Genome-Wide Location and Function of DNA Binding P

Science

290, 2306-2309

DOI: 10.1126/science.290.5500.2306

Citation Report

#	Article	IF	Citations
1	Events at DNA replication origins and genome stability. , 0, , 35-55.		0
3	Regulatory sequence analysis: application to the interpretation of gene expression. European Neuropsychopharmacology, 2001, 11, 399-411.	0.3	20
4	Genome-wide analysis of protein-DNA interactions in living cells. Genome Biology, 2001, 2, reviews1013.1.	13.9	13
5	Making Sense of the Sequence. Science, 2001, 291, 1257-1260.	6.0	26
6	Integrated Genomic and Proteomic Analyses of a Systematically Perturbed Metabolic Network. Science, 2001, 292, 929-934.	6.0	1,921
7	Navigating gene expression using microarrays â€” a technology review. Nature Cell Biology, 2001, 3, E190-E195.	4.6	460
8	Applications of DNA microarrays in microbial systems. Journal of Microbiological Methods, 2001, 47, 257-272.	0.7	170
9	Neuronal promoter of human aromatic l-amino acid decarboxylase gene directs transgene expression to the adult floor plate and aminergic nuclei induced by the isthmus. Molecular Brain Research, 2001, 97, 149-160.	2.5	16
10	Metabolic engineering as an integrating platform for strain development. Current Opinion in Microbiology, 2001, 4, 336-340.	2.3	43
11	Transcription and chromatin converge: lessons from yeast genetics. Current Opinion in Genetics and Development, 2001, 11, 142-147.	1.5	19
12	Spotting the target: microarrays for disease gene discovery. Current Opinion in Genetics and Development, 2001, 11, 258-263.	1.5	51
13	Transcriptomes, transcription activators and microarrays. FEBS Letters, 2001, 498, 140-144.	1.3	30
14	Serial Regulation of Transcriptional Regulators in the Yeast Cell Cycle. Cell, 2001, 106, 697-708.	13.5	604
15	Making Sense of Eukaryotic DNA Replication Origins. Science, 2001, 294, 96-100.	6.0	278
16	Systems Biology: an emerging theme in biological research. Computer Aided Chemical Engineering, 2001, , 55-68.	0.3	1
17	Characterization of Nucleophosmin (B23) as a Myc Target by Scanning Chromatin Immunoprecipitation. Journal of Biological Chemistry, 2001, 276, 48285-48291.	1.6	108
18	A novel in vitro system for analyzing parental allele-specific histone acetylation in genomic imprinting. Journal of Human Genetics, 2001, 46, 626-632.	1.1	17
19	DNA microarrays: new tools in the analysis of plant defence responses. Molecular Plant Pathology, 2001, 2, 177-185.	2.0	35

#	Article	IF	Citations
20	Location analysis of DNA-bound proteins at the whole-genome level: untangling transcriptional regulatory networks. BioEssays, 2001, 23, 473-476.	1.2	21
21	Chipping away at chromatin. Nature Genetics, 2001, 27, 240-241.	9.4	2
22	Chromatin profiling using targeted DNA adenine methyltransferase. Nature Genetics, 2001, 27, 304-308.	9.4	303
23	To bind or not to bind. Nature Genetics, 2001, 28, 303-304.	9.4	22
24	Selection analyses of insertional mutants using subgenic-resolution arrays. Nature Biotechnology, 2001, 19, 1060-1065.	9.4	140
25	Chip on chips. Nature Reviews Genetics, 2001, 2, 88-88.	7.7	2
26	Emerging technologies in yeast genomics. Nature Reviews Genetics, 2001, 2, 302-312.	7.7	96
27	Functional genomics and the study of development, variation and evolution. Nature Reviews Genetics, 2001, 2, 528-537.	7.7	50
28	Modeling Genetic Networks and Their Evolution: A Complex Dynamical Systems Perspective. Biological Chemistry, 2001, 382, 1289-99.	1.2	45
29	Regulation of G Proteinâ€"Initiated Signal Transduction in Yeast: Paradigms and Principles. Annual Review of Biochemistry, 2001, 70, 703-754.	5.0	400
30	Are All DNA Binding and Transcription Regulation by an Activator Physiologically Relevant?. Molecular and Cellular Biology, 2001, 21, 2467-2474.	1.1	24
31	H2A.Z Is Required for Global Chromatin Integrity and for Recruitment of RNA Polymerase II under Specific Conditions. Molecular and Cellular Biology, 2001, 21, 6270-6279.	1.1	206
32	Ceramic Capillaries for Use in Microarray Fabrication. Genome Research, 2001, 11, 1780-1783.	2.4	16
33	Genome-Wide Distribution of ORC and MCM Proteins in S. cerevisiae: High-Resolution Mapping of Replication Origins. Science, 2001, 294, 2357-2360.	6.0	385
34	Analysis of large-scale gene expression data. Briefings in Bioinformatics, 2001, 2, 350-362.	3.2	59
35	DNA REPLICATION: Enhanced: Genomic Views of Genome Duplication. Science, 2001, 294, 2301-2304.	6.0	18
36	Microarrays for microbiologists. Microbiology (United Kingdom), 2001, 147, 1403-1414.	0.7	116
37	Osmotic Stress Signaling and Osmoadaptation in Yeasts. Microbiology and Molecular Biology Reviews, 2002, 66, 300-372.	2.9	1,452

#	Article	IF	Citations
38	Transcriptional Regulation: a Genomic Overview. The Arabidopsis Book, 2002, 1, e0085.	0.5	55
39	From promoter sequence to expression. , 2002, , .		64
40	Detection and Visualization of Compositionally Similar cis-Regulatory Element Clusters in Orthologous and Coordinately Controlled Genes. Genome Research, 2002, 12, 1408-1417.	2.4	86
41	Bayesian methods for elucidating genetic regulatory networks. IEEE Intelligent Systems, 2002, 17, 37-43.	4.0	15
42	Deciphering genetic regulatory codes: A challenge for functional genomics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 546-548.	3.3	61
43	Identification of a Binding Region for Human Origin Recognition Complex Proteins 1 and 2 That Coincides with an Origin of DNA Replication. Molecular and Cellular Biology, 2002, 22, 1036-1048.	1.1	134
44	Differential Transactivation by the p53 Transcription Factor Is Highly Dependent on p53 Level and Promoter Target Sequence. Molecular and Cellular Biology, 2002, 22, 8612-8625.	1.1	175
45	Mcm3 Is Polyubiquitinated during Mitosis before Establishment of the Pre-replication Complex. Journal of Biological Chemistry, 2002, 277, 41706-41714.	1.6	11
46	Analysis of the Innate and Adaptive Phases of Allograft Rejection by Cluster Analysis of Transcriptional Profiles. Journal of Immunology, 2002, 169, 522-530.	0.4	57
47	Transcriptional mechanisms underlying neuropathic pain: DREAM, transcription factors and future pain management?. Expert Review of Neurotherapeutics, 2002, 2, 677-689.	1.4	15
48	DEVELOPMENTALGENOMICAPPROACHES INMODELORGANISMS. Annual Review of Genomics and Human Genetics, 2002, 3, 153-178.	2.5	31
49	Functional Cloning, Sorting, and Expression Profiling of Nucleic Acid-Binding Proteins. Genome Research, 2002, 12, 1175-1184.	2.4	8
50	High-Density Cell Microarrays for Parallel Functional Determinations. Genome Research, 2002, 12, 482-486.	2.4	22
51	GATA-1 binding sites mapped in the Â-globin locus by using mammalian chIp-chip analysis. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2924-2929.	3.3	149
52	Methylation of histone H3 Lys 4 in coding regions of active genes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8695-8700.	3.3	673
53	Discovering regulatory and signalling circuits in molecular interaction networks. Bioinformatics, 2002, 18, S233-S240.	1.8	1,098
54	Anterior-posterior patterning in the Drosophila embryo. Advances in Developmental Biology and Biochemistry, 2002, 12, 155-204.	0.3	43
55	Extracting functional information from microarrays: A challenge for functional genomics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12509-12511.	3.3	21

#	Article	IF	Citations
56	Evolution of Transcription Factor Binding Sites in Mammalian Gene Regulatory Regions: Conservation and Turnover. Molecular Biology and Evolution, 2002, 19, 1114-1121.	3.5	411
57	A hypothesis driven approach to condition specific transcription factor binding site characterization in S.c.. , 2002, , .		0
58	Genomics for Applied Microbiology. Advances in Applied Microbiology, 2002, 51, 201-248e.	1.3	14
59	The Insulin Resistance Syndrome: Mechanisms of Clustering of Cardiovascular Risk. Seminars in Vascular Medicine, 2002, 2, 045-058.	2.1	34
60	Genome-wide location and regulated recruitment of the RSC nucleosome-remodeling complex. Genes and Development, 2002, 16, 806-819.	2.7	239
61	Minreg: Inferring an active regulator set. Bioinformatics, 2002, 18, S258-S267.	1.8	63
62	Genes directly controlled by CtrA, a master regulator of the Caulobacter cell cycle. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4632-4637.	3.3	363
63	Condition specific transcription factor binding site characterization in Saccharomyces cerevisiae. Bioinformatics, 2002, 18, 1289-1296.	1.8	10
64	Identifying transcription factor binding sites through Markov chain optimization. Bioinformatics, 2002, 18, S100-S109.	1.8	71
65	Gcn4p, a Master Regulator of Gene Expression, Is Controlled at Multiple Levels by Diverse Signals of Starvation and Stress. Eukaryotic Cell, 2002, 1, 22-32.	3.4	315
66	Isolating human transcription factor targets by coupling chromatin immunoprecipitation and CpG island microarray analysis. Genes and Development, 2002, 16, 235-244.	2.7	409
67	Microarray Technologies â€“ An Overview. Pharmacogenomics, 2002, 3, 293-297.	0.6	21
68	An ensemble method for identifying regulatory circuits with special reference to the qa gene cluster of Neurospora crassa. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16904-16909.	3.3	110
69	A Genome-wide Screen for Site-specific DNA-binding Proteins. Molecular and Cellular Proteomics, 2002, 1, 538-543.	2.5	22
70	TRANSCRIPTION: Of Chips and ChIPs. Science, 2002, 296, 666-669.	6.0	38
71	Gene Expression Analysis Using c DNA Microarrays. Current Protocols in Neuroscience, 2002, 20, Unit 4.28.	2.6	6
72	Novel Signal Transduction Pathway Utilized by Extracellular HSP70. Journal of Biological Chemistry, 2002, 277, 15028-15034.	1.6	1,370
73	One-step affinity purification of the yeast ribosome and its associated proteins and mRNAs. Rna, 2002, 8, 948-958.	1.6	111

#	ARTICLE	IF	CITATIONS
74	Requirement of Hos2 Histone Deacetylase for Gene Activity in Yeast. Science, 2002, 298, 1412-1414.	6.0	245
75	Subcellular localization of the yeast proteome. Genes and Development, 2002, 16, 707-719.	2.7	667
76	E2F integrates cell cycle progression with DNA repair, replication, and G2/M checkpoints. Genes and Development, 2002, 16, 245-256.	2.7	1,002
77	DNA microarrays in medicine: manufacturing techniques and potential applications. Expert Opinion on Therapeutic Patents, 2002, 12, 1783-1794.	2.4	8
78	Nontargeted Metabolome Analysis by Use of Fourier Transform Ion Cyclotron Mass Spectrometry. OMICS A Journal of Integrative Biology, 2002, 6, 217-234.	1.0	415
79	ChIP-chip: A genomic approach for identifying transcription factor binding sites. Methods in Enzymology, 2002, 350, 469-483.	0.4	151
80	Microarray analysis of orthologous genes: conservation of the translational machinery across species at the sequence and expression level. Genome Biology, 2002, 4, R4.	13.9	19
82	Role of the Leukemia-associated Transcription Factor STAT3 in Platelet Physiology. Leukemia and Lymphoma, 2002, 43, 1461-1467.	0.6	21
83	Perspective: Microarray Technology, Seeing More Than Spots. Endocrinology, 2002, 143, 1983-1989.	1.4	49
84	A Unified Theory of Gene Expression. Cell, 2002, 108, 439-451.	13.5	787
85	Microarray Deacetylation Maps Determine Genome-Wide Functions for Yeast Histone Deacetylases. Cell, 2002, 109, 437-446.	13.5	422
86	Modifying Gene Expression Programs by Altering Core Promoter Chromatin Architecture. Cell, 2002, 110, 261-271.	13.5	168
87	Targeted Stimulation of Meiotic Recombination. Cell, 2002, 111, 173-184.	13.5	97
88	FMR1 silencing and the signals to chromatin: a unified model of transcriptional regulation. Biochemical and Biophysical Research Communications, 2002, 295, 575-581.	1.0	15
89	Identification of unknown target genes of human transcription factors using chromatin immunoprecipitation. Methods, 2002, 26, 37-47.	1.9	315
90	The Genome-Wide Localization of Rsc9, a Component of the RSC Chromatin-Remodeling Complex, Changes in Response to Stress. Molecular Cell, 2002, 9, 563-573.	4.5	135
91	Exchange of RNA Polymerase II Initiation and Elongation Factors during Gene Expression In Vivo. Molecular Cell, 2002, 9, 799-809.	4.5	282
92	Protein Interaction Verification and Functional Annotation by Integrated Analysis of Genome-Scale Data. Molecular Cell, 2002, 9, 1133-1143.	4.5	221

#	ARTICLE	IF	CITATIONS
93	Design and function of transcriptional switches in Drosophila. Insect Biochemistry and Molecular Biology, 2002, 32, 1257-1273.	1.2	14
94	Functional genomics as applied to mapping transcription regulatory networks. Current Opinion in Microbiology, 2002, 5, 313-317.	2.3	71
95	Deciphering gene expression regulatory networks. Current Opinion in Genetics and Development, 2002, 12, 130-136.	1.5	171
96	Exploring genetic regulatory networks in metazoan development: methods and models. Physiological Genomics, 2002, 10, 131-143.	1.0	29
97	Quantitative prediction of NF-ÂB DNA- protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8167-8172.	3.3	102
98	ModÃ©lisation, analyse et simulationdes rÃ©seaux gÃ©nÃ©tiques. Medecine/Sciences, 2002, 18, 492-502.	0.0	2
99	Systems biology. , 2002, , 135-176.		1
100	Transcript elongation on a nucleoprotein template. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2002, 1577, 276-286.	2.4	56
101	Designed transcription factors as tools for therapeutics and functional genomics. Biochemical Pharmacology, 2002, 64, 919-923.	2.0	37
102	â€˜Omicâ€™ approaches for unraveling signaling networks. Current Opinion in Cell Biology, 2002, 14, 173-179.	2.6	73
103	Transcriptional regulatory networks and the yeast cell cycle. Current Opinion in Cell Biology, 2002, 14, 676-683.	2.6	105
104	Wrestling with pleiotropy: Genomic and topological analysis of the yeast gene expression network. BioEssays, 2002, 24, 267-274.	1.2	165
105	Expression profiling in mouse fetal thymus reveals clusters of coordinately expressed genes that mark individual stages of T-cell ontogeny. Immunogenetics, 2002, 54, 469-478.	1.2	4
106	The genomics of yeast responses to environmental stress and starvation. Functional and Integrative Genomics, 2002, 2, 181-192.	1.4	363
107	Yeast genomics: past, present, and future promise. Functional and Integrative Genomics, 2002, 2, 135-137.	1.4	7
108	Global analysis of gene expression in yeast. Functional and Integrative Genomics, 2002, 2, 171-180.	1.4	74
109	Gene function on a genomic scale. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 782, 151-163.	1.2	5
110	Transcriptional control of nutrient partitioning during rice grain filling. Plant Biotechnology Journal, 2002, 1, 59-70.	4.1	131

#	ARTICLE	IF	CITATIONS
111	A chromatin immunoprecipitation (ChIP) approach to isolate genes regulated by AGL15, a MADS domain protein that preferentially accumulates in embryos. Plant Journal, 2002, 32, 831-843.	2.8	82
112	Molecular characterization of MRG19 of Saccharomyces cerevisiae. FEBS Journal, 2002, 269, 5840-5850.	0.2	10
113	Modeling cancer in mice. Oncogene, 2002, 21, 5504-5514.	2.6	36
114	In silico biology through â€œomicsâ€. Nature Biotechnology, 2002, 20, 649-650.	9.4	93
115	Genome-wide internal tagging of bacterial exported proteins. Nature Biotechnology, 2002, 20, 839-842.	9.4	38
116	An algorithm for finding proteinâ€“DNA binding sites with applications to chromatin-Âimmunoprecipitation microarray experiments. Nature Biotechnology, 2002, 20, 835-839.	9.4	617
117	Characterizing the physical genome. Nature Genetics, 2002, 32, 515-521.	9.4	70
118	Topological and causal structure of the yeast transcriptional regulatory network. Nature Genetics, 2002, 31, 60-63.	9.4	550
119	Genome-wide binding map of the histone deacetylase Rpd3 in yeast. Nature Genetics, 2002, 31, 248-254.	9.4	255
120	Regulatory phases of early liver development: paradigms of organogenesis. Nature Reviews Genetics, 2002, 3, 499-512.	7.7	459
121	Treasures and traps in genome-wide data sets: case examples from yeast. Nature Reviews Genetics, 2002, 3, 653-661.	7.7	72
122	Global Approaches to Chromatin. Chemistry and Biology, 2002, 9, 1167-1173.	6.2	17
123	DNA microarrays for functional plant genomics. Plant Molecular Biology, 2002, 48, 99-118.	2.0	158
124	Transcriptional Regulatory Networks in Saccharomyces cerevisiae. Science, 2002, 298, 799-804.	6.0	2,706
125	Modeling and Simulation of Genetic Regulatory Systems: A Literature Review. Journal of Computational Biology, 2002, 9, 67-103.	0.8	2,250
126	Designed transcription factors as structural, functional and therapeutic probes of chromatin in vivo. EMBO Reports, 2002, 3, 610-615.	2.0	22
127	On Learning Gene Regulatory Networks Under the Boolean Network Model. Machine Learning, 2003, 52, 147-167.	3.4	240
128	Genome-wide location of yeast RNA polymerase III transcription machinery. EMBO Journal, 2003, 22, 4738-4747.	3.5	145

#	ARTICLE	IF	CITATIONS
129	Repression of transcription by Rgt1 in the absence of glucose requires Std1 and Mth1. Current Genetics, 2003, 44, 19-25.	0.8	88
130	In silico identification of metazoan transcriptional regulatory regions. Die Naturwissenschaften, 2003, 90, 156-166.	0.6	31
131	Integrated analysis of yeast regulatory sequences for biologically linked clusters of genes. Functional and Integrative Genomics, 2003, 3, 125-134.	1.4	27
132	An array of insights: application of DNA chip technology in the study of cell biologyâˆ—. Trends in Cell Biology, 2003, 13, 151-156.	3.6	56
133	Global analysis of gene expression using GeneChip microarrays. Current Opinion in Plant Biology, 2003, 6, 418-425.	3.5	79
134	Computational approaches for deciphering the transcriptional regulatory network by promoter analysis. Biosilico, 2003, 1, 125-133.	0.5	6
135	Development and validation of a T7 based linear amplification for genomic DNA. BMC Genomics, 2003, 4, 19.	1.2	102
136	Genomic analysis of gene expression relationships in transcriptional regulatory networks. Trends in Genetics, 2003, 19, 422-427.	2.9	238
137	Chromatin remodeling as a guide to transcriptional regulatory networks in mammals. Journal of Cellular Biochemistry, 2003, 88, 684-694.	1.2	34
138	Functional genomics of neural and behavioral plasticity. Journal of Neurobiology, 2003, 54, 272-282.	3.7	133
139	Candida glabrata STE12 is required for wild-type levels of virulence and nitrogen starvation induced filamentation. Molecular Microbiology, 2003, 50, 1309-1318.	1.2	64
140	The Spo0A regulon of Bacillus subtilis. Molecular Microbiology, 2003, 50, 1683-1701.	1.2	466
141	DNA Microarray Analyses of Circadian Timing: The Genomic Basis of Biological Time. Journal of Neuroendocrinology, 2003, 15, 991-1002.	1.2	207
142	Telomere and ribosomal DNA repeats are chromosomal targets of the bloom syndrome DNA helicase. BMC Cell Biology, 2003, 4, 15.	3.0	54
143	Neural crest specification: migrating into genomics. Nature Reviews Neuroscience, 2003, 4, 795-805.	4.9	211
144	S-phase checkpoint proteins Tof1 and Mrc1 form a stable replication-pausing complex. Nature, 2003, 424, 1078-1083.	13.7	614
145	Molecular basis of lithium action: integration of lithium-responsive signaling and gene expression networks. Molecular Psychiatry, 2003, 8, 135-144.	4.1	115
146	Functional genomics as a window on radiation stress signaling. Oncogene, 2003, 22, 5828-5833.	2.6	98

#	Article	IF	Citations
147	Reconstructing genetic networks in yeast. Nature Biotechnology, 2003, 21, 1295-1297.	9.4	14
148	Playing tag with the yeast proteome. Nature Biotechnology, 2003, 21, 1297-1299.	9.4	5
149	Proteomics: the first decade and beyond. Nature Genetics, 2003, 33, 311-323.	9.4	660
150	Chromatin as a Tool for the Study of Genome Function in Cancer. Annals of the New York Academy of Sciences, 2003, 983, 5-21.	1.8	21
151	Changes in the Protein Expression of Yeast as a Function of Carbon Source. Journal of Proteome Research, 2003, 2, 643-649.	1.8	175
152	Analysis of Genome-Wide Histone Acetylation State and Enzyme Binding Using DNA Microarrays. Methods in Enzymology, 2003, 376, 289-304.	0.4	23
153	High-Throughput Screening of Chromatin Immunoprecipitates Using CpG-Island Microarrays. Methods in Enzymology, 2003, 376, 315-334.	0.4	85
154	The Use of Chromatin Immunoprecipitation Assays in Genome-Wide Analyses of Histone Modifications. Methods in Enzymology, 2003, 376, 349-360.	0.4	37
155	Using DNA-Binding Proteins as an Analytical Tool. Journal of the American Chemical Society, 2003, 125, 13451-13454.	6.6	62
156	The Evolution of Transcriptional Regulation in Eukaryotes. Molecular Biology and Evolution, 2003, 20, 1377-1419.	3.5	1,034
157	Correlating Proteinâ€“DNA and Proteinâ€“Protein Interaction Networks. Journal of Molecular Biology, 2003, 333, 75-85.	2.0	34
158	And then there were many: MADS goes genomic. Trends in Plant Science, 2003, 8, 475-483.	4.3	179
159	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. Science, 2003, 302, 842-846.	6.0	853
160	Dissecting the transcription networks of a cell using computational genomics. Current Opinion in Genetics and Development, 2003, 13, 611-616.	1.5	27
161	In vivo characterization of regulatory polymorphisms by allele-specific quantification of RNA polymerase loading. Nature Genetics, 2003, 33, 469-475.	9.4	231
162	Targeted Recruitment of Set1 Histone Methylase by Elongating Pol II Provides a Localized Mark and Memory of Recent Transcriptional Activity. Molecular Cell, 2003, 11, 709-719.	4.5	961
163	Periodic Epi-organization of the Yeast Genome Revealed by the Distribution of Promoter Sites. Journal of Molecular Biology, 2003, 329, 859-865.	2.0	36
164	Program-Specific Distribution of a Transcription Factor Dependent on Partner Transcription Factor and MAPK Signaling. Cell, 2003, 113, 395-404.	13.5	206

#	Article	IF	Citations
165	A global transcriptional regulatory role for c-Myc in Burkitt's lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8164-8169.	3.3	447
166	Egr1 Signaling in Prostate Cancer. Cancer Biology and Therapy, 2003, 2, 615-620.	1.5	47
167	Genomewide histone acetylation microarrays. Methods, 2003, 31, 83-89.	1.9	46
168	In vivo proteinâ€“protein and proteinâ€“DNA crosslinking for genomewide binding microarray. Methods, 2003, 31, 90-95.	1.9	121
169	Finding regulatory sequences. International Journal of Biochemistry and Cell Biology, 2003, 35, 95-103.	1.2	3
170	Dissecting the phytochrome A-dependent signaling network in higher plants. Trends in Plant Science, 2003, 8, 172-178.	4.3	133
171	Subsystem Identification Through Dimensionality Reduction of Large-Scale Gene Expression Data. Genome Research, 2003, 13, 1706-1718.	2.4	200
172	The environmental stress response: a common yeast response to diverse environmental stresses. , 2003, , 11-70.		96
173	Computational prediction of transcription-factor binding site locations. Genome Biology, 2003, 5, 201.	13.9	237
175	Time series analysis of gene expression and location data. , 0, , .		7
176	Chemical approaches to studying transcription. Organic and Biomolecular Chemistry, 2003, 1, 3257.	1.5	11
178	Genome-wide identification of in vivo DrosophilaEngrailed-binding DNA fragments and related target genes. Development (Cambridge), 2003, 130, 1243-1254.	1.2	42
179	Detection of regulatory circuits by integrating the cellular networks of protein-protein interactions and transcription regulation. Nucleic Acids Research, 2003, 31, 6053-6061.	6.5	34
180	ExpressYourself: a modular platform for processing and visualizing microarray data. Nucleic Acids Research, 2003, 31, 3477-3482.	6.5	38
181	From Gene Networks to Gene Function. Genome Research, 2003, 13, 2568-2576.	2.4	142
182	The Stanford Microarray Database: data access and quality assessment tools. Nucleic Acids Research, 2003, 31, 94-96.	6.5	297
183	E2F6 Negatively Regulates BRCA1 in Human Cancer Cells without Methylation of Histone H3 on Lysine 9. Journal of Biological Chemistry, 2003, 278, 42466-42476.	1.6	80
184	Sensitivity and specificity of inferring genetic regulatory interactions from microarray experiments with dynamic Bayesian networks. Bioinformatics, 2003, 19, 2271-2282.	1.8	461

