Berthold Gottgens

List of Publications by Year
in descending order

278 papers	25,352 citations	8755 75 h-index	10157 140 g-index
307 all docs	307 docs citations	307 times ranked	32695 citing authors

#	Article	IF	Citations
1	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
2	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. Genome Biology, 2019, 20, 59.	8.8	911
3	A single-cell molecular map of mouse gastrulation and early organogenesis. Nature, 2019, 566, 490-495.	27.8	658
4	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
5	A single-cell resolution map of mouse hematopoietic stem and progenitor cell differentiation. Blood, 2016, 128, e20-e31.	1.4	608
6	JAK2 phosphorylates histone H3Y41 and excludes HP1α from chromatin. Nature, 2009, 461, 819-822.	27.8	564
7	From haematopoietic stem cells to complex differentiation landscapes. Nature, 2018, 553, 418-426.	27.8	549
8	Epigenomic Profiling of Young and Aged HSCs Reveals Concerted Changes during Aging that Reinforce Self-Renewal. Cell Stem Cell, 2014, 14, 673-688.	11.1	524
9	Functionally Distinct Subsets of Lineage-Biased Multipotent Progenitors Control Blood Production in Normal and Regenerative Conditions. Cell Stem Cell, 2015, 17, 35-46.	11.1	494
10	Single-cell multi-omics analysis of the immune response in COVID-19. Nature Medicine, 2021, 27, 904-916.	30.7	452
11	Genome-wide analysis of repressor element 1 silencing transcription factor/neuron-restrictive silencing factor (REST/NRSF) target genes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10458-10463.	7.1	433
12	The SCL gene specifies haemangioblast development from early mesoderm. EMBO Journal, 1998, 17, 4029-4045.	7.8	412
13	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	27.8	392
14	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	11.1	376
15	Decoding the regulatory network of early blood development from single-cell gene expression measurements. Nature Biotechnology, 2015, 33, 269-276.	17.5	352
16	Esrrb Is a Pivotal Target of the Gsk3/Tcf3 Axis Regulating Embryonic Stem Cell Self-Renewal. Cell Stem Cell, 2012, 11, 491-504.	11.1	348
17	Multi-omics profiling of mouse gastrulation at single-cell resolution. Nature, 2019, 576, 487-491.	27.8	307
18	Reprogramming of T Cells to Natural Killer–Like Cells upon *Bcl11b* Deletion. Science, 2010, 329, 85-89.	12.6	294

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19	Large conserved domains of low DNA methylation maintained by Dnmt3a. Nature Genetics, 2014, 46, 17-23.	21.4	276
20	The Epidermis Comprises Autonomous Compartments Maintained by Distinct Stem Cell Populations. Cell Stem Cell, 2013, 13, 471-482.	11.1	268
21	Proneural bHLH and Brn Proteins Coregulate a Neurogenic Program through Cooperative Binding to a Conserved DNA Motif. Developmental Cell, 2006, 11, 831-844.	7.0	267
22	Genetically tagging endothelial cells in vivo: bone marrow-derived cells do not contribute to tumor endothelium. Blood, 2004, 104, 1769-1777.	1.4	264
23	Resolving early mesoderm diversification through single-cell expression profiling. Nature, 2016, 535, 289-293.	27.8	261
24	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. Nature Cell Biology, 2013, 15, 363-372.	10.3	257
25	Genome-wide Analysis of Simultaneous GATA1/2, RUNX1, FLI1, and SCL Binding in Megakaryocytes Identifies Hematopoietic Regulators. Developmental Cell, 2011, 20, 597-609.	7.0	255
26	Epigenetic silencing by the HUSH complex mediates position-effect variegation in human cells. Science, 2015, 348, 1481-1485.	12.6	250
27	A tripartite transcription factor network regulates primordial germ cell specification in mice. Nature Cell Biology, 2013, 15, 905-915.	10.3	240
