

Aurora Ruiz-Herrera

List of Publications by Year in descending order

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Version: 2024-02-01

64
papers

3,128
citations

172457

29
h-index

182427

51
g-index

68
all docs

68
docs citations

68
times ranked

4443
citing authors

#	ARTICLE	IF	CITATIONS
1	Unpacking chromatin remodelling in germ cells: implications for development and evolution. <i>Trends in Genetics</i> , 2022, 38, 422-425.	6.7	7
2	Strategies for meiotic sex chromosome dynamics and telomeric elongation in Marsupials. <i>PLoS Genetics</i> , 2022, 18, e1010040.	3.5	9
3	Fragile, unfaithful and persistent Ys on how meiosis can shape sex chromosome evolution. <i>Heredity</i> , 2022, 129, 22-30.	2.6	4
4	3D chromatin remodelling in the germ line modulates genome evolutionary plasticity. <i>Nature Communications</i> , 2022, 13, 2608.	12.8	10
5	Chromosomal evolution in <i>Raphicerus antelope</i> suggests divergent X chromosomes may drive speciation through females, rather than males, contrary to Haldane's rule. <i>Scientific Reports</i> , 2021, 11, 3152.	3.3	3
6	The impact of chromosomal fusions on 3D genome folding and recombination in the germ line. <i>Nature Communications</i> , 2021, 12, 2981.	12.8	34
7	Microchromosomes are building blocks of bird, reptile, and mammal chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	84
8	Meiotic Executioner Genes Protect the Y from Extinction. <i>Trends in Genetics</i> , 2020, 36, 728-738.	6.7	19
9	Whole genome sequencing identifies allelic ratio distortion in sperm involving genes related to spermatogenesis in a swine model. <i>DNA Research</i> , 2020, 27, .	3.4	6
10	The Plasticity of Genome Architecture. <i>Genes</i> , 2020, 11, 1413.	2.4	2
11	Chromosomal Differentiation in Genetically Isolated Populations of the Marsh-Specialist <i>Crocidura suaveolens</i> (Mammalia: Soricidae). <i>Genes</i> , 2020, 11, 270.	2.4	2
12	Three-Dimensional Genomic Structure and Cohesin Occupancy Correlate with Transcriptional Activity during Spermatogenesis. <i>Cell Reports</i> , 2019, 28, 352-367.e9.	6.4	112
13	CENP-A binding domains and recombination patterns in horse spermatocytes. <i>Scientific Reports</i> , 2019, 9, 15800.	3.3	10
14	Chromosomics: Bridging the Gap between Genomes and Chromosomes. <i>Genes</i> , 2019, 10, 627.	2.4	79
15	PRDM9 Diversity at Fine Geographical Scale Reveals Contrasting Evolutionary Patterns and Functional Constraints in Natural Populations of House Mice. <i>Molecular Biology and Evolution</i> , 2019, 36, 1686-1700.	8.9	17
16	Per-Nucleus Crossover Covariation and Implications for Evolution. <i>Cell</i> , 2019, 177, 326-338.e16.	28.9	64
17	Detailed analysis of inversions predicted between two human genomes: errors, real polymorphisms, and their origin and population distribution. <i>Human Molecular Genetics</i> , 2017, 26, ddw415.	2.9	12
18	Recombination correlates with synaptonemal complex length and chromatin loop size in bovids insights into mammalian meiotic chromosomal organization. <i>Chromosoma</i> , 2017, 126, 615-631.	2.2	45

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19	Mammalian Meiotic Recombination: A Toolbox for Genome Evolution. <i>Cytogenetic and Genome Research</i> , 2016, 150, 1-16.	1.1	38
20	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , 2016, 17, 251.	8.8	131
21	Meiotic behaviour of evolutionary sex-autosome translocations in Bovidae. <i>Chromosome Research</i> , 2016, 24, 325-338.	2.2	21
22	Mammalian comparative genomics reveals genetic and epigenetic features associated with genome reshuffling in Rodentia. <i>Genome Biology and Evolution</i> , 2016, 8, evw276.	2.5	21
23	Telomere homeostasis in mammalian germ cells: a review. <i>Chromosoma</i> , 2016, 125, 337-351.	2.2	46
24	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
25	Use of targeted SNP selection for an improved anchoring of the melon (<i>Cucumis melo</i> L.) scaffold genome assembly. <i>BMC Genomics</i> , 2015, 16, 4.	2.8	67
26	An Integrative Breakage Model of genome architecture, reshuffling and evolution. <i>BioEssays</i> , 2015, 37, 479-488.	2.5	54
27	On the origin of Robertsonian fusions in nature: evidence of telomere shortening in wild house mice. <i>Journal of Evolutionary Biology</i> , 2015, 28, 241-249.	1.7	18
28	Validation and Genotyping of Multiple Human Polymorphic Inversions Mediated by Inverted Repeats Reveals a High Degree of Recurrence. <i>PLoS Genetics</i> , 2014, 10, e1004208.	3.5	28
29	Genetic recombination variation in wild Robertsonian mice: on the role of chromosomal fusions and <i>Prdm9</i> allelic background. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140297.	2.6	36
30	Telomeric Repeat-Containing RNA (TERRA) and Telomerase Are Components of Telomeres During Mammalian Gametogenesis ¹ . <i>Biology of Reproduction</i> , 2014, 90, 103.	2.7	36
31	Unraveling the effect of genomic structural changes in the rhesus macaque - implications for the adaptive role of inversions. <i>BMC Genomics</i> , 2014, 15, 530.	2.8	24
32	Telomere homeostasis is compromised in spermatocytes from patients with idiopathic infertility. <i>Fertility and Sterility</i> , 2014, 102, 728-738.e1.	1.0	41
33	Recombination Rates and Genomic Shuffling in Human and Chimpanzee—A New Twist in the Chromosomal Speciation Theory. <i>Molecular Biology and Evolution</i> , 2013, 30, 853-864.	8.9	73
34	Evolution of recombination in eutherian mammals: insights into mechanisms that affect recombination rates and crossover interference. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20131945.	2.6	74
35	Telomeric repeat-containing RNA and telomerase in human fetal oocytes. <i>Human Reproduction</i> , 2013, 28, 414-422.	0.9	30
36	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	27.8	768

