

# Hendrik Gerard Stunnenberg

## List of Publications by Year in descending order

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Version: 2024-02-01

294  
papers

48,624  
citations

2696

98  
h-index

2351

205  
g-index

317  
all docs

317  
docs citations

317  
times ranked

69947  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamics of broad H3K4me3 domains uncover an epigenetic switch between cell identity and cancer-related genes. <i>Genome Research</i> , 2022, 32, 1328-1342.	2.4	14
2	CBX2 shapes chromatin accessibility promoting AML via p38 MAPK signaling pathway. <i>Molecular Cancer</i> , 2022, 21, .	7.9	18
3	Recent insights into Histone Acetyltransferase-1: biological function and involvement in pathogenesis. <i>Epigenetics</i> , 2021, 16, 838-850.	1.3	21
4	Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. <i>Haematologica</i> , 2021, 106, 2613-2623.	1.7	12
5	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. <i>Nature Communications</i> , 2021, 12, 651.	5.8	67
6	The Role of Necroptosis: Biological Relevance and Its Involvement in Cancer. <i>Cancers</i> , 2021, 13, 684.	1.7	27
7	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. <i>Genome Research</i> , 2021, 31, 919-933.	2.4	4
8	G1-phase progression in pluripotent stem cells. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 4507-4519.	2.4	6
9	Chronic HIV infection induces transcriptional and functional reprogramming of innate immune cells. <i>JCI Insight</i> , 2021, 6, .	2.3	33
10	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	3.3	34
11	Clonal evolution of acute myeloid leukemia with FLT3-ITD mutation under treatment with midostaurin. <i>Blood</i> , 2021, 137, 3093-3104.	0.6	91
12	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	9.4	96
13	Trained innate immunity, long-lasting epigenetic modulation, and skewed myelopoiesis by heme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
14	p120-catenin-dependent collective brain infiltration by glioma cell networks. <i>Nature Cell Biology</i> , 2020, 22, 97-107.	4.6	79
15	Critical Role for P53 in Regulating the Cell Cycle of Ground State Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2020, 14, 175-183.	2.3	22
16	Controlled Human Malaria Infection Induces Long-Term Functional Changes in Monocytes. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 604553.	1.6	13
17	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	4.2	15
18	STARR-seq identifies active, chromatin-masked, and dormant enhancers in pluripotent mouse embryonic stem cells. <i>Genome Biology</i> , 2020, 21, 243.	3.8	48

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19	Chromatin activation as a unifying principle underlying pathogenic mechanisms in multiple myeloma. <i>Genome Research</i> , 2020, 30, 1217-1227.	2.4	35
20	Dynamic CpG methylation delineates subregions within super-enhancers selectively decommissioned at the exit from naive pluripotency. <i>Nature Communications</i> , 2020, 11, 1112.	5.8	25
21	Rewiring of glucose metabolism defines trained immunity induced by oxidized low-density lipoprotein. <i>Journal of Molecular Medicine</i> , 2020, 98, 819-831.	1.7	59
22	The translational landscape of ground state pluripotency. <i>Nature Communications</i> , 2020, 11, 1617.	5.8	18
23	Chromatin-Based Classification of Genetically Heterogeneous AMLs into Two Distinct Subtypes with Diverse Stemness Phenotypes. <i>Cell Reports</i> , 2019, 26, 1059-1069.e6.	2.9	33
24	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	2.4	85
25	BRD9 binds cell type-specific chromatin regions regulating leukemic cell survival via STAT5 inhibition. <i>Cell Death and Disease</i> , 2019, 10, 338.	2.7	31
26	Epigenetic modulation of a hardwired 3D chromatin landscape in two naive states of pluripotency. <i>Nature Cell Biology</i> , 2019, 21, 568-578.	4.6	55
27	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	5.8	46
28	Combined quantification of intracellular (phospho-)proteins and transcriptomics from fixed single cells. <i>Scientific Reports</i> , 2019, 9, 1469.	1.6	73
29	Extensive epigenomic integration of the glucocorticoid response in primary human monocytes and in vitro derived macrophages. <i>Scientific Reports</i> , 2019, 9, 2772.	1.6	27
30	Epigenetic reader complexes of the human malaria parasite, <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2019, 47, 11574-11588.	6.5	45
31	Inhibition of Histone Demethylases LSD1 and UTX Regulates ER $\alpha$ Signaling in Breast Cancer. <i>Cancers</i> , 2019, 11, 2027.	1.7	34
32	The SMAD2/3 interactome reveals that TGF $\beta$ 2 controls m6A mRNA methylation in pluripotency. <i>Nature</i> , 2018, 555, 256-259.	13.7	283
33	Brd4-independence in ground state pluripotency. <i>Nature Cell Biology</i> , 2018, 20, 513-515.	4.6	0
34	Transcriptional and functional profiling defines human small intestinal macrophage subsets. <i>Journal of Experimental Medicine</i> , 2018, 215, 441-458.	4.2	144
35	BCG Vaccination Protects against Experimental Viral Infection in Humans through the Induction of Cytokines Associated with Trained Immunity. <i>Cell Host and Microbe</i> , 2018, 23, 89-100.e5.	5.1	860
36	RIP1 $\alpha$ -HAT1 $\alpha$ -SIRT Complex Identification and Targeting in Treatment and Prevention of Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 2886-2900.	3.2	40

