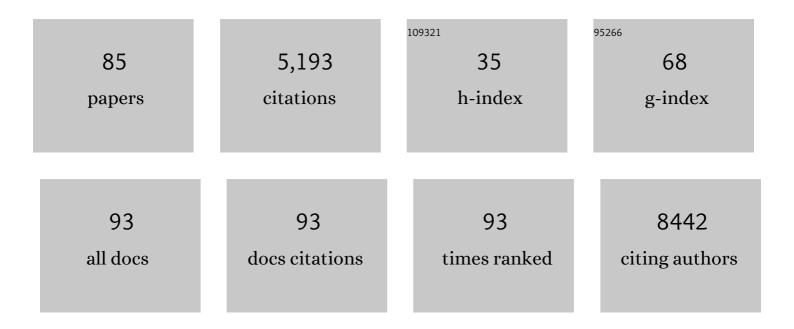
List of Publications by Year in descending order

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Ιομν Ε Ριμανίολ

#	Article	IF	CITATIONS
1	Analysing high-throughput sequencing data in Python with HTSeq 2.0. Bioinformatics, 2022, 38, 2943-2945.	4.1	335
2	Demethylation and Up-Regulation of an Oncogene after Hypomethylating Therapy. New England Journal of Medicine, 2022, 386, 1998-2010.	27.0	25
3	Induction of muscle-regenerative multipotent stem cells from human adipocytes by PDGF-AB and 5-azacytidine. Science Advances, 2021, 7, .	10.3	3
4	Heart on A Chip: Labelâ€Free Isolation and Single Cell Biophysical Phenotyping Analysis of Primary Cardiomyocytes Using Inertial Microfluidics (Small 8/2021). Small, 2021, 17, 2170034.	10.0	0
5	Disruption of a GATA2-TAL1-ERG regulatory circuit promotes erythroid transition in healthy and leukemic stem cells. Blood, 2021, 138, 1441-1455.	1.4	26
6	Targeting an Inducible SALL4-Mediated Cancer Vulnerability with Sequential Therapy. Cancer Research, 2021, 81, 6018-6028.	0.9	13
7	Labelâ€Free Isolation and Single Cell Biophysical Phenotyping Analysis of Primary Cardiomyocytes Using Inertial Microfluidics. Small, 2021, 17, e2006176.	10.0	12
8	<i>DKC1</i> is a transcriptional target of GATA1 and drives upregulation of telomerase activity in normal human erythroblasts. Haematologica, 2020, 105, 1517-1526.	3.5	15
9	Human endogenous retroviruses form a reservoir of T cell targets in hematological cancers. Nature Communications, 2020, 11, 5660.	12.8	55
10	Titans awake: HMAs for virus-driven ATL. Blood, 2020, 136, 777-779.	1.4	1
11	The EMT modulator SNAI1 contributes to AML pathogenesis via its interaction with LSD1. Blood, 2020, 136, 957-973.	1.4	35
12	RNA Splicing Alterations Induce a Cellular Stress Response Associated with Poor Prognosis in Acute Myeloid Leukemia. Clinical Cancer Research, 2020, 26, 3597-3607.	7.0	26
13	Constitutive CHK1 Expression Drives a pSTAT3–CIP2A Circuit that Promotes Glioblastoma Cell Survival and Growth. Molecular Cancer Research, 2020, 18, 709-722.	3.4	15
14	Murine and related chapparvoviruses are nephro-tropic and produce novel accessory proteins in infected kidneys. PLoS Pathogens, 2020, 16, e1008262.	4.7	23
15	Shared roles for Scl and Lyl1 in murine platelet production and function. Blood, 2019, 134, 826-835.	1.4	15
16	Transcriptional networks in acute myeloid leukemia. Genes Chromosomes and Cancer, 2019, 58, 859-874.	2.8	20
17	Scarcity of Recurrent Regulatory Driver Mutations in Colorectal Cancer Revealed by Targeted Deep Sequencing. JNCI Cancer Spectrum, 2019, 3, pkz012.	2.9	2
18	HMGA2 promotes long-term engraftment and myeloerythroid differentiation of human hematopoietic stem and progenitor cells. Blood Advances, 2019, 3, 681-691.	5.2	15

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19	A Menin-MLL Inhibitor Induces Specific Chromatin Changes and Eradicates Disease in Models of MLL-Rearranged Leukemia. Cancer Cell, 2019, 36, 660-673.e11.	16.8	231
20	Granulomonocytic progenitors are key target cells of azacytidine in higher risk myelodysplastic syndromes and acute myeloid leukemia. Leukemia, 2018, 32, 1856-1860.	7.2	7
21	Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. Cancer Cell, 2018, 34, 906-921.e8.	16.8	51
22	A novel role for <i>Lyl1</i> in primitive erythropoiesis. Development (Cambridge), 2018, 145, .	2.5	14
