

CITATION REPORT

List of articles citing

Variation in transcription factor binding among humans

DOI: 10.1126/science.1183621
Science, 2010, 328, 232-5.

Source: <https://exaly.com/paper-pdf/49270671/citation-report.pdf>

Version: 2024-04-23

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

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

#	Paper	IF	Citations
497	Is transcription factor binding site turnover a sufficient explanation for cis-regulatory sequence divergence?. 2010 , 2, 851-8		20
496	Early Career Research Award Lecture. Structure, evolution and dynamics of transcriptional regulatory networks. 2010 , 38, 1155-78		18
495	Transcription factor binding variation in the evolution of gene regulation. 2010 , 26, 468-75		48
494	Evolution of transcription networks--lessons from yeasts. 2010 , 20, R746-53		78
493	The Notch/Hes1 pathway sustains NF- κ B activation through CYLD repression in T cell leukemia. 2010 , 18, 268-81		214
492	Genes, mutations, and human inherited disease at the dawn of the age of personalized genomics. 2010 , 31, 631-55		138
491	Palate morphogenesis: current understanding and future directions. 2010 , 90, 133-54		48
490	Transcriptional and translational control of C/EBPs: the case for "deep" genetics to understand physiological function. 2010 , 32, 680-6		22
489	Next-generation genomics: an integrative approach. 2010 , 11, 476-86		488
488	Genome-wide allele-specific analysis: insights into regulatory variation. 2010 , 11, 533-8		220
487	Evolutionary history of regulatory variation in human populations. 2010 , 19, R197-203		10
486	Identification of epistatic effects using a protein-protein interaction database. 2010 , 19, 4345-52		21
485	Allele-specific DNA methylation: beyond imprinting. 2010 , 19, R210-20		118
484	Experimental strategies for studying transcription factor-DNA binding specificities. 2010 , 9, 362-73		52
483	Evolution of Plant Homeobox Genes. 2010 ,		1
482	Allele-specific and heritable chromatin signatures in humans. 2010 , 19, R204-9		24
481	Coevolution within a transcriptional network by compensatory trans and cis mutations. <i>Genome Research</i> , 2010 , 20, 1672-8	9.7	58

480	Illuminating transcription pathways using fluorescent reporter genes and yeast functional genomics. 2010 , 1, 76-80		3
479	Differential expression analysis for sequence count data. <i>Genome Biology</i> , 2010 , 11, R106	18.3	9952
478	Analysis of active and inactive X chromosome architecture reveals the independent organization of 30 nm and large-scale chromatin structures. 2010 , 40, 397-409		57
477	Production of erythroid cells from human embryonic stem cells (hESC) and human induced pluripotent stem cells (hiPS). 2010 , 17, 104-9		22
476	Uncovering the roles of rare variants in common disease through whole-genome sequencing. 2010 , 11, 415-25		1082
475	Dramatic changes in transcription factor binding over evolutionary time. <i>Genome Biology</i> , 2010 , 11, 122	18.3	7
474	AlleleSeq: analysis of allele-specific expression and binding in a network framework. 2011 , 7, 522		228
473	DNA methylation patterns associate with genetic and gene expression variation in HapMap cell lines. <i>Genome Biology</i> , 2011 , 12, R10	18.3	651
472	Pol III binding in six mammals shows conservation among amino acid isotypes despite divergence among tRNA genes. 2011 , 43, 948-55		67
471	Identification of Transcription Factor-DNA Interactions In Vivo. 2011 , 52, 175-91		5
470	Isochores and the regulation of gene expression in the human genome. 2011 , 3, 1080-9		24
469	A Handbook of Transcription Factors. 2011 ,		11
468	Epstein-Barr virus exploits intrinsic B-lymphocyte transcription programs to achieve immortal cell growth. 2011 , 108, 14902-7		146
467	Bioinformatics challenges for personalized medicine. 2011 , 27, 1741-8		173
466	Integrated approaches reveal determinants of genome-wide binding and function of the transcription factor Pho4. 2011 , 42, 826-36		80
465	Complex systems, evolution, and animal models. 2011 , 42, 542-4		6
464	Regulatory variation within and between species. 2011 , 12, 327-46		52
463	Extensive characterization of NF- κ B binding uncovers non-canonical motifs and advances the interpretation of genetic functional traits. <i>Genome Biology</i> , 2011 , 12, R70	18.3	110

462	A user guide to the encyclopedia of DNA elements (ENCODE). 2011 , 9, e1001046		1060
461	T2DM: Why Epigenetics?. 2011 , 2011, 647514		21
460	Lessons from chimpanzee-based research on human disease: the implications of genetic differences. 2011 , 39, 527-40		15
459	dPORE-miRNA: polymorphic regulation of microRNA genes. <i>PLoS ONE</i> , 2011 , 6, e16657	3-7	29
458	A computational framework discovers new copy number variants with functional importance. <i>PLoS ONE</i> , 2011 , 6, e17539	3-7	14
457	Frontiers in DNA Sequencing: the (R)Evolution of Sequencing Technologies. 2011 ,		
456	Inferring regulatory mechanisms from patterns of evolutionary divergence. 2011 , 7, 530		25
455	Chromatin architecture and the regulation of nuclear receptor inducible transcription. 2011 , 23, 94-106		13
454	Association genetics of complex traits in plants. 2011 , 189, 909-922		218
453	Association of a functional variant downstream of TNFAIP3 with systemic lupus erythematosus. 2011 , 43, 253-8		208
452	High conservation of transcription factor binding and evidence for combinatorial regulation across six <i>Drosophila</i> species. 2011 , 43, 414-20		102
451	The importance of phase information for human genomics. 2011 , 12, 215-23		210
450	Heart failure: advances through genomics. 2011 , 12, 357-62		55
449	Genomic views of STAT function in CD4+ T helper cell differentiation. 2011 , 11, 239-50		213
448	Mapping and analysis of chromatin state dynamics in nine human cell types. 2011 , 473, 43-9		2153
447	A twin approach to unraveling epigenetics. 2011 , 27, 116-25		268
446	Chromatin and heritability: how epigenetic studies can complement genetic approaches. 2011 , 27, 172-6		18
445	Epigenomics of human embryonic stem cells and induced pluripotent stem cells: insights into pluripotency and implications for disease. 2011 , 3, 36		39

444	Identification and regulation of c-Myb target genes in MCF-7 cells. 2011 , 11, 30		62
443	Assessing quality and completeness of human transcriptional regulatory pathways on a genome-wide scale. 2011 , 6, 15		44
442	The institutional review board is an impediment to human research: the result is more animal-based research. 2011 , 6, 12		11
441	Divergence in cis-regulatory sequences surrounding the opsin gene arrays of African cichlid fishes. 2011 , 11, 120		28
440	ChIP-chip versus ChIP-seq: lessons for experimental design and data analysis. 2011 , 12, 134		103
439	Cross species comparison of C/EBP β and PPAR α profiles in mouse and human adipocytes reveals interdependent retention of binding sites. 2011 , 12, 152		74
438	Identifying functional single nucleotide polymorphisms in the human CAzome. 2011 , 43, 1038-48		38
437	Genome-wide identification of conserved regulatory function in diverged sequences. <i>Genome Research</i> , 2011 , 21, 1139-49	9.7	54
436	Association of -27T>C and its haplotype at the putative promoter for IgA-specific receptor gene with IgA nephropathy among the Chinese Han population. 2011 , 26, 2537-44		1
435	Intraspecific phenotypic variation in deer: the role of genetic and epigenetic processes. 2011 , 51, 365		8
434	MPromDb update 2010: an integrated resource for annotation and visualization of mammalian gene promoters and ChIP-seq experimental data. <i>Nucleic Acids Research</i> , 2011 , 39, D92-7	20.1	31
433	What fraction of the human genome is functional?. <i>Genome Research</i> , 2011 , 21, 1769-76	9.7	104
432	Allele-specific distribution of RNA polymerase II on female X chromosomes. 2011 , 20, 3964-73		25
431	Notice of Retraction: Dynamic Nucleosome Positioning around Functional Transcription Factor Binding Sites in the Promoters of Inducible NF-kappaB Target Genes. 2011 ,		
430	Classification and clustering of sequencing data using a Poisson model. 2011 , 5,		97
429	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. <i>Nucleic Acids Research</i> , 2011 , 39, 7058-76	20.1	58
428	Whole-genome analysis reveals that active heat shock factor binding sites are mostly associated with non-heat shock genes in <i>Drosophila melanogaster</i> . <i>PLoS ONE</i> , 2011 , 6, e15934	3.7	57
427	De novo genesis of enhancers in vertebrates. 2011 , 9, e1001188		42