28	Defining the earliest step of cardiovascular lineage segregation by single-cell RNA-seq. Science, 2018, 359, 1177-1181.	12.6	230
29	Establishment of mouse expanded potential stem cells. Nature, 2017, 550, 393-397.	27.8	223
30	A HaemAtlas: characterizing gene expression in differentiated human blood cells. Blood, 2009, 113, e1-e9.	1.4	215
31	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. Developmental Cell, 2016, 36, 572-587.	7.0	213
32	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
33	Single-Cell RNA Sequencing Reveals T Helper Cells Synthesizing Steroids De Novo to Contribute to Immune Homeostasis. Cell Reports, 2014, 7, 1130-1142.	6.4	198
34	Establishing the transcriptional programme for blood: the SCL stem cell enhancer is regulated by a multiprotein complex containing Ets and GATA factors. EMBO Journal, 2002, 21, 3039-3050.	7.8	194
35	Single-cell analysis reveals the continuum of human lympho-myeloid progenitor cells. Nature Immunology, 2018, 19, 85-97.	14.5	193
36	Inducible chronic phase of myeloid leukemia with expansion of hematopoietic stem cells in a transgenic model of BCR-ABL leukemogenesis. Blood, 2005, 105, 324-334.	1.4	192

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37	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. Nature Structural and Molecular Biology, 2010, 17, 617-619.	8.2	192
38	The Endothelial Transcription Factor ERG Promotes Vascular Stability and Growth through Wnt/Î²-Catenin Signaling. Developmental Cell, 2015, 32, 82-96.	7.0	190
39	Local and systemic responses to SARS-CoV-2 infection in children and adults. Nature, 2022, 602, 321-327.	27.8	179
40	GFI1 proteins orchestrate the emergence of haematopoietic stem cells through recruitment of LSD1. Nature Cell Biology, 2016, 18, 21-32.	10.3	172
41	Analysis of vertebrate SCL loci identifies conserved enhancers. Nature Biotechnology, 2000, 18, 181-186.	17.5	162
42	In vivo fate-tracing studies using the Scl stem cell enhancer: embryonic hematopoietic stem cells significantly contribute to adult hematopoiesis. Blood, 2005, 105, 2724-2732.	1.4	162
43	RUNX1 reshapes the epigenetic landscape at the onset of haematopoiesis. EMBO Journal, 2012, 31, 4318-4333.	7.8	158
44	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. Nature Communications, 2013, 4, 2924.	12.8	158
45	A single-cell hematopoietic landscape resolves 8 lineage trajectories and defects in Kit mutant mice. Blood, 2018, 131, e1-e11.	1.4	158
46	Nonlinear partial differential equations and applications: Identification of endoglin as a functional marker that defines long-term repopulating hematopoietic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15468-15473.	7.1	156
47	Myeloid progenitor cluster formation drives emergency and leukaemic myelopoiesis. Nature, 2017, 544, 53-58.	27.8	155
48	Clonal Dynamics Reveal Two Distinct Populations of Basal Cells in Slow-Turnover Airway Epithelium. Cell Reports, 2015, 12, 90-101.	6.4	154
49	Potential Autoregulation of Transcription Factor PU.1 by an Upstream Regulatory Element. Molecular and Cellular Biology, 2005, 25, 2832-2845.	2.3	152
50	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. Nature Biotechnology, 2022, 40, 74-85.	17.5	152
51	GFI1 and GFI1B control the loss of endothelial identity of hemogenic endothelium during hematopoietic commitment. Blood, 2012, 120, 314-322.	1.4	144
52	Fast and sensitive multiple alignment of large genomic sequences. BMC Bioinformatics, 2003, 4, 66.	2.6	134
53	Sustained PU.1 Levels Balance Cell-Cycle Regulators to Prevent Exhaustion of Adult Hematopoietic Stem Cells. Molecular Cell, 2013, 49, 934-946.	9.7	127
