

Hendrik Gerard Stunnenberg

List of Publications by Year in descending order

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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	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
2	Trained immunity: A program of innate immune memory in health and disease. <i>Science</i> , 2016, 352, aaf1098.	12.6	1,809
3	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
4	An oestrogen-receptor-bound human chromatin interactome. <i>Nature</i> , 2009, 462, 58-64.	27.8	1,537
5	mTOR- and HIF-1 α -mediated aerobic glycolysis as metabolic basis for trained immunity. <i>Science</i> , 2014, 345, 1250684.	12.6	1,517
6	Epigenetic programming of monocyte-to-macrophage differentiation and trained innate immunity. <i>Science</i> , 2014, 345, 1251086.	12.6	1,338
7	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
8	A Unified Nomenclature System for the Nuclear Receptor Superfamily. <i>Cell</i> , 1999, 97, 161-163.	28.9	1,083
9	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
10	Identification of a retinoic acid responsive element in the retinoic acid receptor β gene. <i>Nature</i> , 1990, 343, 177-180.	27.8	1,044
11	<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
12	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
13	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
14	The Transcriptional and Epigenomic Foundations of Ground State Pluripotency. <i>Cell</i> , 2012, 149, 590-604.	28.9	774
15	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , 2017, 23, 517-525.	30.7	769
16	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	27.8	749
17	Molecular mechanism of anaerobic ammonium oxidation. <i>Nature</i> , 2011, 479, 127-130.	27.8	707
18	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	27.8	596

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19	Glutaminolysis and Fumarate Accumulation Integrate Immunometabolic and Epigenetic Programs in Trained Immunity. <i>Cell Metabolism</i> , 2016, 24, 807-819.	16.2	584
20	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , 2016, 167, 1398-1414.e24.	28.9	573
21	Quantitative comparison of genome-wide DNA methylation mapping technologies. <i>Nature Biotechnology</i> , 2010, 28, 1106-1114.	17.5	534
22	Heterodimerization of the Drosophila ecdysone receptor with retinoid X receptor and ultraspiracle. <i>Nature</i> , 1993, 362, 471-475.	27.8	512
23	Transcriptional Landscape of Human Tissue Lymphocytes Unveils Uniqueness of Tumor-Infiltrating T Regulatory Cells. <i>Immunity</i> , 2016, 45, 1135-1147.	14.3	510
24	Genome-wide analysis of ETS-family DNA-binding in vitro and in vivo. <i>EMBO Journal</i> , 2010, 29, 2147-2160.	7.8	497
25	Genome-wide profiling of PPAR α :RXR and RNA polymerase II occupancy reveals temporal activation of distinct metabolic pathways and changes in RXR dimer composition during adipogenesis. <i>Genes and Development</i> , 2008, 22, 2953-2967.	5.9	475
26	β -Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance. <i>Cell</i> , 2016, 167, 1354-1368.e14.	28.9	467
27	Rapid and efficient purification of native histidine-tagged protein expressed by recombinant vaccinia virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 8972-8976.	7.1	456
28	N6-methyladenosine (m6A) recruits and repels proteins to regulate mRNA homeostasis. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 870-878.	8.2	432
29	Whole-Genome Bisulfite Sequencing of Two Distinct Interconvertible DNA Methylomes of Mouse Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2013, 13, 360-369.	11.1	424
30	The interplay of epigenetic marks during stem cell differentiation and development. <i>Nature Reviews Genetics</i> , 2017, 18, 643-658.	16.3	414
31	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
32	Repression of transcription mediated at a thyroid hormone response element by the v-erb-A oncogene product. <i>Nature</i> , 1989, 340, 242-244.	27.8	402
33	ChIP-Seq of ER α and RNA polymerase II defines genes differentially responding to ligands. <i>EMBO Journal</i> , 2009, 28, 1418-1428.	7.8	377
34	Sequential ChIP-bisulfite sequencing enables direct genome-scale investigation of chromatin and DNA methylation cross-talk. <i>Genome Research</i> , 2012, 22, 1128-1138.	5.5	344
35	A TFTC/STAGA Module Mediates Histone H2A and H2B Deubiquitination, Coactivates Nuclear Receptors, and Counteracts Heterochromatin Silencing. <i>Molecular Cell</i> , 2008, 29, 92-101.	9.7	331
36	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226.	17.5	323

