Vincenza Colonna

List of Publications by Year
in descending order

44 papers	23,616 citations	304743 22 h-index	276875 41 g-index
57 all docs	57 docs citations	57 times ranked	48389 citing authors

#	Article	IF	Citations
1	Prioritization of putatively detrimental variants in euploid miscarriages. Scientific Reports, 2022, 12, 1997.	3.3	3
2	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	4.1	18
3	Genetic instability and anti-HPV immune response as drivers of infertility associated with HPV infection. Infectious Agents and Cancer, 2021, 16, 29.	2.6	12
4	A global analysis of conservative and non-conservative mutations in SARS-CoV-2 detected in the first year of the COVID-19 world-wide diffusion. Scientific Reports, 2021, 11, 24495.	3.3	5
5	GENOMICS ANALYSIS OF MATERNAL EXOMES REVEALS NEW CANDIDATE GENES AND PATHWAYS FOR THE DIAGNOSIS AND PREDICTION OF RECURRENT PREIMPLANTATION EMBRYO ARREST IN IVF CYCLES. Fertility and Sterility, 2020, 114, e238.	1.0	0
6	Abstract PO-048: Lack of L1CAM increases tumorigenicity, stemness and tumor fibrosis in pancreatic ductal adenocarcinoma. , 2020, , .		0
7	Genomic diversity and novel genome-wide association with fruit morphology in Capsicum, from 746k polymorphic sites. Scientific Reports, 2019, 9, 10067.	3.3	53
8	Identification of sex determination genes and their evolution in Phlebotominae sand flies (Diptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	2.8	10
9	Inter-individual genomic heterogeneity within European population isolates. PLoS ONE, 2019, 14, e0214564.	2.5	3
10	Positive selection in Europeans and East-Asians at the ABCA12 gene. Scientific Reports, 2019, 9, 4843.	3.3	1
11	Overcoming the dichotomy between open and isolated populations using genomic data from a large European dataset. Scientific Reports, 2017, 7, 41614.	3.3	15
12	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	12.8	64
13	An Ethnolinguistic and Genetic Perspective on the Origins of the Dravidian-Speaking Brahui in Pakistan. Man in India, 2017, 97, 267-278.	2.0	3
14	New Cross-Talk Layer between Ultraconserved Non-Coding RNAs, MicroRNAs and Polycomb Protein YY1 in Bladder Cancer. Genes, 2016, 7, 127.	2.4	26
15	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. Blood, 2016, 128, e1-e9.	1.4	49
16	Vitamin B12 ameliorates the phenotype of a mouse model of DiGeorge syndrome. Human Molecular Genetics, 2016, 25, ddw267.	2.9	16
17	Long non-coding RNA containing ultraconserved genomic region 8 promotes bladder cancer tumorigenesis. Oncotarget, 2016, 7, 20636-20654.	1.8	66
18	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998

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19	Abstract 4854: A computational framework for prioritizing noncoding regulatory variants in cancer. Cancer Research, 2015, 75, 4854-4854.	0.9	1
20	Monoamine Oxidase A gene polymorphisms and self reported aggressive behaviour in a Pakistani ethnic group. JPMA the Journal of the Pakistan Medical Association, 2015, 65, 818-24.	0.2	2
21	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. Nature Communications, 2014, 5, 5345.	12.8	60
22	Genetic landscape of populations along the Silk Road: admixture and migration patterns. BMC Genetics, 2014, 15, 131.	2.7	24
23	Revisiting the Thrifty Gene Hypothesis via 65 Loci Associated with Susceptibility to Type 2 Diabetes. American Journal of Human Genetics, 2014, 94, 176-185.	6.2	72
24	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications, 2014, 5, 3934.	12.8	364
25	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biology, 2014, 15, R88.	9.6	72
26	Small effective population size and genetic homogeneity in the Val Borbera isolate. European Journal of Human Genetics, 2013, 21, 89-94.	2.8	32
27	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
28	Modeling the contrasting Neolithic male lineage expansions in Europe and Africa. Investigative Genetics, 2013, 4, 25.	3.3	6
29	Origins and Evolution of the Etruscansâ€™ mtDNA. PLoS ONE, 2013, 8, e55519.	2.5	40
30	IFITM3 restricts the morbidity and mortality associated with influenza. Nature, 2012, 484, 519-523.	27.8	668
31	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	2.9	33
32	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
33	A world in a grain of sand: human history from genetic data. Genome Biology, 2011, 12, 234.	9.6	9
34	Genetic affinity and admixture of northern Thai people along their migration route in northern Thailand: evidence from autosomal STR loci. Journal of Human Genetics, 2011, 56, 130-137.	2.3	19
35	Human genome diversity: frequently asked questions. Trends in Genetics, 2010, 26, 285-295.	6.7	93
36	Subject Index Vol. 70, 2010. Human Heredity, 2010, 70, 303-303.	0.8	0

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37	Long-Range Comparison between Genes and Languages Based on Syntactic Distances. Human Heredity, 2010, 70, 245-254.	0.8	20
38	Comparing population structure as inferred from genealogical versus genetic information. European Journal of Human Genetics, 2009, 17, 1635-1641.	2.8	31
39	Comparing models on the genealogical relationships among Neandertal, Cro-Magnoid and modern Europeans by serial coalescent simulations. Heredity, 2009, 102, 218-225.	2.6	26
40	Isonymy Structure of Buenos Aires City. Human Biology, 2009, 81, 447-461.	0.2	16
41	Identification and Replication of a Novel Obesity Locus on Chromosome 1q24 in Isolated Populations of Cilento. Diabetes, 2008, 57, 783-790.	0.6	16
42	Campora: A Young Genetic Isolate in South Italy. Human Heredity, 2007, 64, 123-135.	0.8	28
43	New susceptibility locus for hypertension on chromosome 8q by efficient pedigree-breaking in an Italian isolate. Human Molecular Genetics, 2006, 15, 1735-1743.	2.9	39
44	The C. elegans pvfâ€1 gene encodes a PDGF/VEGFâ€like factor able to bind mammalian VEGF receptors and to induce angiogenesis. FASEB Journal, 2006, 20, 227-233.	0.5	53