

Joost H A Martens

List of Publications by Year in descending order

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97
papers

15,676
citations

71102

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48315

88
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98
all docs

98
docs citations

98
times ranked

26456
citing authors

#	ARTICLE	IF	CITATIONS
1	ENGINEERING FLOWS IN SMALL DEVICES. Annual Review of Fluid Mechanics, 2004, 36, 381-411.	25.0	3,041
2	mTOR- and HIF-1 α -mediated aerobic glycolysis as metabolic basis for trained immunity. Science, 2014, 345, 1250684.	12.6	1,517
3	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. Science, 2014, 345, 1251086.	12.6	1,338
4	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
5	Partitioning and Plasticity of Repressive Histone Methylation States in Mammalian Chromatin. Molecular Cell, 2003, 12, 1577-1589.	9.7	1,010
6	Candida albicans Infection Affords Protection against Reinfection via Functional Reprogramming of Monocytes. Cell Host and Microbe, 2012, 12, 223-232.	11.0	926
7	The profile of repeat-associated histone lysine methylation states in the mouse epigenome. EMBO Journal, 2005, 24, 800-812.	7.8	594
8	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
9	β -Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. Cell, 2016, 167, 1354-1368.e14.	28.9	467
10	A Chromosomal Memory Triggered by Xist Regulates Histone Methylation in X Inactivation. PLoS Biology, 2004, 2, e171.	5.6	336
11	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	17.5	323
12	Suv39h-Dependent H3K9me3 Marks Intact Retrotransposons and Silences LINE Elements in Mouse Embryonic Stem Cells. Molecular Cell, 2014, 55, 277-290.	9.7	278
13	PML-RAR α /RXR Alters the Epigenetic Landscape in Acute Promyelocytic Leukemia. Cancer Cell, 2010, 17, 173-185.	16.8	276
14	Silenced Tumor Suppressor Genes Reactivated by DNA Demethylation Do Not Return to a Fully Euchromatic Chromatin State. Cancer Research, 2006, 66, 3541-3549.	0.9	266
15	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
16	BLUEPRINT: mapping human blood cell epigenomes. Haematologica, 2013, 98, 1487-1489.	3.5	189
17	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
18	Active and Repressive Chromatin Are Interspersed without Spreading in an Imprinted Gene Cluster in the Mammalian Genome. Molecular Cell, 2007, 27, 353-366.	9.7	138

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19	EZH2 and Histone 3 Trimethyl Lysine 27 Associated with Il4 and Il13 Gene Silencing in TH1 Cells. <i>Journal of Biological Chemistry</i> , 2005, 280, 31470-31477.	3.4	132
20	Non-canonical PRC1.1 Targets Active Genes Independent of H3K27me3 and Is Essential for Leukemogenesis. <i>Cell Reports</i> , 2016, 14, 332-346.	6.4	126
21	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015, 47, 1316-1325.	21.4	119
22	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	5.5	118
23	c-Myc Modulation and Acetylation Is a Key HDAC Inhibitor Target in Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2542-2555.	7.0	105
24	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.4	104
25	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. <i>Cancer Cell</i> , 2016, 30, 806-821.	16.8	103
26	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	6.4	102
27	ERG and FLI1 binding sites demarcate targets for aberrant epigenetic regulation by AML1-ETO in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 4038-4048.	1.4	98
28	Histone modification patterns associated with the human X chromosome. <i>EMBO Reports</i> , 2006, 7, 628-634.	4.5	94
29	The molecular signature of oncofusion proteins in acute myeloid leukemia. <i>FEBS Letters</i> , 2010, 584, 2662-2669.	2.8	88
30	Scaffold/Matrix Attachment Region Elements Interact with a p300 Scaffold Attachment Factor A Complex and Are Bound by Acetylated Nucleosomes. <i>Molecular and Cellular Biology</i> , 2002, 22, 2598-2606.	2.3	87
31	MLL-AF9 and MLL-AF4 oncofusion proteins bind a distinct enhancer repertoire and target the RUNX1 program in 11q23 acute myeloid leukemia. <i>Oncogene</i> , 2017, 36, 3346-3356.	5.9	86
32	Cascade of Distinct Histone Modifications during Collagenase Gene Activation. <i>Molecular and Cellular Biology</i> , 2003, 23, 1808-1816.	2.3	84
33	Large-scale in vitro production of red blood cells from human peripheral blood mononuclear cells. <i>Blood Advances</i> , 2019, 3, 3337-3350.	5.2	70
34	The European Hematology Association Roadmap for European Hematology Research: a consensus document. <i>Haematologica</i> , 2016, 101, 115-208.	3.5	67
35	miR-194-5p/BCLAF1 deregulation in AML tumorigenesis. <i>Leukemia</i> , 2017, 31, 2315-2325.	7.2	66
36	Chromatin accessibility, p300, and histone acetylation define PML-RAR α and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 3058-3068.	1.4	60

