> , 2021, 30, 6144-6161.	3.9	30
2	Evolutionary selection of alleles in the melanophilin gene that impacts on prostate organ function and cancer risk. <i>Evolution, Medicine and Public Health</i> , 2021, 9, 311-321.	2.5	3
3	LeafGo: Leaf to Genome, a quick workflow to produce high-quality de novo plant genomes using long-read sequencing technology. <i>Genome Biology</i> , 2021, 22, 256.	8.8	15
4	LongQC: A Quality Control Tool for Third Generation Sequencing Long Read Data. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 1193-1196.	1.8	80
5	Single cell analysis of clonal architecture in acute myeloid leukaemia. <i>Leukemia</i> , 2019, 33, 1113-1123.	7.2	65
6	Evolutionary dynamics of residual disease in human glioblastoma. <i>Annals of Oncology</i> , 2019, 30, 456-463.	1.2	47
7	The subclonal complexity of STIL-TAL1+ T-cell acute lymphoblastic leukaemia. <i>Leukemia</i> , 2018, 32, 1984-1993.	7.2	26
8	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4763-4770.	7.0	30
9	Zonkey: A simple, accurate and sensitive pipeline to genetically identify equine F1-hybrids in archaeological assemblages. <i>Journal of Archaeological Science</i> , 2017, 78, 147-157.	2.4	44
10	Less effective selection leads to larger genomes. <i>Genome Research</i> , 2017, 27, 1016-1028.	5.5	75
11	Carbon dating cancer: defining the chronology of metastatic progression in colorectal cancer. <i>Annals of Oncology</i> , 2017, 28, 1243-1249.	1.2	25
12	Systematic assessment of the influence of complement gene polymorphisms on kidney transplant outcome. <i>Immunobiology</i> , 2016, 221, 528-534.	1.9	10
13	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	3.3	61
14	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	4.0	142
15	Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. <i>Current Biology</i> , 2015, 25, 2577-2583.	3.9	161
16	Evolutionary Adaptations to Risk of Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 1806.	7.4	11
17	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.	7.1	139
18	Major transitions in human evolution revisited: A tribute to ancient DNA. <i>Journal of Human Evolution</i> , 2015, 79, 4-20.	2.6	37

#	ARTICLE	IF	CITATIONS
19	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	4.0	292
20	Clonal origins of ETV6-RUNX1+ acute lymphoblastic leukemia: studies in monozygotic twins. <i>Leukemia</i> , 2015, 29, 839-846.	7.2	46
21	Positioning the Red Deer ( <i>Cervus elaphus</i> ) Hunted by the Tyrolean Iceman into a Mitochondrial DNA Phylogeny. <i>PLoS ONE</i> , 2014, 9, e100136.	2.5	13
22	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5661-9.	7.1	260
23	Shotgun microbial profiling of fossil remains. <i>Molecular Ecology</i> , 2014, 23, 1780-1798.	3.9	55
24	Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. <i>Nature Protocols</i> , 2014, 9, 1056-1082.	12.0	403
25	Single-cell mutational profiling and clonal phylogeny in cancer. <i>Genome Research</i> , 2013, 23, 2115-2125.	5.5	105
26	Complement polymorphisms: Geographical distribution and relevance to disease. <i>Immunobiology</i> , 2012, 217, 265-271.	1.9	19
27	Phylogenetic Position of a Copper Age Sheep ( <i>Ovis aries</i> ) Mitochondrial DNA. <i>PLoS ONE</i> , 2012, 7, e33792.	2.5	20
28	Common genetic variants in complement genes other than CFH, CD46 and the CFHRs are not associated with aHUS. <i>Molecular Immunology</i> , 2012, 49, 640-648.	2.2	37
29	Composite Single Cell Genetics and Clonal Phylogeny in Acute Lymphoblastic Leukaemia. <i>Blood</i> , 2012, 120, 122-122.	1.4	4
30	Genetic variants in CFH and CD46 are the major susceptibility factors for aHUS – An association study of multiple complement genes. <i>Molecular Immunology</i> , 2011, 48, 1667.	2.2	0
31	Characterization of Nucleotide Misincorporation Patterns in the Iceman's Mitochondrial DNA. <i>PLoS ONE</i> , 2010, 5, e8629.	2.5	18
32	Correcting for Purifying Selection: An Improved Human Mitochondrial Molecular Clock. <i>American Journal of Human Genetics</i> , 2009, 84, 740-759.	6.2	643
33	Complete Mitochondrial Genome Sequence of the Tyrolean Iceman. <i>Current Biology</i> , 2008, 18, 1687-1693.	3.9	101
34	Persistence and decay of the intestinal microbiota's DNA in glacier mummies from the Alps. <i>Journal of Archaeological Science</i> , 2007, 34, 1294-1305.	2.4	21
35	The resolved location of A-tzi's mtDNA within haplogroup K: A reply to Endicott et al.. <i>American Journal of Physical Anthropology</i> , 2007, 132, 591-593.	2.1	3
36	Fine characterization of the Iceman's mtDNA haplogroup. <i>American Journal of Physical Anthropology</i> , 2006, 130, 557-564.	2.1	24

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37	Å-tzi's last meals: DNA analysis of the intestinal content of the Neolithic glacier mummy from the Alps. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12594-12599.	7.1	102
38	DNA Diagenesis: Effect of Environment and Time on Human Bone. Ancient Biomolecules, 2002, 4, 1-7.	0.5	11