

CITATION REPORT

List of articles citing

Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors

DOI: 10.1016/j.cell.2015.11.013
Cell, 2015, 163, 1663-77.

Source: <https://exaly.com/paper-pdf/62747148/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. 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.

#	Paper	IF	Citations
789	Not All Created Equal: Lineage Hard-Wiring in the Production of Blood. <i>Cell</i> , 2015 , 163, 1568-70	56.2	15
788	The Branching Point in Erythro-Myeloid Differentiation. <i>Cell</i> , 2015 , 163, 1655-62	56.2	115
787	Maintenance of hematopoietic stem cell dormancy: yet another role for the macrophage. 2016 , 3, 46		1
786	Cell Fate Decision as High-Dimensional Critical State Transition. 2016 , 14, e2000640		180
785	Unperturbed vs. post-transplantation hematopoiesis: both in vivo but different. 2016 , 23, 295-303		30
784	Developmental regulation of myeloerythroid progenitor function by the Lin28b-let-7-Hmga2 axis. 2016 , 213, 1497-512		44
783	Advancing haematopoietic stem and progenitor cell biology through single-cell profiling. 2016 , 590, 4052-4067		4
782	De Novo Prediction of Stem Cell Identity using Single-Cell Transcriptome Data. 2016 , 19, 266-277		322
781	Hematopoiesis and T-cell specification as a model developmental system. 2016 , 271, 72-97		23
780	Continuous single cell imaging reveals sequential steps of plasmacytoid dendritic cell development from common dendritic cell progenitors. 2016 , 6, 37462		16
779	Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors. <i>Nucleic Acids Research</i> , 2017 , 45, 1281-1296	20.1	31
778	Transcription factor Zeb2 regulates commitment to plasmacytoid dendritic cell and monocyte fate. 2016 , 113, 14775-14780		40
777	Dissecting Immune Circuits by Linking CRISPR-Pooled Screens with Single-Cell RNA-Seq. <i>Cell</i> , 2016 , 167, 1883-1896.e15	56.2	411
776	Human lymphoid organ dendritic cell identity is predominantly dictated by ontogeny, not tissue microenvironment. 2016 , 1,		92
775	Murine Monocytes: Origins, Subsets, Fates, and Functions. 2016 , 4,		35
774	[Quo vadis hematology?]. 2016 , 157, 1819-1829		
773	Robust lineage reconstruction from high-dimensional single-cell data. <i>Nucleic Acids Research</i> , 2016 , 44, e122	20.1	24

772	Regulation of basophil and mast cell development by transcription factors. 2016 , 65, 127-134	22
771	Epigenetic regulation of neutrophil development and function. 2016 , 28, 83-93	29
770	Wishbone identifies bifurcating developmental trajectories from single-cell data. 2016 , 34, 637-45	404
769	Single-cell profiling of human megakaryocyte-erythroid progenitors identifies distinct megakaryocyte and erythroid differentiation pathways. 2016 , 17, 83	92
768	The force awakens: insights into the origin and formation of microglia. 2016 , 39, 30-7	37
767	Single-cell genomics: coming of age. 2016 , 17, 97	58
766	Hematopoietic stem cell lineage specification. 2016 , 23, 311-7	11
765	A genome editing primer for the hematologist. 2016 , 127, 2525-35	21
764	A single-cell resolution map of mouse hematopoietic stem and progenitor cell differentiation. 2016 , 128, e20-31	331
763	Microbiota-myeloid cell crosstalk beyond the gut. 2016 , 100, 865-879	45
762	Haemopedia: An Expression Atlas of Murine Hematopoietic Cells. 2016 , 7, 571-582	61
761	Dissecting stem cell differentiation using single cell expression profiling. 2016 , 43, 78-86	18
760	Multiplexed, targeted profiling of single-cell proteomes and transcriptomes in a single reaction. 2016 , 17, 188	102
759	Chromatin Control of Developmental Dynamics and Plasticity. 2016 , 38, 610-20	75
758	Writ large: Genomic dissection of the effect of cellular environment on immune response. 2016 , 354, 64-68	32
757	TET2 Regulates Mast Cell Differentiation and Proliferation through Catalytic and Non-catalytic Activities. 2016 , 15, 1566-1579	53
756	Epigenetic memory: A macrophage perspective. 2016 , 28, 359-67	23
755	Hematopoietic Lineage Diversification, Simplified. 2016 , 19, 148-150	3

754	Chromatin programming by developmentally regulated transcription factors: lessons from the study of haematopoietic stem cell specification and differentiation. 2016 , 590, 4105-4115		10
753	Clonal analysis of stem cells in differentiation and disease. 2016 , 43, 14-21		8
752	Diffusion pseudotime robustly reconstructs lineage branching. 2016 , 13, 845-8		566
751	Single-cell analysis of mixed-lineage states leading to a binary cell fate choice. 2016 , 537, 698-702		308
750	Regulation of Hematopoiesis and Osteogenesis by Blood Vessel-Derived Signals. 2016 , 32, 649-675		85
749	Granulopoiesis and granules of human neutrophils. 2016 , 273, 11-28		188
748	Single-Cell Transcript Profiles Reveal Multilineage Priming in Early Progenitors Derived from Lgr5(+) Intestinal Stem Cells. 2016 , 16, 2053-2060		56
747	The stem cell niche finds its true north. <i>Development (Cambridge)</i> , 2016 , 143, 2877-81	6.6	4
746	Cellular Barcoding Links B-1a B Cell Potential to a Fetal Hematopoietic Stem Cell State at the Single-Cell Level. <i>Immunity</i> , 2016 , 45, 346-57	32.3	52
745	The Spectrum and Regulatory Landscape of Intestinal Innate Lymphoid Cells Are Shaped by the Microbiome. <i>Cell</i> , 2016 , 166, 1231-1246.e13	56.2	347
744	Myeloid Cell Origins, Differentiation, and Clinical Implications. 2016 , 4,		40
743	Output without input: the lifelong productivity of hematopoietic stem cells. 2016 , 43, 69-77		12
742	Transition states and cell fate decisions in epigenetic landscapes. 2016 , 17, 693-703		188
741	Advances in understanding the mechanisms of erythropoiesis in homeostasis and disease. 2016 , 174, 661-73		33
740	Retracing the in vivo haematopoietic tree using single-cell methods. 2016 , 590, 4068-4083		10
739	Single-cell genome-wide studies give new insight into nongenetic cell-to-cell variability in animals. 2016 , 146, 239-54		4
738	Cellular identity at the single-cell level. 2016 , 12, 2965-79		14
737	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016 , 167, 1415-1429.e19	56.2	637

736	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. 2016 , 19, 808-822		142
735	Human dendritic cells (DCs) are derived from distinct circulating precursors that are precommitted to become CD1c+ or CD141+ DCs. 2016 , 213, 2861-2870		87
734	Challenges in long-term imaging and quantification of single-cell dynamics. 2016 , 34, 1137-1144		118
733	Hematopoietic Stem Cells Count and Remember Self-Renewal Divisions. <i>Cell</i> , 2016 , 167, 1296-1309.e10	56.2	155
732	Mobilisation and dysfunction of haematopoietic stem/progenitor cells after <i>Listonella anguillarum</i> infection in ayu, <i>Plecoglossus altivelis</i> . 2016 , 6, 28082		6
731	Microglia development follows a stepwise program to regulate brain homeostasis. 2016 , 353, aad8670		618
730	Engineering Hematopoietic Stem Cells: Lessons from Development. 2016 , 18, 707-720		57
729	Myelopoiesis Reloaded: Single-Cell Transcriptomics Leads the Way. <i>Immunity</i> , 2016 , 44, 18-20	32.3	9
728	Tissue-Resident Macrophage Ontogeny and Homeostasis. <i>Immunity</i> , 2016 , 44, 439-449	32.3	849
727	Exploring the multifaceted nature of the common lymphoid progenitor compartment. 2016 , 39, 121-6		3
726	STEM CELLS. Potency finds its niches. 2016 , 351, 126-7		4
725	Scaling single-cell genomics from phenomenology to mechanism. 2017 , 541, 331-338		414
724	Chromatin Remodeling in Monocyte and Macrophage Activation. 2017 , 106, 1-15		6
723	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. 2017 , 18, 18		70
722	Studying hematopoiesis using single-cell technologies. 2017 , 10, 27		26
721	Reactive Oxygen Species-Producing Myeloid Cells Act as a Bone Marrow Niche for Sterile Inflammation-Induced Reactive Granulopoiesis. 2017 , 198, 2854-2864		17
720	Non-apoptotic functions of caspases in myeloid cell differentiation. 2017 , 24, 1337-1347		26
719	Single-cell molecular analysis defines therapy response and immunophenotype of stem cell subpopulations in CML. 2017 , 129, 2384-2394		75

718	The chronic myeloid leukemia stem cell: stemming the tide of persistence. 2017 , 129, 1595-1606		171
717	Expression and regulation of C/EBP β in normal myelopoiesis and in malignant transformation. 2017 , 129, 2083-2091		71
716	Single-cell transcriptome conservation in cryopreserved cells and tissues. 2017 , 18, 45		101
715	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017 , 18, 583-593	19.1	189
714	Visualization and analysis of single-cell RNA-seq data by kernel-based similarity learning. 2017 , 14, 414-416		355
713	Power analysis of single-cell RNA-sequencing experiments. 2017 , 14, 381-387		357
712	Epithelial-Mesenchymal Micro-niches Govern Stem Cell Lineage Choices. <i>Cell</i> , 2017 , 169, 483-496.e13	56.2	142
711	Tissue-Specific Diversity and Functions of Conventional Dendritic Cells. 2017 , 134, 89-135		14
710	CBP/Catenin antagonists: Targeting LSCs' Achilles heel. 2017 , 52, 1-11		12
709	Genomic Characterization of Murine Monocytes Reveals C/EBP β Transcription Factor Dependence of Ly6C Cells. <i>Immunity</i> , 2017 , 46, 849-862.e7	32.3	151
708	Structure of Nascent Chromatin Is Essential for Hematopoietic Lineage Specification. 2017 , 19, 295-306		21
707	Comparative transcriptomics in human and mouse. 2017 , 18, 425-440		99
706	JingleBells: A Repository of Immune-Related Single-Cell RNA-Sequencing Datasets. 2017 , 198, 3375-3379		21
705	Innate Immune Landscape in Early Lung Adenocarcinoma by Paired Single-Cell Analyses. <i>Cell</i> , 2017 , 169, 750-765.e17	56.2	629
704	Mapping the human DC lineage through the integration of high-dimensional techniques. 2017 , 356,		301
703	Shaping development by stochasticity and dynamics in gene regulation. 2017 , 7,		9
702	Model-based branching point detection in single-cell data by K-branches clustering. <i>Bioinformatics</i> , 2017 , 33, 3211-3219	7.2	7
701	A Unique Microglia Type Associated with Restricting Development of Alzheimer's Disease. <i>Cell</i> , 2017 , 169, 1276-1290.e17	56.2	1758

