

Constanze Bonifer

List of Publications by Year in descending order

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68
papers

3,333
citations

172457

29
h-index

168389

53
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73
all docs

73
docs citations

73
times ranked

5793
citing authors

#	ARTICLE	IF	CITATIONS
1	Derepression of an endogenous long terminal repeat activates the CSF1R proto-oncogene in human lymphoma. <i>Nature Medicine</i> , 2010, 16, 571-579.	30.7	317
2	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. <i>Developmental Cell</i> , 2016, 36, 572-587.	7.0	213
3	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. <i>Nucleic Acids Research</i> , 2013, 41, e201-e201.	14.5	196
4	<i>PU.1</i> expression is modulated by the balance of functional sense and antisense RNAs regulated by a shared <i>cis</i> -regulatory element. <i>Genes and Development</i> , 2008, 22, 2085-2092.	5.9	169
5	<i>RUNX1</i> reshapes the epigenetic landscape at the onset of haematopoiesis. <i>EMBO Journal</i> , 2012, 31, 4318-4333.	7.8	158
6	<i>GF11</i> and <i>GF11B</i> control the loss of endothelial identity of hemogenic endothelium during hematopoietic commitment. <i>Blood</i> , 2012, 120, 314-322.	1.4	144
7	Subtype-specific regulatory network rewiring in acute myeloid leukemia. <i>Nature Genetics</i> , 2019, 51, 151-162.	21.4	140
8	Two distinct auto-regulatory loops operate at the <i>PU.1</i> locus in B cells and myeloid cells. <i>Blood</i> , 2011, 117, 2827-2838.	1.4	120
9	<i>Sox4</i> Is a Key Oncogenic Target in <i>C/EBPβ</i> Mutant Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2013, 24, 575-588.	16.8	112
10	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML that Regulates Differentiation Block and Self-Renewal. <i>Cell Reports</i> , 2014, 8, 1974-1988.	6.4	106
11	Inducible chromatin priming is associated with the establishment of immunological memory in T cells. <i>EMBO Journal</i> , 2016, 35, 515-535.	7.8	92
12	Small Molecule Inhibitor of <i>CBFβ</i> - <i>RUNX</i> Binding for <i>RUNX</i> Transcription Factor Driven Cancers. <i>EBioMedicine</i> , 2016, 8, 117-131.	6.1	84
13	The Oncogenic Transcription Factor <i>RUNX1/ETO</i> Corrupts Cell Cycle Regulation to Drive Leukemic Transformation. <i>Cancer Cell</i> , 2018, 34, 626-642.e8.	16.8	81
14	The <i>RUNX1</i> - <i>PU.1</i> axis in the control of hematopoiesis. <i>International Journal of Hematology</i> , 2015, 101, 319-329.	1.6	78
15	The Role of the Ubiquitously Expressed Transcription Factor <i>Sp1</i> in Tissue-specific Transcriptional Regulation and in Disease. <i>Yale Journal of Biology and Medicine</i> , 2016, 89, 513-525.	0.2	77
16	Prospective Isolation and Characterization of Genetically and Functionally Distinct AML Subclones. <i>Cancer Cell</i> , 2018, 34, 674-689.e8.	16.8	71
17	The transcriptional regulation of the Colony-Stimulating Factor 1 Receptor (<i>csf1r</i>) gene during hematopoiesis. <i>Frontiers in Bioscience - Landmark</i> , 2008, 13, 549.	3.0	64
18	The mechanism of repression of the myeloid-specific <i>c-fms</i> gene by <i>Pax5</i> during B lineage restriction. <i>EMBO Journal</i> , 2006, 25, 1070-1080.	7.8	63

