Giulio Genovese

List of Publications by Year
in descending order

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41 papers	28,096 citations	159525 30 h-index	254106 43 g-index
58 all docs	58 docs citations	58 times ranked	48843 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	13.9	2,669
3	Schizophrenia risk from complex variation of complement component 4. Nature, 2016, 530, 177-183.	13.7	1,915
4	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	1,305
5	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
6	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
7	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
8	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807
9	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
10	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
11	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427
12	Large multiallelic copy number variations in humans. Nature Genetics, 2015, 47, 296-303.	9.4	357
13	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
14	Increased neutrophil extracellular trap formation promotes thrombosis in myeloproliferative neoplasms. Science Translational Medicine, 2018, 10, .	5.8	299
15	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. Nature, 2018, 559, 350-355.	13.7	279
16	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
17	The Genetic Landscape of Diamond-Blackfan Anemia. American Journal of Human Genetics, 2018, 103, 930-947.	2.6	184
18	Monogenic and polygenic inheritance become instruments for clonal selection. Nature, 2020, 584, 136-141.	13.7	119

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19	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. Nature Medicine, 2021, 27, 1012-1024.	15.2	109
20	Spatiotemporal profile of postsynaptic interactomes integrates components of complex brain disorders. Nature Neuroscience, 2017, 20, 1150-1161.	7.1	104
21	Dynamics of Tumor Heterogeneity Derived from Clonal Karyotypic Evolution. Cell Reports, 2015, 12, 809-820.	2.9	99
22	Mutations in PAX2 Associate with Adult-Onset FSGS. Journal of the American Society of Nephrology: JASN, 2014, 25, 1942-1953.	3.0	96
23	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	2.8	95
24	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90
25	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. American Journal of Human Genetics, 2015, 97, 775-789.	2.6	77
26	Using population admixture to help complete maps of the human genome. Nature Genetics, 2013, 45, 406-414.	9.4	61
27	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
28	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. Nature Communications, 2019, 10, 4719.	5.8	50
29	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
30	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
31	Discovery of new glomerular diseaseâ€“relevant genes by translational profiling of podocytes in vivo. Kidney International, 2014, 86, 1116-1129.	2.6	36
32	Large mosaic copy number variations confer autism risk. Nature Neuroscience, 2021, 24, 197-203.	7.1	36
33	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
34	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. Nature Communications, 2022, 13, .	5.8	22
35	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
36	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15

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37	Improved IBD detection using incomplete haplotype information. BMC Genetics, 2010, 11, 58.	2.7	10
38	Mosaic mutations in blood DNA sequence are associated with solid tumor cancers. Npj Genomic Medicine, 2017, 2, 22.	1.7	10
39	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
40	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
41	Chromosomal phase improves aneuploidy detection in non-invasive prenatal testing at low fetal DNA fractions. Scientific Reports, 2022, 12, .	1.6	1