

CITATION REPORT

List of articles citing

A user's guide to the encyclopedia of DNA elements (ENCODE)

DOI: 10.1371/journal.pbio.1001046
PLoS Biology, 2011, 9, e1001046.

Source: <https://exaly.com/paper-pdf/50426367/citation-report.pdf>

Version: 2024-04-20

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
1181	Genomics in 2011: challenges and opportunities. 2011 , 12, 137		
1180	Developing and implementing an institute-wide data sharing policy. 2011 , 3, 60		27
1179	The human mitochondrial transcriptome. 2011 , 146, 645-58		561
1178	Identifying novel transcriptional components controlling energy metabolism. 2011 , 14, 739-45		20
1177	Animal transcription networks as highly connected, quantitative continua. 2011 , 21, 611-26		231
1176	Cross-regulation between an alternative splicing activator and a transcription repressor controls neurogenesis. 2011 , 43, 843-50		101
1175	Annotating individual human genomes. 2011 , 98, 233-41		17
1174	Look beyond one's own nose: combination of information from publicly available sources reveals an association of GATA4 polymorphisms with plasma triglycerides. 2011 , 219, 698-703		5
1173	Nuclear accumulation of an uncapped RNA produced by Drosha cleavage of a transcript encoding miR-10b and HOXD4. 2011 , 6, e25689		11
1172	Needles in stacks of needles: finding disease-causal variants in a wealth of genomic data. 2011 , 12, 628-40		423
1171	A guided tour of the genome. 2011 , 473, 8-9		
1170	MotifMap: integrative genome-wide maps of regulatory motif sites for model species. 2011 , 12, 495		113
1169	The relationship between transcription initiation RNAs and CCCTC-binding factor (CTCF) localization. 2011 , 4, 13		36
1168	Exploratory analysis of genomic segmentations with Segtools. 2011 , 12, 415		14
1167	Long non-coding RNA modifies chromatin: epigenetic silencing by long non-coding RNAs. 2011 , 33, 830-9		148
1166	What fraction of the human genome is functional?. <i>Genome Research</i> , 2011 , 21, 1769-76	9.7	104
1165	Pyicos: a versatile toolkit for the analysis of high-throughput sequencing data. 2011 , 27, 3333-40		76

1164	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. <i>Nucleic Acids Research</i> , 2011 , 39, 7058-76	20.1	58
1163	Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states. <i>Genome Research</i> , 2011 , 21, 2049-57	9.7	32
1162	Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. <i>Genome Research</i> , 2011 , 21, 1757-67	9.7	391
1161	MicroRNA-driven developmental remodeling in the brain distinguishes humans from other primates. <i>PLoS Biology</i> , 2011 , 9, e1001214	9.7	159
1160	Pybedtools: a flexible Python library for manipulating genomic datasets and annotations. 2011 , 27, 3423-4		223
1159	CTCFBSDB 2.0: a database for CTCF-binding sites and genome organization. <i>Nucleic Acids Research</i> , 2013 , 41, D188-94	20.1	109
1158	Genome-wide localization of protein-DNA binding and histone modification by a Bayesian change-point method with ChIP-seq data. 2012 , 8, e1002613		43
1157	A genome-wide screen for genetic variants that modify the recruitment of REST to its target genes. 2012 , 8, e1002624		15
1156	Controls of nucleosome positioning in the human genome. 2012 , 8, e1003036		196
1155	Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection. 2012 , 8, e1002789		85
1154	Regulatory variation in a TBX5 enhancer leads to isolated congenital heart disease. 2012 , 21, 3255-63		131
1153	Inferring direct DNA binding from ChIP-seq. <i>Nucleic Acids Research</i> , 2012 , 40, e128	20.1	294
1152	Tracking and coordinating an international curation effort for the CCDS Project. 2012 , 2012, bas008		44
1151	Pinstripe: a suite of programs for integrating transcriptomic and proteomic datasets identifies novel proteins and improves differentiation of protein-coding and non-coding genes. 2012 , 28, 3042-50		59
1150	Finding genes and variants for lipid levels after genome-wide association analysis. 2012 , 23, 98-103		39
1149	An in-depth map of polyadenylation sites in cancer. <i>Nucleic Acids Research</i> , 2012 , 40, 8460-71	20.1	106
1148	YY1 associates with the macrosatellite DXZ4 on the inactive X chromosome and binds with CTCF to a hypomethylated form in some male carcinomas. <i>Nucleic Acids Research</i> , 2012 , 40, 1596-608	20.1	16
1147	Decoding the human genome. <i>Genome Research</i> , 2012 , 22, 1599-601	9.7	32

1146	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , 2012 , 22, 1748-59	9.7	538
1145	Systematic elucidation and in vivo validation of sequences enriched in hindbrain transcriptional control. <i>Genome Research</i> , 2012 , 22, 2278-89	9.7	16
1144	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. <i>Genome Research</i> , 2012 , 22, 9-24	9.7	86
1143	Epigenetic priors for identifying active transcription factor binding sites. 2012 , 28, 56-62		82
1142	Sequence and chromatin determinants of cell-type-specific transcription factor binding. <i>Genome Research</i> , 2012 , 22, 1723-34	9.7	152
1141	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. 2012 , 21, 322-33		91
1140	EGFR ligands drive multipotential stromal cells to produce multiple growth factors and cytokines via early growth response-1. 2012 , 21, 2541-51		40
1139	Key principles and clinical applications of "next-generation" DNA sequencing. 2012 , 5, 887-900		149
1138	Innate interferons inhibit allergen and microbial specific T(H)2 responses. 2012 , 90, 974-7		14
1137	Understanding cardiovascular disease: a journey through the genome (and what we found there). 2012 , 5, 434-43		27
1136	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. <i>Genome Research</i> , 2012 , 22, 1698-710	9.7	44
1135	Comparative genome-wide DNA methylation analysis of colorectal tumor and matched normal tissues. 2012 , 7, 1355-67		62
1134	Detecting differential usage of exons from RNA-seq data. <i>Genome Research</i> , 2012 , 22, 2008-17	9.7	882
1133	Androgen deprivation causes epithelial-mesenchymal transition in the prostate: implications for androgen-deprivation therapy. 2012 , 72, 527-36		267
1132	Asking for more. 2012 , 44, 733		22
1131	The tumor suppressor RASSF10 is upregulated upon contact inhibition and frequently epigenetically silenced in cancer. 2012 , 1, e18		34
1130	The genetics of addiction-a translational perspective. 2012 , 2, e140		129
1129	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012 , 22, 1798-812	9.7	596

1128	The UCSC Genome Browser database: extensions and updates 2011. <i>Nucleic Acids Research</i> , 2012 , 40, D918-23	20.1	263
1127	An introduction to decoding genomes. 2012 , 139, 4494-4495		
1126	Global identification of MLL2-targeted loci reveals MLL2's role in diverse signaling pathways. 2012 , 109, 17603-8		75
1125	Evolutionary conservation of histone modifications in mammals. 2012 , 29, 1757-67		37
1124	The UCSC Genome Browser database: extensions and updates 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D64-9	20.1	633
1123	Early growth response genes signaling supports strong paracrine capability of mesenchymal stem cells. 2012 , 2012, 428403		19
1122	Integrated genome-wide analysis of transcription factor occupancy, RNA polymerase II binding and steady-state RNA levels identify differentially regulated functional gene classes. <i>Nucleic Acids Research</i> , 2012 , 40, 148-58	20.1	54
1121	Genome-wide analysis of p63 binding sites identifies AP-2 factors as co-regulators of epidermal differentiation. <i>Nucleic Acids Research</i> , 2012 , 40, 7190-206	20.1	72
1120	The importance of identifying alternative splicing in vertebrate genome annotation. 2012 , 2012, bas014		23
1119	MolBioLib: a C++11 framework for rapid development and deployment of bioinformatics tasks. 2012 , 28, 2412-6		8
1118	A comprehensive molecular cytogenetic analysis of chromosome rearrangements in gibbons. <i>Genome Research</i> , 2012 , 22, 2520-8	9.7	25
1117	An encyclopedia of mouse DNA elements (Mouse ENCODE). 2012 , 13, 418		340
1116	Extraneuronal activities and regulatory mechanisms of the atypical cyclin-dependent kinase Cdk5. 2012 , 84, 985-93		61
1115	Clinical and public health research using methylated DNA immunoprecipitation (MeDIP): a comparison of commercially available kits to examine differential DNA methylation across the genome. 2012 , 7, 106-12		7
1114	Online tools for bioinformatics analyses in nutrition sciences. 2012 , 3, 654-65		12
1113	Facilitators and impediments of the pluripotency reprogramming factors' initial engagement with the genome. 2012 , 151, 994-1004		605
1112	Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. 2012 , 7, 1368-78		55
1111	Genome-wide epigenetic data facilitate understanding of disease susceptibility association studies. <i>Journal of Biological Chemistry</i> , 2012 , 287, 30932-40	5.4	35

1110	5' end-centered expression profiling using cap-analysis gene expression and next-generation sequencing. 2012 , 7, 542-61		182
1109	A novel evolutionarily conserved element is a general transcriptional repressor of p21WAF1/CIP1. 2012 , 72, 6236-46		4
1108	PDGFR blockade is a rational and effective therapy for NPM-ALK-driven lymphomas. 2012 , 18, 1699-704		85
1107	Epigenetic impact of dietary polyphenols in cancer chemoprevention: lifelong remodeling of our epigenomes. 2012 , 65, 565-76		187
1106	Mutant p53 is a transcriptional co-factor that binds to G-rich regulatory regions of active genes and generates transcriptional plasticity. 2012 , 11, 3290-303		49
1105	Genome-wide studies of CCCTC-binding factor (CTCF) and cohesin provide insight into chromatin structure and regulation. <i>Journal of Biological Chemistry</i> , 2012 , 287, 30906-13	5-4	74
1104	EpiExplorer: live exploration and global analysis of large epigenomic datasets. 2012 , 13, R96		63
1103	The mouse DXZ4 homolog retains Ctf binding and proximity to Pls3 despite substantial organizational differences compared to the primate macrosatellite. 2012 , 13, R70		30
1102	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. 2012 , 13, R48		194
1101	Functional analysis of transcription factor binding sites in human promoters. 2012 , 13, R50		110
1100	Introns in UTRs: why we should stop ignoring them. 2012 , 34, 1025-34		89
1099	BioGPS and GXD: mouse gene expression data-the benefits and challenges of data integration. 2012 , 23, 550-8		6
1098	First exon length controls active chromatin signatures and transcription. <i>Cell Reports</i> , 2012 , 2, 62-8	10.6	119
1097	The KRAB-ZFP/KAP1 system contributes to the early embryonic establishment of site-specific DNA methylation patterns maintained during development. <i>Cell Reports</i> , 2012 , 2, 766-73	10.6	104
1096	An integrated encyclopedia of DNA elements in the human genome. 2012 , 489, 57-74		11449
1095	DNase I sensitivity QTLs are a major determinant of human expression variation. 2012 , 482, 390-4		479
1094	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012 , 22, 1813-31	9.7	1211
1093	Identification of novel NRF2-regulated genes by ChIP-Seq: influence on retinoid X receptor alpha. <i>Nucleic Acids Research</i> , 2012 , 40, 7416-29	20.1	377

1092	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012 , 22, 1760-74	9.7	3142
1091	Identifying disease mutations in genomic medicine settings: current challenges and how to accelerate progress. 2012 , 4, 58		56
1090	Cell type-specific eQTLs in the human immune system. 2012 , 44, 478-80		11
1089	Dense fine-mapping study identifies new susceptibility loci for primary biliary cirrhosis. 2012 , 44, 1137-41		214
1088	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1	798
1087	Np63 knockout mice reveal its indispensable role as a master regulator of epithelial development and differentiation. 2012 , 139, 772-82		198
1086	The long-range interaction landscape of gene promoters. 2012 , 489, 109-13		1066
1085	Unsupervised pattern discovery in human chromatin structure through genomic segmentation. 2012 , 9, 473-6		419
1084	Modeling gene expression using chromatin features in various cellular contexts. 2012 , 13, R53		182
1083	Genome-wide in silico prediction of gene expression. 2012 , 28, 2789-96		42
1082	Circuitry and dynamics of human transcription factor regulatory networks. 2012 , 150, 1274-86		328
1081	Applying next-generation sequencing to pancreatic cancer treatment. 2012 , 9, 477-86		37
1080	Decoding the non-coding RNAs in Alzheimer's disease. 2012 , 69, 3543-59		55
1079	Using formaldehyde-assisted isolation of regulatory elements (FAIRE) to isolate active regulatory DNA. 2012 , 7, 256-67		230
1078	Chromatin insulator elements: establishing barriers to set heterochromatin boundaries. <i>Epigenomics</i> , 2012 , 4, 67-80	4.4	51
1077	Waves of retrotransposon expansion remodel genome organization and CTCF binding in multiple mammalian lineages. 2012 , 148, 335-48		390
1076	Base-resolution analysis of 5-hydroxymethylcytosine in the mammalian genome. 2012 , 149, 1368-80		801
1075	Identification and functional characterization of the human EXT1 promoter region. 2012 , 492, 148-59		17

1074	Standard guidelines for the chromosome-centric human proteome project. 2012 , 11, 2005-13		121
1073	The high Nrf2 expression in human acute myeloid leukemia is driven by NF- κ B and underlies its chemo-resistance. 2012 , 120, 5188-98		175
1072	Design and quality control of short interfering RNA. 2012 , 46, 739-754		2
1071	The Ruby UCSC API: accessing the UCSC genome database using Ruby. 2012 , 13, 240		2
1070	Conserved cis-regulatory regions in a large genomic landscape control SHH and BMP-regulated Gremlin1 expression in mouse limb buds. 2012 , 12, 23		30
1069	Optimizing the GATA-3 position weight matrix to improve the identification of novel binding sites. <i>BMC Genomics</i> , 2012 , 13, 416	4-5	5
1068	SERE: single-parameter quality control and sample comparison for RNA-Seq. <i>BMC Genomics</i> , 2012 , 13, 524	4-5	82
1067	Euchromatin islands in large heterochromatin domains are enriched for CTCF binding and differentially DNA-methylated regions. <i>BMC Genomics</i> , 2012 , 13, 566	4-5	33
1066	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. 2012 , 5, 6		13
1065	Identification of rare X-linked neuroligin variants by massively parallel sequencing in males with autism spectrum disorder. 2012 , 3, 8		18
1064	Metazoan promoters: emerging characteristics and insights into transcriptional regulation. 2012 , 13, 233-45		347
1063	HLA typing from RNA-Seq sequence reads. 2012 , 4, 102		140
1062	Identifying functional annotation for noncoding genomic sequences. 2012 , Chapter 1, Unit1.10		5
1061	SWI/SNF chromatin-remodeling factors: multiscale analyses and diverse functions. <i>Journal of Biological Chemistry</i> , 2012 , 287, 30897-905	5-4	121
1060	Thematic minireview series on results from the ENCODE Project: Integrative global analyses of regulatory regions in the human genome. <i>Journal of Biological Chemistry</i> , 2012 , 287, 30885-7	5-4	12
1059	An integrated map of genetic variation from 1,092 human genomes. 2012 , 491, 56-65		6049
1058	Contextual data integration in drug discovery. 2012 , 7, 659-66		1
1057	A common single-nucleotide variant in T is strongly associated with chordoma. 2012 , 44, 1185-7		85

1056	Multiple apical plasma membrane constituents are associated with susceptibility to meconium ileus in individuals with cystic fibrosis. 2012 , 44, 562-9		139
1055	Systematic evaluation of factors influencing ChIP-seq fidelity. 2012 , 9, 609-14		112
1054	Application of a systems approach to study developmental gene regulation. 2012 , 4, 245-253		1
1053	FunciSNP: an R/bioconductor tool integrating functional non-coding data sets with genetic association studies to identify candidate regulatory SNPs. <i>Nucleic Acids Research</i> , 2012 , 40, e139	20.1	83
1052	ENCODE whole-genome data in the UCSC Genome Browser: update 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D912-7	20.1	196
1051	ENCODE data in the UCSC Genome Browser: year 5 update. <i>Nucleic Acids Research</i> , 2013 , 41, D56-63	20.1	580
1050	Omics Era in Stem Cell Research: Data Integration of Multi-regulatory Layers. 2012 , 119-137		
1049	Massively parallel functional dissection of mammalian enhancers in vivo. <i>Nature Biotechnology</i> , 2012 , 30, 265-70	44.5	366
1048	Whole genome studies of Tetrahymena. 2012 , 109, 53-81		27
1047	Using potential master regulator sites and paralogous expansion to construct tissue-specific transcriptional networks. 2012 , 6 Suppl 2, S15		5
1046	Support for calcium channel gene defects in autism spectrum disorders. 2012 , 3, 18		50
1045	Mutational signatures of de-differentiation in functional non-coding regions of melanoma genomes. 2012 , 8, e1002871		10
1044	A novel intracellular isoform of matrix metalloproteinase-2 induced by oxidative stress activates innate immunity. 2012 , 7, e34177		74
1043	Bivalent-like chromatin markers are predictive for transcription start site distribution in human. 2012 , 7, e38112		3
1042	Three-dimensional genome architecture influences partner selection for chromosomal translocations in human disease. 2012 , 7, e44196		87
1041	A global genome segmentation method for exploration of epigenetic patterns. 2012 , 7, e46811		19
1040	Upstream distal regulatory elements contact the Lmo2 promoter in mouse erythroid cells. 2012 , 7, e52880		4
1039	Identifying and characterizing regulatory sequences in the human genome with chromatin accessibility assays. 2012 , 3, 651-70		24