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19	Chronic FLT3-ITD Signaling in Acute Myeloid Leukemia Is Connected to a Specific Chromatin Signature. <i>Cell Reports</i> , 2015, 12, 821-836.	6.4	63
20	RUNX1 positively regulates a cell adhesion and migration program in murine hemogenic endothelium prior to blood emergence. <i>Blood</i> , 2014, 124, e11-e20.	1.4	61
21	Mapping of transcription factor motifs in active chromatin identifies IRF5 as key regulator in classical Hodgkin lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4513-22.	7.1	53
22	The Chicken Lysozyme Locus as a Paradigm for the Complex Developmental Regulation of Eukaryotic Gene Loci. <i>Journal of Biological Chemistry</i> , 1997, 272, 26075-26078.	3.4	51
23	A crucial role for the ubiquitously expressed transcription factor Sp1 at early stages of hematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 2391-2401.	2.5	51
24	Wellington-bootstrap: differential DNase-seq footprinting identifies cell-type determining transcription factors. <i>BMC Genomics</i> , 2015, 16, 1000.	2.8	49
25	RUNX1-ETO and RUNX1-EVI1 Differentially Reprogram the Chromatin Landscape in t(8;21) and t(3;21) AML. <i>Cell Reports</i> , 2017, 19, 1654-1668.	6.4	46
26	Cooperative binding of AP-1 and TEAD4 modulates the balance between vascular smooth muscle and hemogenic cell fate. <i>Development (Cambridge)</i> , 2016, 143, 4324-4340.	2.5	43
27	Chromatin priming of genes in development: Concepts, mechanisms and consequences. <i>Experimental Hematology</i> , 2017, 49, 1-8.	0.4	41
28	In vitro differentiation of c-myb ^{-/-} ES cells reveals that the colony forming capacity of unilineage macrophage precursors and myeloid progenitor commitment are c-Myb independent. <i>Oncogene</i> , 2000, 19, 3343-3351.	5.9	36
29	A FOXO1-induced oncogenic network defines the AML1-ETO preleukemic program. <i>Blood</i> , 2017, 130, 1213-1222.	1.4	36
30	Transcription Factor PU.1 Controls Transcription Start Site Positioning and Alternative TLR4 Promoter Usage. <i>Journal of Biological Chemistry</i> , 2007, 282, 26874-26883.	3.4	33
31	RUNX1/RUNX1T1 mediates alternative splicing and reorganises the transcriptional landscape in leukemia. <i>Nature Communications</i> , 2021, 12, 520.	12.8	27
32	How transcription factors program chromatin—Lessons from studies of the regulation of myeloid-specific genes. <i>Seminars in Immunology</i> , 2008, 20, 257-263.	5.6	26
33	RUNX1-ETO Depletion in t(8;21) AML Leads to C/EBP β - and AP-1-Mediated Alterations in Enhancer-Promoter Interaction. <i>Cell Reports</i> , 2019, 28, 3022-3031.e7.	6.4	25
34	Developmental-stage-dependent transcriptional response to leukaemic oncogene expression. <i>Nature Communications</i> , 2015, 6, 7203.	12.8	24
35	Lineage-inappropriate PAX5 expression in t(8;21) acute myeloid leukemia requires signaling-mediated abrogation of polycomb repression. <i>Blood</i> , 2013, 122, 759-769.	1.4	23
36	Runx1 Structure and Function in Blood Cell Development. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 65-81.	1.6	23

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37	The Co-operation of RUNX1 with LDB1, CDK9 and BRD4 Drives Transcription Factor Complex Relocation During Haematopoietic Specification. <i>Scientific Reports</i> , 2018, 8, 10410.	3.3	22
38	Robust hematopoietic specification requires the ubiquitous Sp1 and Sp3 transcription factors. <i>Epigenetics and Chromatin</i> , 2019, 12, 33.	3.9	21
39	Expression of RUNX1-ETO Rapidly Alters the Chromatin Landscape and Growth of Early Human Myeloid Precursor Cells. <i>Cell Reports</i> , 2020, 31, 107691.	6.4	20
40	Chromatin Mechanisms Regulating Gene Expression in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2011, 711, 12-25.	1.6	20
41	Global long terminal repeat activation participates in establishing the unique gene expression programme of classical Hodgkin lymphoma. <i>Leukemia</i> , 2019, 33, 1463-1474.	7.2	19
42	The transcriptional regulation of normal and malignant blood cell development. <i>FEBS Journal</i> , 2022, 289, 1240-1255.	4.7	19
43	Identification of gene specific cis-regulatory elements during differentiation of mouse embryonic stem cells: An integrative approach using high-throughput datasets. <i>PLoS Computational Biology</i> , 2019, 15, e1007337.	3.2	18
44	Paracrine cyclooxygenase-2 activity by macrophages drives colorectal adenoma progression in the Apc Min/+ mouse model of intestinal tumorigenesis. <i>Scientific Reports</i> , 2017, 7, 6074.	3.3	17
45	Dissecting Clonal Heterogeneity in AML. <i>Cancer Cell</i> , 2020, 38, 782-784.	16.8	16
46	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. <i>Blood</i> , 2022, 139, 1080-1097.	1.4	16
47	Different mutant RUNX1 oncoproteins program alternate haematopoietic differentiation trajectories. <i>Life Science Alliance</i> , 2021, 4, e202000864.	2.8	15
48	C/EBP β overrides epigenetic reprogramming by oncogenic transcription factors in acute myeloid leukemia. <i>Blood Advances</i> , 2018, 2, 271-284.	5.2	14
49	Chromatin programming by developmentally regulated transcription factors: lessons from the study of haematopoietic stem cell specification and differentiation. <i>FEBS Letters</i> , 2016, 590, 4105-4115.	2.8	13
50	Epigenetic mechanisms regulating normal and malignant haematopoiesis: new therapeutic targets for clinical medicine. <i>Expert Reviews in Molecular Medicine</i> , 2010, 12, e6.	3.9	12
51	Isoform-specific and signaling-dependent propagation of acute myeloid leukemia by Wilms tumor 1. <i>Cell Reports</i> , 2021, 35, 109010.	6.4	12
52	Chromatin Structure Profiling Identifies Crucial Regulators of Tumor Maintenance. <i>Trends in Cancer</i> , 2015, 1, 157-160.	7.4	11
53	Epigenetic plasticity of hematopoietic cells. <i>Cell Cycle</i> , 2005, 4, 211-4.	2.6	9
54	RUNX1-EVI1 disrupts lineage determination and the cell cycle by interfering with RUNX1 and EVI1 driven gene regulatory networks. <i>Haematologica</i> , 2021, 106, 1569-1580.	3.5	8