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37	MBD2/NuRD and MBD3/NuRD, Two Distinct Complexes with Different Biochemical and Functional Properties. <i>Molecular and Cellular Biology</i> , 2006, 26, 843-851.	2.3	290
38	Restoring polyamines protects from age-induced memory impairment in an autophagy-dependent manner. <i>Nature Neuroscience</i> , 2013, 16, 1453-1460.	14.8	283
39	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
40	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	21.4	278
41	PML-RAR α /RXR Alters the Epigenetic Landscape in Acute Promyelocytic Leukemia. <i>Cancer Cell</i> , 2010, 17, 173-185.	16.8	276
42	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	12.6	253
43	A comprehensive evaluation of rodent malaria parasite genomes and gene expression. <i>BMC Biology</i> , 2014, 12, 86.	3.8	251
44	Plasmodium falciparum Heterochromatin Protein 1 Marks Genomic Loci Linked to Phenotypic Variation of Exported Virulence Factors. <i>PLoS Pathogens</i> , 2009, 5, e1000569.	4.7	243
45	Whole-genome DNA methylation profiling using MethylCap-seq. <i>Methods</i> , 2010, 52, 232-236.	3.8	243
46	Pcl-PRC2 is needed to generate high levels of H3-K27 trimethylation at Polycomb target genes. <i>EMBO Journal</i> , 2007, 26, 4078-4088.	7.8	236
47	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016, 7, 11383.	12.8	235
48	Tracking the embryonic stem cell transition from ground state pluripotency. <i>Development (Cambridge)</i> , 2017, 144, 1221-1234.	2.5	226
49	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
50	Dynamic binding of RBPJ is determined by Notch signaling status. <i>Genes and Development</i> , 2013, 27, 1059-1071.	5.9	218
51	DNA Methylation Dynamics of Human Hematopoietic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2016, 19, 808-822.	11.1	216
52	Affinity purification of histidine-tagged proteins. <i>Molecular Biology Reports</i> , 1993, 18, 223-230.	2.3	215
53	Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. <i>Molecular and Cellular Biology</i> , 2008, 28, 2732-2744.	2.3	208
54	A Hierarchy of H3K4me3 and H3K27me3 Acquisition in Spatial Gene Regulation in Xenopus Embryos. <i>Developmental Cell</i> , 2009, 17, 425-434.	7.0	206

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55	Genome-Wide Profiling of Liver X Receptor, Retinoid X Receptor, and Peroxisome Proliferator-Activated Receptor β in Mouse Liver Reveals Extensive Sharing of Binding Sites. <i>Molecular and Cellular Biology</i> , 2012, 32, 852-867.	2.3	205
56	H2A.Z Demarcates Intergenic Regions of the <i>Plasmodium falciparum</i> Epigenome That Are Dynamically Marked by H3K9ac and H3K4me3. <i>PLoS Pathogens</i> , 2010, 6, e1001223.	4.7	201
57	Characterization of genome-wide p53-binding sites upon stress response. <i>Nucleic Acids Research</i> , 2008, 36, 3639-3654.	14.5	199
58	Three Members of the 6-cys Protein Family of <i>Plasmodium</i> Play a Role in Gamete Fertility. <i>PLoS Pathogens</i> , 2010, 6, e1000853.	4.7	198
59	Dynamic histone H3 epigenome marking during the intraerythrocytic cycle of <i>Plasmodium falciparum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 9655-9660.	7.1	195
60	Proteomic Profiling of <i>Plasmodium</i> Sporozoite Maturation Identifies New Proteins Essential for Parasite Development and Infectivity. <i>PLoS Pathogens</i> , 2008, 4, e1000195.	4.7	191
61	Roadmap for regulation. <i>Nature</i> , 2015, 518, 314-316.	27.8	190
62	BLUEPRINT: mapping human blood cell epigenomes. <i>Haematologica</i> , 2013, 98, 1487-1489.	3.5	189
63	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
64	Epigenetic Regulation of Learning and Memory by <i>Drosophila</i> EHMT/G9a. <i>PLoS Biology</i> , 2011, 9, e1000569.	5.6	185
65	Biochemical complementation with RNA in the <i>Xenopus</i> oocyte: A small rna is required for the generation of 3' histone mRNA termini. <i>Cell</i> , 1983, 34, 823-828.	28.9	184
66	Coactivation of GR and NF κ B alters the repertoire of their binding sites and target genes. <i>Genome Research</i> , 2011, 21, 1404-1416.	5.5	184
67	A myosin-like dimerization helix and an extra-large homeodomain are essential elements of the tripartite DNA binding structure of LFB1. <i>Cell</i> , 1990, 61, 1225-1236.	28.9	181
68	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
69	Application of Active and Kinase-Deficient Kinome Collection for Identification of Kinases Regulating Hedgehog Signaling. <i>Cell</i> , 2008, 133, 537-548.	28.9	171
70	Genome-Wide Profiling of p63 DNA-Binding Sites Identifies an Element that Regulates Gene Expression during Limb Development in the 7q21 SHFM1 Locus. <i>PLoS Genetics</i> , 2010, 6, e1001065.	3.5	169
71	UTF1, a novel transcriptional coactivator expressed in pluripotent embryonic stem cells and extra-embryonic cells. <i>EMBO Journal</i> , 1998, 17, 2019-2032.	7.8	167
72	Discontinuous transcription or RNA processing of vaccinia virus late messengers results in a poly(A) leader. <i>Cell</i> , 1987, 50, 163-169.	28.9	164