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37	Increased H3K9 methylation and impaired expression of Protocadherins are associated with the cognitive dysfunctions of the Kleeftstra syndrome. <i>Nucleic Acids Research</i> , 2018, 46, 4950-4965.	6.5	32
38	C-terminal BRE overexpression in 11q23-rearranged and t(8;16) acute myeloid leukemia is caused by intragenic transcription initiation. <i>Leukemia</i> , 2018, 32, 828-836.	3.3	6
39	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018, 9, 25647-25660.	0.8	13
40	Epigenetic Repression of Androgen Receptor Transcription in Mutation-Negative Androgen Insensitivity Syndrome (AIS Type II). <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 4617-4627.	1.8	22
41	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. <i>Cell Reports</i> , 2018, 25, 3490-3503.e4.	2.9	41
42	E-cadherin loss induces targetable autocrine activation of growth factor signalling in lobular breast cancer. <i>Scientific Reports</i> , 2018, 8, 15454.	1.6	55
43	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	2.9	104
44	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	15.2	157
45	Immuno-detection by sequencing enables large-scale high-dimensional phenotyping in cells. <i>Nature Communications</i> , 2018, 9, 2384.	5.8	17
46	Mammalian embryo comparison identifies novel pluripotency genes associated with the naïve or primed state. <i>Biology Open</i> , 2018, 7, .	0.6	32
47	Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions via DC-SCRIPT and Dual-Specificity Phosphatase 4. <i>Frontiers in Immunology</i> , 2018, 9, 1420.	2.2	16
48	Combined HAT/EZH2 modulation leads to cancer-selective cell death. <i>Oncotarget</i> , 2018, 9, 25630-25646.	0.8	5
49	c-Myc Modulation and Acetylation Is a Key HDAC Inhibitor Target in Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2542-2555.	3.2	105
50	Jmjd2c/Kdm4c facilitates the assembly of essential enhancer-protein complexes at the onset of embryonic stem cell differentiation. <i>Development (Cambridge)</i> , 2017, 144, 567-579.	1.2	24
51	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017, 49, 341-348.	9.4	75
52	MLL-AF9 and MLL-AF4 oncofusion proteins bind a distinct enhancer repertoire and target the RUNX1 program in 11q23 acute myeloid leukemia. <i>Oncogene</i> , 2017, 36, 3346-3356.	2.6	86
53	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	3.8	97
54	miR-194-5p/BCLAF1 deregulation in AML tumorigenesis. <i>Leukemia</i> , 2017, 31, 2315-2325.	3.3	66