#	ARTICLE	IF	CITATIONS
185	Gene Expression Profiling of the Cellular Transcriptional Network Regulated by Alpha/Beta Interferon and Its Partial Attenuation by the Hepatitis C Virus Nonstructural 5A Protein. Journal of Virology, 2003, 77, 6367-6375.	1.5	103
186	Protein-DNA interaction mapping using genomic tiling path microarrays in Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 9428-9433.	3.3	73
187	A General Strategy to Uncover Transcription Factor Properties Identifies a New Regulator of Drug Resistance in Yeast. Journal of Biological Chemistry, 2003, 278, 11427-11432.	1.6	56
188	In Vivo Cloning and Characterization of a New Growth Suppressor Protein TOE1 as a Direct Target Gene of Egr1. Journal of Biological Chemistry, 2003, 278, 14306-14312.	1.6	32
189	Discovering Novel cis-Regulatory Motifs Using Functional Networks. Genome Research, 2003, 13, 883-895.	2.4	19
190	Quantitative Analysis of GAL Genetic Switch of Saccharomyces cerevisiae Reveals That Nucleocytoplasmic Shuttling of Gal80p Results in a Highly Sensitive Response to Galactose. Journal of Biological Chemistry, 2003, 278, 48764-48769.	1.6	56
191	Additional Targets of the Bacillus subtilis Global Regulator CodY Identified by Chromatin Immunoprecipitation and Genome-Wide Transcript Analysis. Journal of Bacteriology, 2003, 185, 1911-1922.	1.0	265
192	Beyond expression profiling: Next generation uses of high density oligonucleotide arrays. Briefings in Functional Genomics & Proteomics, 2003, 2, 47-56.	3.8	30
193	Genome-wide Mapping of Protein-DNA Interactions by Chromatin Immunoprecipitation and DNA Microarray Hybridization. , 2003, 224, 99-110.		23
194	Continuous-Time Identification of Gene Expression Models. OMICS A Journal of Integrative Biology, 2003, 7, 373-386.	1.0	15
195	Network component analysis: Reconstruction of regulatory signals in biological systems. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 15522-15527.	3.3	550
196	Distribution of NF-ÂB-binding sites across human chromosome 22. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 12247-12252.	3.3	298
197	DNA Arrays: Applications and Implications for Circadian Biology. Journal of Biological Rhythms, 2003, 18, 96-105.	1.4	31
198	cWINNOWER algorithm for finding fuzzy DNA motifs. , 0, , .		14
199	Cotranscriptional Recruitment of the U1 snRNP to Intron-Containing Genes in Yeast. Molecular and Cellular Biology, 2003, 23, 5768-5779.	1.1	107
200	Yaf9, a Novel NuA4 Histone Acetyltransferase Subunit, Is Required for the Cellular Response to Spindle Stress in Yeast. Molecular and Cellular Biology, 2003, 23, 6086-6102.	1.1	92
201	Active repression by unliganded retinoid receptors in development. Journal of Cell Biology, 2003, 161, 223-228.	2.3	117
202	Prediction of regulatory networks: genome-wide identification of transcription factor targets from gene expression data. Bioinformatics, 2003, 19, 1917-1926.	1.8	116

#	ARTICLE	IF	CITATIONS
203	DNA Microarrays and Bacterial Gene Expression. Methods in Enzymology, 2003, 370, 264-278.	0.4	3
204	Genomic targets of the human c-Myc protein. Genes and Development, 2003, 17, 1115-1129.	2.7	819
205	Reconciling Gene Expression Data With Known Genome-Scale Regulatory Network Structures. Genome Research, 2003, 13, 2423-2434.	2.4	96
206	Dominant-Negative Mutants of Helix-Loop-Helix Proteins: Transcriptional Inhibition. Methods in Enzymology, 2003, 370, 454-466.	0.4	5
207	Applications of genomics in the inner ear. Pharmacogenomics, 2003, 4, 735-745.	0.6	3
208	Probing Chromatin Immunoprecipitates with CpG-Island Microarrays to Identify Genomic Sites Occupied by DNA-Binding Proteins. Methods in Enzymology, 2003, 371, 577-596.	0.4	58
209	Array-Based Technologies and their Applications in Proteomics. Current Topics in Medicinal Chemistry, 2003, 3, 705-724.	1.0	55
210	Background rareness-based iterative multiple sequence alignment algorithm for regulatory element detection. Bioinformatics, 2003, 19, 1952-1963.	1.8	19
211	The Dynamics of Chromosome Replication in Yeast. Current Topics in Developmental Biology, 2003, 55, 1-73.	1.0	11
212	Serial Analysis of Gene Expression and Gene Trapping to Identify Nuclear Receptor Target Genes. Methods in Enzymology, 2003, 364, 297-322.	0.4	0
213	Transcription-Based Solenoidal Model of Chromosomes. Complexus, 2003, 1, 171-180.	0.7	31
214	Epigenomic profiling using microarrays. BioTechniques, 2003, 35, 346-357.	0.8	57
215	Methods for Studying Transcription Factors. , 2004, , 23-53.		0
216	Chromatin immunoprecipitation assay. BioTechniques, 2004, 37, 961-969.	0.8	165
217	COMPACTNESS AND CYCLES IN SIGNAL TRANSDUCTION AND TRANSCRIPTIONAL REGULATION NETWORKS: A SIGNATURE OF NATURAL SELECTION?. International Journal of Modeling, Simulation, and Scientific Computing, 2004, 07, 419-432.	0.9	5
218	Characterization of Proteinâ€“DNA Association In Vivo by Chromatin Immunoprecipitation. , 2004, 284, 147-162.		20
221	Chromatin Immunoprecipitation for Determining the Association of Proteins with Specific Genomic Sequences In Vivo. Current Protocols in Molecular Biology, 2004, 65, 21.3.1.	2.9	9
222	Multilevel Modeling and Inference of Transcription Regulation. Journal of Computational Biology, 2004, 11, 357-375.	0.8	10

#	ARTICLE	IF	CITATIONS
223	A Gateway-Compatible Yeast One-Hybrid System. Genome Research, 2004, 14, 2093-2101.	2.4	189
224	Coordination of replication and transcription along a Drosophila chromosome. Genes and Development, 2004, 18, 3094-3105.	2.7	271
225	DBRF-MEGN method: an algorithm for deducing minimum equivalent gene networks from large-scale gene expression profiles of gene deletion mutants. Bioinformatics, 2004, 20, 2662-2675.	1.8	18
226	Identifying gene regulatory elements by genome-wide recovery of DNase hypersensitive sites. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 992-997.	3.3	166
227	In silico identification of transcriptional regulators associated with c-Myc. Nucleic Acids Research, 2004, 32, 4955-4961.	6.5	26
228	Detecting single DNA copy number variations in complex genomes using one nanogram of starting DNA and BAC-array CGH. Nucleic Acids Research, 2004, 32, e112-e112.	6.5	38
229	Revealing modularity and organization in the yeast molecular network by integrated analysis of highly heterogeneous genomewide data. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 2981-2986.	3.3	344
230	Comparative analysis of dioxin response elements in human, mouse and rat genomic sequences. Nucleic Acids Research, 2004, 32, 4512-4523.	6.5	197
231	cWINNOWER ALGORITHM FOR FINDING FUZZY DNA MOTIFS. Journal of Bioinformatics and Computational Biology, 2004, 02, 47-60.	0.3	24
232	Arginine methyltransferase affects interactions and recruitment of mRNA processing and export factors. Genes and Development, 2004, 18, 2024-2035.	2.7	119
233	Silencing of human polycomb target genes is associated with methylation of histone H3 Lys 27. Genes and Development, 2004, 18, 1592-1605.	2.7	447
234	Global Analysis of the Regulatory Network Structure of Gene Expression in Saccharomyces cerevisiae. DNA Research, 2004, 11, 163-177.	1.5	9
235	Saccharomyces cerevisiae Engineered for Xylose Metabolism Exhibits a Respiratory Response. Applied and Environmental Microbiology, 2004, 70, 6816-6825.	1.4	146
236	A model-based optimization framework for the inference on gene regulatory networks from DNA array data. Bioinformatics, 2004, 20, 3221-3235.	1.8	31
237	Global Survey of Chromatin Accessibility Using DNA Microarrays. Genome Research, 2004, 14, 1374-1381.	2.4	28
238	Network motifs in integrated cellular networks of transcription-regulation and protein-protein interaction. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5934-5939.	3.3	479
239	Interaction Networks of the Molecular Machines That Decode, Replicate, and Maintain the Integrity of the Human Genome. Molecular and Cellular Proteomics, 2004, 3, 851-856.	2.5	18
240	Computational inference of transcriptional regulatory networks from expression profiling and transcription factor binding site identification. Nucleic Acids Research, 2004, 32, 179-188.	6.5	99

#	Article	IF	Citations
241	Identifying estrogen receptor Â target genes using integrated computational genomics and chromatin immunoprecipitation microarray. Nucleic Acids Research, 2004, 32, 6627-6635.	6.5	79
242	Regulatory Network Connecting Two Glucose Signal Transduction Pathways in Saccharomyces cerevisiae. Eukaryotic Cell, 2004, 3, 221-231.	3.4	145
243	MesA, a Novel Fungal Protein Required for the Stabilization of Polarity Axes inAspergillus nidulans. Molecular Biology of the Cell, 2004, 15, 3658-3672.	0.9	81
244	Nutrition and Genomics. , 2004, 9, 243-263.		7
245	Basal and luminal breast cancers: Basic or luminous? (Review). International Journal of Oncology, 2004, 25, 249.	1.4	18
246	Genomic identification of direct target genes of LEAFY. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1775-1780.	3.3	185
247	Global network analysis of phenotypic effects: Protein networks and toxicity modulation in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 18006-18011.	3.3	123
248	RECONSTRUCTING GENETIC NETWORKS FROM TIME ORDERED GENE EXPRESSION DATA USING BAYESIAN METHOD WITH GLOBAL SEARCH ALGORITHM. Journal of Bioinformatics and Computational Biology, 2004, 02, 441-458.	0.3	11
249	Histone Fold Protein Dls1p Is Required for Isw2-Dependent Chromatin Remodeling In Vivo. Molecular and Cellular Biology, 2004, 24, 2605-2613.	1.1	44
250	Genomic dissection of the cell-type-specification circuit in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 18069-18074.	3.3	98
251	Changes in genomewide occupancy of core transcriptional regulators during heat stress. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16843-16848.	3.3	69
252	Quantitative modeling of DNA-protein interactions: effects of amino acid substitutions on binding specificity of the Mnt repressor. Nucleic Acids Research, 2004, 32, 4026-4032.	6.5	16
253	DYNAMIC INTEGRATION OF GENE ANNOTATION AND ITS APPLICATION TO MICROARRAY ANALYSIS. Journal of Bioinformatics and Computational Biology, 2004, 01, 627-645.	0.3	4
254	Microarray Data Visualization and Analysis with the Longhorn Array Database (LAD). , 2004, Chapter 7, Unit 7.10.		2
255	Regulatory motif finding by logic regression. Bioinformatics, 2004, 20, 2799-2811.	1.8	52
256	Microarray Platforms: Introduction and Application to Neurobiology. International Review of Neurobiology, 2004, 60, 1-23.	0.9	3
257	Rapid tagging of endogenous mouse genes by recombineering and ES cell complementation of tetraploid blastocysts. Nucleic Acids Research, 2004, 32, e128-e128.	6.5	30
258	PathBLAST: a tool for alignment of protein interaction networks. Nucleic Acids Research, 2004, 32, W83-W88.	6.5	360

#	Article	IF	Citations
259	Quantitative sequential chromatin immunoprecipitation, a method for analyzing co-occupancy of proteins at genomic regions in vivo. Nucleic Acids Research, 2004, 32, e151-e151.	6.5	94
260	Microarray analysis of chromatin-immunoprecipitated DNA identifies specific regions of tobacco genes associated with acetylated histones. Plant Journal, 2004, 37, 789-800.	2.8	31
261	Comparative genomic hybridization (CGH)-arrays pave the way for identification of novel cancer-related genes. Cancer Science, 2004, 95, 559-563.	1.7	130
262	Expression profiling using a hexamer-based universal microarray. Nature Biotechnology, 2004, 22, 418-426.	9.4	33
263	Stochastic yet biased expression of multiple Dscam splice variants by individual cells. Nature Genetics, 2004, 36, 240-246.	9.4	234
264	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. Nature Genetics, 2004, 36, 1331-1339.	9.4	341
265	Design of gene circuits: lessons from bacteria. Nature Reviews Genetics, 2004, 5, 34-42.	7.7	206
266	Novel ChIP-based strategies to uncover transcription factor target genes in the immune system. Nature Reviews Immunology, 2004, 4, 381-386.	10.6	33
267	Cell-cycle progression and the generation of asymmetry in Caulobacter crescentus. Nature Reviews Microbiology, 2004, 2, 325-337.	13.6	151
268	Transcriptional regulatory code of a eukaryotic genome. Nature, 2004, 431, 99-104.	13.7	1,969
269	Growth-regulated recruitment of the essential yeast ribosomal protein gene activator Ifh1. Nature, 2004, 432, 1058-1061.	13.7	203
270	Nickel-induced down-regulation of serpin by hypoxic signaling. Toxicology and Applied Pharmacology, 2004, 194, 60-68.	1.3	22
271	Interrogating the transcriptome. Trends in Biotechnology, 2004, 22, 23-30.	4.9	58
272	Extracting novel information from gene expression data. Trends in Biotechnology, 2004, 22, 381-383.	4.9	6
273	Genomic microarrays in the spotlight. Trends in Genetics, 2004, 20, 87-94.	2.9	155
274	How much expression divergence after yeast gene duplication could be explained by regulatory motif evolution?. Trends in Genetics, 2004, 20, 403-407.	2.9	77
275	Defining transcriptional networks through integrative modeling of mRNA expression and transcription factor binding data. BMC Bioinformatics, 2004, 5, 31.	1.2	212
276	Expression of GAL genes in a mutant strain of Saccharomyces cerevisiae lacking GAL80: quantitative model and experimental verification. Biotechnology and Applied Biochemistry, 2004, 39, 89.	1.4	14

#	ARTICLE	IF	CITATIONS
277	An Arabidopsis Promoter Microarray and its Initial Usage in the Identification of HY5 Binding Targets in Vitro. Plant Molecular Biology, 2004, 54, 683-699.	2.0	35
278	New Approaches forin SilicoIdentification of Cytokine-Modified Î² Cell Gene Networks. Annals of the New York Academy of Sciences, 2004, 1037, 41-58.	1.8	11
279	DNA microarrays â€" techniques and applications in microbial systems. Folia Microbiologica, 2004, 49, 635-64.	1.1	23
280	In silico biotechnology. Current Opinion in Biotechnology, 2004, 15, 50-51.	3.3	26
281	Transcriptional networks controlling pancreatic development and beta cell function. Diabetologia, 2004, 47, 597-613.	2.9	205
282	Molecular evolution in the yeast transcriptional regulation network. The Journal of Experimental Zoology, 2004, 302B, 392-411.	1.4	38
283	A Case Study on Choosing Normalization Methods and Test Statistics for Two-Channel Microarray Data. Comparative and Functional Genomics, 2004, 5, 432-444.	2.0	14
284	Proteomics of calcium-signaling components in plants. Phytochemistry, 2004, 65, 1745-1776.	1.4	230
285	Reconstruction of microbial transcriptional regulatory networks. Current Opinion in Biotechnology, 2004, 15, 70-77.	3.3	149
286	Bioinformatics and cellular signaling. Current Opinion in Biotechnology, 2004, 15, 78-81.	3.3	29
287	Qualitative simulation of genetic regulatory networks using piecewise-linear models. Bulletin of Mathematical Biology, 2004, 66, 301-340.	0.9	309
288	Parallel inactivation of multiple GAL pathway genes and ecological diversification in yeasts. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14144-14149.	3.3	182
289	Quantitative X-ray Photoelectron Spectroscopy and Time-of-Flight Secondary Ion Mass Spectrometry Characterization of the Components in DNA. Analytical Chemistry, 2004, 76, 1114-1122.	3.2	96
290	Sweeping Capillary Electrophoresis:â€‰ A Non-Stopped-Flow Method for Measuring Bimolecular Rate Constant of Complex Formation between Protein and DNA. Journal of the American Chemical Society, 2004, 126, 7166-7167.	6.6	37
291	Common Chromatin Architecture, Common Chromatin Remodeling, and Common Transcription Kinetics of Adr1-Dependent Genes inSaccharomyces cerevisiaeâ€. Biochemistry, 2004, 43, 8878-8884.	1.2	19
292	A systems view of mRNP biology. Genes and Development, 2004, 18, 2845-2860.	2.7	137
293	ChIP Display: novel method for identification of genomic targets of transcription factors. Nucleic Acids Research, 2004, 32, e104-e104.	6.5	28
294	Identification of Target Genes Regulated byFOXC1Using Nickel Agaroseâ€"Based Chromatin Enrichment. , 2004, 45, 3904.		29

#	Article	IF	Citations
295	PLANT GENOMICS: The Third Wave. Annual Review of Genomics and Human Genetics, 2004, 5, 443-477.	2.5	68
296	From sequence to structure and back again: approaches for predicting protein-DNA binding. Proteome Science, 2004, 2, 3.	0.7	21
297	Microarray analysis of transposition targets in Escherichia coli: The impact of transcription. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9780-9785.	3.3	43
298	MONKEY: identifying conserved transcription-factor binding sites in multiple alignments using a binding site-specific evolutionary model. Genome Biology, 2004, 5, R98.	13.9	134
299	Sparse graphical Gaussian modeling of the isoprenoid gene network in Arabidopsis thaliana. Genome Biology, 2004, 5, R92.	13.9	290
300	Global nucleosome occupancy in yeast. Genome Biology, 2004, 5, R62.	13.9	309
301	Identifying combinatorial regulation of transcription factors and binding motifs. Genome Biology, 2004, 5, R56.	13.9	150
302	From co-expression to co-regulation: how many microarray experiments do we need?. Genome Biology, 2004, 5, R48.	13.9	88
303	Enriching for direct regulatory targets in perturbed gene-expression profiles. Genome Biology, 2004, 5, R29.	13.9	10
304	Identifying transcriptional targets. Genome Biology, 2004, 5, 210.	13.9	34
305	Network responses to DNA damaging agents. DNA Repair, 2004, 3, 1123-1132.	1.3	48
306	Progress and challenges in profiling the dynamics of chromatin and transcription factor binding with DNA microarrays. Current Opinion in Genetics and Development, 2004, 14, 697-705.	1.5	97
307	Bioinformatics and Systems Biology, rapidly evolving tools for interpreting plant response to global change. Field Crops Research, 2004, 90, 117-131.	2.3	11
308	Autoregulation of regulatory proteins is key for dynamic operation ofGALswitch inSaccharomyces cerevisiae. FEBS Letters, 2004, 576, 119-126.	1.3	16
309	Learning module networks from genome-wide location and expression data. FEBS Letters, 2004, 578, 297-304.	1.3	48
310	Comparative sequence analysis of Sordaria macrospora and Neurospora crassa as a means to improve genome annotation. Fungal Genetics and Biology, 2004, 41, 285-292.	0.9	51
311	Genome-scale identification of conditionally essential genes in E. coli by DNA microarrays. Biochemical and Biophysical Research Communications, 2004, 322, 347-354.	1.0	34
312	A genome-wide and nonredundant mouse transcription factor database. Biochemical and Biophysical Research Communications, 2004, 322, 787-793.	1.0	137

#	ARTICLE	IF	CITATIONS
313	Detecting DNA-binding of proteins in vivo by UV-crosslinking and immunoprecipitation. Biochemical and Biophysical Research Communications, 2004, 322, 705-711.	1.0	34
314	ChIP-chip: considerations for the design, analysis, and application of genome-wide chromatin immunoprecipitation experiments. Genomics, 2004, 83, 349-360.	1.3	536
315	The MTG proteins: chromatin repression players with a passion for networking. Genomics, 2004, 84, 1-9.	1.3	36
316	A walk-through of the yeast mating pheromone response pathway. Peptides, 2004, 25, 1465-1476.	1.2	236
317	Transcriptional networks: reverse-engineering gene regulation on a global scale. Current Opinion in Microbiology, 2004, 7, 638-646.	2.3	56
318	Cellular Stress Alters the Transcriptional Properties of Promoter-Bound Mot1-TBP Complexes. Molecular Cell, 2004, 14, 479-489.	4.5	41
319	Hot Spots for Modulating Toxicity Identified by Genomic Phenotyping and Localization Mapping. Molecular Cell, 2004, 16, 117-125.	4.5	90
320	Global Position and Recruitment of HATs and HDACs in the Yeast Genome. Molecular Cell, 2004, 16, 199-209.	4.5	212
321	Postreplicative Recruitment of Cohesin to Double-Strand Breaks Is Required for DNA Repair. Molecular Cell, 2004, 16, 1003-1015.	4.5	473
322	Enhanced CPT Sensitivity of Yeast Cells and Selective Relaxation of Gal4 Motif-containing DNA by Novel Gal4â€“Topoisomerase I Fusion Proteins. Journal of Molecular Biology, 2004, 337, 295-305.	2.0	4
323	Constrained Binding Site Diversity within Families of Transcription Factors Enhances Pattern Discovery Bioinformatics. Journal of Molecular Biology, 2004, 338, 207-215.	2.0	157
324	POSaM: a fast, flexible, open-source, inkjet oligonucleotide synthesizer and microarrayer. Genome Biology, 2004, 5, R58.	13.9	79
325	Systems Biology, Proteomics, and the Future of Health Care:Â Toward Predictive, Preventative, and Personalized Medicine. Journal of Proteome Research, 2004, 3, 179-196.	1.8	680
326	Unbiased Mapping of Transcription Factor Binding Sites along Human Chromosomes 21 and 22 Points to Widespread Regulation of Noncoding RNAs. Cell, 2004, 116, 499-509.	13.5	1,047
327	Genome-Wide Localization of the Nuclear Transport Machinery Couples Transcriptional Status and Nuclear Organization. Cell, 2004, 117, 427-439.	13.5	528
328	Chromatin Immunoprecipitation for Determining the Association of Proteins with Specific Genomic Sequences In Vivo. Current Protocols in Cell Biology, 2004, 23, Unit 17.7.	2.3	101
329	Acetylation of Yeast Histone H4 Lysine 16: A Switch for Protein Interactions in Heterochromatin and Euchromatin. Cold Spring Harbor Symposia on Quantitative Biology, 2004, 69, 193-200.	2.0	39
330	Charting gene regulatory networks: strategies, challenges and perspectives. Biochemical Journal, 2004, 381, 1-12.	1.7	73