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37	Molecular cytogenetic and genomic insights into chromosomal evolution. <i>Heredity</i> , 2012, 108, 28-36.	2.6	51
38	Radiobiology and Reproductionâ€™What Can We Learn from Mammalian Females?. <i>Genes</i> , 2012, 3, 521-544.	2.4	5
39	Polymorphic organization of constitutive heterochromatin in <i>Equus asinus</i> (2n = 62) chromosome 1. <i>Hereditas</i> , 2011, 148, 110-113.	1.4	10
40	A comparative study of the recombination pattern in three species of Platyrrhini monkeys (primates). <i>Chromosoma</i> , 2011, 120, 521-530.	2.2	21
41	Gene amplification in human cells knocked down for RAD54. <i>Genome Integrity</i> , 2011, 2, 5.	1.0	19
42	Assessing the Role of Tandem Repeats in Shaping the Genomic Architecture of Great Apes. <i>PLoS ONE</i> , 2011, 6, e27239.	2.5	35
43	Selection against Robertsonian fusions involving housekeeping genes in the house mouse: integrating data from gene expression arrays and chromosome evolution. <i>Chromosome Research</i> , 2010, 18, 801-808.	2.2	8
44	Mammalian Chromosomal Evolution: From Ancestral States to Evolutionary Regions. , 2010, , 143-158.		1
45	Enhanced gene amplification in human cells knocked down for DNA-PKcs. <i>DNA Repair</i> , 2009, 8, 19-28.	2.8	10
46	Defining the ancestral eutherian karyotype: A cladistic interpretation of chromosome painting and genome sequence assembly data. <i>Chromosome Research</i> , 2008, 16, 1133-1141.	2.2	33
47	Dissection of a Y-autosome translocation in <i>Cryptomys hottentotus</i> (Rodentia, Bathyergidae) and implications for the evolution of a meiotic sex chromosome chain. <i>Chromosoma</i> , 2008, 117, 211-217.	2.2	12
48	Evolutionary plasticity and cancer breakpoints in human chromosome 3. <i>BioEssays</i> , 2008, 30, 1126-1137.	2.5	15
49	Telomeric repeats far from the ends: mechanisms of origin and role in evolution. <i>Cytogenetic and Genome Research</i> , 2008, 122, 219-228.	1.1	181
50	Hemiplasy and homoplasy in the karyotypic phylogenies of mammals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14477-14481.	7.1	51
51	Chromosomal instability in Afrotheria: fragile sites, evolutionary breakpoints and phylogenetic inference from genome sequence assemblies. <i>BMC Evolutionary Biology</i> , 2007, 7, 199.	3.2	37
52	Sex chromosomes of basal placental mammals. <i>Chromosoma</i> , 2007, 116, 511-518.	2.2	16
53	Is mammalian chromosomal evolution driven by regions of genome fragility?. <i>Genome Biology</i> , 2006, 7, R115.	9.6	130
54	Dissecting the mammalian genome â€™ new insights into chromosomal evolution. <i>Trends in Genetics</i> , 2006, 22, 297-301.	6.7	32

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55	Genomic instability in rat: Breakpoints induced by ionising radiation and interstitial telomeric-like sequences. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2006, 595, 156-166.	1.0	20
56	Comparative chromosome painting in <i>Aotus</i> reveals a highly derived evolution. <i>American Journal of Primatology</i> , 2005, 65, 73-85.	1.7	23
57	Evolutionary breakpoints are co-localized with fragile sites and intrachromosomal telomeric sequences in primates. <i>Cytogenetic and Genome Research</i> , 2005, 108, 234-247.	1.1	62
58	Evolutionary conserved chromosomal segments in the human karyotype are bounded by unstable chromosome bands. <i>Cytogenetic and Genome Research</i> , 2005, 108, 161-174.	1.1	34
59	Conservation of aphidicolin-induced fragile sites in Papionini (Primates) species and humans. <i>Chromosome Research</i> , 2004, 12, 683-690.	2.2	31
60	New polymorphisms in a <i>Cebus</i> (Platyrrhini, Primates) species. The case of <i>Cebus nigrivittatus</i> . <i>Caryologia</i> , 2004, 57, 206-209.	0.3	2
61	Chromosomal homologies between <i>Cebus</i> and <i>Ateles</i> (Primates) based on ZOO-FISH and C-banding comparisons. <i>American Journal of Primatology</i> , 2002, 57, 177-188.	1.7	33
62	Distribution of intrachromosomal telomeric sequences (ITS) on <i>Macaca fascicularis</i> (Primates) chromosomes and their implication for chromosome evolution. <i>Human Genetics</i> , 2002, 110, 578-586.	3.8	69
63	Fragile sites in human and <i>Macaca fascicularis</i> chromosomes are breakpoints in chromosome evolution. <i>Chromosome Research</i> , 2002, 10, 33-44.	2.2	46
64	Chromosomal homologies between humans and <i>Cebus apella</i> (Primates) revealed by ZOO-FISH. <i>Mammalian Genome</i> , 2000, 11, 399-401.	2.2	38