

Hendrik Gerard Stunnenberg

List of Publications by Year
in descending order

Source: <https://exaly.com/author-pdf/2426052/publications.pdf>

Version: 2024-02-01

294
papers

48,624
citations

2322

98
h-index

2033

205
g-index

317
all docs

317
docs citations

317
times ranked

63556
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.	5.5	14
2	CBX2 shapes chromatin accessibility promoting AML via p38 MAPK signaling pathway. <i>Molecular Cancer</i> , 2022, 21, .	19.2	18
3	Recent insights into Histone Acetyltransferase-1: biological function and involvement in pathogenesis. <i>Epigenetics</i> , 2021, 16, 838-850.	2.7	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.	3.5	12
5	Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. <i>Nature Communications</i> , 2021, 12, 651.	12.8	67
6	The Role of Necroptosis: Biological Relevance and Its Involvement in Cancer. <i>Cancers</i> , 2021, 13, 684.	3.7	27
7	A plug and play microfluidic platform for standardized sensitive low-input chromatin immunoprecipitation. <i>Genome Research</i> , 2021, 31, 919-933.	5.5	4
8	G1-phase progression in pluripotent stem cells. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 4507-4519.	5.4	6
9	Chronic HIV infection induces transcriptional and functional reprogramming of innate immune cells. <i>JCI Insight</i> , 2021, 6, .	5.0	33
10	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. <i>Leukemia</i> , 2021, 35, 2002-2016.	7.2	34
11	Clonal evolution of acute myeloid leukemia with FLT3-ITD mutation under treatment with midostaurin. <i>Blood</i> , 2021, 137, 3093-3104.	1.4	91
12	The Organoid Cell Atlas. <i>Nature Biotechnology</i> , 2021, 39, 13-17.	17.5	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, .	7.1	40
14	p120-catenin-dependent collective brain infiltration by glioma cell networks. <i>Nature Cell Biology</i> , 2020, 22, 97-107.	10.3	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.	4.8	22
16	Controlled Human Malaria Infection Induces Long-Term Functional Changes in Monocytes. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 604553.	3.5	13
17	Blueprint of human thymopoiesis reveals molecular mechanisms of stage-specific TCR enhancer activation. <i>Journal of Experimental Medicine</i> , 2020, 217, .	8.5	15
18	STARR-seq identifies active, chromatin-masked, and dormant enhancers in pluripotent mouse embryonic stem cells. <i>Genome Biology</i> , 2020, 21, 243.	8.8	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.	5.5	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.	12.8	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.	3.9	59
22	The translational landscape of ground state pluripotency. <i>Nature Communications</i> , 2020, 11, 1617.	12.8	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.	6.4	33
24	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	5.5	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.	6.3	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.	10.3	55
27	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	12.8	46
28	Combined quantification of intracellular (phospho-)proteins and transcriptomics from fixed single cells. <i>Scientific Reports</i> , 2019, 9, 1469.	3.3	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.	3.3	27
30	Epigenetic reader complexes of the human malaria parasite, <i>Plasmodium falciparum</i> . <i>Nucleic Acids Research</i> , 2019, 47, 11574-11588.	14.5	45
31	Inhibition of Histone Demethylases LSD1 and UTX Regulates ER \pm Signaling in Breast Cancer. <i>Cancers</i> , 2019, 11, 2027.	3.7	34
32	The SMAD2/3 interactome reveals that TGF β ² controls m6A mRNA methylation in pluripotency. <i>Nature</i> , 2018, 555, 256-259.	27.8	283
33	Brd4-independence in ground state pluripotency. <i>Nature Cell Biology</i> , 2018, 20, 513-515.	10.3	0
34	Transcriptional and functional profiling defines human small intestinal macrophage subsets. <i>Journal of Experimental Medicine</i> , 2018, 215, 441-458.	8.5	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.	11.0	860
36	RIPl α -HAT1 α -SIRT Complex Identification and Targeting in Treatment and Prevention of Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 2886-2900.	7.0	40