1038	Coding exons function as tissue-specific enhancers of nearby genes. <i>Genome Research</i> , 2012 , 22, 1059-68.7	149
1037	A decade of 3C technologies: insights into nuclear organization. 2012 , 26, 11-24	543
1036	Common variants near MBNL1 and NKX2-5 are associated with infantile hypertrophic pyloric stenosis. 2012 , 44, 334-7	33
1035	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. 2011 , 44, 40-6	474
1034	Dissecting genomic regulatory elements in vivo. <i>Nature Biotechnology</i> , 2012 , 30, 504-6	44-5 9
1033	Characterization of enhancer function from genome-wide analyses. 2012 , 13, 29-57	80
1032	Genomic approaches towards finding cis-regulatory modules in animals. 2012 , 13, 469-83	156
1031	Predictive regulatory models in <i>Drosophila melanogaster</i> by integrative inference of transcriptional networks. <i>Genome Research</i> , 2012 , 22, 1334-49	9-7 79
1030	A map of the cis-regulatory sequences in the mouse genome. 2012 , 488, 116-20	1019
1029	Interaction between genetic and epigenetic variation defines gene expression patterns at the asthma-associated locus 17q12-q21 in lymphoblastoid cell lines. 2012 , 131, 1161-71	47
1028	At the crossroads: EGFR and PTHrP signaling in cancer-mediated diseases of bone. 2012 , 100, 109-29	13
1027	A vision for a biomedical cloud. 2012 , 271, 122-30	34
1026	A C9orf72 promoter repeat expansion in a Flanders-Belgian cohort with disorders of the frontotemporal lobar degeneration-amyotrophic lateral sclerosis spectrum: a gene identification study. 2012 , 11, 54-65	489
1025	The influence of assortativity on the robustness of signal-integration logic in gene regulatory networks. 2012 , 296, 21-32	13
1024	Long non-coding RNAs in Huntington's disease neurodegeneration. 2012 , 46, 245-54	302
1023	The epigenome in early vertebrate development. 2012 , 50, 192-206	24
1022	Annotation of the domestic dog genome sequence: finding the missing genes. 2012 , 23, 124-31	10
1021	DNA methylation of distal regulatory sites characterizes dysregulation of cancer genes. 2013 , 14, R21	222

1020	Spatial compartmentalization at the nuclear periphery characterized by genome-wide mapping. 2013 , 6,		78
1019	Genetic modifiers of cystic fibrosis-related diabetes. 2013 , 62, 3627-35		116
1018	Candidate gene association studies: a comprehensive guide to useful in silico tools. 2013 , 14, 39		79
1017	Selective constraint, background selection, and mutation accumulation variability within and between human populations. <i>BMC Genomics</i> , 2013 , 14, 495	4-5	13
1016	Combined CHIP-Seq and transcriptome analysis identifies AP-1/JunD as a primary regulator of oxidative stress and IL-1 β synthesis in macrophages. <i>BMC Genomics</i> , 2013 , 14, 92	4-5	17
1015	PuF, an antimetastatic and developmental signaling protein, interacts with the Alzheimer's amyloid- β precursor protein via a tissue-specific proximal regulatory element (PRE). <i>BMC Genomics</i> , 2013 , 14, 68	4-5	6
1014	A comprehensive analysis of adiponectin QTLs using SNP association, SNP cis-effects on peripheral blood gene expression and gene expression correlation identified novel metabolic syndrome (MetS) genes with potential role in carcinogenesis and systemic inflammation. 2013 , 6, 14		17
1013	Signal transducer and activator of transcription (STAT)-3 regulates microRNA gene expression in chronic lymphocytic leukemia cells. 2013 , 12, 50		44
1012	Dipeptidyl peptidases in atherosclerosis: expression and role in macrophage differentiation, activation and apoptosis. 2013 , 108, 350		61
1011	Pharmacogenetics and Pharmacogenomics. 2013 , 1-27		
1010	Human Gene Mutation in Inherited Disease. 2013 , 1-48		1
1009	Computational methodology for ChIP-seq analysis. 2013 , 1, 54-70		20
1008	Latent regulatory potential of human-specific repetitive elements. 2013 , 49, 262-72		53
1007	Persistently altered epigenetic marks in the mouse uterus after neonatal estrogen exposure. 2013 , 27, 1666-77		76
1006	DNA sequence motif: a jack of all trades for ChIP-Seq data. 2013 , 91, 135-71		6
1005	Identification of functional cis-regulatory polymorphisms in the human genome. 2013 , 34, 735-42		7
1004	Common fragile site profiling in epithelial and erythroid cells reveals that most recurrent cancer deletions lie in fragile sites hosting large genes. <i>Cell Reports</i> , 2013 , 4, 420-8	10.6	134
1003	Identification of novel imprinted differentially methylated regions by global analysis of human-parthenogenetic-induced pluripotent stem cells. 2013 , 1, 79-89		26

1002	Whole-exome sequencing identifies mutated c12orf57 in recessive corpus callosum hypoplasia. 2013 , 92, 392-400		20
1001	Impacts of variation in the human genome on gene regulation. 2013 , 425, 3970-7		97
1000	Testosterone enhances cardiomyogenesis in stem cells and recruits the androgen receptor to the MEF2C and HCN4 genes. 2013 , 60, 164-71		16
999	Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position. 2013 , 10, 1213-8		3263
998	Discovery and refinement of loci associated with lipid levels. 2013 , 45, 1274-1283		1904
997	Distinct properties of cell-type-specific and shared transcription factor binding sites. 2013 , 52, 25-36		197
996	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. 2013 , 15, 1141-1152		62
995	Kraken: a set of tools for quality control and analysis of high-throughput sequence data. 2013 , 63, 41-9		242
994	Semiconductor-based DNA sequencing of histone modification states. <i>Nature Communications</i> , 2013 , 4, 2672	17.4	13
993	Genomic and proteomic analyses of Prdm5 reveal interactions with insulator binding proteins in embryonic stem cells. 2013 , 33, 4504-16		24
992	Variants at multiple loci implicated in both innate and adaptive immune responses are associated with Sjögren's syndrome. 2013 , 45, 1284-92		322
991	Identification of genetic variants that affect histone modifications in human cells. 2013 , 342, 747-9		331
990	Identification of recurrent NAB2-STAT6 gene fusions in solitary fibrous tumor by integrative sequencing. 2013 , 45, 180-5		514
989	Global DNA methylation remodeling accompanies CD8 T cell effector function. 2013 , 191, 3419-29		135
988	De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements. <i>Genome Research</i> , 2013 , 23, 1601-14	9.7	44
987	Integrative functional genomic analyses implicate specific molecular pathways and circuits in autism. 2013 , 155, 1008-21		676
986	A network of epigenetic regulators guides developmental haematopoiesis in vivo. 2013 , 15, 1516-25		62
985	Dynamic regulation of the transcription initiation landscape at single nucleotide resolution during vertebrate embryogenesis. <i>Genome Research</i> , 2013 , 23, 1938-50	9.7	77

984	Animal Models of Metabolic Syndrome. 2013 , 243-264		3
983	Identifying multiple causative genes at a single GWAS locus. <i>Genome Research</i> , 2013 , 23, 1996-2002	9-7	81
982	DNA methylation profiling in human B cells reveals immune regulatory elements and epigenetic plasticity at Alu elements during B-cell activation. <i>Genome Research</i> , 2013 , 23, 2030-41	9-7	75
981	Disclosing the crosstalk among DNA methylation, transcription factors, and histone marks in human pluripotent cells through discovery of DNA methylation motifs. <i>Genome Research</i> , 2013 , 23, 2013-29	9-7	29
980	A genome-wide association analysis identifies novel susceptibility loci for coronary arterial lesions in patients with Kawasaki disease. 2013 , 161, 513-5		11
979	EPITRANS: a database that integrates epigenome and transcriptome data. 2013 , 36, 472-5		6
978	Genome-wide signatures of differential DNA methylation in pediatric acute lymphoblastic leukemia. 2013 , 14, r105		208
977	Gentrepid V2.0: a web server for candidate disease gene prediction. 2013 , 14, 249		4
976	Spatial compartmentalization at the nuclear periphery characterized by genome-wide mapping. <i>BMC Genomics</i> , 2013 , 14, 591	4-5	29
975	NPEBseq: nonparametric empirical bayesian-based procedure for differential expression analysis of RNA-seq data. 2013 , 14, 262		25
974	Limited evidence for evolutionarily conserved targeting of long non-coding RNAs by microRNAs. 2013 , 4, 4		4
973	A compact, in vivo screen of all 6-mers reveals drivers of tissue-specific expression and guides synthetic regulatory element design. 2013 , 14, R72		12
972	DNA methylation and differentiation: HOX genes in muscle cells. 2013 , 6, 25		38
971	REACTIN: regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. <i>BMC Genomics</i> , 2013 , 14, 504	4-5	17
970	Spatial expression of transcription factors in Drosophila embryonic organ development. 2013 , 14, R140		87
969	Discovery of MLL1 binding units, their localization to CpG Islands, and their potential function in mitotic chromatin. <i>BMC Genomics</i> , 2013 , 14, 927	4-5	12
968	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. 2013 , 12, 140		48
967	Aging is associated with highly defined epigenetic changes in the human epidermis. 2013 , 6, 36		62

966	Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. 2013 , 45, 1198-206		350
965	Promiscuous RNA binding by Polycomb repressive complex 2. 2013 , 20, 1250-7		332
964	The lysine specific demethylase-1 (LSD1/KDM1A) regulates VEGF-A expression in prostate cancer. 2013 , 7, 555-66		70
963	The Human Genome Project: big science transforms biology and medicine. 2013 , 5, 79		103
962	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013 , 41, 827-40.1	40.1	383
961	Comparative analysis of affinity-based 5-hydroxymethylation enrichment techniques. <i>Nucleic Acids Research</i> , 2013 , 41, e206	20.1	41
960	Enterocyte-specific regulation of the apical nutrient transporter SLC6A19 (B(0)AT1) by transcriptional and epigenetic networks. <i>Journal of Biological Chemistry</i> , 2013 , 288, 33813-33823	5-4	21
959	Chromatin marks identify critical cell types for fine mapping complex trait variants. 2013 , 45, 124-30		422
958	XACT, a long noncoding transcript coating the active X chromosome in human pluripotent cells. 2013 , 45, 239-41		103
957	eRNAs are required for p53-dependent enhancer activity and gene transcription. 2013 , 49, 524-35		399
956	Analysis of alternative cleavage and polyadenylation by 3' region extraction and deep sequencing. 2013 , 10, 133-9		286
955	Transcriptomics in the RNA-seq era. 2013 , 17, 4-11		211
954	Dynamic DNA methylation across diverse human cell lines and tissues. <i>Genome Research</i> , 2013 , 23, 555-63.7	63.7	500
953	Multilayered chromatin analysis reveals E2f, Smad and Zfx as transcriptional regulators of histones. 2013 , 20, 119-26		34
952	The androgen receptor induces a distinct transcriptional program in castration-resistant prostate cancer in man. 2013 , 23, 35-47		282
951	The Human Genome: A Window on Human Genetics, Biology, and Medicine. 2013 , 4-27		1
950	Regulation of transcription through acetylation of H3K122 on the lateral surface of the histone octamer. 2013 , 152, 859-72		163
949	Mechanisms of formation of structural variation in a fully sequenced human genome. 2013 , 34, 345-54		25

948	Systematic investigation of protein-small molecule interactions. 2013 , 65, 2-8	24
947	Fine mapping of 11q13.5 identifies regions associated with prostate cancer and prostate cancer death. 2013 , 49, 3335-43	5
946	Common genetic variants regulating ADD3 gene expression alter biliary atresia risk. 2013 , 59, 1285-91	53
945	Suppression and epigenetic regulation of MiR-9 contributes to ethanol teratology: evidence from zebrafish and murine fetal neural stem cell models. 2013 , 37, 1657-67	37
944	Cytosine 5-Hydroxymethylation of the LZTS1 Gene Is Reduced in Breast Cancer. 2013 , 6, 715-21	16
943	The influence of assortativity on the robustness and evolvability of gene regulatory networks upon gene birth. 2013 , 330, 26-36	10
942	The Coding and the Non-coding Transcriptome. 2013 , 27-41	2
941	Epigenomics: sequencing the methylome. 2013 , 973, 39-54	2
940	The helix turns at 60: writhing free in chromosomes. 2013 , 20, 251-3	6
939	Transcription-dependent dynamic supercoiling is a short-range genomic force. 2013 , 20, 396-403	209
938	Gene regulation. 2013 , 977, 1-11	5
937	DNase I digestion of isolated nuclei for genome-wide mapping of DNase hypersensitivity sites in chromatin. 2013 , 977, 21-33	19
936	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. 2013 , 45, 385-91, 391e1-2	413
935	Genome-wide profiling of 5-formylcytosine reveals its roles in epigenetic priming. 2013 , 153, 678-91	453
934	Integrated genomic approaches to enhance genetic resistance in chickens. 2013 , 1, 239-60	31
933	Inversion upstream of FOXF1 in a case of lethal alveolar capillary dysplasia with misalignment of pulmonary veins. 2013 , 161A, 764-70	12
932	The vast, conserved mammalian lincRNome. 2013 , 9, e1002917	44
931	New insights from existing sequence data: generating breakthroughs without a pipette. 2013 , 49, 605-17	9

930	DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. 2013 , 45, 852-9	94
929	Global chromatin state analysis reveals lineage-specific enhancers during the initiation of human T helper 1 and T helper 2 cell polarization. 2013 , 38, 1271-84	70
928	A detailed protocol for formaldehyde-assisted isolation of regulatory elements (FAIRE). 2013 , Chapter 21, Unit21.26	27
927	Browsing (Epi)genomes: a guide to data resources and epigenome browsers for stem cell researchers. 2013 , 13, 14-21	16
926	Genome-wide chromatin interactions of the Nanog locus in pluripotency, differentiation, and reprogramming. 2013 , 12, 699-712	161
925	PING 2.0: an R/Bioconductor package for nucleosome positioning using next-generation sequencing data. 2013 , 29, 2049-50	14
924	An integrative approach to understanding the combinatorial histone code at functional elements. 2013 , 29, 2231-7	6
923	Methylomics of gene expression in human monocytes. 2013 , 22, 5065-74	66
922	The Xist lncRNA exploits three-dimensional genome architecture to spread across the X chromosome. 2013 , 341, 1237973	695
921	STAT3 targets suggest mechanisms of aggressive tumorigenesis in diffuse large B-cell lymphoma. 2013 , 3, 2173-85	24
920	Developmental dysplasia of the hip: linkage mapping and whole exome sequencing identify a shared variant in CX3CR1 in all affected members of a large multigeneration family. 2013 , 28, 2540-9	36
919	Informatics and clinical genome sequencing: opening the black box. 2013 , 15, 165-71	30
918	Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs. 2013 , 29, 2300-10	18
917	The genomic landscape of cohesin-associated chromatin interactions. <i>Genome Research</i> , 2013 , 23, 1224-34	85
916	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013 , 23, 800-11	9.7 191
915	Inferring chromatin-bound protein complexes from genome-wide binding assays. <i>Genome Research</i> , 2013 , 23, 1295-306	9.7 28
914	Comprehensive prediction in 78 human cell lines reveals rigidity and compactness of transcription factor dimers. <i>Genome Research</i> , 2013 , 23, 1307-18	9.7 26
913	Transforming Genomes Using MOD Files with Applications. 2013 ,	7

912	An Island-Based Approach for Differential Expression Analysis. 2013 , 2013, 419-429	0
911	Rejuvenation of gene expression pattern of aged human skin by broadband light treatment: a pilot study. 2013 , 133, 394-402	33
910	Inactivation of intergenic enhancers by EBNA3A initiates and maintains polycomb signatures across a chromatin domain encoding CXCL10 and CXCL9. 2013 , 9, e1003638	45
909	Inferring nucleosome positions with their histone mark annotation from ChIP data. 2013 , 29, 2547-54	15
908	Centromere-like regions in the budding yeast genome. 2013 , 9, e1003209	30
907	Asynchronous replication, mono-allelic expression, and long range Cis-effects of ASAR6. 2013 , 9, e1003423	31
906	Linking proteomic and transcriptional data through the interactome and epigenome reveals a map of oncogene-induced signaling. 2013 , 9, e1002887	42
905	Human genome replication proceeds through four chromatin states. 2013 , 9, e1003233	46
904	Computational identification of diverse mechanisms underlying transcription factor-DNA occupancy. 2013 , 9, e1003571	39
903	MBD3 localizes at promoters, gene bodies and enhancers of active genes. 2013 , 9, e1004028	79
902	Grape RNA-Seq analysis pipeline environment. 2013 , 29, 614-21	23
901	Systematically differentiating functions for alternatively spliced isoforms through integrating RNA-seq data. 2013 , 9, e1003314	58
900	CistromeFinder for ChIP-seq and DNase-seq data reuse. 2013 , 29, 1352-4	15
899	NF-Y coassociates with FOS at promoters, enhancers, repetitive elements, and inactive chromatin regions, and is stereo-positioned with growth-controlling transcription factors. <i>Genome Research</i> , 2013 , 23, 1195-209	9.7 99
898	Early de novo DNA methylation and prolonged demethylation in the muscle lineage. 2013 , 8, 317-32	63
897	Long non-coding RNAs and human X-chromosome regulation: a coat for the active X chromosome. 2013 , 10, 1262-5	9
896	Sequence features of yeast and human core promoters that are predictive of maximal promoter activity. <i>Nucleic Acids Research</i> , 2013 , 41, 5569-81	20.1 70
895	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. 2013 , 22, 2520-8	88

894	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. <i>Nucleic Acids Research</i> , 2013 , 41, D171-6	20.1	212
893	HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. <i>Nucleic Acids Research</i> , 2013 , 41, D195-202	20.1	158
892	Genetic variation in the inflammation and innate immunity pathways and colorectal cancer risk. 2013 , 22, 2094-101		15
891	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. <i>Nucleic Acids Research</i> , 2013 , 41, 7220-30	20.1	11
890	Comparative transgenic analysis of enhancers from the human SHOX and mouse Shox2 genomic regions. 2013 , 22, 3063-76		14
889	Transcription factor and chromatin features predict genes associated with eQTLs. <i>Nucleic Acids Research</i> , 2013 , 41, 1450-63	20.1	22
888	Human TREX component Thoc5 affects alternative polyadenylation site choice by recruiting mammalian cleavage factor I. <i>Nucleic Acids Research</i> , 2013 , 41, 7060-72	20.1	43
887	A p53 enhancer region regulates target genes through chromatin conformations in cis and in trans. 2013 , 27, 2433-8		27
886	High-throughput sequencing reveals principles of adeno-associated virus serotype 2 integration. 2013 , 87, 8559-68		28
885	miRspring: a compact standalone research tool for analyzing miRNA-seq data. <i>Nucleic Acids Research</i> , 2013 , 41, e147	20.1	30
884	Several cis-regulatory elements control mRNA stability, translation efficiency, and expression pattern of Prrxl1 (paired related homeobox protein-like 1). <i>Journal of Biological Chemistry</i> , 2013 , 288, 36285-301	5.4	12
883	VlincRNAs controlled by retroviral elements are a hallmark of pluripotency and cancer. 2013 , 14, R73		59
882	The glucocorticoid receptor and KLF15 regulate gene expression dynamics and integrate signals through feed-forward circuitry. 2013 , 33, 2104-15		71
881	Nucleosome maps of the human cytomegalovirus genome reveal a temporal switch in chromatin organization linked to a major IE protein. 2013 , 110, 13126-31		29
880	Signal transducer and activator of transcription 3 limits Epstein-Barr virus lytic activation in B lymphocytes. 2013 , 87, 11438-46		37
879	A pharmacogenomic approach to the treatment of children with GH deficiency or Turner syndrome. 2013 , 169, 277-89		22
878	Deciphering the transcriptional regulation of microRNA genes in humans with ACTLocator. <i>Nucleic Acids Research</i> , 2013 , 41, e5	20.1	11
877	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. 2013 , 110, 17921-6		477

