Citation Report

List of articles citing

An integrated encyclopedia of DNA elements in the human genome

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#	Paper	IF	Citations
2257	Book Notes. **1991**, 3, 166-189		
2256	Gene-environment interaction for hypertension among African American women across generations. **2010**, 12, 149-55		25
2255	Chapter 14: Cancer genome analysis. **2012**, 8, e1002824		12
2254	Impaired Sulfate Metabolism and Epigenetics: Is There a Link in Autism?. **2012**, 14, 1953-1977		14
2253	Long non-coding RNAs and p53 regulation. **2012**, 13, 16708-17		35
2252	Annotation of functional variation in personal genomes using RegulomeDB. **2012**, 22, 1790-7		1723
2251	NCBI GEO: archive for functional genomics data sets--update. **2013**, 41, D991-5		4393
2250	NCBI Epigenomics: what's new for 2013. **2013**, 41, D221-5		19
2249	Decoding the human genome. **2012**, 22, 1599-601		32
2248	Linking disease associations with regulatory information in the human genome. **2012**, 22, 1748-59		538
2247	Understanding CpG methylation in the context of osteoarthritis. **2012**, 4, 593-5		7
2246	Sizing up long non-coding RNAs: do lncRNAs have secondary and tertiary structure?. **2012**, 2, 189-99		98
2245	Personal and population genomics of human regulatory variation. **2012**, 22, 1689-97		87
2244	Developmental control of replication timing defines a new breed of chromosomal domains with a novel mechanism of chromatin unfolding. **2012**, 3, 500-7		16
2243	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. **2012**, 22, 1698-710		44
2242	Decoding ENCODE. **2012**, 8, 871		3
2241	The ENCODE project. **2012**, 9, 1046		51

2240	The implications of ENCODE for diagnostics. **2012**, 30, 1064-5		11
2239	The UCSC Genome Browser database: extensions and updates 2013. **2013**, 41, D64-9		633
2238	Horizontal transfer and the evolution of host-pathogen interactions. **2012**, 2012, 679045		12
2237	THE FUTURE OF GENOME-BASED MEDICINE. **2012**,		
2236	Characteristics and significance of intergenic polyadenylated RNA transcription in Arabidopsis. **2013**, 161, 210-24		18
2235	Coinciding revolutions: how discovery of non-coding DNA and RNA can change our understanding of addiction. **2012**, 3, 271		4
2234	Dynamin 3 and platelet size variation. **2012**, 120, 4666-7		
2233	Direct imaging of DNA fibers: the visage of double helix. **2012**, 12, 6453-8		59
2232	Uniting ENCODE with genome-wide proteomics. **2012**, 30, 1065-7		38
2231	Interpreting noncoding genetic variation in complex traits and human disease. **2012**, 30, 1095-106		347
2230	Somatic copy number mosaicism in human skin revealed by induced pluripotent stem cells. *Nature*, **2012**, 492, 438-42	50.4	299
2229	Genome-wide epigenetic data facilitate understanding of disease susceptibility association studies. **2012**, 287, 30932-40		35
2228	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. **2012**, 26, 2802-16		124
2227	Will SNPs be useful predictors of normal tissue radiosensitivity in the future?. **2012**, 105, 283-8		17
2226	Diagnostic exome sequencing--are we there yet?. **2012**, 367, 1951-3		23
2225	Surveying the epigenomic landscape, one base at a time. **2012**, 13, 250		24
2224	What can epigenomics do for you?. **2012**, 13, 420		7
2223	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. **2012**, 13, R48		194

2222	Analysis of variation at transcription factor binding sites in Drosophila and humans. **2012**, 13, R49		71
2221	The epigenome and its role in diabetes. **2012**, 12, 673-85		22
2220	Long noncoding RNAs in cardiac development and pathophysiology. **2012**, 111, 1349-62		178
2219	Genetics of bipolar disorder: where we are and where we are going. **2012**, 29, 991-3		21
2218	Foxp3 exploits a pre-existent enhancer landscape for regulatory T cell lineage specification. **2012**, 151, 153-66		342
2217	Long noncoding RNAs are rarely translated in two human cell lines. **2012**, 22, 1646-57		292
2216	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. **2012**, 22, 1735-47		129
2215	Evolution of hemoglobin and its genes. **2012**, 2, a011627		85
2214	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. **2012**, 22, 1775-89		3408
2213	Ensembl 2013. **2013**, 41, D48-55		797
2212	Novel conformation of an RNA structural switch. **2012**, 51, 9257-9		14
2211	ENCODE: The human encyclopaedia. *Nature*, **2012**, 489, 46-8	50.4	173
2210	An expansive human regulatory lexicon encoded in transcription factor footprints. *Nature*, **2012**, 489, 83-90	50.4	589
2209	The long-range interaction landscape of gene promoters. *Nature*, **2012**, 489, 109-13	50.4	1066
2208	Evidence of abundant purifying selection in humans for recently acquired regulatory functions. **2012**, 337, 1675-8		151
2207	Modeling gene expression using chromatin features in various cellular contexts. **2012**, 13, R53		182
2206	Genomics: users' guide to the human genome. **2012**, 13, 678		3
2205	Rocking the foundations of molecular genetics. **2012**, 109, 16400-1		24

2204	Authorship: Who's on first?. *Nature*, **2012**, 489, 591-3	50.4	70
2203	Spark: a navigational paradigm for genomic data exploration. **2012**, 22, 2262-9		26
2202	Intronic RNAs constitute the major fraction of the non-coding RNA in mammalian cells. **2012**, 13, 504		87
2201	Limitations and possibilities of low cell number ChIP-seq. **2012**, 13, 645		66
2200	Strategies to identify long noncoding RNAs involved in gene regulation. **2012**, 2, 37		63
2199	Genome empowerment for the Puerto Rican parrot - Amazona vittata. **2012**, 1, 13		6
2198	Wie sich Ameisen in der W□te orientieren. **2012**, 60, 1007-1009		
2197	The UCSC Genome Browser. **2012**, Chapter 1, Unit1.4		69
2196	Genomics: ENCODE explained. *Nature*, **2012**, 489, 52-5	50.4	191
2195	Thematic minireview series on results from the ENCODE Project: Integrative global analyses of regulatory regions in the human genome. **2012**, 287, 30885-7		12
2194	ChIP-seq and beyond: new and improved methodologies to detect and characterize protein-DNA interactions. **2012**, 13, 840-52		524
2193	Nursing Science: Cutting Edge Research. **2012**, 44, 311-312		
2192	What does our genome encode?. **2012**, 22, 1602-11		87
2191	CTCF/cohesin-mediated DNA looping is required for protocadherin □promoter choice. **2012**, 109, 21081-6		176
2190	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
2189	ChIPing away at breast cancer. **2012**, 13, 1185-7		5
2188	Long distance relationships: enhancer-promoter communication and dynamic gene transcription. **2012**, 1819, 1217-27		66
2187	The accessible chromatin landscape of the human genome. *Nature*, **2012**, 489, 75-82	50.4	1900

2186	ENCODE data in the UCSC Genome Browser: year 5 update. **2013**, 41, D56-63		580
2185	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. **2012**, 22, 1658-67		133
2184	Epigenetics: Reading the second genomic code. *Nature*, **2012**, 491, 143-7	50.4	17
2183	Landscape of transcription in human cells. *Nature*, **2012**, 489, 101-8	50.4	3544
2182	iASeq: integrative analysis of allele-specificity of protein-DNA interactions in multiple ChIP-seq datasets. **2012**, 13, 681		20
2181	Genetic "lnc"-age of noncoding RNAs to human disease. **2012**, 122, 3837-40		29
2180	Copy number variants in obesity-related syndromes: review and perspectives on novel molecular approaches. **2012**, 2012, 845480		23
2179	Recruitment of transcription complexes to enhancers and the role of enhancer transcription. **2012**, 1, 778-93		5
2178	CRNDE: A Long Non-Coding RNA Involved in CanceR, Neurobiology, and DEvelopment. **2012**, 3, 270		167
2177	China buys US sequencing firm. *Nature*, **2012**, 489, 485-6	50.4	1
2176	Junk DNA and the identification of new levels of evidence to guide medical practice in 2013 and beyond. **2012**, 197, 672		
2175	Structurally differentiated cis-elements that interact with PU.1 are functionally distinguishable in acute promyelocytic leukemia. **2013**, 6, 25		11
2174	EMu: probabilistic inference of mutational processes and their localization in the cancer genome. **2013**, 14, R39		79
2173	The histone deacetylase inhibitor sodium valproate causes limited transcriptional change in mouse embryonic stem cells but selectively overrides Polycomb-mediated Hoxb silencing. **2013**, 6, 11		27
2172	Whole-genome sequencing in an autism multiplex family. **2013**, 4, 8		58
2171	The Origin of Metazoa: An Algorithmic View of Life. **2013**, 8, 221-231		1
2170	Genetic insights into common pathways and complex relationships among immune-mediated diseases. **2013**, 14, 661-73		394
2169	Short-term memory of danger signals and environmental stimuli in immune cells. **2013**, 14, 777-84		59

2168	Digital quantitation of potential therapeutic target RNAs. **2013**, 23, 188-94		47
2167	CNVs of noncoding cis-regulatory elements in human disease. **2013**, 23, 249-56		35
2166	Genome-wide variation of cytosine modifications between European and African populations and the implications for complex traits. **2013**, 194, 987-96		93
2165	Marker gene screening for human mesenchymal stem cells in early osteogenic response to bone morphogenetic protein 6 with DNA microarray. **2013**, 17, 641-5		1
2164	Infobiotics. **2013**,		27
2163	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. **2013**, 154, 530-40		107
2162	Bringing genome-wide association findings into clinical use. **2013**, 14, 549-58		262
2161	From promises to practical strategies in epigenetic epidemiology. **2013**, 14, 585-94		270
2160	Epigenomic of Aging. **2013**, 02,		0
2159	An atlas of over 90,000 conserved noncoding sequences provides insight into crucifer regulatory regions. **2013**, 45, 891-8		248
2158	Estrogen induced concentration dependent differential gene expression in human breast cancer (MCF7) cells: role of transcription factors. **2013**, 437, 475-81		9
2157	DNA methylation and methylcytosine oxidation in cell fate decisions. **2013**, 25, 152-61		69
2156	The haplotype-resolved genome and epigenome of the aneuploid HeLa cancer cell line. *Nature*, **2013**, 500, 207-11	50.4	236
2155	RelB: an outlier in leukocyte biology. **2013**, 94, 941-51		33
2154	Discovering and mapping chromatin states using a tree hidden Markov model. **2013**, 14 Suppl 5, S4		26
2153	Incorporating phylogenetic-based covarying mutations into RNAalifold for RNA consensus structure prediction. **2013**, 14, 142		6
2152	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. **2013**, 14, 128		2715
2151	MotifLab: a tools and data integration workbench for motif discovery and regulatory sequence analysis. **2013**, 14, 9		22

2150	CpG islands under selective pressure are enriched with H3K4me3, H3K27ac and H3K36me3 histone modifications. **2013**, 13, 145	5
2149	WS-SNPs&GO: a web server for predicting the deleterious effect of human protein variants using functional annotation. **2013**, 14 Suppl 3, S6	159
2148	Discovery of structural alterations in solid tumor oligodendroglioma by single molecule analysis. **2013**, 14, 505	25
2147	Selective constraint, background selection, and mutation accumulation variability within and between human populations. **2013**, 14, 495	13
2146	Genome-wide identification of binding sites for NAC and YABBY transcription factors and co-regulated genes during soybean seedling development by ChIP-Seq and RNA-Seq. **2013**, 14, 477	43
2145	Non-canonical protein-DNA interactions identified by ChIP are not artifacts. **2013**, 14, 254	20
2144	Exome sequencing of senescence-accelerated mice (SAM) reveals deleterious mutations in degenerative disease-causing genes. **2013**, 14, 248	21
2143	TRACER: a resource to study the regulatory architecture of the mouse genome. **2013**, 14, 215	13
2142	Whole human genome proteogenomic mapping for ENCODE cell line data: identifying protein-coding regions. **2013**, 14, 141	45
2141	Open questions: a logic (or lack thereof) of genome organization. **2013**, 11, 58	6
2140	Vitamin D receptor ChIP-seq in primary CD4+ cells: relationship to serum 25-hydroxyvitamin D levels and autoimmune disease. **2013**, 11, 163	47
2139	How life changes itself: the Read-Write (RW) genome. **2013**, 10, 287-323	67
2138	Translational genetics for diagnosis of human disorders of sex development. **2013**, 14, 371-92	45
2137	Long non-coding RNAs: novel targets for nervous system disease diagnosis and therapy. **2013**, 10, 632-46	97
2136	Genetics of dystonia: what's known? What's new? What's next?. **2013**, 28, 899-905	61
2135	Long noncoding RNAs and the genetics of cancer. **2013**, 108, 2419-25	588
2134	Long non-coding RNAs: challenges for diagnosis and therapies. **2013**, 23, 15-20	137
2133	Epigenetic mechanisms and non-coding RNAs in osteoarthritis. **2013**, 15, 353	38

2132	Computational approaches to identify functional genetic variants in cancer genomes. **2013**, 10, 723-9	129
2131	Update in pulmonary vascular diseases 2012. **2013**, 188, 23-8	3
2130	Databases as instruments for analysis of large-scale data sets of interactions between molecular biological objects. **2013**, 40, 233-242	2
2129	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. **2013**, 45, 1150-9	1153
2128	The extent of functionality in the human genome. **2013**, 7,	19
2127	Systems biomedicine: It's your turn. Recent progress in systems biomedicine. **2013**, 1, 140-155	2
2126	Personal genomes, quantitative dynamic omics and personalized medicine. **2013**, 1, 71-90	26
2125	[Personalized urooncology based on molecular uropathology: what is the future?]. **2013**, 52, 976-81	
2124	Variable phenotypes of knockin mice carrying the M712T Gne mutation. **2013**, 15, 180-91	16
2123	Epidemiology and genetic determinants of progressive deterioration of glycaemia in American Indians: the Strong Heart Family Study. **2013**, 56, 2194-202	5
2122	Laparoscopic total gastrectomy and gastric cancer genome architecture: lessons, cautions, and promises. **2013**, 27, 3945-7	1
2121	Two novel aspects of the kinetics of gene expression including miRNAs. **2013**, 11,	1
2120	Latent regulatory potential of human-specific repetitive elements. **2013**, 49, 262-72	53
2119	The non-coding road towards cardiac regeneration. **2013**, 6, 909-23	10
2118	Identification of candidate intergenic risk loci in autism spectrum disorder. **2013**, 14, 499	37
2117	From evolution to revolution: miRNAs as pharmacological targets for modulating cholesterol efflux and reverse cholesterol transport. **2013**, 75, 60-72	36
2116	Phylogeny as the basis for naming histones. **2013**, 29, 499-500	15
2115	Oligonucleotides for upregulating gene expression. **2013**, 2, 215-29	6

2114	Finding the lost treasures in exome sequencing data. **2013**, 29, 593-9	105
2113	ChEA2: Gene-Set Libraries from ChIP-X Experiments to Decode the Transcription Regulome. **2013**, 416-430	9
2112	Selection and adaptation in the human genome. **2013**, 14, 467-89	90
2111	Transcription factor binding in human cells occurs in dense clusters formed around cohesin anchor sites. **2013**, 154, 801-13	253
2110	Advances in therapeutic RNA-targeting. **2013**, 30, 299-301	10
2109	DNA methylation analysis in nonalcoholic fatty liver disease suggests distinct disease-specific and remodeling signatures after bariatric surgery. **2013**, 18, 296-302	298
2108	Next Generation Sequencing in Cancer Research. **2013**,	4
2107	Fine mapping of the Bmgr5 quantitative trait locus for allogeneic bone marrow engraftment in mice. **2013**, 65, 585-96	3
2106	Long noncoding RNAs: new players in prostate cancer. **2013**, 339, 8-14	41
2105	Genome-scale proteome quantification by DEEP SEQ mass spectrometry. **2013**, 4, 2171	80
2104	Sequencing and annotated analysis of the Holstein cow genome. **2013**, 24, 309-21	9
2103	A glimpse into past, present, and future DNA sequencing. **2013**, 110, 3-24	106
2102	Information engineering infrastructure for life sciences and its implementation in China. **2013**, 56, 220-7	
2101	The genetic equidistance result: misreading by the molecular clock and neutral theory and reinterpretation nearly half of a century later. **2013**, 56, 254-61	22
2100	Genes, Exomes, Genomes, Copy Number: What is Their Future in Pediatric Renal Disease. **2013**, 1, 52-59	1
2099	Differentiation and adaptation epigenetic networks: Translational research in gastric carcinogenesis. **2013**, 58, 1-6	15
2098	Dissecting quantitative traits in mice. **2013**, 14, 421-39	24
2097	Major histocompatibility complex genomics and human disease. **2013**, 14, 301-23	381

2096	Diagnostic biomarkers are hidden in the infected host's epigenome. **2013**, 13, 625-37	4
2095	Inherited genetic susceptibility to breast cancer: the beginning of the end or the end of the beginning?. **2013**, 183, 1038-1051	66
2094	Clinical implications of shared genetics and pathogenesis in autoimmune diseases. **2013**, 9, 646-59	86
2093	DNA sequence motif: a jack of all trades for ChIP-Seq data. **2013**, 91, 135-71	6
2092	Roles of long noncoding RNAs in brain development, functional diversification and neurodegenerative diseases. **2013**, 97, 69-80	266
2091	3S: shotgun secondary structure determination of long non-coding RNAs. **2013**, 63, 170-7	47
2090	TALE-mediated modulation of transcriptional enhancers in vivo. **2013**, 10, 762-7	68
2089	Blood pressure regulation via the epithelial sodium channel: from gene to kidney and beyond. **2013**, 40, 495-503	17
2088	Genomics of lymphoid malignancies reveal major activation pathways in lymphocytes. **2013**, 45, 15-23	2
2087	Extensive cooperation of immune master regulators IRF3 and NFB in RNA Pol II recruitment and pause release in human innate antiviral transcription. **2013**, 4, 959-73	57
2086	Radiation-dose response of glycophorin A somatic mutation in erythrocytes associated with gene polymorphisms of p53 binding protein 1. **2013**, 755, 49-54	1
2085	The genetics of complex cholestatic disorders. **2013**, 144, 1357-74	111
2084	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. **2013**, 93, 545-54	145
2083	An aberrant transcription factor network essential for Wnt signaling and stem cell maintenance in glioblastoma. **2013**, 3, 1567-79	187
2082	Early T helper cell programming of gene expression in human. **2013**, 25, 282-90	11
2081	Impacts of variation in the human genome on gene regulation. **2013**, 425, 3970-7	97
2080	Integrative annotation of variants from 1092 humans: application to cancer genomics. **2013**, 342, 1235587	281
2079	Genetic architecture of quantitative traits and complex diseases. **2013**, 23, 678-83	22

2078	Investigation of six testicular germ cell tumor susceptibility genes suggests a parent-of-origin effect in SPRY4. **2013**, 22, 3373-80		25
2077	Molecular consequences of animal breeding. **2013**, 23, 295-301		35
2076	Dial M(RF) for myogenesis. **2013**, 280, 3980-90		66
2075	Beyond BRCA1/2: polygenic, 'polyfunctional' molecular circuitry model to predict breast cancer risk. **2013**, 7, 675-8		2
2074	New insights into the genetic basis of TAR (thrombocytopenia-absent radii) syndrome. **2013**, 23, 316-23		55
2073	Nine things to remember about human genome diversity. **2013**, 82, 155-64		24
2072	Natural antisense transcripts as therapeutic targets. **2013**, 10, e119-e125		11
2071	Virology. Our viral inheritance. **2013**, 340, 820-1		29
2070	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. **2013**, 45, 1353-60		934
2069	Crossing the omic chasm: a time for omic ancillary systems. **2013**, 309, 1237-8		66
2068	Micro- and nanoscale devices for the investigation of epigenetics and chromatin dynamics. **2013**, 8, 709-18		47
2067	Gene Evolution and Human Adaptation. **2013**,		
2066	Mutational analysis of breast cancer: guiding personalized treatments. **2013**, 22 Suppl 2, S19-21		12
2065	What is the point of large-scale collections of human induced pluripotent stem cells?. **2013**, 31, 875-7		51
2064	Mutations in regulators of the epigenome and their connections to global chromatin patterns in cancer. **2013**, 14, 765-80		286
2063	RNA in unexpected places: long non-coding RNA functions in diverse cellular contexts. **2013**, 14, 699-712		1047
2062	Genomics: Comparisons across cancers. *Nature*, **2013**, 502, 306-7	50.4	8
2061	Patterns of Selection in Plant Genomes. **2013**, 44, 31-49		35

2060	A high-resolution map of the three-dimensional chromatin interactome in human cells. *Nature*, **2013**, 503, 290-4	50.4	861
2059	High-throughput microfluidic single-cell digital polymerase chain reaction. **2013**, 85, 7182-90		84
2058	Dynamic trans-acting factor colocalization in human cells. **2013**, 155, 713-24		109
2057	The nexus of chromatin regulation and intermediary metabolism. *Nature*, **2013**, 502, 489-98	50.4	286
2056	Topology of mammalian developmental enhancers and their regulatory landscapes. *Nature*, **2013**, 502, 499-506	50.4	355
2055	A platform for RNA. **2013**, 6, 1151-1151		1
2054	MicroRNAs and other non-coding RNAs as targets for anticancer drug development. **2013**, 12, 847-65		982
2053	Epigenetic reprogramming in cancer. **2013**, 339, 1567-70		518
2052	Dynamics of 1₱25-dihydroxyvitamin D3-dependent chromatin accessibility of early vitamin D receptor target genes. **2013**, 1829, 1266-75		40
2051	microRNAs: small regulators with a big impact on lipid metabolism. **2013**, 54, 1159-60		15
2050	The role of transposable elements in health and diseases of the central nervous system. **2013**, 33, 17577-86		122
2049	Epithelial-mesenchymal transition and tumor suppression are controlled by a reciprocal feedback loop between ZEB1 and Grainyhead-like-2. **2013**, 73, 6299-309		131
2048	Histone modifications for human epigenome analysis. **2013**, 58, 439-45		253
2047	Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. **2013**, 342, 744-7		278
2046	Identification of genetic variants that affect histone modifications in human cells. **2013**, 342, 747-9		331
2045	Extensive variation in chromatin states across humans. **2013**, 342, 750-2		276
2044	Global DNA methylation remodeling accompanies CD8 T cell effector function. **2013**, 191, 3419-29		135
2043	Mapping the HIF Transcription Factor in Cancer by ChIP-Seq Technology. **2013**, 91-117		

2042	Super-enhancers in the control of cell identity and disease. **2013**, 155, 934-47	2053
2041	Cortical evolution: judge the brain by its cover. **2013**, 80, 633-47	352
2040	De novo DNA demethylation and noncoding transcription define active intergenic regulatory elements. **2013**, 23, 1601-14	44
2039	Ancient DNA reveals key stages in the formation of central European mitochondrial genetic diversity. **2013**, 342, 257-61	237
2038	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. **2013**, 14, 441-6	25
2037	A polymorphic p53 response element in KIT ligand influences cancer risk and has undergone natural selection. **2013**, 155, 410-22	100
2036	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. **2013**, 110, 13481-6	127
2035	Bubble-seq analysis of the human genome reveals distinct chromatin-mediated mechanisms for regulating early- and late-firing origins. **2013**, 23, 1774-88	65
2034	Biomarker discovery and validation: the tide is turning. **2013**, 10, 505-7	5
2033	Genetically encoded system to track histone modification in vivo. **2013**, 3, 2436	74
2032	Detectable clonal mosaicism in the human genome. **2013**, 50, 348-59	26
2031	Identifying context-specific transcription factor targets from prior knowledge and gene expression data. **2013**, 12, 142-9	9
2030	Availability, Reliability, and Security in Information Systems and HCI. **2013**,	
2029	Immunological Genome Project and systems immunology. **2013**, 34, 602-9	111
2028	A brief review on the Human Encyclopedia of DNA Elements (ENCODE) project. **2013**, 11, 135-41	74
2027	Reprogramming cellular events by poly(ADP-ribose)-binding proteins. **2013**, 34, 1066-87	115
2026	ceRNA cross-talk in cancer: when ce-bling rivalries go awry. **2013**, 3, 1113-21	505
2025	Beyond gene discovery in inflammatory bowel disease: the emerging role of epigenetics. **2013**, 145, 293-308	206

2024	The evolving epigenome. **2013**, 22, R1-6	49
2023	Rational drug repositioning by medical genetics. **2013**, 31, 1080-2	69
2022	Reply to Rational drug repositioning by medical genetics. **2013**, 31, 1082	4
2021	Deep conservation of cis-regulatory elements in metazoans. **2013**, 368, 20130020	20
2020	Beyond the ENCODE project: using genomics and epigenomics strategies to study enhancer evolution. **2013**, 368, 20130022	14
2019	Pattern recognition in bioinformatics. **2013**, 14, 633-47	46
2018	Osteoarthritis year 2013 in review: genetics and genomics. **2013**, 21, 1443-51	33
2017	Cross-talk between site-specific transcription factors and DNA methylation states. **2013**, 288, 34287-94	136
2016	Genetics. GWAS to therapy by genome edits?. **2013**, 342, 206-7	11
2015	Cardiovascular RNA interference therapy: the broadening tool and target spectrum. **2013**, 113, 588-602	30
2014	Metabolic mechanisms of epigenetic regulation. **2013**, 8, 2607-21	48
2013	Targeted Sequencing Strategies in Cancer Research. **2013**, 137-163	2
2012	Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. **2013**, 155, 1521-31	256
2011	Network analysis of GWAS data. **2013**, 23, 602-10	67
2010	Cell cycle-related genes as modifiers of age of onset of colorectal cancer in Lynch syndrome: a large-scale study in non-Hispanic white patients. **2013**, 34, 299-306	9
2009	Connecting signaling pathways underlying communication to ASD vulnerability. **2013**, 113, 97-133	8
2008	Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. **2013**, 155, 1507-20	255
2007	Understanding the regulatory and transcriptional complexity of the genome through structure. **2013**, 23, 1081-8	55

2006	Epigenetic concerns in assisted reproduction: update and critical review of the current literature. **2013**, 99, 605-6	26
2005	Combining in silico prediction and ribosome profiling in a genome-wide search for novel putatively coding sORFs. **2013**, 14, 648	65
2004	Time for the zebrafish ENCODE. **2013**, 92, 695-701	10
2003	An erythroid enhancer of BCL11A subject to genetic variation determines fetal hemoglobin level. **2013**, 342, 253-7	400
2002	Introduction to Evolutionary Genomics. **2013**,	14
2001	Identification of active regulatory regions from DNA methylation data. **2013**, 41, e155	133
2000	Genetic susceptibility to chronic lymphocytic leukemia. **2013**, 50, 296-302	23
1999	Bidirectional promoters in the transcription of mammalian genomes. **2013**, 78, 335-41	28
1998	Structure prediction and analysis of DNA transposon and LINE retrotransposon proteins. **2013**, 288, 16127-38	10
1997	CruzDB: software for annotation of genomic intervals with UCSC genome-browser database. **2013**, 29, 3003-6	16
1996	Chromatin organization and global regulation of Hox gene clusters. **2013**, 368, 20120367	53
1995	Epigenetics and Complex Traits. **2013**,	1
1994	NGS++: a library for rapid prototyping of epigenomics software tools. **2013**, 29, 1893-4	3
1993	The open chromatin landscape of Kaposi's sarcoma-associated herpesvirus. **2013**, 87, 11831-42	32
1992	snOPY: a small nucleolar RNA orthological gene database. **2013**, 6, 426	64
1991	Deep sequencing reveals increased DNA methylation in chronic rat epilepsy. **2013**, 126, 741-56	134
1990	Expression variation of the porcine ADRB2 has a complex genetic background. **2013**, 288, 615-25	4
1989	A systematic approach identifies FOXA1 as a key factor in the loss of epithelial traits during the epithelial-to-mesenchymal transition in lung cancer. **2013**, 14, 680	43

1988	Defining the contribution of SNPs identified in asthma GWAS to clinical variables in asthmatic children. **2013**, 14, 100	19
1987	Transcriptome analysis of human tissues and cell lines reveals one dominant transcript per gene. **2013**, 14, R70	175
1986	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. **2013**, 15, R92	248
1985	Non-coding RNAs regulate tumor cell plasticity. **2013**, 56, 886-90	12
1984	Large-scale study of long non-coding RNA functions based on structure and expression features. **2013**, 56, 953-9	8
1983	Mapping genome-wide transcription factor binding sites in frozen tissues. **2013**, 6, 30	25
1982	The splice site variant rs11078928 may be associated with a genotype-dependent alteration in expression of GSDMB transcripts. **2013**, 14, 627	18
1981	Efficient digest of high-throughput sequencing data in a reproducible report. **2013**, 14 Suppl 11, S3	5
1980	Efficient alignment of RNA secondary structures using sparse dynamic programming. **2013**, 14, 269	9
1979	Meeting report: Frontiers in genetics: genomics and epigenomics. **2013**, 35, 559-562	
1978	Screening in silico predicted remotely acting NF1 gene regulatory elements for mutations in patients with neurofibromatosis type 1. **2013**, 7, 18	4
1977	Genome-wide analysis of H4K5 acetylation associated with fear memory in mice. **2013**, 14, 539	34
1976	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. **2013**, 6, 26	168
1975	REACTIN: regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. **2013**, 14, 504	17
1974	Discovery of MLL1 binding units, their localization to CpG Islands, and their potential function in mitotic chromatin. **2013**, 14, 927	12
1973	Why are bacteria different from eukaryotes?. **2013**, 11, 119	16
1972	Pathways systematically associated to Hirschsprung's disease. **2013**, 8, 187	14
1971	A platform independent RNA-Seq protocol for the detection of transcriptome complexity. **2013**, 14, 855	4

1970	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B. **2013**, 14, R132		100
1969	The chromatin modification by SUMO-2/3 but not SUMO-1 prevents the epigenetic activation of key immune-related genes during Kaposi's sarcoma associated herpesvirus reactivation. **2013**, 14, 824		24
1968	Long non-coding RNA HOTAIR is an independent prognostic marker of metastasis in estrogen receptor-positive primary breast cancer. **2013**, 142, 529-36		203
1967	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. **2013**, 12, 140		48
1966	Structure-based protein-protein interaction networks and drug design. **2013**, 1, 183-191		7
1965	Identification of novel transcripts and noncoding RNAs in bovine skin by deep next generation sequencing. **2013**, 14, 789		96
1964	Pathway analyses and understanding disease associations. **2013**, 1, 230		9
1963	Synergistic activation of inflammatory cytokine genes by interferon-□nduced chromatin remodeling and toll-like receptor signaling. **2013**, 39, 454-69		176
1962	Cracking the ENCODE: from transcription to therapeutics. **2013**, 57, 2532-5		10
1961	Epigenetic modifications in the pathogenesis of diabetic nephropathy. **2013**, 33, 341-53		63
1960	eRNAs promote transcription by establishing chromatin accessibility at defined genomic loci. **2013**, 51, 606-17		342
1959	Genomic organization of human transcription initiation complexes. *Nature*, **2013**, 502, 53-8	50.4	49
1958	Pathogenic variants in non-protein-coding sequences. **2013**, 84, 422-8		28
1957	Integration of cancer genomics with treatment selection: from the genome to predictive biomarkers. **2013**, 119, 3914-28		13
1956	Deep sequencing and integrative genome analysis: approaching a new class of biomarkers and therapeutic targets for breast cancer. **2013**, 14, 5-8		3
1955	Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, **2013**, 501, 506-511	50.4	1323
1954	Systematic identification of trans eQTLs as putative drivers of known disease associations. **2013**, 45, 1238-1243		1244
1953	Epigenetic memory at embryonic enhancers identified in DNA methylation maps from adult mouse tissues. **2013**, 45, 1198-206		350

