Valentina Iotchkova

List of Publications by Year
in descending order

17 papers	3,807 citations	566801 15 h-index	940134 16 g-index
23 all docs	23 docs citations	23 times ranked	11641 citing authors

#	Article	IF	Citations
1	Multi-Modal Characterization of Monocytes in Idiopathic Pulmonary Fibrosis Reveals a Primed Type I Interferon Immune Phenotype. Frontiers in Immunology, 2021, 12, 623430.	2.2	34
2	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	5.8	32
3	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
4	Monocyte and neutrophil levels are potentially linked to progression to IPF for patients with indeterminate UIP CT pattern. BMJ Open Respiratory Research, 2021, 8, e000899.	1.2	15
5	Incidence of symptomatic, image-confirmed venous thromboembolism following hospitalization for COVID-19 with 90-day follow-up. Blood Advances, 2020, 4, 6230-6239.	2.5	64
6	Mechanisms of Progression of Myeloid Preleukemia to Transformed Myeloid Leukemia in Children with Down Syndrome. Cancer Cell, 2019, 36, 123-138.e10.	7.7	93
7	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	9.4	147
8	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
9	Significant impact of miRNAâ€“target gene networks on genetics of human complex traits. Scientific Reports, 2016, 6, 22223.	1.6	44
10	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
11	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
12	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	13.5	1,052
13	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
14	A multiple-phenotype imputation method for genetic studies. Nature Genetics, 2016, 48, 466-472.	9.4	93
15	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
16	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
17	FORGE: A tool to discover cell specific enrichments of GWAS associated SNPs in regulatory regions. F1000Research, 0, 4, 18.	0.8	16