54	An SCL 3â€² enhancer targets developing endothelium together with embryonic and adult haematopoietic progenitors. Development (Cambridge), 1999, 126, 3891-3904.	2.5	125

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55	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
56	LIF-independent JAK signalling to chromatin in embryonic stem cells uncovered from an adult stem cell disease. Nature Cell Biology, 2011, 13, 13-21.	10.3	121
57	Two distinct auto-regulatory loops operate at the PU.1 locus in B cells and myeloid cells. Blood, 2011, 117, 2827-2838.	1.4	120
58	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. Nature Genetics, 2018, 50, 883-894.	21.4	117
59	A roadmap for the Human Developmental Cell Atlas. Nature, 2021, 597, 196-205.	27.8	114
60	The Proto-Oncogene ERG in Megakaryoblastic Leukemias. Cancer Research, 2005, 65, 7596-7602.	0.9	112
61	CODEX: a next-generation sequencing experiment database for the haematopoietic and embryonic stem cell communities. Nucleic Acids Research, 2015, 43, D1117-D1123.	14.5	112
62	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. Nature Cell Biology, 2018, 20, 127-134.	10.3	112
63	Epigenetic silencing of BIM in glucocorticoid poor-responsive pediatric acute lymphoblastic leukemia, and its reversal by histone deacetylase inhibition. Blood, 2010, 116, 3013-3022.	1.4	110
64	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
65	The transcriptional program controlled by the stem cell leukemia gene Scl/Tal1 during early embryonic hematopoietic development. Blood, 2009, 113, 5456-5465.	1.4	107
66	DNMT3A Loss Drives Enhancer Hypomethylation in FLT3-ITD-Associated Leukemias. Cancer Cell, 2016, 29, 922-934.	16.8	107
67	Signaling from the Sympathetic Nervous System Regulates Hematopoietic Stem Cell Emergence during Embryogenesis. Cell Stem Cell, 2012, 11, 554-566.	11.1	106
68	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. Human Molecular Genetics, 2012, 21, 322-333.	2.9	100
69	Distinct 5â€² SCL Enhancers Direct Transcription to Developing Brain, Spinal Cord, and Endothelium: Neural Expression Is Mediated by GATA Factor Binding Sites. Developmental Biology, 1999, 209, 128-142.	2.0	99
70	Prenatal development of human immunity. Science, 2020, 368, 600-603.	12.6	90
71	Reconstructing blood stem cell regulatory network models from single-cell molecular profiles. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5822-5829.	7.1	89
72	Transcriptional Regulation of the Stem Cell Leukemia Gene (SCL) --- Comparative Analysis of Five Vertebrate SCL Loci. Genome Research, 2002, 12, 749-759.	5.5	87

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73	The scl +18/19 Stem Cell Enhancer Is Not Required for Hematopoiesis: Identification of a 5â€² Bifunctional Hematopoietic-Endothelial Enhancer Bound by Fli-1 and Elf-1. Molecular and Cellular Biology, 2004, 24, 1870-1883.	2.3	83
74	Hard-wired heterogeneity in blood stem cells revealed using a dynamic regulatory network model. Bioinformatics, 2013, 29, i80-i88.	4.1	83
75	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
76	Long-Range Comparison of Human and Mouse <i>SCL</i> Loci: Localized Regions of Sensitivity to Restriction Endonucleases Correspond Precisely with Peaks of Conserved Noncoding Sequences. Genome Research, 2001, 11, 87-97.	5.5	81
77	Genome-wide identification of cis -regulatory sequences controlling blood and endothelial development. Human Molecular Genetics, 2005, 14, 595-601.	2.9	79
78	Lineage-restricted regulation of the murine SCL/TAL-1 promoter. Blood, 1995, 86, 1502-1514.	1.4	78