1952	Towards precision medicine: advances in computational approaches for the analysis of human variants. **2013**, 425, 4047-63	95
1951	Next generation sequencing and rare genetic variants: from human population studies to medical genetics. **2013**, 54, 518-32	8
1950	Genomics in cardiovascular disease. **2013**, 61, 2029-37	24
1949	Population Genomics of Human Adaptation. **2013**, 44, 123-143	66
1948	Ionizing radiation and genetic risks. XVII. Formation mechanisms underlying naturally occurring DNA deletions in the human genome and their potential relevance for bridging the gap between induced DNA double-strand breaks and deletions in irradiated germ cells. **2013**, 753, 114-130	16
1947	The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community. **2013**, 12, 23-7	87
1946	Locus-specific editing of histone modifications at endogenous enhancers. **2013**, 31, 1133-6	295
1945	Cancer omics: from regulatory networks to clinical outcomes. **2013**, 340, 277-83	9
1944	Genome-wide association study identifies two susceptibility loci for osteosarcoma. **2013**, 45, 799-803	156
1943	Building an ENCODE-style data compendium on a shoestring. **2013**, 10, 926	11
1942	ExpressionBlast: mining large, unstructured expression databases. **2013**, 10, 925-6	23
1941	Promiscuous RNA binding by Polycomb repressive complex 2. **2013**, 20, 1250-7	332
1940	Mapping human epigenomes. **2013**, 155, 39-55	405
1939	Genome network medicine: new diagnostics and predictive tools. **2013**, 13, 643-6	5
1938	Support of the histaminergic hypothesis in Tourette syndrome: association of the histamine decarboxylase gene in a large sample of families. **2013**, 50, 760-4	82
1937	Host genomic influences on HIV/AIDS. **2013**, 14, 201	16
1936	Assay of insulator enhancer-blocking activity with the use of transient transfection. **2013**, 78, 895-903	1
1935	Migraine genetics: Part II. **2013**, 53, 1218-29	41

1934	A geometric framework for evaluating rare variant tests of association. **2013**, 37, 345-57	18
1933	The epigenetic basis of behavioral phenotypes: is there reason for continued optimism?. **2013**, 30, 1147-50	4
1932	A modified watermark synchronisation code for robust embedding of data in DNA. **2013**,	4
1931	Diagnostics for personalized medicine: what will change in the era of large-scale genomics studies?. **2013**, 10, 835-848	2
1930	Crowd-funded micro-grants for genomics and "big data": an actionable idea connecting small (artisan) science, infrastructure science, and citizen philanthropy. **2013**, 17, 161-72	29
1929	Genomic approaches for studying craniofacial disorders. **2013**, 163C, 218-31	24
1928	Reading and writing omes. **2013**, 9, 642	
1927	Migraine genetics--a review: Part I. **2013**, 53, 1207-17	8
1926	An Interactive Analysis and Exploration Tool for Epigenomic Data. **2013**, 32, 91-100	9
1925	Fundamental interactions in RNA: Questions answered and remaining. **2013**, 99, 1097-104	13
1924	Neurogenomics of speech and language disorders: the road ahead. **2013**, 14, 204	26
1923	Machine learning and genome annotation: a match meant to be?. **2013**, 14, 205	56
1922	The Human Genome Project: big science transforms biology and medicine. **2013**, 5, 79	103
1921	Genetic architecture of retinal and macular degenerative diseases: the promise and challenges of next-generation sequencing. **2013**, 5, 84	28
1920	Impact of polymorphisms in drug pathway genes on disease-free survival in adults with acute myeloid leukemia. **2013**, 58, 353-61	32
1919	Research in Computational Molecular Biology. **2013**,	9
1918	Why is epigenetics important in understanding the pathogenesis of inflammatory musculoskeletal diseases?. **2013**, 15, 209	18
1917	MANBA, CXCR5, SOX8, RPS6KB1 and ZBTB46 are genetic risk loci for multiple sclerosis. **2013**, 136, 1778-82	47

1916	Novel effects of chromosome Y on cardiac regulation, chromatin remodeling, and neonatal programming in male mice. **2013**, 154, 4746-56	12
1915	Integrative annotation of chromatin elements from ENCODE data. **2013**, 41, 827-41	383
1914	Genomic region operation kit for flexible processing of deep sequencing data. **2013**, 10, 200-6	12
1913	The humankind genome: from genetic diversity to the origin of human diseases. **2013**, 56, 705-16	17
1912	Association of intron loss with high mutation rate in Arabidopsis: implications for genome size evolution. **2013**, 5, 723-33	30
1911	Genome-wide analysis of transcriptional regulators in human HSPCs reveals a densely interconnected network of coding and noncoding genes. **2013**, 122, e12-22	96
1910	Security study of keyed DNA data embedding. **2013**,	0
1909	Human brain evolution: transcripts, metabolites and their regulators. **2013**, 14, 112-27	154
1908	Phenotypic impact of genomic structural variation: insights from and for human disease. **2013**, 14, 125-38	340
1907	Genetics 100 for cardiologists: basics of genome-wide association studies. **2013**, 29, 10-7	27
1906	Transcriptomics in the RNA-seq era. **2013**, 17, 4-11	211
1905	A first step toward completion of a genome-wide characterization of the human proteome. **2013**, 12, 1-5	70
1904	Dressed for success applying chemistry to modulate aptamer functionality. **2013**, 4, 60-67	57
1903	Dynamic DNA methylation across diverse human cell lines and tissues. **2013**, 23, 555-67	500
1902	Genome-wide epigenetic regulation of miRNAs in cancer. **2013**, 73, 473-7	244
1901	Genome-wide chromatin state transitions associated with developmental and environmental cues. **2013**, 152, 642-54	400
1900	Epigenetic studies of schizophrenia: progress, predicaments, and promises for the future. **2013**, 39, 11-6	59
1899	Chromatin organization: form to function. **2013**, 23, 185-90	37

1898	Deciphering the transcriptional cis-regulatory code. **2013**, 29, 11-22	83
1897	Using whole exome sequencing to walk from clinical practice to research and back again. **2013**, 127, 968-70	4
1896	Genotype to phenotype: lessons from model organisms for human genetics. **2013**, 14, 168-78	164
1895	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. **2013**, 23, 169-80	133
1894	Small open reading frames associated with morphogenesis are hidden in plant genomes. **2013**, 110, 2395-400	116
1893	RNA-mediated genome rearrangement: hypotheses and evidence. **2013**, 35, 84-7	15
1892	Non-random mutation: the evolution of targeted hypermutation and hypomutation. **2013**, 35, 123-30	43
1891	Transposable elements as genetic regulatory substrates in early development. **2013**, 23, 218-26	103
1890	A DNA-centric protein interaction map of ultraconserved elements reveals contribution of transcription factor binding hubs to conservation. **2013**, 5, 531-45	23
1889	Genetics of human gene expression. **2013**, 23, 627-34	17
1888	Exploring the effects of polymorphisms on cis-regulatory signal transduction response. **2013**, 19, 99-107	12
1887	Epigenetic Regulation of Gene Expression: Emerging Applications for Horses. **2013**, 33, 288-294	5
1886	FOXO3 selectively amplifies enhancer activity to establish target gene regulation. **2013**, 5, 1664-78	43
1885	Molecular analysis of a deletion hotspot in the NRXN1 region reveals the involvement of short inverted repeats in deletion CNVs. **2013**, 92, 375-86	38
1884	Using chromatin marks to interpret and localize genetic associations to complex human traits and diseases. **2013**, 23, 635-41	30
1883	A comprehensive nuclear receptor network for breast cancer cells. **2013**, 3, 538-51	61
1882	One man's junk is another man's treasure: GWAS, ENCODE, and the search for control of the heart. **2013**, 10, 409-11	
1881	News from the protein mutability landscape. **2013**, 425, 3937-48	55

1880 Two telling tales. **2013**, 23, R213 2

1879 Evaluating risks of insertional mutagenesis by DNA transposons in gene therapy. **2013**, 161, 265-83 68

1878 Dissecting non-coding RNA mechanisms in cellulo by Single-molecule High-Resolution Localization and Counting. **2013**, 63, 188-99 23

1877 Indicators of domestic/intimate partner violence are structured by genetic and nonshared environmental influences. **2013**, 47, 371-6 30

1876 An ACE in the hole: Twin family models for applied behavioral genetics research. **2013**, 24, 572-594 20

1875 Modeling and inference of genetic interactions. **2013**, 3, 453-466

1874 Evolutionary psychology and consumer behavior: A constructive critique. **2013**, 23, 387-399 13

1873 Systems biology approaches to epidemiological studies of complex diseases. **2013**, 5, 677-86 7

1872 Genome-wide association study identifies loci affecting blood copper, selenium and zinc. **2013**, 22, 3998-4006 76

1871 Rare-variant genome-wide association studies: a new frontier in genetic analysis of complex traits. **2013**, 14, 413-24 33

1870 Chromatin Structure and Human Genome Evolution. **2013**,

1869 The epigenetic landscape of B lymphocyte tolerance to self. **2013**, 587, 2067-73 12

1868 Amish revisited: next-generation sequencing studies of psychiatric disorders among the Plain people. **2013**, 29, 412-8 17

1867 Twenty-five years of progress: the view from NIMH and NINDS. **2013**, 80, 561-7 59

1866 Building a genome analysis pipeline to predict disease risk and prevent disease. **2013**, 425, 3993-4005 26

1865 Alec J. Jeffreys Born a scientist. **2013**, 27, 169-170

1864 Unraveling the genetics of common epilepsies: approaches, platforms, and caveats. **2013**, 26, 229-33 10

1863 Epigenomics: the science of no-longer-junk DNA. Why study it in chronic kidney disease?. **2013**, 33, 354-62 21

1862	A tiered hidden Markov model characterizes multi-scale chromatin states. **2013**, 102, 1-7	7
1861	Global analysis of DNA methylation variation in adipose tissue from twins reveals links to disease-associated variants in distal regulatory elements. **2013**, 93, 876-90	269
1860	Cytosine 5-Hydroxymethylation of the LZTS1 Gene Is Reduced in Breast Cancer. **2013**, 6, 715-21	16
1859	Epigenetic changes in histologically normal prostate tissues. **2013**, 189, 2020-1	1
1858	Genotype to phenotype via network analysis. **2013**, 23, 611-21	88
1857	Progression from ductal carcinoma in situ to invasive breast cancer: revisited. **2013**, 7, 859-69	146
1856	Editorial for "non-coding RNA methods". **2013**, 63, 93-4	1
1855	Progress in the genetics of polygenic brain disorders: significant new challenges for neurobiology. **2013**, 80, 578-87	63
1854	Genome-wide studies of nuclear receptors in cell fate decisions. **2013**, 24, 706-15	18
1853	Remodeling of the enhancer landscape during macrophage activation is coupled to enhancer transcription. **2013**, 51, 310-25	462
1852	Cancer genome sequencing: understanding malignancy as a disease of the genome, its conformation, and its evolution. **2013**, 340, 152-60	16
1851	Recent Developments in the Genetic and Genomic Basis of Type 2 Diabetes. **2013**, 7, 66-72	
1850	High-throughput chromatin immunoprecipitation for genome-wide mapping of in vivo protein-DNA interactions and epigenomic states. **2013**, 8, 539-54	180
1849	High-throughput sequencing for biology and medicine. **2013**, 9, 640	186
1848	Genome-wide distribution of DNA methylation and DNA demethylation and related chromatin regulators in cancer. **2013**, 1835, 155-63	17
1847	Genomic modulators of the immune response. **2013**, 29, 74-83	43
1846	Characterization of the genetic variation present in CYP3A4 in three South African populations. **2013**, 4, 17	23
1845	Can ENCODE tell us how much junk DNA we carry in our genome?. **2013**, 430, 1340-3	72

1844 ENCODE and its first impractical application. **2013**, 4, 4

1843 Rise of the RNA machines: exploring the structure of long non-coding RNAs. **2013**, 425, 3731-46 98

1842 Robust shifts in S100a9 expression with aging: a novel mechanism for chronic inflammation. **2013**, 3, 1215 63

1841 Enhancers: five essential questions. **2013**, 14, 288-95 316

1840 Basic concepts of epigenetics. **2013**, 99, 607-15 112

1839 Distinguishing between Genomic Regions Bound by Paralogous Transcription Factors. **2013**, 145-157 1

1838 Cryptococcus neoformans copper detoxification machinery is critical for fungal virulence. **2013**, 13, 265-76 124

1837 Pharmacogenomics of Cytochrome P450 3A4: Recent Progress Toward the "Missing Heritability" Problem. **2013**, 4, 12 145

1836 Population genetic tools for dissecting innate immunity in humans. **2013**, 13, 280-93 87

1835 Epigenetic regulation of macrophage polarization and function. **2013**, 34, 216-23 216

1834 Vitamin D receptor signaling mechanisms: integrated actions of a well-defined transcription factor. **2013**, 78, 127-36 178

1833 Structure and dynamics of molecular networks: a novel paradigm of drug discovery: a comprehensive review. **2013**, 138, 333-408 604

1832 The genetic basis of Gilles de la Tourette Syndrome. **2013**, 37, 1026-39 85

1831 Dynamic integration of splicing within gene regulatory pathways. **2013**, 152, 1252-69 299

1830 CTCF and cohesin: linking gene regulatory elements with their targets. **2013**, 152, 1285-97 280

1829 Transcriptional regulation and its misregulation in disease. **2013**, 152, 1237-51 805

1828 Genome architecture: domain organization of interphase chromosomes. **2013**, 152, 1270-84 522

1827 Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. **2013**, 45, 314-8 314

1826	"Seq-ing" insights into the epigenetics of neuronal gene regulation. **2013**, 77, 606-23	67
1825	A network model of the molecular organization of chromatin in Drosophila. **2013**, 49, 759-71	49
1824	Interpreting the role of de novo protein-coding mutations in neuropsychiatric disease. **2013**, 45, 234-8	64
1823	Next-generation sequencing: from understanding biology to personalized medicine. **2013**, 2, 378-98	25
1822	Functional implications of genome topology. **2013**, 20, 290-9	321
1821	DNA methylation dynamics in health and disease. **2013**, 20, 274-81	405
1820	Epigenetic programming and reprogramming during development. **2013**, 20, 282-9	310
1819	Pan-genomic binding of hypoxia-inducible transcription factors. **2013**, 394, 507-17	56
1818	Long noncoding RNAs: past, present, and future. **2013**, 193, 651-69	1251
1817	Non-Coding RNAs: Functional Aspects and Diagnostic Utility in Oncology. **2013**, 14, 4934-68	25
1816	Interplay between the cancer genome and epigenome. **2013**, 153, 38-55	588
1815	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. **2013**, 45, 385-91, 391e1-2	413
1814	Application of proteomics technology in adipocyte biology. **2013**, 9, 1076-91	15
1813	Next-generation sequencing platforms. **2013**, 6, 287-303	443
1812	Master transcription factors and mediator establish super-enhancers at key cell identity genes. **2013**, 153, 307-19	2252
1811	Methylation-dependent and -independent genomic targeting principles of the MBD protein family. **2013**, 153, 480-92	240
1810	MicroRNA regulation of T-cell differentiation and function. **2013**, 253, 65-81	101
1809	Role of microRNAs and long-non-coding RNAs in CD4(+) T-cell differentiation. **2013**, 253, 82-96	69

1808	The ENCODE project: missteps overshadowing a success. **2013**, 23, R259-61		67
1807	Epigenomics and the regulation of aging. **2013**, 5, 205-27		42
1806	Fatty acid binding protein 3 (fabp3) is associated with insulin, lipids and cardiovascular phenotypes of the metabolic syndrome through epigenetic modifications in a Northern European family population. **2013**, 6, 9		37
1805	SMIM1 underlies the Vel blood group and influences red blood cell traits. **2013**, 45, 542-545		77
1804	H3K9/HP1 and Polycomb: two key epigenetic silencing pathways for gene regulation and embryo development. **2013**, 104, 243-91		38
1803	Modification of enhancer chromatin: what, how, and why?. **2013**, 49, 825-37		859
1802	DNA: Celebrate the unknowns. *Nature*, **2013**, 496, 419-20	50.4	29
1801	Massively-parallel sequencing of genes on a single chromosome: a comparison of solution hybrid selection and flow sorting. **2013**, 14, 253		6
1800	From neural development to cognition: unexpected roles for chromatin. **2013**, 14, 347-59		347
1799	Chromosomal domains: epigenetic contexts and functional implications of genomic compartmentalization. **2013**, 23, 197-203		52
1798	Analysis of sequence variation underlying tissue-specific transcription factor binding and gene expression. **2013**, 34, 1140-8		10
1797	Aptamers: molecules of great potential. **2013**, 31, 1260-74		132
1796	Structural variations, the regulatory landscape of the genome and their alteration in human disease. **2013**, 35, 533-43		49
1795	Systematic study of human long intergenic non-coding RNAs and their impact on cancer. **2013**, 56, 324-34		34
1794	Synthesis and properties of isobicyclo-DNA. **2013**, 19, 6990-7006		10
1793	Clinical applications of the functional connectome. **2013**, 80, 527-40		232
1792	Principles of transcriptome analysis and gene expression quantification: an RNA-seq tutorial. **2013**, 13, 559-72		123
1791	Sherlock: detecting gene-disease associations by matching patterns of expression QTL and GWAS. **2013**, 92, 667-80		173

1790	Management of incidental findings in clinical genomic sequencing. **2013**, Chapter 9, Unit9.23	19
1789	Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data. **2013**, 14, 390-403	762
1788	Genome-wide kinase-chromatin interactions reveal the regulatory network of ERK signaling in human embryonic stem cells. **2013**, 50, 844-55	72
1787	Epigenetic mechanisms of drug addiction. **2013**, 23, 521-8	86
1786	The vast, conserved mammalian lincRNome. **2013**, 9, e1002917	44
1785	Getting to the heart of the matter: long non-coding RNAs in cardiac development and disease. **2013**, 32, 1805-16	85
1784	Human corneal epithelial subpopulations: oxygen dependent ex vivo expansion and transcriptional profiling. **2013**, 91 Thesis 4, 1-34	5
1783	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. **2013**, 45, 730-8	551
1782	Association of serotonin transporter gene (SLC6A4) polymorphisms with schizophrenia susceptibility and symptoms in a Chinese-Han population. **2013**, 44, 290-5	17
1781	Arguments for standardizing transposable element annotation in plant genomes. **2013**, 18, 367-76	19
1780	Genome-wide inference of natural selection on human transcription factor binding sites. **2013**, 45, 723-9	95
1779	LASAGNA: a novel algorithm for transcription factor binding site alignment. **2013**, 14, 108	19
1778	On the stability of [(uracil)2-Cu]2+ complexes in the gas phase. Different pathways for the formation of [(uracil-H)(uracil)-Cu]+ monocations. **2013**, 11, 3862-70	13
1777	Genome organization and long-range regulation of gene expression by enhancers. **2013**, 25, 387-94	118
1776	ZBTB33 binds unmethylated regions of the genome associated with actively expressed genes. **2013**, 6, 13	50
1775	Pathway databases: making chemical and biological sense of the genomic data flood. **2013**, 20, 629-35	18
1774	Progress in understanding the genetics of bronchopulmonary dysplasia. **2013**, 37, 85-93	41
1773	Emerging tools for synthetic genome design. **2013**, 35, 359-70	15

1772	Genome engineering at the dawn of the golden age. **2013**, 14, 135-58		94
1771	New insights from existing sequence data: generating breakthroughs without a pipette. **2013**, 49, 605-17		9
1770	Targeting long non-coding RNA to therapeutically upregulate gene expression. **2013**, 12, 433-46		373
1769	Epigenetic mechanisms in multiple sclerosis: implications for pathogenesis and treatment. **2013**, 12, 195-206		99
1768	Epigenetic abnormalities in cancer find a "home on the range". **2013**, 23, 1-3		14
1767	Genomics: A spruce sequence. *Nature*, **2013**, 497, 569-70	50.4	7
1766	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. **2013**, 45, 836-41		154
1765	Implications of genome-wide association studies in cancer therapeutics. **2013**, 76, 370-80		17
1764	Systems virology: host-directed approaches to viral pathogenesis and drug targeting. **2013**, 11, 455-66		54
1763	Convergent functional genomics of psychiatric disorders. **2013**, 162B, 587-94		17
1762	Genetics and consequences of crop domestication. **2013**, 61, 8267-76		83
1761	Genome-wide quantitative enhancer activity maps identified by STARR-seq. **2013**, 339, 1074-7		603
1760	Helper T-cell identity and evolution of differential transcriptomes and epigenomes. **2013**, 252, 24-40		76
1759	Mobile DNA distributions refine the phylogeny of "matsutake" mushrooms, Tricholoma sect. Caligata. **2013**, 23, 447-61		14
1758	Genetic approaches to neural circuits in the mouse. **2013**, 36, 183-215		146
1757	DNase I-hypersensitive exons colocalize with promoters and distal regulatory elements. **2013**, 45, 852-9		94
1756	Multi-cultural association of the serotonin transporter gene (SLC6A4) with substance use disorder. **2013**, 38, 1737-47		34
1755	DNA methylation data analysis and its application to cancer research. **2013**, 5, 301-16		73

1754	Pediatric systems medicine: evaluating needs and opportunities using congenital heart block as a case study. **2013**, 73, 508-13		7
1753	Browsing (Epi)genomes: a guide to data resources and epigenome browsers for stem cell researchers. **2013**, 13, 14-21		16
1752	Food, nutrigenomics, and neurodegeneration--neuroprotection by what you eat!. **2013**, 48, 353-62		96
1751	The gene for the transcription factor BHLHE40/DEC1/stra13 is a dynamically regulated primary target of the vitamin D receptor. **2013**, 136, 62-7		15
1750	From evolutionary bystander to master manipulator: the emerging roles for the mitochondrial genome as a modulator of nuclear gene expression. **2013**, 21, 1335-7		20
1749	Small RNAs derived from structural non-coding RNAs. **2013**, 63, 76-84		28
1748	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. **2013**, 45, 907-11		191
1747	Prioritization of genetic variants in the microRNA regulome as functional candidates in genome-wide association studies. **2013**, 34, 1049-56		33
1746	ZFN, TALEN, and CRISPR/Cas-based methods for genome engineering. **2013**, 31, 397-405		2526
1745	Ethical, legal, social, and policy implications of behavioral genetics. **2013**, 14, 515-34		17
1744	Regulatory mechanisms of long noncoding RNAs in vertebrate central nervous system development and function. **2013**, 235, 200-14		108
1743	Diverse mechanisms of somatic structural variations in human cancer genomes. **2013**, 153, 919-29		238
1742	The correlation between histone modifications and gene expression. **2013**, 5, 113-6		109
1741	Architecture and evolution of a minute plant genome. *Nature*, **2013**, 498, 94-8	50.4	237
1740	Genetic variants in GPR126 are associated with adolescent idiopathic scoliosis. **2013**, 45, 676-9		172
1739	A rational design of completely random shRNA library. **2013**, 430, 987-92		
1738	Mapping the Functional Genome. **2013**, 28-40		1
1737	Peppy: proteogenomic search software. **2013**, 12, 3019-25		64

1736	Effect of posttranslational modifications on enzyme function and assembly. **2013**, 92, 80-109	61
1735	De novo mutations in the genome organizer CTCF cause intellectual disability. **2013**, 93, 124-31	89
1734	Non-coding transcription at cis-regulatory elements: computational and experimental approaches. **2013**, 63, 66-75	4
1733	Sequencing studies in human genetics: design and interpretation. **2013**, 14, 460-70	200
1732	Translation regulation gets its 'omics' moment. **2013**, 4, 617-30	36
1731	Integrating multiple oestrogen receptor alpha ChIP studies: overlap with disease susceptibility regions, DNase I hypersensitivity peaks and gene expression. **2013**, 6, 45	5
1730	Chromatin-associated ncRNA activities. **2013**, 21, 627-41	31
1729	A peptide-spectrum scoring system based on ion alignment, intensity, and pair probabilities. **2013**, 12, 4240-7	11
1728	How next-generation sequencing is transforming complex disease genetics. **2013**, 29, 23-30	57
1727	Techniques of DNA methylation analysis with nutritional applications. **2013**, 6, 83-96	16
1726	The role of memory-related gene WWC1 (KIBRA) in lifetime posttraumatic stress disorder: evidence from two independent samples from African conflict regions. **2013**, 74, 664-71	20
1725	From human genome to cancer genome: the first decade. **2013**, 23, 1054-62	103
1724	Xq27 FRAXA locus is a strong candidate for dyslexia: evidence from a genome-wide scan in French families. **2013**, 43, 132-40	8
1723	Alternative polyadenylation sites reveal distinct chromatin accessibility and histone modification in human cell lines. **2013**, 29, 1713-7	14
1722	Profiling spatial enrichment of chromatin marks suggests an additional epigenomic dimension in gene regulation. **2013**, 7, 80-87	6
1721	Many human accelerated regions are developmental enhancers. **2013**, 368, 20130025	117
1720	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. **2013**, 45, 1487-93	151
1719	Evolutionary dynamics of repetitive DNA in semaprochilodus (characiformes, prochilodontidae): a fish model for sex chromosome differentiation. **2013**, 7, 325-33	19

1718	Genomic landscape of transcriptional and epigenetic dysregulation in early onset polyglutamine disease. **2013**, 33, 10471-82	54
1717	Genes and cardiovascular risk. **2013**, 34, 949-50	1
1716	Discovery of cell-type specific regulatory elements in the human genome using differential chromatin modification analysis. **2013**, 41, 9230-42	14
1715	Comment on "Evidence of abundant purifying selection in humans for recently acquired regulatory functions". **2013**, 340, 682	15
1714	Widespread selection across coding and noncoding DNA in the pea aphid genome. **2013**, 3, 993-1001	6
1713	Mapping inherited and somatic variation in regulatory DNA: new roadmap for common disease clinical discoveries. **2013**, 13, 519-22	3
1712	Architecture of pharmacogenomic associations: structures with functional foundations or castles made of sand?. **2013**, 14, 1-4	7
1711	A complex V ATP5A1 defect causes fatal neonatal mitochondrial encephalopathy. **2013**, 136, 1544-54	67
1710	Genotype-phenotype correlations in hyperekplexia: apnoeas, learning difficulties and speech delay. **2013**, 136, 3085-95	58
1709	PRISM offers a comprehensive genomic approach to transcription factor function prediction. **2013**, 23, 889-904	25
1708	Patterns of regulatory activity across diverse human cell types predict tissue identity, transcription factor binding, and long-range interactions. **2013**, 23, 777-88	153
1707	SORCS1 contributes to the development of renal disease in rats and humans. **2013**, 45, 720-8	11
1706	Targeting MYCN: a good BET for improving neuroblastoma therapy?. **2013**, 3, 255-7	13
1705	LPS-treated macrophage cytokines repress surfactant protein-B in lung epithelial cells. **2013**, 49, 306-15	12
1704	ABCs of genomics. **2013**, 2013, 316-23	4
1703	ENCODE and a new landscape for psychiatric genetics. **2013**, 203, 84-5	5
1702	Cancer heterogeneity and signaling network-based drug target. **2013**, 14, 1243-6	2
1701	Decoding coronary artery disease: somatic mosaicism and genomics for personal and population risk prediction. **2013**, 7, 189-92	1

1700	Gastric cancer guidelines and genome differences between Japan and the west. **2013**, 9, 1053-6	5
1699	Maps of open chromatin highlight cell type-restricted patterns of regulatory sequence variation at hematological trait loci. **2013**, 23, 1130-41	31
1698	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. **2013**, 23, 2136-48	39
1697	Tissue-specific splicing of a ubiquitously expressed transcription factor is essential for muscle differentiation. **2013**, 27, 1247-59	73
1696	Pharmacogenomic approaches that may guide preeclampsia therapy. **2013**, 14, 591-3	10
1695	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. **2013**, 23, 1522-40	119
1694	Inferring chromatin-bound protein complexes from genome-wide binding assays. **2013**, 23, 1295-306	28
1693	Analysis of variable retroduplications in human populations suggests coupling of retrotransposition to cell division. **2013**, 23, 2042-52	41
1692	Functional transcriptomics in the post-ENCODE era. **2013**, 23, 1961-73	49
1691	Chromatin and epigenetic features of long-range gene regulation. **2013**, 41, 7185-99	87
1690	Practical guidelines for the comprehensive analysis of ChIP-seq data. **2013**, 9, e1003326	166
1689	Genome-wide analysis reveals selection for important traits in domestic horse breeds. **2013**, 9, e1003211	157
1688	Too New for Textbooks. **2013**, 75, 480-485	
1687	Regulatory Roles for Long ncRNA and mRNA. **2013**, 5, 462-90	69
1686	Gene regulatory scenarios of primary 1,25-dihydroxyvitamin d3 target genes in a human myeloid leukemia cell line. **2013**, 5, 1221-41	15
1685	APPRIS: annotation of principal and alternative splice isoforms. **2013**, 41, D110-7	128
1684	The Genomic HyperBrowser: an analysis web server for genome-scale data. **2013**, 41, W133-41	25
1683	Quantifying missing heritability at known GWAS loci. **2013**, 9, e1003993	87

1682	Inactivation of intergenic enhancers by EBNA3A initiates and maintains polycomb signatures across a chromatin domain encoding CXCL10 and CXCL9. **2013**, 9, e1003638	45
1681	Long non-coding RNAs and complex human diseases. **2013**, 14, 18790-808	137
1680	GEMINI: integrative exploration of genetic variation and genome annotations. **2013**, 9, e1003153	271
1679	Contributions of protein-coding and regulatory change to adaptive molecular evolution in murid rodents. **2013**, 9, e1003995	76
1678	CentroidAlign-Web: A Fast and Accurate Multiple Aligner for Long Non-Coding RNAs. **2013**, 14, 6144-56	3
1677	Transposable elements are major contributors to the origin, diversification, and regulation of vertebrate long noncoding RNAs. **2013**, 9, e1003470	437
1676	Pervasive transcription of the human genome produces thousands of previously unidentified long intergenic noncoding RNAs. **2013**, 9, e1003569	498
1675	Ras-induced changes in H3K27me3 occur after those in transcriptional activity. **2013**, 9, e1003698	35
1674	TFcheckpoint: a curated compendium of specific DNA-binding RNA polymerase II transcription factors. **2013**, 29, 2519-20	66
1673	Why precursors matter. **2013**, 22, 518-20	5
1672	Causes and consequences of chromatin variation between inbred mice. **2013**, 9, e1003570	16
1671	Genome-Wide Detection of Gene Coexpression Domains Showing Linkage to Regions Enriched with Polymorphic Retrotransposons in Recombinant Inbred Mouse Strains. **2013**, 3, 597-605	8
1670	ChIP-PED enhances the analysis of ChIP-seq and ChIP-chip data. **2013**, 29, 1182-9	11
1669	Stability selection for regression-based models of transcription factor-DNA binding specificity. **2013**, 29, i117-25	35
1668	Biosemiotic Entropy of the Genome: Mutations and Epigenetic Imbalances Resulting in Cancer. **2013**, 15, 234-261	12
1667	Expression profiling of type 2 diabetes susceptibility genes in the pancreatic islets, adipose tissue and liver of obese mice. **2013**, 121, 413-9	2
1666	Fine-mapping the genetic association of the major histocompatibility complex in multiple sclerosis: HLA and non-HLA effects. **2013**, 9, e1003926	186
1665	Genome-wide signatures of transcription factor activity: connecting transcription factors, disease, and small molecules. **2013**, 9, e1003198	18

