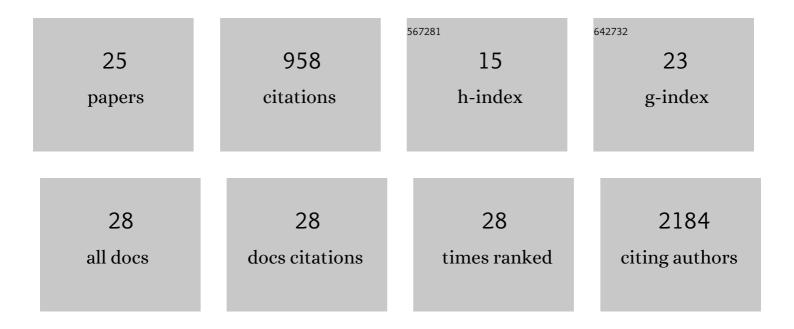
Ana Rio-Machin

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Acquired somatic variants in inherited myeloid malignancies. Leukemia, 2022, 36, 1377-1381.	7.2	8
2	CKS1 inhibition depletes leukemic stem cells and protects healthy hematopoietic stem cells in acute myeloid leukemia. Science Translational Medicine, 2022, 14, .	12.4	8
3	Germline ETV6 variants: not ALL created equally. Blood, 2021, 137, 288-289.	1.4	0
4	AML through the prism of molecular genetics. British Journal of Haematology, 2020, 188, 49-62.	2.5	17
5	Endogenous retroviruses are a source of enhancers with oncogenic potential in acute myeloid leukaemia. Nature Communications, 2020, 11, 3506.	12.8	80
6	A frameshift variant in specificity protein 1 triggers superactivation of Sp1-mediated transcription in familial bone marrow failure. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17151-17155.	7.1	2
7	The complex genetic landscape of familial MDS and AML reveals pathogenic germline variants. Nature Communications, 2020, 11, 1044.	12.8	81
8	Transmission of diffuse large B-cell lymphoma by an allogeneic stem-cell transplant. Haematologica, 2019, 104, e174-e177.	3.5	5
9	Proteomic and genomic integration identifies kinase and differentiation determinants of kinase inhibitor sensitivity in leukemia cells. Leukemia, 2018, 32, 1818-1822.	7.2	36
10	Genomic profiling reveals spatial intra-tumor heterogeneity in follicular lymphoma. Leukemia, 2018, 32, 1261-1265.	7.2	87
11	Genome instability is a consequence of transcription deficiency in patients with bone marrow failure harboring biallelic <i>ERCC6L2</i> variants. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 7777-7782.	7.1	37
12	GATA2 monoallelic expression underlies reduced penetrance in inherited GATA2-mutated MDS/AML. Leukemia, 2018, 32, 2502-2507.	7.2	48
13	Familial CEBPA -mutated acute myeloid leukemia. Seminars in Hematology, 2017, 54, 87-93.	3.4	54
14	Recurrent somatic JAK-STAT pathway variants within a RUNX1-mutated pedigree. European Journal of Human Genetics, 2017, 25, 1020-1024.	2.8	13
15	Proteomic and genomic integration identifies kinase and differentiation determinants of kinase inhibitor sensitivity in leukemia cells. Leukemia, 2017, , .	7.2	0
16	The molecular pathogenesis of the NUP98-HOXA9 fusion protein in acute myeloid leukemia. Leukemia, 2017, 31, 2000-2005.	7.2	28
17	Myelodysplasia and liver disease extend the spectrum of RTEL1 related telomeropathies. Haematologica, 2017, 102, e293-e296.	3.5	15
18	Germline heterozygous DDX41 variants in a subset of familial myelodysplasia and acute myeloid leukemia. Leukemia, 2016, 30, 2083-2086.	7.2	62

#	Article	IF	CITATIONS
19	Differentially expressed small <scp>RNA</scp> s in Arabidopsis galls formed by <i>Meloidogyne javanica</i> : a functional role for miR390 and its <scp>TAS</scp> 3â€derived tasi <scp>RNA</scp> s. New Phytologist, 2016, 209, 1625-1640.	7.3	86
20	<scp>MAPK</scp> 8â€mediated stabilization of <scp>SP</scp> 1 is essential for <scp>RUNX</scp> 1â€ <scp>RUNX</scp> 1T1 – driven leukaemia. British Journal of Haematology, 2016, 172, 807-810.	2.5	2
21	BPTF is required for c-MYC transcriptional activity and in vivo tumorigenesis. Nature Communications, 2016, 7, 10153.	12.8	104
22	Whole-Exome Sequencing Identifies MDH2 as a New Familial Paraganglioma Gene. Journal of the National Cancer Institute, 2015, 107, .	6.3	143
23	Downregulation of specific miRNAs in hyperdiploid multiple myeloma mimics the oncogenic effect of lgH translocations occurring in the non-hyperdiploid subtype. Leukemia, 2013, 27, 925-931.	7.2	31
24	Abrogation of RUNX1 gene expression in de novo myelodysplastic syndrome with t(4;21)(q21;q22). Haematologica, 2012, 97, 534-537.	3.5	5
25	A dual role for the RNA helicase DHX34 in NMD and pre-mRNA splicing and its function in hematopoietic differentiation. Rna, 0, , rna.079277.122.	3.5	4