79	Regulatory network control of blood stem cells. Blood, 2015, 125, 2614-2620.	1.4	77
80	Runx genes are direct targets of Scl/Tal1 in the yolk sac and fetal liver. Blood, 2008, 111, 3005-3014.	1.4	76
81	Cell of Origin in AML: Susceptibility to MN1-Induced Transformation Is Regulated by the MEIS1/AbdB-like HOX Protein Complex. Cancer Cell, 2011, 20, 39-52.	16.8	76
82	T cell cytolytic capacity is independent of initial stimulation strength. Nature Immunology, 2018, 19, 849-858.	14.5	74
83	The Transcription Factor ERG Regulates Super-Enhancers Associated With an Endothelial-Specific Gene Expression Program. Circulation Research, 2019, 124, 1337-1349.	4.5	73
84	Blood and immune development in human fetal bone marrow and Down syndrome. Nature, 2021, 598, 327-331.	27.8	73
85	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
86	The paralogous hematopoietic regulators Lyl1 and Scl are coregulated by Ets and GATA factors, but Lyl1 cannot rescue the early Sclâ€“/â€“ phenotype. Blood, 2007, 109, 1908-1916.	1.4	71
87	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	19.0	71
88	BET protein inhibition shows efficacy against JAK2V617F-driven neoplasms. Leukemia, 2014, 28, 88-97.	7.2	70
89	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. Genome Research, 2017, 27, 1795-1806.	5.5	70
90	Expression of the leukemia oncogene Lmo2 is controlled by an array of tissue-specific elements dispersed over 100 kb and bound by Tal1/Lmo2, Ets, and Gata factors. Blood, 2009, 113, 5783-5792.	1.4	69

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91	The transcription factor Erg regulates expression of histone deacetylase 6 and multiple pathways involved in endothelial cell migration and angiogenesis. Blood, 2012, 119, 894-903.	1.4	69
92	Single-cell RNA-sequencing reveals a distinct population of proglucagon-expressing cells specific to the mouse upper small intestine. Molecular Metabolism, 2017, 6, 1296-1303.	6.5	68
93	Multi-site Neurogenin3 Phosphorylation Controls Pancreatic Endocrine Differentiation. Developmental Cell, 2017, 41, 274-286.e5.	7.0	67
94	MicroRNA-486-5p is an erythroid oncomiR of the myeloid leukemias of Down syndrome. Blood, 2015, 125, 1292-1301.	1.4	66
95	Cytokine‐induced megakaryocytic differentiation is regulated by genome‐wide loss of a <scp>uSTAT</scp> transcriptional program. EMBO Journal, 2016, 35, 580-594.	7.8	66
96	Growth Factor Independence 1 Antagonizes a p53-Induced DNA Damage Response Pathway in Lymphoblastic Leukemia. Cancer Cell, 2013, 23, 200-214.	16.8	65
97	Differentiation of transplanted haematopoietic stem cells tracked by single-cell transcriptomic analysis. Nature Cell Biology, 2020, 22, 630-639.	10.3	65
98	BTR: training asynchronous Boolean models using single-cell expression data. BMC Bioinformatics, 2016, 17, 355.	2.6	63
99	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
100	Single-cell chromatin accessibility maps reveal regulatory programs driving early mouse organogenesis. Nature Cell Biology, 2020, 22, 487-497.	10.3	62
101	The mouse Runx1 +23 hematopoietic stem cell enhancer confers hematopoietic specificity to both Runx1 promoters. Blood, 2009, 113, 5121-5124.	1.4	61
102	Gfi1 Expression Is Controlled by Five Distinct Regulatory Regions Spread over 100 Kilobases, with Scl/Tal1, Gata2, PU.1, Erg, Meis1, and Runx1 Acting as Upstream Regulators in Early Hematopoietic Cells. Molecular and Cellular Biology, 2010, 30, 3853-3863.	2.3	61
103	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. EMBO Journal, 2014, 33, 1212-26.	7.8	61
104	The epigenetic regulators CBP and p300 facilitate leukemogenesis and represent therapeutic targets in acute myeloid leukemia. Oncogene, 2016, 35, 279-289.	5.9	61