#	ARTICLE	IF	CITATIONS
332	Genomic Approaches That Aid in the Identification of Transcription Factor Target Genes. Experimental Biology and Medicine, 2004, 229, 705-721.	1.1	51
333	The Ecdysteroid Receptor. , 2005, , 243-285.		45
334	GÃ©nomique : Nouvelle technologie pour lâ€™obstÃ©trique-gynÃ©cologie. Journal of Obstetrics and Gynaecology Canada, 2005, 27, 69-75.	0.3	0
336	RETIRED: Genomics: New Technology for Obstetrics and Gynaecology. Journal of Obstetrics and Gynaecology Canada, 2005, 27, 63-68.	0.3	11
337	Kinetic methods in capillary electrophoresis and their applications. , 2005, , .		0
338	Transcriptional regulation and metabolism. Biochemical Society Transactions, 2005, 33, 1423-1426.	1.6	6
339	Transcriptional regulation and metabolism. Biochemical Society Transactions, 2005, 33, 1423.	1.6	7
340	Steady-state analysis of glucose repression reveals hierarchical expression of proteins under Mig1p control in Saccharomyces cerevisiae. Biochemical Journal, 2005, 388, 843-849.	1.7	10
341	Identifying Chromosomal Targets of DNAâ€Binding Proteins by Sequence Tag Analysis of Genomic Enrichment (STAGE). Current Protocols in Molecular Biology, 2005, 72, Unit 21.10.	2.9	0
342	A comparative analysis of the genetic switch between not-so-distant cousins: versus. FEMS Yeast Research, 2005, 5, 1115-1128.	1.1	77
343	Fluorescence based assay ofGALsystem in yeastSaccharomyces cerevisiae. FEMS Microbiology Letters, 2005, 244, 105-110.	0.7	19
344	Genomic studies of transcription factorâ€“DNA interactions. Current Opinion in Chemical Biology, 2005, 9, 38-45.	2.8	60
345	"Promoter Array" Studies Identify Cohorts of Genes Directly Regulated by Methylation, Copy Number Change, or Transcription Factor Binding in Human Cancer Cells. Annals of the New York Academy of Sciences, 2005, 1058, 162-185.	1.8	20
346	Easy detection of chromatin binding proteins by the histone association assay. Biological Procedures Online, 2005, 7, 60-69.	1.4	28
347	Targeted discovery tools: proteomics and chromatin immunoprecipitation-on-chip. BJU International, 2005, 96, 16-22.	1.3	8
348	Discovering DNA regulatory elements with bacteria. Nature Biotechnology, 2005, 23, 942-944.	9.4	15
349	Mapping of genetic and epigenetic regulatory networks using microarrays. Nature Genetics, 2005, 37, S18-S24.	9.4	110
350	From signatures to models: understanding cancer using microarrays. Nature Genetics, 2005, 37, S38-S45.	9.4	331

#	Article	IF	Citations
351	Mapping DNA-protein interactions in large genomes by sequence tag analysis of genomic enrichment. Nature Methods, 2005, 2, 47-53.	9.0	108
352	Reconstruction of cellular signalling networks and analysis of their properties. Nature Reviews Molecular Cell Biology, 2005, 6, 99-111.	16.1	472
353	Insights into host responses against pathogens from transcriptional profiling. Nature Reviews Microbiology, 2005, 3, 281-294.	13.6	581
354	Î²-Catenin activates the growth factor endothelin-1 in colon cancer cells. Oncogene, 2005, 24, 597-604.	2.6	90
355	DNA polymerases Î±, Î´, and É› localize and function together at replication forks in Saccharomyces cerevisiae. Genes To Cells, 2005, 10, 297-309.	0.5	29
356	A high-resolution map of active promoters in the human genome. Nature, 2005, 436, 876-880.	13.7	841
357	Learning More from Microarrays: Insights from Modules and Networks. Journal of Investigative Dermatology, 2005, 125, 175-182.	0.3	25
358	Dynamics of transcription and mRNA export. Current Opinion in Cell Biology, 2005, 17, 332-339.	2.6	45
359	Potentials and pitfalls of DNA array analysis of the endothelial stress response. Biochimica Et Biophysica Acta - Molecular Cell Research, 2005, 1746, 73-84.	1.9	10
360	Complex cellular responses to reactive oxygen species. Trends in Cell Biology, 2005, 15, 319-326.	3.6	344
361	Robotic spotting of cDNA and oligonucleotide microarrays. Trends in Biotechnology, 2005, 23, 374-379.	4.9	76
362	Genome-wide analysis of HDAC function. Trends in Genetics, 2005, 21, 608-615.	2.9	111
363	GeneRank: using search engine technology for the analysis of microarray experiments. BMC Bioinformatics, 2005, 6, 233.	1.2	214
364	Measuring similarities between transcription factor binding sites. BMC Bioinformatics, 2005, 6, 237.	1.2	55
365	Fabrication of high quality microarrays. New Biotechnology, 2005, 22, 173-184.	2.7	162
366	A genomic view of eukaryotic DNA replication. Chromosome Research, 2005, 13, 309-326.	1.0	105
367	Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. Chromosome Research, 2005, 13, 259-274.	1.0	72
368	Whole-genome views of chromatin structure. Chromosome Research, 2005, 13, 289-298.	1.0	28

#	ARTICLE	IF	CITATIONS
369	Devising transcriptional regulatory networks operating during the cell cycle and differentiation using ChIP-on-chip. Chromosome Research, 2005, 13, 275-288.	1.0	7
370	A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. Plant Molecular Biology, 2005, 59, 137-149.	2.0	17
371	Predicting transcription factor activities from combined analysis of microarray and ChIP data: a partial least squares approach. Theoretical Biology and Medical Modelling, 2005, 2, 23.	2.1	98
372	Functional genomics inSaccharomyces cerevisiae. , 2005, , .		0
373	Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs. Lecture Notes in Computer Science, 2005, , 65-78.	1.0	9
374	Genetic and pharmacological inactivation of adenosine A2A receptor reveals an Egr-2-mediated transcriptional regulatory network in the mouse striatum. Physiological Genomics, 2005, 23, 89-102.	1.0	17
375	Accessible Protein Interaction Data for Network Modeling. Structure of the Information and Available Repositories. Lecture Notes in Computer Science, 2005, , 1-13.	1.0	3
376	Seven years of yeast microarray analysis. , 2005, , .		1
377	Reverse engineering gene regulatory networks. , 2005, , .		0
378	Functional networks in mammalian cells. , 2005, , .		0
379	Identification in silico of putative damage responsive elements (DRE) in promoter regions of the yeast genome. Genetics and Molecular Biology, 2005, 28, 814-820.	0.6	1
380	Analysis of Gene Regulatory Circuits. , 2005, , 265-276.		0
381	Glucocorticoid Receptor-Dependent Gene Regulatory Networks. PLoS Genetics, 2005, 1, e16.	1.5	207
382	Non-additivity in protein-DNA binding. Bioinformatics, 2005, 21, 2254-2263.	1.8	52
383	Design optimization methods for genomic DNA tiling arrays. Genome Research, 2005, 16, 271-281.	2.4	46
384	Genomic approaches for reconstructing gene networks. Pharmacogenomics, 2005, 6, 245-258.	0.6	17
385	Proteomic and genomic characterization of chromatin complexes at a boundary. Journal of Cell Biology, 2005, 169, 35-47.	2.3	130
386	Variant Histone H2A.Z Is Globally Localized to the Promoters of Inactive Yeast Genes and Regulates Nucleosome Positioning. PLoS Biology, 2005, 3, e384.	2.6	366

#	ARTICLE	IF	CITATIONS
387	Functional Genomics of Blood Pressure Determination: Dissecting and Assembling a Polygenic Trait by Experimental Genetics. Current Hypertension Reviews, 2005, 1, 35-50.	0.5	14
388	Incommensurable Goods, Alternative Possibilities, and the Self-Refutation of the Self-Refutation of Determinism. American Journal of Jurisprudence, 2005, 50, 165-171.	0.4	0
389	DIP-chip: Rapid and accurate determination of DNA-binding specificity. Genome Research, 2005, 15, 421-427.	2.4	82
390	Inference of combinatorial regulation in yeast transcriptional networks: A case study of sporulation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1998-2003.	3.3	95
391	A note on using permutation-based false discovery rate estimates to compare different analysis methods for microarray data. Bioinformatics, 2005, 21, 4280-4288.	1.8	104
392	Systems biology in the cell nucleus. Journal of Cell Science, 2005, 118, 4083-4092.	1.2	34
393	A network of transcriptionally coordinated functional modules in Saccharomyces cerevisiae. Genome Research, 2005, 15, 1298-1306.	2.4	29
394	Inferring network interactions within a cell. Briefings in Bioinformatics, 2005, 6, 380-389.	3.2	26
395	Evidence that the Elongation Factor TFIIS Plays a Role in Transcription Initiation at GAL1 in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2005, 25, 2650-2659.	1.1	47
396	Mapping Global Histone Methylation Patterns in the Coding Regions of Human Genes. Molecular and Cellular Biology, 2005, 25, 4650-4661.	1.1	101
397	Chromatin Immunoprecipitation (ChIP) on Chip Experiments Uncover a Widespread Distribution of NF-Y Binding CCAAT Sites Outside of Core Promoters. Journal of Biological Chemistry, 2005, 280, 13606-13615.	1.6	79
398	Incorporating Biological Information as a Prior in an Empirical Bayes Approach to Analyzing Microarray Data. Statistical Applications in Genetics and Molecular Biology, 2005, 4, Article12.	0.2	19
400	Computational discovery of transcriptional regulatory rules. Bioinformatics, 2005, 21, ii101-ii107.	1.8	15
401	Cell-based microarrays: current progress, future prospects. Pharmacogenomics, 2005, 6, 527-534.	0.6	13
402	Regulation of gene expression: probing DNAâ€"protein interactionsin vivoandin vitro. Expert Review of Proteomics, 2005, 2, 705-718.	1.3	14
403	Combining SELEX with quantitative assays to rapidly obtain accurate models of protein-DNA interactions. Nucleic Acids Research, 2005, 33, e141-e141.	6.5	75
404	PCR amplification from single DNA molecules on magnetic beads in emulsion: application for high-throughput screening of transcription factor targets. Nucleic Acids Research, 2005, 33, e150-e150.	6.5	109
405	Epigenetic Hypothesis Tests for Methylation and Acetylation in a Triple Microarray System. Journal of Computational Biology, 2005, 12, 370-390.	0.8	21

#	ARTICLE	IF	CITATIONS
406	A Statistical Method for Constructing Transcriptional Regulatory Networks Using Gene Expression and Sequence Data. Journal of Computational Biology, 2005, 12, 229-246.	0.8	30
407	Identification of Direct Serum-response Factor Gene Targets during Me2SO-induced P19 Cardiac Cell Differentiation. Journal of Biological Chemistry, 2005, 280, 19115-19126.	1.6	74
408	Direct isolation and identification of promoters in the human genome. Genome Research, 2005, 15, 830-839.	2.4	76
409	PBK/TOPK, a Proliferating Neural Progenitor-Specific Mitogen-Activated Protein Kinase Kinase. Journal of Neuroscience, 2005, 25, 10773-10785.	1.7	90
411	Reliable prediction of transcription factor binding sites by phylogenetic verification. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16945-16950.	3.3	43
412	Identification of the mismatch repair genes PMS2 and MLH1 as p53 target genes by using serial analysis of binding elements. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4813-4818.	3.3	109
413	Global changes in STAT target selection and transcription regulation upon interferon treatments. Genes and Development, 2005, 19, 2953-2968.	2.7	95
414	Developmentally induced changes in transcriptional program alter spatial organization across chromosomes. Genes and Development, 2005, 19, 1188-1198.	2.7	171
415	Making connections between novel transcription factors and their DNA motifs. Genome Research, 2005, 15, 312-320.	2.4	49
416	Constructing transcriptional regulatory networks. Genes and Development, 2005, 19, 1499-1511.	2.7	220
417	Immobilization of Escherichia coli RNA Polymerase and Location of Binding Sites by Use of Chromatin Immunoprecipitation and Microarrays. Journal of Bacteriology, 2005, 187, 6166-6174.	1.0	105
418	Functional Genomic Analysis of the AUXIN RESPONSE FACTOR Gene Family Members in Arabidopsis thaliana: Unique and Overlapping Functions of ARF7 and ARF19 Â. Plant Cell, 2005, 17, 444-463.	3.1	933
419	A data integration methodology for systems biology: Experimental verification. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17302-17307.	3.3	124
420	TIME SERIES ANALYSIS OF GENE EXPRESSION AND LOCATION DATA. International Journal on Artificial Intelligence Tools, 2005, 14, 755-769.	0.7	5
421	Combined Global Localization Analysis and Transcriptome Data Identify Genes That Are Directly Coregulated by Adr1 and Cat8. Molecular and Cellular Biology, 2005, 25, 2138-2146.	1.1	139
422	Genome-wide Analysis Reveals Inositol, Not Choline, as the Major Effector of Ino2p-Ino4p and Unfolded Protein Response Target Gene Expression in Yeast. Journal of Biological Chemistry, 2005, 280, 9106-9118.	1.6	112
423	Regulation of an intergenic transcript controls adjacent gene transcription in Saccharomyces cerevisiae. Genes and Development, 2005, 19, 2695-2704.	2.7	215
424	Topological units of environmental signal processing in the transcriptional regulatory network of Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7841-7846.	3.3	180

#	ARTICLE	IF	CITATIONS
425	The mobile nucleoporin Nup2p and chromatin-bound Prp20p function in endogenous NPC-mediated transcriptional control. Journal of Cell Biology, 2005, 171, 955-965.	2.3	114
426	Genomic Analysis of PIS1 Gene Expression. Eukaryotic Cell, 2005, 4, 604-614.	3.4	13
427	Genome-wide identification of Isw2 chromatin-remodeling targets by localization of a catalytically inactive mutant. Genes and Development, 2005, 19, 942-954.	2.7	100
428	Studies of the distribution of Escherichia coli cAMP-receptor protein and RNA polymerase along the E. coli chromosome. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 17693-17698.	3.3	285
429	Temporal Control of Cell Cycle Gene Expression Mediated by E2F Transcription Factors. Cell Cycle, 2005, 4, 633-636.	1.3	18
430	Identification of Novel p53 Target Genes in Ionizing Radiation Response. Cancer Research, 2005, 65, 7666-7673.	0.4	98
431	Identification of target genes in breast cancer cells directly regulated by the SRC-3/AIB1 coactivator. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1339-1344.	3.3	92
432	CpG Island microarray probe sequences derived from a physical library are representative of CpG Islands annotated on the human genome. Nucleic Acids Research, 2005, 33, 2952-2961.	6.5	89
433	RSIR: regularized sliced inverse regression for motif discovery. Bioinformatics, 2005, 21, 4169-4175.	1.8	61
434	Gene Array Technologies in Biological Investigations. Proceedings of the IEEE, 2005, 93, 737-749.	16.4	3
436	Integrative analysis of genomeâ€wide experiments in the context of a large highâ€throughput data compendium. Molecular Systems Biology, 2005, 1, 2005.0002.	3.2	44
437	Improved understanding of gene expression regulation using systems biology. Expert Review of Proteomics, 2005, 2, 915-924.	1.3	5
438	A hidden Markov model for analyzing ChIP-chip experiments on genome tiling arrays and its application to p53 binding sequences. Bioinformatics, 2005, 21, i274-i282.	1.8	94
439	Metabolic Engineering in the -omics Era: Elucidating and Modulating Regulatory Networks. Microbiology and Molecular Biology Reviews, 2005, 69, 197-216.	2.9	105
440	AREB1 Is a Transcription Activator of Novel ABRE-Dependent ABA Signaling That Enhances Drought Stress Tolerance in Arabidopsis Â. Plant Cell, 2005, 17, 3470-3488.	3.1	826
441	Parallel Profiling of Active Transcription Factors Using an Oligonucleotide Array-Based Transcription Factor Assay (OATFA). Journal of Proteome Research, 2005, 4, 1451-1456.	1.8	19
442	Finding Motifs with Insufficient Number of Strong Binding Sites. Journal of Computational Biology, 2005, 12, 686-701.	0.8	17
443	Tilling the chromatin landscape: emerging methods for the discovery and profiling of proteinâ€"DNA interactions. Biochemistry and Cell Biology, 2005, 83, 525-534.	0.9	28

#	ARTICLE	IF	CITATIONS
444	Defining a Centromere-like Element in Bacillus subtilis by Identifying the Binding Sites for the Chromosome-Anchoring Protein RacA. Molecular Cell, 2005, 17, 773-782.	4.5	93
445	Prediction of cis-regulatory elements using binding site matrices â€” the successes, the failures and the reasons for both. Current Opinion in Genetics and Development, 2005, 15, 395-402.	1.5	57
446	Comparative genomics as a tool in the understanding of eukaryotic transcriptional regulation. Current Opinion in Genetics and Development, 2005, 15, 634-639.	1.5	2
447	The SCAN domain family of zinc finger transcription factors. Gene, 2005, 359, 1-17.	1.0	104
448	Use of a restriction endonuclease cytotoxicity assay to identify inducible GAL1 promoter variants with reduced basal activity. Gene, 2005, 363, 183-192.	1.0	8
449	Acetylation in Histone H3 Globular Domain Regulates Gene Expression in Yeast. Cell, 2005, 121, 375-385.	13.5	362
450	Genome-wide Map of Nucleosome Acetylation and Methylation in Yeast. Cell, 2005, 122, 517-527.	13.5	1,242
451	The Noncanonical Binding Site of the MED-1 GATA Factor Defines Differentially Regulated Target Genes in the C. elegans Mesendoderm. Developmental Cell, 2005, 8, 427-433.	3.1	57
452	Modelling gene networks at different organisational levels. FEBS Letters, 2005, 579, 1859-1866.	1.3	47
453	A walk-through of the yeast mating pheromone response pathway. Peptides, 2005, 26, 339-350.	1.2	319
454	Applications of DNA tiling arrays for whole-genome analysis. Genomics, 2005, 85, 1-15.	1.3	376
455	Evaluation of genome-wide chromatin library of Stat5 binding sites in human breast cancer. Molecular Cancer, 2005, 4, 6.	7.9	27
456	APPLICATIONS OF DNA MICROARRAYS IN BIOLOGY. Annual Review of Biochemistry, 2005, 74, 53-82.	5.0	345
457	Chromatin Immunoprecipitation for Determining the Association of Proteins with Specific Genomic Sequences In Vivo. Current Protocols in Molecular Biology, 2005, 69, Unit 21.3.	2.9	129
458	Survey of Differentially Methylated Promoters in Prostate Cancer Cell Lines. Neoplasia, 2005, 7, 748-IN7.	2.3	92
459	From genome to epigenome. Human Molecular Genetics, 2005, 14, R3-R10.	1.4	154
460	Chipper: discovering transcription-factor targets from chromatin immunoprecipitation microarrays using variance stabilization. Genome Biology, 2005, 6, R96.	13.9	37
461	Genomic analysis of heat-shock factor targets in Drosophila. Genome Biology, 2005, 6, R63.	13.9	76

#	ARTICLE	IF	CITATIONS
462	Title is missing!. Genome Biology, 2005, 6, P7.	13.9	63
463	Genome-wide analysis of the context-dependence of regulatory networks. Genome Biology, 2005, 6, 206.	13.9	13
464	Identification of ciliary and ciliopathy genes in Caenorhabditis elegans through comparative genomics. Genome Biology, 2006, 7, R126.	13.9	86
465	BoCaTFBS: a boosted cascade learner to refine the binding sites suggested by ChIP-chip experiments. Genome Biology, 2006, 7, R102.	13.9	1
467	Mapping the Distribution of Chromatin Proteins by ChIP on Chip. Methods in Enzymology, 2006, 410, 316-341.	0.4	56
468	'Top Down' Approaches for the Study of Single-Cells: Micro-Engineering and Electrical Phenotype. Advances in Science and Technology, 2006, 53, 97-106.	0.2	3
469	Enhancers Located within Two Introns of the Vitamin D Receptor Gene Mediate Transcriptional Autoregulation by 1,25-Dihydroxyvitamin D3. Molecular Endocrinology, 2006, 20, 1231-1247.	3.7	140
470	Genome-wide mapping of Polycomb target genes unravels their roles in cell fate transitions. Genes and Development, 2006, 20, 1123-1136.	2.7	1,098
471	Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression. Genome Research, 2006, 16, 656-668.	2.4	229
472	A Computational Inference Framework for analyzing Gene Regulation Pathway using Microarray Data. , 2006, , .		0
473	Identifying synergistic transcriptional factors involved in the yeast cell cycle using Microarray and ChIP-chip data. , 2006, , .		5
474	Genome-wide analysis of human HSF1 signaling reveals a transcriptional program linked to cellular adaptation and survival. Molecular BioSystems, 2006, 2, 627.	2.9	117
475	Defining the sequence-recognition profile of DNA-binding molecules. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 867-872.	3.3	221
476	High-throughput Biology in the Postgenomic Era. Journal of Vascular and Interventional Radiology, 2006, 17, 1077-1085.	0.2	11
477	Applying whole-genome studies of epigenetic regulation to study human disease. Cytogenetic and Genome Research, 2006, 114, 1-15.	0.6	54
478	A survey of motif discovery methods in an integrated framework. Biology Direct, 2006, 1, 11.	1.9	135
479	Transcriptional Regulatory Elements in the Human Genome. Annual Review of Genomics and Human Genetics, 2006, 7, 29-59.	2.5	724
480	Genome-Wide Analysis of Protein-DNA Interactions. Annual Review of Genomics and Human Genetics, 2006, 7, 81-102.	2.5	148

#	ARTICLE	IF	CITATIONS
481	Genomic Approach for the Understanding of Dynamic Aspect of Chromosome Behavior. Methods in Enzymology, 2006, 409, 389-410.	0.4	60
482	Identifying transcription factor functions and targets by phenotypic activation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12045-12050.	3.3	156
483	Genome-wide Mapping of Histone Modifications by GMAT. Biotechnology and Genetic Engineering Reviews, 2006, 23, 93-104.	2.4	0
484	The emerging science of epigenomics. Human Molecular Genetics, 2006, 15, R95-R101.	1.4	283
485	Step out of the Groove: Epigenetic Gene Control Systems and Engineered Transcription Factors. Advances in Genetics, 2006, 56, 163-204.	0.8	24
486	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. Cell, 2006, 124, 207-219.	13.5	1,060
487	Transcription Factor Target Practice. Cell, 2006, 124, 21-23.	13.5	16
488	RISC-y Memories. Cell, 2006, 124, 23-26.	13.5	4
489	Combinatorial Analysis of Transcription Factor Partners Reveals Recruitment of c-MYC to Estrogen Receptor-Î± Responsive Promoters. Molecular Cell, 2006, 21, 393-404.	4.5	165
490	Isolating Apparently Pure Libraries of Replication Origins from Complex Genomes. Molecular Cell, 2006, 21, 719-726.	4.5	61
491	Yng1 PHD Finger Binding to H3 Trimethylated at K4 Promotes NuA3 HAT Activity at K14 of H3 and Transcription at a Subset of Targeted ORFs. Molecular Cell, 2006, 24, 785-796.	4.5	283
492	A Genome-Wide Analysis Indicates that Yeast Pre-mRNA Splicing Is Predominantly Posttranscriptional. Molecular Cell, 2006, 24, 917-929.	4.5	99
493	Condition-specific coregulation with cis-regulatory motifs and modules in the mouse genome. Genomics, 2006, 87, 500-508.	1.3	6
494	High-throughput methods of regulatory element discovery. BioTechniques, 2006, 41, 673-681.	0.8	49
495	Genome-wide approaches for identification of nuclear receptor target genes. Nuclear Receptor Signaling, 2006, 4, nrs.04018.	1.0	9
496	Mapping cis-acting regulatory variation in recombinant congenic strains. Physiological Genomics, 2006, 25, 294-302.	1.0	20
497	Chromosomal Distribution of PcG Proteins during Drosophila Development. PLoS Biology, 2006, 4, e170.	2.6	218
499	Inference of Genetic Regulatory Networks via Best-Fit Extensions. , 2006, , 259-278.		0

#	Article	IF	Citations
500	The Plant Circadian Clock: Review of a Clockwork Arabidopsis. , 0, , 1-23.		3
501	Cellular Responses to Reactive Oxygen Species. , 2006, , 281-308.		2
502	Single Cell Proteomics: Challenge for Current Analytical Science. Current Analytical Chemistry, 2006, 2, 67-76.	0.6	10
503	Distinct roles for de novo versus hydrolytic pathways of sphingolipid biosynthesis in Saccharomyces cerevisiae. Biochemical Journal, 2006, 393, 733-740.	1.7	41
504	Accuracy and Reproducibility of Proteinâ€"DNA Microarray Technology. , 2007, 104, 87-110.		10
505	Pairedâ€End diTagging for Transcriptome and Genome Analysis. Current Protocols in Molecular Biology, 2006, 75, 21.12.1.	2.9	2
506	Communication between levels of transcriptional control improves robustness and adaptivity. Molecular Systems Biology, 2006, 2, 65.	3.2	29
507	Motion as a phenotype: the use of live-cell imaging and machine visual screening to characterize transcription-dependent chromosome dynamics. BMC Cell Biology, 2006, 7, 19.	3.0	37
508	A biphasic pattern of gene expression during mouse retina development. BMC Developmental Biology, 2006, 6, 48.	2.1	42
509	A library of gene expression signatures to illuminate normal and pathological lymphoid biology. Immunological Reviews, 2006, 210, 67-85.	2.8	189
510	Functional clustering by Bayesian wavelet methods. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2006, 68, 305-332.	1.1	105
511	Computational Biology: Toward Deciphering Gene Regulatory Information in Mammalian Genomes. Biometrics, 2006, 62, 645-663.	0.8	31
512	The Hsp70 member, Ssa1, acts as a DNA-binding transcriptional co-activator of laccase in Cryptococcus neoformans. Molecular Microbiology, 2006, 62, 1090-1101.	1.2	57
513	Development of Arabidopsis whole-genome microarrays and their application to the discovery of binding sites for the TGA2 transcription factor in salicylic acid-treated plants. Plant Journal, 2006, 47, 152-162.	2.8	116
514	Modeling cellular machinery through biological network comparison. Nature Biotechnology, 2006, 24, 427-433.	9.4	492
515	High-resolution computational models of genome binding events. Nature Biotechnology, 2006, 24, 963-970.	9.4	82
516	Genome-scale mapping of DNase I sensitivity in vivo using tiling DNA microarrays. Nature Methods, 2006, 3, 511-518.	9.0	306
517	Reverse engineering cellular networks. Nature Protocols, 2006, 1, 662-671.	5.5	345