876	Fine-mapping of genome-wide association study-identified risk loci for colorectal cancer in African Americans. 2013 , 22, 5048-55		30
875	Patterns of methylation heritability in a genome-wide analysis of four brain regions. <i>Nucleic Acids Research</i> , 2013 , 41, 2095-104	20.1	41
874	High-throughput identification of long-range regulatory elements and their target promoters in the human genome. <i>Nucleic Acids Research</i> , 2013 , 41, 4835-46	20.1	23
873	The Functionality of Prostate Cancer Predisposition Risk Regions Is Revealed by AR Enhancers. 2013 , 59-84		1
872	TCL1A and ATM are co-expressed in chronic lymphocytic leukemia cells without deletion of 11q. 2013 , 98, 269-73		4
871	Common chromosome fragile sites in human and murine epithelial cells and FHIT/FRA3B loss-induced global genome instability. 2013 , 52, 1017-29		46
870	Efficiently identifying significant associations in genome-wide association studies. 2013 , 20, 817-30		3
869	Advancing Renewable Normal Human Cell Assays for Drug Discovery. 2013 , 74, 127-137		2
868	CHIPBase: a database for decoding the transcriptional regulation of long non-coding RNA and microRNA genes from CHIP-Seq data. <i>Nucleic Acids Research</i> , 2013 , 41, D177-87	20.1	256
867	Validation of reported genetic risk factors for periodontitis in a large-scale replication study. 2013 , 40, 563-72		68
866	Transcriptional response to stress in the dynamic chromatin environment of cycling and mitotic cells. 2013 , 110, E3388-97		104
865	Dual roles of the transcription factor grainyhead-like 2 (GRHL2) in breast cancer. <i>Journal of Biological Chemistry</i> , 2013 , 288, 22993-3008	5.4	84
864	Epigenetic regulation of the human genome: coherence between promoter activity and large-scale chromatin environment. 2013 , 7, 44-62		7
863	A far downstream enhancer for murine Bcl11b controls its T-cell specific expression. 2013 , 122, 902-11		89
862	A co-localization model of paired ChIP-seq data using a large ENCODE data set enables comparison of multiple samples. <i>Nucleic Acids Research</i> , 2013 , 41, 54-62	20.1	7
861	Functional characterization of motif sequences under purifying selection. <i>Nucleic Acids Research</i> , 2013 , 41, 2105-20	20.1	2
860	Heterogeneous nuclear ribonucleoprotein (HnRNP) K genome-wide binding survey reveals its role in regulating 3'-end RNA processing and transcription termination at the early growth response 1 (EGR1) gene through XRN2 exonuclease. <i>Journal of Biological Chemistry</i> , 2013 , 288, 24788-98	5.4	23
859	Distinct global shifts in genomic binding profiles of limb malformation-associated HOXD13 mutations. <i>Genome Research</i> , 2013 , 23, 2091-102	9.7	24

858	CpG dinucleotide-specific hypermethylation of the TNS3 gene promoter in human renal cell carcinoma. 2013 , 8, 739-47	15
857	MPN patients harbor recurrent truncating mutations in transcription factor NF-E2. 2013 , 210, 1003-19	50
856	Genetic markers of comorbid depression and alcoholism in women. 2013 , 37, 896-904	32
855	Transcription factor nuclear factor erythroid-2 mediates expression of the cytokine interleukin 8, a known predictor of inferior outcome in patients with myeloproliferative neoplasms. 2013 , 98, 1073-80	23
854	Transcriptional regulation of the Ikzf1 locus. 2013 , 122, 3149-59	26
853	A mechanistic role for DNA methylation in endothelial cell (EC)-enriched gene expression: relationship with DNA replication timing. 2013 , 121, 3531-40	52
852	DNA methylation of Runx1 regulatory regions correlates with transition from primitive to definitive hematopoietic potential in vitro and in vivo. 2013 , 122, 2978-86	16
851	Pathway Analysis of CHIP-Seq-Based NRF1 Target Genes Suggests a Logical Hypothesis of their Involvement in the Pathogenesis of Neurodegenerative Diseases. 2013 , 7, 139-52	71
850	Sequence signatures extracted from proximal promoters can be used to predict distal enhancers. 2013 , 14, R117	30
849	Phenotypic Plasticity, CYP19A1 Pleiotropy, and Maladaptive Selection in Developmental Disorders. 2013 , 3, 215824401348447	
848	Integrative genomic analysis of CREB defines a critical role for transcription factor networks in mediating the fed/fasted switch in liver. <i>BMC Genomics</i> , 2013 , 14, 337	4-5 41
847	Non-coding-regulatory regions of human brain genes delineated by bacterial artificial chromosome knock-in mice. 2013 , 11, 106	3
846	DNA sequencing methods in human genetics and disease research. 2013 , 5, 34	6
845	MicroRNA discovery by similarity search to a database of RNA-seq profiles. 2013 , 4, 133	8
844	Novel hematopoietic target genes in the NRF2-mediated transcriptional pathway. 2013 , 2013, 120305	54
843	Predicting cell types and genetic variations contributing to disease by combining GWAS and epigenetic data. 2013 , 8, e54359	27
842	Transcriptional suppression, DNA methylation, and histone deacetylation of the regulator of G-protein signaling 10 (RGS10) gene in ovarian cancer cells. 2013 , 8, e60185	36
841	ARLTS1 and prostate cancer risk--analysis of expression and regulation. 2013 , 8, e72040	8

840	RNA-Seq reveals spliceosome and proteasome genes as most consistent transcripts in human cancer cells. 2013 , 8, e72884	36
839	Alternative 5' untranslated regions are involved in expression regulation of human heme oxygenase-1. 2013 , 8, e77224	29
838	Comprehensive analysis of long non-coding RNAs in ovarian cancer reveals global patterns and targeted DNA amplification. 2013 , 8, e80306	63
837	RFECs: a random-forest based algorithm for enhancer identification from chromatin state. 2013 , 9, e1002968	160
836	Detection of regulatory SNPs in human genome using CHIP-seq ENCODE data. 2013 , 8, e78833	39
835	Enhancing systems medicine beyond genotype data by dynamic patient signatures: having information and using it too. 2013 , 4, 241	4
834	A review of post-GWAS prioritization approaches. 2013 , 4, 280	60
833	Evidence for site-specific occupancy of the mitochondrial genome by nuclear transcription factors. 2014 , 9, e84713	25
832	Effects of sulforaphane and 3,3'-diindolylmethane on genome-wide promoter methylation in normal prostate epithelial cells and prostate cancer cells. 2014 , 9, e86787	82
831	Characterization of human pseudogene-derived non-coding RNAs for functional potential. 2014 , 9, e93972	42
830	A Bayesian method to incorporate hundreds of functional characteristics with association evidence to improve variant prioritization. 2014 , 9, e98122	24
829	A new IRAK-M-mediated mechanism implicated in the anti-inflammatory effect of nicotine via α 7 nicotinic receptors in human macrophages. 2014 , 9, e108397	43
828	Genetic Dissection of the Physiological Role of Skeletal Muscle in Metabolic Syndrome. 2014 , 2014, 1-21	4
827	Genome-wide DNA Methylation Profiles of Small Intestine and Liver in Fast-growing and Slow-growing Weaning Piglets. 2014 , 27, 1532-9	5
826	Insights from space: potential role of diet in the spatial organization of chromosomes. 2014 , 6, 5724-39	4
825	Myogenic differential methylation: diverse associations with chromatin structure. 2014 , 3, 426-51	8
824	Cooperative interactions between p53 and NF κ B enhance cell plasticity. 2014 , 5, 12111-25	22
823	Notch signaling genes: myogenic DNA hypomethylation and 5-hydroxymethylcytosine. 2014 , 9, 842-50	35

822	Estrogen receptor polymorphism in a species with alternative behavioral phenotypes. 2014 , 111, 1443-8		69
821	MBD4 cooperates with DNMT1 to mediate methyl-DNA repression and protects mammalian cells from oxidative stress. 2014 , 9, 546-56		38
820	CpG island-mediated global gene regulatory modes in mouse embryonic stem cells. <i>Nature Communications</i> , 2014 , 5, 5490	17.4	21
819	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. 2014 , 23, 3045-53		39
818	Gene-environment interaction research in psychiatric epidemiology: a framework and implications for study design. 2014 , 49, 1525-9		7
817	Overexpression of HOX genes is prevalent in Ewing sarcoma and is associated with altered epigenetic regulation of developmental transcription programs. 2014 , 9, 1613-25		36
816	Integrating gene expression and epidemiological data for the discovery of genetic interactions associated with cancer risk. 2014 , 35, 578-85		1
815	De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. <i>BMC Genomics</i> , 2014 , 15, 1047	4.5	9
814	Deciphering miRNA transcription factor feed-forward loops to identify drug repurposing candidates for cystic fibrosis. 2014 , 6, 94		16
813	dCaP: detecting differential binding events in multiple conditions and proteins. <i>BMC Genomics</i> , 2014 , 15 Suppl 9, S12	4.5	3
812	Role of chromatin and transcriptional co-regulators in mediating p63-genome interactions in keratinocytes. <i>BMC Genomics</i> , 2014 , 15, 1042	4.5	22
811	Incorporating functional annotation information in prioritizing disease associated SNPs from genome wide association studies. 2014 , 57, 1072-9		1
810	Demethylation of the human eotaxin-3 gene promoter leads to the elevated expression of eotaxin-3. 2014 , 192, 466-74		19
809	Alteration in basal and depolarization induced transcriptional network in iPSC derived neurons from Timothy syndrome. 2014 , 6, 75		63
808	Genomic and proteomic analysis of transcription factor TFII-I reveals insight into the response to cellular stress. <i>Nucleic Acids Research</i> , 2014 , 42, 7625-41	20.1	14
807	Differentially methylated CpG island within human XIST mediates alternative P2 transcription and YY1 binding. 2014 , 15, 89		22
806	Polymorphisms in the carcinogen detoxification genes CYB5A and CYB5R3 and breast cancer risk in African American women. 2014 , 25, 1513-21		6
805	Mammalian transcriptional hotspots are enriched for tissue specific enhancers near cell type specific highly expressed genes and are predicted to act as transcriptional activator hubs. 2014 , 15, 412		7

804	Tissue specific CTCF occupancy and boundary function at the human growth hormone locus. <i>Nucleic Acids Research</i> , 2014 , 42, 4906-21	20.1	8
803	Biased, non-equivalent gene-proximal and -distal binding motifs of orphan nuclear receptor TR4 in primary human erythroid cells. 2014 , 10, e1004339		6
802	Quantifying the impact of inter-site heterogeneity on the distribution of ChIP-seq data. 2014 , 5, 399		1
801	A cohesin-independent role for NIPBL at promoters provides insights in CdLS. 2014 , 10, e1004153		87
800	Replicon: a software to accurately predict DNA replication timing in metazoan cells. 2014 , 5, 378		5
799	Identification of a regulatory variant that binds FOXA1 and FOXA2 at the CDC123/CAMK1D type 2 diabetes GWAS locus. 2014 , 10, e1004633		62
798	Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association. 2014 , 10, e1004122		26
797	MAS promoter regulation: a role for Sry and tyrosine nitration of the KRAB domain of ZNF274 as a feedback mechanism. 2014 , 126, 727-38		5
796	A meta-analysis of genome-wide association studies for adiponectin levels in East Asians identifies a novel locus near WDR11-FGFR2. 2014 , 23, 1108-19		53
795	Regression analysis of combined gene expression regulation in acute myeloid leukemia. 2014 , 10, e1003908		48
794	The sequence-specific transcription factor c-Jun targets Cockayne syndrome protein B to regulate transcription and chromatin structure. 2014 , 10, e1004284		25
793	Comparison of REST cistromes across human cell types reveals common and context-specific functions. 2014 , 10, e1003671		27
792	Tracing the evolution of lineage-specific transcription factor binding sites in a birth-death framework. 2014 , 10, e1003771		15
791	biomvRhsmm: genomic segmentation with hidden semi-Markov model. 2014 , 2014, 910390		2
790	Host cell factor-1 recruitment to E2F-bound and cell-cycle-control genes is mediated by THAP11 and ZNF143. <i>Cell Reports</i> , 2014 , 9, 967-82	10.6	27
789	Mapping the Shh long-range regulatory domain. 2014 , 141, 3934-43		49
788	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. <i>Nature Communications</i> , 2014 , 5, 4883	17.4	71
787	Application of experimentally verified transcription factor binding sites models for computational analysis of ChIP-Seq data. <i>BMC Genomics</i> , 2014 , 15, 80	4.5	26

786	Immunomic, genomic and transcriptomic characterization of CT26 colorectal carcinoma. <i>BMC Genomics</i> , 2014 , 15, 190	4.5	179
785	Disrupted auto-regulation of the spliceosomal gene SNRPB causes cerebro-costo-mandibular syndrome. <i>Nature Communications</i> , 2014 , 5, 4483	17.4	40
784	Polo-like kinase 4 transcription is activated via CRE and NRF1 elements, repressed by DREAM through CDE/CHR sites and deregulated by HPV E7 protein. <i>Nucleic Acids Research</i> , 2014 , 42, 163-80	20.1	38
783	Two novel type 2 diabetes loci revealed through integration of TCF7L2 DNA occupancy and SNP association data. 2014 , 2, e000052		12
782	Rho-actin signaling to the MRTF coactivators dominates the immediate transcriptional response to serum in fibroblasts. 2014 , 28, 943-58		219
781	Genetic determinants of circulating interleukin-1 receptor antagonist levels and their association with glycemic traits. 2014 , 63, 4343-59		32
780	Genetic variation in regulatory DNA elements: the case of OCA2 transcriptional regulation. 2014 , 27, 169-77		21
779	Application of histone modification-specific interaction domains as an alternative to antibodies. <i>Genome Research</i> , 2014 , 24, 1842-53	9.7	41
778	A chromatin structure-based model accurately predicts DNA replication timing in human cells. 2014 , 10, 722		59
777	Induction of adult levels of β globin in human erythroid cells that intrinsically express embryonic or fetal globin by transduction with KLF1 and BCL11A-XL. 2014 , 99, 1677-85		37
776	Comparing the efficacy of SNP filtering methods for identifying a single causal SNP in a known association region. 2014 , 78, 50-61		12
775	Comparative epigenomics: defining and utilizing epigenomic variations across species, time-course, and individuals. 2014 , 6, 345-52		6
774	A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. 2014 , 159, 1665-80		3824
773	A bioinformatic and computational study of myosin phosphatase subunit diversity. 2014 , 307, R256-70		16
772	Answering the demands of digital genomics. 2014 , 26, 917-928		1
771	Novel type of red blood cell pyruvate kinase hyperactivity predicts a remote regulatory locus involved in PKLR gene expression. 2014 , 89, 380-4		4
770	Building a Pangenome Reference for a Population. 2014 , 207-221		4
769	(Epi)Genetic analyses of age-related macular degeneration: case-control and discordant twin studies. 2014 , 78, 59-72		13

768	Proteomics, genomics and transcriptomics: their emerging roles in the discovery and validation of colorectal cancer biomarkers. 2014 , 11, 179-205		21
767	Human placental transcriptome shows sexually dimorphic gene expression and responsiveness to maternal dietary n-3 long-chain polyunsaturated fatty acid intervention during pregnancy. <i>BMC Genomics</i> , 2014 , 15, 941	4.5	44
766	microRNA-29 negatively regulates EMT regulator N-myc interactor in breast cancer. 2014 , 13, 200		50
765	Functional variants at the 21q22.3 locus involved in breast cancer progression identified by screening of genome-wide estrogen response elements. 2014 , 16, 455		5
764	Sequence specificity incompletely defines the genome-wide occupancy of Myc. 2014 , 15, 482		43
763	The long non-coding RNA Paupar regulates the expression of both local and distal genes. 2014 , 33, 296-311		154
762	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. <i>Nucleic Acids Research</i> , 2014 , 42, 10856-68	20.1	50
761	Spread of X-chromosome inactivation into autosomal sequences: role for DNA elements, chromatin features and chromosomal domains. 2014 , 23, 1211-23		49
760	Advances in lupus genetics and epigenetics. 2014 , 26, 482-92		84
759	FunCoup 3.0: database of genome-wide functional coupling networks. <i>Nucleic Acids Research</i> , 2014 , 42, D380-8	20.1	89
758	Genome-wide profiling reveals stimulus-specific functions of p53 during differentiation and DNA damage of human embryonic stem cells. <i>Nucleic Acids Research</i> , 2014 , 42, 205-23	20.1	75
757	MACE: model based analysis of ChIP-exo. <i>Nucleic Acids Research</i> , 2014 , 42, e156	20.1	59
756	Sphingosine kinase 2 promotes acute lymphoblastic leukemia by enhancing MYC expression. 2014 , 74, 2803-15		60
755	Study of exonic variation identifies incremental information regarding lipid-related and coronary heart disease genes. 2014 , 115, 478-80		1
754	Genome-wide characterization reveals complex interplay between TP53 and TP63 in response to genotoxic stress. <i>Nucleic Acids Research</i> , 2014 , 42, 6270-85	20.1	50
753	A catalog of HLA type, HLA expression, and neo-epitope candidates in human cancer cell lines. 2014 , 3, e954893		54
752	CpG domains downstream of TSSs promote high levels of gene expression. <i>Nucleic Acids Research</i> , 2014 , 42, 3551-64	20.1	21
751	Transcription factors bind negatively selected sites within human mtDNA genes. 2014 , 6, 2634-46		36