700	Reconstructing blood stem cell regulatory network models from single-cell molecular profiles. 2017 , 114, 5822-5829		47
699	Associating cellular epigenetic models with human phenotypes. 2017 , 18, 441-451		176
698	Impact of inflammation on early hematopoiesis and the microenvironment. 2017 , 106, 27-33		20
697	Single-cell analyses to reveal hematopoietic stem cell fate decisions. 2017 , 591, 2195-2212		4
696	Diversity and functions of intestinal mononuclear phagocytes. 2017 , 10, 845-864		105
695	Myeloid progenitor cluster formation drives emergency and leukaemic myelopoiesis. 2017 , 544, 53-58		97
694	MeDeCom: discovery and quantification of latent components of heterogeneous methylomes. 2017 , 18, 55		42
693	Location, function, and ontogeny of pulmonary macrophages during the steady state. 2017 , 469, 561-572		39
692	Human haematopoietic stem cell lineage commitment is a continuous process. 2017 , 19, 271-281		441
691	Runx1 Structure and Function in Blood Cell Development. <i>Advances in Experimental Medicine and Biology</i> , 2017 , 962, 65-81	3.6	14
690	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. 2017 , 114, E327-E336		30
689	Intrinsic transcriptional heterogeneity in B cells controls early class switching to IgE. 2017 , 214, 183-196		35
688	The Human Cell Atlas. 2017 ,		41
687	High-Dimensional Fluorescence Cytometry. 2017 , 119, 5.8.1-5.8.38		20
686	A distinct hematopoietic stem cell population for rapid multilineage engraftment in nonhuman primates. 2017 , 9,		57
685	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017 , 171, 398-413.e21	56.2	50
684	Single-cell RNA-seq reveals a distinct transcriptome signature of aneuploid hematopoietic cells. 2017 , 130, 2762-2773		41
683	Single-cell RNA sequencing reveals developmental heterogeneity among early lymphoid progenitors. <i>EMBO Journal</i> , 2017 , 36, 3619-3633	13	27

682	Reversed graph embedding resolves complex single-cell trajectories. 2017 , 14, 979-982	1207
681	Single Cell Phenotyping Reveals Heterogeneity Among Hematopoietic Stem Cells Following Infection. 2017 , 35, 2292-2304	9
680	Epigenetic Regulation of Dendritic Cell Development and Function. 2017 , 23, 302-307	20
679	Counting the cost of lineage decisions. <i>Nature Immunology</i> , 2017 , 18, 872-873	19.1
678	Delineating biological and technical variance in single cell expression data. 2017 , 90, 161-166	11
677	Dual MET and ERBB inhibition overcomes intratumor plasticity in osimertinib-resistant-advanced non-small-cell lung cancer (NSCLC). 2017 , 28, 2451-2457	43
676	Monocyte-derived alveolar macrophages drive lung fibrosis and persist in the lung over the life span. 2017 , 214, 2387-2404	434
675	The Road Map for Megakaryopoietic Lineage from Hematopoietic Stem/Progenitor Cells. 2017 , 6, 1661-1665	9
674	Simultaneous epitope and transcriptome measurement in single cells. 2017 , 14, 865-868	1068
673	Inflammatory monocytes regulate Th1 oriented immunity to CpG adjuvanted protein vaccines through production of IL-12. 2017 , 7, 5986	19
672	Single-Cell Transcriptomic Characterization of Vertebrate Brain Composition, Development, and Function. 2017 , 437-468	5
671	I am : 7q regulator I am. 2017 , 129, 2210-2212	2
670	Single-cell Hi-C bridges microscopy and genome-wide sequencing approaches to study 3D chromatin organization. 2017 , 39, 1700104	32
669	Polylox barcoding reveals haematopoietic stem cell fates realized in vivo. 2017 , 548, 456-460	202
668	How Single-Cell Genomics Is Changing Evolutionary and Developmental Biology. 2017 , 33, 537-553	57
667	Feature screening in large scale cluster analysis. 2017 , 161, 191-212	1
666	Decoding early myelopoiesis from dynamics of core endogenous network. 2017 , 60, 627-646	13
665	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. <i>Nature Communications</i> , 2017 , 8, 2045	17.4 78

664	Spatial reconstruction of immune niches by combining photoactivatable reporters and scRNA-seq. 2017 , 358, 1622-1626		116
663	Efficient Generation of Transcriptomic Profiles by Random Composite Measurements. <i>Cell</i> , 2017 , 171, 1424-1436.e18	56.2	57
662	Granulocyte-Monocyte Progenitors and Monocyte-Dendritic Cell Progenitors Independently Produce Functionally Distinct Monocytes. <i>Immunity</i> , 2017 , 47, 890-902.e4	32.3	157
661	Lineage specification of human dendritic cells is marked by IRF8 expression in hematopoietic stem cells and multipotent progenitors. <i>Nature Immunology</i> , 2017 , 18, 877-888	19.1	75
660	Transcriptional determination and functional specificity of myeloid cells: making sense of diversity. 2017 , 17, 595-607		41
659	Rewiring of the inferred protein interactome during blood development studied with the tool PPICompare. 2017 , 11, 44		2
658	Challenges and emerging directions in single-cell analysis. 2017 , 18, 84		166
657	The Role of Skeletal Stem Cells in the Reconstruction of Bone Defects. 2017 , 28, 1136-1141		6
656	A Single-Cell Roadmap of Lineage Bifurcation in Human ESC Models of Embryonic Brain Development. 2017 , 20, 120-134		76
655	Concise Review: Stem Cell Population Biology: Insights from Hematopoiesis. 2017 , 35, 80-88		17
654	The hematopoietic stem-cell niche in health and leukemia. 2017 , 74, 579-590		66
653	STRT-seq-2i: dual-index 5' single cell and nucleus RNA-seq on an addressable microwell array. 2017 , 7, 16327		50
652	Illuminating stem cell transcription factor dynamics: long-term single-cell imaging of fluorescent protein fusions. 2017 , 49, 77-83		8
651	Murine Monocytes: Origins, Subsets, Fates, and Functions. 2017 , 141-153		2
650	Myeloid Cell Origins, Differentiation, and Clinical Implications. 2017 , 857-875		1
649	Single cell analysis of the inner ear sensory organs. 2017 , 61, 205-213		2
648	Developmental Control of NRAMP1 (SLC11A1) Expression in Professional Phagocytes. 2017 , 6,		4
647	The Human Cell Atlas. 2017 , 6,		937

646	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. <i>Nucleic Acids Research</i> , 2017 , 45, 9244-9259	20.1	10
645	Immunology, one cell at a time. 2017 , 547, 27-29		26
644	Human megakaryocytes: finding the root. 2017 , 129, 3277-3279		1
643	Probabilistic modeling of bifurcations in single-cell gene expression data using a Bayesian mixture of factor analyzers. 2017 , 2, 19		19
642	Selective Expression of Flt3 within the Mouse Hematopoietic Stem Cell Compartment. 2017 , 18,		18
641	Terminally Differentiating Eosinophils Express Neutrophil Primary Granule Proteins as well as Eosinophil-specific Granule Proteins in a Temporal Manner. 2017 , 17, 410-423		9
640	Dynamics of embryonic stem cell differentiation inferred from single-cell transcriptomics show a series of transitions through discrete cell states. 2017 , 6,		27
639	Population snapshots predict early haematopoietic and erythroid hierarchies. 2018 , 555, 54-60		184
638	Transcription Factor IRF8 Governs Enhancer Landscape Dynamics in Mononuclear Phagocyte Progenitors. 2018 , 22, 2628-2641		26
637	Homeostatic control of dendritic cell numbers and differentiation. 2018 , 96, 463-476		24
636	Stretching the limits: from homeostasis to stem cell plasticity in wound healing and cancer. 2018 , 19, 311-325		87
635	Heterogeneity of Metazoan Cells and Beyond: To Integrative Analysis of Cellular Populations at Single-Cell Level. 2018 , 1745, 3-23		3
634	Fundamental limits on dynamic inference from single-cell snapshots. 2018 , 115, E2467-E2476		138
633	Reconstruction of complex single-cell trajectories using CellRouter. <i>Nature Communications</i> , 2018 , 9, 892	17.4	49
632	Exploring intermediate cell states through the lens of single cells. 2018 , 9, 32-41		35
631	Transcript-indexed ATAC-seq for precision immune profiling. 2018 , 24, 580-590		93
630	Concise Review: Bipotent Megakaryocytic-Erythroid Progenitors: Concepts and Controversies. 2018 , 36, 1138-1145		22
629	FateID infers cell fate bias in multipotent progenitors from single-cell RNA-seq data. 2018 , 15, 379-386		153

628	The changing face of hematopoiesis: a spectrum of options is available to stem cells. 2018 , 96, 898-911		10
627	Myeloid cell heterogeneity in cancer: not a single cell alike. 2018 , 330, 188-201		89
626	The Ontogeny of a Neutrophil: Mechanisms of Granulopoiesis and Homeostasis. 2018 , 82,		88
625	We skip to work: alternative splicing in normal and malignant myelopoiesis. 2018 , 32, 1081-1093		23
624	Proliferation dynamics of acute myeloid leukaemia and haematopoietic progenitors competing for bone marrow space. <i>Nature Communications</i> , 2018 , 9, 519	17.4	41
623	High-throughput single-cell fate potential assay of murine hematopoietic progenitors in vitro. 2018 , 60, 21-29.e3		6
622	From haematopoietic stem cells to complex differentiation landscapes. 2018 , 553, 418-426		311
621	Single-Cell Genomics: A Stepping Stone for Future Immunology Discoveries. <i>Cell</i> , 2018 , 172, 14-21	56.2	108
620	Modulation of Myelopoiesis Progenitors Is an Integral Component of Trained Immunity. <i>Cell</i> , 2018 , 172, 147-161.e12	56.2	417
619	Manifold learning-based methods for analyzing single-cell RNA-sequencing data. 2018 , 7, 36-46		59
618	Immune regulation by monocytes. 2018 , 35, 12-18		56
617	Human dendritic cell subsets: an update. 2018 , 154, 3-20		467
616	Large-Scale Low-Cost NGS Library Preparation Using a Robust Tn5 Purification and Tagmentation Protocol. 2018 , 8, 79-89		54
615	Clonal analysis of lineage fate in native haematopoiesis. 2018 , 553, 212-216		249
614	Phenotypic stability and plasticity in GMP-derived cells as determined by their underlying regulatory network. <i>Bioinformatics</i> , 2018 , 34, 1174-1182	7.2	5
613	Single-Cell Computational Strategies for Lineage Reconstruction in Tissue Systems. 2018 , 5, 539-548		25
612	Causes and Consequences of Hematopoietic Stem Cell Heterogeneity. 2018 , 22, 627-638		118
611	bigScale: an analytical framework for big-scale single-cell data. 2018 , 28, 878-890		45

610	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018 , 173, 1535-1548.e16	56.2	292
609	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. 2018 , 36, 421-427		775
608	Integrating single-cell transcriptomic data across different conditions, technologies, and species. 2018 , 36, 411-420		4181
607	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018 , 173, 90-103.e19	56.2	174
606	Defining the Transcriptional Landscape during Cytomegalovirus Latency with Single-Cell RNA Sequencing. 2018 , 9,		91
605	A single-cell hematopoietic landscape resolves 8 lineage trajectories and defects in Kit mutant mice. 2018 , 131, e1-e11		85
604	Tumor-Induced Generation of Splenic Erythroblast-like Ter-Cells Promotes Tumor Progression. <i>Cell</i> , 2018 , 173, 634-648.e12	56.2	65
603	Breast and pancreatic cancer interrupt IRF8-dependent dendritic cell development to overcome immune surveillance. <i>Nature Communications</i> , 2018 , 9, 1250	17.4	88
602	Molecular transitions in early progenitors during human cord blood hematopoiesis. 2018 , 14, e8041		75
601	The impact of single-cell RNA sequencing on understanding the functional organization of the immune system. 2018 , 17, 265-272		14
600	Impact of DNA methylation programming on normal and pre-leukemic hematopoiesis. 2018 , 51, 89-100		14
599	Single cell analysis of normal and leukemic hematopoiesis. 2018 , 59, 85-94		31
598	Mechanisms underlying the heterogeneity of myelodysplastic syndromes. 2018 , 58, 17-26		10
597	Unsupervised Trajectory Analysis of Single-Cell RNA-Seq and Imaging Data Reveals Alternative Tuft Cell Origins in the Gut. 2018 , 6, 37-51.e9		100
596	Constructing cell lineages from single-cell transcriptomes. 2018 , 59, 95-113		13
595	When the good go bad: Mutant NPM1 in acute myeloid leukemia. 2018 , 32, 167-183		50
594	Systems Biology. 2018 ,		
593	Single-cell analysis reveals the continuum of human lympho-myeloid progenitor cells. <i>Nature Immunology</i> , 2018 , 19, 85-97	19.1	116