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37	Increased H3K9 methylation and impaired expression of Protocadherins are associated with the cognitive dysfunctions of the Kleefstra syndrome. <i>Nucleic Acids Research</i> , 2018, 46, 4950-4965.	14.5	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.	7.2	6
39	Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. <i>Oncotarget</i> , 2018, 9, 25647-25660.	1.8	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.	3.6	22
41	Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. <i>Cell Reports</i> , 2018, 25, 3490-3503.e4.	6.4	41
42	E-cadherin loss induces targetable autocrine activation of growth factor signalling in lobular breast cancer. <i>Scientific Reports</i> , 2018, 8, 15454.	3.3	55
43	Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. <i>Cell Reports</i> , 2018, 24, 2784-2794.	6.4	104
44	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
45	Immuno-detection by sequencing enables large-scale high-dimensional phenotyping in cells. <i>Nature Communications</i> , 2018, 9, 2384.	12.8	17
46	Mammalian embryo comparison identifies novel pluripotency genes associated with the naïve or primed state. <i>Biology Open</i> , 2018, 7, .	1.2	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.	4.8	16
48	Combined HAT/EZH2 modulation leads to cancer-selective cell death. <i>Oncotarget</i> , 2018, 9, 25630-25646.	1.8	5
49	c-Myc Modulation and Acetylation Is a Key HDAC Inhibitor Target in Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 2542-2555.	7.0	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.	2.5	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.	21.4	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.	5.9	86
53	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. <i>Genome Biology</i> , 2017, 18, 18.	8.8	97
54	miR-194-5p/BCLAF1 deregulation in AML tumorigenesis. <i>Leukemia</i> , 2017, 31, 2315-2325.	7.2	66

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55	Tracking the embryonic stem cell transition from ground state pluripotency. Development (Cambridge), 2017, 144, 1221-1234.	2.5	226
56	The non-coding variant rs1800734 enhances DCLK3 expression through long-range interaction and promotes colorectal cancer progression. Nature Communications, 2017, 8, 14418.	12.8	48
57	Uric acid priming in human monocytes is driven by the AKT-PRAS40 autophagy pathway. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5485-5490.	7.1	114
58	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	30.7	769
59	Vitamin C and L-Proline Antagonistic Effects Capture Alternative States in the Pluripotency Continuum. Stem Cell Reports, 2017, 8, 1-10.	4.8	56
60	Distinct Cell-Cycle Control in Two Different States of Mouse Pluripotency. Cell Stem Cell, 2017, 21, 449-455.e4.	11.1	61
61	Time-resolved analysis of DNA-protein interactions in living cells by UV laser pulses. Scientific Reports, 2017, 7, 11725.	3.3	11
62	Blood monocyte transcriptome and epigenome analyses reveal loci associated with human atherosclerosis. Nature Communications, 2017, 8, 393.	12.8	51
63	Transcriptional and epigenetic control in mouse pluripotency: lessons from in vivo and in vitro studies. Current Opinion in Genetics and Development, 2017, 46, 114-122.	3.3	13
64	The interplay of epigenetic marks during stem cell differentiation and development. Nature Reviews Genetics, 2017, 18, 643-658.	16.3	414
65	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	12.8	50
66	Digitalis-like Compounds Facilitate Non-Medullary Thyroid Cancer Redifferentiation through Intracellular Ca ²⁺ , FOS, and Autophagy-Dependent Pathways. Molecular Cancer Therapeutics, 2017, 16, 169-181.	4.1	19
67	I Remember You: Epigenetic Priming in Epithelial Stem Cells. Immunity, 2017, 47, 1019-1021.	14.3	12
68	Integrated transcriptional analysis unveils the dynamics of cellular differentiation in the developing mouse hippocampus. Scientific Reports, 2017, 7, 18073.	3.3	11
69	An efficient method for generation of bi-allelic null mutant mouse embryonic stem cells and its application for investigating epigenetic modifiers. Nucleic Acids Research, 2017, 45, e174-e174.	14.5	7
70	PRC1 Prevents Replication Stress during Chondrogenic Transit Amplification. Epigenomes, 2017, 1, 22.	1.8	0
71	N6-methyladenosine (m6A) recruits and repels proteins to regulate mRNA homeostasis. Nature Structural and Molecular Biology, 2017, 24, 870-878.	8.2	432
72	p63 exerts spatio-temporal control of palatal epithelial cell fate to prevent cleft palate. PLoS Genetics, 2017, 13, e1006828.	3.5	34