426	Relating CNVs to transcriptome data at fine resolution: assessment of the effect of variant size, type, and overlap with functional regions. <i>Genome Research</i> , 2011 , 21, 2004-13	9.7	80
425	Strategic approaches to unraveling genetic causes of cardiovascular diseases. 2011 , 108, 1252-69		68
424	CpG deamination creates transcription factor-binding sites with high efficiency. 2011 , 3, 1304-11		31
423	Targeted isolation of cloned genomic regions by recombineering for haplotype phasing and isogenic targeting. <i>Nucleic Acids Research</i> , 2011 , 39, e137	20.1	13
422	Cooperative transcription factor associations discovered using regulatory variation. 2011 , 108, 13353-8		38
421	Mapping personal functional data to personal genomes. 2011 , 27, 3427-9		5
420	Modularity of CHIP/LDB transcription complexes regulates cell differentiation. 2011 , 5, 200-5		10
419	Genomic analysis reveals a novel nuclear factor- κ B (NF- κ B)-binding site in Alu-repetitive elements. 2011 , 286, 38768-38782		44
418	Prediction of regulatory interactions from genome sequences using a biophysical model for the Arabidopsis LEAFY transcription factor. 2011 , 23, 1293-306		124
417	Gene regulatory networks and the role of robustness and stochasticity in the control of gene expression. <i>Genome Research</i> , 2011 , 21, 645-57	9.7	209
416	Canonical NF- κ B activation is essential for Epstein-Barr virus latent membrane protein 1 TES2/CTAR2 gene regulation. 2011 , 85, 6764-73		31
415	Dynamic chromatin localization of Sirt6 shapes stress- and aging-related transcriptional networks. <i>PLoS Genetics</i> , 2011 , 7, e1002153	6	71
414	Proteome-wide analysis of disease-associated SNPs that show allele-specific transcription factor binding. <i>PLoS Genetics</i> , 2012 , 8, e1002982	6	74
413	Evidence for positive selection on a number of MicroRNA regulatory interactions during recent human evolution. <i>PLoS Genetics</i> , 2012 , 8, e1002578	6	52
412	Genetics and regulatory impact of alternative polyadenylation in human B-lymphoblastoid cells. <i>PLoS Genetics</i> , 2012 , 8, e1002882	6	39
411	DNA breathing dynamics distinguish binding from nonbinding consensus sites for transcription factor YY1 in cells. <i>Nucleic Acids Research</i> , 2012 , 40, 10116-23	20.1	29
410	Widespread site-dependent buffering of human regulatory polymorphism. <i>PLoS Genetics</i> , 2012 , 8, e1002599		53
409	The contribution of RNA decay quantitative trait loci to inter-individual variation in steady-state gene expression levels. <i>PLoS Genetics</i> , 2012 , 8, e1003000	6	80

408	A genome-wide screen for genetic variants that modify the recruitment of REST to its target genes. <i>PLoS Genetics</i> , 2012 , 8, e1002624	6	15
407	Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , 2012 , 22, 1790-7	9.7	1723
406	Genome-wide siRNA screen for mediators of NF- κ B activation. 2012 , 109, 2467-72		80
405	Animal models in an age of personalized medicine. 2012 , 9, 47-64		14
404	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , 2012 , 22, 1748-59	9.7	538
403	Cistrome plasticity and mechanisms of cistrome reprogramming. 2012 , 11, 3199-210		6
402	KLF15 negatively regulates estrogen-induced epithelial cell proliferation by inhibition of DNA replication licensing. 2012 , 109, E1334-43		69
401	Evolutionary conservation of histone modifications in mammals. 2012 , 29, 1757-67		37
400	Massively parallel measurements of molecular interaction kinetics on a microfluidic platform. 2012 , 109, 16540-5		75
399	Modulation of NF- κ B-dependent gene transcription using programmable DNA minor groove binders. 2012 , 109, 1023-8		104
398	Dynamic regulation of glucocorticoid signalling in health and disease. 2012 , 51, 403-12		89
397	The value of twins in epigenetic epidemiology. 2012 , 41, 140-50		73
396	A role of genomic copy number variation in the complex behavioral phenotype of alcohol dependence: a commentary. 2012 , 36, 1483-6		
395	An atlas of the Epstein-Barr virus transcriptome and epigenome reveals host-virus regulatory interactions. 2012 , 12, 233-45		175
394	Interpreting noncoding genetic variation in complex traits and human disease. 2012 , 30, 1095-106		347
393	Whole-genome and whole-exome sequencing in neurological diseases. 2012 , 8, 508-17		79
392	Using epigenetic mechanisms to understand the impact of common disease causing alleles. 2012 , 24, 558-63		19
391	Dissecting the regulatory architecture of gene expression QTLs. <i>Genome Biology</i> , 2012 , 13, R7	18.3	151

390	DNA methylation studies using twins: what are they telling us?. <i>Genome Biology</i> , 2012 , 13, 172	18.3	56
389	Analysis of variation at transcription factor binding sites in Drosophila and humans. <i>Genome Biology</i> , 2012 , 13, R49	18.3	71
388	Functional analysis of transcription factor binding sites in human promoters. <i>Genome Biology</i> , 2012 , 13, R50	18.3	110
387	Genome-wide localization of replication factors. 2012 , 57, 187-95		14
386	DNase I sensitivity QTLs are a major determinant of human expression variation. 2012 , 482, 390-4		479
385	A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals. 2012 , 47, 810-22		299
384	Population genetics of cis-regulatory sequences that operate during embryonic development in the sea urchin <i>Strongylocentrotus purpuratus</i> . 2012 , 14, 152-67		18
383	A role for CTCF and cohesin in subtelomere chromatin organization, TERRA transcription, and telomere end protection. 2012 , 31, 4165-78		115
382	Personal omics profiling reveals dynamic molecular and medical phenotypes. 2012 , 148, 1293-307		921
381	Normalization of ChIP-seq data with control. 2012 , 13, 199		76
380	Simultaneous SNP identification and assessment of allele-specific bias from ChIP-seq data. 2012 , 13, 46		29
379	Sequencing and analysis of a South Asian-Indian personal genome. 2012 , 13, 440		23
378	Epigenetic Epidemiology of Cancer. 2012 , 225-267		
377	ChIP-seq and beyond: new and improved methodologies to detect and characterize protein-DNA interactions. 2012 , 13, 840-52		524
376	Overexpression of androgen receptor enhances the binding of the receptor to the chromatin in prostate cancer. 2012 , 31, 2153-63		100
375	Architecture of the human regulatory network derived from ENCODE data. 2012 , 489, 91-100		1104
374	Sef is an inhibitor of proinflammatory cytokine signaling, acting by cytoplasmic sequestration of NF- κ B. 2012 , 23, 611-23		22
373	Localized and temporal gene regulation in heart development. 2012 , 100, 171-201		8