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73	Mechanisms of transactivation by retinoic acid receptors. <i>BioEssays</i> , 1993, 15, 309-315.	2.5	162
74	Controlled Assembly of Macromolecular β -Sheet Fibrils. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 1968-1971.	13.8	157
75	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , 2018, 24, 868-880.	30.7	157
76	Role of p53 Serine 46 in p53 Target Gene Regulation. <i>PLoS ONE</i> , 2011, 6, e17574.	2.5	154
77	Dnmt3L Antagonizes DNA Methylation at Bivalent Promoters and Favors DNA Methylation at Gene Bodies in ESCs. <i>Cell</i> , 2013, 155, 121-134.	28.9	153
78	De Novo Mutations in the Genome Organizer CTCF Cause Intellectual Disability. <i>American Journal of Human Genetics</i> , 2013, 93, 124-131.	6.2	151
79	A Major Role for the Plasmodium falciparum ApiAP2 Protein PfSIP2 in Chromosome End Biology. <i>PLoS Pathogens</i> , 2010, 6, e1000784.	4.7	150
80	Transcriptional and functional profiling defines human small intestinal macrophage subsets. <i>Journal of Experimental Medicine</i> , 2018, 215, 441-458.	8.5	144
81	Global Histone Analysis by Mass Spectrometry Reveals a High Content of Acetylated Lysine Residues in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Journal of Proteome Research</i> , 2009, 8, 3439-3450.	3.7	140
82	Correctly folded Pfs48/45 protein of <i>Plasmodium falciparum</i> elicits malaria transmission-blocking immunity in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4301-4305.	7.1	138
83	9-cis retinoic acid signaling: changing partners causes some excitement.. <i>Genes and Development</i> , 1995, 9, 1811-1816.	5.9	136
84	Transcription factor p63 bookmarks and regulates dynamic enhancers during epidermal differentiation. <i>EMBO Reports</i> , 2015, 16, 863-878.	4.5	134
85	Cooperativity in transactivation between retinoic acid receptor and TFIID requires an activity analogous to E1A. <i>Cell</i> , 1992, 69, 401-412.	28.9	132
86	Genomic actions of estrogen receptor β : what are the targets and how are they regulated?. <i>Endocrine-Related Cancer</i> , 2009, 16, 1073-1089.	3.1	128
87	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
88	High-resolution analysis of epigenetic changes associated with X inactivation. <i>Genome Research</i> , 2009, 19, 1361-1373.	5.5	122
89	Improved method for PCR-mediated site-directed mutagenesis. <i>Nucleic Acids Research</i> , 1994, 22, 541-542.	14.5	121
90	GATA3-dependent cellular reprogramming requires activation-domain dependent recruitment of a chromatin remodeler. <i>Genome Biology</i> , 2016, 17, 36.	8.8	121

