

Joost H A Martens

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

15,676
citations

81434

41
h-index

54771

88
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98
all docs

98
docs citations

98
times ranked

29405
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. <i>Genome Research</i> , 2022, 32, 1328-1342.	2.4	14
2	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.	0.2	1
3	CBX2 shapes chromatin accessibility promoting AML via p38 MAPK signaling pathway. <i>Molecular Cancer</i> , 2022, 21, .	7.9	18
4	Recent insights into Histone Acetyltransferase-1: biological function and involvement in pathogenesis. <i>Epigenetics</i> , 2021, 16, 838-850.	1.3	21
5	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. <i>Haematologica</i> , 2021, 106, 2613-2623.	1.7	12
6	The Role of Necroptosis: Biological Relevance and Its Involvement in Cancer. <i>Cancers</i> , 2021, 13, 684.	1.7	27
7	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.	1.6	6
8	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	3.3	34
9	The USP7-TRIM27 axis mediates non-canonical PRC1.1 function and is a druggable target in leukemia. <i>IScience</i> , 2021, 24, 102435.	1.9	19
10	Characterization of a genomic region 8Åkb downstream of GFI1B associated with myeloproliferative neoplasms. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2021, 1867, 166259.	1.8	0
11	Stronger induction of trained immunity by mucosal BCG or MTBVAC vaccination compared to standard intradermal vaccination. <i>Cell Reports Medicine</i> , 2021, 2, 100185.	3.3	41
12	The EHA Research Roadmap: Normal Hematopoiesis. <i>HemaSphere</i> , 2021, 5, e669.	1.2	1
13	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	15
14	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. <i>Genome Research</i> , 2020, 30, 1217-1227.	2.4	35
15	CBF $\hat{2}$ -SMMHC Affects Genome-wide Polycomb Repressive Complex 1 Activity in Acute Myeloid Leukemia. <i>Cell Reports</i> , 2020, 30, 299-307.e3.	2.9	6
16	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.	1.7	7
17	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019, 26, 1059-1069.e6.	2.9	33
18	The alarmin S100A9 hampers osteoclast differentiation from human circulating precursors by reducing the expression of RANK. <i>FASEB Journal</i> , 2019, 33, 10104-10115.	0.2	9

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19	The AAA+ATPase RUVBL2 is essential for the oncogenic function of c-MYB in acute myeloid leukemia. <i>Leukemia</i> , 2019, 33, 2817-2829.	3.3	18
20	BRD9 binds cell type-specific chromatin regions regulating leukemic cell survival via STAT5 inhibition. <i>Cell Death and Disease</i> , 2019, 10, 338.	2.7	31
21	CBF $\hat{2}$ -MYH11 interferes with megakaryocyte differentiation via modulating a gene program that includes GATA2 and KLF1. <i>Blood Cancer Journal</i> , 2019, 9, 33.	2.8	7
22	P074â€¦The alarmin S100A9 hampers osteoclast differentiation from circulating precursors by reducing the expression of rank. , 2019, , .		0
23	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.	2.5	27
24	Large-scale in vitro production of red blood cells from human peripheral blood mononuclear cells. <i>Blood Advances</i> , 2019, 3, 3337-3350.	2.5	70
25	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.	2.5	6
26	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.	2.4	46
27	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.	1.1	15
28	Molecular mechanisms of bleeding disorder associated GFI1B ^{Q287*} mutation and its affected pathways in megakaryocytes and platelets. <i>Haematologica</i> , 2019, 104, 1460-1472.	1.7	21
29	Title is missing!. , 2019, 14, e0226435.		0
30	Title is missing!. , 2019, 14, e0226435.		0
31	Title is missing!. , 2019, 14, e0226435.		0
32	Title is missing!. , 2019, 14, e0226435.		0
33	GFI1 is required for RUNX1/ETO positive acute myeloid leukemia. <i>Haematologica</i> , 2018, 103, e395-e399.	1.7	13
34	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.	3.3	6
35	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018, 9, 25647-25660.	0.8	13
36	E-cadherin loss induces targetable autocrine activation of growth factor signalling in lobular breast cancer. <i>Scientific Reports</i> , 2018, 8, 15454.	1.6	55