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55	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development</i> (Cambridge), 2017, 144, 1221-1234.	1.2	226
56	The non-coding variant rs1800734 enhances DCLK3 expression through long-range interaction and promotes colorectal cancer progression. <i>Nature Communications</i> , 2017, 8, 14418.	5.8	48
57	Uric acid priming in human monocytes is driven by the AKT-PRAS40 autophagy pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5485-5490.	3.3	114
58	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , 2017, 23, 517-525.	15.2	769
59	Vitamin C and L-Proline Antagonistic Effects Capture Alternative States in the Pluripotency Continuum. <i>Stem Cell Reports</i> , 2017, 8, 1-10.	2.3	56
60	Distinct Cell-Cycle Control in Two Different States of Mouse Pluripotency. <i>Cell Stem Cell</i> , 2017, 21, 449-455.e4.	5.2	61
61	Time-resolved analysis of DNA-protein interactions in living cells by UV laser pulses. <i>Scientific Reports</i> , 2017, 7, 11725.	1.6	11
62	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. <i>Nature Communications</i> , 2017, 8, 393.	5.8	51
63	Transcriptional and epigenetic control in mouse pluripotency: lessons from in vivo and in vitro studies. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 114-122.	1.5	13
64	The interplay of epigenetic marks during stem cell differentiation and development. <i>Nature Reviews Genetics</i> , 2017, 18, 643-658.	7.7	414
65	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	5.8	50
66	Digitalis-like Compounds Facilitate Non-Medullary Thyroid Cancer Redifferentiation through Intracellular Ca <sup>2+</sup> , FOS, and Autophagy-Dependent Pathways. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 169-181.	1.9	19
67	I Remember You: Epigenetic Priming in Epithelial Stem Cells. <i>Immunity</i> , 2017, 47, 1019-1021.	6.6	12
68	Integrated transcriptional analysis unveils the dynamics of cellular differentiation in the developing mouse hippocampus. <i>Scientific Reports</i> , 2017, 7, 18073.	1.6	11
69	An efficient method for generation of bi-allelic null mutant mouse embryonic stem cells and its application for investigating epigenetic modifiers. <i>Nucleic Acids Research</i> , 2017, 45, e174-e174.	6.5	7
70	PRC1 Prevents Replication Stress during Chondrogenic Transit Amplification. <i>Epigenomes</i> , 2017, 1, 22.	0.8	0
71	N <sup>6</sup> -methyladenosine (m <sup>6</sup> A) recruits and repels proteins to regulate mRNA homeostasis. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 870-878.	3.6	432
72	p63 exerts spatio-temporal control of palatal epithelial cell fate to prevent cleft palate. <i>PLoS Genetics</i> , 2017, 13, e1006828.	1.5	34

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73	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016, 12, 861.	3.2	97
74	Genome-wide epigenomic profiling for biomarker discovery. <i>Clinical Epigenetics</i> , 2016, 8, 122.	1.8	67
75	Recruitment of the Mammalian Histone-modifying EMSY Complex to Target Genes Is Regulated by ZNF131. <i>Journal of Biological Chemistry</i> , 2016, 291, 7313-7324.	1.6	35
76	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016, 17, 36.	3.8	121
77	Dynamic chromatin organization: Role in development and disease. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 76, 119-122.	1.2	4
78	Trained immunity: A program of innate immune memory in health and disease. <i>Science</i> , 2016, 352, aaf1098.	6.0	1,809
79	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760
80	ZMYND8 Co-localizes with NuRD on Target Genes and Regulates Poly(ADP-Ribose)-Dependent Recruitment of GATAD2A/NuRD to Sites of DNA Damage. <i>Cell Reports</i> , 2016, 17, 783-798.	2.9	100
81	Epigenetic memory: A macrophage perspective. <i>Seminars in Immunology</i> , 2016, 28, 359-367.	2.7	49
82	MEIS2 Is an Oncogenic Partner in AML1-ETO-Positive AML. <i>Cell Reports</i> , 2016, 16, 498-507.	2.9	32
83	Glutaminolysis and Fumarate Accumulation Integrate Immunometabolic and Epigenetic Programs in Trained Immunity. <i>Cell Metabolism</i> , 2016, 24, 807-819.	7.2	584
84	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	2.9	102
85	Transcriptional Landscape of Human Tissue Lymphocytes Unveils Uniqueness of Tumor-Infiltrating T Regulatory Cells. <i>Immunity</i> , 2016, 45, 1135-1147.	6.6	510
86	Information recovery from low coverage whole-genome bisulfite sequencing. <i>Nature Communications</i> , 2016, 7, 11306.	5.8	33
87	Decoding the DNA Methylome of Mantle Cell Lymphoma in the Light of the Entire B Cell Lineage. <i>Cancer Cell</i> , 2016, 30, 806-821.	7.7	103
88	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016, 167, 1354-1368.e14.	13.5	467
89	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016, 167, 1369-1384.e19.	13.5	863
90	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	13.5	1,052