750	Genomic architecture of pharmacological efficacy and adverse events. 2014 , 15, 2025-48	18
749	Comparison of sequence variants in transcriptomic control regions across 17 mouse genomes. 2014 , 2014, bau020	3
748	Similarity in targets with REST points to neural and glioblastoma related miRNAs. <i>Nucleic Acids Research</i> , 2014 , 42, 5436-46	20.1 4
747	Considerations for rare variants in drug metabolism genes and the clinical implications. 2014 , 10, 873-84	16
746	Dynamic reprogramming of signaling upon met inhibition reveals a mechanism of drug resistance in gastric cancer. 2014 , 7, ra38	34
745	Suppression of deacetylase SIRT1 mediates tumor-suppressive NOTCH response and offers a novel treatment option in metastatic Ewing sarcoma. 2014 , 74, 6578-88	50
744	Expression of glutamine transporter Slc38a3 (SNAT3) during acidosis is mediated by a different mechanism than tissue-specific expression. 2014 , 33, 1591-606	10
743	Large-scale quality analysis of published ChIP-seq data. 2014 , 4, 209-23	90
742	Epigenetic modifications are associated with inter-species gene expression variation in primates. 2014 , 15, 547	49
741	Highly divergent integration profile of adeno-associated virus serotype 5 revealed by high-throughput sequencing. 2014 , 88, 2481-8	10
740	Longitudinal epigenetic variation of DNA methyltransferase genes is associated with vulnerability to post-traumatic stress disorder. 2014 , 44, 3165-79	40
739	A novel regulatory element for Shh expression in the lung and gut of mouse embryos. 2014 , 131, 127-36	25
738	Copper metabolism domain-containing 1 represses genes that promote inflammation and protects mice from colitis and colitis-associated cancer. 2014 , 147, 184-195.e3	24
737	A genome-wide association study of bronchodilator response in Latinos implicates rare variants. 2014 , 133, 370-8	84
736	A homozygous 237-kb deletion at 1p31 identified as the locus for midline cleft of the upper and lower lip in a consanguineous family. 2014 , 22, 333-7	10
735	Early growth response-2 signaling mediates immunomodulatory effects of human multipotential stromal cells. 2014 , 23, 155-66	12
734	β-chimaerin, a novel member of the chimaerin Rac-GAP family. 2014 , 41, 2067-76	7
733	Bhlhe40 controls cytokine production by T cells and is essential for pathogenicity in autoimmune neuroinflammation. <i>Nature Communications</i> , 2014 , 5, 3551	17.4 97

732	STAT3, STAT4, NFATc1, and CTCF regulate PD-1 through multiple novel regulatory regions in murine T cells. 2014 , 192, 4876-86		90
731	From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. <i>Genome Research</i> , 2014 , 24, 496-510	9-7	363
730	Reconstructing the DNA methylation maps of the Neandertal and the Denisovan. 2014 , 344, 523-7		142
729	Role of DNA sequence based structural features of promoters in transcription initiation and gene expression. 2014 , 25, 77-85		53
728	Identification of a novel Parkinson's disease locus via stratified genome-wide association study. <i>BMC Genomics</i> , 2014 , 15, 118	4-5	45
727	Stable COT-1 repeat RNA is abundant and is associated with euchromatic interphase chromosomes. 2014 , 156, 907-19		121
726	Transcriptionally active chromatin recruits homologous recombination at DNA double-strand breaks. 2014 , 21, 366-74		386
725	Obesity-associated variants within FTO form long-range functional connections with IRX3. 2014 , 507, 371-5		835
724	Subtelomeric CTCF and cohesin binding site organization using improved subtelomere assemblies and a novel annotation pipeline. <i>Genome Research</i> , 2014 , 24, 1039-50	9-7	45
723	Genetics of male infertility. 2014 , 41, 1-17		42
722	B cell differentiation is associated with reprogramming the CCCTC binding factor-dependent chromatin architecture of the murine MHC class II locus. 2014 , 192, 3925-35		20
721	Clinical genetic testing for male factor infertility: current applications and future directions. 2014 , 2, 339-50		94
720	Principles and methods of integrative genomic analyses in cancer. 2014 , 14, 299-313		245
719	Deep RNA sequencing reveals dynamic regulation of myocardial noncoding RNAs in failing human heart and remodeling with mechanical circulatory support. 2014 , 129, 1009-21		297
718	Erythro-megakaryocytic transcription factors associated with hereditary anemia. 2014 , 123, 3080-8		40
717	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. <i>Genome Research</i> , 2014 , 24, 708-17	9-7	66
716	Transcriptional regulation of Munc13-4 expression in cytotoxic lymphocytes is disrupted by an intronic mutation associated with a primary immunodeficiency. 2014 , 211, 1079-91		32
715	Ribosome-omics of the human ribosome. 2014 , 20, 1004-13		41

714	The tissue-specific transcriptomic landscape of the mid-gestational mouse embryo. 2014 , 141, 2325-30	27
713	Identification of latent biomarkers in hepatocellular carcinoma by ultra-deep whole-transcriptome sequencing. 2014 , 33, 4786-94	31
712	Identification of the RNA recognition element of the RBPMS family of RNA-binding proteins and their transcriptome-wide mRNA targets. 2014 , 20, 1090-102	29
711	Broadly permissive intestinal chromatin underlies lateral inhibition and cell plasticity. 2014 , 506, 511-5	164
710	Prioritizing disease-linked variants, genes, and pathways with an interactive whole-genome analysis pipeline. 2014 , 35, 537-47	18
709	Multi-ethnic fine-mapping of 14 central adiposity loci. 2014 , 23, 4738-44	38
708	Pharmacomicrobiomics: the impact of human microbiome variations on systems pharmacology and personalized therapeutics. 2014 , 18, 402-14	89
707	Genome-wide analysis of HPV integration in human cancers reveals recurrent, focal genomic instability. <i>Genome Research</i> , 2014 , 24, 185-99	9.7 259
706	Basal NF- κ B controls IL-7 responsiveness of quiescent naïve T cells. 2014 , 111, 7397-402	21
705	A CHIP-seq-defined genome-wide map of MEF2C binding reveals inflammatory pathways associated with its role in bone density determination. 2014 , 94, 396-402	16
704	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. 2014 , 156, 343-58	96
703	Peroxisome proliferator-activated receptor γ regulates genes involved in insulin/insulin-like growth factor signaling and lipid metabolism during adipogenesis through functionally distinct enhancer classes. <i>Journal of Biological Chemistry</i> , 2014 , 289, 708-22	5.4 32
702	Epigenetic regulation of the RHOX homeobox gene cluster and its association with human male infertility. 2014 , 23, 12-23	36
701	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. 2014 , 46, 136-143	366
700	Genetic manipulation of the ApoF/Stat2 locus supports an important role for type I interferon signaling in atherosclerosis. 2014 , 233, 234-41	15
699	TNF- β blockade induces IL-10 expression in human CD4 ⁺ T cells. <i>Nature Communications</i> , 2014 , 5, 3199	17.4 74
698	Perspectives on the Human Genome. 2014 , 577-595	
697	Sequencing depth and coverage: key considerations in genomic analyses. 2014 , 15, 121-32	799

696	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. <i>Nature Biotechnology</i> , 2014 , 32, 1231-40	44.5	107
695	Embryonic development following somatic cell nuclear transfer impeded by persisting histone methylation. 2014 , 159, 884-95		271
694	EWS-FLI1 utilizes divergent chromatin remodeling mechanisms to directly activate or repress enhancer elements in Ewing sarcoma. 2014 , 26, 668-681		223
693	Genetic association of the tachykinin receptor 1 TACR1 gene in bipolar disorder, attention deficit hyperactivity disorder, and the alcohol dependence syndrome. 2014 , 165B, 373-80		32
692	Age-related variations in the methylome associated with gene expression in human monocytes and T cells. <i>Nature Communications</i> , 2014 , 5, 5366	17.4	116
691	Epigenetics and ocular diseases: from basic biology to clinical study. 2014 , 229, 825-33		21
690	Mechanisms and treatment of ischaemic stroke--insights from genetic associations. 2014 , 10, 723-30		41
689	RARs and microRNAs. 2014 , 70, 151-79		11
688	Genetics of lipid traits: Genome-wide approaches yield new biology and clues to causality in coronary artery disease. 2014 , 1842, 2010-2020		7
687	Characterizing the genetic basis of innate immune response in TLR4-activated human monocytes. <i>Nature Communications</i> , 2014 , 5, 5236	17.4	48
686	Cross-talking noncoding RNAs contribute to cell-specific neurodegeneration in SCA7. 2014 , 21, 955-961		64
685	TRIB1 downregulates hepatic lipogenesis and glycogenesis via multiple molecular interactions. 2014 , 52, 145-58		40
684	Biorepository regulatory frameworks: building parallel resources that both promote scientific investigation and protect human subjects. 2014 , 13, 5319-24		9
683	Functional importance of cardiac enhancer-associated noncoding RNAs in heart development and disease. 2014 , 76, 55-70		98
682	A three-stage genome-wide association study identifies a susceptibility locus for late radiotherapy toxicity at 2q24.1. 2014 , 46, 891-4		92
681	Extreme HOT regions are CpG-dense promoters in <i>C. elegans</i> and humans. <i>Genome Research</i> , 2014 , 24, 1138-46	9.7	41
680	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014 , 5, 3365	17.4	103
679	Understanding the epigenetic syntax for the genetic alphabet in the kidney. 2014 , 25, 10-7		52

678	Regions outside the DNA-binding domain are critical for proper in vivo specificity of an archetypal zinc finger transcription factor. <i>Nucleic Acids Research</i> , 2014 , 42, 276-89	20.1	24
677	A novel estrogen receptor-microRNA 190a-PAR-1-pathway regulates breast cancer progression, a finding initially suggested by genome-wide analysis of loci associated with lymph-node metastasis. 2014 , 23, 355-67		42
676	Lean Big Data integration in systems biology and systems pharmacology. 2014 , 35, 450-60		67
675	Joint association of genome-wide association study-identified susceptibility loci and dietary patterns in risk of renal cell carcinoma among non-Hispanic whites. 2014 , 180, 499-507		16
674	High-throughput functional testing of ENCODE segmentation predictions. <i>Genome Research</i> , 2014 , 24, 1595-602	9.7	162
673	Epigenetics, chromatin and genome organization: recent advances from the ENCODE project. 2014 , 276, 201-14		67
672	Leveraging biological replicates to improve analysis in ChIP-seq experiments. <i>Computational and Structural Biotechnology Journal</i> , 2014 , 9, e201401002	6.8	33
671	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. <i>Genome Research</i> , 2014 , 24, 1854-68	9.7	168
670	A genome-wide association study identifies a novel locus at 6q22.1 associated with ulcerative colitis. 2014 , 23, 6927-34		31
669	The role of chromatin dynamics in immune cell development. 2014 , 261, 9-22		35
668	The long noncoding RNAs NEAT1 and MALAT1 bind active chromatin sites. 2014 , 55, 791-802		421
667	Bcl-6 directly represses the gene program of the glycolysis pathway. 2014 , 15, 957-64		134
666	Identification of TERRA locus unveils a telomere protection role through association to nearly all chromosomes. <i>Nature Communications</i> , 2014 , 5, 4723	17.4	66
665	5mC oxidation by Tet2 modulates enhancer activity and timing of transcriptome reprogramming during differentiation. 2014 , 56, 286-297		226
664	A NOTCH1-driven MYC enhancer promotes T cell development, transformation and acute lymphoblastic leukemia. 2014 , 20, 1130-7		269
663	Roles for helper T cell lineage-specifying transcription factors in cellular specialization. 2014 , 124, 171-206		11
662	Study of cell differentiation by phylogenetic analysis using histone modification data. 2014 , 15, 269		10
661	Conservation in first introns is positively associated with the number of exons within genes and the presence of regulatory epigenetic signals. <i>BMC Genomics</i> , 2014 , 15, 526	4.5	41

660	ChIPseek, a web-based analysis tool for ChIP data. <i>BMC Genomics</i> , 2014 , 15, 539	4-5	51
659	Common variants near ABCA1, AFAP1 and GMDS confer risk of primary open-angle glaucoma. 2014 , 46, 1120-1125		141
658	Aberrant methylation of the MSH3 promoter and distal enhancer in esophageal cancer patients exposed to first-hand tobacco smoke. 2014 , 140, 1825-33		16
657	Genomics of alternative splicing: evolution, development and pathophysiology. 2014 , 133, 679-87		71
656	Junk or functional DNA? ENCODE and the function controversy. 2014 , 29, 807-831		28
655	glbase: a framework for combining, analyzing and displaying heterogeneous genomic and high-throughput sequencing data. 2014 , 3, 1		50
654	The relationship between DNA methylation, genetic and expression inter-individual variation in untransformed human fibroblasts. 2014 , 15, R37		311
653	Genome-wide profiling of transcription factor binding and epigenetic marks in adipocytes by ChIP-seq. 2014 , 537, 261-79		20
652	A common functional regulatory variant at a type 2 diabetes locus upregulates ARAP1 expression in the pancreatic beta cell. 2014 , 94, 186-97		58
651	Epigenome-wide DNA methylation landscape of melanoma progression to brain metastasis reveals aberrations on homeobox D cluster associated with prognosis. 2014 , 23, 226-38		82
650	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. 2014 , 46, 498-502		104
649	Determinants of protein evolutionary rates in light of ENCODE functional genomics. 2014 , 15,		2
648	Analysis of interactions between the epigenome and structural mutability of the genome using Genboree Workbench tools. 2014 , 15 Suppl 7, S2		10
647	Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics. <i>BMC Genomics</i> , 2014 , 15, 319	4-5	6
646	Functional annotation signatures of disease susceptibility loci improve SNP association analysis. <i>BMC Genomics</i> , 2014 , 15, 398	4-5	10
645	Data integration in the era of omics: current and future challenges. 2014 , 8 Suppl 2, I1		230
644	Replication of previous genome-wide association studies of psychiatric diseases in a large schizophrenia case-control sample from Spain. 2014 , 159, 107-13		27
643	Analysis of candidate genes for lineage-specific expression changes in humans and primates. 2014 , 13, 3596-606		5

642	Genomics: Something to swing about. 2014 , 513, 174-5		1
641	Otx2 expression in anterior neuroectoderm and forebrain/midbrain is directed by more than six enhancers. 2014 , 387, 203-13		15
640	Functionally distinct gene classes as bigger or smaller transcription factor traps: a possible stochastic component to sequential gene expression programs in cancer. 2014 , 536, 398-406		18
639	Large hypomethylated domains serve as strong repressive machinery for key developmental genes in vertebrates. 2014 , 141, 2568-80		30
638	Reorganization of enhancer patterns in transition from naive to primed pluripotency. 2014 , 14, 838-53		306
637	Epigenomic comparison reveals activation of "seed" enhancers during transition from naive to primed pluripotency. 2014 , 14, 854-63		109
636	Long range regulation of the sonic hedgehog gene. 2014 , 27, 54-9		23
635	Transcriptional profiling of the human fibrillin/LTBP gene family, key regulators of mesenchymal cell functions. 2014 , 112, 73-83		25
634	Liver Expression Quantitative Trait Loci (eQTL) and Related Approaches in Pharmacogenomic Studies. 2014 , 111-123		1
633	The PRDX2 gene is transcriptionally silenced and de novo methylated in Hodgkin and Reed-Sternberg cells of classical Hodgkin lymphoma. 2014 , 123, 3672-4		12
632	Advancing Transplantation In Silico: Studying Global Gene Expression Using Functional Genomics for Transplantation Research. 2014 , 208-218		
631	Modelling epigenetic regulation of gene expression in 12 human cell types reveals combinatorial patterns of cell-type-specific genes. 2014 , 8, 104-15		3
630	Application of quantitative trait locus mapping and transcriptomics to studies of the senescence-accelerated phenotype in rats. <i>BMC Genomics</i> , 2014 , 15 Suppl 12, S3	4-5	6
629	Novel bayes factors that capture expert uncertainty in prior density specification in genetic association studies. 2015 , 39, 239-48		9
628	Hierarchical folding and reorganization of chromosomes are linked to transcriptional changes in cellular differentiation. 2015 , 11, 852		229
627	MethGo: a comprehensive tool for analyzing whole-genome bisulfite sequencing data. <i>BMC Genomics</i> , 2015 , 16 Suppl 12, S11	4-5	18
626	PRC2 inhibition counteracts the culture-associated loss of engraftment potential of human cord blood-derived hematopoietic stem and progenitor cells. 2015 , 5, 12319		5
625	Integration of extracellular RNA profiling data using metadata, biomedical ontologies and Linked Data technologies. 2015 , 4, 27497		34

624	Improving Cancer Gene Expression Data Quality through a TCGA Data-Driven Evaluation of Identifier Filtering. 2015 , 14, 149-61		2
623	Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: identifying ChIP-quality p300 monoclonal antibodies. 2014 , 4, 5152		30
622	Smoking Gun or Circumstantial Evidence? Comparison of Statistical Learning Methods using Functional Annotations for Prioritizing Risk Variants. 2015 , 5, 13373		5
621	Differential and coherent processing patterns from small RNAs. 2015 , 5, 12062		18
620	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015 , 13, 1493-1504	10.6	25
619	Inferring intra-motif dependencies of DNA binding sites from ChIP-seq data. 2015 , 16, 375		25
618	Copy number loss upstream of RAI1 uncovers gene expression regulatory region that may impact Potocki-Lupski syndrome diagnosis. 2015 , 8, 75		2
617	BIDCHIPS: bias decomposition and removal from ChIP-seq data clarifies true binding signal and its functional correlates. 2015 , 8, 33		13
616	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. 2015 , 16, 236		23
615	TACR1 gene polymorphism and sex differences in postoperative nausea and vomiting. 2015 , 70, 1148-59		11
614	Accurate inference of isoforms from multiple sample RNA-Seq data. <i>BMC Genomics</i> , 2015 , 16 Suppl 2, S15	4.5	8
613	Insights from GWAS: emerging landscape of mechanisms underlying complex trait disease. <i>BMC Genomics</i> , 2015 , 16 Suppl 8, S4	4.5	10
612	Functionally conserved enhancers with divergent sequences in distant vertebrates. <i>BMC Genomics</i> , 2015 , 16, 882	4.5	12
611	cChIP-seq: a robust small-scale method for investigation of histone modifications. <i>BMC Genomics</i> , 2015 , 16, 1083	4.5	10
610	Functionally distinct patterns of nucleosome remodeling at enhancers in glucocorticoid-treated acute lymphoblastic leukemia. 2015 , 8, 53		8
609	Inferring cell type innovations by phylogenetic methods-concepts, methods, and limitations. 2015 , 324, 653-61		8
608	TERT gene harbors multiple variants associated with pancreatic cancer susceptibility. 2015 , 137, 2175-83		46
607	Multilevel-analysis identify a cis-expression quantitative trait locus associated with risk of renal cell carcinoma. 2015 , 6, 4097-109		1

