## Javier Quilez

List of Publications by Year in descending order

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#	Article	lF	CITATIONS
1	C/EBPα mediates the growth inhibitory effect of progestins on breast cancer cells. EMBO Journal, 2019, 38, e101426.	3.5	15
2	Rapid reversible changes in compartments and local chromatin organization revealed by hyperosmotic shock. Genome Research, 2019, 29, 18-28.	2.4	40
3	Arginine Citrullination at the C-Terminal Domain Controls RNA Polymerase II Transcription. Molecular Cell, 2019, 73, 84-96.e7.	4.5	50
4	Hormone-control regions mediate steroid receptor–dependent genome organization. Genome Research, 2019, 29, 29-39.	2.4	49
5	OneD: increasing reproducibility of Hi-C samples with abnormal karyotypes. Nucleic Acids Research, 2018, 46, e49-e49.	6.5	50
6	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. Nature Genetics, 2018, 50, 238-249.	9.4	295
7	Unliganded Progesterone Receptor Governs Estrogen Receptor Gene Expression by Regulating DNA Methylation in Breast Cancer Cells. Cancers, 2018, 10, 371.	1.7	15
8	Parallel sequencing lives, or what makes large sequencing projects successful. GigaScience, 2017, 6, 1-6.	3.3	4
9	Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. BMC Genomics, 2017, 18, 977.	1.2	24
10	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
11	Polymorphic tandem repeats within gene promoters act as modifiers of gene expression and DNA methylation in humans. Nucleic Acids Research, 2016, 44, 3750-3762.	6.5	120
12	Hormoneâ€induced repression of genes requires <scp>BRG</scp> 1â€mediated H1.2 deposition at target promoters. EMBO Journal, 2016, 35, 1822-1843.	3.5	33
13	Germline Methylation Patterns Determine the Distribution of Recombination Events in the Dog Genome. Genome Biology and Evolution, 2015, 7, 522-530.	1.1	16
14	Digital Genotyping of Macrosatellites and Multicopy Genes Reveals Novel Biological Functions Associated with Copy Number Variation of Large Tandem Repeats. PLoS Genetics, 2014, 10, e1004418.	1.5	49
15	Elephant shark genome provides unique insights into gnathostome evolution. Nature, 2014, 505, 174-179.	13.7	689
16	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
17	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17230-17235.	3.3	281
18	Analysis of structural diversity in wolf-like canids reveals post-domestication variants. BMC Genomics, 2014, 15, 465.	1.2	16

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#	Article	IF	CITATIONS
19	Annotated features of domestic cat – Felis catus genome. GigaScience, 2014, 3, 13.	3.3	30
20	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
21	Genetic Control of Canine Leishmaniasis: Genome-Wide Association Study and Genomic Selection Analysis. PLoS ONE, 2012, 7, e35349.	1.1	31
22	A Novel Unstable Duplication Upstream of HAS2 Predisposes to a Breed-Defining Skin Phenotype and a Periodic Fever Syndrome in Chinese Shar-Pei Dogs. PLoS Genetics, 2011, 7, e1001332.	1.5	118
23	Canine leishmaniasis: the key points for qPCR result interpretation. Parasites and Vectors, 2011, 4, 57.	1.0	59
24	A selective sweep of >8 Mb on chromosome 26 in the Boxer genome. BMC Genomics, 2011, 12, 339.	1.2	50
25	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. PLoS Genetics, 2011, 7, e1002316.	1.5	339