105	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. ELife, 2016, 5, e11469.	6.0	61
106	Motif-Blind, Genome-Wide Discovery of cis-Regulatory Modules in Drosophila and Mouse. Developmental Cell, 2009, 17, 568-579.	7.0	60
107	New insights into hematopoietic differentiation landscapes from single-cell RNA sequencing. Blood, 2019, 133, 1415-1426.	1.4	60
108	Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization. Science, 2021, 374, eaba5531.	12.6	60

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109	Transcription of the SCL gene in erythroid and CD34 positive primitive myeloid cells is controlled by a complex network of lineage-restricted chromatin-dependent and chromatin-independent regulatory elements. Oncogene, 1997, 15, 2419-2428.	5.9	58
110	Fli1, Elf1, and Ets1 regulate the proximal promoter of the LMO2 gene in endothelial cells. Blood, 2005, 106, 2680-2687.	1.4	58
111	SCNS: a graphical tool for reconstructing executable regulatory networks from single-cell genomic data. BMC Systems Biology, 2018, 12, 59.	3.0	58
112	Transcriptional Regulation of the Stem Cell Leukemia Gene by PU.1 and Elf-1. Journal of Biological Chemistry, 1998, 273, 29032-29042.	3.4	55
113	Transcriptional Regulation of the SCL Locus: Identification of an Enhancer That Targets the Primitive Erythroid Lineage In Vivo. Molecular and Cellular Biology, 2005, 25, 5215-5225.	2.3	55
114	Three Distinct Patterns of Histone H3Y41 Phosphorylation Mark Active Genes. Cell Reports, 2012, 2, 470-477.	6.4	54
115	A new RNASeq-based reference transcriptome for sugar beet and its application in transcriptome-scale analysis of vernalization and gibberellin responses. BMC Genomics, 2012, 13, 99.	2.8	54
116	Mammalian Transcription Factor Networks: Recent Advances in Interrogating Biological Complexity. Cell Systems, 2017, 5, 319-331.	6.2	54
117	Modeling Reveals Bistability and Low-Pass Filtering in the Network Module Determining Blood Stem Cell Fate. PLoS Computational Biology, 2010, 6, e1000771.	3.2	53
118	An SCL 3' enhancer targets developing endothelium together with embryonic and adult haematopoietic progenitors. Development (Cambridge), 1999, 126, 3891-904.	2.5	52
119	Gene regulatory networks governing haematopoietic stem cell development and identity. International Journal of Developmental Biology, 2010, 54, 1201-1211.	0.6	51
120	The Transcription Factor Erg Controls Endothelial Cell Quiescence by Repressing Activity of Nuclear Factor (NF)-κB p65. Journal of Biological Chemistry, 2012, 287, 12331-12342.	3.4	50
121	The transcription factor Lyl-1 regulates lymphoid specification and the maintenance of early T lineage progenitors. Nature Immunology, 2012, 13, 761-769.	14.5	50
122	Distinct Mechanisms Direct SCL/tal-1 Expression in Erythroid Cells and CD34 Positive Primitive Myeloid Cells. Journal of Biological Chemistry, 1997, 272, 8781-8790.	3.4	49
123	The Flk1-Cre-Mediated Deletion of ETV2 Defines Its Narrow Temporal Requirement During Embryonic Hematopoietic Development. Stem Cells, 2012, 30, 1521-1531.	3.2	49
124	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. Blood, 2016, 127, e12-e23.	1.4	49
125	Iterative Single-Cell Analyses Define the Transcriptome of the First Functional Hematopoietic Stem Cells. Cell Reports, 2020, 31, 107627.	6.4	49
126	Diverse Routes toward Early Somites in the Mouse Embryo. Developmental Cell, 2021, 56, 141-153.e6.	7.0	49

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127	Identification of HSC/MPP expansion units in fetal liver by single-cell spatiotemporal transcriptomics. Cell Research, 2022, 32, 38-53.	12.0	48