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37	The Hematopoietic Transcription Factors RUNX1 and ERG Prevent AML1-ETO Oncogene Overexpression and Onset of the Apoptosis Program in t(8;21) AMLs. <i>Cell Reports</i> , 2016, 17, 2087-2100.	6.4	60
38	E-cadherin loss induces targetable autocrine activation of growth factor signalling in lobular breast cancer. <i>Scientific Reports</i> , 2018, 8, 15454.	3.3	55
39	Genome-wide functions of PML-RAR α in acute promyelocytic leukaemia. <i>British Journal of Cancer</i> , 2011, 104, 554-558.	6.4	54
40	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016, 17, 2101-2111.	6.4	54
41	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	12.8	50
42	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	8.8	48
43	Acute myeloid leukemia: A central role for the ETS factor ERG. <i>International Journal of Biochemistry and Cell Biology</i> , 2011, 43, 1413-1416.	2.8	46
44	HIF1/2-exerted control over glycolytic gene expression is not functionally relevant for glycolysis in human leukemic stem/progenitor cells. <i>Cancer & Metabolism</i> , 2019, 7, 11.	5.0	46
45	The Tetraspanin CD9 Affords High-Purity Capture of All Murine Hematopoietic Stem Cells. <i>Cell Reports</i> , 2013, 4, 642-648.	6.4	42
46	Stronger induction of trained immunity by mucosal BCG or MTBVAC vaccination compared to standard intradermal vaccination. <i>Cell Reports Medicine</i> , 2021, 2, 100185.	6.5	41
47	The oncofusion protein FUS-ERG targets key hematopoietic regulators and modulates the all-trans retinoic acid signaling pathway in t(16;21) acute myeloid leukemia. <i>Oncogene</i> , 2016, 35, 1965-1976.	5.9	39
48	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. <i>Genome Research</i> , 2020, 30, 1217-1227.	5.5	35
49	Characterization of plant proteins that interact with cowpea mosaic virus α 60K protein in the yeast two-hybrid system. <i>Journal of General Virology</i> , 2002, 83, 885-893.	2.9	35
50	The Role of Histone Modifications in Epigenetic Transitions During Normal and Perturbed Development. , 2006, , 1-27.		34
51	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
52	Context-Selective Death of Acute Myeloid Leukemia Cells Triggered by the Novel Hybrid Retinoid-HDAC Inhibitor MC2392. <i>Cancer Research</i> , 2014, 74, 2328-2339.	0.9	33
53	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019, 26, 1059-1069.e6.	6.4	33
54	MEIS2 Is an Oncogenic Partner in AML1-ETO-Positive AML. <i>Cell Reports</i> , 2016, 16, 498-507.	6.4	32

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55	BRD9 binds cell type-specific chromatin regions regulating leukemic cell survival via STAT5 inhibition. <i>Cell Death and Disease</i> , 2019, 10, 338.	6.3	31
56	RUNX1 mutations enhance self-renewal and block granulocytic differentiation in human in vitro models and primary AMLs. <i>Blood Advances</i> , 2019, 3, 320-332.	5.2	27
57	The Role of Necroptosis: Biological Relevance and Its Involvement in Cancer. <i>Cancers</i> , 2021, 13, 684.	3.7	27
58	Genome-wide interplay of nuclear receptors with the epigenome. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2011, 1812, 818-823.	3.8	23
59	AML associated oncofusion proteins PML-RARA, AML1-ETO and CFBF-MYH11 target RUNX/ETS-factor binding sites to modulate H3ac levels and drive leukemogenesis. <i>Oncotarget</i> , 2017, 8, 12855-12865.	1.8	22
60	Molecular mechanisms of bleeding disorder associated GFI1B ^{Q287*} mutation and its affected pathways in megakaryocytes and platelets. <i>Haematologica</i> , 2019, 104, 1460-1472.	3.5	21
61	Recent insights into Histone Acetyltransferase-1: biological function and involvement in pathogenesis. <i>Epigenetics</i> , 2021, 16, 838-850.	2.7	21
62	The USP7-TRIM27 axis mediates non-canonical PRC1.1 function and is a druggable target in leukemia. <i>IScience</i> , 2021, 24, 102435.	4.1	19
63	Dual Promoter Usage as Regulatory Mechanism of let-7c Expression in Leukemic and Solid Tumors. <i>Molecular Cancer Research</i> , 2014, 12, 878-889.	3.4	18
64	The AAA+ATPase RUVBL2 is essential for the oncogenic function of c-MYB in acute myeloid leukemia. <i>Leukemia</i> , 2019, 33, 2817-2829.	7.2	18
65	CBX2 shapes chromatin accessibility promoting AML via p38 MAPK signaling pathway. <i>Molecular Cancer</i> , 2022, 21, .	19.2	18
66	The Decade of the Epigenomes?. <i>Genes and Cancer</i> , 2011, 2, 680-687.	1.9	16
67	The acute myeloid leukemia associated AML1-ETO fusion protein alters the transcriptome and cellular progression in a single-oncogene expressing in vitro induced pluripotent stem cell based granulocyte differentiation model. <i>PLoS ONE</i> , 2019, 14, e0226435.	2.5	15
68	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	15
69	Dynamics of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. <i>Genome Research</i> , 2022, 32, 1328-1342.	5.5	14
70	The genome-wide molecular signature of transcription factors in leukemia. <i>Experimental Hematology</i> , 2014, 42, 637-650.	0.4	13
71	GFI1 is required for RUNX1/ETO positive acute myeloid leukemia. <i>Haematologica</i> , 2018, 103, e395-e399.	3.5	13
72	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018, 9, 25647-25660.	1.8	13

