

# Berthold Gottgens

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/623368/berthold-gottgens-publications-by-year.pdf>

**Version:** 2024-04-18

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

283  
papers

17,644  
citations

71  
h-index

125  
g-index

307  
ext. papers

22,239  
ext. citations

11.5  
avg, IF

6.56  
L-index

#	Paper	IF	Citations
283	Cholinergic signals preserve haematopoietic stem cell quiescence during regenerative haematopoiesis.. <i>Nature Communications</i> , <b>2022</b> , 13, 543	17.4	4
282	Simultaneous Analysis of Single-Cell Transcriptomes and Cell Surface Protein Expression of Human Hematopoietic Stem Cells and Progenitors Using the 10x Genomics Platform. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2386, 189-201	1.4	
281	Coagulation Factor V is a T cell inhibitor expressed by leukocytes in COVID-19.. <i>IScience</i> , <b>2022</b> , 103971	6.1	1
280	The impact of hypoxia on B cells in COVID-19.. <i>EBioMedicine</i> , <b>2022</b> , 77, 103878	8.8	3
279	Cell-by-cell dissection of phloem development links a maturation gradient to cell specialization.. <i>Science</i> , <b>2021</b> , 374, eaba5531	33.3	4
278	CITED2 coordinates key hematopoietic regulatory pathways to maintain the HSC pool in both steady-state hematopoiesis and transplantation. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 2784-2797	8	0
277	How haematopoiesis research became a fertile ground for regulatory network biology as pioneered by Eric Davidson. <i>Current Opinion in Hematology</i> , <b>2021</b> , 28, 1-10	3.3	1
276	Single-cell molecular profiling provides a high-resolution map of basophil and mast cell development. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2021</b> , 76, 1731-1742	9.3	6
275	Reconciling Flux Experiments for Quantitative Modeling of Normal and Malignant Hematopoietic Stem/Progenitor Dynamics. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 741-753	8	1
274	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , <b>2021</b> , 27, 904-916	50.5	101
273	Disruption of a GATA2-TAL1-ERG regulatory circuit promotes erythroid transition in healthy and leukemic stem cells. <i>Blood</i> , <b>2021</b> , 138, 1441-1455	2.2	2
272	Hematopoietic stem cells retain functional potential and molecular identity in hibernation cultures. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 1614-1628	8	2
271	Coordinated changes in gene expression kinetics underlie both mouse and human erythroid maturation. <i>Genome Biology</i> , <b>2021</b> , 22, 197	18.3	6
270	De novo generation of macrophage from placenta-derived hemogenic endothelium. <i>Developmental Cell</i> , <b>2021</b> , 56, 2121-2133.e6	10.2	5
269	Diverse Routes toward Early Somites in the Mouse Embryo. <i>Developmental Cell</i> , <b>2021</b> , 56, 141-153.e6	10.2	12
268	Single-cell transcriptome analysis of CAR T-cell products reveals subpopulations, stimulation, and exhaustion signatures. <i>OncImmunology</i> , <b>2021</b> , 10, 1866287	7.2	8
267	The T-box transcription factor Eomesodermin governs haemogenic competence of yolk sac mesodermal progenitors. <i>Nature Cell Biology</i> , <b>2021</b> , 23, 61-74	23.4	4

266	JMJD6 promotes self-renewal and regenerative capacity of hematopoietic stem cells. <i>Blood Advances</i> , <b>2021</b> , 5, 889-899	7.8	3
265	Identification of HSC/MPP expansion units in fetal liver by single-cell spatiotemporal transcriptomics. <i>Cell Research</i> , <b>2021</b> ,	24.7	9
264	Integration of spatial and single-cell transcriptomic data elucidates mouse organogenesis. <i>Nature Biotechnology</i> , <b>2021</b> ,	44.5	16
263	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , <b>2021</b> , 598, 327-331	50.4	10
262	A roadmap for the Human Developmental Cell Atlas. <i>Nature</i> , <b>2021</b> , 597, 196-205	50.4	18
261	Single-Cell Analysis of Hematopoietic Stem Cells. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2308, 301-337	1.4	0
260	Local and systemic responses to SARS-CoV-2 infection in children and adults.. <i>Nature</i> , <b>2021</b> ,	50.4	17
259	Differentiation of transplanted haematopoietic stem cells tracked by single-cell transcriptomic analysis. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 630-639	23.4	22
258	Iterative Single-Cell Analyses Define the Transcriptome of the First Functional Hematopoietic Stem Cells. <i>Cell Reports</i> , <b>2020</b> , 31, 107627	10.6	17
257	Prenatal development of human immunity. <i>Science</i> , <b>2020</b> , 368, 600-603	33.3	39
256	Lysine acetyltransferase Tip60 is required for hematopoietic stem cell maintenance. <i>Blood</i> , <b>2020</b> , 136, 1735-1747	2.2	11
255	Notch ligand Dll4 impairs cell recruitment to aortic clusters and limits blood stem cell generation. <i>EMBO Journal</i> , <b>2020</b> , 39, e104270	13	18
254	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. <i>Nature Communications</i> , <b>2020</b> , 11, 1407	17.4	6
253	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. <i>Genome Research</i> , <b>2020</b> , 30, 472-484	9.7	11
252	Single-cell chromatin accessibility maps reveal regulatory programs driving early mouse organogenesis. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 487-497	23.4	24
251	Single cell genomics and developmental biology: moving beyond the generation of cell type catalogues. <i>Current Opinion in Genetics and Development</i> , <b>2020</b> , 64, 66-71	4.9	5
250	Advancing Stem Cell Research through Multimodal Single-Cell Analysis. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2020</b> , 12,	10.2	1
249	Gata3 targets Runx1 in the embryonic haematopoietic stem cell niche. <i>IUBMB Life</i> , <b>2020</b> , 72, 45-52	4.7	7