606	An Efficient Method for Electroporation of Small Interfering RNAs into ENCODE Project Tier 1 GM12878 and K562 Cell Lines. 2015 , 26, 142-9	5
605	Personalized Pharmacoeugenomics. 2015 , 351-367	2
604	An epigenetic hypothesis for the genomic memory of pain. 2015 , 9, 88	32
603	The genetic basis of quality of life in healthy Swedish women: a candidate gene approach. 2015 , 10, e0118292	6
602	HIV Tat controls RNA Polymerase II and the epigenetic landscape to transcriptionally reprogram target immune cells. 2015 , 4,	27
601	SETD2 loss-of-function promotes renal cancer branched evolution through replication stress and impaired DNA repair. 2015 , 34, 5699-708	114
600	Examination of Epigenetic and other Molecular Factors Associated with mda-9/Syntenin Dysregulation in Cancer Through Integrated Analyses of Public Genomic Datasets. 2015 , 127, 49-121	21
599	Characterization and dynamics of pericentromere-associated domains in mice. <i>Genome Research</i> , 2015 , 25, 958-69	9-7 54
598	The Human Genome Project: Where Are We Now and Where Are We Going?. 2015 , 7-31	
597	Hepatitis B virus induces RNR-R2 expression via DNA damage response activation. 2015 , 63, 789-96	21
596	Epigenetic silencing of miR-708 enhances NF- κ B signaling in chronic lymphocytic leukemia. 2015 , 137, 1352-61	40
595	Cardiac gene expression data and in silico analysis provide novel insights into human and mouse taste receptor gene regulation. 2015 , 388, 1009-27	19
594	Investigation of Gene Regulatory Networks Associated with Autism Spectrum Disorder Based on MiRNA Expression in China. 2015 , 10, e0129052	35
593	Using the ENCODE Resource for Functional Annotation of Genetic Variants. 2015 , 2015, 522-36	23
592	EWS and FUS bind a subset of transcribed genes encoding proteins enriched in RNA regulatory functions. <i>BMC Genomics</i> , 2015 , 16, 929	4-5 14
591	A parallel algorithm for -way interval set intersection. 2017 , 105, 542-551	2
590	Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders. 2015 , 86, 1189-202	79
589	Identification and computational analysis of gene regulatory elements. 2015 , 2015, pdb.top083642	4

588	Molecular mechanisms regulating the defects in fragile X syndrome neurons derived from human pluripotent stem cells. 2015 , 4, 37-46		67
587	Vision from next generation sequencing: multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. 2015 , 46, 1-30		43
586	Expitope: a web server for epitope expression. 2015 , 31, 1854-6		11
585	Considering the kinetics of mRNA synthesis in the analysis of the genome and epigenome reveals determinants of co-transcriptional splicing. <i>Nucleic Acids Research</i> , 2015 , 43, 699-707	20.1	12
584	Promises and Challenges of Big Data Computing in Health Sciences. 2015 , 2, 2-11		138
583	Genetic analysis of schizophrenia and bipolar disorder reveals polygenicity but also suggests new directions for molecular interrogation. 2015 , 30, 131-8		52
582	Defining CD4 T cell memory by the epigenetic landscape of CpG DNA methylation. 2015 , 194, 1565-79		44
581	Characterization of a REST-Regulated Internal Promoter in the Schizophrenia Genome-Wide Associated Gene MIR137. 2015 , 41, 698-707		29
580	ZNF143 provides sequence specificity to secure chromatin interactions at gene promoters. <i>Nature Communications</i> , 2015 , 2, 6186	17.4	123
579	Chromatin remodelling and autocrine TNF α are required for optimal interleukin-6 expression in activated human neutrophils. <i>Nature Communications</i> , 2015 , 6, 6061	17.4	70
578	Building a pan-genome reference for a population. 2015 , 22, 387-401		41
577	RNA-Sequencing and Methylome Analysis. 2015 , 77-88		0
576	Cellular STAT3 functions via PCBP2 to restrain Epstein-Barr Virus lytic activation in B lymphocytes. 2015 , 89, 5002-11		28
575	Integrative analysis of public ChIP-seq experiments reveals a complex multi-cell regulatory landscape. <i>Nucleic Acids Research</i> , 2015 , 43, e27	20.1	95
574	Identification of functional variants for cleft lip with or without cleft palate in or near PAX7, FGFR2, and NOG by targeted sequencing of GWAS loci. 2015 , 96, 397-411		106
573	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. <i>Nature Communications</i> , 2015 , 6, 6178	17.4	131
572	Genetic changes shaping the human brain. 2015 , 32, 423-34		87
571	Genome-wide CIITA-binding profile identifies sequence preferences that dictate function versus recruitment. <i>Nucleic Acids Research</i> , 2015 , 43, 3128-42	20.1	20

570	Tissue-specific epigenetics in gene neighborhoods: myogenic transcription factor genes. 2015 , 24, 4660-73		16
569	Expression of the vault RNA protects cells from undergoing apoptosis. <i>Nature Communications</i> , 2015 , 6, 7030	17.4	47
568	Sin3A-associated protein, 18 kDa, a novel binding partner of TRIB1, regulates MTTP expression. 2015 , 56, 1145-52		18
567	Global analysis of biogenesis, stability and sub-cellular localization of lncRNAs mapping to intragenic regions of the human genome. 2015 , 12, 877-92		45
566	Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. 2015 , 47, 979-986		1278
565	Single-cell chromatin accessibility reveals principles of regulatory variation. 2015 , 523, 486-90		1110
564	Publisher's Note: Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction. 2015 , 58, 104-19		2
563	Escape from X inactivation varies in mouse tissues. 2015 , 11, e1005079		142
562	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. 2015 , 11, e1004217		15
561	A pooling-based approach to mapping genetic variants associated with DNA methylation. <i>Genome Research</i> , 2015 , 25, 907-17	9.7	18
560	Transcriptome analysis of controlled and therapy-resistant childhood asthma reveals distinct gene expression profiles. 2015 , 136, 638-48		40
559	Human aging in the post-GWAS era: further insights reveal potential regulatory variants. 2015 , 16, 529-41		3
558	STAT3 acts through pre-existing nucleosome-depleted regions bound by FOS during an epigenetic switch linking inflammation to cancer. 2015 , 8, 7		26
557	Analysis of RNA decay factor mediated RNA stability contributions on RNA abundance. <i>BMC Genomics</i> , 2015 , 16, 154	4.5	30
556	Spectacle: fast chromatin state annotation using spectral learning. 2015 , 16, 33		28
555	Cloning, characterization and analysis of the 5' regulatory region of zebrafish xpd gene. 2015 , 185, 47-53		2
554	Enhancers compete with a long non-coding RNA for regulation of the Kcnq1 domain. <i>Nucleic Acids Research</i> , 2015 , 43, 745-59	20.1	27
553	Genome-wide association study of plasma levels of polychlorinated biphenyls disclose an association with the CYP2B6 gene in a population-based sample. 2015 , 140, 95-101		10

552	Origin of cells and network information. 2015 , 7, 535-40		3
551	Epigenetics, Stem Cell Pluripotency and Differentiation. 2015 , 27-43		
550	A global analysis of the complex landscape of isoforms and regulatory networks of p63 in human cells and tissues. <i>BMC Genomics</i> , 2015 , 16, 584	4-5	40
549	Long-Range Chromatin Interactions. 2015 , 7, a019356		147
548	Exploring DNA methylation changes in promoter, intragenic, and intergenic regions as early and late events in breast cancer formation. 2015 , 15, 816		73
547	Genome-wide association study of toxic metals and trace elements reveals novel associations. 2015 , 24, 4739-45		75
546	Inferring 3D chromatin structure using a multiscale approach based on quaternions. 2015 , 16, 234		10
545	Histone Demethylase Expression Enhances Human Somatic Cell Nuclear Transfer Efficiency and Promotes Derivation of Pluripotent Stem Cells. 2015 , 17, 758-766		119
544	Glucocorticoids and the Lung. 2015 , 872, 279-98		14
543	Editorial overview: Behavioral genetics. 2015 , 2, v-vii		
542	A chromatin code for alternative splicing involving a putative association between CTCF and HP1 proteins. 2015 , 13, 31		43
541	STAT3 Regulates Lytic Activation of Kaposi's Sarcoma-Associated Herpesvirus. 2015 , 89, 11347-55		32
540	Functional diversity of CTCFs is encoded in their binding motifs. <i>BMC Genomics</i> , 2015 , 16, 649	4-5	8
539	Phase I dose escalation and pharmacokinetic evaluation of two different schedules of LY2334737, an oral gemcitabine prodrug, in patients with advanced solid tumors. 2015 , 33, 1206-16		9
538	Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". 2015 , 59 Pt B, 123-38		9
537	Proteogenomics Dashboard for the Human Proteome Project. 2015 , 14, 3738-49		9
536	New basal cell carcinoma susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 6825	17.4	49
535	Tumor necrosis factor- α confers cardioprotection through ectopic expression of keratins K8 and K18. 2015 , 21, 1076-84		69

534	Altitude Adaptation: A Glimpse Through Various Lenses. 2015 , 16, 125-37		81
533	PHACTR1: Functional Clues Linking a Genome-Wide Association Study Locus to Coronary Artery Disease. 2015 , 35, 1293-5		2
532	Genome-wide binding and mechanistic analyses of Smchd1-mediated epigenetic regulation. 2015 , 112, E3535-44		63
531	piRNA-like small RNAs mark extended 3'UTRs present in germ and somatic cells. <i>BMC Genomics</i> , 2015 , 16, 462	4-5	14
530	Current transcriptomics in pig immunity research. 2015 , 26, 1-20		30
529	Proteomic analysis and identification of cellular interactors of the giant ubiquitin ligase HERC2. 2015 , 14, 953-66		30
528	Comparative FAIRE-seq analysis reveals distinguishing features of the chromatin structure of ground state- and primed-pluripotent cells. 2015 , 33, 378-91		16
527	Mechanisms of epigenetic and cell-type specific regulation of Hey target genes in ES cells and cardiomyocytes. 2015 , 79, 79-88		18
526	TP53 engagement with the genome occurs in distinct local chromatin environments via pioneer factor activity. <i>Genome Research</i> , 2015 , 25, 179-88	9-7	69
525	Searching for repetitions in biological networks: methods, resources and tools. 2015 , 16, 118-36		21
524	Assaying the epigenome in limited numbers of cells. 2015 , 72, 51-6		15
523	Proteome sequencing goes deep. 2015 , 24, 11-7		77
522	Computational schemes for the prediction and annotation of enhancers from epigenomic assays. 2015 , 72, 86-94		22
521	Molecular signatures of mood stabilisers highlight the role of the transcription factor REST/NRSF. 2015 , 172, 63-73		8
520	Haplotypes of CpG-related SNPs and associations with DNA methylation patterns. 193-207		1
519	RNA-seq based transcriptomic map reveals new insights into mouse salivary gland development and maturation. <i>BMC Genomics</i> , 2016 , 17, 923	4-5	22
518	Modeling Gene Regulation in Liver Hepatocellular Carcinoma with Random Forests. 2016 , 2016, 1035945		4
517	DOT1L promotes angiogenesis through cooperative regulation of VEGFR2 with ETS-1. 2016 , 7, 69674-69687		15

516	Integrated Systems for NGS Data Management and Analysis: Open Issues and Available Solutions. 2016 , 7, 75	27
515	AuPairWise: A Method to Estimate RNA-Seq Replicability through Co-expression. 2016 , 12, e1004868	8
514	Immunoinformatics Cyberinfrastructure for Modeling and Analytics. 2016 , 45-61	
513	Defining the identity of mouse embryonic dermal fibroblasts. 2016 , 54, 415-30	17
512	Omics-based approaches to understand mechanosensitive endothelial biology and atherosclerosis. 2016 , 8, 378-401	12
511	Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. 2016 , 54, 12.13.1-12.13.25	11
510	Identification of Rare Variants in Metabolites of the Carnitine Pathway by Whole Genome Sequencing Analysis. 2016 , 40, 486-91	8
509	Epigenetics of the myotonic dystrophy-associated DMPK gene neighborhood. <i>Epigenomics</i> , 2016 , 8, 13-34.4	17
508	Enhancer RNA-driven looping enhances the transcription of the long noncoding RNA DHRS4-AS1, a controller of the DHRS4 gene cluster. 2016 , 6, 20961	39
507	A benchmark of gene expression tissue-specificity metrics. 2017 , 18, 205-214	153
506	Deep resequencing of in 762 F508del homozygotes reveals clusters of non-coding variants associated with cystic fibrosis disease traits. 2016 , 3, 16038	25
505	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. 2016 , 17, 266	65
504	Long non-coding RNA Databases in Cardiovascular Research. 2016 , 14, 191-9	35
503	Advances in Genetic Testing for Hereditary Cancer Syndromes. 2016 , 205, 1-15	1
502	JBrowse: a dynamic web platform for genome visualization and analysis. 2016 , 17, 66	393
501	Defining the multivalent functions of CTCF from chromatin state and three-dimensional chromatin interactions. <i>Nucleic Acids Research</i> , 2016 , 44, 6200-12	20.1 14
500	Deletion of Amino Acid Transporter ASCT2 (SLC1A5) Reveals an Essential Role for Transporters SNAT1 (SLC38A1) and SNAT2 (SLC38A2) to Sustain Glutaminolysis in Cancer Cells. <i>Journal of Biological Chemistry</i> , 2016 , 291, 13194-205	5-4 124
499	Evolution of Gene Regulation in Humans. 2016 , 17, 45-67	33

498 Techniques and Approaches to Genetic Analyses in Nephrological Disorders. **2016**, 5, 2-14

497 Cre Recombinase and Other Tyrosine Recombinases. **2016**, 116, 12785-12820 63

496 Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. **2016**, 127, e12-23 35

495 Cystic fibrosis gene modifier SLC26A9 modulates airway response to CFTR-directed therapeutics. **2016**, 25, 4590-4600 62

494 RNA-Seq Library Construction Methods for Transcriptome Analysis. **2016**, 1, 197-215 2

493 Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. **2016**, 25, 4835-4846 34

492 GWAS analysis of handgrip and lower body strength in older adults in the CHARGE consortium. **2016**, 15, 792-800 33

491 Incorporating Functional Genomic Information in Genetic Association Studies Using an Empirical Bayes Approach. **2016**, 40, 176-87 12

490 Noncoding somatic and inherited single-nucleotide variants converge to promote ESR1 expression in breast cancer. **2016**, 48, 1260-6 53

489 Genome-Wide Techniques for the Study of Clinical Epigenetic Biomarkers. **2016**, 119-135

488 Data sources for in vivo molecular profiling of human phenotypes. **2016**, 8, 472-484 1

487 Essential control of early B-cell development by Mef2 transcription factors. **2016**, 127, 572-81 43

486 Emerging tools and approaches to biotechnology in the omics era. **2016**, 1-29

485 How should we measure proportionality on relative gene expression data?. **2016**, 135, 21-36 50

484 Deciphering the cross-talking of human competitive endogenous RNAs in K562 chronic myelogenous leukemia cell line. **2016**, 12, 3633-3642 4

483 Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. *Nature Communications*, **2016**, 7, 12048 17.4 82

482 A novel type 2 diabetes risk allele increases the promoter activity of the muscle-specific small ankyrin 1 gene. **2016**, 6, 25105 9

481 Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). **2016**, 6, 32512 16

480	Natural Selection in the Great Apes. 2016 , 33, 3268-3283		44
479	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. <i>Nature Communications</i> , 2016 , 7, 12510	17.4	65
478	Histone H4 lysine 20 acetylation is associated with gene repression in human cells. 2016 , 6, 24318		29
477	DamID-seq: Genome-wide Mapping of Protein-DNA Interactions by High Throughput Sequencing of Adenine-methylated DNA Fragments. 2016 , e53620		6
476	Describing a Transcription Factor Dependent Regulation of the MicroRNA Transcriptome. 2016 ,		
475	Fluorescence ImmunoPrecipitation (FLIP): a Novel Assay for High-Throughput IP. 2016 , 18, 16		4
474	A semi-parametric statistical model for integrating gene expression profiles across different platforms. 2016 , 17 Suppl 1, 5		8
473	The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. 2016 , 2016,		504
472	Rare Variants of the Serotonin Transporter Are Associated With Psychiatric Comorbidity in Irritable Bowel Syndrome. 2016 , 18, 394-400		9
471	A maximum-likelihood approach for building cell-type trees by lifting. <i>BMC Genomics</i> , 2016 , 17 Suppl 1, 14	4.5	4
470	Long noncoding RNAs expressed in human hepatic stellate cells form networks with extracellular matrix proteins. 2016 , 8, 31		41
469	Parent-of-origin-specific signatures of de novo mutations. 2016 , 48, 935-9		174
468	A Computational Drug Repositioning Approach for Targeting Oncogenic Transcription Factors. <i>Cell Reports</i> , 2016 , 15, 2348-56	10.6	25
467	Krüppel-like Factor 3 (KLF3/BKLF) Is Required for Widespread Repression of the Inflammatory Modulator Galectin-3 (Lgals3). <i>Journal of Biological Chemistry</i> , 2016 , 291, 16048-58	5.4	14
466	Salinity-induced changes in gene expression from anterior and posterior gills of <i>Callinectes sapidus</i> (Crustacea: Portunidae) with implications for crustacean ecological genomics. 2016 , 19, 34-44		16
465	Cell fate control by pioneer transcription factors. 2016 , 143, 1833-7		161
464	Establishing an analytic pipeline for genome-wide DNA methylation. 2016 , 8, 45		31
463	Identification of genetic variants in pharmacokinetic genes associated with Ewing Sarcoma treatment outcome. 2016 , 27, 1788-93		8

