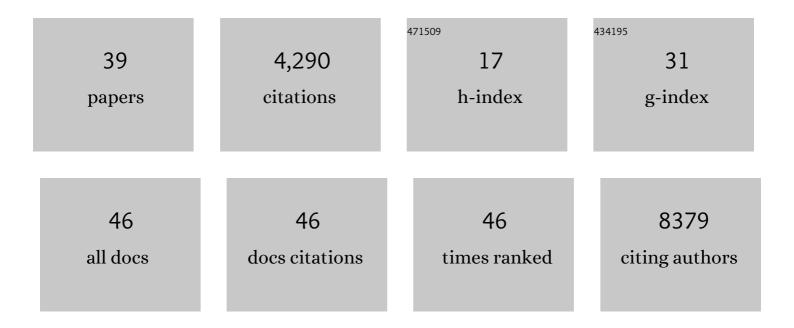
Simon Haas

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2025124/publications.pdf Version: 2024-02-01



SIMON HAAS

#	Article	IF	CITATIONS
1	Transcriptional Heterogeneity and Lineage Commitment in Myeloid Progenitors. Cell, 2015, 163, 1663-1677.	28.9	875
2	Braveheart, a Long Noncoding RNA Required for Cardiovascular Lineage Commitment. Cell, 2013, 152, 570-583.	28.9	839
3	Combined single-cell and spatial transcriptomics reveal the molecular, cellular and spatial bone marrow niche organization. Nature Cell Biology, 2020, 22, 38-48.	10.3	521
4	Identification of Regulatory Networks in HSCs and Their Immediate Progeny via Integrated Proteome, Transcriptome, and DNA Methylome Analysis. Cell Stem Cell, 2014, 15, 507-522.	11.1	439
5	Inflammation-Induced Emergency Megakaryopoiesis Driven by Hematopoietic Stem Cell-like Megakaryocyte Progenitors. Cell Stem Cell, 2015, 17, 422-434.	11.1	353
6	DNMT and HDAC inhibitors induce cryptic transcription start sites encoded in long terminal repeats. Nature Genetics, 2017, 49, 1052-1060.	21.4	235
7	Causes and Consequences of Hematopoietic Stem Cell Heterogeneity. Cell Stem Cell, 2018, 22, 627-638.	11.1	233
8	Myc Depletion Induces a Pluripotent Dormant State Mimicking Diapause. Cell, 2016, 164, 668-680.	28.9	209
9	Decline in IGF1 in the bone marrow microenvironment initiates hematopoietic stem cell aging. Cell Stem Cell, 2021, 28, 1473-1482.e7.	11.1	87
10	Single-cell proteo-genomic reference maps of the hematopoietic system enable the purification and massive profiling of precisely defined cell states. Nature Immunology, 2021, 22, 1577-1589.	14.5	76
11	Identification of leukemic and pre-leukemic stem cells by clonal tracking from single-cell transcriptomics. Nature Communications, 2021, 12, 1366.	12.8	69
12	Identification of DNA methylation changes at <i>cis</i> -regulatory elements during early steps of HSC differentiation using tagmentation-based whole genome bisulfite sequencing. Cell Cycle, 2014, 13, 3476-3487.	2.6	39
13	IFNα-mediated remodeling of endothelial cells in the bone marrow niche. Haematologica, 2017, 102, 445-453.	3.5	35
14	Extracellular matrix protein Matrilin-4 regulates stress-induced HSC proliferation via CXCR4. Journal of Experimental Medicine, 2016, 213, 1961-1971.	8.5	29
15	Antigen presentation safeguards the integrity of the hematopoietic stem cell pool. Cell Stem Cell, 2022, 29, 760-775.e10.	11.1	29
16	Activated SUMOylation restricts MHC class I antigen presentation to confer immune evasion in cancer. Journal of Clinical Investigation, 2022, 132, .	8.2	22
17	Lineage commitment of hematopoietic stem cells and progenitors: insights from recent single cell and lineage tracing technologies. Experimental Hematology, 2020, 88, 1-6.	0.4	21
18	Cancer stem cells: The adventurous journey from hematopoietic to leukemic stem cells. Cell, 2022, 185, 1266-1270.	28.9	19

