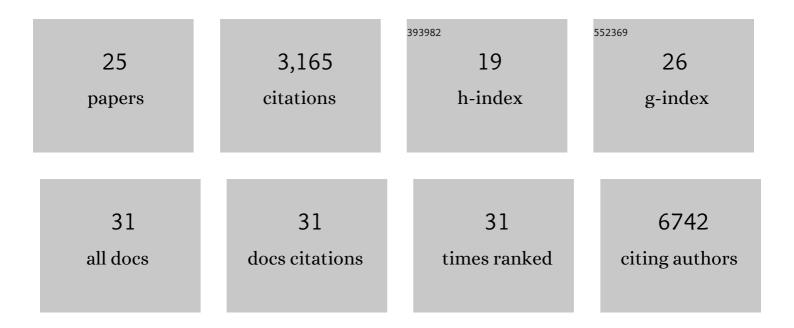
Javier Quilez

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Elephant shark genome provides unique insights into gnathostome evolution. Nature, 2014, 505, 174-179.	13.7	689
2	Identification of Genomic Regions Associated with Phenotypic Variation between Dog Breeds using Selection Mapping. PLoS Genetics, 2011, 7, e1002316.	1.5	339
3	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
4	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
5	Transcription factors orchestrate dynamic interplay between genome topology and gene regulation during cell reprogramming. Nature Genetics, 2018, 50, 238-249.	9.4	295
6	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
7	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
8	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
9	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
10	Canine leishmaniasis: the key points for qPCR result interpretation. Parasites and Vectors, 2011, 4, 57.	1.0	59
11	A selective sweep of >8 Mb on chromosome 26 in the Boxer genome. BMC Genomics, 2011, 12, 339.	1.2	50
12	OneD: increasing reproducibility of Hi-C samples with abnormal karyotypes. Nucleic Acids Research, 2018, 46, e49-e49.	6.5	50
13	Arginine Citrullination at the C-Terminal Domain Controls RNA Polymerase II Transcription. Molecular Cell, 2019, 73, 84-96.e7.	4.5	50
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	Hormone-control regions mediate steroid receptor–dependent genome organization. Genome Research, 2019, 29, 29-39.	2.4	49
16	Rapid reversible changes in compartments and local chromatin organization revealed by hyperosmotic shock. Genome Research, 2019, 29, 18-28.	2.4	40
17	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
18	Genetic Control of Canine Leishmaniasis: Genome-Wide Association Study and Genomic Selection Analysis. PLoS ONE, 2012, 7, e35349.	1.1	31

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#	Article	IF	CITATIONS
19	Annotated features of domestic cat – Felis catus genome. GigaScience, 2014, 3, 13.	3.3	30
20	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
21	Analysis of structural diversity in wolf-like canids reveals post-domestication variants. BMC Genomics, 2014, 15, 465.	1.2	16
22	Germline Methylation Patterns Determine the Distribution of Recombination Events in the Dog Genome. Genome Biology and Evolution, 2015, 7, 522-530.	1.1	16
23	Unliganded Progesterone Receptor Governs Estrogen Receptor Gene Expression by Regulating DNA Methylation in Breast Cancer Cells. Cancers, 2018, 10, 371.	1.7	15
24	C/EBPα mediates the growth inhibitory effect of progestins on breast cancer cells. EMBO Journal, 2019, 38, e101426.	3.5	15
25	Parallel sequencing lives, or what makes large sequencing projects successful. GigaScience, 2017, 6, 1-6.	3.3	4