Giulio Genovese

List of Publications by Year
in descending order

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41 papers	28,096 citations	159358 30 h-index	253896 43 g-index
58 all docs	58 docs citations	58 times ranked	48843 citing authors

#	Article	IF	Citations
1	Whole-genome analysis of human embryonic stem cells enables rational line selection based on genetic variation. Cell Stem Cell, 2022, 29, 472-486.e7.	5.2	27
2	Clonal Hematopoiesis Analyses in Clinical, Epidemiologic, and Genetic Aging Studies to Unravel Underlying Mechanisms of Age-Related Dysfunction in Humans. Frontiers in Aging, 2022, 3, .	1.2	3
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
4	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
5	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010113.	1.5	16
6	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. Nature Communications, 2022, 13, .	5.8	22
7	Chromosomal phase improves aneuploidy detection in non-invasive prenatal testing at low fetal DNA fractions. Scientific Reports, 2022, 12, .	1.6	1
8	Large mosaic copy number variations confer autism risk. Nature Neuroscience, 2021, 24, 197-203.	7.1	36
9	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
10	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
11	Monogenic and polygenic inheritance become instruments for clonal selection. Nature, 2020, 584, 136-141.	13.7	119
12	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. Nature Communications, 2019, 10, 4719.	5.8	50
13	Non-del(5q) myelodysplastic syndromesâ€“associated loci detected by SNP-array genome-wide association meta-analysis. Blood Advances, 2019, 3, 3579-3589.	2.5	7
14	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
15	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
16	Increased neutrophil extracellular trap formation promotes thrombosis in myeloproliferative neoplasms. Science Translational Medicine, 2018, 10, .	5.8	299
17	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. American Journal of Human Genetics, 2018, 102, 760-775.	2.6	57
18	The Genetic Landscape of Diamond-Blackfan Anemia. American Journal of Human Genetics, 2018, 103, 930-947.	2.6	184

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19	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355.	13.7	279
20	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
21	Spatiotemporal profile of postsynaptic interactomes integrates components of complex brain disorders. Nature Neuroscience, 2017, 20, 1150-1161.	7.1	104
22	Mosaic mutations in blood DNA sequence are associated with solid tumor cancers. Npj Genomic Medicine, 2017, 2, 22.	1.7	10
23	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
24	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427
25	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90
26	Schizophrenia risk from complex variation of complement component 4. Nature, 2016, 530, 177-183.	13.7	1,915
27	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	2.6	77
28	Large multiallelic copy number variations in humans. Nature Genetics, 2015, 47, 296-303.	9.4	357
29	Dynamics of Tumor Heterogeneity Derived from Clonal Karyotypic Evolution. Cell Reports, 2015, 12, 809-820.	2.9	99
30	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
31	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
32	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	2.8	95
33	Discovery of new glomerular diseaseâ€“relevant genes by translational profiling of podocytes in vivo. Kidney International, 2014, 86, 1116-1129.	2.6	36
34	Mutations in PAX2 Associate with Adult-Onset FSGS. Journal of the American Society of Nephrology: JASN, 2014, 25, 1942-1953.	3.0	96
35	Exome sequencing and in vitro studies identified podocalyxin as a candidate gene for focal and segmental glomerulosclerosis. Kidney International, 2014, 85, 124-133.	2.6	41
36	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	13.9	2,669

#	Article	IF	Citations
37	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
38	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	2.6	569
39	Mapping the Human Reference Genomeâ€™s Missing Sequence by Three-Way Admixture in Latino Genomes. American Journal of Human Genetics, 2013, 93, 411-421.	2.6	36
40	Using population admixture to help complete maps of the human genome. Nature Genetics, 2013, 45, 406-414.	9.4	61
41	Improved IBD detection using incomplete haplotype information. BMC Genetics, 2010, 11, 58.	2.7	10