462	Cistrome-based Cooperation between Airway Epithelial Glucocorticoid Receptor and NF- κ B Orchestrates Anti-inflammatory Effects. <i>Journal of Biological Chemistry</i> , 2016 , 291, 12673-12687	5-4	33
461	rAAV-compatible MiniPromoters for restricted expression in the brain and eye. 2016 , 9, 52		43
460	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. 2016 , 55, 1-31		39
459	Mapping nucleosome positions using DNase-seq. <i>Genome Research</i> , 2016 , 26, 351-64	9-7	35
458	Np63 regulates IL-33 and IL-31 signaling in atopic dermatitis. 2016 , 23, 1073-85		28
457	CrossHub: a tool for multi-way analysis of The Cancer Genome Atlas (TCGA) in the context of gene expression regulation mechanisms. <i>Nucleic Acids Research</i> , 2016 , 44, e62	20.1	28
456	Intersection of genetics and epigenetics in monozygotic twin genomes. 2016 , 102, 50-6		3
455	Metabolism pathways in chronic lymphocytic leukemia. 2016 , 57, 758-65		32
454	Template-Based Models for Genome-Wide Analysis of Next-Generation Sequencing Data at Base-Pair Resolution. 2016 , 111, 967-987		1
453	MethPat: a tool for the analysis and visualisation of complex methylation patterns obtained by massively parallel sequencing. 2016 , 17, 98		16
452	eQuIPS: eQTL Analysis Using Informed Partitioning of SNPs - A Fully Bayesian Approach. 2016 , 40, 273-83		7
451	ENCODE data at the ENCODE portal. <i>Nucleic Acids Research</i> , 2016 , 44, D726-32	20.1	292
450	From Loci to Biology: Functional Genomics of Genome-Wide Association for Coronary Disease. 2016 , 118, 586-606		36
449	Genetics of Coronary Artery Disease. 2016 , 118, 564-78		185
448	Improving understanding of chromatin regulatory proteins and potential implications for drug discovery. 2016 , 13, 435-45		2
447	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. 2016 , 150, 1633-1645		64
446	Bioinformatic and Genomic Analyses of Cellular Reprogramming and Direct Lineage Conversion. 2016 , 2, 103-112		
445	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. 2016 , 48, 189-94		159

444	Genetic and environmental impacts on DNA methylation levels in twins. <i>Epigenomics</i> , 2016 , 8, 105-17	4.4	17
443	TCGAbiolinks: an R/Bioconductor package for integrative analysis of TCGA data. <i>Nucleic Acids Research</i> , 2016 , 44, e71	20.1	1155
442	Sequence variants in the PTCH1 gene associate with spine bone mineral density and osteoporotic fractures. <i>Nature Communications</i> , 2016 , 7, 10129	17.4	41
441	The genetic association of RUNX3 with ankylosing spondylitis can be explained by allele-specific effects on IRF4 recruitment that alter gene expression. 2016 , 75, 1534-40		37
440	Computational discovery of transcription factors associated with drug response. 2016 , 16, 573-582		12
439	Analysis of the effects of depression associated polymorphisms on the activity of the BICC1 promoter in amygdala neurones. 2016 , 16, 366-74		10
438	Histone H3K4 trimethylation: dynamic interplay with pre-mRNA splicing. 2016 , 94, 1-11		28
437	The epigenetic regulators CBP and p300 facilitate leukemogenesis and represent therapeutic targets in acute myeloid leukemia. 2016 , 35, 279-89		45
436	Antisense transcription of the myotonic dystrophy locus yields low-abundant RNAs with and without (CAG) _n repeat. 2017 , 14, 1374-1388		22
435	Genome-wide association study with additional genetic and post-transcriptional analyses reveals novel regulators of plasma factor XI levels. 2017 , 26, 637-649		27
434	Molecular mechanisms underlying noncoding risk variations in psychiatric genetic studies. 2017 , 22, 497-511		28
433	Single nucleotide-level mapping of DNA double-strand breaks in human HEK293T cells. 2017 , 11, 43-45		
432	Rapid Recall Ability of Memory T cells is Encoded in their Epigenome. 2017 , 7, 39785		26
431	A genome-wide association study yields five novel thyroid cancer risk loci. <i>Nature Communications</i> , 2017 , 8, 14517	17.4	80
430	Human neural progenitors derived from integration-free iPSCs for SCI therapy. 2017 , 19, 55-64		25
429	Nucleome Analysis Reveals Structure-Function Relationships for Colon Cancer. 2017 , 15, 821-830		24
428	Genetic and regulatory mechanism of susceptibility to high-hyperdiploid acute lymphoblastic leukaemia at 10p21.2. <i>Nature Communications</i> , 2017 , 8, 14616	17.4	30
427	Identifying Novel Transcriptional and Epigenetic Features of Nuclear Lamina-associated Genes. 2017 , 7, 100		17

426	Evolutionary re-wiring of p63 and the epigenomic regulatory landscape in keratinocytes and its potential implications on species-specific gene expression and phenotypes. <i>Nucleic Acids Research</i> , 2017 , 45, 8208-8224	20.1	24
425	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. 2017 , 135, 2336-2353		36
424	Identifying low density lipoprotein cholesterol associated variants in the Annexin A2 (ANXA2) gene. 2017 , 261, 60-68		8
423	High-Resolution Genetic Maps Identify Multiple Type 2 Diabetes Loci at Regulatory Hotspots in African Americans and Europeans. 2017 , 100, 803-816		14
422	Association of 5-hydroxymethylation and 5-methylation of DNA cytosine with tissue-specific gene expression. 2017 , 12, 123-138		40
421	Identification of rare nonsynonymous variants in SYNE1/CPG2 in bipolar affective disorder. 2017 , 27, 81-88		4
420	Targeting of Polycomb Repressive Complex 2 to RNA by Short Repeats of Consecutive Guanines. 2017 , 65, 1056-1067.e5		119
419	ChIPBase v2.0: decoding transcriptional regulatory networks of non-coding RNAs and protein-coding genes from ChIP-seq data. <i>Nucleic Acids Research</i> , 2017 , 45, D43-D50	20.1	140
418	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. 2017 , 74, 162-168		66
417	Bioinformatic tools for analysis of CLIP ribonucleoprotein data. 2017 , 8, e1404		8
416	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. 2017 , 100, 51-63		30
415	In Vivo Hepatic Enhancer Elements in the Human ABCG2 Locus. 2017 , 45, 208-215		4
414	Personalized Medicine Through Advanced Genomics. 2017 , 31-48		1
413	Genetic association study identified a 20 kb regulatory element in WLS associated with osteoporosis and bone mineral density in Han Chinese. 2017 , 7, 13668		8
412	Genetic and epigenetic determinants of inter-individual variability in responses to toxicants. 2017 , 6, 50-59		9
411	Common Polymorphisms in Relation to Survival among Small Cell Lung Cancer Patients: A Multicenter Study from the International Lung Cancer Consortium. 2017 , 23, 7550-7557		4
410	Whole genome DNA methylation sequencing of the chicken retina, cornea and brain. 2017 , 4, 170148		14
409	Coordinated Splicing of Regulatory Detained Introns within Oncogenic Transcripts Creates an Exploitable Vulnerability in Malignant Glioma. 2017 , 32, 411-426.e11		99

408 Online resources for studies of genome biology and epigenetics. **2017**, 6, 34-41

407 Association analysis identifies 65 new breast cancer risk loci. **2017**, 551, 92-94 643

406 Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. **2017**, 49, 1767-1778 186

405 Transcriptional response to stress is pre-wired by promoter and enhancer architecture. *Nature Communications*, **2017**, 8, 255 17.4 78

404 RNA sequencing in post-mortem human brains of neuropsychiatric disorders. **2017**, 71, 663-672 11

403 Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. **2017**, 109, 1030-1038 18

402 Parvovirus B19 integration into human CD36+ erythroid progenitor cells. **2017**, 511, 40-48 10

401 A constrained (ell)¹ minimization approach for estimating multiple sparse Gaussian or nonparanormal graphical models. **2017**, 106, 1381-1417 5

400 Integration of DNA methylation and gene transcription across nineteen cell types reveals cell type-specific and genomic region-dependent regulatory patterns. **2017**, 7, 3626 12

399 Integration of VDR genome wide binding and GWAS genetic variation data reveals co-occurrence of VDR and NF- κ B binding that is linked to immune phenotypes. *BMC Genomics*, **2017**, 18, 132 4.5 27

398 Early growth response protein 1 regulates promoter activity of E_{plasma} membrane calcium ATPase 2, a major calcium pump in the brain and auditory system. **2017**, 18, 14 5

397 Links between DNA methylation and nucleosome occupancy in the human genome. **2017**, 10, 18 32

396 Insights into inner ear-specific gene regulation: Epigenetics and non-coding RNAs in inner ear development and regeneration. **2017**, 65, 69-79 24

395 Spatiotemporal regulation of enhancers during cardiogenesis. **2017**, 74, 257-265 4

394 DMAK: A curated pan-cancer DNA methylation annotation knowledgebase. **2017**, 8, 182-190 3

393 It's All in the Brain: A Review of Available Functional Genomic Annotations. **2017**, 81, 478-483 12

392 Peak-Finding Algorithms. **2017**, 2017,

391 Alternative splicing of U2AF1 reveals a shared repression mechanism for duplicated exons. *Nucleic Acids Research*, **2017**, 45, 417-434 20.1 10

390	Genetic Modifiers of Progression-Free Survival in Never-Smoking Lung Adenocarcinoma Patients Treated with First-Line Tyrosine Kinase Inhibitors. 2017 , 195, 663-673	16
389	The vitamin D receptor: contemporary genomic approaches reveal new basic and translational insights. 2017 , 127, 1146-1154	81
388	The Importance of Endophenotypes to Evaluate the Relationship between Genotype and External Phenotype. 2017 , 18,	15
387	Epigenetic Landscape during Coronavirus Infection. 2017 , 6,	61
386	Trans-ethnic predicted expression genome-wide association analysis identifies a gene for estrogen receptor-negative breast cancer. 2017 , 13, e1006727	6
385	Swellix: a computational tool to explore RNA conformational space. 2017 , 18, 504	3
384	CAMKII β suppresses an efferocytosis pathway in macrophages and promotes atherosclerotic plaque necrosis. 2017 , 127, 4075-4089	50
383	CERENKOV. 2017 ,	1
382	Transcriptomics: Next Generation Transcriptome. 2017 , 1-20	
381	Rare Variants in the Promoter Modulate In Vivo Activity. 2018 , 46, 636-642	7
380	From gene networks to drugs: systems pharmacology approaches for AUD. 2018 , 235, 1635-1662	11
379	Developmentally linked human DNA hypermethylation is associated with down-modulation, repression, and upregulation of transcription. 2018 , 13, 275-289	20
378	Widespread enhancer activation via ER α mediates estrogen response in vivo during uterine development. <i>Nucleic Acids Research</i> , 2018 , 46, 5487-5503	20.1 16
377	Evaluation of CpG-SNPs in miRNA promoters and risk of breast cancer. 2018 , 651, 1-8	10
376	Senataxin Mutation Reveals How R-Loops Promote Transcription by Blocking DNA Methylation at Gene Promoters. 2018 , 69, 426-437.e7	83
375	-Omics and Clinical Data Integration. 2018 , 248-273	
374	Autologous iPSC-Based Vaccines Elicit Anti-tumor Responses In Vivo. 2018 , 22, 501-513.e7	78
373	Targeted deletion of a 170-kb cluster of LINE-1 repeats and implications for regional control. <i>Genome Research</i> , 2018 ,	9-7 7

372	Rules governing the mechanism of epigenetic reprogramming memory. <i>Epigenomics</i> , 2018 , 10, 149-174	4.4	8
371	DNA Supercoiling(omics). 2018 , 81-99		
370	dreamBase: DNA modification, RNA regulation and protein binding of expressed pseudogenes in human health and disease. <i>Nucleic Acids Research</i> , 2018 , 46, D85-D91	20.1	38
369	Correlates of evolutionary rates in the murine sperm proteome. 2018 , 18, 35		3
368	Towards a map of cis-regulatory sequences in the human genome. <i>Nucleic Acids Research</i> , 2018 , 46, 5395-5409	25.4	7
367	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. 2018 , 50, 668-681		1301
366	Candidate gene DNA methylation associations with breast cancer characteristics and tumor progression. <i>Epigenomics</i> , 2018 , 10, 367-378	4.4	7
365	Evidence for a second ankylosing spondylitis-associated regulatory polymorphism. 2018 , 4, e000628		12
364	Epigenetic regulation of NFE2 overexpression in myeloproliferative neoplasms. 2018 , 131, 2065-2073		23
363	Functional interrelationship between TFII-I and E2F transcription factors at specific cell cycle gene loci. 2018 , 119, 712-722		7
362	DNA methylation and antipsychotic treatment mechanisms in schizophrenia: Progress and future directions. 2018 , 81, 38-49		44
361	Epigenetics and Epigenomics. 2018 , 17-24		2
360	iDEP: an integrated web application for differential expression and pathway analysis of RNA-Seq data. 2018 , 19, 534		291
359	Endogenous DNA Double-Strand Breaks during DNA Transactions: Emerging Insights and Methods for Genome-Wide Profiling. 2018 , 9,		30
358	Genome-Wide Association Studies of Hypertension and Several Other Cardiovascular Diseases. 2019 , 6, 169-186		19
357	Genomes and Variants. 2018 , 17-33		
356	Automatic detection of genomic regions with informative epigenetic patterns. <i>BMC Genomics</i> , 2018 , 19, 847	4.5	0
355	ZFX Mediates Non-canonical Oncogenic Functions of the Androgen Receptor Splice Variant 7 in Castrate-Resistant Prostate Cancer. 2018 , 72, 341-354.e6		38

354	Biologically anchored knowledge expansion approach uncovers KLF4 as a novel insulin signaling regulator. 2018 , 13, e0204100		3
353	Robust Findings From 25 Years of PTSD Genetics Research. 2018 , 20, 115		23
352	Requirement for NF- κ B in maintenance of molecular and behavioral circadian rhythms in mice. 2018 , 32, 1367-1379		47
351	Principles of Molecular Biology. 2018 , 1-16		
350	Genome-Wide Association Studies of Hypertension and Several Other Cardiovascular Diseases. 2018 , 1-29		0
349	Pharmacogenetic variants and response to neoadjuvant single-agent doxorubicin or docetaxel: a study in locally advanced breast cancer patients participating in the NCT00123929 phase 2 randomized trial. 2018 , 28, 245-250		0
348	N-Acetylglutamate Synthase Deficiency Due to a Recurrent Sequence Variant in the N-acetylglutamate Synthase Enhancer Region. 2018 , 8, 15436		7
347	Pairs of Adjacent Conserved Noncoding Elements Separated by Conserved Genomic Distances Act as Cis-Regulatory Units. 2018 , 10, 2535-2550		0
346	Emerging role of nutrition and the non-coding landscape in type 2 diabetes mellitus: A review of literature. 2018 , 675, 54-61		6
345	Gene Regulatory Network Perturbation by Genetic and Epigenetic Variation. 2018 , 43, 576-592		10
344	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018 , 9, 3121	17.4	74
343	Identification of a Novel Enhancer/Chromatin Opening Element Associated with High-Level β Globin Gene Expression. 2018 , 38,		3
342	H3K4me2 and WDR5 enriched chromatin interacting long non-coding RNAs maintain transcriptionally competent chromatin at divergent transcriptional units. <i>Nucleic Acids Research</i> , 2018 , 46, 9384-9400	20.1	12
341	Genome-Wide Association Studies of Coronary Artery Disease: Recent Progress and Challenges Ahead. 2018 , 20, 47		19
340	Meta-analysis of GWAS in both Chinese and European populations identifies GPR173 as a novel X chromosome susceptibility gene for SLE. 2018 , 20, 92		12
339	Thinking BIG rheumatology: how to make functional genomics data work for you. 2018 , 20, 29		4
338	LncRNA GAS5 Indel Genetic Polymorphism Contributes to Glioma Risk Through Interfering Binding of Transcriptional Factor TFAP2A. 2018 , 37, 750-757		22
337	Challenges and approaches to predicting RNA with multiple functional structures. 2018 , 24, 1615-1624		19

336	Integrative epigenomic analysis in differentiated human primary bronchial epithelial cells exposed to cigarette smoke. 2018 , 8, 12750		8
335	Transfer RNA genes experience exceptionally elevated mutation rates. 2018 , 115, 8996-9001		18
334	Prediction and identification of transcriptional regulatory elements at the lung cancer-specific locus. 2018 , 16, 137-144		2
333	Genome-wide Identification and Characterization of Enhancers Across 10 Human Tissues. 2018 , 14, 1321-1332	10	
332	Promoter methylation of PGC1A and PGC1B predicts cancer incidence in a veteran cohort. <i>Epigenomics</i> , 2018 , 10, 733-743	4-4	7
331	Principled multi-omic analysis reveals gene regulatory mechanisms of phenotype variation. <i>Genome Research</i> , 2018 , 28, 1207-1216	9-7	11
330	An Intergenic Variant rs9268877 Between HLA-DRA and HLA-DRB Contributes to the Clinical Course and Long-term Outcome of Ulcerative Colitis. 2018 , 12, 1113-1121		10
329	Biological Databases. 2018 , 303-337		
328	The in vitro functional analysis of single-nucleotide polymorphisms associated with growth hormone (GH) response in children with GH deficiency. 2019 , 19, 200-210		2
327	Genetic predisposition to B-cell acute lymphoblastic leukemia at 14q11.2 is mediated by a CEBPE promoter polymorphism. 2019 , 33, 1-14		11
326	Population Analysis of Pharmacogenetic Polymorphisms. 2019 , 379-387		
325	Molecular Systems Biology of Neurodevelopmental Disorders, Rett Syndrome as an Archetype. 2019 , 13, 30		7
324	Nascent RNA analyses: tracking transcription and its regulation. 2019 , 20, 705-723		83
323	Extensive transcriptional responses are co-ordinated by microRNAs as revealed by Exon-Intron Split Analysis (EISA). <i>Nucleic Acids Research</i> , 2019 , 47, 8606-8619	20-1	3
322	Bayesian variable selection using partially observed categorical prior information in fine-mapping association studies. 2019 , 43, 690-703		3
321	Toxicology Data Resources to Support Read-Across and (Q)SAR. 2019 , 10, 561		38
320	A protein-RNA interaction atlas of the ribosome biogenesis factor AATF. 2019 , 9, 11071		10
319	Novel Genetic Locus Influencing Retinal Venular Tortuosity Is Also Associated With Risk of Coronary Artery Disease. 2019 , 39, 2542-2552		11