372	Isochores. 2012,		2
371	Genome-Wide Mapping of Protein-DNA Interactions by ChIP-Seq. 2012, 139-151		1
370	Integrative functional genomics identifies an enhancer looping to the SOX9 gene disrupted by the 17q24.3 prostate cancer risk locus. <i>Genome Research</i> , 2012, 22, 1437-46	9.7	107
369	Tumors of the Central Nervous System, Volume 5. 2012,		
368	New methods for separating causes from effects in genomics data. 2012, 13 Suppl 8, S22		16
367	iASeq: integrative analysis of allele-specificity of protein-DNA interactions in multiple ChIP-seq datasets. 2012, 13, 681		20
366	RNA-Seq approach for genetic improvement of meat quality in pig and evolutionary insight into the substrate specificity of animal carbonyl reductases. <i>PLoS ONE</i> , 2012, 7, e42198	3.7	32
365	Mutations and binding sites of human transcription factors. <i>Frontiers in Genetics</i> , 2012, 3, 100	4.5	8
364	Transcription factor binding at enhancers: shaping a genomic regulatory landscape in flux. <i>Frontiers in Genetics</i> , 2012, 3, 195	4.5	29
363	Principles of dimer-specific gene regulation revealed by a comprehensive characterization of NF-B family DNA binding. 2011, 13, 95-102		143
362	Detecting differential binding of transcription factors with ChIP-seq. 2012, 28, 121-2		94
361	Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. 2011, 30, 90-8		447
360	Human genomic disease variants: a neutral evolutionary explanation. <i>Genome Research</i> , 2012, 22, 1383-94	9.7	32
359	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. <i>Genome Research</i> , 2012, 22, 860-9	9.7	113
358	Comparative studies of gene expression and the evolution of gene regulation. 2012, 13, 505-16		272
357	Genomic approaches towards finding cis-regulatory modules in animals. 2012, 13, 469-83		156
356	Epigenetic and genetic disturbance of the imprinted 11p15 region in Beckwith-Wiedemann and Silver-Russell syndromes. 2012, 81, 350-61		52
355	Cis-regulatory elements: molecular mechanisms and evolutionary processes underlying divergence. 2011, 13, 59-69		561

354	Cellular genomics for complex traits. 2012 , 13, 215-20		32
353	Resolving the variable genome and epigenome in human disease. 2012 , 271, 379-91		13
352	It takes two to tango: IBs, the multifunctional partners of NF- κ B. 2012 , 246, 59-76		109
351	Exome and genome analysis as a tool for disease identification and treatment: the 2011 Human Genome Variation Society scientific meeting. 2012 , 33, 586-90		8
350	The B cell transcription program mediates hypomethylation and overexpression of key genes in Epstein-Barr virus-associated proliferative conversion. <i>Genome Biology</i> , 2013 , 14, R3	18.3	42
349	Research progress in allele-specific expression and its regulatory mechanisms. 2013 , 54, 271-83		31
348	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. 2013 , 154, 530-40		107
347	H ₂ O ₂ in the induction of NF- κ B-dependent selective gene expression. 2013 , 528, 173-88		10
346	Computational methodology for ChIP-seq analysis. 2013 , 1, 54-70		20
345	Systems Biology. 2013 ,		8
344	Selection and adaptation in the human genome. 2013 , 14, 467-89		90
343	NBPF is a potential DNA-binding transcription factor that is directly regulated by NF- κ B. 2013 , 45, 2479-90		21
342	Functional Genomics, Proteomics, Metabolomics and Bioinformatics for Systems Biology. 2013 , 3-41		4
341	Impacts of variation in the human genome on gene regulation. 2013 , 425, 3970-7		97
340	Identification of transcription factor binding sites from ChIP-seq data at high resolution. 2013 , 29, 2705-13		45
339	Androgen regulation of the TMPRSS2 gene and the effect of a SNP in an androgen response element. 2013 , 27, 2028-40		85
338	Coordinated effects of sequence variation on DNA binding, chromatin structure, and transcription. <i>Science</i> , 2013 , 342, 744-7	33.3	278
337	Extensive variation in chromatin states across humans. <i>Science</i> , 2013 , 342, 750-2	33.3	276

336	Effect of natural genetic variation on enhancer selection and function. 2013 , 503, 487-92	241
335	Beyond the ENCODE project: using genomics and epigenomics strategies to study enhancer evolution. 2013 , 368, 20130022	14
334	A novel test for selection on cis-regulatory elements reveals positive and negative selection acting on mammalian transcriptional enhancers. 2013 , 30, 2509-18	19
333	ChIP-seq in steatohepatitis and normal liver tissue identifies candidate disease mechanisms related to progression to cancer. 2013 , 6, 50	8
332	Cancer omics: from regulatory networks to clinical outcomes. 2013 , 340, 277-83	9
331	The Human Genome: A Window on Human Genetics, Biology, and Medicine. 2013 , 4-27	1
330	Deciphering the transcriptional cis-regulatory code. 2013 , 29, 11-22	83
329	Chromatin Structure and Human Genome Evolution. 2013 ,	
328	High-throughput sequencing for biology and medicine. 2013 , 9, 640	186
327	Child development and structural variation in the human genome. 2013 , 84, 34-48	17
326	Studying the evolution of transcription factor binding events using multi-species ChIP-Seq data. 2013 , 12, 1-15	3
325	The genome-wide landscape of copy number variations in the MUSGEN study provides evidence for a founder effect in the isolated Finnish population. 2013 , 21, 1411-6	10
324	miRNA regulatory variation in human evolution. 2013 , 29, 116-24	32
323	Analysis of sequence variation underlying tissue-specific transcription factor binding and gene expression. 2013 , 34, 1140-8	10
322	Genome-wide profiling of human cap-independent translation-enhancing elements. 2013 , 10, 747-50	22
321	Genome-wide inference of natural selection on human transcription factor binding sites. 2013 , 45, 723-9	95
320	Characterization of genome-wide binding of NF- κ B in TNF β -stimulated HeLa cells. 2013 , 526, 142-9	23
319	Genome-wide copy number variation analysis in extended families and unrelated individuals characterized for musical aptitude and creativity in music. <i>PLoS ONE</i> , 2013 , 8, e56356	3.7 52

318	Mapping the Functional Genome. 2013 , 28-40		1
317	Variation and genetic control of protein abundance in humans. 2013 , 499, 79-82		272
316	Subset of genes targeted by transcription factor NF- κ B in TNF α -stimulated human HeLa cells. 2013 , 13, 143-54		15
315	STAT3 targets suggest mechanisms of aggressive tumorigenesis in diffuse large B-cell lymphoma. 2013 , 3, 2173-85		24
314	Causes and consequences of chromatin variation between inbred mice. <i>PLoS Genetics</i> , 2013 , 9, e10035706		16
313	Robust prediction of expression differences among human individuals using only genotype information. <i>PLoS Genetics</i> , 2013 , 9, e1003396	6	30
312	Genetic landscape of open chromatin in yeast. <i>PLoS Genetics</i> , 2013 , 9, e1003229	6	18
311	The next generation of transcription factor binding site prediction. <i>PLoS Computational Biology</i> , 2013 , 9, e1003214	5	118
310	Understanding variation in transcription factor binding by modeling transcription factor genome-epigenome interactions. <i>PLoS Computational Biology</i> , 2013 , 9, e1003367	5	23
309	Global properties and functional complexity of human gene regulatory variation. <i>PLoS Genetics</i> , 2013 , 9, e1003501	6	47
308	Extensive divergence of transcription factor binding in <i>Drosophila</i> embryos with highly conserved gene expression. <i>PLoS Genetics</i> , 2013 , 9, e1003748	6	70
307	Junk DNA. 2013 , 149		
306	Arpeggio: harmonic compression of ChIP-seq data reveals protein-chromatin interaction signatures. <i>Nucleic Acids Research</i> , 2013 , 41, e161	20.1	5
305	From remote enhancers to gene regulation: charting the genome's regulatory landscapes. 2013 , 368, 20120358		26
304	Towards an understanding of cell-specific functions of signal-dependent transcription factors. 2013 , 51, T37-50		24
303	Insights into the genetic basis of type 2 diabetes. 2013 , 4, 233-44		44
302	Systematic functional regulatory assessment of disease-associated variants. 2013 , 110, 9607-12		75
301	AHT-ChIP-seq: a completely automated robotic protocol for high-throughput chromatin immunoprecipitation. <i>Genome Biology</i> , 2013 , 14, R124	18.3	24