248	Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. <i>IUBMB Life</i> , <b>2020</b> , 72, 27-38	4.7	3
247	Manipulating niche composition limits damage to haematopoietic stem cells during Plasmodium infection. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 1399-1410	23.4	6
246	The stem/progenitor landscape is reshaped in a mouse model of essential thrombocythemia and causes excess megakaryocyte production. <i>Science Advances</i> , <b>2020</b> , 6,	14.3	3
245	Interactions between lineage-associated transcription factors govern haematopoietic progenitor states. <i>EMBO Journal</i> , <b>2020</b> , 39, e104983	13	7
244	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 23626-23635	11.5	8
243	Machine learning predicts putative hematopoietic stem cells within large single-cell transcriptomics data sets. <i>Experimental Hematology</i> , <b>2019</b> , 78, 11-20	3.1	20
242	Reconstructing Gene Regulatory Networks That Control Hematopoietic Commitment. <i>Methods in Molecular Biology</i> , <b>2019</b> , 1975, 239-249	1.4	2
241	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. <i>Genome Biology</i> , <b>2019</b> , 20, 59	18.3	369
240	The Transcription Factor ERG Regulates Super-Enhancers Associated With an Endothelial-Specific Gene Expression Program. <i>Circulation Research</i> , <b>2019</b> , 124, 1337-1349	15.7	34
239	The pluripotency factor NANOG controls primitive hematopoiesis and directly regulates. <i>EMBO Journal</i> , <b>2019</b> , 38,	13	1
238	New insights into hematopoietic differentiation landscapes from single-cell RNA sequencing. <i>Blood</i> , <b>2019</b> , 133, 1415-1426	2.2	30
237	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. <i>Stem Cell Reports</i> , <b>2019</b> , 13, 515-529	8	12
236	Distinct Molecular Trajectories Converge to Induce Naive Pluripotency. <i>Cell Stem Cell</i> , <b>2019</b> , 25, 388-406	18	16
235	Expanded potential stem cell media as a tool to study human developmental hematopoiesis in vitro. <i>Experimental Hematology</i> , <b>2019</b> , 76, 1-12.e5	3.1	4
234	Decoding human fetal liver haematopoiesis. <i>Nature</i> , <b>2019</b> , 574, 365-371	50.4	200
233	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> , <b>2019</b> , 15, e1007337	5	6
232	A single-cell molecular map of mouse gastrulation and early organogenesis. <i>Nature</i> , <b>2019</b> , 566, 490-495	50.4	316
231	regulates expression at the exit from pluripotency during gastrulation. <i>Biology Open</i> , <b>2019</b> , 8,	2.2	6

230	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. <i>Blood</i> , <b>2019</b> , 134, 2195-2208	2.2	21
229	BNC1 regulates cell heterogeneity in human pluripotent stem cell-derived epicardium. <i>Development (Cambridge)</i> , <b>2019</b> , 146,	6.6	11
228	Discrimination of Dormant and Active Hematopoietic Stem Cells by G Marker Reveals Dormancy Regulation by Cytoplasmic Calcium. <i>Cell Reports</i> , <b>2019</b> , 29, 4144-4158.e7	10.6	11
227	Ontogenic Changes in Hematopoietic Hierarchy Determine Pediatric Specificity and Disease Phenotype in Fusion Oncogene-Driven Myeloid Leukemia. <i>Cancer Discovery</i> , <b>2019</b> , 9, 1736-1753	24.4	19
226	Multi-omics profiling of mouse gastrulation at single-cell resolution. <i>Nature</i> , <b>2019</b> , 576, 487-491	50.4	137
225	Single-cell transcriptional profiling: a window into embryonic cell-type specification. <i>Nature Reviews Molecular Cell Biology</i> , <b>2018</b> , 19, 399-412	48.7	32
224	From haematopoietic stem cells to complex differentiation landscapes. <i>Nature</i> , <b>2018</b> , 553, 418-426	50.4	311
223	Defining the earliest step of cardiovascular lineage segregation by single-cell RNA-seq. <i>Science</i> , <b>2018</b> , 359, 1177-1181	33.3	146
222	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. <i>Nature Cell Biology</i> , <b>2018</b> , 20, 127-134	23.4	75
221	Sorting apples from oranges in single-cell expression comparisons. <i>Nature Methods</i> , <b>2018</b> , 15, 321-322	21.6	
220	A single-cell hematopoietic landscape resolves 8 lineage trajectories and defects in Kit mutant mice. <i>Blood</i> , <b>2018</b> , 131, e1-e11	2.2	85
219	Single-Cell Sequencing in Normal and Malignant Hematopoiesis. <i>HemaSphere</i> , <b>2018</b> , 2, e34	0.3	8
218	A graphical model approach visualizes regulatory relationships between genome-wide transcription factor binding profiles. <i>Briefings in Bioinformatics</i> , <b>2018</b> , 19, 162-173	13.4	1
217	Defining Lineage Potential and Fate Behavior of Precursors during Pancreas Development. <i>Developmental Cell</i> , <b>2018</b> , 46, 360-375.e5	10.2	24
216	T cell cytolytic capacity is independent of initial stimulation strength. <i>Nature Immunology</i> , <b>2018</b> , 19, 849-858	8.5	35
215	Single-cell approaches identify the molecular network driving malignant hematopoietic stem cell self-renewal. <i>Blood</i> , <b>2018</b> , 132, 791-803	2.2	15
214	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. <i>Nature Genetics</i> , <b>2018</b> , 50, 883-894	36.3	73
213	SCNS: a graphical tool for reconstructing executable regulatory networks from single-cell genomic data. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 59	3.5	28