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91	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
92	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	12.8	119
93	E2F transcriptional repressor complexes are critical downstream targets of p19ARF/p53-induced proliferative arrest. <i>Cancer Cell</i> , 2002, 2, 55-65.	16.8	118
94	Whole-epigenome analysis in multiple myeloma reveals DNA hypermethylation of B cell-specific enhancers. <i>Genome Research</i> , 2015, 25, 478-487.	5.5	118
95	High expression of functional adenovirus DNA polymerase and precursor terminal protein using recombinant vaccinia virus. <i>Nucleic Acids Research</i> , 1988, 16, 2431-2444.	14.5	116
96	Uncovering Common Principles in Protein Export of Malaria Parasites. <i>Cell Host and Microbe</i> , 2012, 12, 717-729.	11.0	115
97	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.	7.1	114
98	RAD21 Cooperates with Pluripotency Transcription Factors in the Maintenance of Embryonic Stem Cell Identity. <i>PLoS ONE</i> , 2011, 6, e19470.	2.5	109
99	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
100	Characterization of Lysine 56 of Histone H3 as an Acetylation Site in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 25949-25952.	3.4	105
101	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
102	Dynamics of gene silencing during X inactivation using allele-specific RNA-seq. <i>Genome Biology</i> , 2015, 16, 149.	8.8	104
103	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
104	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
105	SS18 Together with Animal-Specific Factors Defines Human BAF-Type SWI/SNF Complexes. <i>PLoS ONE</i> , 2012, 7, e33834.	2.5	102
106	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. <i>Cell Reports</i> , 2016, 17, 2137-2150.	6.4	102
107	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
108	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

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109	Identification of novel functional TBP-binding sites and general factor repertoires. EMBO Journal, 2007, 26, 944-954.	7.8	97
110	An RNA-Seq Strategy to Detect the Complete Coding and Non-Coding Transcriptome Including Full-Length Imprinted Macro ncRNAs. PLoS ONE, 2011, 6, e27288.	2.5	97
111	Environment-induced epigenetic reprogramming in genomic regulatory elements in smoking mothers and their children. Molecular Systems Biology, 2016, 12, 861.	7.2	97
112	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
113	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	21.4	96
114	The Organoid Cell Atlas. Nature Biotechnology, 2021, 39, 13-17.	17.5	96
115	The Gene Encoding the Acyl-CoA-binding Protein Is Activated by Peroxisome Proliferator-activated Receptor β through an Intronic Response Element Functionally Conserved between Humans and Rodents. Journal of Biological Chemistry, 2002, 277, 26821-26830.	3.4	94
116	Histone modification patterns associated with the human X chromosome. EMBO Reports, 2006, 7, 628-634.	4.5	94
117	Temporal uncoupling of the DNA methylome and transcriptional repression during embryogenesis. Genome Research, 2011, 21, 1313-1327.	5.5	92
118	MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5261-70.	7.1	91
119	Clonal evolution of acute myeloid leukemia with FLT3-ITD mutation under treatment with midostaurin. Blood, 2021, 137, 3093-3104.	1.4	91
120	Isolation and Functional Characterization of Two Distinct Sexual-Stage-Specific Promoters of the Human Malaria Parasite <i>Plasmodium falciparum</i> . Molecular and Cellular Biology, 1999, 19, 967-978.	2.3	89
121	The molecular signature of oncofusion proteins in acute myeloid leukemia. FEBS Letters, 2010, 584, 2662-2669.	2.8	88
122	MLL-AF9 and MLL-AF4 oncofusion proteins bind a distinct enhancer repertoire and target the RUNX1 program in 11q23 acute myeloid leukemia. Oncogene, 2017, 36, 3346-3356.	5.9	86
123	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	5.5	85
124	v-erbA overexpression is required to extinguish c-erbA function in erythroid cell differentiation and regulation of the erbA target gene CAII. Genes and Development, 1991, 5, 2033-2047.	5.9	83
125	Vaccinia virus late transcripts generated in vitro have a poly(A) head. EMBO Journal, 1988, 7, 1183-1190.	7.8	80
126	p120-catenin-dependent collective brain infiltration by glioma cell networks. Nature Cell Biology, 2020, 22, 97-107.	10.3	79