300	jMOSAICS: joint analysis of multiple ChIP-seq datasets. <i>Genome Biology</i> , 2013 , 14, R38	18.3	42
299	Genetic, functional and molecular features of glucocorticoid receptor binding. <i>PLoS ONE</i> , 2013 , 8, e61654	4.7	20
298	Detection of regulatory SNPs in human genome using ChIP-seq ENCODE data. <i>PLoS ONE</i> , 2013 , 8, e78833	3.7	39
297	Animal Models in Drug Development. 2013 ,		6
296	Evidence for site-specific occupancy of the mitochondrial genome by nuclear transcription factors. <i>PLoS ONE</i> , 2014 , 9, e84713	3.7	25
295	C26 cancer-induced muscle wasting is IKK β -dependent and NF-kappaB-independent. <i>PLoS ONE</i> , 2014 , 9, e87776	3.7	29
294	A comprehensive association analysis confirms ZMIZ1 to be a susceptibility gene for vitiligo in Chinese population. 2014 , 51, 345-53		15
293	Genomic mapping of the MHC transactivator CIITA using an integrated ChIP-seq and genetical genomics approach. <i>Genome Biology</i> , 2014 , 15, 494	18.3	26
292	Approaches for establishing the function of regulatory genetic variants involved in disease. 2014 , 6, 92		31
291	De novo prediction of cis-regulatory elements and modules through integrative analysis of a large number of ChIP datasets. 2014 , 15, 1047		9
290	dCaP: detecting differential binding events in multiple conditions and proteins. 2014 , 15 Suppl 9, S12		3
289	Integrative genomics and transcriptomics analysis of human embryonic and induced pluripotent stem cells. 2014 , 7, 32		2
288	SNP-guided identification of monoallelic DNA-methylation events from enrichment-based sequencing data. <i>Nucleic Acids Research</i> , 2014 , 42, e157	20.1	5
287	MYC cofactors: molecular switches controlling diverse biological outcomes. 2014 , 4, a014399		37
286	Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association. <i>PLoS Genetics</i> , 2014 , 10, e1004122	6	26
285	A symbiotic liaison between the genetic and epigenetic code. <i>Frontiers in Genetics</i> , 2014 , 5, 113	4.5	20
284	Quantitative genetics of CTCF binding reveal local sequence effects and different modes of X-chromosome association. <i>PLoS Genetics</i> , 2014 , 10, e1004798	6	38
283	Tracing the evolution of lineage-specific transcription factor binding sites in a birth-death framework. <i>PLoS Computational Biology</i> , 2014 , 10, e1003771	5	15

282	Divergence in a master variator generates distinct phenotypes and transcriptional responses. 2014 , 28, 409-21		12
281	The transcription factor p53: not a repressor, solely an activator. 2014 , 13, 3037-58		84
280	Minireview: Conversing with chromatin: the language of nuclear receptors. 2014 , 28, 3-15		12
279	Regulatory Variants and Disease: The E-Cadherin -160C/A SNP as an Example. 2014 , 2014, 967565		25
278	The NF- κ B genomic landscape in lymphoblastoid B cells. 2014 , 8, 1595-606		112
277	Molecular network of ChIP-Seq-based NF- κ B p65 target genes involves diverse immune functions relevant to the immunopathogenesis of multiple sclerosis. 2014 , 3, 94-106		15
276	Evolution of transcription factor binding in metazoans - mechanisms and functional implications. 2014 , 15, 221-33		143
275	Laying a solid foundation for Manhattan--Getting the functional basis for the post-GWAS era 2014 , 30, 140-9		68
274	Common genetic variants modulate pathogen-sensing responses in human dendritic cells. <i>Science</i> , 2014 , 343, 1246980	33.3	309
273	ISMARA: automated modeling of genomic signals as a democracy of regulatory motifs. <i>Genome Research</i> , 2014 , 24, 869-84	9.7	163
272	Identification and removal of low-complexity sites in allele-specific analysis of ChIP-seq data. 2014 , 30, 165-71		17
271	Genomics meets proteomics: identifying the culprits in disease. 2014 , 133, 689-700		16
270	Relative specificity: all substrates are not created equal. 2014 , 12, 1-7		1
269	Transcriptome sequencing of Chinese and Caucasian population identifies ethnic-associated differential transcript abundance of heterogeneous nuclear ribonucleoprotein K (hnRNPK). 2014 , 103, 56-64		19
268	Principles of regulatory information conservation between mouse and human. 2014 , 515, 371-375		190
267	Spurious transcription factor binding: non-functional or genetically redundant?. 2014 , 36, 798-806		50
266	Whole-genome haplotyping approaches and genomic medicine. 2014 , 6, 73		45
265	DNA recombination. Recombination initiation maps of individual human genomes. <i>Science</i> , 2014 , 346, 1256442	33.3	179

264	The Regulation of Gene Expression. 2014 , 129-208		
263	Cis-regulatory elements and human evolution. 2014 , 29, 81-9		24
262	The role of genetics and epigenetics in the pathogenesis of systemic sclerosis. 2014 , 10, 671-81		85
261	Widespread contribution of transposable elements to the innovation of gene regulatory networks. <i>Genome Research</i> , 2014 , 24, 1963-76	9.7	251
260	Genetic variants within the second intron of the KCNQ1 gene affect CTCF binding and confer a risk of Beckwith-Wiedemann syndrome upon maternal transmission. 2014 , 51, 502-11		12
259	A statistical framework for power calculations in ChIP-seq experiments. 2014 , 30, 753-60		11
258	Leveraging biological replicates to improve analysis in ChIP-seq experiments. 2014 , 9, e201401002		33
257	Natural variation of histone modification and its impact on gene expression in the rat genome. <i>Genome Research</i> , 2014 , 24, 942-53	9.7	42
256	Hemophilia B Leyden and once mysterious cis-regulatory mutations. 2014 , 30, 18-23		18
255	Hormones, Intrauterine Health and Programming. <i>Research and Perspectives in Endocrine Interactions</i> , 2014 ,		
254	Protein-protein interactions and genetic diseases: The interactome. 2014 , 1842, 1971-1980		75
253	Regulatory divergence of X-linked genes and hybrid male sterility in mice. 2014 , 89, 99-108		8
252	WAVELET-BASED GENETIC ASSOCIATION ANALYSIS OF FUNCTIONAL PHENOTYPES ARISING FROM HIGH-THROUGHPUT SEQUENCING ASSAYS. 2015 , 9, 655-686		18
251	Integrative Analysis of Multiple CHIP-X Data Sets Using Correlation Motifs. 110-132		
250	Cis-regulatory somatic mutations and gene-expression alteration in B-cell lymphomas. <i>Genome Biology</i> , 2015 , 16, 84	18.3	33
249	Common Regulatory Variants of CYFIP1 Contribute to Susceptibility for Autism Spectrum Disorder (ASD) and Classical Autism. 2015 , 79, 329-340		29
248	Mechanisms of mutational robustness in transcriptional regulation. <i>Frontiers in Genetics</i> , 2015 , 6, 322	4.5	41
247	Examining the role of components of Slc11a1 (Nramp1) in the susceptibility of New Zealand sea lions (<i>Phocartos hookeri</i>) to disease. <i>PLoS ONE</i> , 2015 , 10, e0122703	3.7	3