212	The Lysine Acetyltransferase Tip60 Is Required for Hematopoietic Stem Cell Maintenance. <i>Blood</i> , <b>2018</b> , 132, 2554-2554	2.2	
211	Single Cell RNA-Seq Characterises Pre-Leukemic Transformation Driven By CEBPA N321D in the Hoxb8-FL Cell Line. <i>Blood</i> , <b>2018</b> , 132, 3887-3887	2.2	
210	Single-cell analysis reveals the continuum of human lympho-myeloid progenitor cells. <i>Nature Immunology</i> , <b>2018</b> , 19, 85-97	19.1	116
209	Neurogenin3 phosphorylation controls reprogramming efficiency of pancreatic ductal organoids into endocrine cells. <i>Scientific Reports</i> , <b>2018</b> , 8, 15374	4.9	13
208	Dysregulation of haematopoietic stem cell regulatory programs in acute myeloid leukaemia. <i>Journal of Molecular Medicine</i> , <b>2017</b> , 95, 719-727	5.5	13
207	Multi-site Neurogenin3 Phosphorylation Controls Pancreatic Endocrine Differentiation. <i>Developmental Cell</i> , <b>2017</b> , 41, 274-286.e5	10.2	45
206	Blood: Education for stem cells. <i>Nature</i> , <b>2017</b> , 545, 415-417	50.4	2
205	Reconstructing blood stem cell regulatory network models from single-cell molecular profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 5822-5829	11.5	47
204	Myeloid progenitor cluster formation drives emergency and leukaemic myelopoiesis. <i>Nature</i> , <b>2017</b> , 544, 53-58	50.4	97
203	Demystifying blood stem cell fates. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 261-263	23.4	4
202	Cell-Specific Computational Modeling of the PIM Pathway in Acute Myeloid Leukemia. <i>Cancer Research</i> , <b>2017</b> , 77, 827-838	10.1	30
201	The Human Cell Atlas <b>2017</b> ,		41
200	Mammalian Transcription Factor Networks: Recent Advances in Interrogating Biological Complexity. <i>Cell Systems</i> , <b>2017</b> , 5, 319-331	10.6	28
199	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , <b>2017</b> , 27, 1795-1806	9.7	39
198	Establishment of mouse expanded potential stem cells. <i>Nature</i> , <b>2017</b> , 550, 393-397	50.4	128
197	Mbd3/NuRD controls lymphoid cell fate and inhibits tumorigenesis by repressing a B cell transcriptional program. <i>Journal of Experimental Medicine</i> , <b>2017</b> , 214, 3085-3104	16.6	12
196	Single-cell RNA-sequencing reveals a distinct population of proglucagon-expressing cells specific to the mouse upper small intestine. <i>Molecular Metabolism</i> , <b>2017</b> , 6, 1296-1303	8.8	52
195	Critical Modulation of Hematopoietic Lineage Fate by Hepatic Leukemia Factor. <i>Cell Reports</i> , <b>2017</b> , 21, 2251-2263	10.6	28

194	The Human Cell Atlas. <i>ELife</i> , <b>2017</b> , 6,	8.9	937
193	Author response: The Human Cell Atlas <b>2017</b> ,		10
192	The epigenetic regulators CBP and p300 facilitate leukemogenesis and represent therapeutic targets in acute myeloid leukemia. <i>Oncogene</i> , <b>2016</b> , 35, 279-89	9.2	45
191	BTR: training asynchronous Boolean models using single-cell expression data. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 355	3.6	31
190	Cytokine-induced megakaryocytic differentiation is regulated by genome-wide loss of a uSTAT transcriptional program. <i>EMBO Journal</i> , <b>2016</b> , 35, 580-94	13	47
189	DNMT3A Loss Drives Enhancer Hypomethylation in FLT3-ITD-Associated Leukemias. <i>Cancer Cell</i> , <b>2016</b> , 29, 922-934	24.3	71
188	Processing, visualising and reconstructing network models from single-cell data. <i>Immunology and Cell Biology</i> , <b>2016</b> , 94, 256-65	5	15
187	Genome-scale definition of the transcriptional programme associated with compromised PU.1 activity in acute myeloid leukaemia. <i>Leukemia</i> , <b>2016</b> , 30, 14-23	10.7	10
186	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. <i>Developmental Cell</i> , <b>2016</b> , 36, 572-87	10.2	136
185	ConBind: motif-aware cross-species alignment for the identification of functional transcription factor binding sites. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e72	20.1	5
184	GFI1 proteins orchestrate the emergence of haematopoietic stem cells through recruitment of LSD1. <i>Nature Cell Biology</i> , <b>2016</b> , 18, 21-32	23.4	125
183	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. <i>ELife</i> , <b>2016</b> , 5, e11469	8.9	47
182	Determining Physical Mechanisms of Gene Expression Regulation from Single Cell Gene Expression Data. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1005072	5	15
181	Advancing haematopoietic stem and progenitor cell biology through single-cell profiling. <i>FEBS Letters</i> , <b>2016</b> , 590, 4052-4067	3.8	4
180	Resolving early mesoderm diversification through single-cell expression profiling. <i>Nature</i> , <b>2016</b> , 535, 289-293	50.4	201
179	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. <i>Blood</i> , <b>2016</b> , 127, e12-23	2.2	35
178	A single-cell resolution map of mouse hematopoietic stem and progenitor cell differentiation. <i>Blood</i> , <b>2016</b> , 128, e20-31	2.2	331
177	Dissecting stem cell differentiation using single cell expression profiling. <i>Current Opinion in Cell Biology</i> , <b>2016</b> , 43, 78-86	9	18

