Sven Heinz

List of Publications by Year
in descending order

45 papers	16,976 citations	126907 33 h-index	243625 44 g-index
49 all docs	49 docs citations	49 times ranked	32713 citing authors

#	Article	IF	Citations
1	Simple Combinations of Lineage-Determining Transcription Factors Prime cis-Regulatory Elements Required for Macrophage and B Cell Identities. Molecular Cell, 2010, 38, 576-589.	9.7	10,215
2	The selection and function of cell type-specific enhancers. Nature Reviews Molecular Cell Biology, 2015, 16, 144-154.	37.0	859
3	Genome evolution in the allotetraploid frog Xenopus laevis. Nature, 2016, 538, 336-343.	27.8	849
4	Remodeling of the Enhancer Landscape during Macrophage Activation Is Coupled to Enhancer Transcription. Molecular Cell, 2013, 51, 310-325.	9.7	616
5	Rev-Erbs repress macrophage gene expression by inhibiting enhancer-directed transcription. Nature, 2013, 498, 511-515.	27.8	480
6	A global network of transcription factors, involving E2A, EBF1 and Foxo1, that orchestrates B cell fate. Nature Immunology, 2010, 11, 635-643.	14.5	475
7	Transcription Elongation Can Affect Genome 3D Structure. Cell, 2018, 174, 1522-1536.e22.	28.9	369
8	Biomimetic Morphogenesis of Fluorapatite-Gelatin Composites: Fractal Growth, the Question of Intrinsic Electric Fields, Core/Shell Assemblies, Hollow Spheres and Reorganization of Denatured Collagen. European Journal of Inorganic Chemistry, 1999, 1999, 1643-1653.	2.0	269
9	Global changes in the nuclear positioning of genes and intra- and interdomain genomic interactions that orchestrate B cell fate. Nature Immunology, 2012, 13, 1196-1204.	14.5	249
10	Liver-Derived Signals Sequentially Reprogram Myeloid Enhancers to Initiate and Maintain Kupffer Cell Identity. Immunity, 2019, 51, 655-670.e8.	14.3	234
11	FoxO1 regulates Tlr4 inflammatory pathway signalling in macrophages. EMBO Journal, 2010, 29, 4223-4236.	7.8	203
12	Species-specific Regulation of Toll-like Receptor 3 Genes in Men and Mice. Journal of Biological Chemistry, 2003, 278, 21502-21509.	3.4	174
13	Mechanisms Establishing TLR4-Responsive Activation States of Inflammatory Response Genes. PLoS Genetics, 2011, 7, e1002401.	3.5	146
14	Topoisomerase 1 inhibition suppresses inflammatory genes and protects from death by inflammation. Science, 2016, 352, aad7993.	12.6	132
15	Two distinct auto-regulatory loops operate at the PU.1 locus in B cells and myeloid cells. Blood, 2011, 117, 2827-2838.	1.4	120
16	Human Promoters Are Intrinsically Directional. Molecular Cell, 2015, 57, 674-684.	9.7	115
17	Macrophage development from HSCs requires PU.1-coordinated microRNA expression. Blood, 2011, 118, 2275-2284.	1.4	113
18	IL-17 signaling in steatotic hepatocytes and macrophages promotes hepatocellular carcinoma in alcohol-related liver disease. Journal of Hepatology, 2020, 72, 946-959.	3.7	113