#	ARTICLE	IF	CITATIONS
518	High-throughput assay for determining specificity and affinity of protein-DNA binding interactions. Nature Protocols, 2006, 1, 215-222.	5.5	42
519	Chromatin immunoprecipitation and microarray-based analysis of protein location. Nature Protocols, 2006, 1, 729-748.	5.5	671
520	Microarray technology: beyond transcript profiling and genotype analysis. Nature Reviews Genetics, 2006, 7, 200-210.	7.7	459
521	Highly parallel genomic assays. Nature Reviews Genetics, 2006, 7, 632-644.	7.7	344
522	Yeast homolog of a cancer-testis antigen defines a new transcription complex. EMBO Journal, 2006, 25, 3576-3585.	3.5	122
523	Yeast Gal4: a transcriptional paradigm revisited. EMBO Reports, 2006, 7, 496-499.	2.0	163
524	Genomeâ€wide natural antisense transcription: coupling its regulation to its different regulatory mechanisms. EMBO Reports, 2006, 7, 1216-1222.	2.0	252
525	Strategies to unravel molecular codes essential for the development of meso-diencephalic dopaminergic neurons. Journal of Physiology, 2006, 575, 397-402.	1.3	6
526	DNA microarray technologies for measuring proteinâ€“DNA interactions. Current Opinion in Biotechnology, 2006, 17, 422-430.	3.3	164
527	Relationships between probabilistic Boolean networks and dynamic Bayesian networks as models of gene regulatory networks. Signal Processing, 2006, 86, 814-834.	2.1	106
528	The benefits of DNA microarrays in fundamental and applied bio-medicine. Materials Science and Engineering C, 2006, 26, 354-359.	3.8	13
529	A perspective of synthetic biology: Assembling building blocks for novel functions. Biotechnology Journal, 2006, 1, 690-699.	1.8	28
530	Histone H3 acetylated at lysine 9 in promoter is associated with low nucleosome density in the vicinity of transcription start site in human cell. Chromosome Research, 2006, 14, 203-211.	1.0	84
531	Organization of interphase chromatin. Chromosoma, 2006, 115, 1-14.	1.0	43
532	Global analysis of gene transcription regulation in prokaryotes. Cellular and Molecular Life Sciences, 2006, 63, 2260-2290.	2.4	49
533	The adaptive filter of the yeast galactose pathway. Journal of Theoretical Biology, 2006, 242, 372-381.	0.8	11
534	Elucidating cis- and trans-regulatory variation using genetical genomics. Trends in Genetics, 2006, 22, 245-250.	2.9	24
535	In Vitro selection of DNA binding sites for transcription factor, PhaR, from Paracoccus denitrificans using genetic library on microbeads and flow cytometry. Journal of Bioscience and Bioengineering, 2006, 101, 440-444.	1.1	16

#	ARTICLE	IF	CITATIONS
536	SimArray: a user-friendly and user-configurable microarray design tool. BMC Bioinformatics, 2006, 7, 102.	1.2	3
537	Computational reconstruction of transcriptional regulatory modules of the yeast cell cycle. BMC Bioinformatics, 2006, 7, 421.	1.2	59
538	Rank-statistics based enrichment-site prediction algorithm developed for chromatin immunoprecipitation on chip experiments. BMC Bioinformatics, 2006, 7, 434.	1.2	9
539	Computational promoter analysis of mouse, rat and human antimicrobial peptide-coding genes. BMC Bioinformatics, 2006, 7, S8.	1.2	26
540	Inferring direct regulatory targets from expression and genome location analyses: a comparison of transcription factor deletion and overexpression. BMC Genomics, 2006, 7, 215.	1.2	18
541	Genome-wide mapping of ORC and Mcm2p binding sites on tiling arrays and identification of essential ARS consensus sequences in S. cerevisiae. BMC Genomics, 2006, 7, 276.	1.2	106
542	Statistical mechanical modeling of genome-wide transcription factor occupancy data by MatrixREDUCE. Bioinformatics, 2006, 22, e141-e149.	1.8	259
543	A clustering property of highly-degenerate transcription factor binding sites in the mammalian genome. Nucleic Acids Research, 2006, 34, 2238-2246.	6.5	58
544	1,25-Dihydroxyvitamin D3 Regulates the Expression of Low-Density Lipoprotein Receptor-Related Protein 5 via Deoxyribonucleic Acid Sequence Elements Located Downstream of the Start Site of Transcription. Molecular Endocrinology, 2006, 20, 2215-2230.	3.7	81
545	Advances in the Discovery of cis-Regulatory Elements. Current Bioinformatics, 2006, 1, 321-336.	0.7	10
546	Polycomb group-dependent Cyclin A repression in Drosophila. Genes and Development, 2006, 20, 501-513.	2.7	52
547	[12] Genomic DNA as a General Cohybridization Standard for Ratiometric Microarrays. Methods in Enzymology, 2006, 410, 237-279.	0.4	6
548	A Survey of Computational Methods Used in Microarray Data Interpretation. Applied Mycology and Biotechnology, 2006, , 161-178.	0.3	8
549	[5] Automated Liquid Handling and Highâ€Throughput Preparation of Polymerase Chain Reactionâ€Amplified DNA for Microarray Fabrication. Methods in Enzymology, 2006, 410, 99-120.	0.4	4
550	[13] Analysis of Sequence Specificities of DNAâ€Binding Proteins with Protein Binding Microarrays. Methods in Enzymology, 2006, 410, 279-299.	0.4	32
551	Establishment and Regulation of Chromatin Domains: Mechanistic Insights from Studies of Hemoglobin Synthesis. Progress in Molecular Biology and Translational Science, 2006, 81, 435-471.	1.9	23
552	Microarray Technology as a Universal Tool for High-Throughput Analysis of Biological Systems. Combinatorial Chemistry and High Throughput Screening, 2006, 9, 365-380.	0.6	105
553	H-NS Mediates the Silencing of Laterally Acquired Genes in Bacteria. PLoS Pathogens, 2006, 2, e81.	2.1	471

#	ARTICLE	IF	CITATIONS
554	Genome-wide location analysis: insights on transcriptional regulation. Human Molecular Genetics, 2006, 15, R1-R7.	1.4	30
555	Iterative Reconstruction of Transcriptional Regulatory Networks: An Algorithmic Approach. PLoS Computational Biology, 2006, 2, e52.	1.5	46
556	Large-Scale Turnover of Functional Transcription Factor Binding Sites in Drosophila. PLoS Computational Biology, 2006, 2, e130.	1.5	231
557	Genome-wide identification of direct targetsof the Drosophila retinal determinationprotein Eyeless. Genome Research, 2006, 16, 466-476.	2.4	103
558	Evidence that Spt2/Sin1, an HMG-Like Factor, Plays Roles in Transcription Elongation, Chromatin Structure, and Genome Stability in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2006, 26, 1496-1509.	1.1	82
559	Target hub proteins serve as master regulators of development in yeast. Genes and Development, 2006, 20, 435-448.	2.7	153
560	Nuclear localization of the Saccharomyces cerevisiae ribonucleotide reductase small subunit requires a karyopherin and a WD40 repeat protein. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1422-1427.	3.3	41
561	Singing Mice, Songbirds, and More: Models for FOXP2 Function and Dysfunction in Human Speech and Language. Journal of Neuroscience, 2006, 26, 10376-10379.	1.7	82
562	The Chinese Hamster Dihydrofolate Reductase Replication Origin Decision Point Follows Activation of Transcription and Suppresses Initiation of Replication within Transcription Units. Molecular and Cellular Biology, 2006, 26, 1051-1062.	1.1	43
563	Histone H1 of Saccharomyces cerevisiae Inhibits Transcriptional Silencing. Genetics, 2006, 173, 579-587.	1.2	20
564	Role of the Transcription Activator Ste12p as a Repressor of PRY3 Expression. Molecular and Cellular Biology, 2006, 26, 7901-7912.	1.1	11
565	Oxidative Stress-Activated Zinc Cluster Protein Stb5 Has Dual Activator/Repressor Functions Required for Pentose Phosphate Pathway Regulation and NADPH Production. Molecular and Cellular Biology, 2006, 26, 6690-6701.	1.1	111
566	[8] Printing Your Own Inkjet Microarrays. Methods in Enzymology, 2006, 410, 168-189.	0.4	19
567	Deciphering the Roles of the Histone H2B N-Terminal Domain in Genome-Wide Transcription. Molecular and Cellular Biology, 2006, 26, 3842-3852.	1.1	77
568	PCR-based tandem epitope tagging system forEscherichia coligenome engineering. BioTechniques, 2006, 40, 67-72.	0.8	52
569	Whole-genome comparison of Leu3 binding in vitro and in vivo reveals the importance of nucleosome occupancy in target site selection. Genome Research, 2006, 16, 1517-1528.	2.4	125
570	TOS9 Regulates White-Opaque Switching in Candida albicans. Eukaryotic Cell, 2006, 5, 1674-1687.	3.4	207
571	Transcription Factor STE12Î± Has Distinct Roles in Morphogenesis, Virulence, and Ecological Fitness of the Primary Pathogenic Yeast Cryptococcus gattii. Eukaryotic Cell, 2006, 5, 1065-1080.	3.4	49

#	Article	IF	Citations
572	Gene Expression From Random Libraries of Yeast Promoters. Genetics, 2006, 172, 2113-2122.	1.2	26
573	Protein Binding Microarrays for the Characterization of DNAâ€"Protein Interactions. , 2007, 104, 65-85.		38
574	Distinct Functions of Dispersed GATA Factor Complexes at an Endogenous Gene Locus. Molecular and Cellular Biology, 2006, 26, 7056-7067.	1.1	135
575	Simple histone acetylation plays a complex role in the regulation of gene expression. Briefings in Functional Genomics & Proteomics, 2006, 5, 190-208.	3.8	113
576	Histone acetylation and transcriptional regulation in the genome of Saccharomyces cerevisiae. Bioinformatics, 2006, 22, 392-399.	1.8	16
577	Bayesian error analysis model for reconstructing transcriptional regulatory networks. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7988-7993.	3.3	44
578	Widespread, but Non-identical, Association of Proteasomal 19 and 20 S Proteins with Yeast Chromatin. Journal of Biological Chemistry, 2006, 281, 27346-27355.	1.6	59
579	Large-scale production of SAGE libraries from microdissected tissues, flow-sorted cells, and cell lines. Genome Research, 2006, 17, 108-116.	2.4	34
580	Pheromone-Induced Degradation of Ste12 Contributes to Signal Attenuation and the Specificity of Developmental Fate. Eukaryotic Cell, 2006, 5, 2147-2160.	3.4	17
581	Locating mammalian transcription factor binding sites: A survey of computational and experimental techniques. Genome Research, 2006, 16, 1455-1464.	2.4	188
582	Studying statistical properties of regulatory DNA sequences, and their use in predicting regulatory regions in the eukaryotic genomes. Briefings in Bioinformatics, 2006, 7, 48-54.	3.2	9
583	Extensive low-affinity transcriptional interactions in the yeast genome. Genome Research, 2006, 16, 962-972.	2.4	222
584	START: an automated tool for serial analysis of chromatin occupancy data. Bioinformatics, 2006, 22, 999-1001.	1.8	5
585	Model-based analysis of tiling-arrays for ChIP-chip. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 12457-12462.	3.3	390
586	Coordinated binding of NF-ÂB family members in the response of human cells to lipopolysaccharide. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 5899-5904.	3.3	157
587	The Galactose Switch in Kluyveromyces lactis Depends on Nuclear Competition between Gal4 and Gal1 for Gal80 Binding. Journal of Biological Chemistry, 2006, 281, 29337-29348.	1.6	31
588	Prediction of Genomic Functional Elements. Annual Review of Genomics and Human Genetics, 2006, 7, 315-338.	2.5	40
589	Linking DNA-binding proteins to their recognition sequences by using protein microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9940-9945.	3.3	63

#	ARTICLE	IF	CITATIONS
590	ChIP-chip Comes of Age for Genome-wide Functional Analysis: Figure 1.. Cancer Research, 2006, 66, 6899-6902.	0.4	136
591	High-resolution ChIP-chip analysis reveals that the Drosophila MSL complex selectively identifies active genes on the male X chromosome. Genes and Development, 2006, 20, 848-857.	2.7	184
592	Quantifying DNA-protein binding specificities by using oligonucleotide mass tags and mass spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3061-3066.	3.3	11
593	SWI/SNF is required for transcriptional memory at the yeast GAL gene cluster. Genes and Development, 2007, 21, 997-1004.	2.7	137
594	Identification of Mycobacterial Ïƒ Factor Binding Sites by Chromatin Immunoprecipitation Assays. Journal of Bacteriology, 2007, 189, 1505-1513.	1.0	87
595	Identification of Genes Directly Regulated by the Oncogene ZNF217 Using Chromatin Immunoprecipitation (ChIP)-Chip Assays. Journal of Biological Chemistry, 2007, 282, 9703-9712.	1.6	71
596	The Autoimmune Regulator Directly Controls the Expression of Genes Critical for Thymic Epithelial Function. Journal of Immunology, 2007, 178, 7173-7180.	0.4	46
597	Genome-wide Analysis of Histone Lysine Methylation Variations Caused by Diabetic Conditions in Human Monocytes. Journal of Biological Chemistry, 2007, 282, 13854-13863.	1.6	161
598	PfGCN5-Mediated Histone H3 Acetylation Plays a Key Role in Gene Expression in Plasmodium falciparum. Eukaryotic Cell, 2007, 6, 1219-1227.	3.4	113
599	The developmental selector <i>AS1</i> is an evolutionarily conserved regulator of the plant immune response. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18795-18800.	3.3	74
600	Approaching a complete repository of sequence-verified protein-encoding clones for Saccharomyces cerevisiae. Genome Research, 2007, 17, 536-543.	2.4	99
601	General transcription factor specified global gene regulation in archaea. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4630-4635.	3.3	105
602	Connecting protein structure with predictions of regulatory sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7068-7073.	3.3	60
603	Discovering Motifs in Ranked Lists of DNA Sequences. PLoS Computational Biology, 2007, 3, e39.	1.5	633
604	Identification and Characterization of Cell Typeâ€"Specific and Ubiquitous Chromatin Regulatory Structures in the Human Genome. PLoS Genetics, 2007, 3, e136.	1.5	196
605	A Nucleosome-Guided Map of Transcription Factor Binding Sites in Yeast. PLoS Computational Biology, 2007, 3, e215.	1.5	85
606	Nuclear receptor ERRÎ± and coactivator PGC-1Î² are effectors of IFN-Î³-induced host defense. Genes and Development, 2007, 21, 1909-1920.	2.7	194
607	TransfactomeDB: a resource for exploring the nucleotide sequence specificity and condition-specific regulatory activity of trans-acting factors. Nucleic Acids Research, 2007, 36, D125-D131.	6.5	24

#	ARTICLE	IF	CITATIONS
609	A Screen for Suppressors of Gross Chromosomal Rearrangements Identifies a Conserved Role for PLP in Preventing DNA Lesions. PLoS Genetics, 2007, 3, e134.	1.5	55
610	Computational and Experimental Approaches for Modeling Gene Regulatory Networks. Current Pharmaceutical Design, 2007, 13, 1415-1436.	0.9	51
611	The Application of Microarray Technology to the Analysis of the Cancer Genome. Current Molecular Medicine, 2007, 7, 103-120.	0.6	53
612	Global Gene Expression in Classification, Pathogenetic Understanding and Identification of Therapeutic Targets in Acute Myeloid Leukemia. Current Pharmaceutical Biotechnology, 2007, 8, 344-354.	0.9	2
613	Functional genomics via multiscale analysis: application to gene expression and ChIP-on-chip data. Bioinformatics, 2007, 23, 314-320.	1.8	5
614	GenomeTrafac: a whole genome resource for the detection of transcription factor binding site clusters associated with conventional and microRNA encoding genes conserved between mouse and human gene orthologs. Nucleic Acids Research, 2007, 35, D116-D121.	6.5	24
615	Structure-based prediction of C2H2 zinc-finger binding specificity: sensitivity to docking geometry. Nucleic Acids Research, 2007, 35, 1085-1097.	6.5	56
616	Identification of an OCT4 and SRY regulatory module using integrated computational and experimental genomics approaches. Genome Research, 2007, 17, 807-817.	2.4	59
617	Meiotic association between Spo11 regulated by Rec102, Rec104 and Rec114. Nucleic Acids Research, 2007, 35, 1119-1133.	6.5	53
618	22 Phylogenetic Footprinting. Methods in Microbiology, 2007, 36, 551-713.	0.4	1
619	Inferring Regulatory Interactions between Transcriptional Factors and Genes by Propagating Known Regulatory Links. , 2007, , .		0
620	CoCo: a web application to display, store and curate ChIP-on-chip data integrated with diverse types of gene expression data. Bioinformatics, 2007, 23, 771-773.	1.8	0
621	Heme Levels Switch the Function of Hap1 of <i>Saccharomyces cerevisiae</i> between Transcriptional Activator and Transcriptional Repressor. Molecular and Cellular Biology, 2007, 27, 7414-7424.	1.1	115
622	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. Science, 2007, 317, 815-819.	6.0	320
624	Integrating multi-source biological data for transcriptional regulatory module discovery. , 2007, , .		0
625	Gene Expression Assays. Advances in Clinical Chemistry, 2007, 44, 247-292.	1.8	32
626	HOXA5 is targeted by cell-type-specific CpG island methylation in normal cells and during the development of acute myeloid leukaemia. Carcinogenesis, 2007, 28, 299-309.	1.3	40
627	Ctk Complex-Mediated Regulation of Histone Methylation by COMPASS. Molecular and Cellular Biology, 2007, 27, 709-720.	1.1	59

#	ARTICLE	IF	CITATIONS
628	Genome-Wide Expression and Location Analyses of the <i>Candida albicans</i> Tac1p Regulon. Eukaryotic Cell, 2007, 6, 2122-2138.	3.4	118
629	Global distribution of negative cofactor 2 subunit-Â on human promoters. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10000-10005.	3.3	20
630	A core transcriptional network for early mesoderm development in Drosophila melanogaster. Genes and Development, 2007, 21, 436-449.	2.7	268
631	MOLECULAR BIOLOGY: Site-Seeing by Sequencing. Science, 2007, 316, 1441-1442.	6.0	29
632	Genome-Wide Redistribution of Meiotic Double-Strand Breaks in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2007, 27, 1868-1880.	1.1	90
633	ORegAnno: an open-access community-driven resource for regulatory annotation. Nucleic Acids Research, 2007, 36, D107-D113.	6.5	227
634	An Embarrassment of Switches. Science, 2007, 317, 758-759.	6.0	6
635	Multiple Basic Helix-Loop-Helix Proteins Regulate Expression of the ENO1 Gene of Saccharomyces cerevisiae. Eukaryotic Cell, 2007, 6, 786-796.	3.4	15
636	Genomic characterization of Gli-activator targets in sonic hedgehog-mediated neural patterning. Development (Cambridge), 2007, 134, 1977-1989.	1.2	256
637	Expansion of adult beta-cell mass in response to increased metabolic demand is dependent on HNF-4Â. Genes and Development, 2007, 21, 756-769.	2.7	145
638	Transcriptional responses to fatty acid are coordinated by combinatorial control. Molecular Systems Biology, 2007, 3, 115.	3.2	58
639	In vitro analysis of DNA-protein interactions by proximity ligation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3067-3072.	3.3	68
640	A General Framework for Designing and Validating Oligomer-Based DNA Microarrays and Its Application to Clostridium acetobutylicum. Applied and Environmental Microbiology, 2007, 73, 4631-4638.	1.4	22
641	24 Bioinformatic Prediction of Yeast Gene Function. Methods in Microbiology, 2007, , 597-628.	0.4	4
642	Msc1 Acts Through Histone H2A.Z to Promote Chromosome Stability in<i>Schizosaccharomyces pombe</i>. Genetics, 2007, 177, 1487-1497.	1.2	34
643	Predictive Modeling of Genome-Wide mRNA Expression: From Modules to Molecules. Annual Review of Biophysics and Biomolecular Structure, 2007, 36, 329-347.	18.3	75
644	Precise physical models of protein-DNA interaction from high-throughput data. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 501-506.	3.3	67
645	Sensitive ChIP-DSL technology reveals an extensive estrogen receptor Â-binding program on human gene promoters. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4852-4857.	3.3	120

#	ARTICLE	IF	CITATIONS
646	Reconstructing dynamic regulatory maps. Molecular Systems Biology, 2007, 3, 74.	3.2	183
648	Calling cards for DNA-binding proteins. Genome Research, 2007, 17, 1202-1209.	2.4	34
649	Wnt/Î²â€catenin â€mediated transcriptional regulation. Advances in Developmental Biology (Amsterdam,) Tj ETQq0 0 0 rgBT /Overlock 1	0.4	11
651	Identifying synergistic regulation involving c-Myc and sp1 in human tissues. Nucleic Acids Research, 2007, 35, 1098-1107.	6.5	33
652	Genome-wide analysis of chromatin status using tiling microarrays. Methods, 2007, 41, 304-311.	1.9	17
653	Analysis of transcription, chromatin dynamics and epigenetic changes in neural genes. Progress in Neurobiology, 2007, 83, 195-210.	2.8	8
654	Molecular profiling of stem cells. Clinica Chimica Acta, 2007, 378, 24-32.	0.5	17
655	Perspectives on mechanisms of gene regulation by 1,25-dihydroxyvitamin D3 and its receptor. Journal of Steroid Biochemistry and Molecular Biology, 2007, 103, 389-395.	1.2	70
656	Epigenetic Regulation of Hematopoietic Differentiation by Gfi-1 and Gfi-1b Is Mediated by the Cofactors CoREST and LSD1. Molecular Cell, 2007, 27, 562-572.	4.5	340
657	Gene Regulation in the Postgenomic Era: Technology Takes the Wheel. Molecular Cell, 2007, 28, 708-714.	4.5	15
658	Residue-level prediction of DNA-binding sites and its application on DNA-binding protein predictions. FEBS Letters, 2007, 581, 1058-1066.	1.3	61
659	Identification of the Transcriptional Targets of FOXP2, a Gene Linked to Speech and Language, in Developing Human Brain. American Journal of Human Genetics, 2007, 81, 1144-1157.	2.6	262
660	PAZAR: a framework for collection and dissemination of cis-regulatory sequence annotation. Genome Biology, 2007, 8, R207.	13.9	89
661	Genomic mapping of Suppressor of Hairy-wing binding sites in Drosophila. Genome Biology, 2007, 8, R167.	13.9	56
662	The Sas3p and Gcn5p histone acetyltransferases are recruited to similar genes. Genome Biology, 2007, 8, R119.	13.9	43
663	Microarray Data Analysis. Methods in Molecular Biology, 2007, , .	0.4	5
664	Microarray Technology and Cancer Gene Profiling. , 2007, , .		6
665	Functional Genomics of the Chickenâ€"A Model Organism. Poultry Science, 2007, 86, 2059-2094.	1.5	95