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73	Environmentâ€nduced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. <i>Molecular Systems Biology</i> , 2016, 12, 861.	7.2	97
74	Genome-wide epigenomic profiling for biomarker discovery. <i>Clinical Epigenetics</i> , 2016, 8, 122.	4.1	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.	3.4	35
76	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016, 17, 36.	8.8	121
77	Dynamic chromatin organization: Role in development and disease. <i>International Journal of Biochemistry and Cell Biology</i> , 2016, 76, 119-122.	2.8	4
78	Trained immunity: A program of innate immune memory in health and disease. <i>Science</i> , 2016, 352, aaf1098.	12.6	1,809
79	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	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.	6.4	100
81	Epigenetic memory: A macrophage perspective. <i>Seminars in Immunology</i> , 2016, 28, 359-367.	5.6	49
82	MEIS2 Is an Oncogenic Partner in AML1-ETO-Positive AML. <i>Cell Reports</i> , 2016, 16, 498-507.	6.4	32
83	Glutaminolysis and Fumarate Accumulation Integrate Immunometabolic and Epigenetic Programs in Trained Immunity. <i>Cell Metabolism</i> , 2016, 24, 807-819.	16.2	584
84	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	6.4	102
85	Transcriptional Landscape of Human Tissue Lymphocytes Unveils Uniqueness of Tumor-Infiltrating T Regulatory Cells. <i>Immunity</i> , 2016, 45, 1135-1147.	14.3	510
86	Information recovery from low coverage whole-genome bisulfite sequencing. <i>Nature Communications</i> , 2016, 7, 11306.	12.8	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.	16.8	103
88	Î²-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016, 167, 1354-1368.e14.	28.9	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.	28.9	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.	28.9	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.	28.9	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.	6.4	60
93	Distinct Trends of DNA Methylation Patterning in the Innate and Adaptive Immune Systems. <i>Cell Reports</i> , 2016, 17, 2101-2111.	6.4	54
94	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822.	11.1	216
95	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	28.9	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.	7.1	54
97	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016, 7, 11383.	12.8	235
98	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	12.8	119
99	Saturation analysis for whole-genome bisulfite sequencing data. <i>Nature Biotechnology</i> , 2016, 34, 691-693.	17.5	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.	9.7	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.	6.4	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.	5.9	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.	1.4	0
104	Whole-Genome Analysis of the Chromatin Structure in Multiple Myeloma. <i>Blood</i> , 2016, 128, 118-118.	1.4	0
105	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. <i>EMBO Reports</i> , 2015, 16, 863-878.	4.5	134
106	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	21.4	278
107	Glucocorticoid receptor and nuclear factor kappa-b affect three-dimensional chromatin organization. <i>Genome Biology</i> , 2015, 16, 264.	8.8	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.	11.1	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.	8.8	104
110	Roadmap for regulation. <i>Nature</i> , 2015, 518, 314-316.	27.8	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.	3.7	32
112	A Me6Age for pluripotency. <i>Science</i> , 2015, 347, 614-615.	12.6	6
113	Whole-genome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	5.5	118
114	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	27.8	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.	21.4	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.	7.1	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.	7.1	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.	2.5	44
120	Inference of RNA Polymerase II Transcription Dynamics from Chromatin Immunoprecipitation Time Course Data. <i>PLoS Computational Biology</i> , 2014, 10, e1003598.	3.2	24
121	MBD2 and MBD3: elusive functions and mechanisms. <i>Frontiers in Genetics</i> , 2014, 5, 428.	2.3	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.	0.9	33
123	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	3.8	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.	2.5	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.	1.9	33
126	Genomics meets proteomics: identifying the culprits in disease. <i>Human Genetics</i> , 2014, 133, 689-700.	3.8	18