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91	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
92	The Hematopoietic Transcription Factors RUNX1 and ERG Prevent AML1-ETO Oncogene Overexpression and Onset of the Apoptosis Program in t(8;21) AMLs. <i>Cell Reports</i> , 2016, 17, 2087-2100.	2.9	60
93	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016, 17, 2101-2111.	2.9	54
94	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822.	5.2	216
95	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	13.5	573
96	Control of embryonic stem cell self-renewal and differentiation via coordinated alternative splicing and translation of YY2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12360-12367.	3.3	54
97	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016, 7, 11383.	5.8	235
98	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	5.8	119
99	Saturation analysis for whole-genome bisulfite sequencing data. <i>Nature Biotechnology</i> , 2016, 34, 691-693.	9.4	26
100	Impairment of DNA Methylation Maintenance Is the Main Cause of Global Demethylation in Naive Embryonic Stem Cells. <i>Molecular Cell</i> , 2016, 62, 848-861.	4.5	189
101	Non-canonical PRC1.1 Targets Active Genes Independent of H3K27me3 and Is Essential for Leukemogenesis. <i>Cell Reports</i> , 2016, 14, 332-346.	2.9	126
102	The oncofusion protein FUS-ERG targets key hematopoietic regulators and modulates the all-trans retinoic acid signaling pathway in t(16;21) acute myeloid leukemia. <i>Oncogene</i> , 2016, 35, 1965-1976.	2.6	39
103	Aberrant Expression of the SOX11 Oncogene in Mantle Cell Lymphoma Is Associated with Activation and De Novo 3D Looping of a Distant Enhancer Element. <i>Blood</i> , 2016, 128, 459-459.	0.6	0
104	Whole-Genome Analysis of the Chromatin Structure in Multiple Myeloma. <i>Blood</i> , 2016, 128, 118-118.	0.6	0
105	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. <i>EMBO Reports</i> , 2015, 16, 863-878.	2.0	134
106	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	9.4	278
107	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	3.8	48
108	Dynamic Reorganization of Extremely Long-Range Promoter-Promoter Interactions between Two States of Pluripotency. <i>Cell Stem Cell</i> , 2015, 17, 748-757.	5.2	179

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109	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <i>Genome Biology</i> , 2015, 16, 149.	3.8	104
110	Roadmap for regulation. <i>Nature</i> , 2015, 518, 314-316.	13.7	190
111	A Quantitative Proteomics Tool To Identify DNA-Protein Interactions in Primary Cells or Blood. <i>Journal of Proteome Research</i> , 2015, 14, 1315-1329.	1.8	32
112	A Me6Age for pluripotency. <i>Science</i> , 2015, 347, 614-615.	6.0	6
113	Whole-genome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	2.4	118
114	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	13.7	749
115	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015, 47, 1316-1325.	9.4	119
116	Genome-wide modeling of transcription kinetics reveals patterns of RNA production delays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13115-13120.	3.3	75
117	MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5261-70.	3.3	91
118	DNA Methylation of the Aryl Hydrocarbon Receptor Repressor Associations With Cigarette Smoking and Subclinical Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 707-716.	5.1	107
119	Genome-Wide Binding of MBD2 Reveals Strong Preference for Highly Methylated Loci. <i>PLoS ONE</i> , 2014, 9, e99603.	1.1	44
120	Inference of RNA Polymerase II Transcription Dynamics from Chromatin Immunoprecipitation Time Course Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003598.	1.5	24
121	MBD2 and MBD3: elusive functions and mechanisms. <i>Frontiers in Genetics</i> , 2014, 5, 428.	1.1	53
122	Context-Selective Death of Acute Myeloid Leukemia Cells Triggered by the Novel Hybrid Retinoid-HDAC Inhibitor MC2392. <i>Cancer Research</i> , 2014, 74, 2328-2339.	0.4	33
123	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	1.7	251
124	Mll2 is required for H3K4 trimethylation on bivalent promoters in embryonic stem cells, whereas Mll1 is redundant. <i>Development (Cambridge)</i> , 2014, 141, 526-537.	1.2	225
125	Transcription regulation and chromatin structure in the pluripotent ground state. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 129-137.	0.9	33
126	Genomics meets proteomics: identifying the culprits in disease. <i>Human Genetics</i> , 2014, 133, 689-700.	1.8	18