1664	Transcription factor binding profiles reveal cyclic expression of human protein-coding genes and non-coding RNAs. **2013**, 9, e1003132	6
1663	Global properties and functional complexity of human gene regulatory variation. **2013**, 9, e1003501	47
1662	Side effects: substantial non-neutral evolution flanking regulatory sites. **2013**, 9, e1003528	1
1661	The gene desert mammary carcinoma susceptibility locus Mcs1a regulates Nr2f1 modifying mammary epithelial cell differentiation and proliferation. **2013**, 9, e1003549	17
1660	Pathways-driven sparse regression identifies pathways and genes associated with high-density lipoprotein cholesterol in two Asian cohorts. **2013**, 9, e1003939	22
1659	Low frequency variants, collapsed based on biological knowledge, uncover complexity of population stratification in 1000 genomes project data. **2013**, 9, e1003959	30
1658	Pathway-based analysis of primary biliary cirrhosis genome-wide association studies. **2013**, 14, 179-86	44
1657	Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. **2013**, 29, 1060-7	98
1656	On the state of scientific English and how to improve it--part 2: define what you mean. **2013**, 35, 497	1
1655	Comparative genomics as a tool to understand evolution and disease. **2013**, 23, 1063-8	106
1654	Alpha-interferon suppresses hepadnavirus transcription by altering epigenetic modification of cccDNA minichromosomes. **2013**, 9, e1003613	112
1653	From Identification to Characterization of the Multiple Sclerosis Susceptibility Gene CLEC16A. **2013** , 14, 4476-97	31
1652	Urinary bladder cancer susceptibility markers. What do we know about functional mechanisms?. **2013**, 14, 12346-66	22
1651	Detecting and comparing non-coding RNAs in the high-throughput era. **2013**, 14, 15423-58	16
1650	Recombination dynamics of a human Y-chromosomal palindrome: rapid GC-biased gene conversion, multi-kilobase conversion tracts, and rare inversions. **2013**, 9, e1003666	44
1649	Deletion of an X-inactivation boundary disrupts adjacent gene silencing. **2013**, 9, e1003952	27
1648	Efficient site-specific transgenesis and enhancer activity tests in medaka using PhiC31 integrase. **2013**, 140, 4287-95	23
1647	Long non-coding RNA targeting and transcriptional de-repression. **2013**, 23, 9-14	34

1646	Trans-ancestral studies fine map the SLE-susceptibility locus TNFSF4. **2013**, 9, e1003554	41
1645	Genome-wide determinants of proviral targeting, clonal abundance and expression in natural HTLV-1 infection. **2013**, 9, e1003271	77
1644	Long non-coding RNAs in haematological malignancies. **2013**, 14, 15386-422	34
1643	Integrated module and gene-specific regulatory inference implicates upstream signaling networks. **2013**, 9, e1003252	38
1642	The majority of primate-specific regulatory sequences are derived from transposable elements. **2013**, 9, e1003504	204
1641	Characterization of the p53 cistrome--DNA binding cooperativity dissects p53's tumor suppressor functions. **2013**, 9, e1003726	69
1640	miR-1/133a clusters cooperatively specify the cardiomyogenic lineage by adjustment of myocardin levels during embryonic heart development. **2013**, 9, e1003793	92
1639	Fending for a Braveheart. **2013**, 32, 1211-3	2
1638	Genome-wide analysis of immune system genes by expressed sequence Tag profiling. **2013**, 190, 5578-87	10
1637	BioCode: two biologically compatible Algorithms for embedding data in non-coding and coding regions of DNA. **2013**, 14, 121	20
1636	Minireview: Obesity and breast cancer: a tale of inflammation and dysregulated metabolism. **2013**, 27, 715-25	60
1635	Comparative annotation of functional regions in the human genome using epigenomic data. **2013**, 41, 4423-32	37
1634	Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development. **2013**, 41, 3600-18	20
1633	A genome-wide association study of central corneal thickness in Latinos. **2013**, 54, 2435-43	45
1632	NF-Y coassociates with FOS at promoters, enhancers, repetitive elements, and inactive chromatin regions, and is stereo-positioned with growth-controlling transcription factors. **2013**, 23, 1195-209	99
1631	Genome-wide association studies in asthma: what they really told us about pathogenesis. **2013**, 13, 112-8	33
1630	Hepatocyte nuclear factors 4□and 1□regulate kidney developmental expression of drug-metabolizing enzymes and drug transporters. **2013**, 84, 808-23	76
1629	Recent advances in understanding the genetics of congenital heart defects. **2013**, 25, 561-6	15

1628	Widespread purifying selection on RNA structure in mammals. **2013**, 41, 8220-36	126
1627	Systems genetics implicates cytoskeletal genes in oocyte control of cloned embryo quality. **2013**, 193, 877-96	14
1626	Advances in blood pressure genomics. **2013**, 112, 1365-79	85
1625	Heterogeneous tempo and mode of conserved noncoding sequence evolution among four mammalian orders. **2013**, 5, 2330-43	21
1624	The causal meaning of Fisher's average effect. **2013**, 95, 89-109	21
1623	Clarity against the odds: standards for describing DNA sequence variants. **2013**, 45, 101-3	
1622	Using microRNA as an alternative treatment for hyperlipidemia and cardiovascular disease: cardio-miRs in the pipeline. **2013**, 62, 247-54	22
1621	Arpeggio: harmonic compression of ChIP-seq data reveals protein-chromatin interaction signatures. **2013**, 41, e161	5
1620	Functional anatomy of distant-acting mammalian enhancers. **2013**, 368, 20120359	30
1619	Effects of gene regulatory reprogramming on gene expression in human and mouse developing hearts. **2013**, 368, 20120366	6
1618	Deciphering cis-regulatory control in inflammatory cells. **2013**, 368, 20120370	13
1617	Evolution of transcriptional enhancers and animal diversity. **2013**, 368, 20130017	47
1616	Alterations to the remote control of Shh gene expression cause congenital abnormalities. **2013**, 368, 20120357	26
1615	The mystery of extreme non-coding conservation. **2013**, 368, 20130021	50
1614	From remote enhancers to gene regulation: charting the genome's regulatory landscapes. **2013**, 368, 20120358	26
1613	Buccals are likely to be a more informative surrogate tissue than blood for epigenome-wide association studies. **2013**, 8, 445-54	118
1612	Progress in genetic association studies of plasma lipids. **2013**, 24, 123-8	10
1611	Nencki Genomics Database--Ensembl funcgen enhanced with intersections, user data and genome-wide TFBS motifs. **2013**, 2013, bat069	18

1610	Segmenting the human genome based on states of neutral genetic divergence. **2013**, 110, 14699-704	14
1609	Characterization of the human ESC transcriptome by hybrid sequencing. **2013**, 110, E4821-30	222
1608	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. **2013**, 23, 1142-54	72
1607	Construction of protein phosphorylation networks by data mining, text mining and ontology integration: analysis of the spindle checkpoint. **2013**, 2013, bat038	12
1606	Loss of heterozygosity preferentially occurs in early replicating regions in cancer genomes. **2013**, 41, 7615-24	20
1605	DNase-seq predicts regions of rotational nucleosome stability across diverse human cell types. **2013**, 23, 1118-29	21
1604	Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. **2013**, 41, D171-6	212
1603	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. **2013**, 41, 9999-10009	11
1602	Antisense transcripts enhanced by camptothecin at divergent CpG-island promoters associated with bursts of topoisomerase I-DNA cleavage complex and R-loop formation. **2013**, 41, 10110-23	46
1601	APR-246/PRIMA-1(MET) rescues epidermal differentiation in skin keratinocytes derived from EEC syndrome patients with p63 mutations. **2013**, 110, 2157-62	31
1600	MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. **2013**, 29, 2529-38	40
1599	Bioinformatics in High Throughput Sequencing: Application in Evolving Genetic Diseases. **2013**, 04,	5
1598	A genome-wide perspective of human diversity and its implications in infectious disease. **2013**, 3, a012450	21
1597	Translational genetics: advancing fronts for craniofacial health. **2013**, 92, 1058-64	9
1596	Genome-wide significant association of ANKRD55 rs6859219 and multiple sclerosis risk. **2013**, 50, 140-3	29
1595	Overview of high throughput sequencing technologies to elucidate molecular pathways in cardiovascular diseases. **2013**, 112, 1613-23	77
1594	The impact of trans-regulation on the evolutionary rates of metazoan proteins. **2013**, 41, 6371-80	6
1593	Towards an understanding of cell-specific functions of signal-dependent transcription factors. **2013**, 51, T37-50	24

1592	The Y chromosome as a regulatory element shaping immune cell transcriptomes and susceptibility to autoimmune disease. **2013**, 23, 1474-85	95
1591	Vertebrate paralogous conserved noncoding sequences may be related to gene expressions in brain. **2013**, 5, 140-50	20
1590	VlincRNAs controlled by retroviral elements are a hallmark of pluripotency and cancer. **2013**, 14, R73	59
1589	Understanding neurological disease mechanisms in the era of epigenetics. **2013**, 70, 703-10	45
1588	PhysBinder: Improving the prediction of transcription factor binding sites by flexible inclusion of biophysical properties. **2013**, 41, W531-4	25
1587	Dysregulation of Long Non-coding RNAs in Human Disease. **2013**, 115-136	
1586	Mechanisms of in vivo binding site selection of the hematopoietic master transcription factor PU.1. **2013**, 41, 6391-402	57
1585	Global analysis of Drosophila Cys2His2 zinc finger proteins reveals a multitude of novel recognition motifs and binding determinants. **2013**, 23, 928-40	56
1584	Wellington: a novel method for the accurate identification of digital genomic footprints from DNase-seq data. **2013**, 41, e201	144
1583	Relating genes to function: identifying enriched transcription factors using the ENCODE ChIP-Seq significance tool. **2013**, 29, 1922-4	49
1582	DEXUS: identifying differential expression in RNA-Seq studies with unknown conditions. **2013**, 41, e198	20
1581	Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. **2013**, 30, 1159-71	58
1580	Enhancer networks revealed by correlated DNAse hypersensitivity states of enhancers. **2013**, 41, 6828-38	19
1579	An inflection point in gene discovery efforts for neurodegenerative diseases: from syndromic diagnoses toward endophenotypes and the epigenome. **2013**, 70, 719-26	14
1578	A dose-response study of arsenic exposure and global methylation of peripheral blood mononuclear cell DNA in Bangladeshi adults. **2013**, 121, 1306-12	45
1577	Molecular dissection of dystrophin identifies the docking site for nNOS. **2013**, 110, 387-8	21
1576	Integrative modeling of eQTLs and cis-regulatory elements suggests mechanisms underlying cell type specificity of eQTLs. **2013**, 9, e1003649	112
1575	Detecting DNA-protein interactions in living cells--ChIP approach. **2013**, 91, 101-33	4

1574	Epigenetics in Friedreich's Ataxia: Challenges and Opportunities for Therapy. **2013**, 2013, 852080	21
1573	Novel gene-by-environment interactions: APOB and NPC1L1 variants affect the relationship between dietary and total plasma cholesterol. **2013**, 54, 1512-20	30
1572	Gene expression 'signature' limitations and genome architecture-based perspectives for robust cancer biomarkers. **2013**, 7, 79-82	1
1571	To replicate or not to replicate: the case of pharmacogenetic studies: Establishing validity of pharmacogenomic findings: from replication to triangulation. **2013**, 6, 409-12; discussion 412	22
1570	Combining Hi-C data with phylogenetic correlation to predict the target genes of distal regulatory elements in human genome. **2013**, 41, 10391-402	15
1569	The essential detail: the genetics and genomics of the primate immune response. **2013**, 54, 181-95	16
1568	Differential principal component analysis of ChIP-seq. **2013**, 110, 6789-94	43
1567	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. **2013**, 110, 17921-6	477
1566	Solving nucleic acid structures by molecular replacement: examples from group II intron studies. **2013**, 69, 2174-85	17
1565	Susceptibility genes are enriched in those of the herpes simplex virus 1/host interactome in psychiatric and neurological disorders. **2013**, 69, 240-61	27
1564	A replication study from Chinese supports association between lupus-risk allele in TNFSF4 and renal disorder. **2013**, 2013, 597921	16
1563	The challenge of increasing Pfam coverage of the human proteome. **2013**, 2013, bat023	16
1562	A quantitative analysis of the impact on chromatin accessibility by histone modifications and binding of transcription factors in DNase I hypersensitive sites. **2013**, 2013, 914971	8
1561	Restoring fertility in sterile childhood cancer survivors by autotransplanting spermatogonial stem cells: are we there yet?. **2013**, 2013, 903142	46
1560	MelanomaDB: A Web Tool for Integrative Analysis of Melanoma Genomic Information to Identify Disease-Associated Molecular Pathways. **2013**, 3, 184	9
1559	Non-Coding RNAs as Potential Neuroprotectants against Ischemic Brain Injury. **2013**, 3, 360-95	31
1558	Inter-Laboratory Variability in Array-Based RNA Quantification Methods. **2013**, 6, 13-24	
1557	High-throughput identification of long-range regulatory elements and their target promoters in the human genome. **2013**, 41, 4835-46	23

1556	Prenatal Programming of Psychopathology: The Role of Epigenetic Mechanisms / PRENATALNO PROGRAMIRANJE PSIHIJATRIJSKIH POREMEĆAJA: ULOGA EPIGENETSKIH MEHANIZAMA. **2013**, 32, 313-324	9
1555	Integrated analysis of long noncoding RNA and coding RNA expression in esophageal squamous cell carcinoma. **2013**, 2013, 480534	36
1554	Expanding the foundation for personalized medicine: implications and challenges for dentistry. **2013**, 92, 3S-10S	36
1553	A lesson learned from the H3.3K27M mutation found in pediatric glioma: a new approach to the study of the function of histone modifications in vivo?. **2013**, 12, 2546-52	42
1552	YY1TargetDB: an integral information resource for Yin Yang 1 target loci. **2013**, 2013, bat007	8
1551	Targeted chromosomal deletions and inversions in zebrafish. **2013**, 23, 1008-17	87
1550	Genomic markers of ovarian reserve. **2013**, 31, 399-415	37
1549	Regional chromatin decompaction in Cornelia de Lange syndrome associated with NIPBL disruption can be uncoupled from cohesin and CTCF. **2013**, 22, 4180-93	28
1548	Lessons from postgenome-wide association studies: functional analysis of cancer predisposition loci. **2013**, 274, 414-24	19
1547	Epigenetic studies in Alzheimer's disease: current findings, caveats, and considerations for future studies. **2013**, 162B, 789-99	58
1546	The simplest explanation: passive DNA demethylation in PGCs. **2013**, 32, 318-21	17
1545	Gene regulation and epigenetics in Friedreich's ataxia. **2013**, 126 Suppl 1, 21-42	42
1544	Individualized genomics and the future of translational medicine. **2013**, 1, 1-3	4
1543	Human Genomics and Anthropology*. **2013**, 20, 1-4	0
1542	Common chromosome fragile sites in human and murine epithelial cells and FHIT/FRA3B loss-induced global genome instability. **2013**, 52, 1017-29	46
1541	Insights into the genetic basis of type 2 diabetes. **2013**, 4, 233-44	44
1540	Next-generation sequence analysis of genes associated with obesity and nonalcoholic fatty liver disease-related cirrhosis in extreme obesity. **2013**, 75, 144-51	18
1539	DNA methylation contributes to natural human variation. **2013**, 23, 1363-72	272

1538	MicroRNAs in platelet production and activation. **2013**, 11 Suppl 1, 340-50	67
1537	A meta-analysis of the genomic and transcriptomic composition of complex life. **2013**, 12, 2061-72	102
1536	Orthologues, Paralogues and Horizontal Gene Transfer in the Human Holobiont. **2013**,	3
1535	Efficiently identifying significant associations in genome-wide association studies. **2013**, 20, 817-30	3
1534	The emerging use of zebrafish to model metabolic disease. **2013**, 6, 1080-8	176
1533	Gene smoking interactions on human brain gene expression: finding common mechanisms in adolescents and adults. **2013**, 54, 1109-19	11
1532	A polymorphism affecting MYB binding within the promoter of the PDCD4 gene is associated with severe asthma in children. **2013**, 34, 1131-9	16
1531	Genetic association analyses of nitric oxide synthase genes and neural tube defects vary by phenotype. **2013**, 98, 365-73	2
1530	Advancing Renewable Normal Human Cell Assays for Drug Discovery. **2013**, 74, 127-137	2
1529	Genome-wide and parental allele-specific analysis of CTCF and cohesin DNA binding in mouse brain reveals a tissue-specific binding pattern and an association with imprinted differentially methylated regions. **2013**, 23, 1624-35	37
1528	Statistical significance of combinatorial regulations. **2013**, 110, 12996-3001	53
1527	Histone H3 lysine methylation in cognition and intellectual disability disorders. **2013**, 20, 570-9	44
1526	Evolutionary analysis of the contact system indicates that kininogen evolved adaptively in mammals and in human populations. **2013**, 30, 1397-408	16
1525	Advances in inflammatory bowel disease pathogenesis: linking host genetics and the microbiome. **2013**, 62, 1505-10	318
1524	Characterization and comparison of human nuclear and cytosolic editomes. **2013**, 110, E2741-7	53
1523	The complexity of thyroid transcription factor 1 with both pro- and anti-oncogenic activities. **2013**, 288, 24992-25000	22
1522	Epigenetic modulation of the immune function: a potential target for tolerance. **2013**, 8, 694-702	61
1521	Two genomic regions of chromosomes 1 and 18 explain most of the stroke susceptibility under salt loading in stroke-prone spontaneously hypertensive rat/Izm. **2013**, 62, 55-61	14

1520	The shared genomic architecture of human nucleolar organizer regions. **2013**, 23, 2003-12	75
1519	Developmental timing of mutations revealed by whole-genome sequencing of twins with acute lymphoblastic leukemia. **2013**, 110, 7429-33	40
1518	Utilizing sequence intrinsic composition to classify protein-coding and long non-coding transcripts. **2013**, 41, e166	879
1517	GWAS3D: Detecting human regulatory variants by integrative analysis of genome-wide associations, chromosome interactions and histone modifications. **2013**, 41, W150-8	86
1516	Recurrent patterns of DNA methylation in the ZNF154, CASP8, and VHL promoters across a wide spectrum of human solid epithelial tumors and cancer cell lines. **2013**, 8, 1355-72	40
1515	Lessons from next-generation sequencing analysis in hematological malignancies. **2013**, 3, e127	40
1514	The Genotype-Tissue Expression (GTEx) project. **2013**, 45, 580-5	4179
1513	Homozygosity for a null allele of SMIM1 defines the Vel-negative blood group phenotype. **2013**, 45, 537-41	66
1512	Convergent functional genomics of stem cell-derived cells. **2013**, 3, e305	1
1511	Novel long noncoding RNAs are regulated by angiotensin II in vascular smooth muscle cells. **2013**, 113, 266-78	218
1510	Transcription factors interfering with dedifferentiation induce cell type-specific transcriptional profiles. **2013**, 110, 6412-7	31
1509	Computational detection of abundant long-range nucleotide covariation in Drosophila genomes. **2013**, 19, 1171-82	5
1508	Epigenetic consequences of a changing human diet. **2013**, 72, 363-71	30
1507	Prognostic microRNA/mRNA signature from the integrated analysis of patients with invasive breast cancer. **2013**, 110, 7413-7	128
1506	Massively parallel in vivo enhancer assay reveals that highly local features determine the cis-regulatory function of ChIP-seq peaks. **2013**, 110, 11952-7	136
1505	Global identification of conserved post-transcriptional regulatory programs in trypanosomatids. **2013**, 41, 8591-600	27
1504	Systematic functional regulatory assessment of disease-associated variants. **2013**, 110, 9607-12	75
1503	Epigenetic regulation of planarian stem cells by the SET1/MLL family of histone methyltransferases. **2013**, 8, 79-91	43

1502	Disentangling two QTL on porcine chromosome 12 for backfat fatty acid composition. **2013**, 24, 168-86	8
1501	Decoding human gene expression signatures in the brain. **2013**, 4, 102-8	7
1500	Molecular Biology of Long Non-coding RNAs. **2013**,	2
1499	Real-time dynamics of methyl-CpG-binding domain protein 3 and its role in DNA demethylation by fluorescence correlation spectroscopy. **2013**, 8, 1089-100	20
1498	Kinases and chromatin structure: who regulates whom?. **2013**, 8, 1008-12	
1497	Regions of unusually high flexibility occur frequently in human genomic DNA. **2013**, 77, 612-7	1
1496	Bidirectional Gene Pairs in the Human Genome. **2013**,	1
1495	Big data challenges and opportunities in high-throughput sequencing. **2013**, 1, 29-34	27
1494	Is junk DNA bunk? A critique of ENCODE. **2013**, 110, 5294-300	273
1493	On the immortality of television sets: "function" in the human genome according to the evolution-free gospel of ENCODE. **2013**, 5, 578-90	340
1492	Life course health care and preemptive approach to non-communicable diseases. **2013**, 89, 462-73	29
1491	Penalized estimation in high-dimensional hidden Markov models with state-specific graphical models. **2013**, 7,	9
1490	Discovery of novel small RNAs in the quest to unravel genome complexity. **2013**, 41, 866-70	6
1489	Genome-wide methylation analyses of primary human leukocyte subsets identifies functionally important cell-type-specific hypomethylated regions. **2013**, 122, e52-60	56
1488	Massively parallel sequencing: the new frontier of hematologic genomics. **2013**, 122, 3268-75	17
1487	MicroRNAs as Oncogenes and Tumor Suppressors. **2013**, 223-243	3
1486	Not Junk After All: Non-Protein-Coding DNA Carries Extensive Biological Information. **2013**,	0
1485	AHT-ChIP-seq: a completely automated robotic protocol for high-throughput chromatin immunoprecipitation. **2013**, 14, R124	24

1484	Development of an Illumina-based ChIP-exonuclease method provides insight into FoxA1-DNA binding properties. **2013**, 14, R147	64
1483	Co-binding by YY1 identifies the transcriptionally active, highly conserved set of CTCF-bound regions in primate genomes. **2013**, 14, R148	50
1482	Sequence signatures extracted from proximal promoters can be used to predict distal enhancers. **2013**, 14, R117	30
1481	BLUEPRINT: mapping human blood cell epigenomes. **2013**, 98, 1487-9	109
1480	MMDiff: quantitative testing for shape changes in ChIP-Seq data sets. **2013**, 14, 826	20
1479	Transcription-factor occupancy at HOT regions quantitatively predicts RNA polymerase recruitment in five human cell lines. **2013**, 14, 720	29
1478	Advances in exercise, fitness, and performance genomics in 2012. **2013**, 45, 824-31	44
1477	Social regulation of human gene expression: mechanisms and implications for public health. **2013**, 103 Suppl 1, S84-92	124
1476	The real informatics challenges of personalized medicine: not just about the number of central processing units. **2013**, 10, 639-645	2
1475	APPLICATIONS OF BIOINFORMATICS TO NON-CODING RNAS IN THE ERA OF NEXT-GENERATION SEQUENCING. **2013**,	
1474	Predicting tissue specific transcription factor binding sites. **2013**, 14, 796	23
1473	An ecological genetic delineation of local seed-source provenance for ecological restoration. **2013**, 3, 2138-49	42
1472	Interaction-based evolution: how natural selection and nonrandom mutation work together. **2013**, 8, 24	20
1471	DNA sequencing methods in human genetics and disease research. **2013**, 5, 34	6
1470	MicroRNA discovery by similarity search to a database of RNA-seq profiles. **2013**, 4, 133	8
1469	DNA demethylation pathways: recent insights. **2013**, 5, 43-9	7
1468	Capturing drug responses by quantitative promoter activity profiling. **2013**, 2, e77	1
1467	A contemporary view of genes and behavior: complex systems and interactions. **2013**, 44, 285-306	2

1466	Cell-Type Specific Determinants of NRAMP1 Expression in Professional Phagocytes. **2013**, 2, 233-83	6
1465	LASAGNA-Search: an integrated web tool for transcription factor binding site search and visualization. **2013**, 54, 141-53	81
1464	The genetic architecture of rheumatoid arthritis: from susceptibility to clinical subphenotype associations. **2013**, 13, 720-31	6
1463	[Role of long non-coding ribonucleic acid in gastrointestinal cancer]. **2013**, 62, 317-26	2
1462	The genetics of multiple sclerosis: review of current and emerging candidates. **2013**, 6, 63-73	29
1461	The First 50 Plant Genomes. **2013**, 6, plantgenome2013.03.0001in	182
1460	Single-molecule fluorescence in situ hybridization: quantitative imaging of single RNA molecules. **2013**, 46, 65-72	54
1459	The genomics of schizophrenia: update and implications. **2013**, 123, 4557-63	73
1458	Epigenetic modifications unlock the milk protein gene loci during mouse mammary gland development and differentiation. **2013**, 8, e53270	42
1457	Efficient and comprehensive representation of uniqueness for next-generation sequencing by minimum unique length analyses. **2013**, 8, e53822	25
1456	5'-Methylcytosine and 5'-hydroxymethylcytosine each provide epigenetic information to the mouse zygote. **2013**, 8, e63689	29
1455	FFPred 2.0: improved homology-independent prediction of gene ontology terms for eukaryotic protein sequences. **2013**, 8, e63754	37
1454	Targeted deep resequencing identifies coding variants in the PEAR1 gene that play a role in platelet aggregation. **2013**, 8, e64179	22
1453	Chromatin accessibility data sets show bias due to sequence specificity of the DNase I enzyme. **2013**, 8, e69853	46
1452	Comprehensive characterization of 10,571 mouse large intergenic noncoding RNAs from whole transcriptome sequencing. **2013**, 8, e70835	46
1451	Two variants of the C-reactive protein gene are associated with risk of pre-eclampsia in an American Indian population. **2013**, 8, e71231	14
1450	An in-depth characterization of the major psoriasis susceptibility locus identifies candidate susceptibility alleles within an HLA-C enhancer element. **2013**, 8, e71690	33
1449	ARLTS1 and prostate cancer risk--analysis of expression and regulation. **2013**, 8, e72040	8

1430	Integrative understanding of macular morphologic patterns in diabetic retinopathy based on self-organizing map. **2014**, 55, 1994-2003	10
1429	Reptile genomes open the frontier for comparative analysis of amniote development and regeneration. **2014**, 58, 863-71	16
1428	Screening of key genes of unruptured intracranial aneurysms by using DNA microarray data analysis techniques. **2014**, 13, 758-67	6
1427	Evidence for site-specific occupancy of the mitochondrial genome by nuclear transcription factors. **2014**, 9, e84713	25
1426	Genome-wide analysis of promoters: clustering by alignment and analysis of regular patterns. **2014**, 9, e85260	4
1425	Expression variants of the lipogenic AGPAT6 gene affect diverse milk composition phenotypes in Bos taurus. **2014**, 9, e85757	44
1424	Computational characterization of modes of transcriptional regulation of nuclear receptor genes. **2014**, 9, e88880	5
1423	Natural antisense transcripts and long non-coding RNA in Neurospora crassa. **2014**, 9, e91353	35
1422	Association of DSC3 mRNA down-regulation in prostate cancer with promoter hypermethylation and poor prognosis. **2014**, 9, e92815	16
1421	Characterization of human pseudogene-derived non-coding RNAs for functional potential. **2014**, 9, e93972	42
1420	From human monocytes to genome-wide binding sites--a protocol for small amounts of blood: monocyte isolation/ChIP-protocol/library amplification/genome wide computational data analysis. **2014**, 9, e94164	4
1419	Drosophila 3' UTRs are more complex than protein-coding sequences. **2014**, 9, e97336	5
1418	A Bayesian method to incorporate hundreds of functional characteristics with association evidence to improve variant prioritization. **2014**, 9, e98122	24
1417	Seminoma and embryonal carcinoma footprints identified by analysis of integrated genome-wide epigenetic and expression profiles of germ cell cancer cell lines. **2014**, 9, e98330	25
1416	A general pairwise interaction model provides an accurate description of in vivo transcription factor binding sites. **2014**, 9, e99015	19
1415	Characterization of genome-methylome interactions in 22 nuclear pedigrees. **2014**, 9, e99313	9
1414	Effective automated feature construction and selection for classification of biological sequences. **2014**, 9, e99982	38
1413	Chromatin accessibility mapping identifies mediators of basal transcription and retinoid-induced repression of OTX2 in medulloblastoma. **2014**, 9, e107156	4

1412	In silico pooling of ChIP-seq control experiments. **2014**, 9, e109691	1
1411	Integrative data mining highlights candidate genes for monogenic myopathies. **2014**, 9, e110888	10
1410	Detection theory in identification of RNA-DNA sequence differences using RNA-sequencing. **2014**, 9, e112040	6
1409	Molecular evolution of the porcine type I interferon family: subtype-specific expression and antiviral activity. **2014**, 9, e112378	29
1408	Identification of highly conserved putative developmental enhancers bound by SOX3 in neural progenitors using ChIP-Seq. **2014**, 9, e113361	19
1407	Association between Expression Quantitative Trait Loci and Metabolic Traits in Two Korean Populations. **2014**, 9, e114128	4
1406	CRISPR reveals a distal super-enhancer required for Sox2 expression in mouse embryonic stem cells. **2014**, 9, e114485	118
1405	BLAT-based comparative analysis for transposable elements: BLATCAT. **2014**, 2014, 730814	
1404	Single nucleotide polymorphisms in microRNA binding sites: implications in colorectal cancer. **2014**, 2014, 547154	21
1403	Molecular systematics of terraranas (Anura: Brachycephaloidea)´with an assessment of the effects of alignment and optimality criteria. **2014**, 3825, 1-132	169
1402	Physics and Financial Economics (1776-2014): Puzzles, Ising and Agent-Based Models. **2014**,	5
1401	Uncovering RNA Editing Sites in Long Non-Coding RNAs. **2014**, 2, 64	34
1400	Comprehensive reconstruction and visualization of non-coding regulatory networks in human. **2014**, 2, 69	20
1399	Genetic code expansion as a tool to study regulatory processes of transcription. **2014**, 2, 7	11
1398	Lessons and Implications from Genome-Wide Association Studies (GWAS) Findings of Blood Cell Phenotypes. **2014**, 5, 51-64	12
1397	Genetic profiling for risk reduction in human cardiovascular disease. **2014**, 5, 214-34	11
1396	Illuminating the Transcriptome through the Genome. **2014**, 5, 235-53	4
1395	Epigenetic variation in monozygotic twins: a genome-wide analysis of DNA methylation in buccal cells. **2014**, 5, 347-65	43