176	Drug target optimization in chronic myeloid leukemia using innovative computational platform. <i>Scientific Reports</i> , <b>2015</b> , 5, 8190	4.9	9
175	Creating cellular diversity through transcription factor competition. <i>EMBO Journal</i> , <b>2015</b> , 34, 691-3	13	1
174	Functionally Distinct Subsets of Lineage-Biased Multipotent Progenitors Control Blood Production in Normal and Regenerative Conditions. <i>Cell Stem Cell</i> , <b>2015</b> , 17, 35-46	18	301
173	Clonal Dynamics Reveal Two Distinct Populations of Basal Cells in Slow-Turnover Airway Epithelium. <i>Cell Reports</i> , <b>2015</b> , 12, 90-101	10.6	116
172	CODEX: a next-generation sequencing experiment database for the haematopoietic and embryonic stem cell communities. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D1117-23	20.1	85
171	Regulatory network control of blood stem cells. <i>Blood</i> , <b>2015</b> , 125, 2614-20	2.2	60
170	MicroRNA-486-5p is an erythroid oncomiR of the myeloid leukemias of Down syndrome. <i>Blood</i> , <b>2015</b> , 125, 1292-301	2.2	56
169	The JAK-STAT signaling pathway is differentially activated in CALR-positive compared with JAK2V617F-positive ET patients. <i>Blood</i> , <b>2015</b> , 125, 1679-81	2.2	24
168	The LMO2 -25 Region Harbours GATA2-Dependent Myeloid Enhancer and RUNX-Dependent T-Lymphoid Repressor Activity. <i>PLoS ONE</i> , <b>2015</b> , 10, e0131577	3.7	0
167	Index sorting resolves heterogeneous murine hematopoietic stem cell populations. <i>Experimental Hematology</i> , <b>2015</b> , 43, 803-11	3.1	38
166	Endoglin potentiates nitric oxide synthesis to enhance definitive hematopoiesis. <i>Biology Open</i> , <b>2015</b> , 4, 819-29	2.2	4
165	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , <b>2015</b> , 16, 712-24	18	286
164	GENE SILENCING. Epigenetic silencing by the HUSH complex mediates position-effect variegation in human cells. <i>Science</i> , <b>2015</b> , 348, 1481-1485	33.3	151
163	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 269-276	44.5	268
162	The endothelial transcription factor ERG promotes vascular stability and growth through Wnt/ $\beta$ -catenin signaling. <i>Developmental Cell</i> , <b>2015</b> , 32, 82-96	10.2	124
161	Function-based identification of mammalian enhancers using site-specific integration. <i>Nature Methods</i> , <b>2014</b> , 11, 566-71	21.6	59
160	Probabilistic PCA of censored data: accounting for uncertainties in the visualization of high-throughput single-cell qPCR data. <i>Bioinformatics</i> , <b>2014</b> , 30, 1867-75	7.2	16
159	Large conserved domains of low DNA methylation maintained by Dnmt3a. <i>Nature Genetics</i> , <b>2014</b> , 46, 17-23	36.3	226



158	Concerted bioinformatic analysis of the genome-scale blood transcription factor compendium reveals new control mechanisms. <i>Molecular BioSystems</i> , <b>2014</b> , 10, 2935-41		
157	TRES predicts transcription control in embryonic stem cells. <i>Bioinformatics</i> , <b>2014</b> , 30, 2983-5	7.2	2
156	BET protein inhibition shows efficacy against JAK2V617F-driven neoplasms. <i>Leukemia</i> , <b>2014</b> , 28, 88-97	10.7	57
155	Epigenomic profiling of young and aged HSCs reveals concerted changes during aging that reinforce self-renewal. <i>Cell Stem Cell</i> , <b>2014</b> , 14, 673-88	18	399
154	Single-cell RNA sequencing reveals T helper cells synthesizing steroids de novo to contribute to immune homeostasis. <i>Cell Reports</i> , <b>2014</b> , 7, 1130-42	10.6	143
153	Shared transcription factors contribute to distinct cell fates. <i>Transcription</i> , <b>2014</b> , 5, e978173	4.8	1
152	Delineating MEIS1 cis-regulatory elements active in hematopoietic cells. <i>Leukemia</i> , <b>2014</b> , 28, 433-6	10.7	2
151	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. <i>EMBO Journal</i> , <b>2014</b> , 33, 1212-26	13	46
150	Transcriptional network control of normal and leukaemic haematopoiesis. <i>Experimental Cell Research</i> , <b>2014</b> , 329, 255-64	4.2	25
149	Constrained transcription factor spacing is prevalent and important for transcriptional control of mouse blood cells. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 13513-24	20.1	14
148	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for PU.1 during haematopoietic specification. <i>Development (Cambridge)</i> , <b>2014</b> , 141, 4018-30	6.6	20
147	Transcriptional mechanisms of cell fate decisions revealed by single cell expression profiling. <i>BioEssays</i> , <b>2014</b> , 36, 419-26	4.1	22
146	A tripartite transcription factor network regulates primordial germ cell specification in mice. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 905-15	23.4	187
145	The epidermis comprises autonomous compartments maintained by distinct stem cell populations. <i>Cell Stem Cell</i> , <b>2013</b> , 13, 471-82	18	210
144	Single site-specific integration targeting coupled with embryonic stem cell differentiation provides a high-throughput alternative to in vivo enhancer analyses. <i>Biology Open</i> , <b>2013</b> , 2, 1229-38	2.2	8
143	Building an ENCODE-style data compendium on a shoestring. <i>Nature Methods</i> , <b>2013</b> , 10, 926	21.6	11
142	Genome-wide analysis of transcriptional regulators in human HSPCs reveals a densely interconnected network of coding and noncoding genes. <i>Blood</i> , <b>2013</b> , 122, e12-22	2.2	96
141	Sustained PU.1 levels balance cell-cycle regulators to prevent exhaustion of adult hematopoietic stem cells. <i>Molecular Cell</i> , <b>2013</b> , 49, 934-46	17.6	92