246	Characterization and identification of hidden rare variants in the human genome. 2015 , 16, 340		17
245	Differences in Histone Modifications Between Individuals. 2015 , 55-82		
244	BinDNase: a discriminatory approach for transcription factor binding prediction using DNase I hypersensitivity data. 2015 , 31, 2852-9		40
243	quantro: a data-driven approach to guide the choice of an appropriate normalization method. <i>Genome Biology</i> , 2015 , 16, 117	18.3	54
242	The selection and function of cell type-specific enhancers. 2015 , 16, 144-54		573
241	The Activation of IL-1-Induced Enhancers Depends on TAK1 Kinase Activity and NF- κ B p65. 2015 , 10, 726-739		29
240	Identification of altered cis-regulatory elements in human disease. 2015 , 31, 67-76		77
239	Lagging-strand replication shapes the mutational landscape of the genome. 2015 , 518, 502-506		156
238	Analysis of genome-wide RNA-sequencing data suggests age of the CEPH/Utah (CEU) lymphoblastoid cell lines systematically biases gene expression profiles. 2015 , 5, 7960		12
237	A framework for incorporating evolutionary genomics into biodiversity conservation and management. 2015 , 2,		110
236	The role of regulatory variation in complex traits and disease. 2015 , 16, 197-212		577
235	Pervasive variation of transcription factor orthologs contributes to regulatory network evolution. <i>PLoS Genetics</i> , 2015 , 11, e1005011	6	13
234	The genetic and mechanistic basis for variation in gene regulation. <i>PLoS Genetics</i> , 2015 , 11, e1004857	6	96
233	A SNP in the HTT promoter alters NF- κ B binding and is a bidirectional genetic modifier of Huntington disease. 2015 , 18, 807-16		70
232	Identifying causal regulatory SNPs in ChIP-seq enhancers. <i>Nucleic Acids Research</i> , 2015 , 43, 225-36	20.1	27
231	Role of transcriptional regulation in the evolution of plant phenotype: A dynamic systems approach. 2015 , 244, 1074-1095		12
230	Involvement of RNA Polymerase III in Immune Responses. 2015 , 35, 1848-59		28
229	Sensitive detection of chromatin-altering polymorphisms reveals autoimmune disease mechanisms. 2015 , 12, 458-64		41

228	Regulatory genomics: Combined experimental and computational approaches. 2015 , 51, 334-352		6
227	Genomic approaches for understanding the genetics of complex disease. <i>Genome Research</i> , 2015 , 25, 1432-41	9-7	55
226	Predicting functional regulatory SNPs in the human antimicrobial peptide genes DEFB1 and CAMP in tuberculosis and HIV/AIDS. 2015 , 59 Pt A, 117-25		7
225	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. <i>Genome Research</i> , 2015 , 25, 1610-21	9-7	115
224	Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. 2015 , 47, 1393-401		160
223	Making the case for chromatin profiling: a new tool to investigate the immune-regulatory landscape. 2015 , 15, 585-94		24
222	Mining the coding and non-coding genome for cancer drivers. 2015 , 369, 307-15		9
221	Removing reference mapping biases using limited or no genotype data identifies allelic differences in protein binding at disease-associated loci. 2015 , 8, 43		9
220	Exploiting genomics and natural genetic variation to decode macrophage enhancers. 2015 , 36, 507-18		26
219	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. 2015 , 162, 1039-50		156
218	Populational landscape of INDELS affecting transcription factor-binding sites in humans. 2015 , 16, 536		5
217	JAMM: a peak finder for joint analysis of NGS replicates. 2015 , 31, 48-55		42
216	SMARTS: reconstructing disease response networks from multiple individuals using time series gene expression data. 2015 , 31, 1250-7		12
215	QuASAR: quantitative allele-specific analysis of reads. 2015 , 31, 1235-42		50
214	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. 2015 , 16, 393-412		38
213	Current trend of annotating single nucleotide variation in humans--A case study on SNVrap. 2015 , 79-80, 32-40		9
212	Candidate SNP Markers of Chronopathologies Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. 2016 , 2016, 8642703		12
211	Epigenetic Research of Neurodegenerative Disorders Using Patient iPSC-Based Models. 2016 , 2016, 9464591		12

210	The Future is The Past: Methylation QTLs in Schizophrenia. 2016 , 7,		20
209	The epigenetics of PBC: The link between genetic susceptibility and environment. 2016 , 40, 650-659		22
208	Novel regulatory variant detected on the VKORC1 haplotype that is associated with warfarin dose. 2016 , 17, 1305-14		1
207	In Silico identification of SNP diversity in cultivated and wild tomato species: insight from molecular simulations. 2016 , 6, 38715		14
206	A functional polymorphism located at transcription factor binding sites, rs6695837 near LAMC1 gene, confers risk of colorectal cancer in Chinese populations. 2017 , 38, 177-183		54
205	Pooled ChIP-Seq Links Variation in Transcription Factor Binding to Complex Disease Risk. 2016 , 165, 730-41		67
204	GenomeRunner web server: regulatory similarity and differences define the functional impact of SNP sets. 2016 , 32, 2256-63		25
203	Broken detailed balance at mesoscopic scales in active biological systems. <i>Science</i> , 2016 , 352, 604-7	33.3	150
202	RNA splicing is a primary link between genetic variation and disease. <i>Science</i> , 2016 , 352, 600-4	33.3	357
201	A systematic, large-scale comparison of transcription factor binding site models. 2016 , 17, 388		10
200	Divergence and rewiring of regulatory networks for neural development between human and other species. 2016 , 3, e1231495		4
199	Deep sequencing of 10,000 human genomes. 2016 , 113, 11901-11906		222
198	Genetic and transcriptional analysis of human host response to healthy gut microbiota. 2016 , 1,		24
197	Common genetic variants of GPC1 gene reduce risk of biliary atresia in a Chinese population. 2016 , 51, 1661-4		6
196	The Genetics of Transcription Factor DNA Binding Variation. 2016 , 166, 538-554		201
195	Regulatory elements and genetic variations in periodontal diseases. 2016 , 72, 106-115		9
194	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. <i>Nature Communications</i> , 2016 , 7, 12092	17.4	70
193	Evaluating the impact of single nucleotide variants on transcription factor binding. <i>Nucleic Acids Research</i> , 2016 , 44, 10106-10116	20.1	25