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127	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. <i>Science</i> , 2014, 345, 1251086.	6.0	1,338
128	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	2.9	66
129	Relationship between genome and epigenome - challenges and requirements for future research. <i>BMC Genomics</i> , 2014, 15, 487.	1.2	24
130	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	6.0	253
131	Dual Promoter Usage as Regulatory Mechanism of let-7c Expression in Leukemic and Solid Tumors. <i>Molecular Cancer Research</i> , 2014, 12, 878-889.	1.5	18
132	mTOR- and HIF-1 $\alpha$ -mediated aerobic glycolysis as metabolic basis for trained immunity. <i>Science</i> , 2014, 345, 1250684.	6.0	1,517
133	A Polymorphic Enhancer near GREM1 Influences Bowel Cancer Risk through Differential CDX2 and TCF7L2 Binding. <i>Cell Reports</i> , 2014, 8, 983-990.	2.9	45
134	Analysis of Chromatin-Nuclear Receptor Interactions by Laser-Chromatin Immunoprecipitation. <i>Methods in Molecular Biology</i> , 2014, 1204, 25-34.	0.4	2
135	Characterization of the DNA Methylome during Human B-Cell Differentiation. <i>Blood</i> , 2014, 124, 4346-4346.	0.6	0
136	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 360-369.	5.2	424
137	Restoring polyamines protects from age-induced memory impairment in an autophagy-dependent manner. <i>Nature Neuroscience</i> , 2013, 16, 1453-1460.	7.1	283
138	Dnmt3L Antagonizes DNA Methylation at Bivalent Promoters and Favors DNA Methylation at Gene Bodies in ESCs. <i>Cell</i> , 2013, 155, 121-134.	13.5	153
139	The Tetraspanin CD9 Affords High-Purity Capture of All Murine Hematopoietic Stem Cells. <i>Cell Reports</i> , 2013, 4, 642-648.	2.9	42
140	SMIM1 underlies the Vel blood group and influences red blood cell traits. <i>Nature Genetics</i> , 2013, 45, 542-545.	9.4	96
141	De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. <i>American Journal of Human Genetics</i> , 2013, 93, 124-131.	2.6	151
142	The class I-specific HDAC inhibitor MS-275 modulates the differentiation potential of mouse embryonic stem cells. <i>Biology Open</i> , 2013, 2, 1070-1077.	0.6	17
143	Dynamic binding of RBPJ is determined by Notch signaling status. <i>Genes and Development</i> , 2013, 27, 1059-1071.	2.7	218
144	Integrative Analysis of Deep Sequencing Data Identifies Estrogen Receptor Early Response Genes and Links ATAD3B to Poor Survival in Breast Cancer. <i>PLoS Computational Biology</i> , 2013, 9, e1003100.	1.5	11

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145	Nontypeable Haemophilus influenzae Carbonic Anhydrase Is Important for Environmental and Intracellular Survival. <i>Journal of Bacteriology</i> , 2013, 195, 2737-2746.	1.0	29
146	<i>Streptococcus pneumoniae</i> Folate Biosynthesis Responds to Environmental CO <sub>2</sub> Levels. <i>Journal of Bacteriology</i> , 2013, 195, 1573-1582.	1.0	31
147	H <sub>2</sub> A <sub>1</sub> Z <sub>1</sub> /H <sub>2</sub> B <sub>1</sub> Z <sub>1</sub> double-strand variant nucleosomes inhabit the AT-rich promoter regions of the <i>Plasmodium falciparum</i> genome. <i>Molecular Microbiology</i> , 2013, 87, 1061-1073.	1.2	66
148	BLUEPRINT: mapping human blood cell epigenomes. <i>Haematologica</i> , 2013, 98, 1487-1489.	1.7	189
149	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. <i>Epigenetics</i> , 2012, 7, 1355-1367.	1.3	67
150	Genome-Wide Profiling of Liver X Receptor, Retinoid X Receptor, and Peroxisome Proliferator-Activated Receptor $\alpha$ in Mouse Liver Reveals Extensive Sharing of Binding Sites. <i>Molecular and Cellular Biology</i> , 2012, 32, 852-867.	1.1	205
151	Chromatin accessibility, p300, and histone acetylation define PML-RAR $\alpha$ and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 3058-3068.	0.6	60
152	ERG and FLI1 binding sites demarcate targets for aberrant epigenetic regulation by AML1-ETO in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 4038-4048.	0.6	98
153	Transcriptome Analysis Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2012, 923, 221-239.	0.4	35
154	<i>Candida albicans</i> Infection Affords Protection against Reinfection via Functional Reprogramming of Monocytes. <i>Cell Host and Microbe</i> , 2012, 12, 223-232.	5.1	926
155	Uncovering Common Principles in Protein Export of Malaria Parasites. <i>Cell Host and Microbe</i> , 2012, 12, 717-729.	5.1	115
156	Placing the <i>Plasmodium falciparum</i> epigenome on the map. <i>Trends in Parasitology</i> , 2012, 28, 486-495.	1.5	35
157	Indole-Derived Psammoplin A Analogues as Epigenetic Modulators with Multiple Inhibitory Activities. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9467-9491.	2.9	48
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