140	Gene set control analysis predicts hematopoietic control mechanisms from genome-wide transcription factor binding data. <i>Experimental Hematology</i> , <b>2013</b> , 41, 354-66.e14	3.1	15
139	Growth factor independence 1 antagonizes a p53-induced DNA damage response pathway in lymphoblastic leukemia. <i>Cancer Cell</i> , <b>2013</b> , 23, 200-14	24.3	55
138	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. <i>Nature Cell Biology</i> , <b>2013</b> , 15, 363-72	23.4	221
137	HOX-mediated LMO2 expression in embryonic mesoderm is recapitulated in acute leukaemias. <i>Oncogene</i> , <b>2013</b> , 32, 5471-80	9.2	10
136	Transcriptional regulation of haematopoietic stem cells. <i>Advances in Experimental Medicine and Biology</i> , <b>2013</b> , 786, 187-212	3.6	40
135	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. <i>Nature Communications</i> , <b>2013</b> , 4, 2924	17.4	124
134	Transcriptional hierarchies regulating early blood cell development. <i>Blood Cells, Molecules, and Diseases</i> , <b>2013</b> , 51, 239-47	2.1	17
133	Impaired in vitro erythropoiesis following deletion of the Scl (Tal1) +40 enhancer is largely compensated for in vivo despite a significant reduction in expression. <i>Molecular and Cellular Biology</i> , <b>2013</b> , 33, 1254-66	4.8	7
132	Hard-wired heterogeneity in blood stem cells revealed using a dynamic regulatory network model. <i>Bioinformatics</i> , <b>2013</b> , 29, i80-8	7.2	53
131	Bivalent promoter marks and a latent enhancer may prime the leukaemia oncogene LMO1 for ectopic expression in T-cell leukaemia. <i>Leukemia</i> , <b>2013</b> , 27, 1348-57	10.7	9
130	Activity of a heptad of transcription factors is associated with stem cell programs and clinical outcome in acute myeloid leukemia. <i>Blood</i> , <b>2013</b> , 121, 2289-300	2.2	54
129	Genome-scale expression and transcription factor binding profiles reveal therapeutic targets in transgenic ERG myeloid leukemia. <i>Blood</i> , <b>2013</b> , 122, 2694-703	2.2	37
128	The Epigenetic Regulators CBP and p300 Facilitate Leukemogenesis and Represent Therapeutic Targets In Acute Myeloid Leukemia (AML). <i>Blood</i> , <b>2013</b> , 122, 3732-3732	2.2	
127	The transcriptional programme controlled by Runx1 during early embryonic blood development. <i>Developmental Biology</i> , <b>2012</b> , 366, 404-19	3.1	38
126	The transcription factor Erg regulates expression of histone deacetylase 6 and multiple pathways involved in endothelial cell migration and angiogenesis. <i>Blood</i> , <b>2012</b> , 119, 894-903	2.2	54
125	GFI1 and GFI1B control the loss of endothelial identity of hemogenic endothelium during hematopoietic commitment. <i>Blood</i> , <b>2012</b> , 120, 314-22	2.2	101
124	A GWAS sequence variant for platelet volume marks an alternative DNMT3 promoter in megakaryocytes near a MEIS1 binding site. <i>Blood</i> , <b>2012</b> , 120, 4859-68	2.2	38
123	Three distinct patterns of histone H3Y41 phosphorylation mark active genes. <i>Cell Reports</i> , <b>2012</b> , 2, 470-710.6		49

122	A new RNASeq-based reference transcriptome for sugar beet and its application in transcriptome-scale analysis of vernalization and gibberellin responses. <i>BMC Genomics</i> , <b>2012</b> , 13, 99	4.5	45
121	Esrrb is a pivotal target of the Gsk3/Tcf3 axis regulating embryonic stem cell self-renewal. <i>Cell Stem Cell</i> , <b>2012</b> , 11, 491-504	18	309
120	Signaling from the sympathetic nervous system regulates hematopoietic stem cell emergence during embryogenesis. <i>Cell Stem Cell</i> , <b>2012</b> , 11, 554-66	18	86
119	The transcription factor Lyl-1 regulates lymphoid specification and the maintenance of early T lineage progenitors. <i>Nature Immunology</i> , <b>2012</b> , 13, 761-9	19.1	39
118	Itga2b regulation at the onset of definitive hematopoiesis and commitment to differentiation. <i>PLoS ONE</i> , <b>2012</b> , 7, e43300	3.7	16
117	Establishing the stem cell state: insights from regulatory network analysis of blood stem cell development. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2012</b> , 4, 285-95	6.6	11
116	The Flk1-Cre-mediated deletion of ETV2 defines its narrow temporal requirement during embryonic hematopoietic development. <i>Stem Cells</i> , <b>2012</b> , 30, 1521-31	5.8	43
115	Deletion of the Scl +19 enhancer increases the blood stem cell compartment without affecting the formation of mature blood lineages. <i>Experimental Hematology</i> , <b>2012</b> , 40, 588-598.e1	3.1	6
114	RUNX1 reshapes the epigenetic landscape at the onset of haematopoiesis. <i>EMBO Journal</i> , <b>2012</b> , 31, 4318-33	3.3	124
113	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 322-33	5.6	91
112	Integration of Elf-4 into stem/progenitor and erythroid regulatory networks through locus-wide chromatin studies coupled with in vivo functional validation. <i>Molecular and Cellular Biology</i> , <b>2012</b> , 32, 763-73	4.8	4
111	Genome-scale technology driven advances to research into normal and malignant haematopoiesis. <i>Scientifica</i> , <b>2012</b> , 2012, 437956	2.6	
110	The transcription factor Erg controls endothelial cell quiescence by repressing activity of nuclear factor (NF)- $\kappa$ B p65. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 12331-42	5.4	38
109	Mapping and functional characterisation of a CTCF-dependent insulator element at the 3' border of the murine Scl transcriptional domain. <i>PLoS ONE</i> , <b>2012</b> , 7, e31484	3.7	6
108	RUNX1 regulates the CD34 gene in haematopoietic stem cells by mediating interactions with a distal regulatory element. <i>EMBO Journal</i> , <b>2011</b> , 30, 4059-70	13	23
107	Genome-wide analysis of simultaneous GATA1/2, RUNX1, FLI1, and SCL binding in megakaryocytes identifies hematopoietic regulators. <i>Developmental Cell</i> , <b>2011</b> , 20, 597-609	10.2	207
106	Maximum parsimony analysis of gene expression profiles permits the reconstruction of developmental cell lineage trees. <i>Developmental Biology</i> , <b>2011</b> , 353, 440-7	3.1	4
105	Two distinct auto-regulatory loops operate at the PU.1 locus in B cells and myeloid cells. <i>Blood</i> , <b>2011</b> , 117, 2827-38	2.2	91