592	Conceptual Challenges of the Systemic Approach in Understanding Cell Differentiation. 2018 , 1702, 27-39	3
591	Single-cell RNA sequencing to explore immune cell heterogeneity. 2018 , 18, 35-45	534
590	Deciphering the differentiation trajectory from hematopoietic stem cells to mast cells. 2018 , 2, 2273-2281	27
589	Flexible fate determination ensures robust differentiation in the hair follicle. 2018 , 20, 1361-1369	24
588	Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. 2018 , 13, 2742-2757	87
587	A track of the clones: new developments in cellular barcoding. 2018 , 68, 15-20	8
586	The Molecular Signature of Megakaryocyte-Erythroid Progenitors Reveals a Role for the Cell Cycle in Fate Specification. 2018 , 25, 2083-2093.e4	27
585	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. 2018 , 7, 656-666.e4	30
584	Single cell dissection of plasma cell heterogeneity in symptomatic and asymptomatic myeloma. 2018 , 24, 1867-1876	105
583	Technical Advances in Single-Cell RNA Sequencing and Applications in Normal and Malignant Hematopoiesis. 2018 , 8, 582	12
582	A Single-Cell Sequencing Guide for Immunologists. 2018 , 9, 2425	89
581	Using single cell analysis for translational studies in immune mediated diseases: Opportunities and challenges. 2018 , 103, 191-199	5
580	Mouse adult hematopoietic stem cells actively synthesize ribosomal RNA. 2018 , 24, 1803-1812	12
579	The Human Cell Atlas bone marrow single-cell interactive web portal. 2018 , 68, 51-61	74
578	The Cellular and Molecular Mechanisms of Hematopoiesis. 2018 , 1-23	0
577	Myelo-lymphoid lineage restriction occurs in the human haematopoietic stem cell compartment before lymphoid-primed multipotent progenitors. <i>Nature Communications</i> , 2018 , 9, 4100	17.4 32
576	Kinetics of adult hematopoietic stem cell differentiation in vivo. 2018 , 215, 2815-2832	38
575	Lung Single-Cell Signaling Interaction Map Reveals Basophil Role in Macrophage Imprinting. <i>Cell</i> , 2018 , 175, 1031-1044.e18	56.2 204

574	Ensemble Estimation of Information Divergence. 2018 , 20,		9
573	Recent advances in understanding dendritic cell development, classification, and phenotype. 2018 , 7,		14
572	Single-Cell Transcriptomics in Cancer Immunobiology: The Future of Precision Oncology. 2018 , 9, 2582		33
571	Maintenance of human haematopoietic stem and progenitor cells in vitro using a chemical cocktail. 2018 , 4, 59		9
570	Bloody Zebrafish: Novel Methods in Normal and Malignant Hematopoiesis. <i>Frontiers in Cell and Developmental Biology</i> , 2018 , 6, 124	5-7	4
569	Developmental and Functional Heterogeneity of Monocytes. <i>Immunity</i> , 2018 , 49, 595-613	32-3	306
568	Cytokine control of megakaryopoiesis. 2018 , 36, 89-103		38
567	Quantitative assessment of cell population diversity in single-cell landscapes. 2018 , 16, e2006687		22
566	DNA methylation 101: what is important to know about DNA methylation and its role in SLE risk and disease heterogeneity. 2018 , 5, e000285		21
565	GraphDDP: a graph-embedding approach to detect differentiation pathways in single-cell-data using prior class knowledge. <i>Nature Communications</i> , 2018 , 9, 3685	17.4	5
564	Power in Numbers: Single-Cell RNA-Seq Strategies to Dissect Complex Tissues. 2018 , 52, 203-221		56
563	Oxidant Signaling Mediated by Nox2 in Neutrophils Promotes Regenerative Myelopoiesis and Tissue Recovery following Ischemic Damage. 2018 , 201, 2414-2426		9
562	Murine Bone Marrow Niches from Hematopoietic Stem Cells to B Cells. 2018 , 19,		21
561	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. 2018 , 7, 284-294.e12		32
560	Deciphering the Evolution of Vertebrate Immune Cell Types with Single-Cell RNA-Seq. 2018 , 95-111		0
559	Macrophages and Cardiovascular Health. 2018 , 98, 2523-2569		39
558	Enhancer and Transcription Factor Dynamics during Myeloid Differentiation Reveal an Early Differentiation Block in Cebpa null Progenitors. 2018 , 23, 2744-2757		18
557	Hematopoietic stem cells can differentiate into restricted myeloid progenitors before cell division in mice. <i>Nature Communications</i> , 2018 , 9, 1898	17.4	26

556	Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. <i>Cell</i> , 2018 , 174, 716-729.e27	56.2	583
555	Comparative transcriptomic analysis of hematopoietic system between human and mouse by Microwell-seq. 2018 , 4, 34		9
554	The Making of Hematopoiesis: Developmental Ancestry and Environmental Nurture. 2018 , 19,		6
553	Dissection of progenitor compartments resolves developmental trajectories in B-lymphopoiesis. 2018 , 215, 1947-1963		12
552	Revealing routes of cellular differentiation by single-cell RNA-seq. 2018 , 11, 9-17		5
551	Lineage marker synchrony in hematopoietic genealogies refutes the PU.1/GATA1 toggle switch paradigm. <i>Nature Communications</i> , 2018 , 9, 2697	17.4	15
550	Differentiation-based model of hematopoietic stem cell functions and lineage pathways. 2018 , 132, 1106-1113	28	
549	From the Human Cell Atlas to dynamic immune maps in human disease. 2018 , 18, 597-598		18
548	Mediated Ablation of Conventional Dendritic Cells Suggests a Lymphoid Path to Generating Dendritic Cells. 2018 , 9, 699		11
547	Single Cell RNA Sequencing of Rare Immune Cell Populations. 2018 , 9, 1553		61
546	The 'TranSeq' 3'-end sequencing method for high-throughput transcriptomics and gene space refinement in plant genomes. 2018 , 96, 223-232		15
545	Single-cell mapping of the thymic stroma identifies IL-25-producing tuft epithelial cells. 2018 , 559, 622-626		122
544	Differences in Cell Cycle Status Underlie Transcriptional Heterogeneity in the HSC Compartment. 2018 , 24, 766-780		23
543	NAMPT: A pleiotropic modulator of monocytes and macrophages. 2018 , 135, 25-36		37
542	Single-Cell Transcriptomics Meets Lineage Tracing. 2018 , 23, 166-179		191
541	Identification of an Early Unipotent Neutrophil Progenitor with Pro-tumoral Activity in Mouse and Human Bone Marrow. 2018 , 24, 2329-2341.e8		88
540	Characterization of Imatinib Resistant CML Leukemic Stem/Initiating Cells and Their Sensitivity to CBP/Catenin Antagonists. 2018 , 11, 113-121		7
539	BGP: identifying gene-specific branching dynamics from single-cell data with a branching Gaussian process. 2018 , 19, 65		15

538	Dissection of Influenza Infection In Vivo by Single-Cell RNA Sequencing. 2018 , 6, 679-691.e4		96
537	Myelopoiesis in the Context of Innate Immunity. 2018 , 10, 365-372		40
536	Single-cell characterization of haematopoietic progenitors and their trajectories in homeostasis and perturbed haematopoiesis. 2018 , 20, 836-846		151
535	Modelling Gene Expression Dynamics with Gaussian Process Inference. 2019 , 879-20		
534	mA RNA Methylation Maintains Hematopoietic Stem Cell Identity and Symmetric Commitment. 2019 , 28, 1703-1716.e6		59
533	Reconstructing complex lineage trees from scRNA-seq data using MERLoT. <i>Nucleic Acids Research</i> , 2019 , 47, 8961-8974	20.1	11
532	Mammary stem cells, where art thou?. 2019 , 8, e357		1
531	Deconvolution of autoencoders to learn biological regulatory modules from single cell mRNA sequencing data. 2019 , 20, 379		10
530	Single-Cell Omics: An Overview. 2019 , 3-19		2
529	Transcriptional Regulation in the Immune System: One Cell at a Time. 2019 , 10, 1355		6
528	Predicting bacterial infection outcomes using single cell RNA-sequencing analysis of human immune cells. <i>Nature Communications</i> , 2019 , 10, 3266	17.4	28
527	Modeling the Hematopoietic Landscape. <i>Frontiers in Cell and Developmental Biology</i> , 2019 , 7, 104	5.7	10
526	Single-Cell Analysis Reveals Regulatory Gene Expression Dynamics Leading to Lineage Commitment in Early T Cell Development. 2019 , 9, 321-337.e9		36
525	Quantifying Drug-Induced Bone Marrow Toxicity Using a Novel Haematopoiesis Systems Pharmacology Model. 2019 , 8, 858-868		10
524	Discovering myeloid cell heterogeneity in the lung by means of next generation sequencing. 2019 , 6, 33		7
523	Combinatorial prediction of marker panels from single-cell transcriptomic data. 2019 , 15, e9005		25
522	RBPJ-dependent Notch signaling initiates the T cell program in a subset of thymus-seeding progenitors. <i>Nature Immunology</i> , 2019 , 20, 1456-1468	19.1	32
521	Mind the Map: Technology Shapes the Myeloid Cell Space. 2019 , 10, 2287		8

520	How Methods of Molecular Biology Shape Our Understanding of the Hematopoietic System. 2019 , 53, 626-637		0
519	Potential Immunotherapeutic Targets on Myeloid Cells for Neurovascular Repair After Ischemic Stroke. 2019 , 13, 758		11
518	Fate Mapping via Ms4a3-Expression History Traces Monocyte-Derived Cells. <i>Cell</i> , 2019 , 178, 1509-1525.e102	10.2	176
517	Single-Cell Analysis of Crohn's Disease Lesions Identifies a Pathogenic Cellular Module Associated with Resistance to Anti-TNF Therapy. <i>Cell</i> , 2019 , 178, 1493-1508.e20	56.2	219
516	A large pool of actively cycling progenitors orchestrates self-renewal and injury repair of an ectodermal appendage. 2019 , 21, 1102-1112		32
515	Machine learning predicts putative hematopoietic stem cells within large single-cell transcriptomics data sets. 2019 , 78, 11-20		20
514	Deterministic column subset selection for single-cell RNA-Seq. 2019 , 14, e0210571		
513	PD-1/PD-L1 checkpoint blockade harnesses monocyte-derived macrophages to combat cognitive impairment in a tauopathy mouse model. <i>Nature Communications</i> , 2019 , 10, 465	17.4	50
512	Integrative single-cell analysis. 2019 , 20, 257-272		501
511	Single-cell RNA-seq denoising using a deep count autoencoder. <i>Nature Communications</i> , 2019 , 10, 390	17.4	314
510	Statistical test of structured continuous trees based on discordance matrix. <i>Bioinformatics</i> , 2019 , 35, 4962-4970	7.2	
509	What Makes a pDC: Recent Advances in Understanding Plasmacytoid DC Development and Heterogeneity. 2019 , 10, 1222		48
508	Hematopoietic progenitor cells as integrative hubs for adaptation to and fine-tuning of inflammation. <i>Nature Immunology</i> , 2019 , 20, 802-811	19.1	93
507	Plasmacytoid dendritic cells develop from Ly6D lymphoid progenitors distinct from the myeloid lineage. <i>Nature Immunology</i> , 2019 , 20, 852-864	19.1	97
506	Granulopoiesis and Neutrophil Homeostasis: A Metabolic, Daily Balancing Act. 2019 , 40, 598-612		29
505	Are transplantable stem cells required for adult hematopoiesis?. 2019 , 75, 1-10		6
504	Human Dendritic Cell Subsets, Ontogeny, and Impact on HIV Infection. 2019 , 10, 1088		43
503	Application of single-cell RNA sequencing methodologies in understanding haematopoiesis and immunology. 2019 , 63, 217-225		11