192	Mechanism of allele specific assembly and disruption of master regulator transcription factor complexes of NF-KBp50, NF-KBp65 and HIF1a on a non-coding FAS SNP. 2016 , 1859, 1411-1428		4
191	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
190	High-throughput allele-specific expression across 250 environmental conditions. <i>Genome Research</i> , 2016 , 26, 1627-1638	9.7	56
189	Non-coding single nucleotide variants affecting estrogen receptor binding and activity. 2016 , 8, 128		4
188	Effects of SNPs in the positioning regions of RNA polymerase II on the TBP/promoter affinity in genes of the human circadian clock. 2016 , 6, 759-770		
187	Whole genome sequencing and its applications in medical genetics. 2016 , 4, 115-128		5
186	Principles of microRNA Regulation Revealed Through Modeling microRNA Expression Quantitative Trait Loci. 2016 , 203, 1629-40		15
185	A roadmap of constitutive NF- κ B activity in Hodgkin lymphoma: Dominant roles of p50 and p52 revealed by genome-wide analyses. 2016 , 8, 28		31
184	Fine-mapping cellular QTLs with RASQUAL and ATAC-seq. 2016 , 48, 206-13		119
183	Allele-specific transcription factor binding to common and rare variants associated with disease and gene expression. 2016 , 135, 485-497		32
182	A novel comparative pattern count analysis reveals a chronic ethanol-induced dynamic shift in immediate early NF- κ B genome-wide promoter binding during liver regeneration. 2016 , 12, 1037-56		3
181	BDNF rs6265 methylation and genotype interact on risk for schizophrenia. 2016 , 11, 11-23		40
180	The Role of the Genetic Code in the DNA Methylation Landscape Formation. 2016 , 1-18		0
179	The Effects of Sequence Variation on Genome-wide NRF2 Binding--New Target Genes and Regulatory SNPs. <i>Nucleic Acids Research</i> , 2016 , 44, 1760-75	20.1	25
178	Identifying genetic modulators of the connectivity between transcription factors and their transcriptional targets. 2016 , 113, E1835-43		6
177	Single nucleotide polymorphisms in clinics: Fantasy or reality for cancer?. 2016 , 53, 29-39		49
176	Toward understanding the evolution of vertebrate gene regulatory networks: comparative genomics and epigenomic approaches. 2016 , 15, 315-21		6
175	Association of oligodendrocytes differentiation regulator gene DUSP15 with autism. 2017 , 18, 143-150		8

174	MeCP2 Promotes Gastric Cancer Progression Through Regulating FOXF1/Wnt5a/ECatenin and MYOD1/Caspase-3 Signaling Pathways. 2017 , 16, 87-100		49
173	Combinatorial function of transcription factors and cofactors. 2017 , 43, 73-81		148
172	Identification of novel NF- κ B transcriptional targets in TNF α -treated HeLa and HepG2 cells. 2017 , 41, 555-569		8
171	Global variation in gene expression and the value of diverse sampling. 2017 , 1, 102-108		19
170	The Promoter and Multiple Enhancers of the pou4f3 Gene Regulate Expression in Inner Ear Hair Cells. 2017 , 54, 5414-5426		6
169	Predatory bacteria: a new therapeutic approach for a post-antibiotic era. 2017 , 12, 469-472		18
168	Genetic-epigenetic interactions in cis: a major focus in the post-GWAS era. <i>Genome Biology</i> , 2017 , 18, 120	18.3	76
167	Genes directly regulated by NF- κ B in human hepatocellular carcinoma HepG2. 2017 , 89, 157-170		7
166	A promoter-proximal transcript targeted by genetic polymorphism controls E-cadherin silencing in human cancers. <i>Nature Communications</i> , 2017 , 8, 15622	17.4	21
165	Transcription factor-DNA binding: beyond binding site motifs. 2017 , 43, 110-119		130
164	BEESEM: estimation of binding energy models using HT-SELEX data. 2017 , 33, 2288-2295		21
163	Mining the Unknown: Assigning Function to Noncoding Single Nucleotide Polymorphisms. 2017 , 33, 34-45		60
162	Targeted next generation sequencing of the entire vitamin D receptor gene reveals polymorphisms correlated with vitamin D deficiency among older Filipino women with and without fragility fracture. 2017 , 41, 98-108		4
161	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution. <i>Nature Communications</i> , 2017 , 8, 1092	17.4	31
160	Effects of short indels on protein structure and function in human genomes. 2017 , 7, 9313		30
159	MeCP2, a target of miR-638, facilitates gastric cancer cell proliferation through activation of the MEK1/2-ERK1/2 signaling pathway by upregulating GIT1. 2017 , 6, e368		43
158	Characterization of noncoding regulatory DNA in the human genome. 2017 , 35, 732-746		50
157	Significance of intronic and synonymous MYBPC3 gene variations in hypertrophic cardiomyopathy. 2017 , 8, 94-99		

156	Candidate SNP markers of social dominance, which may affect the affinity of the TATA-binding protein for human gene promoters. 2017 , 7, 523-537		4
155	Candidate SNP Markers of Familial and Sporadic Alzheimer's Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. 2017 , 9, 231		12
154	Implications of DNA Methylation in Parkinson's Disease. 2017 , 10, 225		48
153	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. <i>PLoS Genetics</i> , 2017 , 13, e1006587	6	24
152	Epigenetic regulation of and risk of childhood asthma symptoms. 2017 , 9, 121		17
151	Human Stakeholders and the Use of Animals in Drug Development. 2018 , 123, 3-58		6
150	Integrative omics for health and disease. 2018 , 19, 299-310		402
149	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. 2018 , 17, 116-137		4
148	Massive GGAs in genomic repetitive sequences serve as a nuclear reservoir of NF- κ B. 2018 , 45, 193-203		2
147	T cells are influenced by a long non-coding RNA in the autoimmune associated PTPN2 locus. 2018 , 90, 28-38		16
146	Whole genome variant analysis in three ethnically diverse Indians. 2018 , 40, 497-510		2
145	Principles and methods of in-silico prioritization of non-coding regulatory variants. 2018 , 137, 15-30		17
144	Candidate SNP markers of reproductive potential are predicted by a significant change in the affinity of TATA-binding protein for human gene promoters. 2018 , 19, 0		15
143	Towards a map of cis-regulatory sequences in the human genome. <i>Nucleic Acids Research</i> , 2018 , 46, 5395-5409	7	7
142	Functional Genomics of Host-Microbiome Interactions in Humans. 2018 , 34, 30-40		41
141	Identification of jointly correlated gene sets. 2018 , 16, 1840019		1
140	Exploring the Impact of Single-Nucleotide Polymorphisms on Translation. <i>Frontiers in Genetics</i> , 2018 , 9, 507	4-5	49
139	An integrative approach for building personalized gene regulatory networks for precision medicine. 2018 , 10, 96		19

138	CpG binding protein (CFP1) occupies open chromatin regions of active genes, including enhancers and non-CpG islands. 2018 , 11, 59		9
137	High-throughput characterization of genetic effects on DNA-protein binding and gene transcription. <i>Genome Research</i> , 2018 , 28, 1701-1708	9.7	13
136	Towards a complete map of the human long non-coding RNA transcriptome. 2018 , 19, 535-548		248
135	Variation in Genome-Wide NF- κ B RELA Binding Sites upon Microbial Stimuli and Identification of a Virus Response Profile. 2018 , 201, 1295-1305		10
134	The Epigenetics of Primary Biliary Cholangitis. 2018 , 251-272		
133	minating the Path of Atherosclerosis Progression: Chaos Theory Suggests a Role for Repeats in the Development of Atherosclerotic Vascular Disease. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	12
132	Cis-regulatory determinants of MyoD function. <i>Nucleic Acids Research</i> , 2018 , 46, 7221-7235	20.1	6
131	Direct measurement of pervasive weak repression by microRNAs and their role at the network level. 2018 , 19, 362		7
130	Functional genetic variants can mediate their regulatory effects through alteration of transcription factor binding. <i>Nature Communications</i> , 2019 , 10, 3472	17.4	19
129	The Impact of Population Variation in the Analysis of microRNA Target Sites. 2019 , 5,		3
128	Atheroprotective roles of smooth muscle cell phenotypic modulation and the TCF21 disease gene as revealed by single-cell analysis. 2019 , 25, 1280-1289		198
127	Mechanistic interpretation of non-coding variants for discovering transcriptional regulators of drug response. 2019 , 17, 62		12
126	Single-cell RNA sequencing of a European and an African lymphoblastoid cell line. 2019 , 6, 112		13
125	Genetic diversity underlying behavioral plasticity in human adaptation. 2019 , 250, 41-58		2
124	Association of the Rheumatoid Arthritis Severity Variant rs26232 with the Invasive Activity of Synovial Fibroblasts. 2019 , 8,		2
123	Mechanistic Characterization of Variants Identifies an hnRNP-K-Regulated Transcriptional Enhancer Contributing to SLE Susceptibility. 2019 , 10, 1066		8
122	Evolution and Embryonic Development. 2019 , 93-144		
121	Phylogeny: Craniates to Humans. 2019 , 207-237		