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37	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	2.9	104
38	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	15.2	157
39	Combined HAT/EZH2 modulation leads to cancer-selective cell death. <i>Oncotarget</i> , 2018, 9, 25630-25646.	0.8	5
40	c-Myc Modulation and Acetylation Is a Key HDAC Inhibitor Target in Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2542-2555.	3.2	105
41	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.	2.6	86
42	miR-194-5p/BCLAF1 deregulation in AML tumorigenesis. <i>Leukemia</i> , 2017, 31, 2315-2325.	3.3	66
43	CBF $\hat{2}$ -SMMHC regulates ribosomal gene transcription and alters ribosome biogenesis. <i>Leukemia</i> , 2017, 31, 1443-1446.	3.3	7
44	Time-resolved analysis of DNA-protein interactions in living cells by UV laser pulses. <i>Scientific Reports</i> , 2017, 7, 11725.	1.6	11
45	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
46	CITED2 affects leukemic cell survival by interfering with p53 activation. <i>Cell Death and Disease</i> , 2017, 8, e3132-e3132.	2.7	11
47	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.	1.1	10
48	AML associated oncofusion proteins PML-RARA, AML1-ETO and CBF β -MYH11 target RUNX/ETS-factor binding sites to modulate H3ac levels and drive leukemogenesis. <i>Oncotarget</i> , 2017, 8, 12855-12865.	0.8	22
49	MEIS2 Is an Oncogenic Partner in AML1-ETO-Positive AML. <i>Cell Reports</i> , 2016, 16, 498-507.	2.9	32
50	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	2.9	102
51	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.	7.7	103
52	$\hat{2}$ -Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016, 167, 1354-1368.e14.	13.5	467
53	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	13.5	1,052
54	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.	2.9	60

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55	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016, 17, 2101-2111.	2.9	54
56	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573
57	The European Hematology Association Roadmap for European Hematology Research: a consensus document. <i>Haematologica</i> , 2016, 101, 115-208.	1.7	67
58	Non-canonical PRC1.1 Targets Active Genes Independent of H3K27me3 and Is Essential for Leukemogenesis. <i>Cell Reports</i> , 2016, 14, 332-346.	2.9	126
59	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.	2.6	39
60	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.	0.6	0
61	Whole-Genome Analysis of the Chromatin Structure in Multiple Myeloma. <i>Blood</i> , 2016, 128, 118-118.	0.6	0
62	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	3.8	48
63	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	2.4	118
64	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.	9.4	119
65	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.	0.4	33
66	The genome-wide molecular signature of transcription factors in leukemia. <i>Experimental Hematology</i> , 2014, 42, 637-650.	0.2	13
67	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. <i>Science</i> , 2014, 345, 1251086.	6.0	1,338
68	Genome-wide binding of transcription factors in inv(16) acute myeloid leukemia. <i>Genomics Data</i> , 2014, 2, 170-172.	1.3	6
69	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	6.0	253
70	Dual Promoter Usage as Regulatory Mechanism of let-7c Expression in Leukemic and Solid Tumors. <i>Molecular Cancer Research</i> , 2014, 12, 878-889.	1.5	18
71	Suv39h-Dependent H3K9me3 Marks Intact Retrotransposons and Silences LINE Elements in Mouse Embryonic Stem Cells. <i>Molecular Cell</i> , 2014, 55, 277-290.	4.5	278
72	mTOR- and HIF-1 α -mediated aerobic glycolysis as metabolic basis for trained immunity. <i>Science</i> , 2014, 345, 1250684.	6.0	1,517