23	Disruption of a â´`35 kb Enhancer Impairs CTCF Binding and <i>MLH1</i> Expression in Colorectal Cells. Clinical Cancer Research, 2018, 24, 4602-4611.	7.0	12
24	Annotating function to differentially expressed LincRNAs in myelodysplastic syndrome using a network-based method. Bioinformatics, 2017, 33, 2622-2630.	4.1	14
25	The non-coding RNA landscape of human hematopoiesis and leukemia. Nature Communications, 2017, 8, 218.	12.8	131
26	Integrative Genomics Identifies the Molecular Basis of Resistance to Azacitidine Therapy in Myelodysplastic Syndromes. Cell Reports, 2017, 20, 572-585.	6.4	99
27	Identification of novel regulators of developmental hematopoiesis using Endoglin regulatory elements as molecular probes. Blood, 2016, 128, 1928-1939.	1.4	6
28	Functional Mutations Form at CTCF-Cohesin Binding Sites in Melanoma Due to Uneven Nucleotide Excision Repair across the Motif. Cell Reports, 2016, 17, 2865-2872.	6.4	61
29	PDGF-AB and 5-Azacytidine induce conversion of somatic cells into tissue-regenerative multipotent stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2306-15.	7.1	40
30	Differential DNA repair underlies mutation hotspots at active promoters in cancer genomes. Nature, 2016, 532, 259-263.	27.8	195
31	A quantitative proteomics approach identifies ETV6 and IKZF1 as new regulators of an <i>ERG</i> -driven transcriptional network. Nucleic Acids Research, 2016, 44, 10644-10661.	14.5	17
32	Integrated Genetic, Epigenetic, and Transcriptional Profiling Identifies Molecular Pathways in the Development of Laterally Spreading Tumors. Molecular Cancer Research, 2016, 14, 1217-1228.	3.4	20
33	An autonomous CEBPA enhancer specific for myeloid-lineage priming and neutrophilic differentiation. Blood, 2016, 127, 2991-3003.	1.4	60
34	Acute Sensitivity of Ph-like Acute Lymphoblastic Leukemia to the SMAC-Mimetic Birinapant. Cancer Research, 2016, 76, 4579-4591.	0.9	20
35	Acute myeloid leukemia requires Hhex to enable PRC2-mediated epigenetic repression of <i>Cdkn2a</i> . Genes and Development, 2016, 30, 78-91.	5.9	30
36	Arrested Hematopoiesis and Vascular Relaxation Defects in Mice with a Mutation in <i>Dhfr</i> . Molecular and Cellular Biology, 2016, 36, 1222-1236.	2.3	6

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37	Clinical significance of cancerous inhibitor of protein phosphatase 2A in human cancers. International Journal of Cancer, 2016, 138, 525-532.	5.1	53
38	Opposing regulation of BIM and BCL2 controls glucocorticoid-induced apoptosis of pediatric acute lymphoblastic leukemia cells. Blood, 2015, 125, 273-283.	1.4	107
39	Endoglin potentiates nitric oxide synthesis to enhance definitive hematopoiesis. Biology Open, 2015, 4, 819-829.	1.2	4
40	Whole-transcriptome analysis of endothelial to hematopoietic stem cell transition reveals a requirement for Gpr56 in HSC generation. Journal of Experimental Medicine, 2015, 212, 93-106.	8.5	105
41	Systematic Screening of Promoter Regions Pinpoints Functional <i>Cis</i> -Regulatory Mutations in a Cutaneous Melanoma Genome. Molecular Cancer Research, 2015, 13, 1218-1226.	3.4	29
42	High-level Gpr56 expression is dispensable for the maintenance and function of hematopoietic stem and progenitor cells in mice. Stem Cell Research, 2015, 14, 307-322.	0.7	26
43	SMAD1 and SMAD5 Expression Is Coordinately Regulated by FLI1 and GATA2 during Endothelial Development. Molecular and Cellular Biology, 2015, 35, 2165-2172.	2.3	11