#	Article	IF	Citations
666	Pairedâ€End diTagging for Transcriptome and Genome Analysis. Current Protocols in Molecular Biology, 2007, 79, Unit 21.12.	2.9	12
667	Chromatin profiling in model organisms. Briefings in Functional Genomics & Proteomics, 2007, 6, 133-140.	3.8	17
668	Transcriptional regulation of protein complexes within and across species. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1283-1288.	3.3	52
669	SVMotif: A Machine Learning Motif Algorithm. , 2007, , .		5
670	ChIPâ€chip for Genomeâ€Wide Analysis of Protein Binding in Mammalian Cells. Current Protocols in Molecular Biology, 2007, 79, Unit 21.13.	2.9	22
671	FAIRE (Formaldehyde-Assisted Isolation of Regulatory Elements) isolates active regulatory elements from human chromatin. Genome Research, 2007, 17, 877-885.	2.4	830
672	Tools for visually exploring biological networks. Bioinformatics, 2007, 23, 2651-2659.	1.8	220
673	Identification of novel androgen receptor target genes in prostate cancer. Molecular Cancer, 2007, 6, 39.	7.9	88
674	Inferring Gene Regulatory Networks. , 0, , 807-827.		1
675	Wide-Scale Analysis of Human Functional Transcription Factor Binding Reveals a Strong Bias towards the Transcription Start Site. PLoS ONE, 2007, 2, e807.	1.1	55
676	Finding cis-regulatory elements using comparative genomics: Some lessons from ENCODE data. Genome Research, 2007, 17, 775-786.	2.4	69
677	ChIPping away at proteinâ€“DNA interactions. Nature Reviews Genetics, 2007, 8, S13-S13.	7.7	1
679	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Nature Precedings, 2007, , .	0.1	0
680	Insights on the Functional Role of Chromatin Remodelers in Osteogenic Cells. Critical Reviews in Eukaryotic Gene Expression, 2007, 17, 103-113.	0.4	9
681	Human stem cells, chromatin, and tissue engineering: Boosting relevancy in developmental toxicity testing. Birth Defects Research Part C: Embryo Today Reviews, 2007, 81, 20-40.	3.6	6
682	Identification of novel Runx2 targets in osteoblasts: Cell type-specific BMP-dependent regulation of Tram2. Journal of Cellular Biochemistry, 2007, 102, 1458-1471.	1.2	25
683	Epigenetics in development. Developmental Dynamics, 2007, 236, 1144-1156.	0.8	227
684	Microbial regulatory and metabolic networks. Current Opinion in Biotechnology, 2007, 18, 360-364.	3.3	29

#	Article	IF	Citations
685	Puces Ã ADN. Irbm, 2007, 28, 210-215.	3.7	6
686	Incorporating prior information via shrinkage: a combined analysis of genome-wide location data and gene expression data. Statistics in Medicine, 2007, 26, 2258-2275.	0.8	4
687	Pituitary tumor transforming gene interacts with Sp1 to modulate G1/S cell phase transition. Oncogene, 2007, 26, 5596-5605.	2.6	82
688	Genome-wide in situ exon capture for selective resequencing. Nature Genetics, 2007, 39, 1522-1527.	9.4	635
689	ChIP-seq: welcome to the new frontier. Nature Methods, 2007, 4, 613-614.	9.0	215
690	Prion biology: the quest for the test. Nature Methods, 2007, 4, 614-616.	9.0	11
691	Integrating physical and genetic maps: from genomes to interaction networks. Nature Reviews Genetics, 2007, 8, 699-710.	7.7	192
692	Identification of novel functional TBP-binding sites and general factor repertoires. EMBO Journal, 2007, 26, 944-954.	3.5	97
693	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
694	Imaging Drosophila gene activation and polymerase pausing in vivo. Nature, 2007, 450, 198-202.	13.7	65
695	Mixture Modeling for Genome-Wide Localization of Transcription Factors. Biometrics, 2007, 63, 10-21.	0.8	38
696	ChIP-chip: Data, Model, and Analysis. Biometrics, 2007, 63, 787-796.	0.8	61
697	Identifying regulatory targets of cell cycle transcription factors using gene expression and ChIP-chip data. BMC Bioinformatics, 2007, 8, 188.	1.2	35
698	Ringo â€" an R/Bioconductor package for analyzing ChIP-chip readouts. BMC Bioinformatics, 2007, 8, 221.	1.2	148
699	Bayesian hierarchical model for transcriptional module discovery by jointly modeling gene expression and ChIP-chip data. BMC Bioinformatics, 2007, 8, 283.	1.2	25
700	Differential analysis for high density tiling microarray data. BMC Bioinformatics, 2007, 8, 359.	1.2	6
701	fREDUCE: Detection of degenerate regulatory elements using correlation with expression. BMC Bioinformatics, 2007, 8, 399.	1.2	14
702	A systematic approach to detecting transcription factors in response to environmental stresses. BMC Bioinformatics, 2007, 8, 473.	1.2	14

#	Article	IF	Citations
703	ChIP on SNP-chip for genome-wide analysis of human histone H4 hyperacetylation. BMC Genomics, 2007, 8, 322.	1.2	13
704	Identification of plant promoter constituents by analysis of local distribution of short sequences. BMC Genomics, 2007, 8, 67.	1.2	142
705	Function and regulation in MAPK signaling pathways: Lessons learned from the yeast Saccharomyces cerevisiae. Biochimica Et Biophysica Acta - Molecular Cell Research, 2007, 1773, 1311-1340.	1.9	523
706	Techniques used in studies of epigenome dysregulation due to aberrant DNA methylation: An emphasis on fetal-based adult diseases. Reproductive Toxicology, 2007, 23, 267-282.	1.3	82
707	Bacterial response regulators: versatile regulatory strategies from common domains. Trends in Biochemical Sciences, 2007, 32, 225-234.	3.7	286
708	Yeast systems biology: modelling the winemaker's art. Trends in Biotechnology, 2007, 25, 349-355.	4.9	35
709	Chromatin structure in the genomics era. Trends in Genetics, 2007, 23, 67-73.	2.9	20
710	A portrait of cisplatin-induced transcriptional changes in mouse embryonic stem cells reveals a dominant p53-like response. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2007, 617, 58-70.	0.4	16
711	PhosphoPepâ€"a phosphoproteome resource for systems biology research in <i>Drosophila</i> Kc167 cells. Molecular Systems Biology, 2007, 3, 139.	3.2	168
712	Paired-End Genomic Signature Tags: A Method for the Functional Analysis of Genomes and Epigenomes. , 2007, 28, 159-173.		16
713	Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms. Functional and Integrative Genomics, 2007, 7, 335-345.	1.4	22
714	Context Specific Transcription Factor Prediction. Annals of Biomedical Engineering, 2007, 35, 1053-1067.	1.3	5
715	Integrative content-driven concepts for bioinformatics â€œbeyond the cellâ€. Journal of Biosciences, 2007, 32, 169-180.	0.5	11
716	Of patterns and pathways: microarray technologies for the analysis of filamentous fungi. Fungal Biology Reviews, 2007, 21, 171-178.	1.9	18
717	Brief review: frontiers in the computational studies of gene regulations. Frontiers of Electrical and Electronic Engineering in China: Selected Publications From Chinese Universities, 2008, 3, 251-259.	0.6	1
718	Transcriptional regulators of seven yeast species: Comparative genome analysis â€" Review. Folia Microbiologica, 2008, 53, 275-287.	1.1	9
719	Better estimation of protein-DNA interaction parameters improve prediction of functional sites. BMC Biotechnology, 2008, 8, 94.	1.7	9
720	Structureâ€based prediction of transcription factor binding sites using a proteinâ€DNA docking approach. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1114-1124.	1.5	39

#	ARTICLE	IF	CITATIONS
721	A systems biology approach to prediction of oncogenes and molecular perturbation targets in Bâ€cell lymphomas. Molecular Systems Biology, 2008, 4, 169.	3.2	191
722	Hierarchical modeling of clinical and expression quantitative trait loci. Heredity, 2008, 101, 271-284.	1.2	10
723	Epigenetic silencing of tumour suppressor gene p15 by its antisense RNA. Nature, 2008, 451, 202-206.	13.7	777
724	Predicting expression patterns from regulatory sequence in Drosophila segmentation. Nature, 2008, 451, 535-540.	13.7	434
725	Global control of cell-cycle transcription by coupled CDK and network oscillators. Nature, 2008, 453, 944-947.	13.7	269
726	Genome-wide mapping of allele-specific protein-DNA interactions in human cells. Nature Methods, 2008, 5, 307-309.	9.0	48
727	BAC TransgeneOmics: a high-throughput method for exploration of protein function in mammals. Nature Methods, 2008, 5, 409-415.	9.0	568
728	'Calling Cards' method for high-throughput identification of targets of yeast DNA-binding proteins. Nature Protocols, 2008, 3, 1569-1577.	5.5	14
729	Analysis of epigenetic modifications of chromatin at specific gene loci by native chromatin immunoprecipitation of nucleosomes isolated using hydroxyapatite chromatography. Nature Protocols, 2008, 3, 398-409.	5.5	92
730	The properties of high-dimensional data spaces: implications for exploring gene and protein expression data. Nature Reviews Cancer, 2008, 8, 37-49.	12.8	483
731	Genome-wide approaches to studying chromatin modifications. Nature Reviews Genetics, 2008, 9, 179-191.	7.7	343
732	The next generation of microarray research: applications in evolutionary and ecological genomics. Heredity, 2008, 100, 141-149.	1.2	50
733	Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. BMC Bioinformatics, 2008, 9, 203.	1.2	35
734	Prediction of regulatory elements in mammalian genomes using chromatin signatures. BMC Bioinformatics, 2008, 9, 547.	1.2	92
735	Genome-wide analysis of alternative promoters of human genes using a custom promoter tiling array. BMC Genomics, 2008, 9, 349.	1.2	50
736	Identifying gene regulatory modules of heat shock response in yeast. BMC Genomics, 2008, 9, 439.	1.2	42
737	All and only CpG containing sequences are enriched in promoters abundantly bound by RNA polymerase II in multiple tissues. BMC Genomics, 2008, 9, 67.	1.2	52
738	Transcriptome profiling of Saccharomyces cerevisiae mutants lacking C2H2 zinc finger proteins. BMC Genomics, 2008, 9, S14.	1.2	8

#	ARTICLE	IF	CITATIONS
739	Stochastic analysis of the GAL genetic switch in Saccharomyces cerevisiae: Modeling and experiments reveal hierarchy in glucose repression. BMC Systems Biology, 2008, 2, 97.	3.0	7
740	Central corticosteroid actions: Search for gene targets. European Journal of Pharmacology, 2008, 583, 272-289.	1.7	132
741	Genome-wide RNA polymerase II: not genes only!. Trends in Biochemical Sciences, 2008, 33, 265-273.	3.7	63
742	The impact of next-generation sequencing technology on genetics. Trends in Genetics, 2008, 24, 133-141.	2.9	1,848
743	Plasmodium in the Postgenomic Era: New Insights into the Molecular Cell Biology of Malaria Parasites. International Review of Cell and Molecular Biology, 2008, 266, 85-156.	1.6	62
744	Gene Expression Analysis of Neural Cells and Tissues Using DNA Microarrays. Current Protocols in Neuroscience, 2008, 45, Unit 4.28.	2.6	8
745	Topoisomerase IIÎ² Activates a Subset of Neuronal Genes that Are Repressed in AT-Rich Genomic Environment. PLoS ONE, 2008, 3, e4103.	1.1	55
746	Model-based Analysis of ChIP-Seq (MACS). Genome Biology, 2008, 9, R137.	13.9	13,517
747	High-resolution analysis of condition-specific regulatory modules in Saccharomyces cerevisiae. Genome Biology, 2008, 9, R2.	13.9	6
749	Genome-wide identification of<i>in vivo</i>protein-DNA binding sites from ChIP-Seq data. Nucleic Acids Research, 2008, 36, 5221-5231.	6.5	500
750	Mediator-Dependent Recruitment of TFIIH Modules in Preinitiation Complex. Molecular Cell, 2008, 31, 337-346.	4.5	131
751	Integrated approaches to uncovering transcription regulatory networks in mammalian cells. Genomics, 2008, 91, 219-231.	1.3	38
752	Applications of next-generation sequencing technologies in functional genomics. Genomics, 2008, 92, 255-264.	1.3	1,013
753	Assessing TF regulatory relationships of divergently transcribed genes. Genomics, 2008, 92, 316-321.	1.3	2
754	Imaging transcription dynamics at endogenous genes in living Drosophila tissues. Methods, 2008, 45, 233-241.	1.9	25
755	A Comparative Study on Computational Two-Block Motif Detection: Algorithms and Applications. Molecular Pharmaceutics, 2008, 5, 3-16.	2.3	17
756	Expanding the specificity of DNA targeting by harnessing cooperative assembly. Biochimie, 2008, 90, 1015-1025.	1.3	24
757	An Extended Transcriptional Network for Pluripotency of Embryonic Stem Cells. Cell, 2008, 132, 1049-1061.	13.5	1,226

#	ARTICLE	IF	CITATIONS
758	Future impact of integrated high-throughput methylome analyses on human health and disease. Journal of Genetics and Genomics, 2008, 35, 391-401.	1.7	41
759	Tackling the epigenome in the pluripotent stem cells. Journal of Genetics and Genomics, 2008, 35, 403-412.	1.7	13
760	Next-Generation DNA Sequencing Methods. Annual Review of Genomics and Human Genetics, 2008, 9, 387-402.	2.5	1,788
761	Global Regulators of Transcription in Escherichia coli: Mechanisms of Action and Methods for Study. Advances in Applied Microbiology, 2008, 65, 93-113.	1.3	29
762	Global organization of replication time zones of the mouse genome. Genome Research, 2008, 18, 1562-1570.	2.4	148
764	Systematic screens for human disease genes, from yeast to human and back. Molecular BioSystems, 2008, 4, 18-29.	2.9	45
765	Steps towards a repertoire of comprehensive maps of human protein interaction networks: the Human Proteotheque Initiative (HuPI)This paper is one of a selection of papers published in this Special Issue, entitled CSBMCB â€" Systems and Chemical Biology, and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2008, 86, 149-156.	0.9	5
766	Incorporating Gene Functions into Regression Analysis of DNA-Protein Binding Data and Gene Expression Data to Construct Transcriptional Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 401-415.	1.9	5
767	Identifying Combinatorial Transcription Factor Interactions with Microarray Data and ChIP-Chip Data. , 2008, , .		0
768	Novel High-Throughput Profiling of Human Transcription Factors and Its Use for Systematic Pathway Mapping. Journal of Proteome Research, 2008, 7, 2769-2779.	1.8	16
769	Fluorescence Recovery Assay for the Detection of Proteinâ˘'DNA Binding. Analytical Chemistry, 2008, 80, 5616-5621.	3.2	48
770	Development of a Novel Oligonucleotide Array-Based Transcription Factor Assay Platform for Genome-Wide Active Transcription Factor Profiling in <i>Saccharomyces cerevisiae</i>. Journal of Proteome Research, 2008, 7, 1315-1325.	1.8	5
771	Evolutionary Conservation and Interacting Preference for Identifying Protein-DNA Interactions. , 2008, , .		0
772	Osteoporosis. Methods in Molecular Biology, 2008, 455, v-vi.	0.4	6
773	Chromatin structure analyses identify miRNA promoters. Genes and Development, 2008, 22, 3172-3183.	2.7	541
774	Using ChIP-chip technology to reveal common principles of transcriptional repression in normal and cancer cells. Genome Research, 2008, 18, 521-532.	2.4	44
775	W-AlignACE: an improved Gibbs sampling algorithm based on more accurate position weight matrices learned from sequence and gene expression/ChIP-chip data. Bioinformatics, 2008, 24, 1121-1128.	1.8	36
776	Integrating quantitative information from ChIP-chip experiments into motif finding. Biostatistics, 2008, 9, 51-65.	0.9	6

#	ARTICLE	IF	CITATIONS
777	Improved genome-wide localization by ChIP-chip using double-round T7 RNA polymerase-based amplification. Nucleic Acids Research, 2008, 36, e21-e21.	6.5	35
778	Model-based deconvolution of genome-wide DNA binding. Bioinformatics, 2008, 24, 396-403.	1.8	44
779	Histone Methylation Patterns Are Cell-Type Specific in Human Monocytes and Lymphocytes and Well Maintained at Core Genes. Journal of Immunology, 2008, 180, 2264-2269.	0.4	41
780	<i>Saccharomyces cerevisiae</i> Yta7 Regulates Histone Gene Expression. Genetics, 2008, 179, 291-304.	1.2	42
781	Statistical Methods in Integrative Analysis for Gene Regulatory Modules. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article 28.	0.2	3
782	Global histone acetylation induces functional genomic reorganization at mammalian nuclear pore complexes. Genes and Development, 2008, 22, 627-639.	2.7	165
783	A Bayesian approach to assessing differential expression of microarray data. Journal of Statistical Computation and Simulation, 2008, 78, 179-191.	0.7	1
784	Whole Genome Amplification by T7-Based Linear Amplification of DNA (TLAD): Overview. Cold Spring Harbor Protocols, 2008, 2008, pdb.top42-pdb.top42.	0.2	8
785	Lymphocytes From Patients With Type 1 Diabetes Display a Distinct Profile of Chromatin Histone H3 Lysine 9 Dimethylation. Diabetes, 2008, 57, 3189-3198.	0.3	236
787	Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. Molecular and Cellular Biology, 2008, 28, 2732-2744.	1.1	208
788	Yeast linker histone Hho1p is required for efficient RNA polymerase I processivity and transcriptional silencing at the ribosomal DNA. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11703-11708.	3.3	22
789	Characterization of genome-wide p53-binding sites upon stress response. Nucleic Acids Research, 2008, 36, 3639-3654.	6.5	199
790	Genome-Wide Analysis of the Homeobox C6 Transcriptional Network in Prostate Cancer. Cancer Research, 2008, 68, 1988-1996.	0.4	62
791	Binding Characteristics and Regulatory Mechanisms of the Transcription Factors Controlling Oleate-responsive Genes in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2008, 283, 10264-10275.	1.6	33
792	Genome-wide analysis of Fis binding in <i>Escherichia coli</i> indicates a causative role for A-/AT-tracts. Genome Research, 2008, 18, 900-910.	2.4	164
793	Statistical Modeling of Transcription Factor Binding Affinities Predicts Regulatory Interactions. PLoS Computational Biology, 2008, 4, e1000039.	1.5	54
794	Modeling ChIP Sequencing In Silico with Applications. PLoS Computational Biology, 2008, 4, e1000158.	1.5	70
795	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. PLoS Biology, 2008, 6, e256.	2.6	172

#	Article	IF	Citations
796	Nuclear Receptor Location Analyses in Mammalian Genomes: From Gene Regulation to Regulatory Networks. Molecular Endocrinology, 2008, 22, 1999-2011.	3.7	33
797	A Feature-Based Approach to Modeling Proteinâ€"DNA Interactions. PLoS Computational Biology, 2008, 4, e1000154.	1.5	89
798	Myc Oncogene-Induced Genomic Instability: DNA Palindromes in Bursal Lymphomagenesis. PLoS Genetics, 2008, 4, e1000132.	1.5	25
799	Epigenetic Reprogramming by Adenovirus e1a. Science, 2008, 321, 1086-1088.	6.0	207
800	Transcription Factors Bind Thousands of Active and Inactive Regions in the Drosophila Blastoderm. PLoS Biology, 2008, 6, e27.	2.6	428
801	A high-throughput percentage-of-binding strategy to measure binding energies in DNAâ€"protein interactions: application to genome-scale site discovery. Nucleic Acids Research, 2008, 36, 4863-4871.	6.5	21
802	Fast network component analysis (FastNCA) for gene regulatory network reconstruction from microarray data. Bioinformatics, 2008, 24, 1349-1358.	1.8	77
803	Poisson approximation for significance in genome-wide ChIP-chip tiling arrays. Bioinformatics, 2008, 24, 2825-2831.	1.8	11
804	Genomics of mRNA turnover. Briefings in Functional Genomics & Proteomics, 2008, 6, 282-291.	3.8	23
805	Afi1p Functions as an Arf3p Polarization-specific Docking Factor for Development of Polarity. Journal of Biological Chemistry, 2008, 283, 16915-16927.	1.6	12
806	Clustering of yeast tRNA genes is mediated by specific association of condensin with tRNA gene transcription complexes. Genes and Development, 2008, 22, 2204-2214.	2.7	200
807	Epigenetics meets next-generation sequencing. Epigenetics, 2008, 3, 318-321.	1.3	36
808	Antisense Masking Reveals Contributions of mRNA-rRNA Base Pairing to Translation of Gtx and FGF2 mRNAs. Journal of Biological Chemistry, 2008, 283, 33087-33093.	1.6	15
809	Systems biology at the Institute for Systems Biology. Briefings in Functional Genomics & Proteomics, 2008, 7, 239-248.	3.8	65
810	Structural systems identification of genetic regulatory networks. Bioinformatics, 2008, 24, 553-560.	1.8	17
811	Genome-wide location analysis reveals a role of TFIIS in RNA polymerase III transcription. Genes and Development, 2008, 22, 1934-1947.	2.7	59
812	Statistical methods to infer cooperative binding among transcription factors in <i>Saccharomyces cerevisiae</i>. Bioinformatics, 2008, 24, 545-552.	1.8	26
813	Optimization of experimental design parameters for high-throughput chromatin immunoprecipitation studies. Nucleic Acids Research, 2008, 36, e144-e144.	6.5	28

#	ARTICLE	IF	CITATIONS
815	Transcriptional enhancement by GATA1-occupied DNA segments is strongly associated with evolutionary constraint on the binding site motif. Genome Research, 2008, 18, 1896-1905.	2.4	29
816	Machine Learning for Protein Structure and Function Prediction. Annual Reports in Computational Chemistry, 2008, , 41-66.	0.9	6
817	High-throughput evaluation of aryl hydrocarbon receptor-binding sites selected via chromatin immunoprecipitation-based screening in Hepa-1c1c7 cells stimulated with 2,3,7,8-tetrachlorodibenzo-p-dioxin. Genes and Genetic Systems, 2008, 83, 455-468.	0.2	16
819	Methods for studying global patterns of DNA binding by bacterial transcription factors and RNA polymerase. Biochemical Society Transactions, 2008, 36, 754-757.	1.6	16
820	Next-generation sequencing: applications beyond genomes. Biochemical Society Transactions, 2008, 36, 1091-1096.	1.6	111
821	From Eâ€MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. Molecular Systems Biology, 2008, 4, 209.	3.2	69
822	Epigenomics. Current Drug Metabolism, 2008, 9, 232-237.	0.7	7
825	Complex networks: the key to systems biology. Genetics and Molecular Biology, 2008, 31, 591-601.	0.6	71
826	ChromaSig: A Probabilistic Approach to Finding Common Chromatin Signatures in the Human Genome. PLoS Computational Biology, 2008, 4, e1000201.	1.5	135
827	Identification of Direct Target Genes Using Joint Sequence and Expression Likelihood with Application to DAF-16. PLoS ONE, 2008, 3, e1821.	1.1	8
828	Inferring Condition-Specific Modulation of Transcription Factor Activity in Yeast through Regulon-Based Analysis of Genomewide Expression. PLoS ONE, 2008, 3, e3112.	1.1	35
829	METHODS FOR STUDYING TRANSCRIPTION FACTORS. , 2008, , 29-67.		0
831	An integrated workflow for analysis of ChIP-chip data. BioTechniques, 2008, 45, 131-140.	0.8	17
832	ChIP-Seq: Mapping of Proteinâ€“DNA Interactions. , 0, , 201-215.		1
835	Understanding the regulatory genome. International Journal of Developmental Biology, 2009, 53, 1367-1378.	0.3	19
836	Recent Advances in the Computational Discovery of Transcription Factor Binding Sites. Algorithms, 2009, 2, 582-605.	1.2	22
837	A Noncanonical Bromodomain in the AAA ATPase Protein Yta7 Directs Chromosomal Positioning and Barrier Chromatin Activity. Molecular and Cellular Biology, 2009, 29, 4604-4611.	1.1	34
838	Cooperative Transcriptional Regulation of the Essential Pancreatic Islet Gene NeuroD1 (Beta2) by Nkx2.2 and Neurogenin 3. Journal of Biological Chemistry, 2009, 284, 31236-31248.	1.6	55

#	ARTICLE	IF	CITATIONS
839	High-throughput molecular analysis in lung cancer: insights into biology and potential clinical applications. European Respiratory Journal, 2009, 34, 489-506.	3.1	44
840	Incorporating nucleosomes into thermodynamic models of transcription regulation. Genome Research, 2009, 19, 1480-1496.	2.4	87
841	Chromatin Immunoprecipitation (ChIP). Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5279.	0.2	203
842	A single transcription factor regulates evolutionarily diverse but functionally linked metabolic pathways in response to nutrient availability. Molecular Systems Biology, 2009, 5, 282.	3.2	55
843	Repression of DNA-binding dependent glucocorticoid receptor-mediated gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16598-16603.	3.3	94
844	Duality of Enhancer Functioning Mode Revealed in a Reduced TCRÎ² Gene Enhancer Knockin Mouse Model. Journal of Immunology, 2009, 183, 7939-7948.	0.4	13
845	Flynet: a genomic resource for <i>Drosophila melanogaster</i> transcriptional regulatory networks. Bioinformatics, 2009, 25, 3001-3004.	1.8	3
846	Silencing of Host Cell<i>CYBB</i>Gene Expression by the Nuclear Effector AnkA of the Intracellular Pathogen<i>Anaplasma phagocytophilum</i>. Infection and Immunity, 2009, 77, 2385-2391.	1.0	136
847	Reconstructing transcriptional regulatory networks through genomics data. Statistical Methods in Medical Research, 2009, 18, 595-617.	0.7	19
848	Prevalence of transcription promoters within archaeal operons and coding sequences. Molecular Systems Biology, 2009, 5, 285.	3.2	114
849	Comparative study on ChIP-seq data: normalization and binding pattern characterization. Bioinformatics, 2009, 25, 2334-2340.	1.8	56
850	Detecting Gene Regulatory Networks from Microarray Data Using Fuzzy Logic. Studies in Fuzziness and Soft Computing, 2009, , 141-163.	0.6	6
851	CoCAS: a ChIP-on-chip analysis suite. Bioinformatics, 2009, 25, 954-955.	1.8	25
852	Genome-Wide Analysis of Histone H3 Lysine 4 Trimethylation in Peripheral Blood Mononuclear Cells of Minimal Change Nephrotic Syndrome Patients. American Journal of Nephrology, 2009, 30, 505-513.	1.4	15
853	Genome-wide de novo prediction of cis-regulatory binding sites in prokaryotes. Nucleic Acids Research, 2009, 37, e72-e72.	6.5	29
854	Identification of new Rel/NFÎºB regulatory networks by focused genome location analysis. Cell Cycle, 2009, 8, 2093-2100.	1.3	36
855	Epigenetic patterns of embryonic and adult stem cells. Cell Cycle, 2009, 8, 809-817.	1.3	50
856	Distinguishing direct versus indirect transcription factorâ€“DNA interactions. Genome Research, 2009, 19, 2090-2100.	2.4	128