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55	NFATc1 releases BCL6-dependent repression of CCR2 agonist expression in peritoneal macrophages from <i>Saccharomyces cerevisiae</i> infected mice. <i>European Journal of Immunology</i> , 2016, 46, 634-646.	2.9	7
56	Rewiring of the Transcription Factor Network in Acute Myeloid Leukemia. <i>Cancer Informatics</i> , 2019, 18, 117693511985986.	1.9	7
57	Molecular Basis of Hematological Disease Caused by Inherited or Acquired RUNX1 Mutations. <i>Experimental Hematology</i> , 2022, 111, 1-12.	0.4	7
58	t(8;21) Acute Myeloid Leukemia as a Paradigm for the Understanding of Leukemogenesis at the Level of Gene Regulation and Chromatin Programming. <i>Cells</i> , 2020, 9, 2681.	4.1	5
59	Protocol for the Generation of Definitive Hematopoietic Progenitors from Human Pluripotent Stem Cells. <i>STAR Protocols</i> , 2020, 1, 100130.	1.2	5
60	Chronic growth factor receptor signaling and lineage inappropriate gene expression in AML: The polycomb connection. <i>Cell Cycle</i> , 2013, 12, 2159-2160.	2.6	4
61	Why detailed model gene studies in higher eukaryotes are still necessary. <i>Immunology</i> , 2013, 139, 158-160.	4.4	3
62	The hematopoietic master regulator RUNX1 reshapes the epigenetic landscape at the onset of hematopoiesis. <i>Epigenetics and Chromatin</i> , 2013, 6, O18.	3.9	2
63	Modelling t(8;21) acute myeloid leukaemia -What have we learned?. <i>MedComm</i> , 2020, 1, 260-269.	7.2	2
64	RUNX1/ETO and mutant KIT both contribute to programming the transcriptional and chromatin landscape in t(8;21) acute myeloid leukemia. <i>Experimental Hematology</i> , 2020, 92, 62-74.	0.4	2
65	Reduction in the resident intestinal myelomonocytic cell population occurs during ApcMin/+ mouse intestinal tumorigenesis. <i>Oncology Letters</i> , 2021, 21, 263.	1.8	1
66	The Leukaemia-Associated AML1-ETO Fusion Protein Acts as a Sequence Specific Transcriptional Repressor in vivo by Altering the Chromatin Structure of Target Genes. <i>Clinical Science</i> , 2003, 104, 30P-30P.	0.0	0
67	Cytokine and proinflammatory gene expression in classical Hodgkin lymphoma: Its more than NF- κ B!. <i>Cytokine</i> , 2015, 72, 115-117.	3.2	0
68	Standing at odds: mutated RAS and hematopoietic stem cells. <i>Haematologica</i> , 2019, 104, 2125-2128.	3.5	0