44	A novel mouse model identifies cooperating mutations and therapeutic targets critical for chronic myeloid leukemia progression. Journal of Experimental Medicine, 2015, 212, 1551-1569.	8.5	35
45	CIP2A is a candidate therapeutic target in clinically challenging prostate cancer cell populations. Oncotarget, 2015, 6, 19661-19670.	1.8	26
46	Epigenetic inactivation of the candidate tumor suppressor <i>USP44</i> is a frequent and early event in colorectal neoplasia. Epigenetics, 2014, 9, 1092-1100.	2.7	42
47	OncoCis: annotation of cis-regulatory mutations in cancer. Genome Biology, 2014, 15, 485.	8.8	22
48	BloodChIP: a database of comparative genome-wide transcription factor binding profiles in human blood cells. Nucleic Acids Research, 2014, 42, D172-D177.	14.5	43
49	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells InÂVivo. Cancer Cell, 2014, 25, 794-808.	16.8	272
50	Keeping GBM in check by targeting CHK1-CIP2A axis Journal of Clinical Oncology, 2014, 32, 2036-2036.	1.6	0
51	Identification of a Prognostic Gene Expression Signature for AZA Response in MDS and CMML Patients. Blood, 2014, 124, 4601-4601.	1.4	0
52	Chk1 Targeting Reactivates PP2A Tumor Suppressor Activity in Cancer Cells. Cancer Research, 2013, 73, 6757-6769.	0.9	41
53	Genome-wide analysis of transcriptional regulators in human HSPCs reveals a densely interconnected network of coding and noncoding genes. Blood, 2013, 122, e12-e22.	1.4	123
54	Mathematical model of a gene regulatory network reconciles effects of genetic perturbations on hematopoietic stem cell emergence. Developmental Biology, 2013, 379, 258-269.	2.0	21

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55	Reassembly of Nucleosomes at the MLH1 Promoter Initiates Resilencing Following Decitabine Exposure. PLoS Genetics, 2013, 9, e1003636.	3.5	19
56	Cancerous Inhibitor of Protein Phosphatase 2A, an Emerging Human Oncoprotein and a Potential Cancer Therapy Target. Cancer Research, 2013, 73, 6548-6553.	0.9	135
57	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. Blood, 2013, 121, 2289-2300.	1.4	72
58	Genome-scale expression and transcription factor binding profiles reveal therapeutic targets in transgenic ERG myeloid leukemia. Blood, 2013, 122, 2694-2703.	1.4	44
59	Relative Distribution of Folate Species Is Associated with Global DNA Methylation in Human Colorectal Mucosa. Cancer Prevention Research, 2012, 5, 921-929.	1.5	19
60	Cell signalling pathways that mediate haematopoietic stem cell specification. International Journal of Biochemistry and Cell Biology, 2012, 44, 2175-2184.	2.8	12
61	Concise Review: Blood Relatives: Formation and regulation of hematopoietic stem cells by the basic helix-loop-helix transcription factors stem cell leukemia and lymphoblastic leukemia-derived sequence 1. Stem Cells, 2012, 30, 1053-1058.	3.2	25
62	Pdgfrα and Flk1 are direct target genes of Mixl1 in differentiating embryonic stem cells. Stem Cell Research, 2012, 8, 165-179.	0.7	15
63	ERG dependence distinguishes developmental control of hematopoietic stem cell maintenance from hematopoietic specification. Genes and Development, 2011, 25, 251-262.	5.9	99
64	Adult Cardiac-Resident MSC-like Stem Cells with a Proepicardial Origin. Cell Stem Cell, 2011, 9, 527-540.	11.1	358