502	Persistent stimulation with Mycobacterium tuberculosis antigen impairs the proliferation and transcriptional program of hematopoietic cells in bone marrow. 2019 , 112, 115-122	3
501	MARS-seq2.0: an experimental and analytical pipeline for indexed sorting combined with single-cell RNA sequencing. 2019 , 14, 1841-1862	85
500	PAGA: graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells. 2019 , 20, 59	369
499	Efficient integration of heterogeneous single-cell transcriptomes using Scanorama. 2019 , 37, 685-691	233
498	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. 2019 , 8,	12
497	GATA-1 isoforms differently contribute to the production and compartmentation of reactive oxygen species in the myeloid leukemia cell line K562. 2019 , 234, 20829-20846	4
496	ATP turnover and glucose dependency in hematopoietic stem/progenitor cells are increased by proliferation and differentiation. 2019 , 514, 287-294	6
495	Single Cell Methods. 2019 ,	2
494	A Bioinformatic Toolkit for Single-Cell mRNA Analysis. 2019 , 1979, 433-455	
493	Characterization of cell fate probabilities in single-cell data with Palantir. 2019 , 37, 451-460	126
492	Clonal and Quantitative In Vivo Assessment of Hematopoietic Stem Cell Differentiation Reveals Strong Erythroid Potential of Multipotent Cells. 2019 , 12, 801-815	23
491	Single-Cell Analysis of Diverse Pathogen Responses Defines a Molecular Roadmap for Generating Antigen-Specific Immunity. 2019 , 8, 109-121.e6	24
490	Multidimensional Single-Cell Analyses in Organ Development and Maintenance. 2019 , 29, 477-486	3
489	Trib1 regulates eosinophil lineage commitment and identity by restraining the neutrophil program. 2019 , 133, 2413-2426	20
488	Interrogation of human hematopoiesis at single-cell and single-variant resolution. 2019 , 51, 683-693	77
487	Droplet-based single cell RNAseq tools: a practical guide. 2019 , 19, 1706-1727	45
486	The bone marrow microenvironment at single-cell resolution. 2019 , 569, 222-228	347
485	Cell lineage and communication network inference via optimization for single-cell transcriptomics. <i>Nucleic Acids Research</i> , 2019 , 47, e66	20.1 51

484	Tree-ensemble analysis assesses presence of multifurcations in single cell data. 2019 , 15, e8552	1
483	Identification of a novel enhancer of CEBPE essential for granulocytic differentiation. 2019 , 133, 2507-2517	11
482	Revolutionizing immunology with single-cell RNA sequencing. 2019 , 16, 242-249	59
481	New insights into hematopoietic differentiation landscapes from single-cell RNA sequencing. 2019 , 133, 1415-1426	30
480	EZH2 Inhibitor GSK126 Suppresses Antitumor Immunity by Driving Production of Myeloid-Derived Suppressor Cells. 2019 , 79, 2009-2020	64
479	Unravelling Intratumoral Heterogeneity through High-Sensitivity Single-Cell Mutational Analysis and Parallel RNA Sequencing. 2019 , 73, 1292-1305.e8	113
478	Combined quantification of intracellular (phospho-)proteins and transcriptomics from fixed single cells. 2019 , 9, 1469	37
477	Arc/Arg3.1 defines dendritic cells and Langerhans cells with superior migratory ability independent of phenotype and ontogeny in mice. 2019 , 49, 724-736	4
476	Heterogeneity of neutrophils. 2019 , 19, 255-265	207
475	Emerging Principles in Myelopoiesis at Homeostasis and during Infection and Inflammation. <i>Immunity</i> , 2019 , 50, 288-301	32.3 51
474	Early lineage specification defines alveolar epithelial ontogeny in the murine lung. 2019 , 116, 4362-4371	57
473	Dendritic Cell Regulation of Graft-Vs.-Host Disease: Immunostimulation and Tolerance. 2019 , 10, 93	25
472	Understanding blood and its components. 2019 ,	
471	Entendiendo la sangre y sus componentes. 2019 ,	
470	Dropout imputation and batch effect correction for single-cell RNA sequencing data. 2019 , 2, 169-177	0
469	Sptlc1 is essential for myeloid differentiation and hematopoietic homeostasis. 2019 , 3, 3635-3649	2
468	To be red or white: lineage commitment and maintenance of the hematopoietic system by the "inner myeloid". 2019 , 104, 1919-1927	14
467	Transcriptional control of dendritic cell development and functions. 2019 , 349, 55-151	29

466	Growing old in the age of heterogeneity: the perils of shifting clonality. 2019 , 26, 222-227		1
465	Emerging single-cell tools are primed to reveal functional and molecular heterogeneity in malignant hematopoietic stem cells. 2019 , 26, 214-221		6
464	Theory of cell fate. 2020 , 12, e1471		6
463	Exploring single-cell data with deep multitasking neural networks. 2019 , 16, 1139-1145		98
462	Ontogenic Changes in Hematopoietic Hierarchy Determine Pediatric Specificity and Disease Phenotype in Fusion Oncogene-Driven Myeloid Leukemia. 2019 , 9, 1736-1753		19
461	Visualizing structure and transitions in high-dimensional biological data. 2019 , 37, 1482-1492		199
460	CD45 expression discriminates waves of embryonic megakaryocytes in the mouse. 2019 , 104, 1853-1865		6
459	Single-Cell Transcriptomic Analysis of Human Lung Provides Insights into the Pathobiology of Pulmonary Fibrosis. 2019 , 199, 1517-1536		470
458	BloodSpot: a database of healthy and malignant haematopoiesis updated with purified and single cell mRNA sequencing profiles. <i>Nucleic Acids Research</i> , 2019 , 47, D881-D885	20.1	76
457	Single-cell RNA sequencing in facioscapulohumeral muscular dystrophy disease etiology and development. 2019 , 28, 1064-1075		27
456	The Myeloid Cell Compartment-Cell by Cell. 2019 , 37, 269-293		72
455	A topological view of human CD34 cell state trajectories from integrated single-cell output and proteomic data. 2019 , 133, 927-939		8
454	Single-cell screening using microfluidic systems. 2019 , 353-367		2
453	Single-cell analyses demonstrate that a heme-GATA1 feedback loop regulates red cell differentiation. 2019 , 133, 457-469		13
452	DensityPath: an algorithm to visualize and reconstruct cell state-transition path on density landscape for single-cell RNA sequencing data. <i>Bioinformatics</i> , 2019 , 35, 2593-2601	7.2	12
451	Erythropoiesis, EPO, macrophages, and bone. 2019 , 119, 36-41		20
450	Systems immunology allows a new view on human dendritic cells. 2019 , 86, 15-23		11
449	Human dendritic cell immunodeficiencies. 2019 , 86, 50-61		16

448	New paradigms on hematopoietic stem cell differentiation. 2020 , 11, 34-44		47
447	Learning Low-Dimensional Latent Graph Structures: A Density Estimation Approach. 2020 , 31, 1098-1112		2
446	LSD1-mediated repression of GFI1 super-enhancer plays an essential role in erythroleukemia. 2020 , 34, 746-758		10
445	BEM: Mining Coregulation Patterns in Transcriptomics via Boolean Matrix Factorization. <i>Bioinformatics</i> , 2020 , 36, 4030-4037	7.2	6
444	Role of Dendritic Cells in Exposing Latent HIV-1 for the Kill. 2019 , 12,		4
443	Realistic in silico generation and augmentation of single-cell RNA-seq data using generative adversarial networks. <i>Nature Communications</i> , 2020 , 11, 166	17.4	48
442	scRNA-seq assessment of the human lung, spleen, and esophagus tissue stability after cold preservation. 2019 , 21, 1		161
441	Tracking the immune response with single-cell genomics. 2020 , 38, 4487-4490		5
440	Revealing dynamics of gene expression variability in cell state space. 2020 , 17, 45-49		26
439	The complexity of neutrophils in health and disease: Focus on cancer. 2020 , 48, 101409		10
438	A new lymphoid-primed progenitor marked by Dach1 downregulation identified with single cell multi-omics. <i>Nature Immunology</i> , 2020 , 21, 1574-1584	19.1	4
437	Single-cell molecular profiling provides a high-resolution map of basophil and mast cell development. 2021 , 76, 1731-1742		6
436	The Whole Body as the System in Systems Immunology. 2020 , 23, 101509		12
435	Iterative transfer learning with neural network for clustering and cell type classification in single-cell RNA-seq analysis. 2020 , 2, 607-618		23
434	Neutrophil diversity and plasticity in tumour progression and therapy. 2020 , 20, 485-503		178
433	Hematopoietic Stem Cells in Health and Disease Insights from Single-Cell Multi-omic Approaches. 2020 , 6, 67-76		7
432	Single-cell lineage tracing unveils a role for TCF15 in haematopoiesis. 2020 , 583, 585-589		41
431	The stem/progenitor landscape is reshaped in a mouse model of essential thrombocythemia and causes excess megakaryocyte production. 2020 , 6,		3

430	Basophils and their effector molecules in allergic disorders. 2021 , 76, 1693-1706		5
429	Comprehensive analysis of single-cell RNA sequencing data from healthy human marrow hematopoietic cells. 2020 , 13, 514		0
428	Negative Regulation of the Differentiation of Flk2 CD34 LSK Hematopoietic Stem Cells by EKLF/KLF1. 2020 , 21,		0
427	Wnt-5A/B Signaling in Hematopoiesis throughout Life. 2020 , 9,		2
426	Coupled scRNA-Seq and Intracellular Protein Activity Reveal an Immunosuppressive Role of TREM2 in Cancer. <i>Cell</i> , 2020 , 182, 872-885.e19	56.2	106
425	Network Approaches for Dissecting the Immune System. 2020 , 23, 101354		11
424	The Role of Dendritic Cells During Infections Caused by Highly Prevalent Viruses. 2020 , 11, 1513		16
423	Control of GM-CSF-Dependent Dendritic Cell Differentiation and Maturation by DEF6 and SWAP-70. 2020 , 205, 1306-1317		2
422	Differential IRF8 Transcription Factor Requirement Defines Two Pathways of Dendritic Cell Development in Humans. <i>Immunity</i> , 2020 , 53, 353-370.e8	32.3	61
421	Single-cell transcriptome profiling reveals neutrophil heterogeneity in homeostasis and infection. <i>Nature Immunology</i> , 2020 , 21, 1119-1133	19.1	94
420	Plasticity of monocyte development and monocyte fates. 2020 , 227, 66-78		10
419	Efferocytic Defects in Early Atherosclerosis Are Driven by GATA2 Overexpression in Macrophages. 2020 , 11, 594136		8
418	M. tuberculosis Reprograms Hematopoietic Stem Cells to Limit Myelopoiesis and Impair Trained Immunity. <i>Cell</i> , 2020 , 183, 752-770.e22	56.2	60
417	Constructing and deconstructing GATA2-regulated cell fate programs to establish developmental trajectories. 2020 , 217,		8
416	Single-Cell Analysis of Neonatal HSC Ontogeny Reveals Gradual and Uncoordinated Transcriptional Reprogramming that Begins before Birth. 2020 , 27, 732-747.e7		17
415	Infrapatellar Fat Pad/Synovium Complex in Early-Stage Knee Osteoarthritis: Potential New Target and Source of Therapeutic Mesenchymal Stem/Stromal Cells. 2020 , 8, 860		21
414	Unraveling Hematopoiesis through the Lens of Genomics. <i>Cell</i> , 2020 , 182, 1384-1400	56.2	39
413	Transfer learning efficiently maps bone marrow cell types from mouse to human using single-cell RNA sequencing. 2020 , 3, 736		5