104	ERG promotes T-acute lymphoblastic leukemia and is transcriptionally regulated in leukemic cells by a stem cell enhancer. <i>Blood</i> , <b>2011</b> , 117, 7079-89	2.2	64
103	Nuclear JAK2. <i>Blood</i> , <b>2011</b> , 118, 6987-8	2.2	5
102	LIF-independent JAK signalling to chromatin in embryonic stem cells uncovered from an adult stem cell disease. <i>Nature Cell Biology</i> , <b>2011</b> , 13, 13-21	23.4	101
101	A compendium of genome-wide hematopoietic transcription factor maps supports the identification of gene regulatory control mechanisms. <i>Experimental Hematology</i> , <b>2011</b> , 39, 531-41	3.1	40
100	Deciphering transcriptional control mechanisms in hematopoiesis: the impact of high-throughput sequencing technologies. <i>Experimental Hematology</i> , <b>2011</b> , 39, 961-8	3.1	8
99	Cell of origin in AML: susceptibility to MN1-induced transformation is regulated by the MEIS1/AbdB-like HOX protein complex. <i>Cancer Cell</i> , <b>2011</b> , 20, 39-52	24.3	68
98	Transcriptional regulation of haematopoietic transcription factors. <i>Stem Cell Research and Therapy</i> , <b>2011</b> , 2, 6	8.3	26
97	The transcriptional coactivator Cbp regulates self-renewal and differentiation in adult hematopoietic stem cells. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 5046-60	4.8	39
96	Maps of open chromatin guide the functional follow-up of genome-wide association signals: application to hematological traits. <i>PLoS Genetics</i> , <b>2011</b> , 7, e1002139	6	34
95	A Runx1-Smad6 rheostat controls Runx1 activity during embryonic hematopoiesis. <i>Molecular and Cellular Biology</i> , <b>2011</b> , 31, 2817-26	4.8	18
94	Genome-wide analysis of transcriptional reprogramming in mouse models of acute myeloid leukaemia. <i>PLoS ONE</i> , <b>2011</b> , 6, e16330	3.7	27
93	Ontogeny of haematopoiesis: recent advances and open questions. <i>British Journal of Haematology</i> , <b>2010</b> , 148, 343-55	4.5	18
92	Molecular basis of histone H3K36me3 recognition by the PWWP domain of Brpf1. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 617-9	17.6	164
91	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. <i>Oncogene</i> , <b>2010</b> , 29, 5796-808	9.2	31
90	Gene regulatory networks governing haematopoietic stem cell development and identity. <i>International Journal of Developmental Biology</i> , <b>2010</b> , 54, 1201-11	1.9	45
89	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. <i>Molecular and Cellular Biology</i> , <b>2010</b> , 30, 3853-63	4.8	50
88	cis-Regulatory remodeling of the SCL locus during vertebrate evolution. <i>Molecular and Cellular Biology</i> , <b>2010</b> , 30, 5741-51	4.8	14
87	Transcriptional regulation of Elf-1: locus-wide analysis reveals four distinct promoters, a tissue-specific enhancer, control by PU.1 and the importance of Elf-1 downregulation for erythroid maturation. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, 6363-74	20.1	14

86	Modeling reveals bistability and low-pass filtering in the network module determining blood stem cell fate. <i>PLoS Computational Biology</i> , <b>2010</b> , 6, e1000771	5	48
85	Combinatorial transcriptional control in blood stem/progenitor cells: genome-wide analysis of ten major transcriptional regulators. <i>Cell Stem Cell</i> , <b>2010</b> , 7, 532-44	18	508
84	Enhanced hematovascular contribution of SCL3Qenhancer expressing fetal liver cells uncovers their potential to integrate in extramedullary adult niches. <i>Stem Cells</i> , <b>2010</b> , 28, 100-12	5.8	4
83	Aberrant induction of LMO2 by the E2A-HLF chimeric transcription factor and its implication in leukemogenesis of B-precursor ALL with t(17;19). <i>Blood</i> , <b>2010</b> , 116, 962-70	2.2	33
82	Epigenetic silencing of BIM in glucocorticoid poor-responsive pediatric acute lymphoblastic leukemia, and its reversal by histone deacetylase inhibition. <i>Blood</i> , <b>2010</b> , 116, 3013-22	2.2	95
81	Reprogramming of T cells to natural killer-like cells upon Bcl11b deletion. <i>Science</i> , <b>2010</b> , 329, 85-9	33.3	239
80	BloodExpress: a database of gene expression in mouse haematopoiesis. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D873-9	20.1	30
79	JAK2 phosphorylates histone H3Y41 and excludes HP1alpha from chromatin. <i>Nature</i> , <b>2009</b> , 461, 819-22	50.4	480
78	Motif-blind, genome-wide discovery of cis-regulatory modules in Drosophila and mouse. <i>Developmental Cell</i> , <b>2009</b> , 17, 568-79	10.2	51
77	From genes to cells to tissues--modelling the haematopoietic system. <i>Molecular BioSystems</i> , <b>2009</b> , 5, 1413-20		11
76	ID1 promotes expansion and survival of primary erythroid cells and is a target of JAK2V617F-STAT5 signaling. <i>Blood</i> , <b>2009</b> , 114, 1820-30	2.2	38
75	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , <b>2009</b> , 113, e1-92.2		193
74	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. <i>Blood</i> , <b>2009</b> , 113, 5783-92	2.2	64
73	The mouse Runx1 +23 hematopoietic stem cell enhancer confers hematopoietic specificity to both Runx1 promoters. <i>Blood</i> , <b>2009</b> , 113, 5121-4	2.2	55
72	The transcriptional program controlled by the stem cell leukemia gene Scl/Tal1 during early embryonic hematopoietic development. <i>Blood</i> , <b>2009</b> , 113, 5456-65	2.2	100
71	Transcriptional regulatory networks in haematopoiesis. <i>Current Opinion in Genetics and Development</i> , <b>2008</b> , 18, 530-5	4.9	25
70	A novel mode of enhancer evolution: the Tal1 stem cell enhancer recruited a MIR element to specifically boost its activity. <i>Genome Research</i> , <b>2008</b> , 18, 1422-32	9.7	28
69	Runx genes are direct targets of Scl/Tal1 in the yolk sac and fetal liver. <i>Blood</i> , <b>2008</b> , 111, 3005-14	2.2	68