1394	Pharmacogenomics: Current State-of-the-Art. **2014**, 5, 430-43	43
1393	Hope for GWAS: relevant risk genes uncovered from GWAS statistical noise. **2014**, 15, 17601-21	2
1392	Trans-regulation of RNA-binding protein motifs by microRNA. **2014**, 5, 79	14
1391	miRNA gene counts in chromosomes vary widely in a species and biogenesis of miRNA largely depends on transcription or post-transcriptional processing of coding genes. **2014**, 5, 100	60
1390	Functional implications of long non-coding RNAs in the pancreatic islets of Langerhans. **2014**, 5, 209	34
1389	The social brain meets the reactive genome: neuroscience, epigenetics and the new social biology. **2014**, 8, 309	87
1388	MicroRNA-138 is a potential regulator of memory performance in humans. **2014**, 8, 501	38
1387	Exome sequencing: what clinicians need to know. **2014**, 15	3
1386	The Future of Prenatal Diagnosis and Screening. **2014**, 3, 1291-301	6
1385	A statistical comparison of written language and nonlinguistic symbol systems. **2014**, 90, 457-481	11
1384	Potential of antibody-drug conjugates and novel therapeutics in breast cancer management. **2014**, 7, 491-500	17
1383	Genome-Wide Mapping of Chromatin State of Mouse Forelimbs. **2014**, 6, 1-11	4
1382	Quantum Perspectives of Consciousness, Cognition and Creativity: The Dirac Equation in a New Contour Integral Model of Brain Plasticity. **2014**, 03,	1
1381	Multi-species, multi-transcription factor binding highlights conserved control of tissue-specific biological pathways. **2014**, 3, e02626	62
1380	Insights into the next generation of cancer stem cell research. **2014**, 19, 1015-27	6
1379	Long non-coding RNAs in stem cells and cancer. **2014**, 5, 134-41	84
1378	7th Santorini Conference Biologie Prospective Systems Medicine, Personalized Health and Therapy in collaboration with ESPT. **2014**, 29,	
1377	. **2014**,	3

1376 Towards understanding RNA-mediated neurological disorders. **2014**, 41, 473-84 13

1375 Radiogenomics: the search for genetic predictors of radiotherapy response. **2014**, 10, 2391-406 54

1374 Dissection of thousands of cell type-specific enhancers identifies dinucleotide repeat motifs as general enhancer features. **2014**, 24, 1147-56 93

1373 Heterochromatin and sibling species of Simulium praelargum s.l. (Diptera: Simuliidae). **2014**, 57, 223-32 3

1372 Genome-wide scans of genetic variants for psychophysiological endophenotypes: a methodological overview. **2014**, 51, 1207-24 22

1371 Variation in vertebrate cis-regulatory elements in evolution and disease. **2014**, 5, e28848 14

1370 Long noncoding RNAs: versatile players in biologcial processes and human disorders. **2014**, 6, 375-9 10

1369 References. **2014**, 201-205

1368 Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. **2014**, 23, 3045-53 39

1367 A novel colorectal cancer risk locus at 4q32.2 identified from an international genome-wide association study. **2014**, 35, 2512-9 25

1366 Ensembl 2014. **2014**, 42, D749-55 1087

1365 The UCSC Genome Browser database: 2014 update. **2014**, 42, D764-70 537

1364 Targeted transgene integration overcomes variability of position effects in zebrafish. **2014**, 141, 715-24 30

1363 PePr: a peak-calling prioritization pipeline to identify consistent or differential peaks from replicated ChIP-Seq data. **2014**, 30, 2568-75 73

1362 Identification of non-coding RNAs with a new composite feature in the Hybrid Random Forest Ensemble algorithm. **2014**, 42, e93 29

1361 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

1360 Epigenetics: an accessible mechanism through which to track and respond to an obesogenic environment. **2014**, 9, 605-614 5

1359 Genetic markers associated with plasma protein C level in African Americans: the atherosclerosis risk in communities (ARIC) study. **2014**, 38, 709-13 6

1358	Integrated analysis of transcript-level regulation of metabolism reveals disease-relevant nodes of the human metabolic network. **2014**, 42, 1474-96	35
1357	The emerging roles of eRNAs in transcriptional regulatory networks. **2014**, 11, 106-10	23
1356	TNF-signalling primes chromatin for NF-B binding and induces rapid and widespread nucleosome repositioning. **2014**, 15, 536	22
1355	PD_NGSAtlas: a reference database combining next-generation sequencing epigenomic and transcriptomic data for psychiatric disorders. **2014**, 7, 71	9
1354	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. **2014**, 15, 494	26
1353	A simple metric of promoter architecture robustly predicts expression breadth of human genes suggesting that most transcription factors are positive regulators. **2014**, 15, 413	17
1352	Approaches for establishing the function of regulatory genetic variants involved in disease. **2014**, 6, 92	31
1351	Analysis of pattern overlaps and exact computation of P-values of pattern occurrences numbers: case of Hidden Markov Models. **2014**, 9, 25	1
1350	The parasite Trichomonas´vaginalis expresses thousands of pseudogenes and long non-coding RNAs independently from functional neighbouring genes. **2014**, 15, 906	27
1349	Identifying and mapping cell-type-specific chromatin programming of gene expression. **2014**, 111, E645-54	21
1348	Dynamic sequencing of circulating tumor DNA: novel noninvasive cancer biomarker. **2014**, 8, 629-32	4
1347	Dissecting the chromatin interactome of microRNA genes. **2014**, 42, 3028-43	22
1346	Functional chromatin features are associated with structural mutations in cancer. **2014**, 15, 1013	6
1345	Restraining the enhancers from straying. **2014**, 39, 739-40	
1344	Two ways to fold the genome during the cell cycle: insights obtained with chromosome conformation capture. **2014**, 7, 25	60
1343	OncoCis: annotation of cis-regulatory mutations in cancer. **2014**, 15, 485	19
1342	dCaP: detecting differential binding events in multiple conditions and proteins. **2014**, 15 Suppl 9, S12	3
1341	Genome-wide profiling of mouse RNA secondary structures reveals key features of the mammalian transcriptome. **2014**, 15, 491	87

1340	FunSeq2: a framework for prioritizing noncoding regulatory variants in cancer. **2014**, 15, 480	209
1339	Linking polymorphic p53 response elements with gene expression in airway epithelial cells of smokers and cancer risk. **2014**, 133, 1467-76	3
1338	A PTCH1 homolog transcriptionally activated by p53 suppresses Hedgehog signaling. **2014**, 289, 33020-31	22
1337	Systems biology approaches to enhance our understanding of drug hypersensitivity reactions. **2014** , 44, 1461-72	8
1336	Genetic variation in the GCG and in the GLP1R genes and antipsychotic-induced weight gain. **2014**, 15, 423-31	11
1335	Large differences in global transcriptional regulatory programs of normal and tumor colon cells. **2014**, 14, 708	25
1334	Alteration in basal and depolarization induced transcriptional network in iPSC derived neurons from Timothy syndrome. **2014**, 6, 75	63
1333	VAS: a convenient web portal for efficient integration of genomic features with millions of genetic variants. **2014**, 15, 886	1
1332	Comparative DNA methylome analysis of endometrial carcinoma reveals complex and distinct deregulation of cancer promoters and enhancers. **2014**, 15, 868	45
1331	Fundamental diversity of human CpG islands at multiple biological levels. **2014**, 9, 483-91	24
1330	Genomic and proteomic analysis of transcription factor TFII-I reveals insight into the response to cellular stress. **2014**, 42, 7625-41	14
1329	VEGF: a potential target for hydrocephalus. **2014**, 358, 667-83	6
1328	PI3K pathway activation in high-grade ductal carcinoma in situ--implications for progression to invasive breast carcinoma. **2014**, 20, 2326-37	37
1327	STAT1-induced ASPP2 transcription identifies a link between neuroinflammation, cell polarity, and tumor suppression. **2014**, 111, 9834-9	20
1326	Chromatin accessibility: a window into the genome. **2014**, 7, 33	221
1325	Transcriptome-wide signatures of tumor stage in kidney renal clear cell carcinoma: connecting copy number variation, methylation and transcription factor activity. **2014**, 6, 117	7
1324	An investigation of biomarkers derived from legacy microarray data for their utility in the RNA-seq era. **2014**, 15, 523	95
1323	Global loss of DNA methylation uncovers intronic enhancers in genes showing expression changes. **2014**, 15, 469	108

1322	Are common fragile sites merely structural domains or highly organized "functional" units susceptible to oncogenic stress?. **2014**, 71, 4519-44	43
1321	Differences in DNA methylation between human neuronal and glial cells are concentrated in enhancers and non-CpG sites. **2014**, 42, 109-27	131
1320	Tissue specific CTCF occupancy and boundary function at the human growth hormone locus. **2014**, 42, 4906-21	8
1319	Transcriptome-wide investigation of genomic imprinting in chicken. **2014**, 42, 3768-82	51
1318	Genome-based approaches for the diagnosis of breast cancer: a review with perspective. **2014**, 3, 173-193	
1317	Explicit DNase sequence bias modeling enables high-resolution transcription factor footprint detection. **2014**, 42, 11865-78	48
1316	Discovering functional DNA elements using population genomic information: a proof of concept using human mtDNA. **2014**, 6, 1542-8	2
1315	Splice variants of MDM2 in oncogenesis. **2014**, 85, 247-61	13
1314	FineSplice, enhanced splice junction detection and quantification: a novel pipeline based on the assessment of diverse RNA-Seq alignment solutions. **2014**, 42, e71	26
1313	Epigenetic modifications as novel therapeutic targets for Huntington's disease. **2014**, 6, 287-97	13
1312	Current status and new features of the Consensus Coding Sequence database. **2014**, 42, D865-72	122
1311	Effect of estrogen receptor □binding on functional DNA methylation in breast cancer. **2014**, 9, 523-32	26
1310	Defining functional DNA elements in the human genome. **2014**, 111, 6131-8	490
1309	Tissue-specific RNA-Seq in human evoked inflammation identifies blood and adipose LincRNA signatures of cardiometabolic diseases. **2014**, 34, 902-12	60
1308	Fine mapping genetic determinants of the highly variably expressed MHC gene ZFP57. **2014**, 22, 568-71	12
1307	Human colorectal cancer-specific CCAT1-L lncRNA regulates long-range chromatin interactions at the MYC locus. **2014**, 24, 513-31	471
1306	De-repressing LncRNA-Targeted Genes to Upregulate Gene Expression: Focus on Small Molecule Therapeutics. **2014**, 3, e196	47
1305	THEISTIC EVOLUTION IN THE POSTGENOMIC ERA. **2014**, 49, 829-854	

1304	miRNA-based therapies: strategies and delivery platforms for oligonucleotide and non-oligonucleotide agents. **2014**, 6, 1967-84	159
1303	Evolution of wild emmer wheat and crop improvement. **2014**, 52, 673-696	29
1302	. **2014**, 2, 1396-1408	12
1301	A functional synonymous coding variant in the IL1RN gene is associated with survival in septic shock. **2014**, 190, 656-64	28
1300	Stem Cell Transcriptional Networks. **2014**,	3
1299	Analyzing the global chromatin structure of keratinocytes by MNase-seq. **2014**, 1195, 49-59	10
1298	How can genetics and epigenetics help the nephrologist improve the diagnosis and treatment of chronic kidney disease patients?. **2014**, 29, 972-80	12
1297	Functions of noncoding sequences in mammalian genomes. **2014**, 79, 1442-69	37
1296	Methodologies in the Era of Cardiovascular □mics□**2014**, 15-55	
1295	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. **2014**, 33, 1212-26	46
1294	Little boxes. **2014**, 46, 659	4
1293	Regulation of the dynamic chromatin architecture of the epidermal differentiation complex is mediated by a c-Jun/AP-1-modulated enhancer. **2014**, 134, 2371-2380	23
1292	Open chromatin in plant genomes. **2014**, 143, 18-27	15
1291	Pharmacogenomics in Drug Discovery and Development. **2014**,	1
1290	The distribution of word matches between Markovian sequences with periodic boundary conditions. **2014**, 21, 41-63	4
1289	SNAI2 controls the undifferentiated state of human epidermal progenitor cells. **2014**, 32, 3209-18	47
1288	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. **2014**, 9, 1382-96	222
1287	The lncRNA-MYC regulatory network in cancer. **2014**, 35, 9497-503	33

1286	Comprehensive functional annotation of 77 prostate cancer risk loci. **2014**, 10, e1004102	132
1285	The association of the vanin-1 N131S variant with blood pressure is mediated by endoplasmic reticulum-associated degradation and loss of function. **2014**, 10, e1004641	14
1284	Systematic dissection of coding exons at single nucleotide resolution supports an additional role in cell-specific transcriptional regulation. **2014**, 10, e1004592	26
1283	Pleiotropy constrains the evolution of protein but not regulatory sequences in a transcription regulatory network influencing complex social behaviors. **2014**, 5, 431	26
1282	ECplot: an online tool for making standardized plots from large datasets for bioinformatics publications. **2014**, 30, 1467-8	
1281	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. **2014**, 23, 6607-15	11
1280	Emergence and evolutionary analysis of the human DDR network: implications in comparative genomics and downstream analyses. **2014**, 31, 940-61	15
1279	Mind the gap: why many geneticists and psychological scientists have discrepant views about gene-environment interaction (GE) research. **2014**, 69, 249-68	101
1278	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). **2014**, 2014, bau022	52
1277	iRegulon: from a gene list to a gene regulatory network using large motif and track collections. **2014**, 10, e1003731	463
1276	Intrapopulation genome size variation in D. melanogaster reflects life history variation and plasticity. **2014**, 10, e1004522	47
1275	Transcriptome sequencing from diverse human populations reveals differentiated regulatory architecture. **2014**, 10, e1004549	35
1274	Histone methyltransferase MMSET/NSD2 alters EZH2 binding and reprograms the myeloma epigenome through global and focal changes in H3K36 and H3K27 methylation. **2014**, 10, e1004566	137
1273	Functional analysis of long noncoding RNAs in development and disease. **2014**, 825, 129-58	51
1272	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. **2014**, 5, 5068	160
1271	Estimating the activity of transcription factors by the effect on their target genes. **2014**, 30, i401-7	37
1270	WiggleTools: parallel processing of large collections of genome-wide datasets for visualization and statistical analysis. **2014**, 30, 1008-9	44
1269	Identification of a regulatory variant that binds FOXA1 and FOXA2 at the CDC123/CAMK1D type 2 diabetes GWAS locus. **2014**, 10, e1004633	62

1268	Identification of rare causal variants in sequence-based studies: methods and applications to VPS13B, a gene involved in Cohen syndrome and autism. **2014**, 10, e1004729	34
1267	Long noncoding RNAs in prostate cancer: mechanisms and applications. **2014**, 1, e963469	13
1266	8.2% of the Human genome is constrained: variation in rates of turnover across functional element classes in the human lineage. **2014**, 10, e1004525	124
1265	Global quantitative modeling of chromatin factor interactions. **2014**, 10, e1003525	26
1264	The Human Epigenome Project. **2014**,	
1263	Variation and constraints in species-specific promoter sequences. **2014**, 363, 357-66	1
1262	microRNA Profiling: An Overview of Current Technologies and Applications. **2014**, 64, 23-46	1
1261	Transcriptional network control of normal and leukaemic haematopoiesis. **2014**, 329, 255-64	25
1260	Looking for CDKN1C enhancers. **2014**, 22, 442-3	17
1259	Next-Generation Sequencing for the Diagnosis of Monogenic Diabetes and Discovery of Novel Aetiologies. **2014**, 71-86	2
1258	Noncoding RNAs and the control of hormonal signaling via nuclear receptor regulation. **2014**, 53, R61-70	9
1257	Minireview: mechanisms of growth hormone-mediated gene regulation. **2014**, 28, 1012-25	79
1256	Evolving Genomics of Pulmonary Fibrosis. **2014**, 379-402	1
1255	dbPSHP: a database of recent positive selection across human populations. **2014**, 42, D910-6	32
1254	Constrained transcription factor spacing is prevalent and important for transcriptional control of mouse blood cells. **2014**, 42, 13513-24	14
1253	Linking the genetic architecture of cytosine modifications with human complex traits. **2014**, 23, 5893-905	30
1252	Integrating functional data to prioritize causal variants in statistical fine-mapping studies. **2014**, 10, e1004722	305
1251	A symbiotic liaison between the genetic and epigenetic code. **2014**, 5, 113	20

1250	Targeted H3R26 deimination specifically facilitates estrogen receptor binding by modifying nucleosome structure. **2014**, 10, e1004613	31
1249	Quantitative genetics of CTCF binding reveal local sequence effects and different modes of X-chromosome association. **2014**, 10, e1004798	38
1248	Current status of long non-coding RNAs in human cancer with specific focus on colorectal cancer. **2014**, 15, 13993-4013	46
1247	Abnormal dosage of ultraconserved elements is highly disfavored in healthy cells but not cancer cells. **2014**, 10, e1004646	15
1246	A genetic variant in the region of MMP-9 is associated with serum levels and progression of joint damage in rheumatoid arthritis. **2014**, 73, 1163-9	41
1245	Chromatin loops as allosteric modulators of enhancer-promoter interactions. **2014**, 10, e1003867	82
1244	The case for junk DNA. **2014**, 10, e1004351	146
1243	Subtle changes in motif positioning cause tissue-specific effects on robustness of an enhancer's activity. **2014**, 10, e1004060	35
1242	Evolution and genetic architecture of chromatin accessibility and function in yeast. **2014**, 10, e1004427	13
1241	Universal count correction for high-throughput sequencing. **2014**, 10, e1003494	12
1240	Towards structural systems pharmacology to study complex diseases and personalized medicine. **2014**, 10, e1003554	47
1239	Histone modifications are associated with transcript isoform diversity in normal and cancer cells. **2014**, 10, e1003611	18
1238	The functional consequences of variation in transcription factor binding. **2014**, 10, e1004226	135
1237	Combinatorial interactions are required for the efficient recruitment of pho repressive complex (PhoRC) to polycomb response elements. **2014**, 10, e1004495	40
1236	Meta-analysis of genome-wide association studies in African Americans provides insights into the genetic architecture of type 2 diabetes. **2014**, 10, e1004517	151
1235	Hydroxymethylated cytosines are associated with elevated C to G transversion rates. **2014**, 10, e1004585	28
1234	Methylation QTLs are associated with coordinated changes in transcription factor binding, histone modifications, and gene expression levels. **2014**, 10, e1004663	187
1233	GPA: a statistical approach to prioritizing GWAS results by integrating pleiotropy and annotation. **2014**, 10, e1004787	137

1232	Association mapping across numerous traits reveals patterns of functional variation in maize. **2014**, 10, e1004845	133
1231	Genome-wide (over)view on the actions of vitamin D. **2014**, 5, 167	86
1230	Transcriptome interrogation of human myometrium identifies differentially expressed sense-antisense pairs of protein-coding and long non-coding RNA genes in spontaneous labor at term. **2014**, 27, 1397-408	21
1229	Type I Interferon Regulates the Expression of Long Non-Coding RNAs. **2014**, 5, 548	43
1228	MicroRNAs, genomic instability and cancer. **2014**, 15, 14475-91	40
1227	LANA binds to multiple active viral and cellular promoters and associates with the H3K4methyltransferase hSET1 complex. **2014**, 10, e1004240	50
1226	Epigenetics: Introduction, Caveats, and Historic Overview. **2014**,	
1225	Identification of TNF-□responsive promoters and enhancers in the intestinal epithelial cell model Caco-2. **2014**, 21, 569-83	11
1224	Proteomic approaches and identification of novel therapeutic targets for alcoholism. **2014**, 39, 104-30	28
1223	Rare variant testing of imputed data: an analysis pipeline typified. **2014**, 78, 164-78	2
1222	Small-molecule control of cytokine function: new opportunities for treating immune disorders. **2014**, 23, 23-30	16
1221	Ancient origins of vertebrate-specific innate antiviral immunity. **2014**, 31, 140-53	39
1220	CCAT: Combinatorial Code Analysis Tool for transcriptional regulation. **2014**, 42, 2833-47	16
1219	SPIB and BATF provide alternate determinants of IRF4 occupancy in diffuse large B-cell lymphoma linked to disease heterogeneity. **2014**, 42, 7591-610	23
1218	Long non-coding RNA-dependent transcriptional regulation in neuronal development and disease. **2014**, 5, 164	120
1217	Insights into ?-Cell Biology and Type 2 Diabetes Pathogenesis from Studies of the Islet Transcriptome. **2014**, 111-121	
1216	Epigenetic mechanisms in Alzheimer's disease. **2014**, 4, 85-102	7
1215	Nuclear and mitochondrial tRNA-lookalikes in the human genome. **2014**, 5, 344	28

1214	Noncoding RNAs and cancer. **2014**, 38, 817-828	5
1213	Molecular mechanisms underlying the role of microRNAs in the chemoresistance of pancreatic cancer. **2014**, 2014, 678401	35
1212	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. **2014**, 1, 140021	21
1211	and mRNA expression in 17Ëstradiol-treated MCF7 cells. **2014**, 2, 101-104	2
1210	Integrating diverse datasets improves developmental enhancer prediction. **2014**, 10, e1003677	115
1209	Approximation to the distribution of fitness effects across functional categories in human segregating polymorphisms. **2014**, 10, e1004697	41
1208	Bionimbus: a cloud for managing, analyzing and sharing large genomics datasets. **2014**, 21, 969-75	56
1207	. **2014**,	
1206	Realistic artificial DNA sequences as negative controls for computational genomics. **2014**, 42, e99	17
1205	The roles of Jumonji-type oxygenases in human disease. **2014**, 6, 89-120	122
1204	Emerging role of MicroRNAs and long noncoding RNAs in respiratory disease. **2014**, 146, 193-204	112
1203	The Hippo signal transduction network in skeletal and cardiac muscle. **2014**, 7, re4	58
1202	Future clinical implications emerging from recent genome-wide expression studies in asthma. **2014**, 10, 985-1004	9
1201	Robust validation of methylation levels association at CPT1A locus with lipid plasma levels. **2014**, 55, 1189-91	25
1200	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. **2014**, 24, 177-84	99
1199	A workflow for the computational identification of candidate regulatory elements in noncoding DNA. **2014**,	1
1198	A novel MMP12 locus is associated with large artery atherosclerotic stroke using a genome-wide age-at-onset informed approach. **2014**, 10, e1004469	63
1197	On the threshold from genome-wide association studies to whole-genome sequencing. Looking for signal in all the right places. **2014**, 189, 381-3	1

1196	SHEAR: sample heterogeneity estimation and assembly by reference. **2014**, 15, 84	6
1195	Divergent functions of hematopoietic transcription factors in lineage priming and differentiation during erythro-megakaryopoiesis. **2014**, 24, 1932-44	67
1194	Alignathon: a competitive assessment of whole-genome alignment methods. **2014**, 24, 2077-89	74
1193	Regulation of gene expression by 1,25-dihydroxyvitamin D3 in bone cells: exploiting new approaches and defining new mechanisms. **2014**, 3, 482	54
1192	Bench-top sequencing and clinical implementation: diagnostics and biomarkers challenges. **2014**, 8, 221-4	
1191	From linear 'dogma' and trastuzumab-emtansine to future transcriptional circuitry-based drug discovery for breast cancer. **2014**, 10, 145-8	1
1190	GATA-dependent regulatory switches establish atrioventricular canal specificity during heart development. **2014**, 5, 3680	68
1189	Investigating genomic structure using changept: A Bayesian segmentation model. **2014**, 10, 107-15	9
1188	Beyond GWAS in COPD: probing the landscape between gene-set associations, genome-wide associations and protein-protein interaction networks. **2014**, 78, 131-9	15
1187	Genome-Wide Association Studies in Type 2 Diabetes. **2014**, 1-13	
1186	Large-scale identification of coregulated enhancer networks in the adult human brain. **2014**, 9, 767-79	64
1185	Two novel type 2 diabetes loci revealed through integration of TCF7L2 DNA occupancy and SNP association data. **2014**, 2, e000052	12
1184	Transcription factor binding predicts histone modifications in human cell lines. **2014**, 111, 13367-72	74
1183	Reduced expression of TLR3, TLR10 and TREM1 by human macrophages in Chronic cavitary pulmonary aspergillosis, and novel associations of VEGFA, DENND1B and PLAT. **2014**, 20, O960-8	28
1182	A Sox2 distal enhancer cluster regulates embryonic stem cell differentiation potential. **2014**, 28, 2699-711	104
1181	Nuclear receptors and chromatin: an inducible couple. **2014**, 52, R137-49	32
1180	The 253-kb inversion and deep intronic mutations in UNC13D are present in North American patients with familial hemophagocytic lymphohistiocytosis 3. **2014**, 61, 1034-40	24
1179	Genome-wide association identifies regulatory Loci associated with distinct local histogram emphysema patterns. **2014**, 190, 399-409	62

1178	Take your PICS: moving from GWAS to immune function. **2014**, 41, 883-5	5
1177	Epigenomics Understanding the Epigenetic Landscape of Cells. **2014**,	
1176	Genome-wide analysis of the human p53 transcriptional network unveils a lncRNA tumour suppressor signature. **2014**, 5, 5812	137
1175	Genome-wide interrogation of longitudinal FEV1 in children with asthma. **2014**, 190, 619-27	14
1174	A prominent role for the IL1 pathway and IL15 in susceptibility to chronic cavitary pulmonary aspergillosis. **2014**, 20, O480-8	26
1173	Modeling transcriptional networks regulating secondary growth and wood formation in forest trees. **2014**, 151, 156-63	13
1172	Transcriptional and epigenetic regulation of T-helper lineage specification. **2014**, 261, 62-83	76
1171	Physics, emergence, and the connectome. **2014**, 83, 1253-5	5
1170	DNA G-quadruplex and its potential as anticancer drug target. **2014**, 57, 1605-1614	41
1169	The impact of large-scale genomic methods in orthopaedic disorders: insights from genome-wide association studies. **2014**, 96, e38	3
1168	Translating human genetics into mouse: the impact of ultra-rapid in vivo genome editing. **2014**, 56, 34-45	28
1167	Metadata Standard and Data Exchange Specifications to Describe, Model, and Integrate Complex and Diverse High-Throughput Screening Data from the Library of Integrated Network-based Cellular Signatures (LINCS). **2014**, 19, 803-16	62
1166	RDoC: a roadmap to pathogenesis?. **2014**, 13, 43-4	10
1165	Discovering enhancers directly by activity. **2014**, 11, 491-2	1
1164	Mapping of long-range INS promoter interactions reveals a role for calcium-activated chloride channel ANO1 in insulin secretion. **2014**, 111, 16760-5	24
1163	Methodology for the analysis of rare genetic variation in genome-wide association and re-sequencing studies of complex human traits. **2014**, 13, 362-70	15
1162	A statistical model of ChIA-PET data for accurate detection of chromatin 3D interactions. **2014**, 42, e143	38
1161	Nonsyndromic cleft lip with or without cleft palate: Increased burden of rare variants within Gremlin-1, a component of the bone morphogenetic protein 4 pathway. **2014**, 100, 493-8	16

1160	The journey from RDC/DSM diagnoses toward RDoC dimensions. **2014**, 13, 44-6	19
1159	Global and disease-associated genetic variation in the human Fanconi anemia gene family. **2014**, 23, 6815-25	9
1158	Non-referenced genome assembly from epigenomic short-read data. **2014**, 9, 1329-38	3
1157	LncRNA-regulated infection and inflammation pathways associated with pregnancy loss: genome wide differential expression of lncRNAs in early spontaneous abortion. **2014**, 72, 359-75	42
1156	Single nucleotide variations: biological impact and theoretical interpretation. **2014**, 23, 1650-66	64
1155	Revisiting the identification of canonical splice isoforms through integration of functional genomics and proteomics evidence. **2014**, 14, 2709-18	28
1154	Conserved higher-order chromatin regulates NMDA receptor gene expression and cognition. **2014**, 84, 997-1008	60
1153	A rare functional noncoding variant at the GWAS-implicated MIR137/MIR2682 locus might confer risk to schizophrenia and bipolar disorder. **2014**, 95, 744-53	72
1152	DNA Microarrays Technology: Overview and Current Status. **2014**, 63, 1-23	4
1151	Understanding genetic variation - the value of systems biology. **2014**, 77, 597-605	46
1150	Heritable variation of mRNA decay rates in yeast. **2014**, 24, 2000-10	6
1149	Traceless semisynthesis of a set of histone 3 species bearing specific lysine methylation marks. **2014**, 15, 2071-5	16
1148	Chromatin remodeling mediated by the FOXA1/A2 transcription factors activates CFTR expression in intestinal epithelial cells. **2014**, 9, 557-65	38
1147	Common distal elements orchestrate CIITA isoform-specific expression in multiple cell types. **2014**, 15, 543-55	12
1146	Rare single nucleotide polymorphisms in the regulatory regions of the superoxide dismutase genes in autism spectrum disorder. **2014**, 7, 138-44	19
1145	Genomics and Proteomics for Clinical Discovery and Development. **2014**,	2
1144	The holist tradition in twentieth century genetics. Wilhelm Johannsen's genotype concept. **2014**, 592, 2431-8	10
1143	Pathway analysis approaches for rare and common variants: insights from Genetic Analysis Workshop 18. **2014**, 38 Suppl 1, S86-91	10

1142	The role of the interactome in the maintenance of deleterious variability in human populations. **2014**, 10, 752	25
1141	Translating the ENCyclopedia Of DNA Elements Project findings to the clinic: ENCODE's implications for eye disease. **2014**, 42, 78-83	14
1140	Post-translational Modifications in the Human Proteome. **2014**, 101-136	2
1139	The worm has turned: unexpected similarities between the transcription of enhancers and promoters in the worm and mammalian genomes. **2014**, 36, 157-62	
1138	The Influences of Genetic and Environmental Factors on Methylome-wide Association Studies for Human Diseases. **2014**, 2, 261-270	16
1137	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. **2014**, 5, 4613	62
1136	Distinct patterns of genetic variations in potential functional elements in long noncoding RNAs. **2014**, 35, 192-201	12
1135	Brain-specific noncoding RNAs are likely to originate in repeats and may play a role in up-regulating genes in cis. **2014**, 54, 331-7	15
1134	On the Nature and Evolutionary Impact of Phenotypic Robustness Mechanisms. **2014**, 45, 496-517	58
1133	Human diseases caused by germline and somatic abnormalities in microRNA and microRNA-related genes. **2014**, 54, 12-21	25
1132	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. **2014**, 23, 3054-68	78
1131	Obstacles and opportunities for the future of genomic medicine. **2014**, 2, 205-9	10
1130	Genome-Wide Association Studies of Obesity. **2014**, 33-53	2
1129	A genetic variant in microRNA-122 regulatory region confers risk for chronic hepatitis B virus infection and hepatocellular carcinoma in Han Chinese. **2014**, 86, 1669-74	11
1128	Summary of results and discussions from the gene-based tests group at Genetic Analysis Workshop 18. **2014**, 38 Suppl 1, S44-8	6
1127	Epigenetic and Developmental Basis of Risk of Obesity and Metabolic Disease. **2014**, 111-132	2
1126	A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping. **2014**, 159, 1665-80	3824
1125	DNA methylation dynamics of a maternally methylated DMR in the mouse Dlk1-Dio3 domain. **2014**, 588, 4665-71	6