128	Regulation of the stem cell leukemia (SCL) gene: A tale of two fishes. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 6747-6752.	7.1	47
129	Transcriptional Regulation of Haematopoietic Stem Cells. Advances in Experimental Medicine and Biology, 2013, 786, 187-212.	1.6	47
130	The Transcriptional Coactivator Cbp Regulates Self-Renewal and Differentiation in Adult Hematopoietic Stem Cells. Molecular and Cellular Biology, 2011, 31, 5046-5060.	2.3	46
131	Critical Modulation of Hematopoietic Lineage Fate by Hepatic Leukemia Factor. Cell Reports, 2017, 21, 2251-2263.	6.4	46
132	Single-cell transcriptional profiling: a window into embryonic cell-type specification. Nature Reviews Molecular Cell Biology, 2018, 19, 399-412.	37.0	46
133	Cell-Specific Computational Modeling of the PIM Pathway in Acute Myeloid Leukemia. Cancer Research, 2017, 77, 827-838.	0.9	45
134	Analysis of Multiple Genomic Sequence Alignments: A Web Resource, Online Tools, and Lessons Learned From Analysis of Mammalian SCL Loci. Genome Research, 2004, 14, 313-318.	5.5	44
135	A GWAS sequence variant for platelet volume marks an alternative DNM3 promoter in megakaryocytes near a MEIS1 binding site. Blood, 2012, 120, 4859-4868.	1.4	44
136	Genome-scale expression and transcription factor binding profiles reveal therapeutic targets in transgenic ERG myeloid leukemia. Blood, 2013, 122, 2694-2703.	1.4	44
137	Index sorting resolves heterogeneous murine hematopoietic stemÂcellÂpopulations. Experimental Hematology, 2015, 43, 803-811.	0.4	44
138	GATA transcription in a small rhodamine 123lowCD34+ subpopulation of a peripheral bloodâ€"derived CD34â˜¯CD105+ mesenchymal cell line. Experimental Hematology, 2002, 30, 887-895.	0.4	43
139	A compendium of genome-wide hematopoietic transcription factor maps supports the identification of gene regulatory control mechanisms. Experimental Hematology, 2011, 39, 531-541.	0.4	43
140	The transcriptional programme controlled by Runx1 during early embryonic blood development. Developmental Biology, 2012, 366, 404-419.	2.0	43
141	Comparative and functional analyses of LYL1 loci establish marsupial sequences as a model for phylogenetic footprintingâˇ† âˇ†Sequence data from this article have been deposited with the DDBJ/EMBL/GenBank Data Libraries under Accession No. AL731834.. Genomics, 2003, 81, 249-259.	2.9	42
142	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
143	Singleâ€cell molecular profiling provides a highâ€resolution map of basophil and mast cell development. Allergy: European Journal of Allergy and Clinical Immunology, 2021, 76, 1731-1742.	5.7	42
144	ID1 promotes expansion and survival of primary erythroid cells and is a target of JAK2V617F-STAT5 signaling. Blood, 2009, 114, 1820-1830.	1.4	40

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145	Notch ligand Dll4 impairs cell recruitment to aortic clusters and limits blood stem cell generation. EMBO Journal, 2020, 39, e104270.	7.8	40
146	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. Genome Biology, 2021, 22, 197.	8.8	40
147	The *SCL* +40 Enhancer Targets the Midbrain Together with Primitive and Definitive Hematopoiesis and Is Regulated by SCL and GATA Proteins. Molecular and Cellular Biology, 2007, 27, 7206-7219.	2.3	39
148	A previously unrecognized promoter of LMO2 forms part of a transcriptional regulatory circuit mediating LMO2 expression in a subset of T-acute lymphoblastic leukaemia patients. Oncogene, 2010, 29, 5796-5808.	5.9	39
149	Machine learning predicts putative hematopoietic stem cells within large single-cell transcriptomics data sets. Experimental Hematology, 2019, 78, 11-20.	0.4	39