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73	The Tetraspanin CD9 Affords High-Purity Capture of All Murine Hematopoietic Stem Cells. <i>Cell Reports</i> , 2013, 4, 642-648.	2.9	42
74	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.	0.2	0
75	BLUEPRINT: mapping human blood cell epigenomes. <i>Haematologica</i> , 2013, 98, 1487-1489.	1.7	189
76	Chromatin accessibility, p300, and histone acetylation define PML-RAR \pm and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 3058-3068.	0.6	60
77	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.	0.6	98
78	<i>Candida albicans</i> Infection Affords Protection against Reinfection via Functional Reprogramming of Monocytes. <i>Cell Host and Microbe</i> , 2012, 12, 223-232.	5.1	926
79	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	9.4	323
80	Acute myeloid leukemia: A central role for the ETS factor ERG. <i>International Journal of Biochemistry and Cell Biology</i> , 2011, 43, 1413-1416.	1.2	46
81	Genome-wide interplay of nuclear receptors with the epigenome. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2011, 1812, 818-823.	1.8	23
82	Genome-wide functions of PML-RAR \pm in acute promyelocytic leukaemia. <i>British Journal of Cancer</i> , 2011, 104, 554-558.	2.9	54
83	The Decade of the Epigenomes?. <i>Genes and Cancer</i> , 2011, 2, 680-687.	0.6	16
84	PML-RAR \pm /RXR Alters the Epigenetic Landscape in Acute Promyelocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 173-185.	7.7	276
85	The molecular signature of oncofusion proteins in acute myeloid leukemia. <i>FEBS Letters</i> , 2010, 584, 2662-2669.	1.3	88
86	Active and Repressive Chromatin Are Interspersed without Spreading in an Imprinted Gene Cluster in the Mammalian Genome. <i>Molecular Cell</i> , 2007, 27, 353-366.	4.5	138
87	Silenced Tumor Suppressor Genes Reactivated by DNA Demethylation Do Not Return to a Fully Euchromatic Chromatin State. <i>Cancer Research</i> , 2006, 66, 3541-3549.	0.4	266
88	Histone modification patterns associated with the human X chromosome. <i>EMBO Reports</i> , 2006, 7, 628-634.	2.0	94
89	The Role of Histone Modifications in Epigenetic Transitions During Normal and Perturbed Development. , 2006, , 1-27.		34
90	The profile of repeat-associated histone lysine methylation states in the mouse epigenome. <i>EMBO Journal</i> , 2005, 24, 800-812.	3.5	594

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91	EZH2 and Histone 3 Trimethyl Lysine 27 Associated with Il4 and Il13 Gene Silencing in TH1 Cells. Journal of Biological Chemistry, 2005, 280, 31470-31477.	1.6	132
92	A Chromosomal Memory Triggered by Xist Regulates Histone Methylation in X Inactivation. PLoS Biology, 2004, 2, e171.	2.6	336
93	ENGINEERING FLOWS IN SMALL DEVICES. Annual Review of Fluid Mechanics, 2004, 36, 381-411.	10.8	3,041
94	Partitioning and Plasticity of Repressive Histone Methylation States in Mammalian Chromatin. Molecular Cell, 2003, 12, 1577-1589.	4.5	1,010
95	Cascade of Distinct Histone Modifications during Collagenase Gene Activation. Molecular and Cellular Biology, 2003, 23, 1808-1816.	1.1	84
96	Scaffold/Matrix Attachment Region Elements Interact with a p300 - Scaffold Attachment Factor A Complex and Are Bound by Acetylated Nucleosomes. Molecular and Cellular Biology, 2002, 22, 2598-2606.	1.1	87
97	Characterization of plant proteins that interact with cowpea mosaic virus $\hat{\sim}60\text{K}\hat{\sim}$ protein in the yeast two-hybrid system. Journal of General Virology, 2002, 83, 885-893.	1.3	35