1124	The PHD finger of p300 influences its ability to acetylate histone and non-histone targets. **2014**, 426, 3960-3972	19
1123	A genome-wide association study identifies a LEPR gene as a novel predisposing factor for childhood fasting plasma glucose. **2014**, 104, 594-8	2
1122	Comparative genomics reveals insights into avian genome evolution and adaptation. **2014**, 346, 1311-20	628
1121	Core and region-enriched networks of behaviorally regulated genes and the singing genome. **2014**, 346, 1256780	81
1120	Generalised empirical Bayesian methods for discovery of differential data in high-throughput biology. **2014**,	1
1119	A novel reannotation strategy for dissecting DNA methylation patterns of human long intergenic non-coding RNAs in cancers. **2014**, 42, 8258-70	34
1118	A bioinformatic and computational study of myosin phosphatase subunit diversity. **2014**, 307, R256-70	16
1117	The evolution of comparative genomics. **2014**, 2, 363-8	1
1116	HBx induces hypomethylation of distal intragenic CpG islands required for active expression of developmental regulators. **2014**, 111, 9555-60	44
1115	From the era of genome analysis to the era of genomic drug discovery: a pioneering example of rheumatoid arthritis. **2014**, 86, 432-40	12
1114	Identification of species-specific novel transcripts in pig reproductive tissues using RNA-seq. **2014**, 45, 198-204	19
1113	A general efficient and flexible approach for genome-wide association analyses of imputed genotypes in family-based designs. **2014**, 38, 560-71	22
1112	Genomics of cardiac electrical function. **2014**, 13, 39-50	1
1111	Molecular network analysis enhances understanding of the biology of mental disorders. **2014**, 36, 606-16	13
1110	Epidermal Cells. **2014**,	
1109	Comparison of the transcriptional landscapes between human and mouse tissues. **2014**, 111, 17224-9	239
1108	Genome dynamics of the human embryonic kidney 293 lineage in response to cell biology manipulations. **2014**, 5, 4767	275
1107	Research Highlights. **2014**, 32, 753-753	

1106	The future of neuroepigenetics in the human brain. **2014**, 128, 199-228	10
1105	Genetic architecture of cognitive traits. **2014**, 55, 255-62	12
1104	Effects of negative stressors on DNA methylation in the brain: implications for mood and anxiety disorders. **2014**, 165B, 541-54	24
1103	Regulatory network decoded from epigenomes of surface ectoderm-derived cell types. **2014**, 5, 5442	22
1102	In search of rare variants: preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. **2014**, 51, 1309-20	24
1101	Genome network medicine: innovation to overcome huge challenges in cancer therapy. **2014**, 6, 201-8	6
1100	Environmentally Induced Epigenetic Modifications and Transgenerational Effects. **2014**, 166-193	
1099	Can genome engineering be used to target cancer-associated enhancers?. **2014**, 6, 493-501	7
1098	MicroRNAs in diabetes - are they perpetrators in disguise or just epiphenomena?. **2014**, 1,	
1097	Cfp1 is required for gene expression-dependent H3K4 trimethylation and H3K9 acetylation in embryonic stem cells. **2014**, 15, 451	47
1096	Potential non-B DNA regions in the human genome are associated with higher rates of nucleotide mutation and expression variation. **2014**, 42, 12367-79	28
1095	Chronic cocaine-regulated epigenomic changes in mouse nucleus accumbens. **2014**, 15, R65	108
1094	FISH Oracle 2: a web server for integrative visualization of genomic data in cancer research. **2014**, 4, 5	5
1093	Choice of transcripts and software has a large effect on variant annotation. **2014**, 6, 26	125
1092	Impact of sequencing depth in ChIP-seq experiments. **2014**, 42, e74	49
1091	DNA copy number analysis of fresh and formalin-fixed specimens by shallow whole-genome sequencing with identification and exclusion of problematic regions in the genome assembly. **2014**, 24, 2022-32	210
1090	Variation in genes involved in epigenetic processes offers insights into tropically adapted cattle diversity. **2014**, 5, 89	1
1089	Introduction to Genomics and Proteomics for Clinical Discovery and Development. **2014**, 1-6	

1088 High resolution mapping of modified DNA nucleobases using excision repair enzymes. **2014**, 24, 1534-42 65

1087 MicroRNAs in Alcohol Abuse and Toxicity. **2014**, 497-521 1

1086 Ligand-dependent corepressor contributes to transcriptional repression by C2H2 zinc-finger transcription factor ZBRK1 through association with KRAB-associated protein-1. **2014**, 42, 7012-27 14

1085 Analysis of chromatin-state plasticity identifies cell-type-specific regulators of H3K27me3 patterns. **2014**, 111, E344-53 56

1084 The ETS family member GABP modulates androgen receptor signalling and mediates an aggressive phenotype in prostate cancer. **2014**, 42, 6256-69 26

1083 Transcription factor regulation and chromosome dynamics during pseudohyphal growth. **2014**, 25, 2669-76 9

1082 CGAT: computational genomics analysis toolkit. **2014**, 30, 1290-1 44

1081 Long non-coding RNA INXS is a critical mediator of BCL-XS induced apoptosis. **2014**, 42, 8343-55 49

1080 Databases for lncRNAs: a comparative evaluation of emerging tools. **2014**, 20, 1655-65 72

1079 Drake's rule as a consequence of approaching channel capacity. **2014**, 101, 939-54 2

1078 Hypothesis Generation from Heterogeneous Datasets. **2014**, 81-98

1077 Proteomics, genomics and transcriptomics: their emerging roles in the discovery and validation of colorectal cancer biomarkers. **2014**, 11, 179-205 21

1076 Copy number polymorphisms near SLC2A9 are associated with serum uric acid concentrations. **2014** , 15, 81 14

1075 RNA-Seq gene expression profiling of HepG2 cells: the influence of experimental factors and comparison with liver tissue. **2014**, 15, 1108 28

1074 Systematic exploration of autonomous modules in noisy microRNA-target networks for testing the generality of the ceRNA hypothesis. **2014**, 15, 1178 9

1073 Differential motif enrichment analysis of paired ChIP-seq experiments. **2014**, 15, 752 17

1072 A low-density SNP array for analyzing differential selection in freshwater and marine populations of threespine stickleback (Gasterosteus aculeatus). **2014**, 15, 867 15

1071 Retinal transcriptome profiling at transcription start sites: a cap analysis of gene expression early after axonal injury. **2014**, 15, 982 13

1070	Epigenetics in rheumatic diseases. **2014**, 12,	1
1069	A comparison of RNA-seq and exon arrays for whole genome transcription profiling of the L5 spinal nerve transection model of neuropathic pain in the rat. **2014**, 10, 7	68
1068	Meta-analysis of human methylomes reveals stably methylated sequences surrounding CpG islands associated with high gene expression. **2014**, 7, 28	60
1067	High-resolution genome-wide DNA methylation maps of mouse primary female dermal fibroblasts and keratinocytes. **2014**, 7, 35	10
1066	Predicting expression: the complementary power of histone modification and transcription factor binding data. **2014**, 7, 36	31
1065	ExpaRNA-P: simultaneous exact pattern matching and folding of RNAs. **2014**, 15, 404	11
1064	A framework for modelling gene regulation which accommodates non-equilibrium mechanisms. **2014**, 12, 102	39
1063	Deletions of chromosomal regulatory boundaries are associated with congenital disease. **2014**, 15, 423	108
1062	MUSIC: identification of enriched regions in ChIP-Seq experiments using a mappability-corrected multiscale signal processing framework. **2014**, 15, 474	46
1061	Sequence specificity incompletely defines the genome-wide occupancy of Myc. **2014**, 15, 482	43
1060	SuRFing the genomics wave: an R package for prioritising SNPs by functionality. **2014**, 6, 79	13
1059	Computational approaches to interpreting genomic sequence variation. **2014**, 6, 87	28
1058	Creating and validating cis-regulatory maps of tissue-specific gene expression regulation. **2014**, 42, 11000-10	12
1057	Role of STAT5 and epigenetics in lactation-associated upregulation of multidrug transporter ABCG2 in the mammary gland. **2014**, 307, E596-610	7
1056	Conceptual and empirical challenges of ascribing functions to transposable elements. **2014**, 184, 14-24	23
1055	The long non-coding RNA Paupar regulates the expression of both local and distal genes. **2014**, 33, 296-311	154
1054	The eGenVar data management system--cataloguing and sharing sensitive data and metadata for the life sciences. **2014**, 2014, bau027	7
1053	Biophysics of protein evolution and evolutionary protein biophysics. **2014**, 11, 20140419	144

1052	Profile of differential promoter activity by nucleotide substitution at GWAS signals for multiple sclerosis. **2014**, 93, e281	4
1051	Interrogation of allelic chromatin states in human cells by high-density ChIP-genotyping. **2014**, 9, 1238-51	6
1050	Epigenetic and genetic mechanisms in red cell biology. **2014**, 21, 155-64	5
1049	Epigenetic effects of electroconvulsive seizures. **2014**, 30, 152-9	17
1048	Genetics of juvenile idiopathic arthritis: new tools bring new approaches. **2014**, 26, 579-84	11
1047	Noncoding RNAs in vascular disease. **2014**, 29, 199-206	27
1046	ETS1 is a genome-wide effector of RAS/ERK signaling in epithelial cells. **2014**, 42, 11928-40	72
1045	BloodChIP: a database of comparative genome-wide transcription factor binding profiles in human blood cells. **2014**, 42, D172-7	34
1044	Analysis of an artificial zinc finger epigenetic modulator: widespread binding but limited regulation. **2014**, 42, 10856-68	50
1043	Aberrant transcriptional regulations in cancers: genome, transcriptome and epigenome analysis of lung adenocarcinoma cell lines. **2014**, 42, 13557-72	74
1042	The study of severe cutaneous drug hypersensitivity reactions from a systems biology perspective. **2014**, 14, 301-6	5
1041	Systems biology in inflammatory bowel diseases: ready for prime time. **2014**, 30, 339-46	31
1040	Architectural proteins CTCF and cohesin have distinct roles in modulating the higher order structure and expression of the CFTR locus. **2014**, 42, 9612-22	31
1039	Kinetochore genes are coordinately up-regulated in human tumors as part of a FoxM1-related cell division program. **2014**, 25, 1983-94	36
1038	Control of VEGF-A transcriptional programs by pausing and genomic compartmentalization. **2014**, 42, 12570-84	34
1037	Purifying selection on splice-related motifs, not expression level nor RNA folding, explains nearly all constraint on human lincRNAs. **2014**, 31, 3164-83	44
1036	The future for genetic studies in reproduction. **2014**, 20, 1-14	34
1035	Negative regulation of the interferon response by an interferon-induced long non-coding RNA. **2014**, 42, 10668-80	143

1034	Genomic and phenotypic characterization of a wild medaka population: towards the establishment of an isogenic population genetic resource in fish. **2014**, 4, 433-45	34
1033	Common variation near ROBO2 is associated with expressive vocabulary in infancy. **2014**, 5, 4831	54
1032	Evolutionary analysis identifies an MX2 haplotype associated with natural resistance to HIV-1 infection. **2014**, 31, 2402-14	18
1031	Small and Long Regulatory RNAs in the Immune System and Immune Diseases. **2014**, 5, 513	33
1030	Potential for genomic instability associated with retrotranspositionally-incompetent L1 loci. **2014**, 42, 10488-502	28
1029	Multiple novel promoter-architectures revealed by decoding the hidden heterogeneity within the genome. **2014**, 42, 12388-403	8
1028	Characterizing multi-omic data in systems biology. **2014**, 799, 15-38	21
1027	VAP: a versatile aggregate profiler for efficient genome-wide data representation and discovery. **2014**, 42, W485-93	25
1026	LASAGNA-Search 2.0: integrated transcription factor binding site search and visualization in a browser. **2014**, 30, 1923-5	42
1025	Modeling DNA methylation dynamics with approaches from phylogenetics. **2014**, 30, i408-14	14
1024	Transcriptional and Epigenetic Mechanisms Regulating Normal and Aberrant Blood Cell Development. **2014**,	1
1023	MicroRNAs and ethanol toxicity. **2014**, 115, 245-84	23
1022	Transcription factors bind negatively selected sites within human mtDNA genes. **2014**, 6, 2634-46	36
1021	Sequence variation in TMEM18 in association with body mass index: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. **2014**, 7, 344-9	5
1020	Natural variation in the histone demethylase, KDM4C, influences expression levels of specific genes including those that affect cell growth. **2014**, 24, 52-63	16
1019	Furore over genome function. *Nature*, **2014**, 512, 9-9	50.4
1018	Transcription restores DNA repair to heterochromatin, determining regional mutation rates in cancer genomes. **2014**, 9, 1228-34	77
1017	EGFR Inhibitors as Therapeutic Agents in Head and Neck Cancer. **2014**, 55-90	3

1016	In Situ Hybridization Protocols. **2014**,	0
1015	An improved predictive recognition model for Cys(2)-His(2) zinc finger proteins. **2014**, 42, 4800-12	53
1014	Regulation of LINE-1 in mammals. **2014**, 5, 409-28	14
1013	Meta-analysis of genome-wide association studies in multiethnic Asians identifies two loci for age-related nuclear cataract. **2014**, 23, 6119-28	28
1012	The Human Genome, Gene Regulation, and Genomic Variation. **2014**, 41-56	0
1011	Translational Bioinformatics. **2014**, 721-754	1
1010	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. **2014**, 42, 2856-69	19
1009	Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. **2014**, 42, 2976-87	302
1008	Whole Genome and Exome Sequencing of Type 2 Diabetes. **2014**, 29-41	
1007	Basic Genetics: The Cell, Mitosis and Meiosis, and Mendelian Laws. **2014**, 29-40	
1006	Mining for single nucleotide variants (SNVs) at the kallikrein locus with predicted functional consequences. **2014**, 395, 1037-50	3
1005	Nucleosome regulatory dynamics in response to TGF□**2014**, 42, 6921-34	6
1004	Vespucci: a system for building annotated databases of nascent transcripts. **2014**, 42, 2433-47	14
1003	Introduction to genetics and genomics in asthma: genetics of asthma. **2014**, 795, 125-55	23
1002	Genome-wide association and admixture analysis of glaucoma in the Women's Health Initiative. **2014**, 23, 6634-43	17
1001	JASPAR 2014: an extensively expanded and updated open-access database of transcription factor binding profiles. **2014**, 42, D142-7	795
1000	Impacts of pretranscriptional DNA methylation, transcriptional transcription factor, and posttranscriptional microRNA regulations on protein evolutionary rate. **2014**, 6, 1530-41	20
999	The interaction of MYC with the trithorax protein ASH2L promotes gene transcription by regulating H3K27 modification. **2014**, 42, 6901-20	32

998	Charting Brachyury-mediated developmental pathways during early mouse embryogenesis. **2014**, 111, 4478-83	53
997	Connecting the dots: potential of data integration to identify regulatory SNPs in late-onset Alzheimer's disease GWAS findings. **2014**, 9, e95152	36
996	Regulation of Cardiac Cell Fate by microRNAs: Implications for Heart Regeneration. **2014**, 3, 996-1026	23
995	A pan-cancer modular regulatory network analysis to identify common and cancer-specific network components. **2014**, 13, 69-84	14
994	Genome-wide and single-cell analyses reveal a context dependent relationship between CBP recruitment and gene expression. **2014**, 42, 11363-82	30
993	TF2LncRNA: identifying common transcription factors for a list of lncRNA genes from ChIP-Seq data. **2014**, 2014, 317642	35
992	Nucleosomal packaging of eukaryotic DNA and regulation of transcription. **2014**, 30, 413-425	1
991	Large-scale quality analysis of published ChIP-seq data. **2014**, 4, 209-23	90
990	Genome-wide analysis of histone modifications in human endometrial stromal cells. **2014**, 28, 1656-69	38
989	Discovery and validation of novel expression signature for postcystectomy recurrence in high-risk bladder cancer. **2014**, 106,	36
988	Opportunities-and hard work-ahead. **2015**, 107, 398	1
987	DNA methylation is associated with an increased level of conservation at nondegenerate nucleotides in mammals. **2014**, 31, 387-96	8
986	Parallel profiling of the transcriptome, cistrome, and epigenome in the cellular response to ionizing radiation. **2014**, 7, rs3	45
985	Creation of a federated database of blood proteins: a powerful new tool for finding and characterizing biomarkers in serum. **2014**, 11, 3	14
984	Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. **2014**, 15, R48	30
983	Insulator function and topological domain border strength scale with architectural protein occupancy. **2014**, 15, R82	195
982	Human-specific epigenetic variation in the immunological Leukotriene B4 Receptor (LTB4R/BLT1) implicated in common inflammatory diseases. **2014**, 6, 19	17
981	Localized, non-random differences in chromatin accessibility between homologous metaphase chromosomes. **2014**, 7, 70	7

980	Epigenetic modifications are associated with inter-species gene expression variation in primates. **2014**, 15, 547	49
979	Association of levels of fasting glucose and insulin with rare variants at the chromosome 11p11.2-MADD locus: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. **2014**, 7, 374-382	9
978	Updates to BioSamples database at European Bioinformatics Institute. **2014**, 42, D50-2	30
977	Gramene 2013: comparative plant genomics resources. **2014**, 42, D1193-9	143
976	COUGER--co-factors associated with uniquely-bound genomic regions. **2014**, 42, W461-7	
975	MYC and EGR1 synergize to trigger tumor cell death by controlling NOXA and BIM transcription upon treatment with the proteasome inhibitor bortezomib. **2014**, 42, 10433-47	43
974	Sequence-level mechanisms of human epigenome evolution. **2014**, 6, 1758-71	13
973	Haplotype-specific modulation of a SOX10/CREB response element at the Charcot-Marie-Tooth disease type 4C locus SH3TC2. **2014**, 23, 5171-87	20
972	The spring-loaded genome: nucleosome redistributions are widespread, transient, and DNA-directed. **2014**, 24, 251-9	24
971	A mobile insulator system to detect and disrupt cis-regulatory landscapes in vertebrates. **2014**, 24, 487-95	8
970	Intergenic polymorphisms in the amphiregulin gene region as biomarkers in metastatic colorectal cancer patients treated with anti-EGFR plus irinotecan. **2014**, 14, 256-62	12
969	Long non-coding RNAs: modulators of nuclear structure and function. **2014**, 26, 10-8	199
968	The fall and rise of pharmacology--(re-)defining the discipline?. **2014**, 87, 4-24	23
967	Navigating and mining modENCODE data. **2014**, 68, 38-47	14
966	The 5p12 breast cancer susceptibility locus affects MRPS30 expression in estrogen-receptor positive tumors. **2014**, 8, 273-84	21
965	Genome-wide profiling of long noncoding ribonucleic acid expression patterns in ovarian endometriosis by microarray. **2014**, 101, 1038-46.e7	41
964	Regulation of microRNAs and their role in liver development, regeneration and disease. **2014**, 54, 288-303	45
963	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. **2014**, 94, 349-60	131

962	Expression profiling of leukemia patients: key lessons and future directions. **2014**, 42, 651-60	33
961	Cloning and characterization of the promoter regions from the parent and paralogous creatine transporter genes. **2014**, 533, 488-93	9
960	Joint analysis of functional genomic data and genome-wide association studies of 18 human traits. **2014**, 94, 559-73	400
959	Systematic identification of regulatory elements in conserved 3' UTRs of human transcripts. **2014**, 7, 281-92	48
958	Calcium, channels, intracellular signaling and autoimmunity. **2014**, 10, 43-7	31
957	Transitioning from genotypes to epigenotypes: why the time has come for medulloblastoma epigenomics. **2014**, 264, 171-85	36
956	Identification of differentially expressed microRNAs across the developing human brain. **2014**, 19, 848-52	151
955	IB4-binding sensory neurons in the adult rat express a novel 3' UTR-extended isoform of CaMK4 that is associated with its localization to axons. **2014**, 522, 308-36	12
954	Epigenetic mechanisms of drug addiction. **2014**, 76 Pt B, 259-68	274
953	Genetics of disc-related disorders: current findings and lessons from other complex diseases. **2014**, 23 Suppl 3, S354-63	19
952	Early growth response-2 signaling mediates immunomodulatory effects of human multipotential stromal cells. **2014**, 23, 155-66	12
951	Integrative biological analysis for neuropsychopharmacology. **2014**, 39, 5-23	16
950	Circadian pathway genes in relation to glioma risk and outcome. **2014**, 25, 25-32	35
949	Reduced mRNA expression levels of MBD2 and MBD3 in gastric carcinogenesis. **2014**, 35, 3447-53	23
948	Advances in IBD genetics. **2014**, 11, 372-85	105
947	MutationTaster2: mutation prediction for the deep-sequencing age. **2014**, 11, 361-2	2455
946	Transcriptional enhancers: from properties to genome-wide predictions. **2014**, 15, 272-86	820
945	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. **2014**, 23, 2481-9	23

944	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. **2014**, 9, 989-1009		116
943	Cell isolation induces fate changes of bone marrow mesenchymal cells leading to loss or alternatively to acquisition of new differentiation potentials. **2014**, 32, 2008-20		11
942	Coffin-Siris syndrome: phenotypic evolution of a novel SMARCA4 mutation. **2014**, 164A, 1808-14		5
941	From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. **2014**, 24, 496-510		363
940	Long non-coding RNA GHET1 promotes gastric carcinoma cell proliferation by increasing c-Myc mRNA stability. **2014**, 281, 802-13		175
939	Comparative primate genomics: emerging patterns of genome content and dynamics. **2014**, 15, 347-59		180
938	A genetic program theory of aging using an RNA population model. **2014**, 13, 46-54		6
937	Single nucleotide polymorphisms in microRNA binding sites of oncogenes: implications in cancer and pharmacogenomics. **2014**, 18, 142-54		34
936	Interactive visualization and analysis of large-scale sequencing datasets using ZENBU. **2014**, 32, 217-9		124
935	The grammar of transcriptional regulation. **2014**, 133, 701-11		54
934	Molecular neuroanatomy: a generation of progress. **2014**, 37, 106-23		26
933	A rat RNA-Seq transcriptomic BodyMap across 11 organs and 4 developmental stages. **2014**, 5, 3230		225
932	Finding genomic function for genetic associations in nicotine addiction research: the ENCODE project's role in future pharmacogenomic analysis. **2014**, 123, 34-44		8
931	A promoter-level mammalian expression atlas. *Nature*, **2014**, 507, 462-70	50.4	1301
930	An HIV-encoded antisense long noncoding RNA epigenetically regulates viral transcription. **2014**, 22, 1164-1175		118
929	Computational approaches and resources in single amino acid substitutions analysis toward clinical research. **2014**, 94, 365-423		19
928	Laparoscopic resections and ENCODE-guided genomics to advance surgery and oncology. **2014**, 28, 2244-6		2
927	Prediction and classification of ncRNAs using structural information. **2014**, 15, 127		63

926	Genome-enabled prediction of quantitative traits in chickens using genomic annotation. **2014**, 15, 109		31
925	Protected amine labels: a versatile molecular scaffold for multiplexed nominal mass and sub-Da isotopologue quantitative proteomic reagents. **2014**, 25, 636-50		4
924	Disruption of long-range gene regulation in human genetic disease: a kaleidoscope of general principles, diverse mechanisms and unique phenotypic consequences. **2014**, 133, 815-45		25
923	Accumulation of CTCF-binding sites drives expression divergence between tandemly duplicated genes in humans. **2014**, 15 Suppl 1, S8		6
922	Computational prediction of transcription factor binding sites based on an integrative approach incorporating genomic and epigenomic features. **2014**, 36, 25-30		
921	Bidirectional promoters are the major source of gene activation-associated non-coding RNAs in mammals. **2014**, 15, 35		78
920	A genome-wide association study of prostate cancer in West African men. **2014**, 133, 509-21		56
919	Evaluation of genome-wide loci of iron metabolism in hereditary hemochromatosis identifies PCSK7 as a host risk factor of liver cirrhosis. **2014**, 23, 3883-90		36
918	Changing interpretation of chromosomal microarray over time in a community cohort with intellectual disability. **2014**, 164A, 377-85		34
917	Contributions from emerging transcriptomics technologies and computational strategies for drug discovery. **2014**, 32, 1316-9		5
916	An epigenetic mechanism of resistance to targeted therapy in T cell acute lymphoblastic leukemia. **2014**, 46, 364-70		263
915	An atlas of active enhancers across human cell types and tissues. *Nature*, **2014**, 507, 455-461	50.4	1595
914	CAGExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. **2014**, 30, 1183-1184		5
913	Single-molecule dynamics of enhanceosome assembly in embryonic stem cells. **2014**, 156, 1274-1285		390
912	Dissecting the causal genetic mechanisms of coronary heart disease. **2014**, 16, 406		10
911	CLOCK:BMAL1 is a pioneer-like transcription factor. **2014**, 28, 8-13		134
910	Transposable elements and psychiatric disorders. **2014**, 165B, 201-16		29
909	Evolution of transcription factor binding in metazoans - mechanisms and functional implications. **2014**, 15, 221-33		143

908	Regulation of gene expression programmes by serine-arginine rich splicing factors. **2014**, 32, 11-21	70
907	Laying a solid foundation for Manhattan--'setting the functional basis for the post-GWAS era'. **2014**, 30, 140-9	68
906	Looping back to leap forward: transcription enters a new era. **2014**, 157, 13-25	333
905	Locus-specific databases in cancer: what future in a post-genomic era? The TP53 LSDB paradigm. **2014**, 35, 643-53	14
904	Function-based identification of mammalian enhancers using site-specific integration. **2014**, 11, 566-71	59
903	Recessive mutations in a distal PTF1A enhancer cause isolated pancreatic agenesis. **2014**, 46, 61-64	187
902	Enhancer biology and enhanceropathies. **2014**, 21, 210-9	187
901	Genetics of male infertility. **2014**, 41, 1-17	42
900	X-linked sideroblastic anemia due to ALAS2 intron 1 enhancer element GATA-binding site mutations. **2014**, 89, 315-9	33
899	Common genetic variants modulate pathogen-sensing responses in human dendritic cells. **2014**, 343, 1246980	309
898	Elements and machinery of non-coding RNAs: toward their taxonomy. **2014**, 15, 489-507	63
897	Role of non-coding RNAs in pancreatic beta-cell development and physiology. **2014**, 211, 273-84	55
896	Long noncoding RNA in liver diseases. **2014**, 60, 744-53	144
895	Somatic mutations found in the healthy blood compartment of a 115-yr-old woman demonstrate oligoclonal hematopoiesis. **2014**, 24, 733-42	108
894	Epigenetics and depression: return of the repressed. **2014**, 155, 1-12	85
893	Pack, unpack, bend, twist, pull, push: the physical side of gene expression. **2014**, 25, 74-84	41
892	Innate immune activity conditions the effect of regulatory variants upon monocyte gene expression. **2014**, 343, 1246949	507
891	A novel RNA motif mediates the strict nuclear localization of a long noncoding RNA. **2014**, 34, 2318-29	106

890	Characterization of enhancers active in the mouse embryonic cerebral cortex suggests Sox/Pou cis-regulatory logics and heterogeneity of cortical progenitors. **2014**, 24, 2822-34		11
889	Natural selection and infectious disease in human populations. **2014**, 15, 379-93		255
888	The rise of regulatory RNA. **2014**, 15, 423-37		897
887	Long noncoding RNA in prostate, bladder, and kidney cancer. **2014**, 65, 1140-51		471
886	Genome-wide association study reveals two new risk loci for bipolar disorder. **2014**, 5, 3339		248
885	Epigenetics, plasticity, and evolution: How do we link epigenetic change to phenotype?. **2014**, 322, 208-20		142
884	Epigenetics: a new way to look at kidney diseases. **2014**, 29, 1821-7		42
883	Fish genomics: casting the net wide. **2014**, 13, 79-81		2
882	Erythro-megakaryocytic transcription factors associated with hereditary anemia. **2014**, 123, 3080-8		40
881	Integrating the roles of long and small non-coding RNA in brain function and disease. **2014**, 19, 410-6		110
880	The Significance of Transcriptome Sequencing in Personalized Cancer Medicine. **2014**, 49-64		1
879	The Role of MicroRNAs and Ultraconserved Non-Coding RNAs in Cancer. **2014**, 435-447		2
878	Comparative epigenomics in distantly related teleost species identifies conserved cis-regulatory nodes active during the vertebrate phylotypic period. **2014**, 24, 1075-85		38
877	ENCODE debate revived online. *Nature*, **2014**, 509, 137-137	50.4	0
876	Distinguishing between "function" and "effect" in genome biology. **2014**, 6, 1234-7		59
875	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. **2014**, 24, 708-17		66
874	Genome-wide analysis reveals characteristics of off-target sites bound by the Cas9 endonuclease. **2014**, 32, 677-83		553
873	Cis-regulatory variation: significance in biomedicine and evolution. **2014**, 356, 495-505		5

872	Functional interpretation of non-coding sequence variation: concepts and challenges. **2014**, 36, 191-9	38
871	Determining causality and consequence of expression quantitative trait loci. **2014**, 133, 727-35	34
870	Translational genomics. Targeting the host immune response to fight infection. **2014**, 344, 807-8	20
869	The emerging role of pseudogene expressed non-coding RNAs in cellular functions. **2014**, 54, 350-5	48
868	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. **2014**, 46, 533-42	175
867	Missing links in cardiology: long non-coding RNAs enter the arena. **2014**, 466, 1177-87	14
866	The tissue-specific transcriptomic landscape of the mid-gestational mouse embryo. **2014**, 141, 2325-30	27
865	No gene in the genome makes sense except in the light of evolution. **2014**, 15, 71-92	14
864	Genome-scale neurogenetics: methodology and meaning. **2014**, 17, 756-63	74
863	Incidentalomas in genomics and radiology. **2014**, 370, 988-90	20
862	RAID: a comprehensive resource for human RNA-associated (RNA-RNA/RNA-protein) interaction. **2014**, 20, 989-93	51
861	Parseq: reconstruction of microbial transcription landscape from RNA-Seq read counts using state-space models. **2014**, 30, 1409-16	8
860	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. **2014**, 46, 558-66	203
859	Comparative BAC-based physical mapping of Oryza sativa ssp. indica var. 93-11 and evaluation of the two rice reference sequence assemblies. **2014**, 77, 795-805	14
858	Multi-ethnic fine-mapping of 14 central adiposity loci. **2014**, 23, 4738-44	38
857	rSNPBase: a database for curated regulatory SNPs. **2014**, 42, D1033-9	89
856	Next-generation technologies and data analytical approaches for epigenomics. **2014**, 55, 155-70	48
855	Comparative population genomics: power and principles for the inference of functionality. **2014**, 30, 133-9	32

854	Extraordinarily low evolutionary rates of short wavelength-sensitive opsin pseudogenes. **2014**, 534, 93-9		4
853	IBD genetics: focus on (dys) regulation in immune cells and the epithelium. **2014**, 146, 896-9		8
852	A draft map of the human proteome. *Nature*, **2014**, 509, 575-81	50.4	1520
851	The role of de novo mutations in the genetics of autism spectrum disorders. **2014**, 15, 133-41		261
850	Supercomputing for the parallelization of whole genome analysis. **2014**, 30, 1508-13		41
849	DNA-binding specificities of plant transcription factors and their potential to define target genes. **2014**, 111, 2367-72		423
848	Motif-based analysis of large nucleotide data sets using MEME-ChIP. **2014**, 9, 1428-50		124
847	The birth and development of the DNA theory of inheritance: sixty years since the discovery of the structure of DNA. **2014**, 93, 293-302		21
846	Physics and financial economics (1776-2014): puzzles, Ising and agent-based models. **2014**, 77, 062001		140
845	Comparative epigenetic analyses reveal distinct patterns of oncogenic pathways activation in breast cancer subtypes. **2014**, 23, 5378-93		27
844	Guidelines for investigating causality of sequence variants in human disease. *Nature*, **2014**, 508, 469-76	50.4	910
843	The emerging role of epigenetics in rheumatic diseases. **2014**, 53, 406-14		10
842	Long noncoding RNAs: fresh perspectives into the RNA world. **2014**, 39, 35-43		271
841	New viruses for cancer therapy: meeting clinical needs. **2014**, 12, 23-34		187
840	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. **2014**, 35, 1012-9		121
839	Transposon mutagenesis identifies genes driving hepatocellular carcinoma in a chronic hepatitis B mouse model. **2014**, 46, 24-32		92
838	A large-scale screen for coding variants predisposing to psoriasis. **2014**, 46, 45-50		148
837	Inherited arrhythmia syndromes: exome sequencing opens a new door to diagnosis. **2014**, 63, 267-8		6

