Mattia Frontini

List of Publications by Year
in descending order

25	4,862	394286 19	610775 24
papers	citations	h-index	g-index

35	35	35	13402
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Unique molecular and functional features of extramedullary hematopoietic stem and progenitor cell reservoirs in humans. Blood, 2022, 139, 3387-3401.	0.6	26
2	Nonâ€coding genetic variation in regulatory elements determines thrombosis and hemostasis phenotypes. Journal of Thrombosis and Haemostasis, 2022, 20, 1759-1765.	1.9	2
3	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. Haematologica, 2021, 106, 2613-2623.	1.7	12
4	A rare coding mutation in the MAST2 gene causes venous thrombosis in a French family with unexplained thrombophilia: The Breizh MAST2 Arg89Gln variant. PLoS Genetics, 2021, 17, e1009284.	1.5	2
5	Transcriptional characterization of human megakaryocyte polyploidization and lineage commitment. Journal of Thrombosis and Haemostasis, 2021, 19, 1236-1249.	1.9	15
6	Assessment of a complete and classified platelet proteome from genome-wide transcripts of human platelets and megakaryocytes covering platelet functions. Scientific Reports, 2021, 11, 12358.	1.6	40
7	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. Blood, 2020, 136, 1956-1967.	0.6	34
8	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	13.7	338
9	Activated Î±IIbÎ²3 on platelets mediates flow-dependent NETosis via SLC44A2. ELife, 2020, 9, .	2.8	68
10	Breaking barriers: Quebec platelet disorder. Blood, 2020, 136, 2603-2604.	0.6	0
11	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. Blood, 2019, 134, 2070-2081.	0.6	29
12	High-throughput elucidation of thrombus formation reveals sources of platelet function variability. Haematologica, 2019, 104, 1256-1267.	1.7	70
13	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell Reports, 2018, 24, 2784-2794.	2.9	104
14	Detection of Atherosclerotic Inflammation by 68 Ga-DOTATATE PET Compared to [18 F]FDG PET Imaging. Journal of the American College of Cardiology, 2017, 69, 1774-1791.	1.2	321
15	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	5.8	50
16	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. Genome Biology, 2017, 18, 165.	3.8	68
17	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
18	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66

#	Article	IF	Citations
19	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	13.5	863
20	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
21	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
22	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. Cell Stem Cell, 2016, 19, 808-822.	5.2	216
23	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
24	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
25	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	9.4	96