412	Characterization and generation of human definitive multipotent hematopoietic stem/progenitor cells. 2020 , 6, 89		8
411	Androgen Receptor Signaling Positively Regulates Monocytic Development. 2020 , 11, 519383		2
410	A rank-based marker selection method for high throughput scRNA-seq data. 2020 , 21, 477		6
409	Predicting single-cell gene expression profiles of imaging flow cytometry data with machine learning. <i>Nucleic Acids Research</i> , 2020 , 48, 11335-11346	20.1	6
408	Differentiation of transplanted haematopoietic stem cells tracked by single-cell transcriptomic analysis. 2020 , 22, 630-639		22
407	The quest for faithful in vitro models of human dendritic cells types. 2020 , 123, 40-59		6
406	Two-Faced Roles of Tumor-Associated Neutrophils in Cancer Development and Progression. 2020 , 21,		32
405	Temporal expression of MOF acetyltransferase primes transcription factor networks for erythroid fate. 2020 , 6, eaaz4815		12
404	One too many: the surprising heterogeneity of Drosophila macrophages. <i>EMBO Journal</i> , 2020 , 39, e105199		2
403	Reconstructing human DC, monocyte and macrophage development in utero using single cell technologies. 2020 , 123, 1-6		1
402	Deep learning enables accurate clustering with batch effect removal in single-cell RNA-seq analysis. <i>Nature Communications</i> , 2020 , 11, 2338	17.4	58
401	Single-cell technologies in hepatology: new insights into liver biology and disease pathogenesis. 2020 , 17, 457-472		44
400	Targeted Perturb-seq enables genome-scale genetic screens in single cells. 2020 , 17, 629-635		41
399	Towards the better understanding of myelopoiesis using single-cell technologies. 2020 , 122, 186-192		8
398	In-vivo differentiation of adult hematopoietic stem cells from a single-cell point of view. 2020 , 27, 241-247		2
397	Single-molecule imaging of transcription dynamics in somatic stem cells. 2020 , 583, 431-436		20
396	Transcriptional, Epigenetic and Metabolic Programming of Tumor-Associated Macrophages. 2020 , 12,		29
395	Gene regulation inference from single-cell RNA-seq data with linear differential equations and velocity inference. <i>Bioinformatics</i> , 2020 , 36, 4774-4780	7.2	20

394	Quantitative proteomics reveals specific metabolic features of acute myeloid leukemia stem cells. 2020 , 136, 1507-1519		22
393	Understanding immune system development: An epigenetic perspective. 2020 , 39-76		
392	Advances in single-cell epigenomics of the immune system. 2020 , 185-216		0
391	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. <i>Nature Communications</i> , 2020 , 11, 1407	17.4	6
390	Inferring Causal Gene Regulatory Networks from Coupled Single-Cell Expression Dynamics Using Scribe. 2020 , 10, 265-274.e11		36
389	Imputation of single-cell gene expression with an autoencoder neural network. 2020 , 8, 78-94		16
388	Trajectory-based differential expression analysis for single-cell sequencing data. <i>Nature Communications</i> , 2020 , 11, 1201	17.4	86
387	Dissecting cellular crosstalk by sequencing physically interacting cells. 2020 , 38, 629-637		77
386	FB5P-seq: FACS-Based 5-Prime End Single-Cell RNA-seq for Integrative Analysis of Transcriptome and Antigen Receptor Repertoire in B and T Cells. 2020 , 11, 216		11
385	Human Intestinal Mononuclear Phagocytes in Health and Inflammatory Bowel Disease. 2020 , 11, 410		25
384	Dendritic cell development in infection. 2020 , 121, 111-117		13
383	DNA methylation disruption reshapes the hematopoietic differentiation landscape. 2020 , 52, 378-387		63
382	A conserved dendritic-cell regulatory program limits antitumour immunity. 2020 , 580, 257-262		179
381	MicroRNAs organize intrinsic variation into stem cell states. 2020 , 117, 6942-6950		10
380	Robust and Scalable Learning of Complex Intrinsic Dataset Geometry via ELPiGraph. 2020 , 22,		16
379	Transcriptional and Functional Analysis of CD1c Human Dendritic Cells Identifies a CD163 Subset Priming CD8CD103 T Cells. <i>Immunity</i> , 2020 , 53, 335-352.e8	32.3	91
378	Flexible experimental designs for valid single-cell RNA-sequencing experiments allowing batch effects correction. <i>Nature Communications</i> , 2020 , 11, 3274	17.4	7
377	Single-cell analyses and machine learning define hematopoietic progenitor and HSC-like cells derived from human PSCs. 2020 , 136, 2893-2904		16

376	The Source and Dynamics of Adult Hematopoiesis: Insights from Lineage Tracing. 2020 , 36, 529-550		12
375	scIGANs: single-cell RNA-seq imputation using generative adversarial networks. <i>Nucleic Acids Research</i> , 2020 , 48, e85	20.1	24
374	Exploring Epigenetic Drugs in the Regulation of Inflammatory Autoimmune Diseases. 2020 ,		1
373	Cancer-associated fibroblast compositions change with breast cancer progression linking the ratio of S100A4 and PDPN CAFs to clinical outcome.. 2020 , 1, 692-708		53
372	Poincaré maps for analyzing complex hierarchies in single-cell data. <i>Nature Communications</i> , 2020 , 11, 2966	17.4	18
371	The Molecular Anatomy of Mouse Skin during Hair Growth and Rest. 2020 , 26, 441-457.e7		69
370	The ontogenetic path of human dendritic cells. 2020 , 120, 122-129		19
369	Immunology in the Era of Single-Cell Technologies. 2020 , 38, 727-757		27
368	Quantifying Hematopoietic Stem Cell Clonal Diversity by Selecting Informative Amplicon Barcodes. 2020 , 10, 2153		1
367	Advancing Stem Cell Research through Multimodal Single-Cell Analysis. 2020 , 12,		1
366	A benchmark of batch-effect correction methods for single-cell RNA sequencing data. 2020 , 21, 12		238
365	Transcriptional regulation of neutrophil differentiation and function during inflammation. 2020 , 107, 419-430		11
364	Molecular and cellular mechanisms of tooth development, homeostasis and repair. <i>Development (Cambridge)</i> , 2020 , 147,	6.6	49
363	Differentiation of c-Kit CD24 natural killer cells into myeloid cells in a GATA-2-dependent manner. 2020 , 34, 4462-4481		3
362	Neutrophils as emerging therapeutic targets. 2020 , 19, 253-275		177
361	Insights from Patients with Dendritic Cell Immunodeficiency. 2020 , 122, 116-123		3
360	Macrophages: The Potent Immunoregulatory Innate Immune Cells. 2020 ,		19
359	Normal myeloid progenitor cell subset-associated gene signatures for acute myeloid leukaemia subtyping with prognostic impact. 2020 , 15, e0229593		2

358	Hematopoiesis and Cardiovascular Disease. 2020 , 126, 1061-1085	37
357	SMNN: batch effect correction for single-cell RNA-seq data via supervised mutual nearest neighbor detection. 2021 , 22,	8
356	Systems analysis of hematopoiesis using single-cell lineage tracing. 2021 , 28, 18-27	3
355	A primer on single-cell genomics in myeloid biology. 2021 , 28, 11-17	
354	Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. 2021 , 28, 472-487.e7	44
353	Follicular lymphoma dynamics. 2021 , 150, 43-103	4
352	Cancer Cells Resistance Shaping by Tumor Infiltrating Myeloid Cells. 2021 , 13,	6
351	Systems Immunology Approaches for Understanding of Primary Dendritic Cell Subpopulations in the Past, Present and Future. 2021 , 501-510	3
350	Deepgmd: a graph-neural-network-based method to detect gene regulator module. 2021 , PP,	
349	Longitudinal single-cell RNA-seq of hESCs-derived retinal organoids. 2021 , 64, 1661-1676	4
348	Integrated decoding hematopoiesis and leukemogenesis using single-cell sequencing and its medical implication. 2021 , 7, 2	14
347	Functional change along cellular trajectories. <i>Nature Computational Science</i> , 2021 , 1, 102-103	
346	Independent component analysis based gene co-expression network inference (ICAnet) to decipher functional modules for better single-cell clustering and batch integration. <i>Nucleic Acids Research</i> , 2021 , 49, e54	20.1 6
345	Single-cell RNA-seq reveals a concomitant delay in differentiation and cell cycle of aged hematopoietic stem cells. 2021 , 19, 19	2
344	Enabling single-cell trajectory network enrichment. <i>Nature Computational Science</i> , 2021 , 1, 153-163	2
343	Lhx6 regulates canonical Wnt signaling to control the fate of mesenchymal progenitor cells during mouse molar root patterning. 2021 , 17, e1009320	2
342	Identification of resistance pathways and therapeutic targets in relapsed multiple myeloma patients through single-cell sequencing. 2021 , 27, 491-503	27
341	Re-investigation of classic T cell subsets and identification of novel cell subpopulations by single-cell RNA sequencing.	1

340	Squidpy: a scalable framework for spatial single cell analysis.		26
339	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states.		2
338	Macrophages and Their Organ Locations Shape Each Other in Development and Homeostasis - A Perspective. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 630272	5-7	3
337	Leveraging the cell lineage to predict cell-type specificity of regulatory variation from bulk genomics. 2021 , 217,		
336	Identification of leukemic and pre-leukemic stem cells by clonal tracking from single-cell transcriptomics. <i>Nature Communications</i> , 2021 , 12, 1366	17.4	26
335	Connecting the Dots: Resolving the Bone Marrow Niche Heterogeneity. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 622519	5-7	14
334	Single-cell insights into the hematopoietic generation of T-lymphocyte precursors in mouse and human. 2021 , 95, 1-12		3
333	Application of single-cell transcriptomics to kinetoplastid research. 2021 , 148, 1223-1236		6
332	The dynamic interactive network of long non-coding RNAs and chromatin accessibility facilitates erythroid differentiation.		1
331	ACE2 protein expression within isogenic cell lines is heterogeneous and associated with distinct transcriptomes. 2021 ,		1
330	oCEM: Automatic detection and analysis of overlapping co-expressed gene modules.		
329	DTFLOW: Inference and Visualization of Single-cell Pseudotime Trajectory Using Diffusion Propagation. 2021 , 19, 306-318		0
328	High-throughput enrichment and isolation of megakaryocyte progenitor cells from the mouse bone marrow. 2021 , 11, 8268		0
327	PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data. 2021 , 22, 124		4
326	iSMNN: batch effect correction for single-cell RNA-seq data via iterative supervised mutual nearest neighbor refinement. 2021 , 22,		3
325	Hierarchical chromatin regulation during blood formation uncovered by single-cell sortChIC.		1
324	Identification and characterization of human CD34+ and CD34dim/- neutrophil-committed progenitors.		
323	A high-resolution cell atlas of the domestic pig lung and an online platform for exploring lung single-cell data. 2021 , 48, 411-425		4