120	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. 2019 , 104, 879-895		21
119	Natural Selection Equally Supports the Human Tendencies in Subordination and Domination: A Genome-Wide Study With Confirmation and Validation in Mice. <i>Frontiers in Genetics</i> , 2019 , 10, 73	4.5	7
118	Gain of transcription factor binding sites is associated to changes in the expression signature of human brain and testis and is correlated to genes with higher expression breadth. 2019 , 62, 526-534		
117	Extensive epigenetic and transcriptomic variability between genetically identical human B-lymphoblastoid cells with implications in pharmacogenomics research. 2019 , 9, 4889		9
116	Mucosal RNA and protein expression as the next frontier in IBS: abnormal function despite morphologically intact small intestinal mucosa. 2019 , 316, G701-G719		4
115	The proinflammatory cytokine TNF α induces DNA demethylation-dependent and -independent activation of expression. 2019 , 294, 6785-6795		10
114	Single Nucleotide Polymorphisms at a Distance from Aryl Hydrocarbon Receptor (AHR) Binding Sites Influence AHR Ligand-Dependent Gene Expression. 2019 , 47, 983-994		3
113	Anchor: trans-cell type prediction of transcription factor binding sites. <i>Genome Research</i> , 2019 , 29, 281-297		30
112	Functional microRNA binding site variants. <i>Molecular Oncology</i> , 2019 , 13, 4-8	7.9	16
111	Simple tricks of convolutional neural network architectures improve DNA-protein binding prediction. 2019 , 35, 1837-1843		15
110	Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences Using Deep Neural Networks. 2020 , 17, 657-667		6
109	pathway mapping identifies wild-type as a targetable metabolic node in gastric cancer. 2020 , 69, 231-242		12
108	Predicting the effects of SNPs on transcription factor binding affinity. 2020 , 36, 364-372		20
107	Insights about collective decision-making at the genetic level. 2020 , 12, 19-24		1
106	MyoD1 suppresses cell migration and invasion by inhibiting FUT4 transcription in human gastric cancer cells. 2020 , 27, 773-784		6
105	Population-scale study of eRNA transcription reveals bipartite functional enhancer architecture. <i>Nature Communications</i> , 2020 , 11, 5963	17.4	13
104	Deep conservation of the enhancer regulatory code in animals. <i>Science</i> , 2020 , 370,	33.3	21
103	Disruptive natural selection by male reproductive potential prevents underexpression of protein-coding genes on the human Y chromosome as a self-domestication syndrome. 2020 , 21, 89		4

102	Ranbow: A fast and accurate method for polyploid haplotype reconstruction. <i>PLoS Computational Biology</i> , 2020 , 16, e1007843	5	11
101	Epigenetic biomarkers and preterm birth. 2020 , 6, dvaa005		6
100	Candidate SNP Markers of Atherogenesis Significantly Shifting the Affinity of TATA-Binding Protein for Human Gene Promoters show stabilizing Natural Selection as a Sum of Neutral Drift Accelerating Atherogenesis and Directional Natural Selection Slowing It. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	2
99	Functional effects of variation in transcription factor binding highlight long-range gene regulation by epromoters. <i>Nucleic Acids Research</i> , 2020 , 48, 2866-2879	20.1	11
98	Upregulation of through NF- κ B and Its Target MiR-1276 Contributed to TNF α -promoted Apoptosis of Cancer Cells Induced by Doxorubicin. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	5
97	-acting variation is common across regulatory layers but is often buffered during embryonic development. <i>Genome Research</i> , 2020 ,	9.7	2
96	Robustness and Evolvability in Transcriptional Regulation. 2021 , 197-219		
95	Conserved regulatory logic at accessible and inaccessible chromatin during the acute inflammatory response in mammals. <i>Nature Communications</i> , 2021 , 12, 567	17.4	5
94	Prioritization of regulatory variants with tissue-specific function in the non-coding regions of human genome. <i>Nucleic Acids Research</i> , 2021 ,	20.1	0
93	GRAFIMO: variant and haplotype aware motif scanning on pangenome graphs.		1
92	Genetic Variants in Transcription Factor Binding Sites in Humans: Triggered by Natural Selection and Triggers of Diseases. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
91	Circadian clock dysfunction in human omental fat links obesity to metabolic inflammation. <i>Nature Communications</i> , 2021 , 12, 2388	17.4	16
90	From bedside to bench: regulation of host factors in SARS-CoV-2 infection. <i>Experimental and Molecular Medicine</i> , 2021 , 53, 483-494	12.8	1
89	Genetic determinants of chromatin reveal prostate cancer risk mediated by context-dependent gene regulation.		0
88	Association between Genetic Variants in , , and Genes and Risk of Childhood Autism Spectrum Disorder. <i>Behavioural Neurology</i> , 2021 , 2021, 4150926	3	1
87	Disruptive Selection of Human Immunostimulatory and Immunosuppressive Genes Both Provokes and Prevents Rheumatoid Arthritis, Respectively, as a Self-Domestication Syndrome. <i>Frontiers in Genetics</i> , 2021 , 12, 610774	4.5	3
86	In Vitro Methods Used to Study DNA \propto Protein Interactions. <i>Biology Bulletin Reviews</i> , 2021 , 11, 344-357	0.9	0
85	Mechanisms of Binding Specificity among bHLH Transcription Factors. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	6

84	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. <i>PLoS Computational Biology</i> , 2021 , 17, e1009444	5	1
83	System drift and speciation. <i>Evolution; International Journal of Organic Evolution</i> , 2021 ,	3.8	2
82	Estimating the functional impact of INDELS in transcription factor binding sites: a genome-wide landscape.		1
81	Deep Sequencing of 10,000 Human Genomes.		4
80	Model-based analysis of polymorphisms in an enhancer reveals cis-regulatory mechanisms.		2
79	System drift and speciation.		8
78	Population-scale study of eRNA transcription reveals bipartite functional enhancer architecture.		6
77	Early origin and deep conservation of enhancers in animals.		1
76	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. <i>PLoS Computational Biology</i> , 2015 , 11, e1004491	5	7
75	Dynamics of Transcription Factor Binding Site Evolution. <i>PLoS Genetics</i> , 2015 , 11, e1005639	6	58
74	A linear model for transcription factor binding affinity prediction in protein binding microarrays. <i>PLoS ONE</i> , 2011 , 6, e20059	3.7	36
73	The genome sequence of the North-European cucumber (<i>Cucumis sativus</i> L.) unravels evolutionary adaptation mechanisms in plants. <i>PLoS ONE</i> , 2011 , 6, e22728	3.7	80
72	Genotype-based test in mapping cis-regulatory variants from allele-specific expression data. <i>PLoS ONE</i> , 2012 , 7, e38667	3.7	6
71	PPARG binding landscapes in macrophages suggest a genome-wide contribution of PU.1 to divergent PPARG binding in human and mouse. <i>PLoS ONE</i> , 2012 , 7, e48102	3.7	15
70	Single-nucleotide mutation matrix: a new model for predicting the NF- κ B DNA binding sites. <i>PLoS ONE</i> , 2014 , 9, e101490	3.7	3
69	Purifying selection in deeply conserved human enhancers is more consistent than in coding sequences. <i>PLoS ONE</i> , 2014 , 9, e103357	3.7	7
68	Regulatory evolution and voltage-gated ion channel expression in squid axon: selection-mutation balance and fitness cliffs. <i>PLoS ONE</i> , 2015 , 10, e0120785	3.7	2
67	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. <i>PLoS ONE</i> , 2015 , 10, e0126911	3.7	15