150	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. Blood, 2019, 134, 2195-2208.	1.4	39
151	Maps of Open Chromatin Guide the Functional Follow-Up of Genome-Wide Association Signals: Application to Hematological Traits. PLoS Genetics, 2011, 7, e1002139.	3.5	38
152	Defining Lineage Potential and Fate Behavior of Precursors during Pancreas Development. Developmental Cell, 2018, 46, 360-375.e5.	7.0	38
153	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	5.5	38
154	Ontogenic Changes in Hematopoietic Hierarchy Determine Pediatric Specificity and Disease Phenotype in Fusion Oncogene–Driven Myeloid Leukemia. Cancer Discovery, 2019, 9, 1736-1753.	9.4	37
155	Transcriptional regulation of haematopoietic transcription factors. Stem Cell Research and Therapy, 2011, 2, 6.	5.5	36
156	Transgenic Analysis of the Stem Cell Leukemia +19 Stem Cell Enhancer in Adult and Embryonic Hematopoietic and Endothelial Cells. Stem Cells, 2005, 23, 1378-1388.	3.2	35
157	Aberrant induction of LMO2 by the E2A-HLF chimeric transcription factor and its implication in leukemogenesis of B-precursor ALL with t(17;19). Blood, 2010, 116, 962-970.	1.4	35
158	The JAK-STAT signaling pathway is differentially activated in CALR-positive compared with JAK2V617F-positive ET patients. Blood, 2015, 125, 1679-1681.	1.4	35
159	Identifying gene regulatory elements by genomic microarray mapping of DNaseI hypersensitive sites. Genome Research, 2006, 16, 1310-1319.	5.5	34
160	Distinct Molecular Trajectories Converge to Induce Naive Pluripotency. Cell Stem Cell, 2019, 25, 388-406.e8.	11.1	33
161	Lysine acetyltransferase Tip60 is required for hematopoietic stem cell maintenance. Blood, 2020, 136, 1735-1747.	1.4	33
162	Transcriptional regulatory networks in haematopoiesis. Current Opinion in Genetics and Development, 2008, 18, 530-535.	3.3	32

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163	Transcriptional network control of normal and leukaemic haematopoiesis. Experimental Cell Research, 2014, 329, 255-264.	2.6	32
164	A novel mode of enhancer evolution: The Tal1 stem cell enhancer recruited a MIR element to specifically boost its activity. Genome Research, 2008, 18, 1422-1432.	5.5	31
165	BloodExpress: a database of gene expression in mouse haematopoiesis. Nucleic Acids Research, 2009, 37, D873-D879.	14.5	31
166	Lineage-restricted regulation of the murine SCL/TAL-1 promoter. Blood, 1995, 86, 1502-14.	1.4	31
167	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. Stem Cell Reports, 2019, 13, 515-529.	4.8	27
168	Discrimination of Dormant and Active Hematopoietic Stem Cells by G0 Marker Reveals Dormancy Regulation by Cytoplasmic Calcium. Cell Reports, 2019, 29, 4144-4158.e7.	6.4	27
169	Genome-Wide Analysis of Transcriptional Reprogramming in Mouse Models of Acute Myeloid Leukaemia. PLoS ONE, 2011, 6, e16330.	2.5	27
170	The Role of the Stem Cell Leukemia (SCL) Gene in Hematopoietic and Endothelial Lineage Specification. Journal of Hematotherapy and Stem Cell Research, 2002, 11, 195-206.	1.8	26
171	RUNX1 regulates theCD34gene in haematopoietic stem cells by mediating interactions with a distal regulatory element. EMBO Journal, 2011, 30, 4059-4070.	7.8	26
172	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for *PU.1* during haematopoietic specification. Development (Cambridge), 2014, 141, 4018-4030.	2.5	26
173	Manipulating niche composition limits damage to haematopoietic stem cells during Plasmodium infection. Nature Cell Biology, 2020, 22, 1399-1410.	10.3	26
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