

# 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  
g-index

73  
all docs

73  
docs citations

73  
times ranked

5793  
citing authors

#	ARTICLE	IF	CITATIONS
1	The transcriptional regulation of normal and malignant blood cell development. FEBS Journal, 2022, 289, 1240-1255.	4.7	19
2	PLCG1 is required for AML1-ETO leukemia stem cell self-renewal. Blood, 2022, 139, 1080-1097.	1.4	16
3	Molecular Basis of Hematological Disease Caused by Inherited or Acquired RUNX1 Mutations. Experimental Hematology, 2022, 111, 1-12.	0.4	7
4	RUNX1-EVI1 disrupts lineage determination and the cell cycle by interfering with RUNX1 and EVI1 driven gene regulatory networks. Haematologica, 2021, 106, 1569-1580.	3.5	8
5	Reduction in the resident intestinal myelomonocytic cell population occurs during ApcMin/+ mouse intestinal tumorigenesis. Oncology Letters, 2021, 21, 263.	1.8	1
6	Isoform-specific and signaling-dependent propagation of acute myeloid leukemia by Wilms tumor 1. Cell Reports, 2021, 35, 109010.	6.4	12
7	Different mutant RUNX1 oncoproteins program alternate haematopoietic differentiation trajectories. Life Science Alliance, 2021, 4, e202000864.	2.8	15
8	RUNX1/RUNX1T1 mediates alternative splicing and reorganises the transcriptional landscape in leukemia. Nature Communications, 2021, 12, 520.	12.8	27
9	Dissecting Clonal Heterogeneity in AML. Cancer Cell, 2020, 38, 782-784.	16.8	16
10	t(8;21) Acute Myeloid Leukemia as a Paradigm for the Understanding of Leukemogenesis at the Level of Gene Regulation and Chromatin Programming. Cells, 2020, 9, 2681.	4.1	5
11	Protocol for the Generation of Definitive Hematopoietic Progenitors from Human Pluripotent Stem Cells. STAR Protocols, 2020, 1, 100130.	1.2	5
12	Modelling t(8;21) acute myeloid leukaemia - What have we learned?. MedComm, 2020, 1, 260-269.	7.2	2
13	RUNX1/ETO and mutant KIT both contribute to programming the transcriptional and chromatin landscape in t(8;21) acute myeloid leukemia. Experimental Hematology, 2020, 92, 62-74.	0.4	2
14	Expression of RUNX1-ETO Rapidly Alters the Chromatin Landscape and Growth of Early Human Myeloid Precursor Cells. Cell Reports, 2020, 31, 107691.	6.4	20
15	Rewiring of the Transcription Factor Network in Acute Myeloid Leukemia. Cancer Informatics, 2019, 18, 117693511985986.	1.9	7
16	Identification of gene specific cis-regulatory elements during differentiation of mouse embryonic stem cells: An integrative approach using high-throughput datasets. PLoS Computational Biology, 2019, 15, e1007337.	3.2	18
17	RUNX1-ETO Depletion in t(8;21) AML Leads to C/EBP $\beta$ - and AP-1-Mediated Alterations in Enhancer-Promoter Interaction. Cell Reports, 2019, 28, 3022-3031.e7.	6.4	25
18	Robust hematopoietic specification requires the ubiquitous Sp1 and Sp3 transcription factors. Epigenetics and Chromatin, 2019, 12, 33.	3.9	21