322	MAT2: Manifold alignment of single-cell transcriptomes with cell triplets. <i>Bioinformatics</i> , 2021 ,	7.2	2
321	Mesenchymal stem cell subpopulations and their heterogeneity of response to inductions revealed by single-cell RNA-seq.		1
320	The neutrotime transcriptional signature defines a single continuum of neutrophils across biological compartments. <i>Nature Communications</i> , 2021 , 12, 2856	17.4	23
319	G2S3: A gene graph-based imputation method for single-cell RNA sequencing data. 2021 , 17, e1009029		4
318	Data-driven modeling predicts gene regulatory network dynamics during the differentiation of multipotential progenitors.		
317	Dissection of floral transition by single-meristem transcriptomes at high temporal resolution. 2021 , 7, 800-813		6
316	Gene expression at a single-molecule level: implications for myelodysplastic syndromes and acute myeloid leukemia. 2021 , 138, 625-636		1
315	The Impact of Representation on the Optimization of Marker Panels for Single-cell RNA Data. 2021 ,		0
314	Single-cell technologies and analyses in hematopoiesis and hematological malignancies. 2021 , 98, 1-13		2
313	Quantitative single-cell proteomics as a tool to characterize cellular hierarchies. <i>Nature Communications</i> , 2021 , 12, 3341	17.4	53
312	Gata2-L359V impairs primitive and definitive hematopoiesis and blocks cell differentiation in murine chronic myelogenous leukemia model. 2021 , 12, 568		1
311	Commitment to dendritic cells and monocytes. 2021 , 33, 815-819		0
310	Non-parametric modelling of temporal and spatial counts data from RNA-seq experiments. <i>Bioinformatics</i> , 2021 ,	7.2	8
309	Assessment of medullary and extramedullary myelopoiesis in cardiovascular diseases. 2021 , 169, 105663		0
308	Distinct transcription factor networks control neutrophil-driven inflammation. <i>Nature Immunology</i> , 2021 , 22, 1093-1106	19.1	14
307	Exploiting Single-Cell Tools in Gene and Cell Therapy. 2021 , 12, 702636		4
306	CD14 Expressing Precursors Give Rise to Highly Functional Conventional Dendritic Cells for Use as Dendritic Cell Vaccine. 2021 , 13,		0
305	Niches that regulate stem cells and hematopoiesis in adult bone marrow. 2021 , 56, 1848-1860		26

304	ACE2 protein expression within isogenic cell lines is heterogeneous and associated with distinct transcriptomes. 2021 , 11, 15900	3
303	Heterogeneity of germinal center B cells: New insights from single-cell studies. 2021 , 51, 2555-2567	2
302	Early megakaryocyte lineage-committed progenitors in adult mouse bone marrow.	
301	Naked Mole-Rat Hematopoietic Stem and Progenitors are Highly Quiescent with an Inherent Myeloid Bias.	0
300	. 2021 , 67, 5963-5996	1
299	The Genetic Network of Forkhead Gene Family in Development of Brown Planthoppers. 2021 , 10,	1
298	Differential requirement for the Polycomb repressor complex 2 in dendritic cell and tissue-resident myeloid cell homeostasis. 2021 , 6, eabf7268	0
297	Efficient production of human neutrophils from iPSCs that prevent murine lethal infection with immune cell recruitment. 2021 ,	1
296	Unraveling the Heterogeneity and Ontogeny of Dendritic Cells Using Single-Cell RNA Sequencing. 2021 , 12, 711329	0
295	Secretory MPP3 reinforce myeloid differentiation trajectory and amplify myeloid cell production.	1
294	Hematopoietic Stem Cells in Wound Healing Response. 2021 ,	0
293	Single-cell analysis at the protein level delineates intracellular signaling dynamic during hematopoiesis. 2021 , 19, 201	1
292	The emerging tale of microglia in psychiatric disorders. 2021 , 131, 1-29	14
291	Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data. 2021 , 17, e1008569	6
290	Probabilistic harmonization and annotation of single-cell transcriptomics data with deep generative models. 2021 , 17, e9620	39
289	Normal Hematopoiesis and Blood Cell Maturation. 2021 , 1-12	
288	Regulatory Dynamics of Cell Differentiation Revealed by True Time Series From Multinucleate Single Cells. 2020 , 11, 612256	2
287	Methods for Single-Cell Isolation and Preparation. <i>Advances in Experimental Medicine and Biology</i> , 2020 , 1255, 7-27	3.6 4

286	Hematopoietic Hierarchy - An Updated Roadmap. 2018 , 28, 976-986	67
285	Visualization and analysis of single-cell RNA-seq data by kernel-based similarity learning.	8
284	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis.	1
283	Integrated time-lapse and single-cell transcription studies highlight the variable and dynamic nature of human hematopoietic cell fate commitment.	1
282	Single-cell epigenomics maps the continuous regulatory landscape of human hematopoietic differentiation.	7
281	Reversed graph embedding resolves complex single-cell developmental trajectories.	32
280	MAGIC: A diffusion-based imputation method reveals gene-gene interactions in single-cell RNA-sequencing data.	42
279	Large-scale simultaneous measurement of epitopes and transcriptomes in single cells.	9
278	Visualizing Structure and Transitions for Biological Data Exploration.	20
277	STRT-seq-2i: dual-index 5' single cell and nucleus RNA-seq on an addressable microwell array.	2
276	Mapping Human Hematopoietic Hierarchy at Single Cell Resolution by Microwell-seq.	1
275	Column subset selection for single-cell RNA-Seq clustering.	1
274	Integrated analysis of single cell transcriptomic data across conditions, technologies, and species.	36
273	Correcting batch effects in single-cell RNA sequencing data by matching mutual nearest neighbours.	13
272	BGP: Branched Gaussian processes for identifying gene-specific branching dynamics in single cell data.	3
271	Cell Lineage and Communication Network Inference via Optimization for Single-cell Transcriptomics.	3
270	Fundamental limits on dynamic inference from single cell snapshots.	7
269	bigScale: An Analytical Framework for Big-Scale Single-Cell Data.	6

268	Assessment of batch-correction methods for scRNA-seq data with a new test metric.	15
267	Heme induces innate immune memory.	4
266	Mapping biology from mouse to man using transfer learning.	2
265	Cancer-associated fibroblast compositions change with breast-cancer progression linking S100A4 and PDPN ratios with clinical outcome.	5
264	scIGANs: single-cell RNA-seq imputation using generative adversarial networks.	4
263	Capybara: A computational tool to measure cell identity and fate transitions.	3
262	CellOracle: Dissecting cell identity via network inference and in silico gene perturbation.	16
261	Optimal tuning of weighted kNN- and diffusion-based methods for denoising single cell genomics data.	0
260	G2S3: a gene graph-based imputation method for single-cell RNA sequencing data.	1
259	Concurrent stem- and lineage-affiliated chromatin programs precede hematopoietic lineage restriction.	1
258	Integrative Single-cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Haematopoiesis.	2
257	Single-cell RNA-seq reveals a concomitant delay in differentiation and cell cycle of aged hematopoietic stem cell.	2
256	CITEseq analysis of non-small-cell lung cancer lesions reveals an axis of immune cell activation associated with tumor antigen load and TP53 mutations.	6
255	Non-parametric modelling of temporal and spatial counts data from RNA-seq experiments.	2
254	singlecellVR: interactive visualization of single-cell data in virtual reality.	1
253	Dimension reduction and denoising of single-cell RNA sequencing data in the presence of observed confounding variables.	4
252	Hematopoietic stem cells self-renew symmetrically or gradually proceed to differentiation.	3
251	Nabo framework to define leukemia-initiating cells and differentiation in single-cell RNA-sequencing data.	1

250	Single-cell multimodal profiling of proteins and chromatin accessibility using PHAGE-ATAC.	7
249	PseudotimeDE: inference of differential gene expression along cell pseudotime with well-calibrated p-values from single-cell RNA sequencing data.	2
248	Graph abstraction reconciles clustering with trajectory inference through a topology preserving map of single cells.	23
247	FateID infers cell fate bias in multipotent progenitors from single-cell RNA-seq data.	2
246	Beyond pseudotime: Following T-cell maturation in single-cell RNAseq time series.	2
245	Exploring Single-Cell Data with Deep Multitasking Neural Networks.	9
244	Interrogation of human hematopoiesis at single-cell and single-variant resolution.	7
243	Reconstructing complex lineage trees from scRNA-seq data using MERLoT.	6
242	FASTGenomics: An analytical ecosystem for single-cell RNA sequencing data.	4
241	DensityPath: a level-set algorithm to visualize and reconstruct cell developmental trajectories for large-scale single-cell RNAseq data.	1
240	Single cell RNA-seq denoising using a deep count autoencoder.	16
239	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data.	4
238	matchScore: Matching Single-Cell Phenotypes Across Tools and Experiments.	8
237	Panoramic stitching of heterogeneous single-cell transcriptomic data.	16
236	Palantir characterizes cell fate continuities in human hematopoiesis.	9
235	Towards inferring causal gene regulatory networks from single cell expression Measurements.	13
234	High throughput droplet single-cell Genotyping of Transcriptomes (GoT) reveals the cell identity dependency of the impact of somatic mutations.	4
233	Gene regulation inference from single-cell RNA-seq data with linear differential equations and velocity inference.	5

232	RISC: robust integration of single-cell RNA-seq datasets with different extents of cell cluster overlap.	1
231	Imputation of single-cell gene expression with an autoencoder neural network.	2
230	Probabilistic Harmonization and Annotation of Single-cell Transcriptomics Data with Deep Generative Models.	14
229	Trajectory-based differential expression analysis for single-cell sequencing data.	9
228	A Human Liver Cell Atlas: Revealing Cell Type Heterogeneity and Adult Liver Progenitors by Single-Cell RNA-sequencing.	1
227	Fate mapping via Ms4a3 expression history traces monocyte-derived cells.	3
226	Combinatorial prediction of marker panels from single-cell transcriptomic data.	1
225	A mechanistic model for the negative binomial distribution of single-cell mRNA counts.	11
224	SMNN: Batch Effect Correction for Single-cell RNA-seq data via Supervised Mutual Nearest Neighbor Detection.	2
223	Identification of drugs for leukaemia differentiation therapy by network pharmacology.	3
222	Combined single-cell and spatial transcriptomics reveals the molecular, cellular and spatial bone marrow niche organization.	3
221	Lung, spleen and oesophagus tissue remains stable for scRNAseq in cold preservation.	6
220	Quantitative Single-Cell Proteomics as a Tool to Characterize Cellular Hierarchies.	12
219	Molecular Cross-Validation for Single-Cell RNA-seq.	9
218	Single-cell transcriptome profiling reveals neutrophil heterogeneity and orchestrated maturation during homeostasis and bacterial infection.	8
217	FB5P-seq: FACS-based 5-prime end single-cell RNAseq for integrative analysis of transcriptome and antigen receptor repertoire in B and T cells.	4
216	The hematopoietic landscape at single-cell resolution reveals unexpected stem cell features in naked mole-rats.	2
215	Integrated time-lapse and single-cell transcription studies highlight the variable and dynamic nature of human hematopoietic cell fate commitment. 2017 , 15, e2001867	26

214	Clonal dominance and transplantation dynamics in hematopoietic stem cell compartments. 2017 , 13, e1005803		14
213	In Vivo Deletion of the Cebpa +37 kb Enhancer Markedly Reduces Cebpa mRNA in Myeloid Progenitors but Not in Non-Hematopoietic Tissues to Impair Granulopoiesis. 2016 , 11, e0150809		17
212	Deciphering the regulatory landscape of fetal and adult T-cell development at single-cell resolution. <i>EMBO Journal</i> , 2020 , 39, e104159	13	12
211	Stat5 deficiency decreases transcriptional heterogeneity and supports emergence of hematopoietic sub-populations. 2017 , 8, 22477-22482		2
210	Visualizing Structure and Transitions for Biological Data Exploration.		7
209	The beneficial effects of varicella zoster virus. 2019 , 3, 016-049		4
208	Clonal tracking of erythropoiesis in rhesus macaques. 2020 , 105, 1813-1824		1
207	The epigenetic landscape of innate immunity. 2017 , 4, 110-139		2
206	Genome-Wide Transcriptional Analysis Reveals Novel AhR Targets That Regulate Dendritic Cell Function during Influenza A Virus Infection. 2019 , 3, 219-235		5
205	The Adaptability of Somatic Stem Cells: A Review. 2017 , 13, 3-13		14
204	Discovering sparse transcription factor codes for cell states and state transitions during development. 2017 , 6,		20
203	Murine HSCs contribute actively to native hematopoiesis but with reduced differentiation capacity upon aging. 2018 , 7,		34
202	Single cell analysis reveals human cytomegalovirus drives latently infected cells towards an anergic-like monocyte state. 2020 , 9,		23
201	Integration of single cell data by disentangled representation learning. <i>Nucleic Acids Research</i> , 2021 ,	20.1	0
200	Regulatory association of long noncoding RNAs and chromatin accessibility facilitates erythroid differentiation. 2021 , 5, 5396-5409		1
199	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. 2021 ,		6
198	Inference of cell state transitions and cell fate plasticity from single-cell with MARGARET.		0
197	Robustness of Visualization Methods in Preserving the Continuous and Discrete Latent Structures of High-Dimensional Single-Cell Data. 2021 ,		0

