

Irene Hernando-Herraez

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7752455/publications.pdf>

Version: 2024-02-01

18
papers

3,006
citations

471509

17
h-index

839539

18
g-index

22
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22
docs citations

22
times ranked

5614
citing authors

#	ARTICLE	IF	CITATIONS
1	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768
2	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013, 23, 1363-1372.	5.5	353
3	Multi-tissue DNA methylation age predictor in mouse. <i>Genome Biology</i> , 2017, 18, 68.	8.8	341
4	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. <i>Cell Reports</i> , 2017, 20, 1215-1228.	6.4	290
5	Single cell transcriptome analysis of human, marmoset and mouse embryos reveals common and divergent features of preimplantation development. <i>Development (Cambridge)</i> , 2018, 145, .	2.5	167
6	Ageing affects DNA methylation drift and transcriptional cell-to-cell variability in mouse muscle stem cells. <i>Nature Communications</i> , 2019, 10, 4361.	12.8	157
7	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003763.	3.5	118
8	A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. <i>ELife</i> , 2015, 4, e07103.	6.0	114
9	The Time Scale of Recombination Rate Evolution in Great Apes. <i>Molecular Biology and Evolution</i> , 2016, 33, 928-945.	8.9	92
10	A comparison of gene expression and DNA methylation patterns across tissues and species. <i>Genome Research</i> , 2020, 30, 250-262.	5.5	91
11	DNA Methylation: Insights into Human Evolution. <i>PLoS Genetics</i> , 2015, 11, e1005661.	3.5	90
12	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	7.1	75
13	Multi-omic rejuvenation of human cells by maturation phase transient reprogramming. <i>ELife</i> , 2022, 11, .	6.0	75
14	The interplay between DNA methylation and sequence divergence in recent human evolution. <i>Nucleic Acids Research</i> , 2015, 43, 8204-8214.	14.5	67
15	A Single-Cell Transcriptomics CRISPR-Activation Screen Identifies Epigenetic Regulators of the Zygotic Genome Activation Program. <i>Cell Systems</i> , 2020, 11, 25-41.e9.	6.2	59
16	Rates and patterns of great ape retrotransposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13457-13462.	7.1	57
17	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. <i>BMC Genomics</i> , 2013, 14, 363.	2.8	48
18	Transcriptome and epigenome diversity and plasticity of muscle stem cells following transplantation. <i>PLoS Genetics</i> , 2020, 16, e1009022.	3.5	22