#	ARTICLE	IF	CITATIONS
857	The Euchromatic and Heterochromatic Landscapes Are Shaped by Antagonizing Effects of Transcription on H2A.Z Deposition. PLoS Genetics, 2009, 5, e1000687.	1.5	117
858	Epigenetic Silencing of Host Cell Defense Genes Enhances Intracellular Survival of the Rickettsial Pathogen Anaplasma phagocytophilum. PLoS Pathogens, 2009, 5, e1000488.	2.1	125
859	UniPROBE: an online database of protein binding microarray data on protein-DNA interactions. Nucleic Acids Research, 2009, 37, D77-D82.	6.5	325
860	How eukaryotic genes are transcribed. Critical Reviews in Biochemistry and Molecular Biology, 2009, 44, 117-141.	2.3	129
861	Genome-Wide Promoter Analysis of the <i>SOX4</i> Transcriptional Network in Prostate Cancer Cells. Cancer Research, 2009, 69, 709-717.	0.4	176
862	Double error shrinkage method for identifying protein binding sites observed by tiling arrays with limited replication. Bioinformatics, 2009, 25, 2486-2491.	1.8	1
863	W-ChIPMotifs: a web application tool for <i>de novo</i> motif discovery from ChIP-based high-throughput data. Bioinformatics, 2009, 25, 3191-3193.	1.8	42
864	Utilizing gene pair orientations for HMM-based analysis of promoter array ChIP-chip data. Bioinformatics, 2009, 25, 2118-2125.	1.8	7
865	ChIP-on-chip significance analysis reveals large-scale binding and regulation by human transcription factor oncogenes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 244-249.	3.3	74
866	Functional diversity for REST (NRSF) is defined by in vivo binding affinity hierarchies at the DNA sequence level. Genome Research, 2009, 19, 994-1005.	2.4	73
867	Serial Analysis of Binding Elements for Transcription Factors. Methods in Molecular Biology, 2009, 567, 113-132.	0.4	0
868	Primary sequence and epigenetic determinants of in vivo occupancy of genomic DNA by GATA1. Nucleic Acids Research, 2009, 37, 7024-7038.	6.5	29
869	Histone H2A.Z is essential for estrogen receptor signaling. Genes and Development, 2009, 23, 1522-1533.	2.7	133
870	Hierarchical hidden Markov model with application to joint analysis of ChIP-chip and ChIP-seq data. Bioinformatics, 2009, 25, 1715-1721.	1.8	33
871	High-resolution DNA-binding specificity analysis of yeast transcription factors. Genome Research, 2009, 19, 556-566.	2.4	365
872	Temporal Induction Pattern of STAT4 Target Genes Defines Potential for Th1 Lineage-Specific Programming. Journal of Immunology, 2009, 183, 3839-3847.	0.4	64
873	Predicting functionality of proteinâ€“DNA interactions by integrating diverse evidence. Bioinformatics, 2009, 25, i137-i144.	1.8	38
874	Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. Current Opinion in Plant Biology, 2009, 12, 107-118.	3.5	261

#	ARTICLE	IF	CITATIONS
875	Improved ChIP-chip analysis by a mixture model approach. BMC Bioinformatics, 2009, 10, 173.	1.2	5
876	Evaluation of a microarray-hybridization based method applicable for discovery of single nucleotide polymorphisms (SNPs) in the Pseudomonas aeruginosa genome. BMC Genomics, 2009, 10, 29.	1.2	22
877	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. BMC Genomics, 2009, 10, 37.	1.2	137
878	A functional analysis of the CREB signaling pathway using HaloCHIP-chip and high throughput reporter assays. BMC Genomics, 2009, 10, 497.	1.2	25
879	Upstream sequence elements direct post-transcriptional regulation of gene expression under stress conditions in yeast. BMC Genomics, 2009, 10, 7.	1.2	87
880	An integrative ChIP-chip and gene expression profiling to model SMAD regulatory modules. BMC Systems Biology, 2009, 3, 73.	3.0	62
881	A dynamic network of transcription in LPS-treated human subjects. BMC Systems Biology, 2009, 3, 78.	3.0	36
882	A comprehensive analysis of recruitment and transactivation potential of K-Rta and K-bZIP during reactivation of Kaposi's sarcoma-associated herpesvirus. Virology, 2009, 387, 76-88.	1.1	50
883	Specialized Sugar Sensing in Diverse Fungi. Current Biology, 2009, 19, 436-441.	1.8	46
884	Identifying differentially expressed pathways via a mixed integer linear programming model. IET Systems Biology, 2009, 3, 475-486.	0.8	26
887	Analysis of epigenetic alterations to chromatin during development. Genesis, 2009, 47, 559-572.	0.8	42
888	From sextant to GPS: Twentyâ€five years of mapping the genome with ChIP. Journal of Cellular Biochemistry, 2009, 107, 6-10.	1.2	7
889	Genomic location analysis by ChIPâ€Seq. Journal of Cellular Biochemistry, 2009, 107, 11-18.	1.2	153
890	Genome-wide analysis of histone H3 lysine 27 trimethylation by ChIP-chip in gastric cancer patients. Journal of Gastroenterology, 2009, 44, 305-312.	2.3	40
891	Cross-talks of sensory transcription networks in response to various environmental stresses. Interdisciplinary Sciences, Computational Life Sciences, 2009, 1, 46-54.	2.2	10
892	Quadruple 9-mer-based protein binding microarray with DsRed fusion protein. BMC Molecular Biology, 2009, 10, 91.	3.0	20
893	Novel sequential ChIP and simplified basic ChIP protocols for promoter co-occupancy and target gene identification in human embryonic stem cells. BMC Biotechnology, 2009, 9, 59.	1.7	17
894	Effect of hydroxyurea on the promoter occupancy profiles of tumor suppressor p53 and p73. BMC Biology, 2009, 7, 35.	1.7	2

#	ARTICLE	IF	CITATIONS
895	Chromatin maps, histone modifications and leukemia. Leukemia, 2009, 23, 1243-1251.	3.3	54
896	Genomic views of distant-acting enhancers. Nature, 2009, 461, 199-205.	13.7	549
897	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. Nature Biotechnology, 2009, 27, 66-75.	9.4	514
898	Genome-wide identification of post-translational modulators of transcription factor activity in human B cells. Nature Biotechnology, 2009, 27, 829-837.	9.4	226
899	Differential chromatin marking of introns and expressed exons by H3K36me3. Nature Genetics, 2009, 41, 376-381.	9.4	592
900	Cost-effective strategies for completing the interactome. Nature Methods, 2009, 6, 55-61.	9.0	88
901	Global mapping of protein-DNA interactions in vivo by digital genomic footprinting. Nature Methods, 2009, 6, 283-289.	9.0	533
902	Universal protein-binding microarrays for the comprehensive characterization of the DNA-binding specificities of transcription factors. Nature Protocols, 2009, 4, 393-411.	5.5	322
903	ChIPâ€“seq: advantages and challenges of a maturing technology. Nature Reviews Genetics, 2009, 10, 669-680.	7.7	1,728
904	Reconstruction of biochemical networks in microorganisms. Nature Reviews Microbiology, 2009, 7, 129-143.	13.6	797
905	Application of 'next-generation' sequencing technologies to microbial genetics. Nature Reviews Microbiology, 2009, 7, 96-97.	13.6	269
906	The role of predictive modelling in rationally re-engineering biological systems. Nature Reviews Microbiology, 2009, 7, 297-305.	13.6	55
907	In the News. Nature Reviews Microbiology, 2009, 7, 260-261.	13.6	158
908	Systems biology of innate immunity. Immunological Reviews, 2009, 227, 264-282.	2.8	139
909	Developmental and activityâ€dependent genomic occupancy profiles of CREB in monkey area V1. Genes, Brain and Behavior, 2009, 8, 149-160.	1.1	4
910	Transcriptomics analyses reveal global roles of the regulator AveI inStreptomyces avermitilis. FEMS Microbiology Letters, 2009, 298, 199-207.	0.7	24
911	Regulation by transcription factors in bacteria: beyond description. FEMS Microbiology Reviews, 2009, 33, 133-151.	3.9	185
912	Activatorâ€binding domains of the SWI/SNF chromatin remodeling complex characterized <i>inâ€ƒvitro</i> are required for its recruitment to promoters <i>inâ€ƒvivo</i>. FEBS Journal, 2009, 276, 2557-2565.	2.2	18

#	ARTICLE	IF	CITATIONS
913	Inferring Gene Networks: Dream or Nightmare?. Annals of the New York Academy of Sciences, 2009, 1158, 246-256.	1.8	23
914	CSIâ€“FID: High throughput label-free detection of DNA binding molecules. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 3779-3782.	1.0	24
915	Microarray methods to identify factors determining breast cancer progression: Potentials, limitations, and challenges. Critical Reviews in Oncology/Hematology, 2009, 70, 1-11.	2.0	18
916	Gene interaction â€“ An evolutionary biclustering approach. Information Fusion, 2009, 10, 242-249.	11.7	27
917	Gene regulatory network inference: Data integration in dynamic modelsâ€”A review. BioSystems, 2009, 96, 86-103.	0.9	663
918	ChIPing away at the genome: the new frontier travel guide. Molecular BioSystems, 2009, 5, 1421.	2.9	16
919	RNA Immunoprecipitation to Determine RNA-Protein Associations In Vivo. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5234.	0.2	54
920	Integrating Proteomic, Transcriptional, and Interactome Data Reveals Hidden Components of Signaling and Regulatory Networks. Science Signaling, 2009, 2, ra40.	1.6	161
921	Robust-Linear-Model Normalization To Reduce Technical Variability in Functional Protein Microarrays. Journal of Proteome Research, 2009, 8, 5451-5464.	1.8	77
922	Epigenomic profiling of cancer cells. International Journal of Biochemistry and Cell Biology, 2009, 41, 127-135.	1.2	42
923	The role of histone H2A and H2B post-translational modifications in transcription: A genomic perspective. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2009, 1789, 37-44.	0.9	49
924	Transcriptomics: Unravelling the biology of transcription factors and chromatin remodelers during development and differentiation. Seminars in Cell and Developmental Biology, 2009, 20, 835-841.	2.3	10
925	ChIP-seq: Using high-throughput sequencing to discover proteinâ€“DNA interactions. Methods, 2009, 48, 240-248.	1.9	455
926	Isolation of active regulatory elements from eukaryotic chromatin using FAIRE (Formaldehyde) Tj ETQq1 1 0.784314 rgBT /Overlock 10	1.9	178
927	RNA-Seqâ€”quantitative measurement of expression through massively parallel RNA-sequencing. Methods, 2009, 48, 249-257.	1.9	414
928	Cell Cycle Regulatory Effects of Retinoic Acid and Forskolin Are Mediated by the Cyclin C Gene. Journal of Molecular Biology, 2009, 393, 261-271.	2.0	11
929	Rearrangements of the transcriptional regulatory networks of metabolic pathways in fungi. Current Opinion in Microbiology, 2009, 12, 655-663.	2.3	75
930	Protein Occupancy Landscape of a Bacterial Genome. Molecular Cell, 2009, 35, 247-253.	4.5	107

#	Article	IF	Citations
931	The SAGA Continuesâ€¦to the End. Molecular Cell, 2009, 35, 256-258.	4.5	3
932	Can the Protein Occupancy Landscape Show the Topologically Isolated Chromosomal Domains in the E.Âcoli Genome?: An Exciting Prospect. Molecular Cell, 2009, 35, 255-256.	4.5	3
933	Protein-binding microarrays: probing disease markers at the interface of proteomics and genomics. Trends in Molecular Medicine, 2009, 15, 352-358.	3.5	14
934	Genome-Wide High-Resolution Chromatin Immunoprecipitation of Meiotic Chromosomal Proteins in Saccharomyces cerevisiae. Methods in Molecular Biology, 2009, 557, 285-304.	0.4	3
935	Strategies for Epigenome Analysis. , 2009, , 3-18.		7
936	Next-generation DNA sequencing of paired-end tags (PET) for transcriptome and genome analyses. Genome Research, 2009, 19, 521-532.	2.4	286
937	Quantitative Detection of Small Molecule/DNA Complexes Employing a Force-Based and Label-Free DNA-Microarray. Biophysical Journal, 2009, 96, 4661-4671.	0.2	19
938	Mechanisms and Constraints on Yeast MAPK Signaling Specificity. Biophysical Journal, 2009, 96, 4755-4763.	0.2	7
939	The State-of-the-Art of Chromatin Immunoprecipitation. Methods in Molecular Biology, 2009, 567, 1-25.	0.4	32
940	Genomic Tools for Analyzing Transcriptional Regulatory Networks. , 2009, , 119-136.		0
941	Next-Generation Sequencing: From Basic Research to Diagnostics. Clinical Chemistry, 2009, 55, 641-658.	1.5	668
942	Auditory and Vestibular Research. Methods in Molecular Biology, 2009, , .	0.4	1
943	DNA Replication. Methods in Molecular Biology, 2009, , .	0.4	7
944	Structural Properties of Gene Regulatory Networks: Definitions and Connections. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 158-170.	1.9	6
945	Fuzzy Systems in Bioinformatics and Computational Biology. Studies in Fuzziness and Soft Computing, 2009, , .	0.6	10
946	Protein Networks and Pathway Analysis. Methods in Molecular Biology, 2009, 563, v-vii.	0.4	33
947	Computational Systems Biology. Methods in Molecular Biology, 2009, , .	0.4	5
948	Network-Based Models in Molecular Biology. , 2009, , 35-56.		1

#	ARTICLE	IF	CITATIONS
950	ChIP'ing the mammalian genome: technical advances and insights into functional elements. Genome Medicine, 2009, 1, 89.	3.6	16
951	Advances in the identification and analysis of allele-specific expression. Genome Medicine, 2009, 1, 56.	3.6	35
952	Introduction to Microarray Technology. Methods in Molecular Biology, 2009, 529, 1-22.	0.4	42
953	Chromatin Immunoprecipitation Assays. Methods in Molecular Biology, 2009, , .	0.4	6
954	Genomic regulatory blocks in vertebrates and implications in human disease. Briefings in Functional Genomics & Proteomics, 2009, 8, 333-342.	3.8	27
955	Advantages of next-generation sequencing versus the microarray in epigenetic research. Briefings in Functional Genomics & Proteomics, 2009, 8, 174-183.	3.8	218
956	Scoring overlapping and adjacent signals from genome-wide ChIP and DamID assays. Molecular BioSystems, 2009, 5, 1429.	2.9	13
957	Structural and functional map of a bacterial nucleoid. Genome Biology, 2009, 10, 247.	13.9	13
958	Reagentless, Electrochemical Approach for the Specific Detection of Double- and Single-Stranded DNA Binding Proteins. Analytical Chemistry, 2009, 81, 1608-1614.	3.2	72
959	Effect of false positive and false negative rates on inference of binding target conservation across different conditions and species from ChIP-chip data. BMC Bioinformatics, 2009, 10, 23.	1.2	1
960	Sites of Differential DNA Methylation between Placenta and Peripheral Blood. American Journal of Pathology, 2009, 174, 1609-1618.	1.9	107
961	High-throughput Biology in the Postgenomic Era. Journal of Vascular and Interventional Radiology, 2009, 20, S488-S496.	0.2	1
962	Identifying cell cycle regulators and combinatorial interactions among transcription factors with microarray data and ChIP-chip data. International Journal of Bioinformatics Research and Applications, 2009, 5, 625.	0.1	0
963	Transcription Regulatory Networks Analysis Using CAGE. , 2009, , 153-168.		0
965	Uncovering Transcriptional Regulatory Networks by Sparse Bayesian Factor Model. Eurasip Journal on Advances in Signal Processing, 2010, 2010, .	1.0	6
968	Behind the scenes: Unravelling the molecular mechanisms of p53 target gene selectivity (Review). International Journal of Oncology, 2010, 37, 1061-70.	1.4	10
969	Single Molecule Epigenetic Analysis in a Nanofluidic Channel. Analytical Chemistry, 2010, 82, 2480-2487.	3.2	110
970	Omics-based Medicine and Systems Pathology. Methods of Information in Medicine, 2010, 49, 173-185.	0.7	29

#	Article	IF	Citations
971	Analysis of DNAâ€"protein interactions: from nitrocellulose filter binding assays to microarray studies. Analytical and Bioanalytical Chemistry, 2010, 398, 2551-2561.	1.9	42
972	Electrochemical probe for the monitoring of DNAâ€"protein interactions. Biosensors and Bioelectronics, 2010, 25, 2598-2602.	5.3	25
973	The Current State of Chromatin Immunoprecipitation. Molecular Biotechnology, 2010, 45, 87-100.	1.3	224
974	Investigating micronutrients and epigenetic mechanisms in relation to inflammatory bowel disease. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2010, 690, 71-80.	0.4	36
975	Starr: Simple Tiling ARRay analysis of Affymetrix ChIP-chip data. BMC Bioinformatics, 2010, 11, 194.	1.2	28
976	Detecting disease associated modules and prioritizing active genes based on high throughput data. BMC Bioinformatics, 2010, 11, 26.	1.2	70
977	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. BMC Bioinformatics, 2010, 11, 369.	1.2	94
978	An effective approach for identification of in vivo protein-DNA binding sites from paired-end ChIP-Seq data. BMC Bioinformatics, 2010, 11, 81.	1.2	21
979	Stability analysis of the GAL regulatory network in Saccharomyces cerevisiae and Kluyveromyces lactis. BMC Bioinformatics, 2010, 11, S43.	1.2	13
980	ChIP on Chip: surprising results are often artifacts. BMC Genomics, 2010, 11, 414.	1.2	65
981	Combination of genomic approaches with functional genetic experiments reveals two modes of repression of yeast middle-phase meiosis genes. BMC Genomics, 2010, 11, 478.	1.2	10
982	Systematic identification of conserved motif modules in the human genome. BMC Genomics, 2010, 11, 567.	1.2	28
983	Inference of hierarchical regulatory network of estrogen-dependent breast cancer through ChIP-based data. BMC Systems Biology, 2010, 4, 170.	3.0	40
984	PPARÎ³ in adipocyte differentiation and metabolism â€" Novel insights from genomeâ€wide studies. FEBS Letters, 2010, 584, 3242-3249.	1.3	330
985	High-throughput screening of DNA binding sites for transcription factor AmyR from Aspergillus nidulans using DNA beads display system. Journal of Bioscience and Bioengineering, 2010, 109, 519-525.	1.1	10
986	Global analysis of <i>in vivo</i> EGR1â€binding sites in erythroleukemia cell using chromatin immunoprecipitation and massively parallel sequencing. Electrophoresis, 2010, 31, 2936-2943.	1.3	15
987	Model organisms â€" A historical perspective. Journal of Proteomics, 2010, 73, 2054-2063.	1.2	76
988	Model organism proteomics. Journal of Proteomics, 2010, 73, 2051-2053.	1.2	4

#	Article	IF	Citations
989	Comparison of optimization techniques for sequence pattern discovery by maximum-likelihood. Pattern Recognition Letters, 2010, 31, 2147-2160.	2.6	6
990	Epigenomics of T cell activation, differentiation, and memory. Current Opinion in Immunology, 2010, 22, 341-347.	2.4	91
991	Maintaining Cell Identity through Global Control of Genomic Organization. Immunity, 2010, 33, 12-24.	6.6	187
992	Multiplex parallel pairâ€endâ€ditag sequencing approaches in system biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 224-234.	6.6	4
993	Circuitry of mRNA regulation. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 245-251.	6.6	20
994	Genomeâ€wide maps of transcription regulatory elements. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2010, 2, 422-437.	6.6	22
995	Multiple bHLH proteins regulate <i>CIT2</i> expression in <i>Saccharomyces cerevisiae</i>. Yeast, 2010, 27, 345-359.	0.8	12
996	A Bayesian approach to joint modeling of proteinâ€"DNA binding, gene expression and sequence data. Statistics in Medicine, 2010, 29, 489-503.	0.8	9
997	Prokaryotic genome regulation: multifactor promoters, multitarget regulators and hierarchic networks. FEMS Microbiology Reviews, 2010, 34, 628-645.	3.9	209
998	Systematic identification of fragile sites via genome-wide location analysis of Î³-H2AX. Nature Structural and Molecular Biology, 2010, 17, 299-305.	3.6	167
999	Coordinate control of gene expression noise and interchromosomal interactions in a MAP kinase pathway. Nature Cell Biology, 2010, 12, 954-962.	4.6	59
1000	Role of STAT5 in controlling cell survival and immunoglobulin gene recombination during pro-B cell development. Nature Immunology, 2010, 11, 171-179.	7.0	247
1001	Next-generation genomics: an integrative approach. Nature Reviews Genetics, 2010, 11, 476-486.	7.7	554
1002	Annotating non-coding regions of the genome. Nature Reviews Genetics, 2010, 11, 559-571.	7.7	398
1003	Network-based genomic discovery: application and comparison of Markov random-field models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2010, 59, 105-125.	0.5	19
1005	Chromatin Remodeling. , 2010, , 359-375.		1
1006	DamIP: A novel method to identify DNA binding sites in vivo. Nuclear Receptor Signaling, 2010, 8, nrs.08003.	1.0	14
1007	Systems Approaches to Unraveling Nitric Oxide Response Networks in Prokaryotes. , 2010, , 103-136.		3

#	Article	IF	Citations
1008	Systems Biology and Personalized Medicine in Cancer. Current Pharmacogenomics and Personalized Medicine, 2010, 8, 64-72.	0.2	2
1009	Regulation of Cell Cycle Genes and Induction of Senescence by Overexpression of OTX2 in Medulloblastoma Cell Lines. Molecular Cancer Research, 2010, 8, 1344-1357.	1.5	45
1010	Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation. Genome Research, 2010, 20, 1719-1729.	2.4	111
1011	Defining the budding yeast chromatinâ€associated interactome. Molecular Systems Biology, 2010, 6, 448.	3.2	58
1012	Using deep sequencing to characterize the biophysical mechanism of a transcriptional regulatory sequence. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9158-9163.	3.3	283
1013	On the detection and refinement of transcription factor binding sites using ChIP-Seq data. Nucleic Acids Research, 2010, 38, 2154-2167.	6.5	91
1014	JAMIE: joint analysis of multiple ChIP-chip experiments. Bioinformatics, 2010, 26, 1864-1870.	1.8	12
1015	HRTBLDb: an informative data resource for hormone receptors target binding loci. Nucleic Acids Research, 2010, 38, D676-D681.	6.5	11
1016	Integrating multiple evidence sources to predict transcription factor binding in the human genome. Genome Research, 2010, 20, 526-536.	2.4	85
1017	Experimental strategies for studying transcription factor-DNA binding specificities. Briefings in Functional Genomics, 2010, 9, 362-373.	1.3	77
1018	Computational inference of transcription factor cooperation by fuzzy frequent itemset mining. , 2010, , .		0
1019	Derepression of<i>INO1</i>Transcription Requires Cooperation between the Ino2p-Ino4p Heterodimer and Cbf1p and Recruitment of the ISW2 Chromatin-Remodeling Complex. Eukaryotic Cell, 2010, 9, 1845-1855.	3.4	24
1020	A dynamic Bayesian network for identifying protein-binding footprints from single molecule-based sequencing data. Bioinformatics, 2010, 26, i334-i342.	1.8	43
1021	Expression in Aneuploid Drosophila S2 Cells. PLoS Biology, 2010, 8, e1000320.	2.6	161
1022	Variable Transcription Factor Binding: A Mechanism of Evolutionary Change. PLoS Biology, 2010, 8, e1000342.	2.6	23
1023	DSIF and RNA Polymerase II CTD Phosphorylation Coordinate the Recruitment of Rpd3S to Actively Transcribed Genes. PLoS Genetics, 2010, 6, e1001173.	1.5	122
1024	Quantitative Analysis of the Drosophila Segmentation Regulatory Network Using Pattern Generating Potentials. PLoS Biology, 2010, 8, e1000456.	2.6	69
1025	Nuclear Pore Proteins Nup153 and Megator Define Transcriptionally Active Regions in the Drosophila Genome. PLoS Genetics, 2010, 6, e1000846.	1.5	218