318	Predicting HLA class II antigen presentation through integrated deep learning. <i>Nature Biotechnology</i> , 2019 , 37, 1332-1343	44.5	112
317	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. 2019 , 6, 256		13
316	Coagulation FXIII-A Protein Expression Defines Three Novel Sub-populations in Pediatric B-Cell Progenitor Acute Lymphoblastic Leukemia Characterized by Distinct Gene Expression Signatures. 2019 , 9, 1063		5
315	Cistrome Partitioning Reveals Convergence of Somatic Mutations and Risk Variants on Master Transcription Regulators in Primary Prostate Tumors. 2019 , 36, 674-689.e6		21
314	Meta-Analysis of Gene Expression Changes in the Blood of Patients with Mild Cognitive Impairment and Alzheimer's Disease Dementia. 2019 , 20,		15
313	Comprehensive analysis of long noncoding RNA (lncRNA)-chromatin interactions reveals lncRNA functions dependent on binding diverse regulatory elements. <i>Journal of Biological Chemistry</i> , 2019 , 294, 15613-15622	5.4	18
312	Mitigation of off-target toxicity in CRISPR-Cas9 screens for essential non-coding elements. <i>Nature Communications</i> , 2019 , 10, 4063	17.4	49
311	in Cancer: Mechanisms of Altered Expression and Function, and Clinical Implications. <i>Cancers</i> , 2019 , 11,	6.6	18
310	Quartet-based inference of cell differentiation trees from ChIP-Seq histone modification data. 2019 , 14, e0221270		1
309	Governmental and Academic Efforts to Advance the Field of Pharmacogenomics. 2019 , 55-80		
308	Silencing of Transcription Factor Sp1 Promotes SN1 Transporter Regulation by Ammonia in Mouse Cortical Astrocytes. 2019 , 20,		1
307	Tissue-specific epigenetics of atherosclerosis-related ANGPT and ANGPTL genes. <i>Epigenomics</i> , 2019 , 11, 169-186	4.4	17
306	Single-cell technologies in reproductive immunology. 2019 , 82, e13157		3
305	Long Noncoding RNA: Genomics and Relevance to Physiology. 2019 , 9, 933-946		13
304	ImmuneRegulation: a web-based tool for identifying human immune regulatory elements. <i>Nucleic Acids Research</i> , 2019 , 47, W142-W150	20.1	2
303	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. 2019 , 177, 1035-1049.e19		237
302	Mouse ANKRD31 Regulates Spatiotemporal Patterning of Meiotic Recombination Initiation and Ensures Recombination between X and Y Sex Chromosomes. 2019 , 74, 1069-1085.e11		38
301	Perspectives on gene expression regulation techniques in Drosophila. 2019 , 46, 213-220		4

300	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. 2019 , 177, 162-183		166
299	TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. <i>Genome Research</i> , 2019 , 29, 564-575	9.7	30
298	Epigenetics and Epigenomics Analysis for Autoimmune Diseases. 2019 , 365-395		
297	CERENKOV2: improved detection of functional noncoding SNPs using data-space geometric features. 2019 , 20, 63		4
296	Meta-analysis and prioritization of human skin pigmentation-associated GWAS-SNPs using ENCODE data-based web-tools. 2019 , 311, 163-171		4
295	Epigenetic profiles capturing breast cancer stemness for triple negative breast cancer control. <i>Epigenomics</i> , 2019 , 11, 1811-1825	4.4	5
294	Identification of four novel associations for B-cell acute lymphoblastic leukaemia risk. <i>Nature Communications</i> , 2019 , 10, 5348	17.4	29
293	Human Genomic Variants and Inherited Disease: Molecular Mechanisms and Clinical Consequences. 2019 , 125-200		0
292	Inherent DNA-binding specificities of the HIF-1 α and HIF-2 α transcription factors in chromatin. 2019 , 20,		81
291	De novo pattern discovery enables robust assessment of functional consequences of non-coding variants. 2019 , 35, 1453-1460		1
290	Genome-wide functional association networks: background, data & state-of-the-art resources. 2020 , 21, 1224-1237		5
289	Genome-wide association study of INDELs identified four novel susceptibility loci associated with lung cancer risk. 2020 , 146, 2855-2864		2
288	Metabolic dysregulation in the Wilson's disease mouse model. 2020 , 117, 2076-2083		17
287	STAT3 imparts BRCAness by impairing homologous recombination repair in Epstein-Barr virus-transformed B lymphocytes. 2020 , 16, e1008849		1
286	A systematic evaluation of the design and context dependencies of massively parallel reporter assays. 2020 , 17, 1083-1091		28
285	Genetic background of coronary artery disease: clinical implications and perspectives. 2020 , 5, 135-144		
284	LINC00473 as an Immediate Early Gene under the Control of the EGR1 Transcription Factor. 2020 , 6,		0
283	A Multi-Source Data Fusion Framework for Revealing the Regulatory Mechanism of Breast Cancer Immune Evasion. 2020 , 11, 595324		2

282	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth. 2020 , 6,	9
281	Perspectives on ENCODE. 2020 , 583, 693-698	61
280	Expanded encyclopaedias of DNA elements in the human and mouse genomes. 2020 , 583, 699-710	360
279	5-Formylcytosine landscapes of human preimplantation embryos at single-cell resolution. <i>PLoS Biology</i> , 2020 , 18, e3000799	9-7 3
278	Recent advancements in understanding the role of epigenetics in the auditory system. 2020 , 761, 144996	2
277	Frequency spectra characterization of noncoding human genomic sequences. 2020 , 42, 1215-1226	1
276	Genome Wide Analysis Points towards Subtype-Specific Diseases in Different Genetic Forms of Amyotrophic Lateral Sclerosis. 2020 , 21,	2
275	Elucidating the Basis for Permissivity of the MT-4 T-Cell Line to Replication of an HIV-1 Mutant Lacking the gp41 Cytoplasmic Tail. 2020 , 94,	2
274	Gene co-expression and histone modification signatures are associated with melanoma progression, epithelial-to-mesenchymal transition, and metastasis. 2020 , 12, 127	2
273	Dynamical gene regulatory networks are tuned by transcriptional autoregulation with microRNA feedback. 2020 , 10, 12960	5
272	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. 2020 , 52, 969-983	33
271	Alteration of Proteotranscriptomic Landscape Reveals the Transcriptional Regulatory Circuits Controlling Key-Signaling Pathways and Metabolic Reprogramming During Tumor Evolution. 2020 , 8, 586479	1
270	A Comparison of Gene Expression Changes in the Blood of Individuals Consuming Diets Supplemented with Olives, Nuts or Long-Chain Omega-3 Fatty Acids. 2020 , 12,	5
269	Identification and characterization of key long non-coding RNAs in the mouse cochlea. 2021 , 18, 1160-1169	1
268	Lung Function in African American Children with Asthma Is Associated with Novel Regulatory Variants of the KIT Ligand and Gene-By-Air-Pollution Interaction. 2020 , 215, 869-886	3
267	SZDB2.0: an updated comprehensive resource for schizophrenia research. 2020 , 139, 1285-1297	16
266	Bioinformatic Analysis Reveals Phosphodiesterase 4D-Interacting Protein as a Key Frontal Cortex Dementia Switch Gene. 2020 , 21,	6
265	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 1330-1341	6.8 8

264	Identifying branch-specific positive selection throughout the regulatory genome using an appropriate proxy neutral. <i>BMC Genomics</i> , 2020 , 21, 359	4.5	1
263	Multi-omics analysis reveals the functional transcription and potential translation of enhancers. 2020 , 147, 2210-2224		6
262	Transcription Factor KLF14 and Metabolic Syndrome. 2020 , 7, 91		11
261	Transcriptomic and Network Analysis Identifies Shared and Unique Pathways across Dementia Spectrum Disorders. 2020 , 21,		7
260	Capturing functional epigenomes for insight into metabolic diseases. 2020 , 38, 100936		8
259	Cell type- and stage-specific expression of Otx2 is regulated by multiple transcription factors and -regulatory modules in the retina. 2020 , 147,		15
258	Formaldehyde-assisted isolation of regulatory DNA elements from Arabidopsis leaves. 2020 , 15, 713-733		4
257	Osteoporosis- and obesity-risk interrelationships: an epigenetic analysis of GWAS-derived SNPs at the developmental gene. 2020 , 15, 728-749		4
256	Quantification of aminobutyric acids and their clinical applications as biomarkers for osteoporosis. 2020 , 3, 39		17
255	Gene regulatory landscape of the sonic hedgehog locus in embryonic development. 2020 , 62, 334-342		4
254	Two novel pleiotropic loci associated with osteoporosis and abdominal obesity. 2020 , 139, 1023-1035		3
253	Sci-fate characterizes the dynamics of gene expression in single cells. <i>Nature Biotechnology</i> , 2020 , 38, 980-988	44.5	34
252	Regulatory CDH4 Genetic Variants Associate With Risk to Develop Capecitabine-Induced Hand-Foot Syndrome. 2021 , 109, 462-470		0
251	Genetic Predictors of Severe Skin Toxicity in Patients with Stage III Colon Cancer Treated with Cetuximab: NCCTG N0147 (Alliance). 2021 , 30, 404-411		0
250	Revisiting Schizophrenia from an Evolutionary Perspective: An Association Study of Recent Evolutionary Markers and Schizophrenia. 2021 , 47, 827-836		3
249	Transcriptional enhancers: from prediction to functional assessment on a genome-wide scale. 2021 , 64, 426-448		2
248	Hemodynamics mediated epigenetic regulators in the pathogenesis of vascular diseases. 2021 , 476, 125-143		4
247	SPONGEdb: a pan-cancer resource for competing endogenous RNA interactions. 2021 , 3, zcaa042		5

246	Targeting Lymphotoxin Beta and Paired Box 5: a potential therapeutic strategy for soft tissue sarcoma metastasis. 2021 , 21, 3		
245	Polygenic Scores for ADHD: A Meta-Analysis. 2021 , 49, 297-310		2
244	Epigenetic landscape of stress surfeit disorders: Key role for DNA methylation dynamics. 2021 , 156, 127-183		1
243	FOXO1 and FOXO3 cooperatively regulate innate lymphoid cell development.		
242	Epigenetic changes with age primes mammary luminal epithelia for cancer initiation.		2
241	Identification of Stemness-Related Genes for Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma by Integrated Bioinformatics Analysis. 2021 , 9, 642724		0
240	seqQscorer: automated quality control of next-generation sequencing data using machine learning. 2021 , 22, 75		1
239	An ancient, conserved gene regulatory network led to the rise of oral venom systems. 2021 , 118,		6
238	Adenosine integrates light and sleep signalling for the regulation of circadian timing in mice. <i>Nature Communications</i> , 2021 , 12, 2113	17.4	17
237	Fish-Ing for Enhancers in the Heart. 2021 , 22,		0
236	Differentiation of exhausted CD8 T cells after termination of chronic antigen stimulation stops short of achieving functional T cell memory.		1
235	Stress-induced transcriptional memory accelerates promoter-proximal pause release and decelerates termination over mitotic divisions. 2021 , 81, 1715-1731.e6		7
234	Np63 is a pioneer factor that binds inaccessible chromatin and elicits chromatin remodeling. 2021 , 14, 20		5
233	The Murine MHC Class II Super Enhancer Contains a Functionally Redundant CTCF-Binding Component and a Novel Element Critical for Maximal Expression. 2021 , 206, 2221-2232		
232	Current advances of epigenetics in periodontology from ENCODE project: a review and future perspectives. 2021 , 13, 92		7
231	Induction of OCT2 contributes to regulate the gene expression program in human neutrophils activated via TLR8. <i>Cell Reports</i> , 2021 , 35, 109143	10.6	2
230	Chrom-Lasso: a lasso regression-based model to detect functional interactions using Hi-C data. 2021 , 22,		0
229	Pluripotent stem cell-derived endometrial stromal fibroblasts in a cyclic, hormone-responsive, coculture model of human decidua. <i>Cell Reports</i> , 2021 , 35, 109138	10.6	7

228	TNF- α /NF- κ B signaling epigenetically represses PSD4 transcription to promote alcohol-related hepatocellular carcinoma progression. 2021 , 10, 3346-3357		2
227	From Open Data to Open Science. 2021 , 8, e2020EA001562		6
226	Dysregulation of long non-coding RNAs and their mechanisms in Huntington's disease. 2021 , 99, 2074-2090		1
225	Spatial-transcriptomics reveals unique defining molecular features of fluorescence-sorted 5-aminolevulinic acid+ infiltrative tumor cells associated with glioblastoma recurrence and poor survival.		
224	Glucocorticoid-Induced Exacerbation of Mycobacterial Infection Is Associated With a Reduced Phagocytic Capacity of Macrophages. <i>Frontiers in Immunology</i> , 2021 , 12, 618569	8.4	4
223	An Omics Analysis Search and Information System (OASIS) for Enabling Biological Discovery in the Old Order Amish.		0
222	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. <i>Nature Communications</i> , 2021 , 12, 2524	17.4	6
221	Genome-wide binding analysis of 195 DNA binding proteins reveals "reservoir" promoters and human specific SVA-repeat family regulation. 2021 , 16, e0237055		0
220	Deep Learning Approach to Genomic Breakage Study from Primary Sequence.		
219	RNA-Seq reveals changes in human placental metabolism, transport and endocrinology across the first-second trimester transition. 2021 , 10,		4
218	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021 , 12, 4198	17.4	1
217	VEGFA's distal enhancer regulates its alternative splicing in CML. 2021 , 3, zcab029		1
216	Genome-wide gene-smoking interaction study identified novel susceptibility loci for non-small cell lung cancer in Chinese populations. 2021 , 42, 1154-1161		0
215	Differentiation of exhausted CD8 T cells after termination of chronic antigen stimulation stops short of achieving functional T cell memory. 2021 , 22, 1030-1041		9
214	From Junk to Function: LncRNAs in CNS Health and Disease. 2021 , 14, 714768		3
213	PCRMS: a database of predicted cis-regulatory modules and constituent transcription factor binding sites in genomes.		0
212	Statistical guidelines for quality control of next-generation sequencing techniques. 2021 , 4,		0
211	Identification of genes, pathways and transcription factor-miRNA-target gene networks and experimental verification in venous thromboembolism. 2021 , 11, 16352		0

210	Quantifying RNA Synthesis at Rate-Limiting Steps of Transcription Using Nascent RNA-Sequencing Data.	
209	Vision, challenges and opportunities for a Plant Cell Atlas. 2021 , 10,	8
208	FusionAI: Predicting fusion breakpoint from DNA sequence with deep learning. 2021 , 24, 103164	2
207	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. 2021 , 13, eabj1578	10
206	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro.	0
205	ssvQC: an integrated CUT&RUN quality control workflow for histone modifications and transcription factors. 2021 , 14, 366	0
204	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. 2021 , 53, 1300-1310	60
203	Drives Cancer Cell Proliferation Through an Positive Feedback Loop in Glioblastoma. 2021 , 14, 145-155	4
202	VEGFA β distal enhancer regulates its alternative splicing in CML.	
201	First insights into the molecular basis association between promoter polymorphisms of the IL1B gene and Helicobacter pylori infection in the Sudanese population: computational approach. 2021 , 21, 16	2
200	Spatial clustering for identification of CHIP-enriched regions (SICER) to map regions of histone methylation patterns in embryonic stem cells. 2014 , 1150, 97-111	144
199	Considerations on Experimental Design and Data Analysis of Chromatin Immunoprecipitation Experiments. 2018 , 1689, 9-28	3
198	A guide to the current Web-based resources in pharmacogenomics. 2013 , 1015, 293-310	5
197	Characterization of DNA-Protein Interactions: Design and Analysis of CHIP-Seq Experiments. 2016 , 223-260	2
196	Phylogenetic Analysis of Cell Types Using Histone Modifications. 2013 , 326-337	1
195	Genome-wide Study Identifies Association between HLA-B55:01 and Self-Reported Penicillin Allergy. 2020 , 107, 612-621	17
194	Evaluation of Chromatin Accessibility in Prefrontal Cortex of Schizophrenia Cases and Controls.	5
193	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder.	21

192	Cell type- and stage-specific expression of Otx2 is coordinated by a cohort of transcription factors and multiple cis-regulatory modules in the retina.	1
191	Transcriptome and regulatory maps of decidua-derived stromal cells inform gene discovery in preterm birth.	3
190	An Atlas of Gene Regulatory Elements in Adult Mouse Cerebrum.	15
189	Crinet: A computational tool to infer genome-wide competing endogenous RNA (ceRNA) interactions.	1
188	Genome-wide binding analysis of 195 DNA Binding Proteins reveals Reservoir Promoters and human specific SVA-repeat family regulation.	0
187	Cardiac Cell Type-Specific Gene Regulatory Programs and Disease Risk Association.	1
186	Hypermethylation of human DNA: Fine-tuning transcription associated with development.	1
185	Assessment of the CTCF Binding Sites and Repeat-Positions Upstream the Human H19 Gene.	2
184	Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis.	175
183	ImmuneRegulation: A web-based tool for identifying human immune regulatory elements.	3
182	A systematic evaluation of the design, orientation, and sequence context dependencies of massively parallel reporter assays.	8
181	Stress-Induced Transcriptional Memory Accelerates Promoter-Proximal Pause-Release and Decelerates Termination over Mitotic Divisions.	2
180	Admixture/fine-mapping in Brazilians reveals a West African associated potential regulatory variant (rs114066381) with a strong female-specific effect on body mass- and fat mass-indexes.	1
179	Nicotinamide metabolism regulates glioblastoma stem cell maintenance. 2017 , 2,	51
178	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. 2017 , 127, 1798-1812	68
177	TCGA Workflow: Analyze cancer genomics and epigenomics data using Bioconductor packages. 5, 1542	78
176	: Analyze cancer genomics and epigenomics data using Bioconductor packages. 2016 , 5, 1542	74
175	Tissue-Specificity of Gene Expression Diverges Slowly between Orthologs, and Rapidly between Paralogs. 2016 , 12, e1005274	35

174	Comprehensive Identification of Long Non-coding RNAs in Purified Cell Types from the Brain Reveals Functional LncRNA in OPC Fate Determination. 2015 , 11, e1005669	63
173	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. 2017 , 13, e1006760	38
172	Comprehensive identification and annotation of cell type-specific and ubiquitous CTCF-binding sites in the human genome. 2012 , 7, e41374	89
171	Mechanisms of dietary response in mice and primates: a role for EGR1 in regulating the reaction to human-specific nutritional content. 2012 , 7, e43915	3
170	Discovery and characterization of human exonic transcriptional regulatory elements. 2012 , 7, e46098	11
169	diffReps: detecting differential chromatin modification sites from ChIP-seq data with biological replicates. 2013 , 8, e65598	212
168	DNA methylation of alternative promoters directs tissue specific expression of Epac2 isoforms. 2013 , 8, e67925	35
167	Genome-wide analysis reveals coating of the mitochondrial genome by TFAM. 2013 , 8, e74513	39
166	Structural variation-associated expression changes are paralleled by chromatin architecture modifications. 2013 , 8, e79973	23
165	A new family of predicted Krüppel-like factor genes and pseudogenes in placental mammals. 2013 , 8, e81109	28
164	Sebnif: an integrated bioinformatics pipeline for the identification of novel large intergenic noncoding RNAs (lincRNAs)--application in human skeletal muscle cells. 2014 , 9, e84500	18
163	Molecular evolution of multiple-level control of heme biosynthesis pathway in animal kingdom. 2014 , 9, e86718	3
162	Characterisation of genetic variation in ST8SIA2 and its interaction region in NCAM1 in patients with bipolar disorder. 2014 , 9, e92556	22
161	The histone lysine demethylase JMJD3/KDM6B is recruited to p53 bound promoters and enhancer elements in a p53 dependent manner. 2014 , 9, e96545	51
160	Allele frequencies of variants in ultra conserved elements identify selective pressure on transcription factor binding. 2014 , 9, e110692	4
159	Tissue-Specific Evolution of Protein Coding Genes in Human and Mouse. 2015 , 10, e0131673	26
158	Tissue-Specific Enrichment of Lymphoma Risk Loci in Regulatory Elements. 2015 , 10, e0139360	5
157	Inferring RBP-Mediated Regulation in Lung Squamous Cell Carcinoma. 2016 , 11, e0155354	3