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127	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. Science, 2014, 345, 1251086.	12.6	1,338
128	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. Cell Reports, 2014, 8, 743-753.	6.4	66
129	Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487.	2.8	24
130	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
131	Dual Promoter Usage as Regulatory Mechanism of let-7c Expression in Leukemic and Solid Tumors. Molecular Cancer Research, 2014, 12, 878-889.	3.4	18
132	mTOR- and HIF-1 α -mediated aerobic glycolysis as metabolic basis for trained immunity. Science, 2014, 345, 1250684.	12.6	1,517
133	A Polymorphic Enhancer near GREM1 Influences Bowel Cancer Risk through Differential CDX2 and TCF7L2 Binding. Cell Reports, 2014, 8, 983-990.	6.4	45
134	Analysis of Chromatin-Nuclear Receptor Interactions by Laser-Chromatin Immunoprecipitation. Methods in Molecular Biology, 2014, 1204, 25-34.	0.9	2
135	Characterization of the DNA Methylome during Human B-Cell Differentiation. Blood, 2014, 124, 4346-4346.	1.4	0
136	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. Cell Stem Cell, 2013, 13, 360-369.	11.1	424
137	Restoring polyamines protects from age-induced memory impairment in an autophagy-dependent manner. Nature Neuroscience, 2013, 16, 1453-1460.	14.8	283
138	Dnmt3L Antagonizes DNA Methylation at Bivalent Promoters and Favors DNA Methylation at Gene Bodies in ESCs. Cell, 2013, 155, 121-134.	28.9	153
139	The Tetraspanin CD9 Affords High-Purity Capture of All Murine Hematopoietic Stem Cells. Cell Reports, 2013, 4, 642-648.	6.4	42
140	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	21.4	96
141	De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. American Journal of Human Genetics, 2013, 93, 124-131.	6.2	151
142	The class I-specific HDAC inhibitor MS-275 modulates the differentiation potential of mouse embryonic stem cells. Biology Open, 2013, 2, 1070-1077.	1.2	17
143	Dynamic binding of RBPJ is determined by Notch signaling status. Genes and Development, 2013, 27, 1059-1071.	5.9	218
144	Integrative Analysis of Deep Sequencing Data Identifies Estrogen Receptor Early Response Genes and Links ATAD3B to Poor Survival in Breast Cancer. PLoS Computational Biology, 2013, 9, e1003100.	3.2	11

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145	Nontypeable <i>Haemophilus influenzae</i> Carbonic Anhydrase Is Important for Environmental and Intracellular Survival. <i>Journal of Bacteriology</i> , 2013, 195, 2737-2746.	2.2	29
146	<i>Streptococcus pneumoniae</i> Folate Biosynthesis Responds to Environmental CO ₂ Levels. <i>Journal of Bacteriology</i> , 2013, 195, 1573-1582.	2.2	31
147	<i>H2AZ</i> double-strand variant nucleosomes inhabit the <i>AT-rich</i> promoter regions of the <i>Plasmodium falciparum</i> genome. <i>Molecular Microbiology</i> , 2013, 87, 1061-1073.	2.5	66
148	BLUEPRINT: mapping human blood cell epigenomes. <i>Haematologica</i> , 2013, 98, 1487-1489.	3.5	189
149	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. <i>Epigenetics</i> , 2012, 7, 1355-1367.	2.7	67
150	Genome-Wide Profiling of Liver X Receptor, Retinoid X Receptor, and Peroxisome Proliferator-Activated Receptor α in Mouse Liver Reveals Extensive Sharing of Binding Sites. <i>Molecular and Cellular Biology</i> , 2012, 32, 852-867.	2.3	205
151	Chromatin accessibility, p300, and histone acetylation define PML-RAR α and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 3058-3068.	1.4	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.	1.4	98
153	Transcriptome Analysis Using RNA-Seq. <i>Methods in Molecular Biology</i> , 2012, 923, 221-239.	0.9	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.	11.0	926
155	Uncovering Common Principles in Protein Export of Malaria Parasites. <i>Cell Host and Microbe</i> , 2012, 12, 717-729.	11.0	115
156	Placing the <i>Plasmodium falciparum</i> epigenome on the map. <i>Trends in Parasitology</i> , 2012, 28, 486-495.	3.3	35
157	Indole-Derived Psammoplin A Analogues as Epigenetic Modulators with Multiple Inhibitory Activities. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 9467-9491.	6.4	48
158	The Transcriptional and Epigenomic Foundations of Ground State Pluripotency. <i>Cell</i> , 2012, 149, 590-604.	28.9	774
159	Bacille Calmette-Guérin induces NOD2-dependent nonspecific protection from reinfection via epigenetic reprogramming of monocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17537-17542.	7.1	1,294
160	Comparative Genomics of Two Independently Enriched <i>Candidatus Kuenenia stuttgartiensis</i> Anaerobic Bacteria. <i>Frontiers in Microbiology</i> , 2012, 3, 307.	3.5	51
161	SS18 Together with Animal-Specific Factors Defines Human BAF-Type SWI/SNF Complexes. <i>PLoS ONE</i> , 2012, 7, e33834.	2.5	102
162	The Human EKC/KEOPS Complex Is Recruited to Cullin2 Ubiquitin Ligases by the Human Tumour Antigen PRAME. <i>PLoS ONE</i> , 2012, 7, e42822.	2.5	41

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