#	Article	IF	Citations
1026	Identifying a Transcription Factor's Regulatory Targets from its Binding Targets. Gene Regulation and Systems Biology, 2010, 4, GRSB.S6458.	2.3	3
1027	Many sequence-specific chromatin modifying protein-binding motifs show strong positional preferences for potential regulatory regions in the Saccharomyces cerevisiae genome. Nucleic Acids Research, 2010, 38, 1772-1779.	6.5	21
1028	Association of Tat with Promoters of PTEN and PP2A Subunits Is Key to Transcriptional Activation of Apoptotic Pathways in HIV-Infected CD4+ T Cells. PLoS Pathogens, 2010, 6, e1001103.	2.1	48
1029	GINS motion reveals replication fork progression is remarkably uniform throughout the yeast genome. Molecular Systems Biology, 2010, 6, 353.	3.2	116
1030	An effective model for natural selection in promoters. Genome Research, 2010, 20, 685-692.	2.4	24
1031	Statistical Issues in the Analysis of ChIP-Seq and RNA-Seq Data. Genes, 2010, 1, 317-334.	1.0	17
1032	ChIPâ€Seq: A Method for Global Identification of Regulatory Elements in the Genome. Current Protocols in Molecular Biology, 2010, 91, Unit 21.19.1-14.	2.9	49
1033	Biochemical Methods Used to Study the Gene Expression and Protein Complexes in the Filamentous Fungus Neurospora crassa. Methods in Molecular Biology, 2010, 638, 189-200.	0.4	7
1034	Next Generation DNA Sequencing and the Future of Genomic Medicine. Genes, 2010, 1, 38-69.	1.0	60
1035	Computational Analysis of ChIP-seq Data. Methods in Molecular Biology, 2010, 674, 143-159.	0.4	6
1036	Statistical Methods for Integrating Multiple Types of High-Throughput Data. Methods in Molecular Biology, 2010, 620, 511-529.	0.4	5
1038	High throughput generation of promoter reporter (GFP) transgenic lines of low expressing genes in Arabidopsis and analysis of their expression patterns. Plant Methods, 2010, 6, 18.	1.9	27
1039	Function of Protein Phosphatase-1, Glc7, in Saccharomyces cerevisiae. Advances in Applied Microbiology, 2010, 73, 27-59.	1.3	36
1040	Electric Field Destabilizes Noncovalent Proteinâ^'DNA Complexes. Journal of the American Chemical Society, 2010, 132, 13639-13641.	6.6	15
1041	Why Does Binding of Proteins to DNA or Proteins to Proteins Not Necessarily Spell Function?. ACS Chemical Biology, 2010, 5, 265-272.	1.6	27
1042	Integrating one-dimensional and three-dimensional maps of genomes. Journal of Cell Science, 2010, 123, 1979-1988.	1.2	63
1043	Nuclear Receptors and ATP Dependent Chromatin Remodeling: A Complex Story. , 2010, , 345-363.		0
1044	Comparative Genomics. , 2010, , 557-587.		0

#	ARTICLE	IF	CITATIONS
1045	Review of microarray studies for hostâ€"intracellular pathogen interactions. Journal of Microbiological Methods, 2010, 81, 81-95.	0.7	19
1046	Hormones in synergy: Regulation of the pituitary gonadotropin genes. Molecular and Cellular Endocrinology, 2010, 314, 192-203.	1.6	143
1047	A Myc Network Accounts for Similarities between Embryonic Stem and Cancer Cell Transcription Programs. Cell, 2010, 143, 313-324.	13.5	606
1048	Bioinformatic and Computational Analysis for Genomic Medicine. , 2010, , 111-130.		0
1049	Statistical Methods in Molecular Biology. Methods in Molecular Biology, 2010, , .	0.4	16
1050	An Omics Perspective on Cancer Research. , 2010, , .		20
1051	Integrating multiple â€˜omicsâ€™ analysis for microbial biology: application and methodologies. Microbiology (United Kingdom), 2010, 156, 287-301.	0.7	430
1053	Setdb1 Histone Methyltransferase Regulates Mood-Related Behaviors and Expression of the NMDA Receptor Subunit NR2B. Journal of Neuroscience, 2010, 30, 7152-7167.	1.7	104
1055	Evidence-ranked motif identification. Genome Biology, 2010, 11, R19.	13.9	77
1056	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	13.9	255
1057	Genome-wide prediction of transcription factor binding sites using an integrated model. Genome Biology, 2010, 11, R7.	13.9	100
1058	The Genetics of Obsessive-Compulsive Disorder and Tourette Syndrome: An Epidemiological and Pathway-Based Approach for Gene Discovery. Journal of the American Academy of Child and Adolescent Psychiatry, 2010, 49, 810-819.e2.	0.3	31
1059	Sensitive and Visual Detection of Sequence-Specific DNA-Binding Protein via a Gold Nanoparticle-Based Colorimetric Biosensor. Analytical Chemistry, 2010, 82, 6015-6024.	3.2	117
1060	Integrative genome-wide approaches in embryonic stem cell research. Integrative Biology (United) Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	7
1061	Relational database index choices for genome annotation data. , 2010, , .		3
1062	Model-based method for transcription factor target identification with limited data. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7793-7798.	3.3	87
1063	Whole genome identification of target genes of transcription factors. , 2010, , .		0
1064	A Structural Perspective on the Where, How, Why, and What of Nucleosome Positioning. Journal of Biomolecular Structure and Dynamics, 2010, 27, 803-820.	2.0	51

#	ARTICLE	IF	CITATIONS
1065	A hybridization model for tiling array analysis. , 2010, , .		0
1066	Actin organization and dynamics in filamentous fungi. Nature Reviews Microbiology, 2011, 9, 876-887.	13.6	142
1067	Epigenetic mechanisms in diabetic vascular complications. Cardiovascular Research, 2011, 90, 421-429.	1.8	178
1068	hmChIP: a database and web server for exploring publicly available human and mouse ChIP-seq and ChIP-chip data. Bioinformatics, 2011, 27, 1447-1448.	1.8	49
1069	Characterization of Protein-DNA Interactions Using Protein Microarrays. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5614-pdb.prot5614.	0.2	12
1070	Identification of Transcription Factorâ€“DNA Interactions In Vivo. Sub-Cellular Biochemistry, 2011, 52, 175-191.	1.0	7
1071	Interactions of Transcription Factors with Chromatin. Sub-Cellular Biochemistry, 2011, 52, 223-259.	1.0	4
1072	Genomic-Wide Methods to Evaluate Transcription Rates in Yeast. Methods in Molecular Biology, 2011, 734, 25-44.	0.4	11
1073	Joint Binding of OTX2 and MYC in Promotor Regions Is Associated with High Gene Expression in Medulloblastoma. PLoS ONE, 2011, 6, e26058.	1.1	24
1074	Using CisGenome to Analyze ChIPâ€chip and ChIPâ€seq Data. Current Protocols in Bioinformatics, 2011, 33, Unit2.13.	25.8	34
1076	Processing ChIP-Chip Data: From the Scanner to the Browser. Methods in Molecular Biology, 2011, 719, 251-268.	0.4	2
1077	PeakRanger: A cloud-enabled peak caller for ChIP-seq data. BMC Bioinformatics, 2011, 12, 139.	1.2	142
1078	Constructing gene regulatory networks for long term photosynthetic light acclimation in Arabidopsis thaliana. BMC Bioinformatics, 2011, 12, 335.	1.2	18
1079	Epigenetic Aspects of Chronic Diseases. , 2011, , .		3
1080	A Handbook of Transcription Factors. Sub-Cellular Biochemistry, 2011, , .	1.0	14
1081	Role of ZBP-89 in human globin gene regulation and erythroid differentiation. Blood, 2011, 118, 3684-3693.	0.6	26
1082	Cell-Based Microarrays: Overview. Methods in Molecular Biology, 2011, 706, 1-12.	0.4	1
1083	Techniques to Study DNA Methylation and Histone Modification. , 2011, , 21-39.		3

#	ARTICLE	IF	CITATIONS
1084	Network Biology. Methods in Molecular Biology, 2011, , .	0.4	3
1085	A high throughput molecular force assay for proteinâ€“DNA interactions. Lab on A Chip, 2011, 11, 856.	3.1	18
1086	Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium. Genome Biology, 2011, 12, R99.	13.9	49
1087	Cistrome: an integrative platform for transcriptional regulation studies. Genome Biology, 2011, 12, R83.	13.9	598
1089	Comprehensive Genome-wide Protein-DNA Interactions Detected at Single-Nucleotide Resolution. Cell, 2011, 147, 1408-1419.	13.5	684
1090	A genomic view of mRNA turnover in yeast. Comptes Rendus - Biologies, 2011, 334, 647-654.	0.1	6
1091	Animal Transcription Networks as Highly Connected, Quantitative Continua. Developmental Cell, 2011, 21, 611-626.	3.1	275
1092	H3K4 tri-methylation provides an epigenetic signature of active enhancers. EMBO Journal, 2011, 30, 4198-4210.	3.5	265
1093	Epigenetic methodologies for behavioral scientists. Hormones and Behavior, 2011, 59, 407-416.	1.0	13
1094	Methods for Analysis of Transcription Factor DNA-Binding Specificity In Vitro. Sub-Cellular Biochemistry, 2011, 52, 155-173.	1.0	27
1095	Mapping E. coli RNA Polymerase and Associated Transcription Factors and Identifying Promoters Genome-Wide. Methods in Enzymology, 2011, 498, 449-471.	0.4	22
1096	Dynamic chromatin states in human ES cells reveal potential regulatory sequences and genes involved in pluripotency. Cell Research, 2011, 21, 1393-1409.	5.7	91
1097	Chromatin Modifications Distinguish Genomic Features and Physical Organization of the Nucleus. , 2011, , 159-171.		0
1098	An Integrated Framework to Model Cellular Phenotype as a Component of Biochemical Networks. Advances in Bioinformatics, 2011, 2011, 1-14.	5.7	0
1099	The Dynamical Systems Properties of the HOG Signaling Cascade. Journal of Signal Transduction, 2011, 2011, 1-12.	2.0	22
1100	Grand Challenge: Accelerating Discovery through Technology Development. Frontiers in Plant Science, 2011, 2, 41.	1.7	3
1101	Mayday SeaSight: Combined Analysis of Deep Sequencing and Microarray Data. PLoS ONE, 2011, 6, e16345.	1.1	17
1102	Computational Identification of Transcriptional Regulators in Human Endotoxemia. PLoS ONE, 2011, 6, e18889.	1.1	18

#	Article	IF	Citations
1103	Dia2 Controls Transcription by Mediating Assembly of the RSC Complex. PLoS ONE, 2011, 6, e21172.	1.1	6
1104	Sequence-Specific Capture of Protein-DNA Complexes for Mass Spectrometric Protein Identification. PLoS ONE, 2011, 6, e26217.	1.1	30
1105	DamIP: Using Mutant DNA Adenine Methyltransferase to Study DNAâ€Protein Interactions In Vivo. Current Protocols in Molecular Biology, 2011, 94, Unit21.21.	2.9	9
1106	The RNA polymerase subunits E/F from the Antarctic archaeon <i>Methanococcoides burtonii</i> bind to specific species of mRNA. Environmental Microbiology, 2011, 13, 2039-2055.	1.8	4
1107	Improved proteinâ€binding microarrays for the identification of DNAâ€binding specificities of transcription factors. Plant Journal, 2011, 66, 700-711.	2.8	117
1108	The quorumâ€hindered transcription factor YenR of <i>Yersinia enterocolitica</i> inhibits pheromone production and promotes motility via a small nonâ€coding RNA. Molecular Microbiology, 2011, 80, 556-571.	1.2	22
1109	Unravelling the complexity of metastasis â€” molecular understanding and targeted therapies. Nature Reviews Cancer, 2011, 11, 735-748.	12.8	318
1110	Genomic views of STAT function in CD4+ T helper cell differentiation. Nature Reviews Immunology, 2011, 11, 239-250.	10.6	251
1111	A cis-regulatory map of the Drosophila genome. Nature, 2011, 471, 527-531.	13.7	477
1112	Unraveling the Glioma Epigenomeâ€”From Molecular Mechanisms to Novel Biomarkers and Therapeutic Targets. Brain Pathology, 2011, 21, 619-632.	2.1	38
1113	Histone modification: cause or cog?. Trends in Genetics, 2011, 27, 389-396.	2.9	415
1114	Simple detection of nucleic acids with a single-walled carbon-nanotube-based electrochemical biosensor. Biosensors and Bioelectronics, 2011, 28, 257-262.	5.3	31
1115	Epigenetic regulation by nuclear receptors. Epigenomics, 2011, 3, 59-72.	1.0	29
1116	The opposing transcriptional functions of Sin3a and c-Myc are required to maintain tissue homeostasis. Nature Cell Biology, 2011, 13, 1395-1405.	4.6	57
1117	Deciphering the regulatory codes in bacterial genomes. Biotechnology Journal, 2011, 6, 1052-1063.	1.8	9
1118	Genetic Variation in the KIAA0319 5â€² Region as a Possible Contributor to Dyslexia. Behavior Genetics, 2011, 41, 77-89.	1.4	31
1119	Systematic characterization of protein-DNA interactions. Cellular and Molecular Life Sciences, 2011, 68, 1657-1668.	2.4	33
1120	Analysis of phage Mu DNA transposition by whole-genome Escherichia coli tiling arrays reveals a complex relationship to distribution of target selection protein B, transcription and chromosome architectural elements. Journal of Biosciences, 2011, 36, 587-601.	0.5	17

#	Article	IF	Citations
1121	Ste11p MEKK signals through HOG, mating, calcineurin and PKC pathways to regulate the FKS2 gene. BMC Molecular Biology, 2011, 12, 51.	3.0	11
1122	Bayesian non-negative factor analysis for reconstructing transcription factor mediated regulatory networks. Proteome Science, 2011, 9, S9.	0.7	7
1123	Pinpointing transcription factor binding sites from ChIP-seq data with SeqSite. BMC Systems Biology, 2011, 5, S3.	3.0	6
1124	A transcriptional dynamic network during Arabidopsis thaliana pollen development. BMC Systems Biology, 2011, 5, S8.	3.0	18
1125	Genome-wide analysis of chromatin features identifies histone modification sensitive and insensitive yeast transcription factors. Genome Biology, 2011, 12, R111.	13.9	16
1126	Reconstructing genome-wide regulatory network of E. coli using transcriptome data and predicted transcription factor activities. BMC Bioinformatics, 2011, 12, 233.	1.2	54
1127	ChIP-chip versus ChIP-seq: Lessons for experimental design and data analysis. BMC Genomics, 2011, 12, 134.	1.2	128
1128	The differential disease regulome. BMC Genomics, 2011, 12, 353.	1.2	9
1129	The mouse RANKL gene locus is defined by a broad pattern of histone H4 acetylation and regulated through distinct distal enhancers. Journal of Cellular Biochemistry, 2011, 112, 2030-2045.	1.2	33
1130	A sub-space greedy search method for efficient Bayesian Network inference. Computers in Biology and Medicine, 2011, 41, 763-770.	3.9	2
1131	Profiling a Caenorhabditis elegans behavioral parametric dataset with a supervised K-means clustering algorithm identifies genetic networks regulating locomotion. Journal of Neuroscience Methods, 2011, 197, 315-323.	1.3	12
1132	Genomic approaches for the discovery of<i>CFTR</i>regulatory elements. Transcription, 2011, 2, 23-27.	1.7	4
1133	Calling Cards enable multiplexed identification of the genomic targets of DNA-binding proteins. Genome Research, 2011, 21, 748-755.	2.4	45
1134	Two transcription factors are necessary for iron homeostasis in a salt-dwelling archaeon. Nucleic Acids Research, 2011, 39, 2519-2533.	6.5	31
1135	EpiChIP: gene-by-gene quantification of epigenetic modification levels. Nucleic Acids Research, 2011, 39, e27-e27.	6.5	36
1136	Sensitive and accurate identification of protein-DNA binding events in ChIP-chip assays using higher order derivative analysis. Nucleic Acids Research, 2011, 39, 1656-1665.	6.5	5
1137	Whole-Genome Analysis Reveals That Active Heat Shock Factor Binding Sites Are Mostly Associated with Non-Heat Shock Genes in Drosophila melanogaster. PLoS ONE, 2011, 6, e15934.	1.1	78
1138	Oxidative Stresses and Ageing. Sub-Cellular Biochemistry, 2011, 57, 13-54.	1.0	28

#	Article	IF	Citations
1139	In vitro DNA-binding profile of transcription factors: methods and new insights. Journal of Endocrinology, 2011, 210, 15-27.	1.2	27
1140	Sequential Recruitment of SAGA and TFIID in a Genomic Response to DNA Damage in <i>Saccharomyces cerevisiae</i>. Molecular and Cellular Biology, 2011, 31, 190-202.	1.1	29
1141	A Novel Specificity Protein 1 (SP1)-like Gene Regulating Protein Kinase C-1 (Pkc1)-dependent Cell Wall Integrity and Virulence Factors in Cryptococcus neoformans. Journal of Biological Chemistry, 2011, 286, 20977-20990.	1.6	47
1142	The Conserved Foot Domain of RNA Pol II Associates with Proteins Involved in Transcriptional Initiation and/or Early Elongation. Genetics, 2011, 189, 1235-1248.	1.2	17
1143	Beyond genetics: epigenetic code in chronic kidney disease. Kidney International, 2011, 79, 23-32.	2.6	112
1144	Medusa structure of the gene regulatory network: dominance of transcription factors in cancer subtype classification. Experimental Biology and Medicine, 2011, 236, 628-636.	1.1	20
1145	Direct measurement of DNA affinity landscapes on a high-throughput sequencing instrument. Nature Biotechnology, 2011, 29, 659-664.	9.4	186
1146	CpG Array Analysis of Histone H3 Lysine 4 Trimethylation in Peripheral Blood Mononuclear Cells of Uremia Patients. DNA and Cell Biology, 2011, 30, 179-186.	0.9	4
1147	ChIPâ€onâ€chip analysis reveals angiopoietin 2 (Ang2, ANGPT2) as a novel target of steroidogenic factorâ€1 (SFâ€1, NR5A1) in the human adrenal gland. FASEB Journal, 2011, 25, 1166-1175.	0.2	27
1148	Discovering Transcription Factor Binding Sites in Highly Repetitive Regions of Genomes with Multi-Read Analysis of ChIP-Seq Data. PLoS Computational Biology, 2011, 7, e1002111.	1.5	73
1149	Trade-off between Responsiveness and Noise Suppression in Biomolecular System Responses to Environmental Cues. PLoS Computational Biology, 2011, 7, e1002091.	1.5	16
1150	FlyFactorSurvey: a database of Drosophila transcription factor binding specificities determined using the bacterial one-hybrid system. Nucleic Acids Research, 2011, 39, D111-D117.	6.5	202
1151	Innovative technology for cancer risk analysis. Annals of Oncology, 2011, 22, i37-i43.	0.6	2
1152	Young intragenic miRNAs are less coexpressed with host genes than old ones: implications of miRNAâ€"host gene coevolution. Nucleic Acids Research, 2012, 40, 4002-4012.	6.5	63
1153	Analysis of High Dimensionality Yeast Gene Expression Data Using Data Mining. Applied Mechanics and Materials, 2012, 197, 515-522.	0.2	0
1154	Genome-Wide Localization of Protein-DNA Binding and Histone Modification by a Bayesian Change-Point Method with ChIP-seq Data. PLoS Computational Biology, 2012, 8, e1002613.	1.5	68
1155	Characterizing the roles of Met31 and Met32 in coordinating Met4-activated transcription in the absence of Met30. Molecular Biology of the Cell, 2012, 23, 1928-1942.	0.9	25
1156	A rapid assay for affinity and kinetics of molecular interactions with nucleic acids. Nucleic Acids Research, 2012, 40, e48-e48.	6.5	30

#	Article	IF	Citations
1157	YeTFaSCo: a database of evaluated yeast transcription factor sequence specificities. Nucleic Acids Research, 2012, 40, D169-D179.	6.5	195
1158	Improved Models for Transcription Factor Binding Site Identification Using Nonindependent Interactions. Genetics, 2012, 191, 781-790.	1.2	123
1159	Toward the identification and regulation of the Arabidopsis thaliana ABI3 regulon. Nucleic Acids Research, 2012, 40, 8240-8254.	6.5	145
1160	<i>De novo</i> motif discovery facilitates identification of interactions between transcription factors in <i>Saccharomyces cerevisiae</i>. Bioinformatics, 2012, 28, 701-708.	1.8	15
1161	Experimental and Computational Challenges from Array-Based to Sequence-Based ChIP Techniques. Current Bioinformatics, 2012, 7, 447-453.	0.7	2
1162	Uncovering Transcription Factor Modules Using One- and Three-dimensional Analyses. Journal of Biological Chemistry, 2012, 287, 30914-30921.	1.6	7
1163	A workflow for genome-wide mapping of archaeal transcription factors with ChIP-seq. Nucleic Acids Research, 2012, 40, e74-e74.	6.5	53
1164	INFERRING THE REGULATORY INTERACTION MODELS OF TRANSCRIPTION FACTORS IN TRANSCRIPTIONAL REGULATORY NETWORKS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250012.	0.3	5
1165	Make way for the â€˜next generationâ€™: application and prospects for genome-wide, epigenome-specific technologies in endocrine research. Journal of Molecular Endocrinology, 2012, 49, R19-R27.	1.1	19
1166	Analysis of Gal4-directed transcription activation using Tra1 mutants selectively defective for interaction with Gal4. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1997-2002.	3.3	28
1167	Considerations for creating and annotating the budding yeast Genome Map at SGD: a progress report. Database: the Journal of Biological Databases and Curation, 2012, 2012, bar057-bar057.	1.4	10
1168	A novel ab initio identification system of transcriptional regulation motifs in genome DNA sequences based on direct comparison scheme of signal/noise distributions. Nucleic Acids Research, 2012, 40, 8835-8848.	6.5	7
1169	Omics Approaches to Meat Quality Management. , 2012, , 266-299.		0
1170	Prokaryotic genome regulation: A revolutionary paradigm. Proceedings of the Japan Academy Series B: Physical and Biological Sciences, 2012, 88, 485-508.	1.6	86
1171	Insect Genomics. , 2012, , 1-29.		0
1172	Bridging Omics Technologies with Synthetic Biology in Yeast Industrial Biotechnology. , 2012, , 271-327.		2
1173	Genome-wide Epigenetic Data Facilitate Understanding of Disease Susceptibility Association Studies. Journal of Biological Chemistry, 2012, 287, 30932-30940.	1.6	49
1174	A negative feedback loop at the nuclear periphery regulates <i>GAL</i> gene expression. Molecular Biology of the Cell, 2012, 23, 1367-1375.	0.9	50

#	Article	IF	Citations
1175	Differential network biology. Molecular Systems Biology, 2012, 8, 565.	3.2	689
1176	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. Genome Biology, 2012, 13, R48.	13.9	233
1177	ChAP-MS: A Method for Identification of Proteins and Histone Posttranslational Modifications at a Single Genomic Locus. Cell Reports, 2012, 2, 198-205.	2.9	110
1178	Lrp of Corynebacterium glutamicum controls expression of the brnFE operon encoding the export system for l-methionine and branched-chain amino acids. Journal of Biotechnology, 2012, 158, 231-241.	1.9	78
1179	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
1180	Highly sensitive detection of DNA-binding proteins based on a cationic conjugated polymer via a target-mediated fluorescence resonance energy transfer (TMFRET) strategy. Polymer Chemistry, 2012, 3, 703.	1.9	16
1181	Two Hybrid Technologies. Methods in Molecular Biology, 2012, 812, v-vi.	0.4	4
1182	Gene-Centered Yeast One-Hybrid Assays. Methods in Molecular Biology, 2012, 812, 189-208.	0.4	16
1183	Profiles of Epigenetic Histone Post-translational Modifications at Type 1 Diabetes Susceptible Genes. Journal of Biological Chemistry, 2012, 287, 16335-16345.	1.6	90
1184	Characterization of interactions between organotin compounds and human serum albumin by capillary electrophoresis coupled with inductively coupled plasma mass spectrometry. Talanta, 2012, 93, 239-244.	2.9	22
1185	Exploring the application of high-throughput genomics technologies in the field of maternal-embryo communication. Theriogenology, 2012, 77, 717-737.	0.9	6
1186	Regulation of gene expression in atherosclerosis: insights from microarray studies in monocytes/macrophages. Pharmacogenomics, 2012, 13, 477-495.	0.6	12
1187	Interpreting the regulatory genome: the genomics of transcription factor function in Drosophila melanogaster. Briefings in Functional Genomics, 2012, 11, 336-346.	1.3	4
1188	Using formaldehyde-assisted isolation of regulatory elements (FAIRE) to isolate active regulatory DNA. Nature Protocols, 2012, 7, 256-267.	5.5	274
1189	Histone modification profiles characterize function-specific gene regulation. Journal of Theoretical Biology, 2012, 310, 132-142.	0.8	12
1190	A Recently Evolved Transcriptional Network Controls Biofilm Development in Candida albicans. Cell, 2012, 148, 126-138.	13.5	607
1191	Selective binding of nuclear alpha-synuclein to the PGC1alpha promoter under conditions of oxidative stress may contribute to losses in mitochondrial function: Implications for Parkinsonâ€™s disease. Free Radical Biology and Medicine, 2012, 53, 993-1003.	1.3	152
1192	Are clustered genes in the genomes of Arabidopsis and Drosophila regulated differently?. Gene, 2012, 491, 284-288.	1.0	0