156	Prediction and Validation of Transcription Factors Modulating the Expression of Sestrin3 Gene Using an Integrated Computational and Experimental Approach. 2016 , 11, e0160228	4
155	Bayesian Correlation Analysis for Sequence Count Data. 2016 , 11, e0163595	8
154	SnoVault and encodedD: A novel object-based storage system and applications to ENCODE metadata. 2017 , 12, e0175310	9
153	PEREGRINE: A genome-wide prediction of enhancer to gene relationships supported by experimental evidence. 2020 , 15, e0243791	3
152	Role of global aberrant alternative splicing events in papillary thyroid cancer prognosis. 2019 , 11, 2082-2097	22
151	Understanding the role of NRF2-regulated miRNAs in human malignancies. 2013 , 4, 1130-42	48
150	KMT2D maintains neoplastic cell proliferation and global histone H3 lysine 4 monomethylation. 2013 , 4, 2144-53	91
149	Top associated SNPs in prostate cancer are significantly enriched in cis-expression quantitative trait loci and at transcription factor binding sites. 2014 , 5, 6168-77	18
148	On the presence and role of human gene-body DNA methylation. 2012 , 3, 462-74	295
147	Comprehensive nucleosome mapping of the human genome in cancer progression. 2016 , 7, 13429-45	13
146	Hierarchical regulation of the genome: global changes in nucleosome organization potentiate genome response. 2016 , 7, 6460-75	10
145	Noncoding Variants Functional Prioritization Methods Based on Predicted Regulatory Factor Binding Sites. 2017 , 18, 322-331	2
144	Transcriptional Regulation of Human by Alternate Promoters in Embryonic Stem Cells. 2012 , Suppl 10, 009	1
143	ENCODE: A Sourcebook of Epigenomes and Chromatin Language. 2013 , 11, 2-6	23
142	Human Transcriptome and Chromatin Modifications: An ENCODE Perspective. 2013 , 11, 60-7	4
141	Nuclear receptor LRH-1/NR5A2 is required and targetable for liver endoplasmic reticulum stress resolution. 2014 , 3, e01694	44
140	Two-signal requirement for growth-promoting function of Yap in hepatocytes. 2015 , 4,	38
139	Combinatorial bZIP dimers display complex DNA-binding specificity landscapes. 2017 , 6,	56

138	System wide analyses have underestimated protein abundances and the importance of transcription in mammals. 2014 , 2, e270	193
137	An atlas of gene regulatory elements in adult mouse cerebrum. 2021 , 598, 129-136	8
136	Asthma-associated genetic variants induce IL33 differential expression through an enhancer-blocking regulatory region. <i>Nature Communications</i> , 2021 , 12, 6115	17.4 5
135	Long-range regulatory effects of Neandertal DNA in modern humans.	
134	Differentially accessible, single copy sequences form contiguous domains along metaphase chromosomes that are conserved among multiple tissues. 2021 , 14, 49	
133	ENCODE (Encyclopedia of DNA Elements). 2004 ,	
132	Novel Methods in the Study of the Breast Cancer Genome: Towards a Better Understanding of the Disease of Breast Cancer. 2012 , 03, 797-809	
131	Genome-Associated Data. 2012 ,	
130	Epigenomic and Noncoding RNA Regulation in Addictive Processes. 2013 , 115-165	
129	Measuring Reproducibility of High-Throughput Deep-Sequencing Experiments Based on Self-adaptive Mixture Copula. 2013 , 301-313	0
128	Efficiently Identifying Significant Associations in Genome-Wide Association Studies. 2013 , 118-131	1
127	Blood Pressure Genomics. 2015 , 685-694	
126	Identification of HOT Regions in the Human Genome Using Differential Chromatin Modifications. 2016 , 856-861	
125	SnoVault and encodedD: A novel object-based storage system and applications to ENCODE metadata.	0
124	Genome-wide association study of asthma in individuals of African ancestry reveals novel asthma susceptibility loci.	
123	Novel locus influencing retinal venular tortuosity is also associated with risk of coronary artery disease.	
122	Principled Multi-Omic Analysis Reveals Gene Regulatory Mechanisms Of Phenotype Variation.	1
121	Dynamic-BM: multispecies Dynamic BodyMap database from temporal RNA-seq data. 2018 , 19, 1302-1309	1

- 120 Transfer RNA genes experience exceptionally elevated mutation rates.
- 119 TET2 binding to enhancers facilitates transcription factor recruitment in hematopoietic cells. 2
- 118 Mutant p63 affects epidermal cell identity through rewiring the enhancer landscape. 0
- 117 MafK mediates chromatin remodeling to silence IRF8 expression in non-immune cells in a lineage-specific manner.
- 116 A protein-RNA interaction atlas of the ribosome biogenesis factor AATF.
- 115 GWAS-driven Pathway Analyses and Functional Validation Suggest GLIS1 as a Susceptibility Gene for Mitral Valve Prolapse.
- 114 Identification and mitigation of pervasive off-target activity in CRISPR-Cas9 screens for essential non-coding elements. 1
- 113 Applications of Supercomputers in Sequence Analysis and Genome Annotation. **2019**, 625-652
- 112 Encyclopedia of Animal Cognition and Behavior. **2019**, 1-5
- 111 STATegra: a comprehensive multi-omics dataset of B-cell differentiation in mouse.
- 110 DNA shape complements sequence-based representations of transcription factor binding sites.
- 109 Motif elucidation in ChIP-seq datasets with a knockout control.
- 108 Identifying branch-specific positive selection throughout the regulatory genome using an appropriate neutral proxy. 0
- 107 Osteoporosis- and obesity-risk interrelationships: An epigenetic analysis of GWAS-derived SNPs at the developmental gene TBX15.
- 106 Automated quality control of next generation sequencing data using machine learning.
- 105 Epigenetics of skeletal muscle-associated genes in the ASB, LRRC, TMEM, and OSBPL gene families.
- 104 Integrated profiling of single cell epigenomic and transcriptomic landscape of Parkinson's disease mouse brain. 0
- 103 Apolipoprotein E expression pattern in human induced pluripotent stem cells during neural induction. **2020**, 9, 353

- 102 Elucidating the basis for permissivity of the MT-4 T-cell line to replication of an HIV-1 mutant lacking the gp41 cytoplasmic tail.
- 101 Human and rat skeletal muscle single-nuclei multi-omic integrative analyses nominate causal cell types, regulatory elements, and SNPs for complex traits. 0
- 100 The impact of different negative training data on regulatory sequence predictions. 0
- 99 Apolipoprotein E expression pattern in human induced pluripotent stem cells during in vitro neural induction. **2020**, 9, 353 0
- 98 An ancient, conserved gene regulatory network led to the rise of oral venom systems.
- 97 Analysis of multiple gene co-expression networks to discover interactions favoring CFTR biogenesis and Δ 508-CFTR rescue. **2021**, 14, 258 0
- 96 Genomic Marks Associated with Chromatin Compartments in the CTCF, RNAPII Loop and Genomic Windows. **2021**, 22,
- 95 Colocalization highlights genes in hypothalamic-pituitary-gonadal axis as potentially mediating polycystic ovary syndrome risk.
- 94 Coding Variants are Relevant to the Expression of Obesity-Related Genes for Pediatric Adiposity. **2021**, 29, 194-203 0
- 93 The impact of different negative training data on regulatory sequence predictions. **2020**, 15, e0237412 0
- 92 Precision Medicine in Critical Illness: Sepsis and Acute Respiratory Distress Syndrome. **2020**, 267-288 0
- 91 Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy. 2
- 90 Novel KITLG/SCF regulatory variants are associated with lung function in African American children with asthma.
- 89 Identification and characterization of key long non-coding RNAs in the mouse cochlea.
- 88 Applications of Supercomputers in Sequence Analysis and Genome Annotation. 149-175
- 87 Identifying Genetic Sources of Phenotypic Heterogeneity in Orofacial Clefts by Targeted Sequencing. **2017**,
- 86 Asthma-associated variants induce IL33 differential expression through a novel regulatory region.
- 85 Role of Pnn in alternative splicing of a specific subset of lncRNAs of the corneal epithelium. **2014**, 20, 1629-42 11

84	Accumulation of cholesterol and increased demand for zinc in serum-deprived RPE cells. 2016 , 22, 1387-1404	4
83	DNA Hypomethylation in Intragenic and Intergenic Enhancer Chromatin of Muscle-Specific Genes Usually Correlates with their Expression. 2016 , 89, 441-455	19
82	Specific correlation between the major chromosome 10q26 haplotype conferring risk for age-related macular degeneration and the expression of. 2017 , 23, 318-333	10
81	Systems biology and big data analytics. 2022 , 425-442	
80	insertion variants alter gene transcript levels. <i>Genome Research</i> , 2021 ,	9.7 1
79	From quiescence to repair: C/EBPβ as a regulator of muscle stem cell function in health and disease. <i>FEBS Journal</i> , 2021 ,	5.7
78	Quantifying RNA synthesis at rate-limiting steps of transcription using nascent RNA-sequencing data.. <i>STAR Protocols</i> , 2022 , 3, 101036	1.4 0
77	Identification of functional tumor necrosis factor-alpha promoter variants associated with infection in the Sudanese population: Computational approach.. <i>World Journal of Gastroenterology</i> , 2022 , 28, 242-262	5.6
76	Exploring genomic data coupled with 3D chromatin structures using the WashU Epigenome Browser.	
75	The RNA helicase DDX39B activates FOXP3 RNA splicing to control T regulatory cell fate.	
74	GFI1-Dependent Repression of Increases Multiple Myeloma Cell Survival.. <i>Cancers</i> , 2022 , 14,	6.6 1
73	Human transcription factor protein interaction networks.. <i>Nature Communications</i> , 2022 , 13, 766	17.4 6
72	Identification of cis-regulatory modules for adeno-associated virus-based cell type-specific targeting in the retina and brain.. <i>Journal of Biological Chemistry</i> , 2022 , 101674	5.4 0
71	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro.. <i>Nature Biotechnology</i> , 2022 ,	44.5 1
70	Risks and rewards of big-data in epigenomics research: an interview with Melanie Ehrlich.. <i>Epigenomics</i> , 2022 ,	4.4 1
69	Key Genes and Biochemical Networks in Various Brain Regions Affected in Alzheimer's Disease.. <i>Cells</i> , 2022 , 11,	7.9 1
68	Representation Learning for Multi-omics Data with Heterogeneous Gene Regulatory Network. 2021 ,	1
67	Along the Bos Taurus genome, uncover candidate Imprinting Control Regions.	0

66 WashU Epigenome Browser update 2022.. *Nucleic Acids Research*, **2022**,

20.1 3

65 Data_Sheet_1.pdf. **2020**,

64 Table_1.XLSX. **2020**,

63 Table_10.XLSX. **2020**,

62 Table_2.XLSX. **2020**,

61 Table_3.XLSX. **2020**,

60 Table_4.XLSX. **2020**,

59 Table_5.XLSX. **2020**,

58 Table_6.XLSX. **2020**,

57 Table_7.XLSX. **2020**,

56 Table_8.XLSX. **2020**,

55 Table_9.XLSX. **2020**,

54 Table_1.docx. **2019**,

53 Table_2.docx. **2019**,

52 Table_3.docx. **2019**,

51 Data_Sheet_1.docx. **2019**,

50 Data_Sheet_2.xlsx. **2019**,

49 Data_Sheet_3.xlsx. **2019**,

48	SUMOylation controls the rapid transcriptional reprogramming induced by anthracyclines in Acute Myeloid Leukemias.		
47	Topologically associating domains are disrupted by evolutionary genome rearrangements forming species-specific enhancer connections in mice and humans.. <i>Cell Reports</i> , 2022 , 39, 110769	10.6	o
46	Genome Project. 2022 , 2918-2922		
45	Integrated proteogenomic characterization of urothelial carcinoma of the bladder. <i>Journal of Hematology and Oncology</i> , 2022 , 15,	22.4	o
44	FOXO1 and FOXO3 Cooperatively Regulate Innate Lymphoid Cell Development. <i>Frontiers in Immunology</i> , 13,	8.4	o
43	Predicting 3D chromatin interactions from DNA sequence using Deep Learning. <i>Computational and Structural Biotechnology Journal</i> , 2022 ,	6.8	o
42	Integrating 3D genomic and epigenomic data to enhance target gene discovery and drug repurposing in transcriptome-wide association studies. <i>Nature Communications</i> , 2022 , 13,	17.4	o
41	Bcl11a and the Correlated Key Genes Ascribable to Globin Switching: An In-silico Study.. <i>Cardiovascular & Hematological Disorders Drug Targets</i> , 2022 , 22,	1.1	
40	Along the Bos taurus genome, uncover candidate imprinting control regions. <i>BMC Genomics</i> , 2022 , 23,	4.5	
39	Systems Immunology Analyses of STAT1 Gain-of-Function Immune Phenotypes Reveal Heterogeneous Response to IL-6 and Broad Immunometabolic Roles for STAT1. <i>ImmunoHorizons</i> , 2022 , 6, 447-464	2.7	1
38	The emerging roles of PHOSPHO1 and its regulated phospholipid homeostasis in metabolic disorders. 13,		1
37	Proteomic and phosphoproteomic measurements enhance ability to predict ex vivo drug response in AML. 2022 , 19,		1
36	Scalable Bayesian functional GWAS method accounting for multivariate quantitative functional annotations with applications to studying Alzheimer's disease.		
35	Profiling human pathogenic repeat expansion regions by synergistic and multi-level impacts on molecular connections.		
34	Single-nucleus chromatin accessibility profiling highlights distinct astrocyte signatures in progressive supranuclear palsy and corticobasal degeneration.		
33	Using empirical biological knowledge to infer regulatory networks from multi-omics data. 2022 , 23,		1
32	Prostate Cancer Epigenetic Plasticity and Enhancer Heterogeneity: Molecular Causes, Consequences and Clinical Implications. 2022 , 255-275		o
31	Early Signaling Events in Renal Compensatory Hypertrophy Revealed by Multi-Omics.		o

- 30 Identification of conserved skeletal enhancers associated with craniosynostosis risk genes. ○
- 29 Identification of Cytoprotective Small-Molecule Inducers of Heme-Oxygenase-1. **2022**, 11, 1888 ○
- 28 A scalable Bayesian functional GWAS method accounting for multivariate quantitative functional annotations with applications for studying Alzheimer disease. **2022**, 3, 100143 ○
- 27 HiChIPdb: a comprehensive database of HiChIP regulatory interactions. 1
- 26 Promoter-adjacent DNA hypermethylation can downmodulate gene expression: TBX15 in the muscle lineage. ○
- 25 Exploration of Common Genomic Signatures of Systemic Juvenile Rheumatoid Arthritis and Type 1 Diabetes. ○
- 24 Retrotransposon insertions associated with risk of neurologic and psychiatric diseases. ○
- 23 Profiling human pathogenic repeat expansion regions by synergistic and multi-level impacts on molecular connections. ○
- 22 Bidirectional epigenetic editing reveals hierarchies in gene regulation. ○
- 21 ZNF521 / EBF1 axis regulates AKR1B1 to promote the proliferation, migration, and invasion of gastric cancer cells. ○
- 20 HELIOS: High-speed sequence alignment in optics. **2022**, 18, e1010665 ○
- 19 New roles for AP-1/JUNB in cell cycle control and tumorigenic cell invasion via regulation of cyclin E1 and TGF- β . **2022**, 23, ○
- 18 Transcriptome profiling of celery petiole tissues reveals peculiarities of the collenchyma cell wall formation. **2023**, 257, ○
- 17 Cross-tissue patterns of DNA hypomethylation reveal genetically distinct histories of cell development. ○
- 16 Bayesian model and selection signature analyses reveal risk factors for canine atopic dermatitis. **2022**, 5, 1
- 15 Long-range regulatory effects of Neandertal DNA in modern humans. ○
- 14 Reduced methylation corresponds with diabetic nephropathy risk in type 1 diabetes reduced methylation corresponds with diabetic nephropathy risk. ○
- 13 Genome-wide inference reveals that feedback regulations constrain promoter-dependent transcriptional burst kinetics. **2023**, 51, 68-83 ○

- 12 The histone demethylase JMJD2C constitutes a novel NFE2 target gene that is required for the survival of JAK2V617F mutated cells. ○
- 11 Single-cell multi-omic topic embedding reveals cell-type-specific and COVID-19 severity-related immune signatures. ○
- 10 Analysis of genomesII. **2023**, 65-87 ○
- 9 HGCA2.0: An RNA-Seq Based Webtool for Gene Coexpression Analysis in Homo sapiens. **2023**, 12, 388 ○
- 8 Multi-ancestry and multi-trait genome-wide association meta-analyses inform clinical risk prediction for systemic lupus erythematosus. **2023**, 14, ○
- 7 Dissecting cell state transitions by causal inference. ○
- 6 Integration of single sample and population analysis for understanding immune evasion mechanisms of lung cancer. **2023**, 9, ○
- 5 Investigation of autism-related transcription factors underlying sex differences in the effects of bisphenol A on transcriptome profiles and synaptogenesis in the offspring hippocampus. **2023**, 14, 1
- 4 Transcriptional buffering and 3'UTR lengthening are shaped during human neurodevelopment by shifts in mRNA stability and microRNA load. ○
- 3 Epigenetic Regulation of Inflammatory Mechanisms and a Psychological Symptom Cluster in Patients Receiving Chemotherapy. **2023**, 72, 200-210 ○
- 2 Global detection of human variants and isoforms by deep proteome sequencing. ○
- 1 Connectome and regulatory hubs of CAGE highly active enhancers. **2023**, 13, ○