Francesca Antonacci

List of Publications by Year
in descending order

42 papers	6,486 citations	172457 29 h-index	276875 41 g-index
44 all docs	44 docs citations	44 times ranked	10369 citing authors

#	Article	IF	Citations
1	Mapping and sequencing of structural variation from eight human genomes. Nature, 2008, 453, 56-64.	27.8	983
2	Resolving the complexity of the human genome using single-molecule sequencing. Nature, 2015, 517, 608-611.	27.8	714
3	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	21.4	656
4	Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646.	12.6	609
5	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	21.4	539
6	Evolution of Human-Specific Neural SRGAP2 Genes by Incomplete Segmental Duplication. Cell, 2012, 149, 912-922.	28.9	341
7	Reconstructing complex regions of genomes using long-read sequencing technology. Genome Research, 2014, 24, 688-696.	5.5	222
8	Evolutionary toggling of the MAPT 17q21.31 inversion region. Nature Genetics, 2008, 40, 1076-1083.	21.4	176
9	Evolution and diversity of copy number variation in the great ape lineage. Genome Research, 2013, 23, 1373-1382.	5.5	161
10	Programmed loss of millions of base pairs from a vertebrate genome. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11212-11217.	7.1	151
11	Characterization of missing human genome sequences and copy-number polymorphic insertions. Nature Methods, 2010, 7, 365-371.	19.0	138
12	Evolutionary Formation of New Centromeres in Macaque. Science, 2007, 316, 243-246.	12.6	136
13	Structural diversity and African origin of the 17q21.31 inversion polymorphism. Nature Genetics, 2012, 44, 872-880.	21.4	129
14	The evolution and population diversity of human-specific segmental duplications. Nature Ecology and Evolution, 2017, 1, 69.	7.8	123
15	Characterization of six human disease-associated inversion polymorphisms. Human Molecular Genetics, 2009, 18, 2555-2566.	2.9	118
16	Autosomal Dominant Familial Dyskinesia and Facial Myokymia. Archives of Neurology, 2012, 69, 630.	4.5	109
17	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	12.6	105
18	Emergence of a Homo sapiens-specific gene family and chromosome 16p11.2 CNV susceptibility. Nature, 2016, 536, 205-209.	27.8	102

#	Article	IF	Citations
19	Palindromic GOLGA8 core duplicons promote chromosome 15q13.3 microdeletion and evolutionary instability. Nature Genetics, 2014, 46, 1293-1302.	21.4	96
20	Death and Resurrection of the Human IRGM Gene. PLoS Genetics, 2009, 5, e1000403.	3.5	93
21	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. Nature Genetics, 2010, 42, 745-750.	21.4	89
22	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. Genome Research, 2011, 21, 137-145.	5.5	78
23	Copy number variation analysis in singleâ€suture craniosynostosis: Multiple rare variants including RUNX2 duplication in two cousins with metopic craniosynostosis. American Journal of Medical Genetics, Part A, 2010, 152A, 2203-2210.	1.2	69
24	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
25	Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. Science, 2019, 366, .	12.6	65
26	New Insights into Centromere Organization and Evolution from the White-Cheeked Gibbon and Marmoset. Molecular Biology and Evolution, 2009, 26, 1889-1900.	8.9	45
27	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
28	The birth of a human-specific neural gene by incomplete duplication and gene fusion. Genome Biology, 2017, 18, 49.	8.8	39
29	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
30	Identification of a novel recurrent 1q42.2â€1qter deletion in high risk MYCN single copy 11q deleted neuroblastomas. International Journal of Cancer, 2012, 130, 2599-2606.	5.1	37
31	Inversion variants in human and primate genomes. Genome Research, 2018, 28, 910-920.	5.5	34
32	Rapid and accurate large-scale genotyping of duplicated genes and discovery of interlocus gene conversions. Nature Methods, 2013, 10, 903-909.	19.0	31
33	Unusual 8p inverted duplication deletion with telomere capture from 8q. European Journal of Medical Genetics, 2009, 52, 31-36.	1.3	26
34	Identification of 2 putative critical segments of 17q gain in neuroblastoma through integrative genomics. International Journal of Cancer, 2008, 122, 1177-1182.	5.1	22
35	Discovery of large genomic inversions using long range information. BMC Genomics, 2017, 18, 65.	2.8	18
36	Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. PLoS Genetics, 2019, 15, e1008075.	3.5	17

#	Article	IF	Citations
37	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. BMC Evolutionary Biology, 2011, 11, 23.	3.2	16
38	Single-cell strand sequencing of a macaque genome reveals multiple nested inversions and breakpoint reuse during primate evolution. Genome Research, 2020, 30, 1680-1693.	5.5	16
39	Hominoid fission of chromosome 14/15 and the role of segmental duplications. Genome Research, 2013, 23, 1763-1773.	5.5	14
40	Mapping of 5q35 chromosomal rearrangements within a genomically unstable region. Journal of Medical Genetics, 2008, 45, 672-678.	3.2	7
41	Evolutionary Dynamics of the POTE Gene Family in Human and Nonhuman Primates. Genes, 2020, 11, 213.	2.4	7
42	Cytogenetic and Array-CGH Characterization of a Simple Case of Reciprocal t(3;10) Translocation Reveals a Hidden Deletion at 5q12. Genes, 2021, 12, 877.	2.4	1