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19	Identification of Lineage-Specific Transcription Factors That Prevent Activation of Hepatic Stellate Cells and Promote Fibrosis Resolution. Gastroenterology, 2020, 158, 1728-1744.e14.	1.3	112
20	Identification and dynamic quantification of regulatory elements using total RNA. Genome Research, 2019, 29, 1836-1846.	5.5	102
21	Heterochromatin-Encoded Satellite RNAs Induce Breast Cancer. Molecular Cell, 2018, 70, 842-853.e7.	9.7	96
22	Transcription Factor Tfec Contributes to the IL-4-Inducible Expression of a Small Group of Genes in Mouse Macrophages Including the Granulocyte Colony-Stimulating Factor Receptor. Journal of Immunology, 2005, 174, 7111-7122.	0.8	81
23	Paradoxical association of TET loss of function with genome-wide DNA hypomethylation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16933-16942.	7.1	81
24	TOP1 inhibition therapy protects against SARS-CoV-2-induced lethal inflammation. Cell, 2021, 184, 2618-2632.e17.	28.9	80
25	Active DNA demethylation in human postmitotic cells correlates with activating histone modifications, but not transcription levels. Genome Biology, 2010, 11, R63.	9.6	75
26	Genomic Decoding of Neuronal Depolarization by Stimulus-Specific NPAS4 Heterodimers. Cell, 2019, 179, 373-391.e27.	28.9	73
27	Mesothelin/mucin 16 signaling in activated portal fibroblasts regulates cholestatic liver fibrosis. Journal of Clinical Investigation, 2017, 127, 1254-1270.	8.2	69
28	Serum Response Factor Utilizes Distinct Promoter- and Enhancer-Based Mechanisms To Regulate Cytoskeletal Gene Expression in Macrophages. Molecular and Cellular Biology, 2011, 31, 861-875.	2.3	56
29	Interleukin-4 induction of the CC chemokine TARC (CCL17) in murine macrophages is mediated by multiple STAT6 sites in the TARC gene promoter. BMC Molecular Biology, 2006, 7, 45.	3.0	50
30	Senataxin suppresses the antiviral transcriptional response and controls viral biogenesis. Nature Immunology, 2015, 16, 485-494.	14.5	50
31	Control of VEGF-A transcriptional programs by pausing and genomic compartmentalization. Nucleic Acids Research, 2014, 42, 12570-12584.	14.5	47
32	Deconvolution of pro- and antiviral genomic responses in Zika virus-infected and bystander macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E9172-E9181.	7.1	44
33	Roles of Lineage-Determining Transcription Factors in Establishing Open Chromatin: Lessons From High-Throughput Studies. Current Topics in Microbiology and Immunology, 2011, 356, 1-15.	1.1	36
34	Circular synthesized CRISPR/Cas gRNAs for functional interrogations in the coding and noncoding genome. ELife, 2019, 8, .	6.0	34
35	Exploiting genomics and natural genetic variation to decode macrophage enhancers. Trends in Immunology, 2015, 36, 507-518.	6.8	32
36	ARTDeco: automatic readthrough transcription detection. BMC Bioinformatics, 2020, 21, 214.	2.6	21

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37	Genomic Organization of the Human Gene HEP27: Alternative Promoter Usage in HepG2 Cells and Monocyte-Derived Dendritic Cells. Genomics, 2002, 79, 608-615.	2.9	20
38	Perspectives on Unidirectional versus Divergent Transcription. Molecular Cell, 2015, 60, 348-349.	9.7	19
39	Ncor2/PPARÎ±-Dependent Upregulation of MCUb in the Type 2 Diabetic Heart Impacts Cardiac Metabolic Flexibility and Function. Diabetes, 2021, 70, 665-679.	0.6	17
40	Research Resource: Comparative Nuclear Receptor Atlas: Basal and Activated Peritoneal B-1 and B-2 Cells. Molecular Endocrinology, 2011, 25, 529-545.	3.7	12
41	Purification of mouse hepatic non-parenchymal cells or nuclei for use in ChIP-seq and other next-generation sequencing approaches. STAR Protocols, 2021, 2, 100363.	1.2	12
42	An optimized protocol for rapid, sensitive and robust on-bead ChIP-seq from primary cells. STAR Protocols, 2021, 2, 100358.	1.2	11
43	Characterization of MAX.3 antigen, a glycoprotein expressed on mature macrophages, dendritic cells and blood platelets: identity with CD84. Biochemical Journal, 2000, 346, 729.	3.7	9
44	Generating a Three-Dimensional Genome from Xenopus with Hi-C. Cold Spring Harbor Protocols, 2019, 2019, pdb.prot098343.	0.3	1
45	Negative Regulation of Enhancerâ€Associated RNA in Macrophages. FASEB Journal, 2012, 26, 912.1.	0.5	0