68	Endoglin expression in blood and endothelium is differentially regulated by modular assembly of the Ets/Gata hemangioblast code. <i>Blood</i> , <b>2008</b> , 112, 4512-22	2.2	40
67	Temporal regulation of Cre-recombinase activity in Scl-positive neurons of the central nervous system. <i>Genesis</i> , <b>2007</b> , 45, 145-51	1.9	5
66	Inference, validation, and dynamic modeling of transcription networks in multipotent hematopoietic cells. <i>Annals of the New York Academy of Sciences</i> , <b>2007</b> , 1106, 30-40	6.5	12
65	CoMoDis: composite motif discovery in mammalian genomes. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, e1	20.1	11
64	Gata2, Fli1, and Scl form a recursively wired gene-regulatory circuit during early hematopoietic development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 17692-7	11.5	184
63	The SCL +40 enhancer targets the midbrain together with primitive and definitive hematopoiesis and is regulated by SCL and GATA proteins. <i>Molecular and Cellular Biology</i> , <b>2007</b> , 27, 7206-19	4.8	37
62	Real-time PCR mapping of DNaseI-hypersensitive sites using a novel ligation-mediated amplification technique. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, e56	20.1	17
61	The SCL transcriptional network and BMP signaling pathway interact to regulate RUNX1 activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 840-5	11.5	96
60	The paralogous hematopoietic regulators Lyl1 and Scl are coregulated by Ets and GATA factors, but Lyl1 cannot rescue the early Scl <sup>-/-</sup> phenotype. <i>Blood</i> , <b>2007</b> , 109, 1908-16	2.2	62
59	Differentiation of murine committed megakaryocytic progenitors isolated by a novel strategy reveals the complexity of GATA and Ets factor involvement in megakaryocytopoiesis and an unexpected potential role for GATA-6. <i>Experimental Hematology</i> , <b>2006</b> , 34, 654-63	3.1	21
58	The SCL 3Q enhancer responds to Hedgehog signaling during hemangioblast specification. <i>Experimental Hematology</i> , <b>2006</b> , 34, 1643-50	3.1	5
57	Transcriptional link between blood and bone: the stem cell leukemia gene and its +19 stem cell enhancer are active in bone cells. <i>Molecular and Cellular Biology</i> , <b>2006</b> , 26, 2615-25	4.8	16
56	Identifying gene regulatory elements by genomic microarray mapping of DNaseI hypersensitive sites. <i>Genome Research</i> , <b>2006</b> , 16, 1310-9	9.7	33
55	Evolution of candidate transcriptional regulatory motifs since the human-chimpanzee divergence. <i>Genome Biology</i> , <b>2006</b> , 7, R52	18.3	12
54	Proneural bHLH and Brn proteins coregulate a neurogenic program through cooperative binding to a conserved DNA motif. <i>Developmental Cell</i> , <b>2006</b> , 11, 831-44	10.2	226
53	Endoglin expression in the endothelium is regulated by Fli-1, Erg, and Elf-1 acting on the promoter and a -8-kb enhancer. <i>Blood</i> , <b>2006</b> , 107, 4737-45	2.2	57
52	TFBScluster web server for the identification of mammalian composite regulatory elements. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W524-8	20.1	8
51	Protocol: precision engineering of plant gene loci by homologous recombination cloning in <i>Escherichia coli</i> . <i>Plant Methods</i> , <b>2005</b> , 1, 6	5.8	2

50	The proto-oncogene ERG in megakaryoblastic leukemias. <i>Cancer Research</i> , <b>2005</b> , 65, 7596-602	10.1	99
49	Inducible chronic phase of myeloid leukemia with expansion of hematopoietic stem cells in a transgenic model of BCR-ABL leukemogenesis. <i>Blood</i> , <b>2005</b> , 105, 324-34	2.2	168
48	In vivo fate-tracing studies using the Scl stem cell enhancer: embryonic hematopoietic stem cells significantly contribute to adult hematopoiesis. <i>Blood</i> , <b>2005</b> , 105, 2724-32	2.2	127
47	Fli1, Elf1, and Ets1 regulate the proximal promoter of the LMO2 gene in endothelial cells. <i>Blood</i> , <b>2005</b> , 106, 2680-7	2.2	52
46	Transgenic analysis of the stem cell leukemia +19 stem cell enhancer in adult and embryonic hematopoietic and endothelial cells. <i>Stem Cells</i> , <b>2005</b> , 23, 1378-88	5.8	35
45	Genome-wide identification of cis-regulatory sequences controlling blood and endothelial development. <i>Human Molecular Genetics</i> , <b>2005</b> , 14, 595-601	5.6	75
44	TFBSCluster: a resource for the characterization of transcriptional regulatory networks. <i>Bioinformatics</i> , <b>2005</b> , 21, 3058-9	7.2	24
43	Potential autoregulation of transcription factor PU.1 by an upstream regulatory element. <i>Molecular and Cellular Biology</i> , <b>2005</b> , 25, 2832-45	4.8	138
42	Transcriptional regulation of the SCL locus: identification of an enhancer that targets the primitive erythroid lineage in vivo. <i>Molecular and Cellular Biology</i> , <b>2005</b> , 25, 5215-25	4.8	53
41	TRANSCRIPTIONAL REGULATION OF BLOOD STEM CELLS <b>2005</b> , 29-38		
40	Analysis of multiple genomic sequence alignments: a web resource, online tools, and lessons learned from analysis of mammalian SCL loci. <i>Genome Research</i> , <b>2004</b> , 14, 313-8	9.7	40
39	The scl +18/19 stem cell enhancer is not required for hematopoiesis: identification of a 5Q bifunctional hematopoietic-endothelial enhancer bound by Fli-1 and Elf-1. <i>Molecular and Cellular Biology</i> , <b>2004</b> , 24, 1870-83	4.8	73
38	Improved arteriogenesis with simultaneous skeletal muscle repair in ischemic tissue by SCL(+) multipotent adult progenitor cell clones from peripheral blood. <i>Journal of Vascular Research</i> , <b>2004</b> , 41, 422-31	1.9	21
37	Genome-wide analysis of repressor element 1 silencing transcription factor/neuron-restrictive silencing factor (REST/NRSF) target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 10458-63	11.5	378
36	Transcriptional regulation of haematopoiesis. <i>Vox Sanguinis</i> , <b>2004</b> , 87 Suppl1, 15-9	3.1	3
35	Genetically tagging endothelial cells in vivo: bone marrow-derived cells do not contribute to tumor endothelium. <i>Blood</i> , <b>2004</b> , 104, 1769-77	2.2	242
34	In Vivo Fate Tracing Studies Using the SCL Stem Cell Enhancer: Embryonic Hematopoietic Stem Cells Significantly Contribute to Adult Hematopoiesis.. <i>Blood</i> , <b>2004</b> , 104, 559-559	2.2	
33	Transcriptional Regulation of Hematopoietic Stem Cells <b>2004</b> , 309-322		4