- 196 Single Cell Transcriptome Conservation in Cryopreserved Cells and Tissues.
- 195 Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms.
- 194 Probabilistic inference of bifurcations in single-cell data using a hierarchical mixture of factor analysers.
- 193 Single Cell Phenotyping Reveals Heterogeneity among Haematopoietic Stem Cells Following Infection.
- 192 Model-based branching point detection in single-cell data by K-Branches clustering.
- 191 Composite measurements and molecular compressed sensing for highly efficient transcriptomics. 3
- 190 Single-cell RNA-Sequencing uncovers transcriptional states and fate decisions in haematopoiesis.
- 189 Challenges and emerging directions in single-cell analysis. 1
- 188 FORKS: Finding Orderings Robustly using k-means and Steiner trees. 1
- 187 Existing and Emerging Molecular Technologies in Myeloid Neoplasms. **2018**, 369-412
- 186 Tree-ensemble analysis tests for presence of multifurcations in single cell data.
- 185 Defining the Transcriptional Landscape during Cytomegalovirus Latency with Single-Cell RNA Sequencing.
- 184 Robust expression variability testing reveals heterogeneous T cell responses. 1
- 183 Hematopoietic stem cells differentiate into restricted myeloid progenitors before cell division.
- 182 Recovering Gene Interactions from Single-Cell Data Using Data Diffusion. 7
- 181 Emergence of the erythroid lineage from multipotent hematopoiesis. 1
- 180 Longitudinal single cell fate of hematopoiesis in vivo using cellular barcoding and DiSNE movie visualization.
- 179 Visualizing and interpreting single-cell gene expression datasets with Similarity Weighted Nonnegative Embedding. 1

178	Combined quantification of intracellular (phospho-)proteins and transcriptomics from fixed single cells.	1
177	Single-cell Transcriptomic Landscape of Nucleated Cells in Umbilical Cord Blood.	0
176	HSCs Contribute Actively to Native Multilineage Hematopoiesis but With Reduced Differentiation Capacity Upon Aging.	
175	Identification of leukemic and pre-leukemic stem cells by clonal tracking from single-cell transcriptomics.	
174	Cell type purification by single-cell transcriptome-trained sorting.	
173	Single-cell analysis of Crohn's disease lesions identifies a pathogenic cellular module associated with resistance to anti-TNF therapy.	0
172	Flexible Experimental Designs for Valid Single-cell RNA-sequencing Experiments Allowing Batch Effects Correction.	0
171	Combination Image Flow Cytometry Reveals Novel Methods for Isolating Megakaryocyte Progenitor Cells.	
170	High-throughput enrichment and isolation of megakaryocyte progenitor cells from the mouse bone marrow.	
169	Single cell transcriptome analysis reveals markers of naïve and lineage-primed hematopoietic progenitors derived from human pluripotent stem cells.	0
168	Information Theoretic Feature Selection Methods for Single Cell RNA-Sequencing.	1
167	Networks of enhancers and microRNAs drive variation in cell states.	
166	Comparison of marker selection methods for high throughput scRNA-seq data.	0
165	GATA2 Expression by Intima-Infiltrating Macrophages Drives Early Atheroma Formation.	
164	Mathematical modeling with single-cell sequencing data.	2
163	Poincaré Maps for Analyzing Complex Hierarchies in Single-Cell Data.	1
162	Single-cell molecular profiling provides a high-resolution map of basophil and mast cell differentiation.	
161	Prokaryotic Single-Cell RNA Sequencing by In Situ Combinatorial Indexing.	3

160	Integrated decoding hematopoiesis and leukemogenesis at single-cell resolution and its clinical implication.	0
159	Nested Stochastic Block Models Applied to the Analysis of Single Cell Data.	1
158	singlecellVR: Interactive Visualization of Single-Cell Data in Virtual Reality. 2021 , 12, 764170	1
157	An analytical framework for interpretable and generalizable single-cell data analysis. 2021 , 18, 1317-1321	1
156	High-resolution Cell Atlas of Domestic Pig Lung and Online Platform Exploring for Lung Single Cell.	0
155	Overlapping Definitive Progenitor Waves Divide and Conquer to Build a Layered Hematopoietic System.	2
154	In Silico Modeling of Metabolic State in Single Th17 Cells Reveals Novel Regulators of Inflammation and Autoimmunity.	6
153	Dendritic Cell-Regulated T Cell Immunity and Tolerance against Acute Myeloid Leukemia. 2020 , 279-296	
152	Regulatory mechanism of megakaryocyte-lineage differentiation in hematopoietic stem cells. 2020 , 31, 479-484	
151	Single cell transcriptional characterization of human megakaryocyte lineage commitment and maturation.	0
150	Multistage hematopoietic stem cell regulation in the mouse: A combined biological and mathematical approach. 2021 , 24, 103399	0
149	Epigenetic plasticity of erythroid progenitors. 2021 , 138, 1646-1648	
148	Deciphering the role of Wnt signaling in acute myeloid leukemia prognosis: how alterations in DNA methylation come into play in patients' prognosis. 2020 , 146, 3097-3109	0
147	DTFLOW: Inference and Visualization of Single-cell Pseudo-temporal Trajectories Using Diffusion Propagation.	
146	True time series of gene expression from multinucleate single cells reveal essential information on the regulatory dynamics of cell differentiation.	
145	iSMNN: Batch Effect Correction for Single-cell RNA-seq data via Iterative Supervised Mutual Nearest Neighbor Refinement.	1
144	Single-Cell Transcriptomic Analysis of Hematopoietic Cells. 2021 , 2185, 135-158	0
143	Single cell sequencing reveals cell populations that predict primary resistance to imatinib in chronic myeloid leukemia. 2020 , 12, 25337-25355	1

142	Dirichlet Process Mixture Model for Correcting Technical Variation in Single-Cell Gene Expression Data. 2016 , 48, 1070-1079		38
141	Diversity of human NK cell developmental pathways defined by single-cell analyses. 2021 , 74, 106-111		0
140	Macrophages in Microbial Pathogenesis: Commonalities of Defense Evasion Mechanisms. 2021 , IAI0029121		
139	Single-Cell Genomics: Enabling the Functional Elucidation of Infectious Diseases in Multi-Cell Genomes. 2021 , 10,		
138	Nested Stochastic Block Models applied to the analysis of single cell data. 2021 , 22, 576		0
137	AWGAN: A Powerful Batch Correction Model for scRNA-seq Data.		
136	Single-cell analysis of human non-small cell lung cancer lesions refines tumor classification and patient stratification. <i>Cancer Cell</i> , 2021 ,	24.3	15
135	The EHA Research Roadmap: Normal Hematopoiesis. 2021 , 5, e669		0
134	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states. <i>Nature Immunology</i> , 2021 , 22, 1577-1589	19.1	14
133	CD62L expression level determines the cell fate of myeloid progenitors. 2021 ,		1
132	Adversarial domain translation networks enable fast and accurate large-scale atlas-level single-cell data integration.		0
131	Hematopoiesis under telomere attrition at the single-cell resolution. <i>Nature Communications</i> , 2021 , 12, 6850	17.4	1
130	Evaluating microglial phenotypes using single-cell technologies. 2021 ,		1
129	Comprehensive mapping of the alternative polyadenylation site usage and its dynamics at single cell resolution.		
128	Secretory MPP3 Reinforce Myeloid Differentiation Trajectory and Amplify Myeloid Cell Production.		
127	oCEM: Automatic detection and analysis of overlapping co-expressed gene modules.. 2022 , 23, 39		2
126	Ensemble Feature Selection for Single Cell Chromatin Conformation Analysis. 2021 ,		
125	Isolation of Murine Myeloid Progenitor Populations by CD34/CD150 Surface Markers.. 2022 , 11,		0

124	Revisiting hematopoiesis: applications of the bulk and single-cell transcriptomics dissecting transcriptional heterogeneity in hematopoietic stem cells.. 2022,		1
123	The journey of neutropoiesis: how complex landscapes in bone marrow guide continuous neutrophil lineage determination.. 2022,		0
122	Data-driven modeling predicts gene regulatory network dynamics during the differentiation of multipotential hematopoietic progenitors.. 2022, 18, e1009779		0
121	Chemokines as Regulators of Neutrophils: Focus on Tumors, Therapeutic Targeting, and Immunotherapy.. 2022, 14,		0
120	Single-Cell Sequencing Facilitates Elucidation of HIV Immunopathogenesis: A Review of Current Literature.. 2022, 13, 828860		0
119	Single-Cell Technologies to Decipher the Immune Microenvironment in Myeloid Neoplasms: Perspectives and Opportunities.. 2021, 11, 796477		
118	A Proteomic Platform Enables to Test for AML Normalization .. 2022, 10, 826346		0
117	The horizon of bone organoid: A perspective on construction and application.. 2022, 18, 15-25		7
116	SpatialCorr: Identifying Gene Sets with Spatially Varying Correlation Structure.		0
115	From nasal to basal: single-cell sequencing of the bursa of Fabricius highlights the IBDV infection mechanism in chickens.. 2021, 11, 212		1
114	Enlightenment From Biology of Postnatal Limb Development on Pathology of Osteoarthritis.		
113	Oncogenes and the Origins of Leukemias.. 2022, 23,		1
112	Ulcerative colitis is characterized by a plasmablast-skewed humoral response associated with disease activity.. 2022,		2
111	HOTTIP-dependent R-loop formation regulates CTCF boundary activity and TAD integrity in leukemia.. 2022, 82, 833-851.e11		3
110	Single-cell RNA sequencing data analysis based on non-uniform neighborhood network.. <i>Bioinformatics, 2022,</i>	7.2	1
109	Dictionary learning for integrative, multimodal, and scalable single-cell analysis.		0
108	Deciphering the Heterogeneity of Mitochondrial Functions During Hematopoietic Lineage Differentiation.. 2022, 1		0
107	Single-cell immunology: Past, present, and future.. <i>Immunity, 2022, 55, 393-404</i>	32.3	7

106	Protein Tyrosine Phosphatase PTPRO Signaling Couples Metabolic States to Control the Development of Granulocyte Progenitor Cells.. 2022 ,		1
105	HMGA1 Chromatin Regulators Induce Transcriptional Networks Involved in GATA2 and Proliferation During MPN Progression.. 2022 ,		0
104	Impact of duration of neoadjuvant aromatase inhibitors on molecular expression profiles in estrogen receptor positive breast cancers.. 2021 ,		0
103	Degree of Freedom of Gene Expression in <i>Saccharomyces cerevisiae</i> .. 2022 , e0083821		
102	Integrating transcription-factor abundance with chromatin accessibility in human erythroid lineage commitment.. 2022 , 2,		1
101	Single-cell data analysis in the browser.		0
100	Capybara: A computational tool to measure cell identity and fate transitions.. 2022 ,		1
99	Statistical and machine learning methods to study human CD4 T cell proteome profiles.. 2022 , 245, 8-17		0
98	Integration of Multiple scRNA-Seq Datasets on the Autoencoder Latent Space. 2021 ,		1
97	Neutrophil Homeostasis and Emergency Granulopoiesis: The Example of Systemic Juvenile Idiopathic Arthritis.. 2021 , 12, 766620		1
96	CellVGAE: an unsupervised scRNA-seq analysis workflow with graph attention networks. <i>Bioinformatics</i> , 2021 ,	7.2	1
95	Single-cell multi-omic velocity infers dynamic and decoupled gene regulation.		0
94	Reinvestigation of Classic T Cell Subsets and Identification of Novel Cell Subpopulations by Single-Cell RNA Sequencing.. 2021 ,		2
93	Deep learning tackles single-cell analysis-a survey of deep learning for scRNA-seq analysis.. 2021 ,		0
92	Alzheimer's disease modification mediated by bone marrow-derived macrophages via a TREM2-independent pathway in mouse model of amyloidosis. 2022 , 2, 60-73		2
91	One Cell At a Time (OCAT): a unified framework to integrate and analyze single-cell RNA-seq data.. 2022 , 23, 102		0
90	Table_1.DOCX. 2018 ,		
89	Data_Sheet_1.ZIP. 2021 ,		