66	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , 2016 , 7, 7381-9	3.9	7
65	[DNA-binding profiles of mammalian transcription factors]. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , 2012 , 34, 950-68	1.4	1
64	Expression quantitative trait analyses to identify causal genetic variants for type 2 diabetes susceptibility. <i>World Journal of Diabetes</i> , 2014 , 5, 97-114	4.7	15
63	Evidence for a common evolutionary rate in metazoan transcriptional networks. <i>ELife</i> , 2015 , 4,	8.9	19
62	Uncoupling evolutionary changes in DNA sequence, transcription factor occupancy and enhancer activity. <i>ELife</i> , 2017 , 6,	8.9	24
61	Intrinsic cooperativity potentiates parallel -regulatory evolution. <i>ELife</i> , 2018 , 7,	8.9	7
60	The evolutionary history and genomics of European blackcap migration. <i>ELife</i> , 2020 , 9,	8.9	10
59	UBTF facilitates melanoma progression via modulating MEK1/2-ERK1/2 signalling pathways by promoting GIT1 transcription. <i>Cancer Cell International</i> , 2021 , 21, 543	6.4	0
58	Epigenetic readers and lung cancer: the rs2427964C>T variant of the bromodomain and extraterminal domain gene BRD3 is associated with poorer survival outcome in NSCLC. <i>Molecular Oncology</i> , 2021 ,	7.9	
57	Characterizing batch effects and binding site-specific variability in ChIP-seq data. <i>NAR Genomics and Bioinformatics</i> , 2021 , 3, lqab098	3.7	2
56	Epilepsy-Associated Gangliogliomas: Identification of Genes with Altered Expression. 2012 , 267-273		
55	Contribution of transcription factor binding site motif variants to condition-specific gene expression patterns in budding yeast. <i>PLoS ONE</i> , 2012 , 7, e32274	3.7	
54	Human Fetal Growth Disorders and Imprinting Anomalies. <i>Research and Perspectives in Endocrine Interactions</i> , 2014 , 101-129		
53	Discussion. <i>Springer Theses</i> , 2015 , 89-120	0.1	
52	Genetic and transcriptional analysis of human host response to healthy gut microbiome.		
51	Interplay of cis and trans mechanisms driving transcription factor binding and gene expression evolution.		
50	The detection of covariation of mRNA levels of large sets of genes across multiple human populations.		
49	Probe Efficient Feature Representation of Gapped K-mer Frequency Vectors from Sequences using Deep Neural Networks.		0

48	Altered transcription factor binding events predict personalized gene expression and confer insight into functional cis-regulatory variants.		
47	Variation in Genome-wide NF-kappaB RELA Binding Sites upon Microbial Stimuli and Identification of a Virus Response Profile.		
46	High throughput characterization of genetic effects on DNA:protein binding and gene transcription.		1
45	Intrinsic cooperativity potentiates parallel cis-regulatory evolution.		
44	IMPACT: Genomic annotation of cell-state-specific regulatory elements inferred from the epigenome of bound transcription factors.		1
43	Mechanistic interpretation of non-coding variants helps discover transcriptional regulators of drug response.		
42	Mechanistic characterization of RASGRP1 variants identifies an hnRNP K-regulated transcriptional enhancer contributing to SLE susceptibility.		
41	Predicting the effects of SNPs on transcription factor binding affinity.		0
40	Variation in PU.1 binding and chromatin looping at neutrophil enhancers influences autoimmune disease susceptibility.		1
39	Functional effects of variation in transcription factor binding highlight long-range gene regulation by epromoters.		
38	The impact of population variation in the analysis of microRNA target sites.		
37	Cis acting variation is common, can propagates across multiple regulatory layers, but is often buffered in developmental programs.		0
36	Laboratory evolution of anticipatory gene regulation in Escherichia coli.		
35	Monitoring the Levels of Cellular NF- κ B Activation States. <i>Cancers</i> , 2021 , 13,	6.6	2
34	Drawing inferences from photographs. 2020 , 29-66		
33	Drawing inferences from absences of data values. 2020 , 67-103		
32	Associations between polymorphisms of SLC22A7, NGFR, ARNTL and PPP2R2B genes and Milk production traits in Chinese Holstein. <i>BMC Genomic Data</i> , 2021 , 22, 47	0	0
31	A novel method to identify cell-type specific regulatory variants and their role in cancer risk.		0

30 The classification of life. **2022**, 251-341

29 MeCP2 Increases Cisplatin Resistance in Human Gastric Cancer through the Activation of the AKT Pathway by Facilitating PDK-1 Transcription.. *Current Cancer Drug Targets*, **2022**, 2.8 0

28 Stress Reactivity, Susceptibility to Hypertension, and Differential Expression of Genes in Hypertensive Compared to Normotensive Patients.. *International Journal of Molecular Sciences*, **2022**, 23, 6.3 1

27 The importance of considering regulatory domains in genome-wide analyses - the nearest gene is often wrong!. *Biology Open*, **2022**, 11, 2.2 0

26 Characterization of sequence determinants of enhancer function using natural genetic variation. 0

25 A leukemia-protective germline variant mediates chromatin module formation via transcription factor nucleation.. *Nature Communications*, **2022**, 13, 2042 17.4 1

24 Presentation_1.pptx. **2019**,

23 Table_1.xlsx. **2019**,

22 Data_Sheet_1.PDF. **2019**,

21 Data_Sheet_2.PDF. **2019**,

20 Data_Sheet_3.PDF. **2019**,

19 Data_Sheet_4.PDF. **2019**,

18 Data_Sheet_5.PDF. **2019**,

17 Data_Sheet_6.PDF. **2019**,

16 Evolution of transcription factor binding through sequence variations and turnover of binding sites. *Genome Research*, **2022**, 32, 1099-1111 9.7 0

15 Precise modulation of transcription factor levels reveals drivers of dosage sensitivity. 0

14 Gene structure heterogeneity drives transcription noise within human chromosomes. 0

13 DeCAF: a novel method to identify cell-type specific regulatory variants and their role in cancer risk. *Genome Biology*, **2022**, 23, 18.3

- 12 Chromatin state modeling across individuals reveals global patterns of histone modifications.
- 11 Single Nucleotide Polymorphisms of ALDH18A1 and MAT2A Genes and Their Genetic Associations with Milk Production Traits of Chinese Holstein Cows. **2022**, 13, 1437 ○
- 10 Genetic determinants of chromatin reveal prostate cancer risk mediated by context-dependent gene regulation. **2022**, 54, 1364-1375 2
- 9 Characterization of sequence determinants of enhancer function using natural genetic variation. 11, ○
- 8 Multi-species analysis of inflammatory response elements reveals ancient and lineage-specific contributions of transposable elements to NF- κ B binding. ○
- 7 Integrating Multimorbidity into a Whole-Body Understanding of Disease Using Spatial Genomics. **2022**, 157-187 ○
- 6 Limited conservation in cross-species comparison of GLK transcription factor binding suggested wide-spread cisome divergence. **2022**, 13, ○
- 5 Identification of Genetic Effects of ACADVL and IRF6 Genes with Milk Production Traits of Holstein Cattle in China. **2022**, 13, 2393 ○
- 4 Genetic marker identification of SEC13 gene for milk production traits in Chinese holstein. 13, ○
- 3 Genetic Variation in Transcription Factor Binding Sites. **2023**, 24, 5038 ○
- 2 Statistical Analysis in ChIP-seq-Related Applications. **2023**, 169-181 ○
- 1 Precise modulation of transcription factor levels identifies features underlying dosage sensitivity. ○