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73	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. <i>Haematologica</i> , 2021, 106, 2613-2623.	3.5	12
74	Time-resolved analysis of DNA-protein interactions in living cells by UV laser pulses. <i>Scientific Reports</i> , 2017, 7, 11725.	3.3	11
75	CITED2 affects leukemic cell survival by interfering with p53 activation. <i>Cell Death and Disease</i> , 2017, 8, e3132-e3132.	6.3	11
76	BRD3/4 inhibition and FLT3-ligand deprivation target pathways that are essential for the survival of human MLL-AF9+ leukemic cells. <i>PLoS ONE</i> , 2017, 12, e0189102.	2.5	10
77	The alarmin S100A9 hampers osteoclast differentiation from human circulating precursors by reducing the expression of RANK. <i>FASEB Journal</i> , 2019, 33, 10104-10115.	0.5	9
78	CBF β -SMMHC regulates ribosomal gene transcription and alters ribosome biogenesis. <i>Leukemia</i> , 2017, 31, 1443-1446.	7.2	7
79	CBF β -MYH11 interferes with megakaryocyte differentiation via modulating a gene program that includes GATA2 and KLF1. <i>Blood Cancer Journal</i> , 2019, 9, 33.	6.2	7
80	CD34 ⁺ acute myeloid leukemia cells with low levels of reactive oxygen species show increased expression of stemness genes and can be targeted by the BCL2 inhibitor venetoclax. <i>Haematologica</i> , 2020, 105, e399-e403.	3.5	7
81	Genome-wide binding of transcription factors in inv(16) acute myeloid leukemia. <i>Genomics Data</i> , 2014, 2, 170-172.	1.3	6
82	C-terminal BRE overexpression in 11q23-rearranged and t(8;16) acute myeloid leukemia is caused by intragenic transcription initiation. <i>Leukemia</i> , 2018, 32, 828-836.	7.2	6
83	Ring sideroblasts in AML are associated with adverse risk characteristics and have a distinct gene expression pattern. <i>Blood Advances</i> , 2019, 3, 3111-3122.	5.2	6
84	CBF β -SMMHC Affects Genome-wide Polycomb Repressive Complex 1 Activity in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2020, 30, 299-307.e3.	6.4	6
85	Potential impact of celiac disease genetic risk factors on T cell receptor signaling in gluten-specific CD4+ T cells. <i>Scientific Reports</i> , 2021, 11, 9252.	3.3	6
86	Combined HAT/EZH2 modulation leads to cancer-selective cell death. <i>Oncotarget</i> , 2018, 9, 25630-25646.	1.8	5
87	The EHA Research Roadmap: Normal Hematopoiesis. <i>HemaSphere</i> , 2021, 5, e669.	2.7	1
88	Presence of mutant p53 increases stem cell frequency and is associated with reduced binding to classic TP53 binding sites in cell lines and primary AMLs. <i>Experimental Hematology</i> , 2022, 110, 39-46.	0.4	1
89	CBFB-MYH11/RUNX1 together with a compendium of hematopoietic regulators, chromatin modifiers and basal transcription factors occupies self-renewal genes in inv(16) acute myeloid leukemia. <i>Experimental Hematology</i> , 2013, 41, S50.	0.4	0
90	P074â€¦The alarmin S100A9 hampers osteoclast differentiation from circulating precursors by reducing the expression of rank. , 2019, , .		0

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91	Characterization of a genomic region 8Åkb downstream of GF11B associated with myeloproliferative neoplasms. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166259.	3.8	0
92	Aberrant Expression of the SOX11 Oncogene in Mantle Cell Lymphoma Is Associated with Activation and De Novo 3D Looping of a Distant Enhancer Element. <i>Blood</i> , 2016, 128, 459-459.	1.4	0
93	Whole-Genome Analysis of the Chromatin Structure in Multiple Myeloma. <i>Blood</i> , 2016, 128, 118-118.	1.4	0
94	Title is missing!. , 2019, 14, e0226435.		0
95	Title is missing!. , 2019, 14, e0226435.		0
96	Title is missing!. , 2019, 14, e0226435.		0
97	Title is missing!. , 2019, 14, e0226435.		0