88	Data_Sheet_2.PDF. 2021 ,		
87	Data_Sheet_1.pdf. 2020 ,		
86	DataSheet_1.pdf. 2020 ,		
85	data_sheet_1.PDF. 2018 ,		
84	table_1.xlsx. 2018 ,		
83	table_2.docx. 2018 ,		
82	Presentation_1.pdf. 2020 ,		
81	CD66bCD64CD115 cells in the human bone marrow represent neutrophil-committed progenitors.. <i>Nature Immunology</i> , 2022 ,	19.1	2
80	Stem Cells, Hematopoiesis and Lineage Tracing: Transplantation-Centric Views and Beyond.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 903528	5.7	1
79	The origins and roles of osteoclasts in bone development, homeostasis and repair.. <i>Development (Cambridge)</i> , 2022 , 149,	6.6	2
78	Beyond Pairwise Interactions: Higher-Order Dynamics in Protein Interaction Networks.		
77	DAE-TPGM: A deep autoencoder network based on a two-part-gamma model for analyzing single-cell RNA-seq data.. <i>Computers in Biology and Medicine</i> , 2022 , 146, 105578	7	0
76	Tumor-directed dysregulation of erythroid progenitors drives immunosuppressive myeloid cells. <i>Cancer Cell</i> , 2022 ,	24.3	0
75	Tumor-induced erythroid precursor-differentiated myeloid cells mediate immunosuppression and curtail anti-PD-1/PD-L1 treatment efficacy. <i>Cancer Cell</i> , 2022 ,	24.3	2
74	Adversarial domain translation networks for integrating large-scale atlas-level single-cell datasets. <i>Nature Computational Science</i> , 2022 , 2, 317-330		0
73	Lack of evidence for increased transcriptional noise in aged tissues.		0
72	Toll-like receptor 9 deficiency induces osteoclastic bone loss via gut microbiota-associated systemic chronic inflammation. <i>Bone Research</i> , 2022 , 10,	13.3	3
71	Comparison of cell state models derived from single-cell RNA sequencing data: graph versus multi-dimensional space. <i>Mathematical Biosciences and Engineering</i> , 2022 , 19, 8505-8536	2.1	

70	Inference of cell state transitions and cell fate plasticity from single-cell with MARGARET. <i>Nucleic Acids Research</i> ,	20.1	0
69	A comparison of marker gene selection methods for single-cell RNA sequencing data.		1
68	Forest Fire Clustering for single-cell sequencing combines iterative label propagation with parallelized Monte Carlo simulations. <i>Nature Communications</i> , 2022 , 13,	17.4	
67	Characterization of naked mole-rat hematopoiesis reveals unique stem and progenitor cell patterns and neotenic traits. <i>EMBO Journal</i> ,	13	0
66	Ly6D+Siglec-H+ precursors contribute to conventional dendritic cells via a Zbtb46+Ly6D+ intermediary stage. <i>Nature Communications</i> , 2022 , 13,	17.4	2
65	Microfluidics for Cancer Biomarker Discovery, Research, and Clinical Application. <i>Advances in Experimental Medicine and Biology</i> , 2022 , 499-524	3.6	0
64	Intratumoral mregDC and CXCL13 T helper niches enable local differentiation of CD8 T cells following PD-1 blockade.		1
63	ResPAN: a powerful batch correction model for scRNA-seq data through residual adversarial networks. <i>Bioinformatics</i> ,	7.2	
62	A deep matrix factorization based approach for single-cell RNA-seq data clustering. <i>Methods</i> , 2022 , 205, 114-122	4.6	0
61	Transcription factors TCF-1 and GATA3 are key factors for the epigenetic priming of early innate lymphoid progenitors toward distinct cell fates. <i>Immunity</i> , 2022 ,	32.3	0
60	Cas9+ conditionally immortalized neutrophil progenitors as a tool for genome wide CRISPR screening for neutrophil differentiation and function.		
59	ACUTE AND SUSTAINED ALTERATIONS TO THE BONE MARROW IMMUNE MICROENVIRONMENT FOLLOWING POLYMICROBIAL INFECTION. 2022 , 58, 45-55		
58	SlowMoMan: A web app for discovery of important features along user-drawn trajectories in 2D embeddings.		
57	Targeting the EIF2AK1 signaling pathway rescues red blood cell production in SF3B1-mutant myelodysplastic syndromes with ringed sideroblasts.		0
56	Identification of the Differentiation Stages of Living Cells from the Six Most Immature Murine Hematopoietic Cell Populations by Multivariate Analysis of Single-Cell Raman Spectra.		
55	Nucleotide depletion promotes cell fate transitions by inducing DNA replication stress.		0
54	Biologics and airway remodeling in severe asthma.		2
53	A Deep Learning Pipeline for the Automatic cell type Assignment of scRNA-seq Data. 2022 ,		

52	Multi-objective Optimization for Marker Panel Identification in Single-cell Data. 2022,	
51	SMaSH: a scalable, general marker gene identification framework for single-cell RNA-sequencing. 2022, 23,	1
50	Dimensionality reduction for visualizing high-dimensional biological data. 2022, 220, 104749	0
49	The Role of Epigenetics in Autoimmune Disorders. 2023, 715-736	0
48	Joint Analysis of Transcriptome and Proteome Measurements in Single Cells with totalVI. 2022, 63-85	0
47	Clonally resolved single-cell multi-omics identifies routes of cellular differentiation in acute myeloid leukemia.	0
46	Image-seq: spatially-resolved single cell sequencing guided by in situ and in vivo imaging.	0
45	Murine fetal bone marrow does not support functional hematopoietic stem and progenitor cells until birth. 2022, 13,	0
44	Protein Arginine Methyltransferase 1 in the Generation of Immune Megakaryocytes: A Perspective Review. 2022, 102517	0
43	Splenic red pulp macrophages provide a niche for CML stem cells and induce therapy resistance.	0
42	Single Cell Genomics - a new chapter in how technological advances propel Hemato-Oncology.	0
41	A unified framework of realistic in silico data generation and statistical model inference for single-cell and spatial omics.	0
40	EBF1 primes B-lymphoid enhancers and limits the myeloid bias in murine multipotent progenitors. 2022, 219,	1
39	A time and single-cell resolved model of hematopoiesis.	0
38	Defining mast cell differentiation and heterogeneity through single-cell transcriptomics analysis. 2022, 150, 739-747	1
37	Robust and easy-to-use one pot workflow for label free single cell proteomics.	0
36	Expression of terminal deoxynucleotidyl transferase (TdT) identifies lymphoid-primed progenitors in human bone marrow.	0
35	Multi-omic single-cell velocity models epigenome-transcriptome interactions and improves cell fate prediction.	0

34	Revealing key regulators of neutrophil function during inflammation by re-analysing single-cell RNA-seq. 2022 , 17, e0276460	1
33	Single Cell Transcriptomics to Understand HSC Heterogeneity and Its Evolution upon Aging. 2022 , 11, 3125	1
32	SPEED: Single-cell Pan-species atlas in the light of Ecology and Evolution for Development and Diseases.	2
31	Alignment of single-cell trajectory trees with CAPITAL. 2022 , 13,	0
30	Notch activation during early mesoderm induction modulates emergence of the T/NK cell lineage from human iPSCs. 2022 ,	0
29	A Myb enhancer-guided analysis of basophil and mast cell differentiation. 2022 , 13,	0
28	Image-seq: spatially resolved single-cell sequencing guided by in situ and in vivo imaging. 2022 , 19, 1622-1633	0
27	Role of YAP as a Mechanosensing Molecule in Stem Cells and Stem Cell-Derived Hematopoietic Cells. 2022 , 23, 14634	0
26	Quo Vadis? Immunodynamics of Myeloid Cells after Myocardial Infarction. 2022 , 23, 15814	1
25	SCIBER: a simple method for removing batch effects from single-cell RNA-sequencing data.	0
24	Integration of scATAC-Seq with scRNA-Seq Data. 2023 , 293-310	0
23	SpatialCorr identifies gene sets with spatially varying correlation structure. 2022 , 2, 100369	1
22	Bone Microenvironment. 2023 , 1-41	0
21	Hypergraph geometry reflects higher-order dynamics in protein interaction networks. 2022 , 12,	0
20	Single-cell sortChIC identifies hierarchical chromatin dynamics during hematopoiesis.	0
19	MAGNET: A web-based application for gene set enrichment analysis using macrophage data sets. 2023 , 18, e0272166	0
18	Deciphering postnatal limb development at single-cell resolution. 2023 , 26, 105808	0
17	Lack of evidence for increased transcriptional noise in aged tissues. 11,	1

16	Epigenetic remodeling of the immune landscape in cancer: therapeutic hurdles and opportunities. 2023 , 30,	1
15	Into the multi-omics era: Progress of T cells profiling in the context of solid organ transplantation. 14,	0
14	Metabolically Primed Multipotent Hematopoietic Progenitors Fuel Innate Immunity.	0
13	Hemopoietic Stem Cell and Initial Stages of Hemopoiesis: Research Methods and Modern Concepts. 2022 , 53, 389-404	0
12	Repurposing the Memory-promoting Meclofenoxate Hydrochloride as a Treatment for Parkinson's Disease through Integrative Multi-omics analysis.	0
11	MicroRNA-221/222-expression in HSC and MPP safeguards their quiescence and multipotency by downregulating stress-independent and dependent expression of IEG and of several myelo/granulopoiesis-enhancing target genes.	0
10	Dissecting cell identity via network inference and in silico gene perturbation. 2023 , 614, 742-751	1
9	The Application of Single-Cell RNA Sequencing in the Inflammatory Tumor Microenvironment. 2023 , 13, 344	0
8	GATA1 knockout in human pluripotent stem cells generates enhanced neutrophils to investigate extracellular trap formation.	0
7	Robust and Easy-to-Use One-Pot Workflow for Label-Free Single-Cell Proteomics. 2023 , 95, 4435-4445	1
6	Complex hierarchical structures in single-cell genomics data unveiled by deep hyperbolic manifold learning. 2023 , 33, 232-246	0
5	Temporal multimodal single-cell profiling of native hematopoiesis illuminates altered differentiation trajectories with age. 2023 , 42, 112304	0
4	Targeting MCL1-driven anti-apoptotic pathways to overcome hypomethylating agent resistance in RAS-mutated chronic myelomonocytic leukemia.	0
3	RNA binding protein SYNCRIP maintains proteostasis and self-renewal of hematopoietic stem and progenitor cells. 2023 , 14,	0
2	Secretory MPP3 reinforce myeloid differentiation trajectory and amplify myeloid cell production. 2023 , 220,	0
1	Origin and Heterogeneity of Tissue Myeloid Cells: A Focus on GMP-Derived Monocytes and Neutrophils. 2023 , 41, 375-404	0