836	Genome sequencing and population genomics in non-model organisms. **2014**, 29, 51-63		420
835	Novel region discovery method for Infinium 450K DNA methylation data reveals changes associated with aging in muscle and neuronal pathways. **2014**, 13, 142-55		59
834	Pheochromocytoma and paraganglioma pathogenesis: learning from genetic heterogeneity. **2014**, 14, 108-19		354
833	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. **2014**, 156, 343-58		96
832	The evolution of lncRNA repertoires and expression patterns in tetrapods. *Nature*, **2014**, 505, 635-40	50.4	672
831	The genetics of cognitive epigenetics. **2014**, 80, 83-94		61
830	Applications of alignment-free methods in epigenomics. **2014**, 15, 419-30		30
829	Genetics of sudden cardiac death caused by ventricular arrhythmias. **2014**, 11, 96-111		52
828	Discovery of directional and nondirectional pioneer transcription factors by modeling DNase profile magnitude and shape. **2014**, 32, 171-178		314
827	Evolutionary transitions in individuality: insights from transposable elements. **2014**, 29, 90-6		31
826	Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. **2014**, 46, 205-12		331
825	Resurrecting surviving Neandertal lineages from modern human genomes. **2014**, 343, 1017-21		378
824	Systems biology for hepatologists. **2014**, 60, 736-43		9
823	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. **2014**, 46, 136-143		366
822	Application of a 5-tiered scheme for standardized classification of 2,360 unique mismatch repair gene variants in the InSiGHT locus-specific database. **2014**, 46, 107-115		332
821	Personalized medicine in neurodegenerative diseases: how far away?. **2014**, 18, 17-24		17
820	A genomic portrait of the genetic architecture and regulatory impact of microRNA expression in response to infection. **2014**, 24, 850-9		49
819	Relative specificity: all substrates are not created equal. **2014**, 12, 1-7		1

818	Functional annotation of noncoding sequence variants. **2014**, 11, 294-6		368
817	Genome recognition by MYC. **2014**, 4,		60
816	A general framework for estimating the relative pathogenicity of human genetic variants. **2014**, 46, 310-5		3626
815	TNF-□blockade induces IL-10 expression in human CD4+ T cells. **2014**, 5, 3199		74
814	Fundamentals of vitamin D hormone-regulated gene expression. **2014**, 144 Pt A, 5-11		86
813	Calcium, Channels, Intracellular Signaling and Autoimmunity. **2014**, 10, 43-47		3
812	Enhancer mutations and phenotype modularity. **2014**, 46, 3-4		19
811	Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification. **2014**, 11, 73-78		160
810	Translational paradigms in pharmacology and drug discovery. **2014**, 87, 189-210		31
809	Distal enhancers: new insights into heart development and disease. **2014**, 24, 294-302		32
808	Gene-centric meta-analyses for central adiposity traits in up to 57 412 individuals of European descent confirm known loci and reveal several novel associations. **2014**, 23, 2498-510		22
807	Functional and topological characteristics of mammalian regulatory domains. **2014**, 24, 390-400		279
806	Emerging roles of miR-210 and other non-coding RNAs in the hypoxic response. **2014**, 46, 220-32		60
805	A prostate cancer susceptibility allele at 6q22 increases RFX6 expression by modulating HOXB13 chromatin binding. **2014**, 46, 126-35		142
804	Idiopathic Pulmonary Fibrosis. **2014**,		1
803	The multilayered complexity of ceRNA crosstalk and competition. *Nature*, **2014**, 505, 344-52	50.4	2295
802	Big data in biomedicine. **2014**, 19, 433-40		195
801	Revisiting the thrifty gene hypothesis via 65 loci associated with susceptibility to type 2 diabetes. **2014**, 94, 176-85		59

800	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. **2014**, 46, 116-25	244
799	Regulation of the neuronal transcription factor NPAS4 by REST and microRNAs. **2014**, 1839, 13-24	22
798	Familial and Somatic Mutations of Histone-Modifying Enzymes in Cancer. **2014**, 65-85	
797	The Genetics of Obesity. **2014**,	
796	Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. **2014**, 24, 14-24	371
795	The ENCODE project and perspectives on pathways. **2014**, 38, 275-80	31
794	A systems biology analysis for the whole genome sequencing data. **2014**,	
793	Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. **2014**, 32, 1231-40	107
792	Sequencing the mouse Y chromosome reveals convergent gene acquisition and amplification on both sex chromosomes. **2014**, 159, 800-13	192
791	Early life adversity, genomic plasticity, and psychopathology. **2014**, 1, 461-6	95
790	Embryonic development following somatic cell nuclear transfer impeded by persisting histone methylation. **2014**, 159, 884-95	271
789	Identifying causal variants at loci with multiple signals of association. **2014**, 198, 497-508	266
788	Integrative transcriptome sequencing identifies trans-splicing events with important roles in human embryonic stem cell pluripotency. **2014**, 24, 25-36	74
787	Analytical tools and current challenges in the modern era of neuroepigenomics. **2014**, 17, 1476-90	75
786	Epigenetic control of Ccr7 expression in distinct lineages of lung dendritic cells. **2014**, 193, 4904-13	18
785	Systematic analysis of noncoding somatic mutations and gene expression alterations across 14 tumor types. **2014**, 46, 1258-63	215
784	Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. **2014**, 46, 1311-20	399
783	Complex genetics and the etiology of human congenital heart disease. **2014**, 4, a013953	93

782	p62/SQSTM1 upregulation constitutes a survival mechanism that occurs during granulocytic differentiation of acute myeloid leukemia cells. **2014**, 21, 1852-61		45
781	EWS-FLI1 utilizes divergent chromatin remodeling mechanisms to directly activate or repress enhancer elements in Ewing sarcoma. **2014**, 26, 668-681		223
780	When genetics meets epigenetics: deciphering the mechanisms controlling inter-individual variation in immune responses to infection. **2014**, 29, 119-26		6
779	A comprehensive resequence-analysis of 250 kb region of 8q24.21 in men of African ancestry. **2014**, 74, 579-89		12
778	Widespread genetic epistasis among cancer genes. **2014**, 5, 4828		45
777	Host genetic studies in adult pulmonary tuberculosis. **2014**, 26, 445-53		33
776	Enhancer alterations in cancer: a source for a cell identity crisis. **2014**, 6, 77		36
775	Spurious transcription factor binding: non-functional or genetically redundant?. **2014**, 36, 798-806		50
774	Role of Rare and Common Genetic Variation in SCN5A in Cardiac Electrical Function and Arrhythmia. **2014**, 6, 665-677		1
773	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. **2014**, 95, 535-52		411
772	Beyond single-nucleotide polymorphisms: genetics, genomics, and other 'omic approaches to acute respiratory distress syndrome. **2014**, 35, 673-84		12
771	The dilemma of choosing the ideal permutation strategy while estimating statistical significance of genome-wide enrichment. **2014**, 15, 919-28		16
770	SRF regulates craniofacial development through selective recruitment of MRTF cofactors by PDGF signaling. **2014**, 31, 332-344		32
769	Adenovirus small E1A employs the lysine acetylases p300/CBP and tumor suppressor Rb to repress select host genes and promote productive virus infection. **2014**, 16, 663-76		72
768	Genomics: mice in the ENCODE spotlight. *Nature*, **2014**, 515, 346-7	50.4	10
767	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
766	Macrophages: Biology and Role in the Pathology of Diseases. **2014**,		8
765	Mouse regulatory DNA landscapes reveal global principles of cis-regulatory evolution. **2014**, 346, 1007-12		184

764	Topologically associating domains are stable units of replication-timing regulation. *Nature*, **2014**, 515, 402-5	50.4	563
763	Methods for collapsing multiple rare variants in whole-genome sequence data. **2014**, 38 Suppl 1, S13-20		16
762	Repeat-associated non-AUG translation and its impact in neurodegenerative disease. **2014**, 11, 721-31		31
761	Regulatory variation: an emerging vantage point for cancer biology. **2014**, 6, 37-59		4
760	The chromatin landscape of the moss Physcomitrella patens and its dynamics during development and drought stress. **2014**, 79, 67-81		56
759	Allelic expression mapping across cellular lineages to establish impact of non-coding SNPs. **2014**, 10, 754		16
758	RNA sequencing identifies dysregulation of the human pancreatic islet transcriptome by the saturated fatty acid palmitate. **2014**, 63, 1978-93		174
757	The potential of a data centred approach & knowledge graph data representation in chemical safety and drug design. **2022**, 20, 4837-4849		0
756	Transcriptional and Epigenomic Regulation of Lymphocytes. **2022**,		0
755	Comprehensive Evaluation of BERT Model for DNA-Language for Prediction of DNA Sequence Binding Specificities in Fine-Tuning Phase. **2022**, 92-102		0
754	MAB21L4 Deficiency Drives Squamous Cell Carcinoma via Activation of RET. **2022**, 82, 3143-3157		0
753	FOXR2 Is an Epigenetically Regulated Pan-Cancer Oncogene That Activates ETS Transcriptional Circuits. **2022**, 82, 2980-3001		1
752	Measuring transcription factor binding and gene expression using barcoded self-reporting transposon calling cards and transcriptomes. **2022**, 4,		0
751	A Genome-Wide Association Study Reveals Two Genetic Markers for Chondromalacia. **2022**, 13, 194760352211217		2
750	Computational identification of signals predictive for nuclear RNA exosome degradation pathway targeting. **2022**, 4,		0
749	Circular RNAs: New Players in Cardiomyopathy. **2022**, 13, 1537		0
748	WhichTF is functionally important in your open chromatin data?. **2022**, 18, e1010378		0
747	Accumulation and maintenance of information in evolution. **2022**, 119,		1

746	Aberrant paracrine signalling for bone remodelling underlies the mutant histone-driven giant cell tumour of bone.	0
745	Interaction of Nanomaterials with Protein-Peptide. **2022**, 23, 548-562	0
744	Computational prediction and CRISPR-Cas12a knockout and rescue assays identify many functionally conserved lncRNAs from zebrafish to human.	0
743	Human Umbilical Cord Mesenchymal Stem Cell-Derived Conditioned Medium Promotes Human Endometrial Cell Proliferation through Wnt/Catenin Signaling. **2022**, 2022, 1-10	0
742	False-positive IRESes from Hoxa9 and other genes resulting from errors in mammalian 5? UTR annotations. **2022**, 119,	1
741	Polymorphisms in Cytokine Receptor and Regulator Genes are Associated with Levels of Exercise in Women Prior to Breast Cancer Surgery. 109980042211200	0
740	Enhancer RNAs step forward: new insights into enhancer function. **2022**, 149,	1
739	Parallel recovery of chromatin accessibility and gene expression dynamics from frozen human Regulatory T cells.	0
738	A bipartite function of ESRRB can integrate signaling over time to balance self-renewal and differentiation.	0
737	Gene essentiality and variability: What is the link? A within- and between-species perspective. 2200132	0
736	Updated review of advances in microRNAs and complex diseases: experimental results, databases, webservers and data fusion.	3
735	Temporal dynamics of the multi-omic response to endurance exercise training across tissues.	0
734	CRISPR/Cas9 and FLP-FRT mediated multi-modular engineering of the cis-regulatory landscape of the bithorax complex of Drosophila melanogaster.	0
733	Identification of NHLRC1 as a Novel AKT Activator from a Lung Cancer Epigenome-Wide Association Study (EWAS). **2022**, 23, 10699	0
732	Editorial: Coding and non-coding RNA-based complexes in organismal development and disease pathogenesis. 13,	0
731	Bioinformatics and systems biology approach to identify the pathogenetic link of Long COVID and Myalgic Encephalomyelitis/Chronic Fatigue Syndrome. 13,	0
730	PRC2-indepdendent actions of H3.3K27M in embryonic stem cell differentiation.	0
729	NUDT21 limits CD19 levels through alternative mRNA polyadenylation in B cell acute lymphoblastic leukemia.	1

728	Signatures 1 and 17 show increased propensity to create mutational hotspots in the human genome.	1
727	Where Nanosensors Meet Machine Learning: Prospects and Challenges in Detecting Disease X. **2022**, 16, 13279-13293	3
726	ONECUT2 restricts Microfold cell numbers in the small intestine; a multi-omics study.	0
725	Building integrative functional maps of gene regulation.	0
724	Regulation of CIRP by genetic factors of SP1 related to cold sensitivity. 13,	0
723	Multinomial Convolutions for Joint Modeling of Regulatory Motifs and Sequence Activity Readouts. **2022**, 13, 1614	0
722	Massively parallel genomic perturbations with multi-target CRISPR interrogates Cas9 activity and DNA repair at endogenous sites. **2022**, 24, 1433-1444	0
721	Emerging Roles of miRNA, lncRNA, circRNA, and Their Cross-Talk in Pituitary Adenoma. **2022**, 11, 2920	0
720	Two-layer design protects genes from mutations in their enhancers. **2022**, 609, 477-478	0
719	Identification of conserved skeletal enhancers associated with craniosynostosis risk genes.	0
718	Multiplexed functional genomic assays to decipher the noncoding genome.	0
717	Scalable Functional Assays for the Interpretation of Human Genetic Variation. **2022**, 56,	0
716	Plexins promote hedgehog signaling through their cytoplasmic GAP activity. 11,	0
715	Insights from multi-omics integration in complex disease primary tissues. **2022**,	0
714	Progenitor Hierarchy of Chronic Myelomonocytic Leukemia Identifies Inflammatory Monocytic-Biased Trajectory Linked to Worse Outcomes. OF1-OF18	1
713	Improving stem cell-derived pancreatic islets using single-cell multiome-inferred regulomes.	0
712	Peaksat: An R package for ChIP-seq peak saturation analysis.	0
711	Deciphering multi-way interactions in the human genome. **2022**, 13,	0

710	Major Contribution of Myeloid Cells In TB specific Host Gene Signature: Revelations from Re-Analysis of Publicly Available Datasets.	0
709	3D genome alterations in T cells associated with disease activity of systemic lupus erythematosus. annrheumdis-2022-2	0
708	Genome architecture plasticity underlies DNA replication timing dynamics in cell differentiation. 13,	0
707	Regulatory variants in a novel distal enhancer regulate the expression of CYP3A4 and CYP3A5.	0
706	Best practices for single-cell histone modification analysis.	0
705	Exploring the association of interleukin polymorphisms with aggression and internalizing behaviors in children and adolescents.	1
704	Increased lncRNA AFAP1-AS1 expression predicts poor prognosis in gastric cancer: Evidence from published studies and followed up verification.	0
703	Individual Genetic Heterogeneity. **2022**, 13, 1626	0
702	Genomic data integration and user-defined sample-set extraction for population variant analysis. **2022**, 23,	0
701	MYPT1-PP1δ phosphatase negatively regulates both chromatin landscape and co-activator recruitment for beige adipogenesis. **2022**, 13,	0
700	Effect of genomic and cellular environments on gene expression noise.	0
699	eccDB: a comprehensive repository for eccDNA-mediated chromatin contacts in multi-species.	0
698	Promotion or remission: a role of noncoding RNAs in colorectal cancer resistance to anti-EGFR therapy. **2022**, 20,	0
697	Differential expression of m5C RNA methyltransferase genes NSUN6 and NSUN7 in Alzheimer's disease and Traumatic Brain Injury.	0
696	Expression profile analysis of long noncoding RNA and messenger RNA during mouse cementoblast mineralization.	0
695	Noncoding RNAs as additional mediators of epigenetic regulation in nonalcoholic fatty liver disease. **2022**, 28, 5111-5128	1
694	NRF2 shortage in human skin fibroblasts dysregulates matrisome gene expression and affects collagen fibrillogenesis. **2022**,	0
693	Sensitive and reproducible cell-free methylome quantification with synthetic spike-in controls. **2022**, 2, 100294	0

692	Single-cell multi-omics of human clonal hematopoiesis reveals that DNMT3A R882 mutations perturb early progenitor states through selective hypomethylation. **2022**, 54, 1514-1526	1
691	Promoting validation and cross-phylogenetic integration in model organism research. **2022**, 15,	2
690	CTCF and cohesin promote focal detachment of DNA from the nuclear lamina. **2022**, 23,	1
689	Predicting 3D genome architecture directly from the nucleotide sequence with DNA-DDA.	0
688	Novel clinical, molecular and bioinformatics insights into the genetic background of autism. **2022**, 16,	0
687	G-quadruplexes Mark Sites of Methylation Instability Associated with Ageing and Cancer. **2022**, 13, 1665	1
686	Positional motif analysis reveals the extent of specificity of protein-RNA interactions observed by CLIP. **2022**, 23,	0
685	Multiple parameters shape the 3D chromatin structure of single nuclei at the doc locus in Drosophila. **2022**, 13,	1
684	Interpretation of the role of germline and somatic non-coding mutations in cancer: expression and chromatin conformation informed analysis. **2022**, 14,	0
683	Statistical learning quantifies transposable element-mediated cis-regulation.	0
682	The regulation and potential roles of m6A modifications in early embryonic development and immune tolerance at the maternal-fetal interface. 13,	0
681	A Novel Strategy for Identifying NSCLC MicroRNA Biomarkers and Their Mechanism Analysis Based on a Brand-New CeRNA-Hub-FFL Network. **2022**, 23, 11303	0
680	Transcriptional dynamics of transposable elements in the type I IFN response in Myotis lucifugus cells. **2022**, 13,	2
679	Spatial Transcriptomics Using Multiplexed Deterministic Barcoding in Tissue.	0
678	3D Chromatin Structure in Chondrocytes Identifies Putative Osteoarthritis Risk Genes.	0
677	Probing Nascent RNA with Metabolic Incorporation of Modified Nucleosides. **2022**, 55, 2647-2659	1
676	Identifying enhancer properties associated with genetic risk for complex traits using regulome-wide association studies. **2022**, 18, e1010430	0
675	POLD2 is activated by E2F1 to promote triple-negative breast cancer proliferation. 12,	1

674	Systematic Epigenome Editing Captures the Context-dependent Instructive Function of Chromatin Modifications.	0
673	Tumor purity adjusted beta values improve biological interpretability of high-dimensional DNA methylation data. **2022**, 17, e0265557	0
672	Assessment of small in-frame indels and C-terminal nonsense variants of BRCA1 using a validated functional assay. **2022**, 12,	1
671	Deleterious, protein-altering variants in the X-linked transcriptional coregulator ZMYM3 in 22 individuals with a neurodevelopmental delay phenotype.	0
670	Reversible epigenetic alterations regulate class I HLA loss in prostate cancer. **2022**, 5,	0
669	Learning probabilistic proteinDNA recognition codes from DNA-binding specificities using structural mappings. **2022**, 32, 1776-1786	0
668	Hedgehog signaling activates a mammalian heterochronic gene regulatory network controlling differentiation timing across lineages. **2022**, 57, 2181-2203.e9	0
667	Regulatory chromatin rewiring promotes metabolic switching during adaptation to oncogenic receptor tyrosine kinase inhibition.	1
666	A Genome Scale Transcriptional Regulatory Model of the Human Placenta.	0
665	Current sequence-based models capture gene expression determinants in promoters but mostly ignore distal enhancers.	0
664	Enhancer Reprogramming in Melanoma Immune Checkpoint Therapy Resistance.	0
663	How noncoding RNAs began to leave the junkyard.	0
662	Hypothesis-driven probabilistic modelling enables a principled perspective of genomic compartments.	0
661	Translatome and transcriptome co-profiling reveals a role of TPRXs in human zygotic genome activation. **2022**, 378,	2
660	Roles of super enhancers and enhancer RNAs in skeletal muscle development and disease. 1-11	1
659	Bibliometric analysis of artificial intelligence for biotechnology and applied microbiology: Exploring research hotspots and frontiers. 10,	1
658	A cis-regulatory lexicon of DNA motif combinations mediating cell-type-specific gene regulation. **2022**, 100191	0
657	Cell type deconvolution of methylated cell-free DNA at the resolution of individual reads.	0

656 Gene Therapy for Human Diseases: Recent Achievements and Near-Term Development Prospects. **2022**, 12, 363-369 0

655 Genetic evidence for the dopamine hypothesis of bipolar disorder 0

654 Epigenetic regulation of MIR145 core promoter controls miR-143/145 cluster in bladder cancer progression and treatment outcome. **2022**, 0

653 Associations of RPEL1 and miR-1307 gene polymorphisms with disease susceptibility, glucocorticoid efficacy, anxiety, depression, and health-related quality of life in Chinese systemic lupus erythematosus patients. 096120332211311 0

652 Nuclear position modulates long-range chromatin interactions. **2022**, 18, e1010451 0

651 Sex-dependent placental mQTL provide insight into the prenatal origins of childhood-onset traits and conditions. 0

650 A MYC-ZNF148-ID1/3 regulatory axis modulating cancer stem cell traits in aggressive breast cancer. **2022**, 11, 0

649 The role of long noncoding RNA (lncRNA) nuclear-enriched abundant transcript 1 (NEAT1) in immune diseases. **2022**, 75, 101716 0

648 Gene-Regulatory Networks in Brain Development. **2022**, 239-253 0

647 Long Non-coding RNAs, Lnc(ing) RNA Metabolism to Cancer Biology. **2022**, 175-199 0

646 Dynamic alternative polyadenylation during iPSC differentiation into cardiomyocytes. **2022**, 20, 5859-5869 0

645 MiRNA Gene Activity Interaction Networks (miGAIN): Integrated Joint Models of miRNA Gene Targeting and Disturbance in Signaling Pathways. **2022**, 3-21 0

644 A Comprehensive Approach for the Conceptual Modeling of Genomic Data. **2022**, 194-208 0

643 Non-coding antisense transcripts: fine regulation of gene expression in cancer. **2022**, 20, 5652-5660 0

642 Enhancer RNA (eRNA) in Human Diseases. **2022**, 23, 11582 0

641 New insights of liquid biopsy in ovarian cancer. **2022**, 5, 001-011 0

640 Polygenic architecture of a novel MRI endophenotype: the Hemochromatosis brain 0

639 Live slow-frozen human tumor tissues viable for 2D, 3D, ex vivo cultures and single-cell RNAseq. **2022**, 5, 0

638	Integrated multi-omics approach revealed cellular senescence landscape.	0
637	MIR retrotransposons link the epigenome and the transcriptome of coding genes in acute myeloid leukemia. **2022**, 13,	0
636	A comprehensive SARS-CoV-2–human protein–protein interactome reveals COVID-19 pathobiology and potential host therapeutic targets.	1
635	Identifying Genetic Regulatory Variants that Affect Transcription Factor Activity.	0
634	Enhancer and super-enhancer landscape in polycystic kidney disease. **2022**,	0
633	Differential Regulation of mTor signaling defines subtypes ofcblXsyndrome.	0
632	Targeted profiling of human extrachromosomal DNA by CRISPR-CATCH.	2
631	Molecular Characteristics and Promoter Analysis of Porcine COL1A1. **2022**, 13, 1971	0
630	EGFL7 drives the evolution of resistance to EGFR inhibitors in lung cancer by activating NOTCH signaling. **2022**, 13,	1
629	Structure-based screening for functional non-coding RNAs in fission yeast identifies a factor repressing untimely initiation of sexual differentiation.	0
628	Genetic variants associated with psychiatric disorders are enriched at epigenetically active sites in lymphoid cells. **2022**, 13,	0
627	Flnc: Machine Learning Improves the Identification of Novel Long Noncoding RNAs from Stand-Alone RNA-Seq Data. **2022**, 8, 70	0
626	3D genome organization links non-coding disease-associated variants to genes. 10,	0
625	Computational methods to explore chromatin state dynamics.	0
624	SARS-CoV-2 N protein potentiates host NPM1-snoRNA translation machinery to enhance viral replication. **2022**, 7,	0
623	JAK/BCL2 inhibition acts synergistically with LSD1 inhibitors to selectively target ETP-ALL.	0
622	COOBoostR: an extreme gradient boosting-based tool for robust tissue or cell-of-origin prediction of tumors.	0
621	HNRNPH1 regulates the neuroprotective cold-shock protein RBM3 expression through poison exon exclusion.	0

620	Testis-specific serine kinase 3 is required for sperm morphogenesis and male fertility.	0
619	MEPP: more transparent motif enrichment by profiling positional correlations. **2022**, 4,	0
618	A Pilot Study of Associations Between the Occurrence of Palpitations and Cytokine Gene Variations in Women Prior to Breast Cancer Surgery. 109980042211346	0
617	Multi-histone ChIP-Seq Analysis with DecoDen.	0
616	Pseudogenes limit the identification of novel common transcripts generated by their parent genes.	0
615	Single-cell transcriptome analyses reveal distinct gene expression signatures of severe COVID-19 in the presence of clonal hematopoiesis.	0
614	Discovering DNA Methylation, the History and Future of the Writing on DNA.	0
613	SMAD4 loss induces c-MYC-mediated NLE1 upregulation to support protein biosynthesis, colorectal cancer growth and metastasis.	0
612	Whole genome sequence analysis of blood lipid levels in >66,000 individuals. **2022**, 13,	1
611	The splicing switch of SLK controls tumor progression partiallyviadifferent associations with occludin.	0
610	ClampFISH 2.0 enables rapid, scalable amplified RNA detection in situ. **2022**, 19, 1403-1410	0
609	Current updates of CRISPR/Cas9-mediated genome editing and targeting within tumor cells: an innovative strategy of cancer management.	1
608	Genome-wide chromatin accessibility analysis unveils open chromatin convergent evolution during polyploidization in cotton. **2022**, 119,	1
607	Glycation-Associated Diabetic Nephropathy and the Role of Long Noncoding RNAs. **2022**, 10, 2623	0
606	Systematic discovery of recombinases for efficient integration of large DNA sequences into the human genome.	1
605	5-Hydroxymethylation alterations in cell-free DNA reflect molecular distinctions of diffuse large B cell lymphoma at different primary sites. **2022**, 14,	0
604	A multi-omic analysis of MCF10A cells provides a resource for integrative assessment of ligand-mediated molecular and phenotypic responses. **2022**, 5,	0
603	The dynseq browser track shows context-specific features at nucleotide resolution.	0

602	Modified nucleotides for chemical and enzymatic synthesis of therapeutic RNA. **2022**, 30,	1
601	The HUNT study: A population-based cohort for genetic research. **2022**, 2, 100193	0
600	Potential Misrepresentation of Inherited Breast Cancer Risk by Common Germline Alleles.	0
599	EUGENe: A Python toolkit for predictive analyses of regulatory sequences.	0
598	Mapping genetic variants for nonsense-mediated mRNA decay regulation across human tissues.	0
597	Multifactorial profiling of epigenetic landscapes at single-cell resolution using MulTI-Tag.	1
596	Discovery of 42 genome-wide significant loci associated with dyslexia.	2
595	A Novel apaQTL-SNP for the Modification of Non-Small-Cell Lung Cancer Susceptibility across Histological Subtypes. **2022**, 14, 5309	0
594	The association of ARRB1 polymorphisms with response to antidepressant treatment in depressed patients. 13,	0
593	The trans-regulatory landscape of gene networks in plants.	0
592	Transcription factor expression is the main determinant of variability in gene co-activity.	0
591	LncRNA Gm43843 Promotes Cardiac Hypertrophy via miR-153-3p/Cacna1c Axis. **2022**, 2022, 1-13	0
590	Epigenetics of neural differentiation: Spotlight on enhancers. 10,	0
589	Navigating the Multiverse of Antisense RNAs: The Transcription- and RNA-Dependent Dimension. **2022**, 8, 74	0
588	Development and validation of an AI/ML platform for the discovery of splice-switching oligonucleotide targets.	0
587	Lineage Landscape: a comprehensive database that records lineage commitment across species.	0
586	Suppression of the Testis-Specific Transcription of the <i>ZBTB32</i> and <i>ZNF473</i> Genes in Germ Cell Tumors. **2022**, 14, 85-94	0
585	Model-based characterization of the equilibrium dynamics of transcription initiation and promoter-proximal pausing in human cells.	0

584	Widespread chromatin context-dependencies of DNA double-strand break repair proteins.	0
583	Accurate Identification of DNA Replication Origin by Fusing Epigenomics and Chromatin Interaction Information. **2022**, 2022, 1-14	0
582	Ancestry-related differences in chromatin accessibility and gene expression ofAPOE4are associated with Alzheimer disease risk.	0
581	PlantCADB: A Comprehensive Plant Chromatin Accessibility Database. **2022**,	0
580	A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies.	1
579	Dynamic chromosomal interactions and control of heterochromatin positioning by Ki-67.	0
578	Local CpG density affects the trajectory and variance of age-associated DNA methylation changes. **2022**, 23,	0
577	Distinctive aspects of the placental epigenome and theories as to how they arise. **2022**, 79,	0
576	Relative importance of composition structures and biologically meaningful logics in bipartite Boolean models of gene regulation. **2022**, 12,	0
575	The co-evolution of the genome and epigenome in colorectal cancer.	3
574	The Role of Dynamic DNA Methylation in Liver Transplant Rejection in Children. **2022**, 8, e1394	0
573	Examining the role of EGR1 during viral infections. 13,	0
572	Comparing 10x Genomics single-cell 3′ and 5′ assay in short-and long-read sequencing.	0
571	Multiomics analysis reveals that hepatocyte nuclear factor 1β regulates axon guidance genes in the developing mouse kidney. **2022**, 12,	0
570	Global population genetics and diversity in the TAS2R bitter taste receptor family. 13,	1
569	Expression of alternative transcription factor 4 mRNAs and protein isoforms in the developing and adult rodent and human tissues. 15,	0
568	Common and rare variants of EGF increase the genetic risk of Alzheimer's disease as revealed by targeted sequencing of growth factors in Han Chinese. **2022**,	0
567	Implementation of a combined bioinformatics and experimental approach to address lncRNA mechanism of action: The example of NRIR. 9,	0

566	The landscape of hervRNAs transcribed from human endogenous retroviruses across human body sites. **2022**, 23,	0
565	RNA-mediated double-strand break repair in human cells.	0
564	The Rb/E2F axis is a key regulator of the molecular signatures instructing the quiescent and activated adult neural stem cell state. **2022**, 41, 111578	0
563	Nuclear Respiratory Factor 1 drives hepatocellular carcinoma progression by forming a positive feedback loop with LPCAT1-ERK1/2-CREB axis.	0
562	Using Genomic Structural Equation Modeling to Partition the Genetic Covariance Between Birthweight and Cardiometabolic Risk Factors into Maternal and Offspring Components in the Norwegian HUNT Study.	0
561	Low-Molecular Weight Small Molecules Can Potently Bind RNA and Affect Oncogenic Pathways in Cells.	0
560	HIF1□AS1 is a DNA:DNA:RNA triplex-forming lncRNA interacting with the HUSH complex. **2022**, 13,	2
559	ERK-dependent DICER1 phosphorylation promotes open chromatin state and lineage plasticity to mediate tumor progression.	0
558	Tissue-specific enhancer-gene maps from multimodal single-cell data identify causal disease alleles.	0
557	A therapeutically targetable NOTCH1-SIRT1-KAT7 axis in T-cell Leukemia.	0
556	Multi-omics approach dissects cis-regulatory mechanisms underlying North Carolina macular dystrophy, a retinal enhanceropathy. **2022**, 109, 2029-2048	0
555	Transcriptional and functional consequences of alterations to MEF2C and its topological organization in neuronal models. **2022**, 109, 2049-2067	2
554	Are Antisense Long Non-Coding RNA Related to COVID-19?. **2022**, 10, 2770	0
553	SEdb 2.0: a comprehensive super-enhancer database of human and mouse.	2
552	Variation in histone configurations correlates with gene expression across nine inbred strains of mice.	0
551	Nucleosome breathing facilitates cooperative binding of pluripotency factors Sox2 and Oct4 to DNA. **2022**,	0
550	A Systems Biology Approach on the Regulatory Footprint of Human Endogenous Retroviruses (HERVs). **2022**, 10, 98	1
549	IL-6 production through repression of UBASH3A gene via epigenetic dysregulation of super-enhancer in CD4+ T cells in rheumatoid arthritis. **2022**, 42,	0

