

# Marta FarrÃ

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

2,334  
citations

394421  
19  
h-index

377865  
34  
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34  
all docs

34  
docs citations

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times ranked

3910  
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel mtDNA haplotypes represented in the European captive population of the Endangered François's langur ( <i>Trachypithecus francoisi</i> ). <i>International Journal of Primatology</i> , 2022, 43, 533-537.	1.9	3
2	3D chromatin remodelling in the germ line modulates genome evolutionary plasticity. <i>Nature Communications</i> , 2022, 13, 2608.	12.8	10
3	Mitochondrial Genome Evolution, Genetic Diversity, and Population Structure in British Water Voles ( <i>Arvicola amphibius</i> ). <i>Genes</i> , 2021, 12, 138.	2.4	4
4	Identification of sequence changes in myosin II that adjust muscle contraction velocity. <i>PLoS Biology</i> , 2021, 19, e3001248.	5.6	9
5	Preimplantation Genetic Testing for Aneuploidy Improves Live Birth Rates with In Vitro Produced Bovine Embryos: A Blind Retrospective Study. <i>Cells</i> , 2021, 10, 2284.	4.1	14
6	The Plasticity of Genome Architecture. <i>Genes</i> , 2020, 11, 1413.	2.4	2
7	An integrated chromosome-scale genome assembly of the Masai giraffe ( <i>Giraffa camelopardalis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10	6.4	13
8	The Red Fox Y-Chromosome in Comparative Context. <i>Genes</i> , 2019, 10, 409.	2.4	6
9	A Near Chromosome Assembly of the Dromedary Camel Genome. <i>Frontiers in Genetics</i> , 2019, 10, 32.	2.3	7
10	Evolution of gene regulation in ruminants differs between evolutionary breakpoint regions and homologous synteny blocks. <i>Genome Research</i> , 2019, 29, 576-589.	5.5	39
11	Comparative Chromosome Mapping of Musk Ox and the X Chromosome among Some Bovidae Species. <i>Genes</i> , 2019, 10, 857.	2.4	8
12	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, .	6.4	138
13	Reconstruction of avian ancestral karyotypes reveals differences in the evolutionary history of macro- and microchromosomes. <i>Genome Biology</i> , 2018, 19, 155.	8.8	44
14	Chromosome-level assembly reveals extensive rearrangement in saker falcon and budgerigar, but not ostrich, genomes. <i>Genome Biology</i> , 2018, 19, 171.	8.8	65
15	Reconstruction of the diapsid ancestral genome permits chromosome evolution tracing in avian and non-avian dinosaurs. <i>Nature Communications</i> , 2018, 9, 1883.	12.8	60
16	Construction of Red Fox Chromosomal Fragments from the Short-Read Genome Assembly. <i>Genes</i> , 2018, 9, 308.	2.4	14
17	Upgrading short-read animal genome assemblies to chromosome level using comparative genomics and a universal probe set. <i>Genome Research</i> , 2017, 27, 875-884.	5.5	97
18	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.	7.1	94

#	ARTICLE	IF	CITATIONS
19	X Chromosome Evolution in Cetartiodactyla. <i>Genes</i> , 2017, 8, 216.	2.4	24
20	Novel Insights into Chromosome Evolution in Birds, Archosaurs, and Reptiles. <i>Genome Biology and Evolution</i> , 2016, 8, 2442-2451.	2.5	66
21	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
22	An Integrative Breakage Model of genome architecture, reshuffling and evolution. <i>BioEssays</i> , 2015, 37, 479-488.	2.5	54
23	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
24	Population structure and history of the Welsh sheep breeds determined by whole genome genotyping. <i>BMC Genetics</i> , 2015, 16, 65.	2.7	69
25	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
26	Reconstruction of gross avian genome structure, organization and evolution suggests that the chicken lineage most closely resembles the dinosaur avian ancestor. <i>BMC Genomics</i> , 2014, 15, 1060.	2.8	71
27	Global Gene Expression and Focused Knockout Analysis Reveals Genes Associated with Fungal Fruiting Body Development in <i>Neurospora crassa</i> . <i>Eukaryotic Cell</i> , 2014, 13, 154-169.	3.4	66
28	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
29	Genome-wide adaptive complexes to underground stresses in blind mole rats <i>Spalax</i> . <i>Nature Communications</i> , 2014, 5, 3966.	12.8	124
30	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
31	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
32	Assessing the Role of Tandem Repeats in Shaping the Genomic Architecture of Great Apes. <i>PLoS ONE</i> , 2011, 6, e27239.	2.5	35
33	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