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127	Peroxisome Proliferator-activated Receptor $\hat{3}$ Regulates Expression of the Anti-lipolytic G-protein-coupled Receptor 81 (GPR81/Gpr81). <i>Journal of Biological Chemistry</i> , 2009, 284, 26385-26393.	3.4	76
128	Sequence requirements for the export of the <i>Plasmodium falciparum</i> Maurer's clefts protein REX2. <i>Molecular Microbiology</i> , 2009, 71, 1003-1017.	2.5	76
129	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
130	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
131	Peroxisome Proliferator-Activated Receptor Subtype- and Cell-Type-Specific Activation of Genomic Target Genes upon Adenoviral Transgene Delivery. <i>Molecular and Cellular Biology</i> , 2006, 26, 5698-5714.	2.3	74
132	<i>Plasmodium falciparum</i> centromeres display a unique epigenetic makeup and cluster prior to and during schizogony. <i>Cellular Microbiology</i> , 2012, 14, 1391-1401.	2.1	74
133	Combined quantification of intracellular (phospho-)proteins and transcriptomics from fixed single cells. <i>Scientific Reports</i> , 2019, 9, 1469.	3.3	73
134	Linear amplification for deep sequencing. <i>Nature Protocols</i> , 2011, 6, 1026-1036.	12.0	72
135	Epitope Analysis of the Malaria Surface Antigen Pfs48/45 Identifies a Subdomain That Elicits Transmission Blocking Antibodies. <i>Journal of Biological Chemistry</i> , 2007, 282, 17148-17156.	3.4	70
136	5-Hydroxymethylcytosine: a new kid on the epigenetic block?. <i>Molecular Systems Biology</i> , 2011, 7, 562.	7.2	69
137	Uncleaved TFIIA Is a Substrate for Taspase 1 and Active in Transcription. <i>Molecular and Cellular Biology</i> , 2006, 26, 2728-2735.	2.3	67
138	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. <i>Epigenetics</i> , 2012, 7, 1355-1367.	2.7	67
139	Genome-wide epigenomic profiling for biomarker discovery. <i>Clinical Epigenetics</i> , 2016, 8, 122.	4.1	67
140	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
141	Fibril Formation by Triblock Copolymers of Silklike $\hat{2}$ -Sheet Polypeptides and Poly(ethylene glycol). <i>Macromolecules</i> , 2006, 39, 2989-2997.	4.8	66
142	H ₂ A ₂ Z/H ₂ B ₂ Z double-stranded nucleosomes inhabit the AT-rich promoter regions of the <i>Plasmodium falciparum</i> genome. <i>Molecular Microbiology</i> , 2013, 87, 1061-1073.	2.5	66
143	Regulation of DNA Methylation Patterns by CK2-Mediated Phosphorylation of Dnmt3a. <i>Cell Reports</i> , 2014, 8, 743-753.	6.4	66
144	miR-194-5p/BCLAF1 deregulation in AML tumorigenesis. <i>Leukemia</i> , 2017, 31, 2315-2325.	7.2	66

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145	Residues in the TATA-binding protein required to mediate a transcriptional response to retinoic acid in EC cells. <i>Nature</i> , 1993, 365, 562-566.	27.8	65
146	Promoter melting by a stage-specific vaccinia virus transcription factor is independent of the presence of RNA polymerase. <i>Cell</i> , 1991, 65, 105-113.	28.9	62
147	Distinct Cell-Cycle Control in Two Different States of Mouse Pluripotency. <i>Cell Stem Cell</i> , 2017, 21, 449-455.e4.	11.1	61
148	Bioassay for components regulating eukaryotic gene expression: a chromosomal factor involved in the generation of histone mRNA 3' termini.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1982, 79, 6201-6204.	7.1	60
149	Chromatin accessibility, p300, and histone acetylation define PML-RAR \pm and AML1-ETO binding sites in acute myeloid leukemia. <i>Blood</i> , 2012, 120, 3058-3068.	1.4	60
150	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
151	Retinoid-dependent in vitro transcription mediated by the RXR/RAR heterodimer.. <i>Genes and Development</i> , 1994, 8, 3068-3079.	5.9	59
152	The tumour antigen PRAME is a subunit of a Cul2 ubiquitin ligase and associates with active NFY promoters. <i>EMBO Journal</i> , 2011, 30, 3786-3798.	7.8	59
153	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
154	Vitamin C and l-Proline Antagonistic Effects Capture Alternative States in the Pluripotency Continuum. <i>Stem Cell Reports</i> , 2017, 8, 1-10.	4.8	56
155	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
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