548	Nucleosomes and flipons exchange energy to alter chromatin conformation, the readout of genomic information, and cell fate. 2200166	2
547	Use of cerebral organoids to model environmental and gene x environment interactions in the developing fetus and neurodegenerative disorders. **2023**, 173-200	0
546	Genetic and epigenetic links to asthma. **2023**, 173-194	0
545	Human transcriptome profiling: applications in health and disease. **2023**, 373-395	0
544	Genetics of Keratoconus. **2023**, 33-50	0
543	The Role of DNA Methylation and DNA Methyltransferases in Cancer. **2022**, 317-348	1
542	Integrating Multimorbidity into a Whole-Body Understanding of Disease Using Spatial Genomics. **2022**, 157-187	0
541	PERSPEKTYWY ZASTOSOWANIA TERAPEUTYCZNEGO EGZOSOMÓW W NAJCZĘŚCIEJ WYSTĘPUJĄCYCH NOWOTWORACH. **2019**, 17, 29-35	0
540	Identification of non-coding silencer elements and their regulation of gene expression.	1
539	Sex modulates the human genome regulatory network during heart failure and aging..	0
538	MethylSeqLogo: DNA methylation smart sequence logos.	0
537	Hi-TrAC reveals division of labor of transcription factors in organizing chromatin loops. **2022**, 13,	1
536	Methyl-SNP-seq reveals dual readouts of methylome and variome at molecule resolution while enabling target enrichment. gr.277080.122	0
535	ERR-activated GPR35 promotes immune infiltration level of macrophages in gastric cancer tissues. **2022**, 8,	0
534	Stress-induced transcriptional readthrough into neighboring genes is linked to intron retention. **2022**, 105543	0
533	Krüppel-like factor 9 (KLF9) links hormone dysregulation and circadian disruption to breast cancer pathogenesis.	0
532	CRISPR nuclease off-target activity and mitigation strategies. 4,	0
531	ARID2 mitigates hepatic steatosis via promoting the ubiquitination of JAK2.	0

530	Genome-wide single-molecule analysis of long-read DNA methylation reveals heterogeneous patterns at heterochromatin.	0
529	BCL6 regulates the endothelial pro-immunogenic phenotype relevant to organ transplant rejection.	0
528	Network reconstruction for trans acting genetic loci using multi-omics data and prior information. **2022**, 14,	0
527	Non-coding RNAs: The link between maternal malnutrition and offspring metabolism. 9,	0
526	Learning the histone codes with large genomic windows and three-dimensional chromatin interactions using transformer. **2022**, 13,	1
525	Functional inhibition of MEF2 by C/EBP is a possible mechanism of leukemia development by CEBP-IGH fusion gene.	0
524	Genome-wide contribution of common short-tandem repeats to Parkinson disease genetic risk.	0
523	Three-dimensional microenvironment regulates gene expression, function, and tight junction dynamics of iPSC-derived blood brain barrier microvessels. **2022**, 19,	1
522	memento: Generalized differential expression analysis of single-cell RNA-seq with method of moments estimation and efficient resampling.	0
521	Pilot genome-wide association study of antibody response to inactivated SARS-CoV-2 vaccines. 13,	0
520	Context-Dependent Function of Long Noncoding RNA PURPL in Transcriptome Regulation during p53 Activation.	0
519	A clinician guide to bioinformatics for next-generation sequencing. **2022**,	0
518	Improved discovery of RNA-binding protein binding sites in eCLIP data using DEWSeq.	0
517	Whole-body gene expression atlas of an adult metazoan.	0
516	A comparative atlas of single-cell chromatin accessibility in the human brain.	0
515	Lentiviral Gene Therapy for X-Linked Chronic Granulomatous Disease Recapitulates Endogenous CYBB Regulation and Expression.	1
514	Type 1 diabetes risk genes mediate pancreatic beta cell survival in response to proinflammatory cytokines. **2022**, 100214	0
513	Genome-wide association and multi-trait analyses characterize the common genetic architecture of heart failure. **2022**, 13,	0

512	Current trends and future perspectives in the treatment of PBC and PSC: A review. **2022**, 100065	0
511	Architecture of the outbred brown fat proteome defines regulators of metabolic physiology. **2022**,	1
510	Fully automated virtual screening pipeline of FDA-approved drugs using CaverWeb. **2022**,	0
509	Involvement of circRNAs in the Development of Heart Failure. **2022**, 23, 14129	0
508	Multi-omics HeCaToS dataset of repeated dose toxicity for cardiotoxic & hepatotoxic compounds. **2022**, 9,	0
507	Rare tandem repeat expansions associate with genes involved in synaptic and neuronal signaling functions in schizophrenia.	0
506	Deep learning-assisted genome-wide characterization of massively parallel reporter assays.	0
505	Computational drug discovery under RNA times. 1-21	0
504	Regulation of ATAD2B bromodomain binding activity by the histone code.	0
503	The 3D enhancer network of the developing T cell genome is shaped by SATB1. **2022**, 13,	0
502	Customized genomes for human and mouse ribosomal DNA mapping.	0
501	FORGEdb: systematic analysis of candidate causal variants to uncover target genes and mechanisms in complex traits..	0
500	A framework for group-wise summarization and comparison of chromatin state annotations.	0
499	De novo and inherited variants in coding and regulatory regions in genetic cardiomyopathies. **2022**, 16,	1
498	From the reference human genome to human pangenome: Premise, promise and challenge. 13,	0
497	IL-1 expression driven by androgen receptor absence or inactivation promotes prostate cancer bone metastasis.	0
496	Dynamics of Viral and Host 3D Genome Structure upon Infection. **2022**,	1
495	Analysis of DNMT1 Gene Variants in Progression of Neural Tube Defects- an insilico to invitro approach.	0

494	Transcription Factor DNA Complexes. **2022**, 195-211	0
493	Circular RNA circPTPRF promotes the progression of GBM via sponging miR-1208 to up-regulate YY1. **2022**, 22,	0
492	Germline determinants of the prostate tumor genome.	0
491	Neoepitopes prediction strategies: an integration of cancer genomics and immunoinformatics approaches.	0
490	Regulatory de novo mutations underlying intellectual disability.	0
489	The RNA editing landscape in Acute Myeloid Leukaemia reveals associations with disease mutations and clinical outcome. **2022**, 105622	0
488	GTF3A mutations predispose to herpes simplex encephalitis by disrupting biogenesis of the host-derived RIG-I ligand RNA5SP141. **2022**, 7,	0
487	Hnf1b renal expression directed by a distal enhancer responsive to Pax8. **2022**, 12,	0
486	Glucocorticoids unmask silent non-coding genetic risk variants for common diseases.	0
485	Structure and disorder: protein functions depend on this new binary transforming lock-and-key into structure-function continuum. **2023**, 127-148	0
484	Role of plasticity and disorder in protein moonlighting: blurring of lines between biocatalysts and other biologically active proteins. **2023**, 279-301	0
483	Decoding protein binding landscape on circular RNAs with base-resolution Transformer models.	0
482	Widespread Increase in Enhancer-Promoter Interactions during Developmental Enhancer Activation in Mammals.	0
481	An Automatized Workflow to Study Mechanistic Indicators for Driver Gene Prediction with Moonlight.	0
480	Estimation of Tumor Immune Signatures from Transcriptomics Data. **2022**, 311-338	0
479	Ensemble learning based assessment of the role of transcription factors in gene expression. **2023**, 152, 106455	0
478	Temporal regulation of head-on transcription at replication initiation sites. **2023**, 26, 105791	0
477	Combining multi-omics approaches to prioritize the variant-regulated functional long non-coding RNAs in autism spectrum disorder. **2023**, 80, 103357	0

476	A peptide-centric approach to analyse quantitative proteomics data- an application to prostate cancer biomarker discovery. **2023**, 272, 104774	0
475	Comprehensive 100-bp resolution genome-wide epigenomic profiling data for the hg38 human reference genome. **2023**, 46, 108827	0
474	Abnormal methylation in the NDUFA13 gene promoter of breast cancer cells breaks the cooperative DNA recognition by transcription factors. **2022**, 3,	0
473	Cell Type-Specific Analysis for High-throughput Data. **2022**, 271-283	0
472	Comprehensive comparison of gene expression diversity among a variety of human stem cells. **2022**, 4,	0
471	Back to Chromatin: ENCODE and the Dynamic Epigenome. **2022**, 17, 235-242	0
470	NetREX-CF integrates incomplete transcription factor data with gene expression to reconstruct gene regulatory networks. **2022**, 5,	0
469	Unique functions of two overlappingPAX6retinal enhancers.	0
468	The RNA binding proteins hnRNP H and F regulate splicing of a MYC dependent HRAS exon in Prostate Cancer Cells.	0
467	Cross-regulome profiling of RNA polymerases highlights the regulatory role of polymerase III on mRNA transcription by maintaining local chromatin architecture. **2022**, 23,	0
466	Accurate prediction of cohesin-mediated 3D genome organization from 2D chromatin features.	0
465	MoDLE: high-performance stochastic modeling of DNA loop extrusion interactions. **2022**, 23,	0
464	Interpretable deep learning translation of GWAS and multi-omics findings to identify pathobiology and drug repurposing in Alzheimer disease. **2022**, 41, 111717	0
463	Emerging Role of Interferon-Induced Noncoding RNA in Innate Antiviral Immunity. **2022**, 14, 2607	0
462	Scalable transcriptomics analysis with Dask: applications in data science and machine learning. **2022** , 23,	0
461	Whole genome DNA and RNA sequencing of whole blood elucidates the genetic architecture of gene expression underlying a wide range of diseases. **2022**, 12,	0
460	Mechanism of KIT gene regulation by GATA1 lacking the N-terminal domain in Down syndrome elated myeloid disorders. **2022**, 12,	0
459	Functional analysis of structural variants in single cells using Strand-seq.	0

458	KLF4 inhibits early neural differentiation of ESCs by coordinating specific 3D chromatin structure. **2022**, 50, 12235-12250	0
457	Single-cell transcriptomics in bone marrow delineates CD56dimGranzymeK+ subset as intermediate stage in NK cell differentiation. 13,	0
456	Insights on variant analysis in silico tools for pathogenicity prediction. 13,	1
455	Quantitative assessment of association between noncoding variants and transcription factor binding.	0
454	Role of Adipose Tissue microRNAs in the Onset of Metabolic Diseases and Implications in the Context of the DOHaD. **2022**, 11, 3711	1
453	PI3K/AKT signaling allows for MAPK/ERK pathway independency mediating dedifferentiation-driven treatment resistance in melanoma. **2022**, 20,	1
452	Integration of 3D genome topology and local chromatin features uncovers enhancers underlying craniofacial-specific cartilage defects. **2022**, 8,	0
451	Widespread hypertranscription in aggressive human cancers. **2022**, 8,	1
450	In Situ Hybridization as a Method to Examine Gene Regulatory Activity In Vivo. **2023**, 241-254	0
449	Automated high-throughput genome editing platform with an AI learning in situ prediction model. **2022**, 13,	0
448	Kinetics of mRNA nuclear export regulate innate immune response gene expression. **2022**, 13,	0
447	Anin vivomassively parallel platform for deciphering tissue-specific regulatory function.	0
446	KARAJ: An Efficient Adaptive Multi-Processor Tool to Streamline Genomic and Transcriptomic Sequence Data Acquisition. **2022**, 23, 14418	1
445	A non-coding GWAS variant impacts anthracycline-induced cardiotoxic phenotypes in human iPSC-derived cardiomyocytes. **2022**, 13,	0
444	An Epigenetic LINE-1-Based Mechanism in Cancer. **2022**, 23, 14610	0
443	MYC regulates a pan-cancer network of co-expressed oncogenic splicing factors. **2022**, 41, 111704	1
442	Chromatin activity identifies differential gene regulation across human ancestries.	0
441	Efficient Selection of Enhancers and Promoters from MIA PaCa-2 Pancreatic Cancer Cells by ChIP-lentiMPRA. **2022**, 23, 15011	0

440	Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. **2022**, 185, 4587-4603.e23	1
439	The integrated transcriptome bioinformatics analysis identifies key genes and cellular components for proliferative diabetic retinopathy. **2022**, 17, e0277952	0
438	Postnatal expansion of mesenteric lymph node stromal cells towards reticular and CD34+ stromal cell subsets. **2022**, 13,	0
437	Complexity of enhancer networks predicts cell identity and disease genes revealed by single-cell multi-omics analysis.	0
436	Generalized nuclear localization of retroelement transcripts. **2022**, 13,	0
435	Data analysis guidelines for single-cell RNA-seq in biomedical studies and clinical applications. **2022**, 9,	0
434	Single-cell chromatin landscapes of mouse skin development. **2022**, 9,	0
433	Incorporation of DNA methylation quantitative trait loci (mQTLs) in epigenome-wide association analysis: application to birthweight effects in neonatal whole blood. **2022**, 14,	0
432	New Insights into lncRNAs in A Cascade Hypothesis of Alzheimer's Disease. **2022**, 12, 1802	0
431	Detection and genomic analysis of BRAF fusions in Juvenile Pilocytic Astrocytoma through the combination and integration of multi-omic data. **2022**, 22,	0
430	The impact of sex and physical activity on the local immune response to muscle pain.	0
429	The Chromatin Structure at the MECP2 Gene and In Silico Prediction of Potential Coding and Non-Coding MECP2 Splice Variants. **2022**, 23, 15643	0
428	Genomic characterization and therapeutic utilization of IL-13-responsive sequences in asthma. **2022**, 100229	0
427	Limited conservation in cross-species comparison of GLK transcription factor binding suggested wide-spread cistrome divergence. **2022**, 13,	0
426	Biochemical activity is the default DNA state in eukaryotes.	0
425	Noncoding RNAs in Vascular Cell Biology and Restenosis. **2023**, 12, 24	0
424	CRISPR screens in sister chromatid cohesion defective cells reveal PAXIP1-PAGR1 as regulator of chromatin association of cohesin.	0
423	CircNTNG1 inhibits renal cell carcinoma progression via HOXA5-mediated epigenetic silencing of Slug. **2022**, 21,	1

422	RNA out of the mist. **2022**,	0
421	Global chromatin landscapes identify candidate noncoding modifiers of cardiac rhythm.	0
420	Integrated analysis of transcriptome and metabolome revealed biological basis of sows from estrus to lactation. **2022**, 105825	0
419	Parent-of-origin detection and chromosome-scale haplotyping using long-read DNA methylation sequencing and Strand-seq. **2022**, 100233	0
418	Bayesian model and selection signature analyses reveal risk factors for canine atopic dermatitis. **2022**, 5,	1
417	Specialized cells for building tissue bridges. **2022**, 29, 1615-1616	0
416	SNHG18 inhibits bladder cancer cell proliferation by increasing p21 transcription through destabilizing c-Myc protein.	0
415	The Idiopathic Pulmonary Fibrosis-Associated Single Nucleotide Polymorphism RS35705950 Is Transcribed in a MUC5B Promoter Associated Long Non-Coding RNA (AC061979.1). **2022**, 8, 83	0
414	HNF4a Acts as Upstream Functional Regulator of Intestinal Wnt3 and Paneth Cell Fate. **2022**,	1
413	Multiplex profiling of developmental enhancers with quantitative, single-cell expression reporters.	0
412	Construction of an lncRNA model for prognostic prediction of bladder cancer. **2022**, 15,	0
411	Insights into the cell fate decision-making processes from chromosome structural reorganizations. **2022**, 3, 041402	0
410	Multiplexed transcriptome discovery of RNA-binding protein binding sites by antibody-barcode eCLIP.	0
409	An Autoimmune Transcriptional Circuit Driving Foxp3+Regulatory T cell Dysfunction.	1
408	Reversal of splicing infidelity is a pre-activation step in B cell differentiation. 13,	0
407	Transcriptional Responses of Cancer Cells to Heat Shock-Inducing Stimuli Involve Amplification of Robust HSF1 Binding.	0
406	DiffDomain enables identification of structurally reorganized topologically associating domains.	0
405	Interplay Between the Histone Variant H2A.Z and the Epigenome in Pancreatic Cancer. **2022**, 53, 840-858	0

404	Reference panel guided topological structure annotation of Hi-C data. **2022**, 13,	0
403	Transposable elements as tissue-specific enhancers in cancers of endodermal lineage.	0
402	CHD8 suppression impacts on histone H3 lysine 36 trimethylation and alters RNA alternative splicing.	0
401	Nanobody-tethered transposition enables multifactorial chromatin profiling at single-cell resolution.	1
400	Disruption of Multiple Overlapping Functions Following Stepwise Inactivation of the Extended Myc Network. **2022**, 11, 4087	0
399	DeepTSS: multi-branch convolutional neural network for transcription start site identification from CAGE data. **2022**, 23,	0
398	Universal chromatin state annotation of the mouse genome.	0
397	CRAG: de novo characterization of cell-free DNA fragmentation hotspots in plasma whole-genome sequencing. **2022**, 14,	0
396	Genetic variation in histone modifications and gene expression identifies regulatory variants in the mammary gland of cattle. **2022**, 23,	1
395	Genome-wide differential DNA methylation analysis of MDA-MB-231 breast cancer cells treated with curcumin derivatives, ST08 and ST09. **2022**, 23,	0
394	Immune Response Serves as a Bridge between Abnormal Lipid and Bone Metabolism: A Differential Expression Genes Profile Analysis Based on Clinical Data-mining.	0
393	Transcriptional regulation of Satb1 in mouse trophoblast stem cells. 10,	0
392	Regression convolutional neural network models implicate peripheral immune regulatory variants in the predisposition to Alzheimer disease.	0
391	Plant Transcriptomics: Data-driven Global Approach to Understand Cellular Processes and Their Regulation in Model and Non-Model Plants. **2022**, 10-29	0
390	CanMethdb: a database for genome-wide DNA methylation annotation in cancers.	0
389	ACTR5 controls CDKN2A and tumor progression in an INO80-independent manner. **2022**, 8,	0
388	Integrating extrusion complex-associated pattern to predict cell type-specific long-range chromatin loops. **2022**, 25, 105687	0
387	Multi-center integrated analysis of non-coding CRISPR screens.	0

386	Strategies for activity analysis of single nucleotide polymorphisms associated with human diseases.	0
385	Heme-dependent induction of mitophagy program during differentiation of murine erythroid cells. **2022**,	0
384	Quantifying negative selection in human 3′UTRs uncovers constrained targets of RNA-binding proteins.	0
383	The complete sequence of a human Y chromosome.	0
382	scTensor detects many-to-many cell–cell interactions from single cell RNA-sequencing data.	0
381	Comparing Genomic and Epigenomic Features across Species Using the WashU Comparative Epigenome Browser.	0
380	Noncoding RNAs associated with IgA nephropathy.	0
379	Deep generative modeling and clustering of single cell Hi-C data.	0
378	Massively parallel reporter assays and variant scoring identified functional variants and target genes for melanoma loci and highlighted cell-type specificity. **2022**, 109, 2210-2229	0
377	Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. **2022**, 82, 4627-4646.e14	1
376	LncRNA LENGA acts as a tumor suppressor in gastric cancer through BRD7/TP53 signaling. **2023**, 80,	0
375	ACAP1 Deficiency Predicts Inferior Immunotherapy Response in Solid Tumors. **2022**, 14, 5951	0
374	Enhancer-driven gene regulatory networks inference from single-cell RNA-seq and ATAC-seq data.	0
373	Gene Therapy and Cardiovascular Diseases. **2023**, 235-254	0
372	Altered and allele-specific open chromatin landscape reveals epigenetic and genetic regulators of innate immunity in COVID-19. **2022**, 100232	1
371	Liver RBFOX2 regulates cholesterol homeostasis via Scarb1 alternative splicing in mice. **2022**, 4, 1812-1829	1
370	Circular RNA circPLOD2 regulates pericyte function by targeting the transcription factor KLF4.	0
369	Diverse silent chromatin states modulate genome compartmentalization and loop extrusion barriers.	0

368	Multimodal learning of noncoding variant effects using genome sequence and chromatin structure.	0
367	Multiscale genetic architecture of donor-recipient differences reveals intronic LIMS1 locus mismatches associated with long-term renal transplant survival.	0
366	Enhancer turnover in cancer and species evolution are associated with DNA replication timing.	0
365	Evaluating deep learning for predicting epigenomic profiles. **2022**, 4, 1088-1100	0
364	DNA methylation entropy is associated with DNA sequence features and developmental epigenetic divergence.	0
363	The sound of silence: Transgene silencing in mammalian cell engineering. **2022**, 13, 950-973	0
362	Boosting tissue-specific prediction of active cis-regulatory regions through deep learning and Bayesian optimization techniques. **2022**, 23,	0
361	GATA4 regulates mitochondrial biogenesis and functions during cardiac development and rescues cardiac and mitochondrial functions impaired by TKIs.	0
360	Recurrent repeat expansions in human cancer genomes.	0
359	Tumor Cell-Intrinsic BTLA Receptor Inhibits the Proliferation of Tumor Cells via ERK1/2. **2022**, 11, 4021	1
358	Distinct binding pattern of EZH2 and JARID2 on RNAs and DNAs in hepatocellular carcinoma development. 12,	0
357	The lncRNA landscape of cardiac resident macrophages and identification ofSchlafenlncas a regulator of macrophage migratory function.	0
356	Computational prediction and characterization of cell-type-specific and shared binding sites.	0
355	RefTM: reference-guided topic modeling of single-cell chromatin accessibility data.	0
354	CONGA: Copy number variation genotyping in ancient genomes and low-coverage sequencing data. **2022**, 18, e1010788	0
353	Structural variants drive context-dependent oncogene activation in cancer. **2022**, 612, 564-572	2
352	Whole-genome functional characterization of RE1 silencers using a modified massively parallel reporter assay. **2022**, 100234	0
351	DANCR promotes glioma cell autophagy and proliferation via the miR-33b/DLX6/ATG7 axis. **2023**, 49,	0

350	cis-Regulatory Elements in Plant Development, Adaptation, and Evolution. **2023**, 74,	0
349	Emerging regulatory mechanisms of noncoding RNAs in topologically associating domains. **2023**,	0
348	Long non-coding RNAs: definitions, functions, challenges and recommendations.	5
347	Coding roles of long non-coding RNAs in breast cancer: Emerging molecular diagnostic biomarkers and potential therapeutic targets with special reference to chemotherapy resistance. 13,	0
346	Unsupervised Contrastive Peak Caller for ATAC-seq.	0
345	Identification and Characterization of novel long non-coding RNAs in vascular smooth cells.	0
344	Interactomes-Scaffolds of Cellular Systems. **2016**, 430-443	0
343	Distant Activation of Transcription by Enhancers. **2016**, 617-624	0
342	Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. **2023**, 23,	1
341	ChIATAC is an efficient strategy for multi-omics mapping of 3D epigenomes from low-cell inputs. **2023**, 14,	0
340	Identification of kinases activated by multiple pro-angiogenic growth factors. 13,	0
339	Multi-functional gene ZNF281 identified as a molecular biomarker in soft tissue regeneration and pan-cancer progression. 13,	0
338	Ten simple rules for using public biological data for your research. **2023**, 19, e1010749	0
337	The human pre-replication complex is an open complex. **2023**, 186, 98-111.e21	0
336	Osteocyte Egln1/Phd2 links oxygen sensing and biomineralization via FGF23. **2023**, 11,	1
335	Metadata retrieval from sequence databases with ffq.	0
334	Quantifying propagation of DNA methylation and hydroxymethylation with iDEMS.	0
333	Cancer plasticity: Investigating the causes for this agility. **2023**, 88, 138-156	0

332	The junctional mechanosensor AmotL2 regulates YAP promotor accessibility.	0
331	Emerging roles and potential application of PIWI-interacting RNA in urological tumors. 13,	0
330	The significance of the crosstalk between ubiquitination or deubiquitination and ncRNAs in non-small cell lung cancer. 12,	0
329	Functional impact of multi-omic interactions in breast cancer subtypes. 13,	1
328	Application of massive parallel reporter analysis in biotechnology and medicine.	0
327	Haplotype-aware pantranscriptome analyses using spliced pangenome graphs.	0
326	DiPRO1 dependent transcriptional and epigenetic regulation distinctly controls the fate of muscle and mesenchymal cancer cells.	0
325	Genome-wide landscape of RNA-binding protein (RBP) networks as potential molecular regulators of psychiatric co-morbidities: a computational analysis. **2023**, 24,	0
324	Emerging roles of non-coding RNAs in colorectal cancer oxaliplatin resistance and liquid biopsy potential. 29, 1-18	0
323	SAMStat 2: quality control for next generation sequencing data.	0
322	Celiac disease-associated loci show considerable genetic overlap with neuropsychiatric diseases but with limited transethnic applicability. **2023**, 102,	0
321	Hypothesis-driven probabilistic modelling enables a principled perspective of genomic compartments.	0
320	CRISPR screens reveal genetic determinants of PARP inhibitor sensitivity and resistance in prostate cancer. **2023**, 14,	1
319	High expression of RNF169 is associated with poor prognosis in pancreatic adenocarcinoma by regulating tumour immune infiltration. 13,	0
318	Transient loss of Polycomb components induces an epigenetic cancer fate.	0
317	Identifying strengths and weaknesses of methods for computational network inference from single cell RNA-seq data.	0
316	ONECUT2 regulates RANKL-dependent enterocyte and microfold cell differentiation in the small intestine; a multi-omics study.	0
315	Current advances in primate genomics: novel approaches for understanding evolution and disease.	0

314	A multicolour polymer model for the prediction of 3D structure and transcription in human chromatin.	0
313	Identification of Novel Genetic Risk Factors for Focal Segmental Glomerulosclerosis in Children: Results From the Chronic Kidney Disease in Children (CKiD) Cohort. **2023**,	0
312	Matching queried single-cell open-chromatin profiles to large pools of single-cell transcriptomes and epigenomes for reference supported analysis. gr.277015.122	0
311	Candidate targets of copy number deletion events across 17 cancer types. 13,	0
310	Prolyl-tRNA synthetase as a novel therapeutic target in multiple myeloma. **2023**, 13,	0
309	Insulin determines the effects of TGF-□n HNF4□transcription and epithelial-to-mesenchymal transition in hepatocytes.	0
308	DNA fragility at the KMT2A / MLL locus: insights from old and new technologies. **2023**, 13,	0
307	Applications of deep learning in understanding gene regulation. **2023**, 100384	0
306	Genetic Redundancy in Rye Shows in a Variety of Ways. **2023**, 12, 282	0
305	Hooked Up from a Distance: Charting Genome-Wide Long-Range Interaction Maps in Neural Cells Chromatin to Identify Novel Candidate Genes for Neurodevelopmental Disorders. **2023**, 24, 1164	1
304	X Or Y Cancer: An Extensive Analysis of Sex Differences in Lung Adenocarcinoma. **2023**, 30, 1395-1415	0
303	Integration of single-cell multiomic measurements across disease states with genetics identifies mechanisms of beta cell dysfunction in type 2 diabetes.	0
302	Vitamin C boosts DNA demethylation in TET2 germline mutation carriers. **2023**, 15,	0
301	The methylome and cell-free DNA: current applications in medicine and pediatric disease.	0
300	A p53-TLR3 axis ameliorates pulmonary hypertension by inducing BMPR2 via IRF3. **2023**, 26, 105935	0
299	Chromatin-bound protein colocalization analysis using bedGraph2Cluster and PanChIP. **2023**, 4, 101991	0
298	From Challenges to Opportunities and Open Questions. **2023**, 87-130	0
297	PGAM4 silencing inhibited glycolysis and chemoresistance to temozolomide in glioma cells.	0

296	Long Non-Coding RNAs as Epigenetic Regulators of Immune Checkpoints in Cancer Immunity. **2023**, 15, 184	0
295	Metagenomic analysis of viral genes integrated in whole genome sequencing data of Thai patients with Brugada syndrome. **2022**, 20, e44	0
294	Exploring the contribution of ARMS2 and HTRA1 genetic risk factors in age-related macular degeneration. **2022**, 101159	1
293	SATB2 organizes the 3D genome architecture of cognition in cortical neurons.	0
292	Investigation of Rare Non-Coding Variants in Familial Multiple Myeloma. **2023**, 12, 96	0
291	Generation of Induced Pluripotent Stem Cells from Lymphoblastoid Cell Lines by Electroporation of Episomal Vectors. **2022**,	0
290	LncReader: identification of dual functional long noncoding RNAs using a multi-head self-attention mechanism. **2023**, 24,	0
289	Sparse canonical correlation to identify breast cancer related genes regulated by copy number aberrations. **2022**, 17, e0276886	1
288	Pioneer transcription factors coordinate active and repressive gene expression states to regulate cell fate.	0
287	A new type of transcriptional reprogramming by an IRF4 mutation in lymphoma.	0
286	The autism risk factor CHD8 is a chromatin activator in human neurons and functionally dependent on the ERK-MAPK pathway effector ELK1. **2022**, 12,	0
285	Loci2Tissue: Ranking tissues by the e3xpression of disease-associated genes reveals insights of the underlying mechanisms of complex diseases and traits. **2022**,	0
284	Deleterious, protein-altering variants in the transcriptional coregulator ZMYM3 in 27 individuals with a neurodevelopmental delay phenotype. **2022**,	0
283	Predicting transcription factor binding sites by dual-stream multiple instance learning network. **2022**,	0
282	COOBoostR: An Extreme Gradient Boosting-Based Tool for Robust Tissue or Cell-of-Origin Prediction of Tumors. **2023**, 13, 71	0
281	Early transcriptional and epigenetic divergence of CD8+ T cells responding to acute versus chronic infection. **2023**, 21, e3001983	0
280	Identification of the MALAT1/miR-106a-5p/ZNF148 feedback loop in regulating HaCaT cell proliferation, migration and apoptosis.	0
279	Epigenetic and transcriptional regulations prime cell fate before division during human pluripotent stem cell differentiation. **2023**, 14,	0

