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	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	28.9	67
2	A high-quality bonobo genome refines the analysis of hominid evolution. Nature, 2021, 594, 77-81.	27.8	39
3	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
4	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
5	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	12.6	105
6	Recurrent inversion toggling and great ape genome evolution. Nature Genetics, 2020, 52, 849-858.	21.4	40
7	Evolutionary Dynamics of the POTE Gene Family in Human and Nonhuman Primates. Genes, 2020, 11, 213.	2.4	7
8	Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. Science, 2019, 366, .	12.6	65
9	Genomic inversions and GOLGA core duplicons underlie disease instability at the 15q25 locus. PLoS Genetics, 2019, 15, e1008075.	3.5	17
10	Inversion variants in human and primate genomes. Genome Research, 2018, 28, 910-920.	5.5	34
11	The evolution and population diversity of human-specific segmental duplications. Nature Ecology and Evolution, 2017, 1, 69.	7.8	123
12	The birth of a human-specific neural gene by incomplete duplication and gene fusion. Genome Biology, 2017, 18, 49.	8.8	39
13	Discovery of large genomic inversions using long range information. BMC Genomics, 2017, 18, 65.	2.8	18
14	Emergence of a Homo sapiens-specific gene family and chromosome 16p11.2 CNV susceptibility. Nature, 2016, 536, 205-209.	27.8	102
15	Resolving the complexity of the human genome using single-molecule sequencing. Nature, 2015, 517, 608-611.	27.8	714
16	Reconstructing complex regions of genomes using long-read sequencing technology. Genome Research, 2014, 24, 688-696.	5.5	222
17	Palindromic GOLGA8 core duplicons promote chromosome 15q13.3 microdeletion and evolutionary instability. Nature Genetics, 2014, 46, 1293-1302.	21.4	96
18	Hominoid fission of chromosome 14/15 and the role of segmental duplications. Genome Research, 2013, 23, 1763-1773.	5.5	14

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19	Evolution and diversity of copy number variation in the great ape lineage. Genome Research, 2013, 23, 1373-1382.	5.5	161
20	Rapid and accurate large-scale genotyping of duplicated genes and discovery of interlocus gene conversions. Nature Methods, 2013, 10, 903-909.	19.0	31
21	Autosomal Dominant Familial Dyskinesia and Facial Myokymia. Archives of Neurology, 2012, 69, 630.	4.5	109
22	Evolution of Human-Specific Neural SRGAP2 Genes by Incomplete Segmental Duplication. Cell, 2012, 149, 912-922.	28.9	341
23	Structural diversity and African origin of the 17q21.31 inversion polymorphism. Nature Genetics, 2012, 44, 872-880.	21.4	129
24	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
25	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. BMC Evolutionary Biology, 2011, 11, 23.	3.2	16
26	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. Genome Research, 2011, 21, 137-145.	5.5	78
27	Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646.	12.6	609
28	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
29	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	21.4	539
30	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. Nature Genetics, 2010, 42, 745-750.	21.4	89
31	Characterization of missing human genome sequences and copy-number polymorphic insertions. Nature Methods, 2010, 7, 365-371.	19.0	138
32	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
33	Characterization of six human disease-associated inversion polymorphisms. Human Molecular Genetics, 2009, 18, 2555-2566.	2.9	118
34	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
35	Death and Resurrection of the Human IRGM Gene. PLoS Genetics, 2009, 5, e1000403.	3.5	93
36	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	21.4	656

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37	Unusual 8p inverted duplication deletion with telomere capture from 8q. European Journal of Medical Genetics, 2009, 52, 31-36.	1.3	26
38	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
39	Mapping and sequencing of structural variation from eight human genomes. Nature, 2008, 453, 56-64.	27.8	983
40	Evolutionary toggling of the MAPT 17q21.31 inversion region. Nature Genetics, 2008, 40, 1076-1083.	21.4	176
41	Mapping of 5q35 chromosomal rearrangements within a genomically unstable region. Journal of Medical Genetics, 2008, 45, 672-678.	3.2	7
42	Evolutionary Formation of New Centromeres in Macaque. Science, 2007, 316, 243-246.	12.6	136