65	ERG promotes T-acute lymphoblastic leukemia and is transcriptionally regulated in leukemic cells by a stem cell enhancer. Blood, 2011, 117, 7079-7089.	1.4	81
66	A Runx1-Smad6 Rheostat Controls Runx1 Activity during Embryonic Hematopoiesis. Molecular and Cellular Biology, 2011, 31, 2817-2826.	2.3	21
67	Gene regulatory networks governing haematopoietic stem cell development and identity. International Journal of Developmental Biology, 2010, 54, 1201-1211.	0.6	51
68	Phosphorylation and Acetylation of Histone H3 and Autoregulation by Early Growth Response 1 Mediate Interleukin 1β Induction of Early Growth Response 1 Transcription. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 536-545.	2.4	42
69	Combinatorial Transcriptional Control In Blood Stem/Progenitor Cells: Genome-wide Analysis of Ten Major Transcriptional Regulators. Cell Stem Cell, 2010, 7, 532-544.	11.1	623
70	Epigenetic Silencing of the Pro-Apoptotic Bim Gene in Glucocorticoid Poor-Responsive Pediatric Acute Lymphoblastic Leukemia, and Its Reversal by Histone Deacetylase Inhibition Blood, 2009, 114, 939-939.	1.4	1
71	Runx genes are direct targets of Scl/Tal1 in the yolk sac and fetal liver. Blood, 2008, 111, 3005-3014.	1.4	76
72	Endoglin expression in blood and endothelium is differentially regulated by modular assembly of the Ets/Gata hemangioblast code. Blood, 2008, 112, 4512-4522.	1.4	42

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73	Gata2, Fli1, and Scl form a recursively wired gene-regulatory circuit during early hematopoietic development. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17692-17697.	7.1	208
74	The SCL transcriptional network and BMP signaling pathway interact to regulate RUNX1 activity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 840-845.	7.1	107
75	The paralogous hematopoietic regulators Lyl1 and Scl are coregulated by Ets and GATA factors, but Lyl1 cannot rescue the early Scl–/– phenotype. Blood, 2007, 109, 1908-1916.	1.4	71
76	A common origin of the 4143insA ADAMTS13 mutation. Thrombosis and Haemostasis, 2006, 96, 3-6.	3.4	74
77	Endoglin expression in the endothelium is regulated by Fli-1, Erg, and Elf-1 acting on the promoter and a –8-kb enhancer. Blood, 2006, 107, 4737-4745.	1.4	62
78	Transcriptional Link between Blood and Bone: the Stem Cell Leukemia Gene and Its +19 Stem Cell Enhancer Are Active in Bone Cells. Molecular and Cellular Biology, 2006, 26, 2615-2625.	2.3	17
79	The Proto-Oncogene ERG in Megakaryoblastic Leukemias. Cancer Research, 2005, 65, 7596-7602.	0.9	112
80	Role of Thrombospondin-1 in Control of von Willebrand Factor Multimer Size in Mice. Journal of Biological Chemistry, 2004, 279, 21439-21448.	3.4	51
81	Congenital thrombotic thrombocytopenic purpura in association with a mutation in the second CUB domain of ADAMTS13. Blood, 2004, 103, 627-629.	1.4	84
82	A perspective on the measurement of ADAMTS13 in thrombotic thrombocytopaenic purpura. European Journal of Haematology, 2003, 70, 257-262.	2.2	6
83	The von Willebrand factor–reducing activity of thrombospondin-1 is located in the calcium-binding/C-terminal sequence and requires a free thiol at position 974. Blood, 2002, 100, 2832-2838.	1.4	34
84	Control of von Willebrand factor multimer size and implications for disease. Blood Reviews, 2002, 16, 185-192.	5.7	18
85	p57Kip2 regulates embryonic blood stem cells by controlling sympathoadrenal progenitor expansion. Blood, 0, , .	1.4	3