278	Computational approaches to understand transcription regulation in development.	1
277	T-REX17 is a transiently expressed non-coding RNA essential for human endoderm formation. 12,	0
276	Epigenomic charting and functional annotation of risk loci in renal cell carcinoma. **2023**, 14,	0
275	Transcriptome Profiling of the Liver in Nellore Cattle Phenotypically Divergent for RFI in Two Genetic Groups. **2023**, 13, 359	0
274	m7G-related gene NUDT4 as a novel biomarker promoting cancer cell proliferation in lung adenocarcinoma. 12,	0
273	A genome-wide association study of germline variation and melanoma prognosis. 12,	0
272	CRISPR/Cas9 and FLP-FRT mediated regulatory dissection of the BX-C of Drosophila melanogaster. **2023**, 31,	0
271	Specificity Guides Interpretation: On H3K4 Methylation at Enhancers and Broad Promoters.	0
270	Quantitative Comparison of Multiple Chromatin Immunoprecipitation-Sequencing (ChIP-seq) Experiments with spikChIP. **2023**, 55-72	0
269	An atlas of lamina-associated chromatin across twelve human cell types reveals an intermediate chromatin subtype. **2023**, 24,	2
268	Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons.	0
267	Novel Genetic Variants Associated with Chronic Kidney Disease Progression. **2023**, Publish Ahead of Print,	0
266	Integration of genetic fine-mapping and multi-omics data reveals candidate effector genes for hypertension.	0
265	An intrinsically interpretable neural network architecture for sequence to function learning.	0
264	High tissue-specificity of lncRNAs maximises the prediction of tissue of origin of circulating DNA.	0
263	Seeing the trees for the wood: reducing heterogeneity in genomic studies of asthma. **2023**, 61, 2201931	0
262	peaksat: an R package for ChIP-seq peak saturation analysis. **2023**, 24,	0
261	How does precursor RNA structure influence RNA processing and gene expression?.	0

260	TRIM24 controls induction of latent HIV-1 by stimulating transcriptional elongation. **2023**, 6,	0
259	Characterization of proteome-size scaling by integrative omics reveals mechanisms of proliferation control in cancer. **2023**, 9,	0
258	Characterizing Primary transcriptional responses to short term heat shock in paired fraternal lymphoblastoid lines with and without Down syndrome.	0
257	SNORA14A inhibits hepatoblastoma cell proliferation by regulating SDHB-mediated succinate metabolism. **2023**, 9,	0
256	ChromDL: A Next-Generation Regulatory DNA Classifier.	0
255	The adapted Activity-By-Contact model for enhancer-gene assignment and its application to single-cell data.	0
254	Multiallelic Copy Number Variation in ORM1 is Associated with Plasma Cell-Free DNA Levels as an Intermediate Phenotype for Venous Thromboembolism.	0
253	DNA Double-Strand Break-Related Competitive Endogenous RNA Network of Noncoding RNA in Bovine Cumulus Cells. **2023**, 14, 290	1
252	DEtail-seq is an ultra-efficient and convenient method for meiotic DNA break profiling in multiple organisms.	0
251	Bayesian mixed model analysis uncovered 21 risk loci for chronic kidney disease in boxer dogs. **2023** , 19, e1010599	0
250	maxATAC: Genome-scale transcription-factor binding prediction from ATAC-seq with deep neural networks. **2023**, 19, e1010863	0
249	Noncoding RNAs and their role in bacterial infections. **2023**, 617-622	0
248	Imaging-Based In Situ Analysis of 5-Methylcytosine at Low Repetitive Single Gene Loci with Transcription-Activator-Like Effector Probes.	0
247	Single cell cortical bone transcriptomics define novel osteolineage gene sets altered in chronic kidney disease. 14,	0
246	FIMICS: A panel of long noncoding RNAs for cardiovascular conditions. **2023**, 9, e13087	0
245	A temporal in vivo catalogue of chromatin accessibility and expression profiles in pineoblastoma reveals a prevalent role for repressor elements. gr.277037.122	0
244	Combinatorial single-cell profiling of all major chromatin types with MAbID.	0
243	A Comprehensive Investigation of Genomic Variants in Prostate Cancer Reveals 30 Putative Regulatory Variants. **2023**, 24, 2472	0

242	LncCat: An ORF attention model to identify LncRNA based on ensemble learning strategy and fused sequence information. **2023**, 21, 1433-1447	0
241	LRphase: an efficient method for assigning haplotype identity to long reads.	0
240	Promoter-pervasive transcription causes RNA polymerase II pausing to boost DOG1 expression in response to salt.	0
239	The Multi-State Epigenetic Pacemaker enables the identification of combinations of factors that influence DNA methylation.	0
238	Epigenetic control of cellular crosstalk defines gastrointestinal organ fate and function. **2023**, 14,	0
237	Integrated, Longitudinal Analysis of Cell-Free DNA in Uveal Melanoma.	0
236	Utilizing Large Functional and Population Genomics Resources for CRISPR/Cas Perturbation Experiment Design. **2023**, 63-73	0
235	Cardiovascular Disease Causes Proinflammatory Microvascular Changes in the Human Right Atrium.	0
234	lncHUB2: aggregated and inferred knowledge about human and mouse lncRNAs. **2023**, 2023,	0
233	The TERT Promoter: A Key Player in the Fight for Cancer Cell Immortality. **2023**, 88, S21-S38	0
232	Databases and prospects of dynamic gene regulation in eukaryotes: A mini review. **2023**, 21, 2147-2159	0
231	Global hypomethylation in childhood asthma identified by genome-wide DNA-methylation sequencing preferentially affects enhancer regions.	0
230	Transcription factor binding sites are frequently under accelerated evolution in primates. **2023**, 14,	0
229	Spatial transcriptomics using multiplexed deterministic barcoding in tissue. **2023**, 14,	0
228	Application of PCR-based approaches for evaluation of cell-free DNA fragmentation in colorectal cancer. 10,	0
227	Widespread allele-specific topological domains in the human genome are not confined to imprinted gene clusters. **2023**, 24,	0
226	Global identification of direct SWI/SNF targets reveals compensation by EP400.	0
225	Modeling cross-cell typecis-regulatory patterns via hierarchical deep neural network and gene expression prediction.	0

224	The Type 2 Diabetes Knowledge Portal: An open access genetic resource dedicated to type 2 diabetes and related traits. **2023**, 35, 695-710.e6	0
223	3D genome organization and its study in livestock breeding. **2023**,	0
222	Comparative genomics analyses reveal sequence determinants underlying interspecies variations in injury-responsive enhancers. **2023**, 24,	0
221	Missense and nonsense mutations of the zebrafish hcfc1a gene result in contrasting mTor and radial glial phenotypes. **2023**, 864, 147290	0
220	HTLV-1 bZIP factor impairs DNA mismatch repair system. **2023**, 657, 43-49	0
219	LncRNA HOXB-AS3 binding to PTBP1 protein regulates lipid metabolism by targeting SREBP1 in endometrioid carcinoma. **2023**, 320, 121512	0
218	Dangerous sugars: Structural diversity and functional significance of acylsugar-like defense compounds in flowering plants. **2023**, 73, 102348	0
217	The impact of sex and physical activity on the local immune response to muscle pain. **2023**, 111, 4-20	0
216	Large-scale Integrative Analysis of Juvenile Idiopathic Arthritis for New Insight into Its Pathogenesis.	0
215	The Function and Therapeutic Potential of lncRNAs in Cardiac Fibrosis. **2023**, 12, 154	0
214	Epigenetic regulation of T cell lineages in skin and blood following hematopoietic stem cell transplantation. **2023**, 248, 109245	0
213	EGRE: Calculating Enrichment Between Genomic Regions. **2022**, 67-79	0
212	L0segmentation enables data-driven concise representations of diverse epigenomic data.	0
211	CCR4 + CD8 + T cells clonally expand to differentiated effectors in murine psoriasis and in human psoriatic arthritis. **2023**, 53,	0
210	Exploring the genetic basis of coronary artery disease using functional genomics. **2023**,	0
209	Pan-cancer molecular subtypes of metastasis reveal distinct and evolving transcriptional programs. **2023**, 4, 100932	1
208	Epigenetic signals that direct cell type‐specific interferon beta response in mouse cells. **2023**, 6, e202201823	0
207	Decoding the genetic and epigenetic basis of asthma. **2023**, 78, 940-956	0

206	Myelodysplastic Syndrome associated TET2 mutations affect NK cell function and genome methylation. **2023**, 14,	0
205	Correspondence between functional scores from deep mutational scans and predicted effects on protein stability.	0
204	Functional genomics identify causal variant underlying the protective CTSH locus for Alzheimer disease.	0
203	The role of lysine-specific demethylase 6A (KDM6A) in tumorigenesis and its therapeutic potentials in cancer therapy. **2023**, 133, 106409	0
202	Neuron Glia-Ratio-Like Approach Evidenced for Limited Variability and In-Aggregate Circadian Shifts in Cortical Cell-Specific Transcriptomes. **2023**, 73, 159-170	0
201	PTBP1 controls intestinal epithelial regeneration through post-transcriptional regulation of gene expression. **2023**, 51, 2397-2414	0
200	Cooperation of local features and global representations by a dual-branch network for transcription factor binding sites prediction. **2023**, 24,	0
199	Cell-specific expression of the FAP gene is regulated by enhancer elements. 10,	0
198	Multi-ancestry and multi-trait genome-wide association meta-analyses inform clinical risk prediction for systemic lupus erythematosus. **2023**, 14,	0
197	Role of the Gut-Brain Axis in the Shared Genetic Etiology Between Gastrointestinal Tract Diseases and Psychiatric Disorders. **2023**, 80, 360	0
196	400. Quantifying the functional conservation between human and pig using artificial neural networks. **2022**,	0
195	Circular RNAs New Kids on the Block in Cancer Pathophysiology and Management. **2023**, 12, 552	0
194	545. Multi-dimensional functional annotation of bovine genome for the BovReg project. **2022**,	0
193	PopTradeOff: a database for exploring population-specific trade-offs between adaptive evolution, disease susceptibility, and drug responsiveness.	0
192	Transposable elements and their role in aging. **2023**, 86, 101881	0
191	Comparative Hypothalamic Transcriptome Analysis Reveals Crucial mRNAs, lncRNAs, and circRNAs Affecting Litter Size in Goats. **2023**, 14, 444	0
190	On augmenting topological graph representations for attributed graphs. **2023**, 136, 110104	0
189	SARS-CoV-2 NSP5 Antagonizes MHC II Expression by Subverting Histone Deacetylase 2.	0

188	Unveiling the Machinery behind Chromosome Folding by Polymer Physics Modeling. **2023**, 24, 3660	0
187	Androgen Signaling Restricts Glutaminolysis to Drive Sex-Specific Th17 Metabolism.	0
186	Gut virome-colonisingOrthohepadnavirusgenus is associated with ulcerative colitis pathogenesis and induces intestinal inflammationin vivo. gutjnl-2022-328375	0
185	Cis-regulatory landscapes of the fat-tailed dunnart and mouse provide insights into the drivers of craniofacial heterochrony.	0
184	Integrative analysis of uterine leiomyoma genetics, epigenomics, and single-cell transcriptomics reveals causal genetic variants, gene targets, and cell types.	0
183	Synthetic analysis of chromatin tracing and live-cell imaging indicates pervasive spatial coupling between genes. 12,	0
182	Integrative multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci.	0
181	Male Contributory Factors in Recurrent Pregnancy Loss.	0
180	A NPAS4NuA4 complex couples synaptic activity to DNA repair. **2023**, 614, 732-741	1
179	AMLs harboring DNMT3A-destabilizing variants show increased intratumor DNA methylation heterogeneity at bivalent chromatin domains.	0
178	Rare genetic variants underlie outlying levels of DNA methylation and gene-expression.	0
177	Selective concurrence of the long non-coding RNA MALAT1 and the Polycomb Repressive Complex 2 to promoter regions of active genes in MCF7 breast cancer cells.	0
176	Transcription factors regulating vasculogenesis and angiogenesis.	0
175	Structures of G-Quadruplexes and Their Drug Interactions. **2023**, 1-30	0
174	Luteolin directly binds to KDM4C and attenuates ovarian cancer stemness via epigenetic suppression of PPP2CA/YAP axis. **2023**, 160, 114350	0
173	Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons.	0
172	Mini-review: Gene regulatory network benefits from three-dimensional chromatin conformation and structural biology. **2023**, 21, 1728-1737	0
171	Low Gut Microbial Diversity Augments Estrogen-driven Pulmonary Fibrosis in Female-Predominant Interstitial Lung Disease.	0

170	Computational prediction of human deep intronic variation.	0
169	Increased alcohol dehydrogenase 1 activity promotes longevity. **2023**, 33, 1036-1046.e6	0
168	RNA independent fragment partition method based on deep learning for RNA secondary structure prediction. **2023**, 13,	0
167	A shared vulnerability code underpins varying sources of DNA damage throughout paternal germline transmission in mouse. **2023**, 51, 2319-2332	0
166	The Host Non-Coding RNA Response to Alphavirus Infection. **2023**, 15, 562	0
165	SETD2 regulates chromatin accessibility and transcription to suppress lung tumorigenesis. **2023**, 8,	0
164	Quantification and Mapping of Alkylation in the Human Genome Reveal Single Nucleotide Resolution Precursors of Mutational Signatures. **2023**, 9, 362-372	1
163	Delta.EPI: a probabilistic voting-based enhancer promoter interaction prediction platform. **2023**,	0
162	Integrative analysis of a Novel six methylated pseudogene Prognostic signature in patients with glioma.	0
161	Nutrient regulation of the islet epigenome controls adaptive insulin secretion. **2023**, 133,	0
160	ChIP-seq profiling of H3K4me3 and H3K27me3 in an invasive insect, Bactroceradorsalis. 14,	0
159	Krppel-like factor 9 (KLF9) links hormone dysregulation and circadian disruption to breast cancer pathogenesis. **2023**, 23,	0
158	Spatial transcriptomics reveals niche-specific enrichment and vulnerabilities of radial glial stem-like cells in malignant gliomas. **2023**, 14,	0
157	The genetic and evolutionary basis of gene expression variation in East Africans. **2023**, 24,	0
156	DeepFormer: a hybrid network based on convolutional neural network and flow-attention mechanism for identifying the function of DNA sequences. **2023**, 24,	0
155	The Role of Non-coding RNAs in Cerebellar Development. **2023**, 111-128	0
154	Long non-coding RNA-derived peptides are immunogenic and drive a potent anti-tumour response. **2023**, 14,	2
153	Mycobacterium tuberculosis methyltransferase perturbs host epigenetic programming to promote bacterial survival.	0

152	Pretraining strategies for effective promoter-driven gene expression prediction.	0
151	A neurodevelopmental epigenetic programme mediated by SMARCD3–DAB1–Reelin signalling is hijacked to promote medulloblastoma metastasis. **2023**, 25, 493-507	0
150	Integrated Stress Response signaling acts as a metabolic sensor in fat tissues to regulate oocyte maturation and ovulation.	0
149	CRISPR/Cas9 screen uncovers functional translation of cryptic lncRNA-encoded open reading frames in human cancer. **2023**, 133,	1
148	Simultaneous Single-Cell Profiling of the Transcriptome and Accessible Chromatin Using SHARE-seq. **2023**, 187-230	0
147	Profiling Chromatin Accessibility on Replicated DNA with repli-ATAC-Seq. **2023**, 71-84	0
146	Genome-Wide Mapping of Active Regulatory Elements Using ATAC-seq. **2023**, 3-19	0
145	Regulatory de novo mutations underlying intellectual disability. **2023**, 6, e202201843	0
144	Low Gut Microbial Diversity Augments Estrogen-Driven Pulmonary Fibrosis in Female-Predominant Interstitial Lung Disease. **2023**, 12, 766	0
143	Genetic features and genomic targets of human KRAB-Zinc Finger Proteins.	0
142	Tcf21 marks visceral adipose mesenchymal progenitors and functions as a rate-limiting factor during visceral adipose tissue development. **2023**, 42, 112166	0
141	Whole-genome sequencing reveals a complex African population demographic history and signatures of local adaptation. **2023**, 186, 923-939.e14	1
140	Fine mapping spatiotemporal mechanisms of genetic variants underlying cardiac traits and disease. **2023**, 14,	0
139	Regulatory roles of ferroptosis-related non-coding RNAs and their research progress in urological malignancies. 14,	0
138	Genomes: Molecular Maps of Living Organisms. **2023**, 35-45	0
137	Processing genome-wide association studies within a repository of heterogeneous genomic datasets. **2023**, 24,	0
136	Predicting CRISPR-Cas12a guide efficiency for targeting using Machine Learning.	0
135	Validation of the new EPIC DNA methylation microarray (900K EPIC v2) for high-throughput profiling of the human DNA methylome. **2023**, 18,	0

134	Identifying promoter sequence architectures via a chunking-based algorithm using non-negative matrix factorisation.	0
133	An econometric lens resolves cell-state parallax.	0
132	Prevalent use and evolution of exonic regulatory sequences in the human genome. **2023**, 3,	0
131	Microtubule-associated protein 4 promotes epithelial mesenchymal transition in hepatocellular cancer cells via regulating GSK3/β-catenin pathway. **2023**, 9, e14309	0
130	Zbtb46coordinates angiogenesis and immunity to control tumor outcome.	0
129	EGR1 drives cell proliferation by directly stimulating TFEB transcription in response to starvation. **2023**, 21, e3002034	0
128	Specificity Proteins (Sp) and Cancer. **2023**, 24, 5164	0
127	Empowering Beginners in Bioinformatics with ChatGPT.	0
126	The molecular consequences of androgen activity in the human breast. **2023**, 3, 100272	0
125	Technologies, strategies, and cautions when deconvoluting genome-wide association signals: FTO in focus. **2023**, 24,	0
124	MAPTexpression is mediated by long-range interactions withcis-regulatory elements.	0
123	The Network Zoo: a multilingual package for the inference and analysis of gene regulatory networks. **2023**, 24,	0
122	Massively parallel characterization of transcriptional regulatory elements in three diverse human cell types.	0
121	MYC determines lineage commitment in kras driven primary liver cancer development. **2023**,	0
120	The CGG triplet repeat binding protein 1 counteracts DNA secondary structure-induced transcription-replication conflicts.	0
119	Analysis of histone antibody specificity directly in sequencing data using siQ-ChIP.	0
118	Identifying polymorphic cis-regulatory variants as risk markers for lung carcinogenesis and chemotherapy responses in tobacco smokers from eastern India. **2023**, 13,	0
117	KRAB zinc finger proteins ZNF587/ZNF417 protect lymphoma cells from replicative stress-induced inflammation.	0

116	An atlas of gene regulatory networks for memory CD4+T cells in youth and old age.	0
115	Dynamic network-guided CRISPRi screen reveals CTCF loop-constrained nonlinear enhancer-gene regulatory activity in cell state transitions.	0
114	Epigenome editing based on CRISPR/dCas9p300 facilitates transdifferentiation of human fibroblasts into Leydig-like cells. **2023**, 425, 113551	0
113	Epigenetic misactivation of a distal developmental enhancer cluster drivesSOX2overexpression in breast and lung cancer.	0
112	GenoPipe: identifying the genotype of origin within (epi)genomic datasets.	0
111	Cis-regulatory control of transcriptional timing and noise in response to estrogen.	0
110	Statistical Analysis in ChIP-seq-Related Applications. **2023**, 169-181	0
109	Femtosecond laser microdissection for isolation of regenerating C. elegans neurons for single-cell RNA sequencing. **2023**, 20, 590-599	0
108	Motif elucidation in ChIP-seq datasets with a knockout control. **2023**, 3,	0
107	Asparagine starvation suppresses histone demethylation through iron depletion. **2023**, 26, 106425	0
106	NOMe-HiC: joint profiling of genetic variant, DNA methylation, chromatin accessibility, and 3D genome in the same DNA molecule. **2023**, 24,	0
105	SNHG18 inhibits bladder cancer cell proliferation by increasing p21 transcription through destabilizing c-Myc protein. **2023**, 23,	0
104	Statistical Methods for Disease Risk Prediction with Genotype Data. **2023**, 331-347	0
103	Epigenetic Regulation of Inflammatory Mechanisms and a Psychological Symptom Cluster in Patients Receiving Chemotherapy. **2023**, 72, 200-210	0
102	Combinatorial effects on gene expression at the Lbx1/Fgf8 locus resolve split-hand/foot malformation type 3. **2023**, 14,	0
101	Identification of mammalian transcription factors that bind to inaccessible chromatin.	0
100	m6A-driven SF3B1 translation control steers splicing to direct genome integrity and leukemogenesis. **2023**, 83, 1165-1179.e11	0
99	Opportunities and challenges in sharing and reusing genomic interval data. 14,	0

98	The Genomics of Diabetic Neuropathy. **2023**, 239-251	0
97	Genetic variants of NEUROD1 target genes are associated with clinical outcomes of small-cell lung cancer patients.	0
96	PAPET: a collection of performant algorithms to identify 5-methyl cytosine from PacBio SequelII data.	0
95	Correlation between large FBN1 deletions and severe cardiovascular phenotype in Marfan syndrome: Analysis of two novel cases and analytical review of the literature.	0
94	A transcriptionally distinct subset of influenza-specific effector memory B cells predicts long-lived antibody responses to vaccination in humans. **2023**, 56, 847-863.e8	0
93	Regulatory and coding sequences of TRNP1 co-evolve with brain size and cortical folding in mammals. 12,	0
92	Evidence for the role of transcription factors in the co-transcriptional regulation of intron retention. **2023**, 24,	0
91	Mitigation of chromosome loss in clinical CRISPR-Cas9-engineered T cells.	0
90	Primate protein-ligand interfaces exhibit significant conservation and unveil human-specific evolutionary drivers. **2023**, 19, e1010966	0
89	Aid or Antagonize: Nuclear Long Noncoding RNAs Regulate Host Responses and Outcomes of Viral Infections. **2023**, 12, 987	0
88	Noncoding RNAs in diabetic nephropathy. **2022**, 2, 39-51	0
87	Cancer Spheroids and Organoids as Novel Tools for Research and Therapy: State of the Art and Challenges to Guide Precision Medicine. **2023**, 12, 1001	0
86	Landscape and significance of human super enhancer-driven core transcription regulatory circuitry. **2023**, 32, 385-401	0
85	SP1 transcriptionally regulates UBE2N expression to promote lung adenocarcinoma progression. **2023**, 4,	0
84	Normal and cancer tissues are accurately characterised by intergenic transcription at RNA polymerase 2 binding sites.	0
83	Epigenomic mapping identifies an enhancer repertoire that regulates cell identity in bladder cancer through distinct transcription factor networks.	0
82	Transcription factor NKX2-1 drives serine and glycine synthesis addiction in cancer.	0
81	Disrupting the phase separation of KAT8-IRF1 diminishes PD-L1 expression and promotes antitumor immunity. **2023**, 4, 382-400	0

80	Longitudinal single-cell profiling of chemotherapy response in acute myeloid leukemia. **2023**, 14,	0
79	Snapshot: a package for clustering and visualizing epigenetic history during cell differentiation. **2023**, 24,	0
78	Dynamics of histone acetylation during human early embryogenesis. **2023**, 9,	0
77	Research trends of omics in ulcerative colitis: A bibliometric analysis. 10,	0
76	Current sequence-based models capture gene expression determinants in promoters but mostly ignore distal enhancers. **2023**, 24,	0
75	Measuring the impact of chromatin context on transcription factor binding affinities.	0
74	Toward a comprehensive catalog of regulatory elements.	0
73	A regulatory variant at 19p13.3 is associated with primary biliary cholangitis risk and ARID3A expression. **2023**, 14,	0
72	BIND&MODIFY: a long-range method for single-molecule mapping of chromatin modifications in eukaryotes. **2023**, 24,	0
71	Massively Parallel Reporter Assays for High-Throughput In Vivo Analysis of Cis-Regulatory Elements. **2023**, 10, 144	0
70	Ornithine aminotransferase supports polyamine synthesis in pancreatic cancer. **2023**, 616, 339-347	0
69	In silico prioritisation of microRNA-associated common variants in multiple sclerosis. **2023**, 17,	0
68	Transfer learning identifies sequence determinants of cell-type specific regulatory element accessibility. **2023**, 5,	0
67	The EN-TEx resource of multi-tissue personal epigenomes´& variant-impact models. **2023**, 186, 1493-1511.e40	
66	Chemical modulation of Schistosoma mansoni lysine specific demethylase 1 (SmLSD1) induces wide-scale biological and epigenomic changes. 8, 146	0
65	Fatty Acid Induced Hypermethylation in the Slc2a4 Gene in Visceral Adipose Tissue Is Associated to Insulin-Resistance and Obesity. **2023**, 24, 6417	0
64	Reprogramming anchorage dependency by adherent-to-suspension transition promotes metastatic dissemination. **2023**, 22,	0
63	Computational approaches for detecting disease-associated alternative splicing events.	0

62	Integration of epigenetic and genetic profiles identifies multiple sclerosis disease-critical cell types and genes. **2023**, 6,	0
61	Recent advances of long non-coding RNAs in control of hepatic gluconeogenesis. 14,	0
60	MYC reshapes CTCF-mediated chromatin architecture in prostate cancer. **2023**, 14,	0
59	Light-activated macromolecular phase separation modulates transcription by reconfiguring chromatin interactions. **2023**, 9,	0
58	A method for extracting effective interactions from Hi-C data with applications to interphase chromosomes and inverted nuclei.	0
57	Genetic impacts on DNA methylation help elucidate regulatory genomic processes.	0
56	Cross-species regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes.	0
55	Detailed profiling with MaChIAto reveals various genomic and epigenomic features affecting the efficacy of knock-out, short homology-based knock-in and Prime Editing.	0
54	Parallel recovery of chromatin accessibility and gene expression dynamics from frozen human regulatory T cells. **2023**, 13,	0
53	NAGS, CPS1, and SLC25A13 (Citrin) at the Crossroads of Arginine and Pyrimidines Metabolism in Tumor Cells. **2023**, 24, 6754	0
52	Male-pattern hair loss: Comprehensive identification of the associated genes as a basis for understanding pathophysiology. **2023**, 35, 3-14	0
51	Connectome and regulatory hubs of CAGE highly active enhancers. **2023**, 13,	0
50	Condensed but liquid-like domain organization of active chromatin regions in living human cells. **2023**, 9,	0
49	Acetylation of histone H2B marks active enhancers and predicts CBP/p300 target genes. **2023**, 55, 679-692	0
48	GWAS for Systemic Sclerosis Identified six novel susceptibility loci including penetrating FcEReceptor Region.	0
47	Identification of Liver Cancer Driver Mutations from COSMIC Data. **2023**, 16,	0
46	Noncoding RNA-chromatin association: Functions and mechanisms. **2023**,	0
45	LncRNA CASC19: a novel oncogene involved in human cancer.	0

44	DNA architectural protein CTCF facilitates subset-specific chromatin interactions to limit the formation of memory CD8+ T´cells. **2023**,	0
43	Understanding cell fate acquisition in stem-cell-derived pancreatic islets using single-cell multiome-inferred regulomes. **2023**,	0
42	MYC activation impairs cell-intrinsic IFN signaling and confers resistance to anti-PD1/PD-L1 therapy in lung cancer. **2023**, 4, 101006	0
41	Dysregulated long non coding RNA as biomarkers for diagnosis of Mesothelioma: A Systematic Review.	0
40	Ancestry-related differences in chromatin accessibility and gene expression of APOE 4 are associated with Alzheimer's disease risk.	0
39	Capture Methylation-Sensitive Restriction Enzyme Sequencing (Capture MRE-Seq) for Methylation Analysis of Highly Degraded DNA Samples. **2023**, 73-89	0
38	Comparative analysis of myoglobin in Cetaceans and humans reveals novel regulatory elements and evolutionary flexibility.	0
37	Functional similarity of non-coding regions is revealed in phylogenetic average motif score representations.	0
36	Animal Transgenesis and Cloning: Combined Development and Future Perspectives. **2023**, 121-149	0
35	Modeling single cell DNA replication dynamics and aneuploidy in genomically unstable cancers.	0
34	The origins and functional effects of postzygotic mutations throughout the human life span. **2023**, 380,	0
33	Chromatin context-dependent regulation and epigenetic manipulation of prime editing.	0
32	Celiac Disease Is a Risk Factor for Mature T and NK Cell Lymphoma: A Mendelian Randomization Study. **2023**, 24, 7216	0
31	From observational to actionable: rethinking omics in biologics production. **2023**,	0
30	The Genetic Heterogeneity of Multimodal Human Brain Age.	0
29	A revamped rat reference genome improves the discovery of genetic diversity in laboratory rats.	0
28	Improved analysis of (e)CLIP data with RCRUNCH yields a compendium of RNA-binding protein binding sites and motifs. **2023**, 24,	0
27	Chromatin structure and context-dependent sequence features control prime editing efficiency.	0

26	Integrative identification of non-coding regulatory regions driving metastatic prostate cancer.	0
25	Haplotype mapping of H3K27me3-associated chromatin interactions defines topological regulation of gene silencing in rice. **2023**, 42, 112350	0
24	A systems biology approach uncovers novel disease mechanisms in age-related macular degeneration. **2023**, 100302	0
23	Gray-Level Co-occurrence Matrix Analysis of Nuclear Textural Patterns in Laryngeal Squamous Cell Carcinoma: Focus on Artificial Intelligence Methods.	0
22	Genome-Wide Principles of Gene Regulation. **2023**, 145-159	0
21	Nucleosome reorganisation in breast cancer tissues.	0
20	Association ofACE Gene Polymorphisms with In-Stent Restenosis by Stent Type (Biomime, Supraflex, Xience).	0
19	Mapping genomic regulation of kidney disease and traits through high-resolution and interpretable eQTLs. **2023**, 14,	0
18	Hsa_circ_0105040 promotes Cutbacterium acnes biofilm induced inflammatory via sponge miR-146a in human keratinocyte.	0
17	The landscape of exosomal non-coding RNAs in breast cancer drug resistance, focusing on underlying molecular mechanisms. 14,	0
16	Circ_0067934 as a novel therapeutic target in cancer: From mechanistic to clinical perspectives. **2023**, 154469	0
15	Experimental Validation and Prediction of Super-Enhancers: Advances and Challenges. **2023**, 12, 1191	0
14	Multi-omics data of gastric cancer cell lines. **2023**, 24,	0
13	MyBrain-Seq: A Pipeline for MiRNA-Seq Data Analysis in Neuropsychiatric Disorders. **2023**, 11, 1230	0
12	Systematic elucidation of genetic mechanisms underlying cholesterol uptake. **2023**, 100304	0
11	Genome-wide cross-trait analysis and Mendelian randomization reveal a shared genetic etiology and causality between COVID-19 and venous thromboembolism. **2023**, 6,	0
10	Evaluating The Infinium Human MethylationEPIC v2 BeadChip.	0
9	The Principles and Applications of High-Throughput Sequencing Technologies. **2023**, 27, 9-24	0

8	Transcription factor binding site orientation and order are major drivers of gene regulatory activity. **2023**, 14,	0
7	Critical Considerations for Investigating MicroRNAs during Tumorigenesis: A Case Study in Conceptual and Contextual Nuances of miR-211-5p in Melanoma. **2023**, 7, 9	0
6	The HIV-1 Capsid-Targeted Inhibitor GSK878 Alters Selection of Target Sites for HIV DNA Integration.	0
5	Discovery of 36 loci significantly associated with stuttering.	0
4	Esrrb guides naive pluripotent cells through the formative transcriptional programme. **2023**, 25, 643-657	0
3	Identification of lncRNAs involved in response to ionizing radiation in fibroblasts of long-term survivors of childhood cancer and cancer-free controls. 13,	0
2	Mapping PTBP2 binding in human brain identifies SYNGAP1 as a target for therapeutic splice switching. **2023**, 14,	0
1	Epigenomic profiling at genome scale: from assays and analysis to clinical insights. **2023**, 143-174	0