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#	Article	IF	CITATIONS
19	Technical considerations for the use of CRISPR/Cas9 in hematology research. Experimental Hematology, 2017, 54, 4-11.	0.4	18
20	Single-cell and spatial transcriptomics approaches of the bone marrow microenvironment. Current Opinion in Oncology, 2020, 32, 146-153.	2.4	18
21	An Intrinsic Interferon Program Protects Stem Cells from Viral Infection. Developmental Cell, 2018, 44, 279-280.	7.0	8
22	Hematopoietic Stem Cells in Health and Disease—Insights from Single-Cell Multi-omic Approaches. Current Stem Cell Reports, 2020, 6, 67-76.	1.6	8
23	Single-cell lineage tracing approaches in hematology research: technical considerations. Experimental Hematology, 2020, 89, 26-36.	0.4	3
24	A Stem Cell-Based Epigenetic Memory Mediates Interferon Response-Heterogeneity within the Hematopoietic System. Blood, 2017, 130, 634-634.	1.4	3
25	Combined Single-Cell and Spatial Transcriptomics to Deconvolute the Hematopoietic Stem Cell Niche. Blood, 2018, 132, 876-876.	1.4	2
26	The Bone Marrow Microenvironment of Multiple Myeloma Long-Term Survivors at Single Cell Resolution. Blood, 2020, 136, 32-33.	1.4	2
27	Stem Cell-like Megakaryocyte Progenitors As Driving Forces of IFN-Induced Emergency Megakaryopooesis. Blood, 2015, 126, 2391-2391.	1.4	1
28	Ifnα Mediated Remodeling of the Bone Marrow Stem Cell Vascular Niche. Blood, 2016, 128, 2667-2667.	1.4	1
29	No Evidence for Hematopoietic Stem Cell Self-Renewal in-Vivo Following Inflammatory Challenge. Blood, 2019, 134, 456-456.	1.4	1
30	Inflammation-driven fast-track differentiation of HSCs into the megakaryocytic lineage. Experimental Hematology, 2014, 42, S14.	0.4	0
31	Human haematopoietic stem cell differentiation follows a continuous waddington-like landscape. Experimental Hematology, 2016, 44, S77.	0.4	0
32	Multi-Layered Single-Cell Transcriptional Profiling of All Bone and Bone Marrow Populations Provides a Systems View of the Mesenchymal and Hematopoietic Stem Cell Niche. Experimental Hematology, 2018, 64, S47-S48.	0.4	0
33	Hematopoietic Stem Cells Fail to Regenerate In Vivo Following Inflammatory Stress. Blood, 2016, 128, 1472-1472.	1.4	0
34	Epigenetic Drug Treatment Globally Induces Cryptic Transcription Start Sites Encoded in Long Terminal Repeats. Blood, 2016, 128, 3931-3931.	1.4	0
35	Human haematopoietic stem cell differentiation follows a continuous waddington-like landscape. Experimental Hematology, 2017, 53, S101.	0.4	0
36	2006 – STEM CELL BASED HETEROGENEITY OF INTERFERON SIGNALING DURING HEMATOPOIETIC DEVELOPMENT. Experimental Hematology, 2020, 88, S29.	0.4	0

#	Article	IF	CITATIONS
37	3037 – COMBINED SINGLE-CELL DNA METHYLOME AND TRANSCRIPTOME ANALYSIS IDENTIFIES MOLECULAR STATES OF EARLY LINEAGE COMMITMENT. Experimental Hematology, 2020, 88, S50.	0.4	0
38	ATACing single cells with phages. Molecular Cell, 2022, 82, 234-236.	9.7	0
39	3071 – HEALTHY AND MALIGNANT HEMATOPOIETIC STEM CELLS ACT AS IMMUNOREGULATORY ANTIGEN PRESENTING CELLS. Experimental Hematology, 2021, 100, S76.	0.4	0