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19	Standing at odds: mutated RAS and hematopoietic stem cells. <i>Haematologica</i> , 2019, 104, 2125-2128.	3.5	0
20	Subtype-specific regulatory network rewiring in acute myeloid leukemia. <i>Nature Genetics</i> , 2019, 51, 151-162.	21.4	140
21	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
22	The Oncogenic Transcription Factor RUNX1/ETO Corrupts Cell Cycle Regulation to Drive Leukemic Transformation. <i>Cancer Cell</i> , 2018, 34, 626-642.e8.	16.8	81
23	Prospective Isolation and Characterization of Genetically and Functionally Distinct AML Subclones. <i>Cancer Cell</i> , 2018, 34, 674-689.e8.	16.8	71
24	C/EBP $\beta$ overrides epigenetic reprogramming by oncogenic transcription factors in acute myeloid leukemia. <i>Blood Advances</i> , 2018, 2, 271-284.	5.2	14
25	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
26	Chromatin priming of genes in development: Concepts, mechanisms and consequences. <i>Experimental Hematology</i> , 2017, 49, 1-8.	0.4	41
27	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
28	Runx1 Structure and Function in Blood Cell Development. <i>Advances in Experimental Medicine and Biology</i> , 2017, 962, 65-81.	1.6	23
29	A FOXO1-induced oncogenic network defines the AML1-ETO preleukemic program. <i>Blood</i> , 2017, 130, 1213-1222.	1.4	36
30	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
31	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
32	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
33	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
34	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
35	Small Molecule Inhibitor of CBF $\beta$ -RUNX Binding for RUNX Transcription Factor Driven Cancers. <i>EBioMedicine</i> , 2016, 8, 117-131.	6.1	84
36	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. <i>Developmental Cell</i> , 2016, 36, 572-587.	7.0	213

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37	The Role of the Ubiquitously Expressed Transcription Factor Sp1 in Tissue-specific Transcriptional Regulation and in Disease. <i>Yale Journal of Biology and Medicine</i> , 2016, 89, 513-525.	0.2	77
38	Chromatin Structure Profiling Identifies Crucial Regulators of Tumor Maintenance. <i>Trends in Cancer</i> , 2015, 1, 157-160.	7.4	11
39	Wellington-bootstrap: differential DNase-seq footprinting identifies cell-type determining transcription factors. <i>BMC Genomics</i> , 2015, 16, 1000.	2.8	49
40	Developmental-stage-dependent transcriptional response to leukaemic oncogene expression. <i>Nature Communications</i> , 2015, 6, 7203.	12.8	24
41	Cytokine and proinflammatory gene expression in classical Hodgkin lymphoma: Its more than NF- $\kappa$ B!. <i>Cytokine</i> , 2015, 72, 115-117.	3.2	0
42	The RUNX1-PU.1 axis in the control of hematopoiesis. <i>International Journal of Hematology</i> , 2015, 101, 319-329.	1.6	78
43	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
44	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
45	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
46	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
47	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
48	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
49	Sox4 Is a Key Oncogenic Target in C/EBP $\beta$ Mutant Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2013, 24, 575-588.	16.8	112
50	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
51	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
52	Why detailed model gene studies in higher eukaryotes are still necessary. <i>Immunology</i> , 2013, 139, 158-160.	4.4	3
53	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
54	RUNX1 reshapes the epigenetic landscape at the onset of haematopoiesis. <i>EMBO Journal</i> , 2012, 31, 4318-4333.	7.8	158

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55	GFI1 and GFI1B control the loss of endothelial identity of hemogenic endothelium during hematopoietic commitment. <i>Blood</i> , 2012, 120, 314-322.	1.4	144
56	Two distinct auto-regulatory loops operate at the PU.1 locus in B cells and myeloid cells. <i>Blood</i> , 2011, 117, 2827-2838.	1.4	120
57	Chromatin Mechanisms Regulating Gene Expression in Health and Disease. <i>Advances in Experimental Medicine and Biology</i> , 2011, 711, 12-25.	1.6	20
58	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
59	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
60	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
61	<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
62	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
63	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
64	The mechanism of repression of the myeloid-specific <i>c-fms</i> gene by Pax5 during B lineage restriction. <i>EMBO Journal</i> , 2006, 25, 1070-1080.	7.8	63
65	Epigenetic plasticity of hematopoietic cells. <i>Cell Cycle</i> , 2005, 4, 211-4.	2.6	9
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	In vitro differentiation of <i>c-myb</i> <sup>-/-</sup> ES cells reveals that the colony forming capacity of unilineage macrophage precursors and myeloid progenitor commitment are <i>c-Myb</i> independent. <i>Oncogene</i> , 2000, 19, 3343-3351.	5.9	36
68	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