32	Manipulation of mouse hematopoietic progenitors by specific retroviral infection. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 43556-63	5.4	12
31	Fast and sensitive multiple alignment of large genomic sequences. <i>BMC Bioinformatics</i> , <b>2003</b> , 4, 66	3.6	112
30	Comparative and functional analyses of LYL1 loci establish marsupial sequences as a model for phylogenetic footprinting. <i>Genomics</i> , <b>2003</b> , 81, 249-59	4.3	38
29	GATA transcription in a small rhodamine 123(low)CD34(+) subpopulation of a peripheral blood-derived CD34(-)CD105(+) mesenchymal cell line. <i>Experimental Hematology</i> , <b>2002</b> , 30, 887-95	3.1	41
28	Establishing the transcriptional programme for blood: the SCL stem cell enhancer is regulated by a multiprotein complex containing Ets and GATA factors. <i>EMBO Journal</i> , <b>2002</b> , 21, 3039-50	13	184
27	The role of the stem cell leukemia (SCL) gene in hematopoietic and endothelial lineage specification. <i>Journal of Hematotherapy and Stem Cell Research</i> , <b>2002</b> , 11, 195-206		23
26	Identification of endoglin as a functional marker that defines long-term repopulating hematopoietic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 15468-73	11.5	141
25	Transcriptional regulation of the stem cell leukemia gene (SCL)--comparative analysis of five vertebrate SCL loci. <i>Genome Research</i> , <b>2002</b> , 12, 749-59	9.7	80
24	Rescue of the lethal scl(-/-) phenotype by the human SCL locus. <i>Blood</i> , <b>2002</b> , 99, 3931-8	2.2	8
23	Regulation of the stem cell leukemia (SCL) gene: a tale of two fishes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2001</b> , 98, 6747-52	11.5	43
22	Long-range comparison of human and mouse SCL loci: localized regions of sensitivity to restriction endonucleases correspond precisely with peaks of conserved noncoding sequences. <i>Genome Research</i> , <b>2001</b> , 11, 87-97	9.7	71
21	Analysis of vertebrate SCL loci identifies conserved enhancers. <i>Nature Biotechnology</i> , <b>2000</b> , 18, 181-6	44.5	150
20	Chromatin structure and transcriptional regulation of the stem cell leukaemia (SCL) gene in mast cells. <i>Leukemia</i> , <b>1999</b> , 13, 750-9	10.7	12
19	The stem cell leukaemia (SCL) gene: a critical regulator of haemopoietic and vascular development. <i>International Journal of Biochemistry and Cell Biology</i> , <b>1999</b> , 31, 1193-207	5.6	14
18	Tdr2, a new zebrafish transposon of the Tc1 family. <i>Gene</i> , <b>1999</b> , 239, 373-9	3.8	10
17	Distinct 5' SCL enhancers direct transcription to developing brain, spinal cord, and endothelium: neural expression is mediated by GATA factor binding sites. <i>Developmental Biology</i> , <b>1999</b> , 209, 128-42	3.1	91
16	An SCL 3' enhancer targets developing endothelium together with embryonic and adult haematopoietic progenitors. <i>Development (Cambridge)</i> , <b>1999</b> , 126, 3891-3904	6.6	104
15	An SCL 3' enhancer targets developing endothelium together with embryonic and adult haematopoietic progenitors. <i>Development (Cambridge)</i> , <b>1999</b> , 126, 3891-904	6.6	52



14	The SCL gene specifies haemangioblast development from early mesoderm. <i>EMBO Journal</i> , <b>1998</b> , 17, 4029-45	13	375
13	The pufferfish SLP-1 gene, a new member of the SCL/TAL-1 family of transcription factors. <i>Genomics</i> , <b>1998</b> , 48, 52-62	4.3	11
12	Transcriptional regulation of the stem cell leukemia gene by PU.1 and Elf-1. <i>Journal of Biological Chemistry</i> , <b>1998</b> , 273, 29032-42	5.4	48
11	Distinct mechanisms direct SCL/tal-1 expression in erythroid cells and CD34 positive primitive myeloid cells. <i>Journal of Biological Chemistry</i> , <b>1997</b> , 272, 8781-90	5.4	43
10	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. <i>Oncogene</i> , <b>1997</b> , 15, 2419-28	9.2	56
9	Lineage-restricted regulation of the murine SCL/TAL-1 promoter. <i>Blood</i> , <b>1995</b> , 86, 1502-1514	2.2	71
8	Discordant regulation of SCL/TAL-1 mRNA and protein during erythroid differentiation. <i>Oncogene</i> , <b>1995</b> , 11, 131-9	9.2	21
7	Lineage-restricted regulation of the murine SCL/TAL-1 promoter. <i>Blood</i> , <b>1995</b> , 86, 1502-14	2.2	25
6	Chromatin structure and transcriptional regulation of the stem cell leukaemia (SCL) gene in mast cells. <i>Leukemia</i> , <b>1995</b> , 13, 750-759	10.7	6
5	Highly multiplexed spatially resolved gene expression profiling of mouse organogenesis		7
4	Coordinated Changes in Gene Expression Kinetics Underlie both Mouse and Human Erythroid Maturation		2
3	Graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells		23
2	The local and systemic response to SARS-CoV-2 infection in children and adults		3
1	Mapping interindividual dynamics of innate immune response at single-cell resolution		1