#	Article	IF	Citations
1193	Hepatitis B viral core protein disrupts human host gene expression by binding to promoter regions. BMC Genomics, 2012, 13, 563.	1.2	50
1194	Identifying targets of multiple co-regulating transcription factors from expression time-series by Bayesian model comparison. BMC Systems Biology, 2012, 6, 53.	3.0	20
1196	Next Generation Microarray Bioinformatics. Methods in Molecular Biology, 2012, , .	0.4	8
1197	A computational pipeline for comparative ChIP-seq analyses. Nature Protocols, 2012, 7, 45-61.	5.5	110
1198	ChIP-Seq Data Analysis: Identification of Proteinâ€"DNA Binding Sites with SISSRs Peak-Finder. Methods in Molecular Biology, 2012, 802, 305-322.	0.4	38
1199	A pipeline for the identification and characterization of chromatin modifications derived from ChIP-Seq datasets. Biochimie, 2012, 94, 2353-2359.	1.3	6
1200	Genome-Wide Mapping of Nucleosome Occupancy, Histone Modifications, and Gene Expression Using Next-Generation Sequencing Technology. Methods in Enzymology, 2012, 513, 297-313.	0.4	24
1202	Potassium-doped graphene enhanced electrochemiluminescence of SiO2@CdS nanocomposites for sensitive detection of TATA-binding protein. Chemical Communications, 2012, 48, 6429.	2.2	38
1203	Nonspecific Protein-DNA Binding Is Widespread in the Yeast Genome. Biophysical Journal, 2012, 102, 1881-1888.	0.2	20
1204	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	2.4	166
1205	Gene Regulatory Networks. Methods in Molecular Biology, 2012, , .	0.4	4
1208	Sensitive Detection of Transcription Factors by Isothermal Exponential Amplification-Based Colorimetric Assay. Analytical Chemistry, 2012, 84, 9544-9549.	3.2	115
1209	Exploiting ancestral mammalian genomes for the prediction of human transcription factor binding sites. BMC Bioinformatics, 2012, 13, S2.	1.2	1
1210	Genomic insights of protein arginine methyltransferase Hmt1 binding reveals novel regulatory functions. BMC Genomics, 2012, 13, 728.	1.2	8
1211	MISCORE: a new scoring function for characterizing DNA regulatory motifs in promoter sequences. BMC Systems Biology, 2012, 6, S4.	3.0	10
1212	Systems Metabolic Engineering. , 2012, , .		11
1213	Macro-level Modeling of the Response of C. elegans Reproduction to Chronic Heat Stress. PLoS Computational Biology, 2012, 8, e1002338.	1.5	33
1214	Genome-Wide Analyses of Nkx2-1 Binding to Transcriptional Target Genes Uncover Novel Regulatory Patterns Conserved in Lung Development and Tumors. PLoS ONE, 2012, 7, e29907.	1.1	42

#	Article	IF	Citations
1215	Widespread mRNA Association with Cytoskeletal Motor Proteins and Identification and Dynamics of Myosin-Associated mRNAs in S. cerevisiae. PLoS ONE, 2012, 7, e31912.	1.1	16
1216	Cooperativity of Stress-Responsive Transcription Factors in Core Hypoxia-Inducible Factor Binding Regions. PLoS ONE, 2012, 7, e45708.	1.1	46
1217	When One and One Gives More than Two: Challenges and Opportunities of Integrative Omics. Frontiers in Genetics, 2012, 2, 105.	1.1	30
1218	Genome-wide ChIP-DSL profiling of promoter methylation patterns associated with cancer and stem cell differentiation. , 0, , 210-222.		0
1219	Using Self-Organizing Maps to Visualize, Filter and Cluster Multidimensional Bio-Omics Data. , 0, , .		4
1220	PLANT EPIGENETICS: BEYOND THE DOUBLE HELIX. Acta Horticulturae, 2012, , 315-325.	0.1	1
1221	CpG Array Analysis of Histone H3 Lysine 4 Trimethylation by Chromatin Immunoprecipitation Linked to Microarrays Analysis in Peripheral Blood Mononuclear Cells of IgA Nephropathy Patients. Yonsei Medical Journal, 2012, 53, 377.	0.9	3
1222	Reverseâ€engineering human regulatory networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 311-325.	6.6	44
1223	A Database of Annotated Promoters of Genes Associated with Common Respiratory and Related Diseases. American Journal of Respiratory Cell and Molecular Biology, 2012, 47, 112-119.	1.4	7
1224	Genome-Wide Occupancy Analysis by ChIP-chip and ChIP-Seq. Advances in Experimental Medicine and Biology, 2012, 723, 753-759.	0.8	5
1225	Characterization of Enhancer Function from Genome-Wide Analyses. Annual Review of Genomics and Human Genetics, 2012, 13, 29-57.	2.5	86
1226	DNAâ€"Protein Interaction Analysis (ChIP-Seq). , 2012, , 127-149.		0
1227	Genomic approaches towards finding cis-regulatory modules in animals. Nature Reviews Genetics, 2012, 13, 469-483.	7.7	200
1228	Organogenesis and functional genomics of the endocrine pancreas. Cellular and Molecular Life Sciences, 2012, 69, 2109-2123.	2.4	10
1229	Exploring the role of the epigenome in multiple sclerosis: A window onto cell-specific transcriptional potential. Journal of Neuroimmunology, 2012, 248, 2-9.	1.1	3
1230	Fish welfare and genomics. Fish Physiology and Biochemistry, 2012, 38, 43-60.	0.9	44
1231	A novel methyl-binding domain protein enrichment method for identifying genome-wide tissue-specific DNA methylation from nanogram DNA samples. Epigenetics and Chromatin, 2013, 6, 17.	1.8	17
1232	Chromatin tandem affinity purification sequencing. Nature Protocols, 2013, 8, 1525-1534.	5.5	13

#	ARTICLE	IF	CITATIONS
1233	Global Mapping of Transcription Factor Binding Sites by Sequencing Chromatin Surrogates: a Perspective on Experimental Design, Data Analysis, and Open Problems. Statistics in Biosciences, 2013, 5, 156-178.	0.6	4
1234	ChIPXpress: using publicly available gene expression data to improve ChIP-seq and ChIP-chip target gene ranking. BMC Bioinformatics, 2013, 14, 188.	1.2	15
1235	An improved sequence based prediction protocol for DNA-binding proteins using SVM and comprehensive feature analysis. BMC Bioinformatics, 2013, 14, 90.	1.2	70
1236	A genome-wide cis-regulatory element discovery method based on promoter sequences and gene co-expression networks. BMC Genomics, 2013, 14, S4.	1.2	13
1237	Pluripotent Stem Cells. Methods in Molecular Biology, 2013, , .	0.4	5
1238	Advances in Enzyme Biotechnology. , 2013, , .		9
1239	Combining genomic and proteomic approaches for epigenetics research. Epigenomics, 2013, 5, 439-452.	1.0	31
1240	Identification of transcription factor binding sites from ChIP-seq data at high resolution. Bioinformatics, 2013, 29, 2705-2713.	1.8	58
1241	A Robust Elicitation Algorithm for Discovering DNA Motifs Using Fuzzy Self-Organizing Maps. IEEE Transactions on Neural Networks and Learning Systems, 2013, 24, 1677-1688.	7.2	14
1242	Cell-type and transcription factor specific enrichment of transcriptional cofactor motifs in ENCODE ChIP-seq data. BMC Genomics, 2013, 14, S2.	1.2	12
1243	Experimental characterization of the human non-sequence-specific nucleic acid interactome. Genome Biology, 2013, 14, R81.	13.9	7
1244	Inferring functional transcription factor-gene binding pairs by integrating transcription factor binding data with transcription factor knockout data. BMC Systems Biology, 2013, 7, S13.	3.0	9
1245	Genome-wide profiling reveals epigenetic inactivation of the PU.1 pathway by histone H3 lysine 27 trimethylation in cytogenetically normal myelodysplastic syndrome. Leukemia, 2013, 27, 1291-1300.	3.3	12
1246	A functional autophagy pathway is required for rapamycin-induced degradation of the Sgs1 helicase in <i>Saccharomyces cerevisiae</i>. Biochemistry and Cell Biology, 2013, 91, 123-130.	0.9	3
1247	Learning a nonlinear dynamical system model of gene regulation: A perturbed steady-state approach. Annals of Applied Statistics, 2013, 7, .	0.5	19
1248	Machine learning and genome annotation: a match meant to be?. Genome Biology, 2013, 14, 205.	13.9	72
1249	Research in Computational Molecular Biology. Lecture Notes in Computer Science, 2013, , .	1.0	17
1250	Time delay estimation in gene regulatory networks. , 2013, , .		3

#	Article	IF	Citations
1251	Next-generation sequencing technologies and their impact on microbial genomics. Briefings in Functional Genomics, 2013, 12, 440-453.	1.3	65
1252	Genome-wide identification of Polycomb target genes in human embryonic stem cells. Gene, 2013, 518, 425-430.	1.0	3
1253	RIP-chip enrichment analysis. Bioinformatics, 2013, 29, 77-83.	1.8	12
1254	OTX2 sustains a bivalent-like state of OTX2-bound promoters in medulloblastoma by maintaining their H3K27me3 levels. Acta Neuropathologica, 2013, 125, 385-394.	3.9	42
1255	Gene Regulatory Networks. , 2013, , 65-88.		4
1256	LinkNMF: Identification of histone modification modules in the human genome using nonnegative matrix factorization. Gene, 2013, 518, 215-221.	1.0	4
1257	Fabrication of a colorimetric biosensing platform for the detection of proteinâ€"DNA interaction. Biosensors and Bioelectronics, 2013, 46, 108-112.	5.3	4
1258	Reconstruction of Genome-Scale Metabolic Networks. , 2013, , 229-250.		1
1259	Distinguishing between Genomic Regions Bound by Paralogous Transcription Factors. Lecture Notes in Computer Science, 2013, , 145-157.	1.0	1
1260	Regulations of sugar transporters: insights from yeast. Current Genetics, 2013, 59, 1-31.	0.8	98
1261	Isolation of Intracellular Protein â€" DNA Complexes Using HaloCHIP, an Antibody-Free Alternative to Chromatin Immunoprecipitation. Methods in Molecular Biology, 2013, 977, 111-124.	0.4	4
1262	Discovery of Posttranscriptional Regulatory RNAs Using Next Generation Sequencing Technologies. Methods in Molecular Biology, 2013, 985, 269-295.	0.4	18
1263	Translational Bioinformatics for Genomic Medicine. , 2013, , 272-286.		4
1264	Epigenetic Control of Cytokine Gene Expression. Advances in Immunology, 2013, 118, 37-128.	1.1	60
1265	Detection of epigenetic changes using ANOVA with spatially varying coefficients. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 189-205.	0.2	3
1266	DNA methylation data analysis and its application to cancer research. Epigenomics, 2013, 5, 301-316.	1.0	82
1267	Systems Metabolic Engineering. Methods in Molecular Biology, 2013, , .	0.4	3
1268	Bridging epigenomics and complex disease: the basics. Cellular and Molecular Life Sciences, 2013, 70, 1609-1621.	2.4	31

#	ARTICLE	IF	CITATIONS
1269	Epigenome Analysis of Pluripotent Stem Cells. Methods in Molecular Biology, 2013, 997, 203-216.	0.4	2
1271	Non-coding transcription at cis-regulatory elements: Computational and experimental approaches. Methods, 2013, 63, 66-75.	1.9	6
1272	An ultrasensitive label-free biosensor for assaying of sequence-specific DNA-binding protein based on amplifying fluorescent conjugated polymer. Biosensors and Bioelectronics, 2013, 41, 218-224.	5.3	43
1273	Amplified electrochemiluminescence detection of DNA-binding protein based on the synergy effect of electron and energy transfer between CdS nanocrystals and gold nanoparticles. Biosensors and Bioelectronics, 2013, 41, 615-620.	5.3	41
1274	Subset of genes targeted by transcription factor NF-Î°B in TNFÎ±-stimulated human HeLa cells. Functional and Integrative Genomics, 2013, 13, 143-154.	1.4	16
1275	Mapping Yeast Transcriptional Networks. Genetics, 2013, 195, 9-36.	1.2	72
1277	Genome-wide analysis of Staufen-associated mRNAs identifies secondary structures that confer target specificity. Nucleic Acids Research, 2013, 41, 9438-9460.	6.5	69
1278	ChIP-PED enhances the analysis of ChIP-seq and ChIP-chip data. Bioinformatics, 2013, 29, 1182-1189.	1.8	12
1279	Sparsely correlated hidden Markov models with application to genome-wide location studies. Bioinformatics, 2013, 29, 533-541.	1.8	15
1280	Transcription Factor Binding Profiles Reveal Cyclic Expression of Human Protein-coding Genes and Non-coding RNAs. PLoS Computational Biology, 2013, 9, e1003132.	1.5	7
1281	Navigating the transcriptional roadmap regulating plant secondary cell wall deposition. Frontiers in Plant Science, 2013, 4, 325.	1.7	124
1282	Divergent Transcriptional Regulatory Logic at the Intersection of Tissue Growth and Developmental Patterning. PLoS Genetics, 2013, 9, e1003753.	1.5	41
1283	DNA motif elucidation using belief propagation. Nucleic Acids Research, 2013, 41, e153-e153.	6.5	53
1284	MuMoD: a Bayesian approach to detect multiple modes of proteinâ€“DNA binding from genome-wide ChIP data. Nucleic Acids Research, 2013, 41, 21-32.	6.5	55
1285	Systematic measurement of transcription factor-DNA interactions by targeted mass spectrometry identifies candidate gene regulatory proteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3645-3650.	3.3	31
1286	Integrative analysis of C. elegans modENCODE ChIP-seq data sets to infer gene regulatory interactions. Genome Research, 2013, 23, 941-953.	2.4	30
1287	Purification of a specific native genomic locus for proteomic analysis. Nucleic Acids Research, 2013, 41, e195-e195.	6.5	49
1288	The twilight zone of cis element alignments. Nucleic Acids Research, 2013, 41, 1438-1449.	6.5	11

#	Article	IF	Citations
1289	NanobodyÂ®-based chromatin immunoprecipitation/micro-array analysis for genome-wide identification of transcription factor DNA binding sites. Nucleic Acids Research, 2013, 41, e59-e59.	6.5	25
1290	Lightâ€dependent, plastomeâ€wide association of the plastidâ€encoded <scp>RNA</scp> polymerase with chloroplast <scp>DNA</scp>. Plant Journal, 2013, 76, 849-860.	2.8	26
1291	Cellâ€specific integration of nuclear receptor function at the genome. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2013, 5, 615-629.	6.6	12
1292	Structure of the transcriptional network controlling whiteâ€opaque switching in <scp><i>C</i></scp><i>andida albicans</i>. Molecular Microbiology, 2013, 90, 22-35.	1.2	118
1293	RNA-sequencing analysis of high glucose-treated monocytes reveals novel transcriptome signatures and associated epigenetic profiles. Physiological Genomics, 2013, 45, 287-299.	1.0	28
1294	Mod5 protein binds to tRNA gene complexes and affects local transcriptional silencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3081-9.	3.3	33
1295	Early Colony Establishment in Neurospora crassa Requires a MAP Kinase Regulatory Network. Genetics, 2013, 195, 883-898.	1.2	59
1296	Pro-inflammatory cytokines can act as intracellular modulators of commensal bacterial virulence. Open Biology, 2013, 3, 130048.	1.5	28
1297	Predicting tissue specific transcription factor binding sites. BMC Genomics, 2013, 14, 796.	1.2	25
1298	Oxidative stress and neurodegeneration: the yeast model system. Frontiers in Bioscience - Landmark, 2013, 18, 1174.	3.0	16
1299	Understanding the Dynamics of Gene Regulatory Systems; Characterisation and Clinical Relevance of cis-Regulatory Polymorphisms. Biology, 2013, 2, 64-84.	1.3	8
1300	STEME: A Robust, Accurate Motif Finder for Large Data Sets. PLoS ONE, 2014, 9, e90735.	1.1	15
1301	An Optimized Protocol for Isolating Primary Epithelial Cell Chromatin for ChIP. PLoS ONE, 2014, 9, e100099.	1.1	19
1302	A Method for Obtaining Epigenomic Data. , 2014, , 773-776.		0
1303	Condensing Biochemistry into Gene Regulatory Networks. International Journal of Natural Computing Research, 2014, 4, 1-25.	0.5	0
1304	The hierarchic network of metal-response transcription factors in <i>Escherichia coli</i>. Bioscience, Biotechnology and Biochemistry, 2014, 78, 737-747.	0.6	11
1305	Chromatin Immunoprecipitation and Multiplex Sequencing (ChIP-Seq) to Identify Global Transcription Factor Binding Sites in the Nematode Caenorhabditis Elegans. Methods in Enzymology, 2014, 539, 89-111.	0.4	7
1306	Epigenetics and Cardiovascular Disease. , 2014, , 747-782.		0

#	Article	IF	Citations
1307	Discrimination between thermodynamic models of<i>cis</i>-regulation using transcription factor occupancy data. Nucleic Acids Research, 2014, 42, 2224-2234.	6.5	10
1308	Learning proteinâ€“DNA interaction landscapes by integrating experimental data through computational models. Bioinformatics, 2014, 30, 2868-2874.	1.8	12
1309	YTRP: a repository for yeast transcriptional regulatory pathways. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau014-bau014.	1.4	19
1310	Structure-based prediction of transcription factor binding sites. Tsinghua Science and Technology, 2014, 19, 568-577.	4.1	8
1311	Role of ChIP-seq in the discovery of transcription factor binding sites, differential gene regulation mechanism, epigenetic marks and beyond. Cell Cycle, 2014, 13, 2847-2852.	1.3	119
1312	Assessing quality standards for ChIP-seq and related massive parallel sequencing-generated datasets: When rating goes beyond avoiding the crisis. Genomics Data, 2014, 2, 268-273.	1.3	7
1313	CisMiner: Genome-Wide In-Silico Cis-Regulatory Module Prediction by Fuzzy Itemset Mining. PLoS ONE, 2014, 9, e108065.	1.1	10
1314	Covariation between homeodomain transcription factors and the shape of their DNA binding sites. Nucleic Acids Research, 2014, 42, 430-441.	6.5	54
1315	Enzymatic Fabrication of Highâ€Density RNA Arrays. Angewandte Chemie - International Edition, 2014, 53, 13514-13517.	7.2	24
1316	Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. Nucleic Acids Research, 2014, 42, 2976-2987.	6.5	421
1317	Large-Scale Quality Analysis of Published ChIP-seq Data. G3: Genes, Genomes, Genetics, 2014, 4, 209-223.	0.8	125
1318	DPRP: a database of phenotype-specific regulatory programs derived from transcription factor binding data. Nucleic Acids Research, 2014, 42, D178-D183.	6.5	2
1319	Binding site discovery from nucleic acid sequences by discriminative learning of hidden Markov models. Nucleic Acids Research, 2014, 42, 12995-13011.	6.5	24
1320	Histone Modification Patterns and Their Responses to Environment. Current Environmental Health Reports, 2014, 1, 11-21.	3.2	36
1321	Inferring transcription factor collaborations in gene regulatory networks. BMC Systems Biology, 2014, 8, S1.	3.0	10
1322	An unexpected journey: Lysine methylation across the proteome. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 1395-1403.	0.9	83
1323	Ancestral Resurrection of the Drosophila S2E Enhancer Reveals Accessible Evolutionary Paths through Compensatory Change. Molecular Biology and Evolution, 2014, 31, 903-916.	3.5	18
1324	footprintDB: a database of transcription factors with annotated cis elements and binding interfaces. Bioinformatics, 2014, 30, 258-265.	1.8	72

#	Article	IF	Citations
1325	Two Novel Ternary Dicopper(II) Î¼-Guanazole Complexes with Aromatic Amines Strongly Activated by Quantum Dots for DNA Cleavage. Inorganic Chemistry, 2014, 53, 578-593.	1.9	20
1326	High-resolution mapping of transcription factor binding sites on native chromatin. Nature Methods, 2014, 11, 203-209.	9.0	170
1327	Applications of alignment-free methods in epigenomics. Briefings in Bioinformatics, 2014, 15, 419-430.	3.2	40
1328	Mapping Argonaute and conventional RNA-binding protein interactions with RNA at single-nucleotide resolution using HITS-CLIP and CIMS analysis. Nature Protocols, 2014, 9, 263-293.	5.5	272
1329	Topology and Control of the Cell-Cycle-Regulated Transcriptional Circuitry. Genetics, 2014, 196, 65-90.	1.2	71
1330	ChIP for Hox Proteins from Drosophila Imaginal Discs. Methods in Molecular Biology, 2014, 1196, 241-253.	0.4	5
1331	A Functional and Evolutionary Perspective on Transcription Factor Binding in <i>Arabidopsis thaliana</i>. Plant Cell, 2014, 26, 3894-3910.	3.1	102
1332	Architecture based on the integration of intermolecular G-quadruplex structure with sticky-end pairing and colorimetric detection of DNA hybridization. Nanoscale, 2014, 6, 2218.	2.8	15
1333	Histone Deacetylases and Phosphorylated Polymerase II C-Terminal Domain Recruit Spt6 for Cotranscriptional Histone Reassembly. Molecular and Cellular Biology, 2014, 34, 4115-4129.	1.1	25
1334	LEVERAGING BIOLOGICAL REPLICATES TO IMPROVE ANALYSIS IN CHIP-SEQ EXPERIMENTS. Computational and Structural Biotechnology Journal, 2014, 9, e201401002.	1.9	57
1335	Kin28 regulates the transient association of Mediator with core promoters. Nature Structural and Molecular Biology, 2014, 21, 449-455.	3.6	127
1336	Genome-Wide Profiling of Transcription Factor Binding and Epigenetic Marks in Adipocytes by ChIP-seq. Methods in Enzymology, 2014, 537, 261-279.	0.4	23
1337	The future of genomeâ€scale modeling of yeast through integration of a transcriptional regulatory network. Quantitative Biology, 2014, 2, 30-46.	0.3	8
1338	Dynamic remodeling of histone modifications in response to osmotic stress in Saccharomyces cerevisiae. BMC Genomics, 2014, 15, 247.	1.2	22
1339	Absence of a simple code: how transcription factors read the genome. Trends in Biochemical Sciences, 2014, 39, 381-399.	3.7	447
1341	Large-scale imaginal disc sorting: A protocol for â€œomicsâ€•approaches. Methods, 2014, 68, 260-264.	1.9	7
1342	The ICY1 gene from Saccharomyces cerevisiae affects nitrogen consumption during alcoholic fermentation. Electronic Journal of Biotechnology, 2014, 17, 150-155.	1.2	14
1343	Fructose bisphosphate aldolase is involved in the control of RNA polymerase III-directed transcription. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 1103-1110.	1.9	32

#	ARTICLE	IF	CITATIONS
1344	A computational method of predicting regulatory interactions in Arabidopsis based on gene expression data and sequence information. Computational Biology and Chemistry, 2014, 51, 36-41.	1.1	7
1345	An electrochemical sensing platform based on local repression of electrolyte diffusion for single-step, reagentless, sensitive detection of a sequence-specific DNA-binding protein. Analyst, The, 2014, 139, 2193-2198.	1.7	3
1346	Pseudomonas Methods and Protocols. Methods in Molecular Biology, 2014, 1149, v.	0.4	78
1347	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. Briefings in Bioinformatics, 2014, 15, 592-611.	3.2	30
1349	Chromatin Interaction Analysis with Paired-End Tag (ChIA-PET) sequencing technology and application. BMC Genomics, 2014, 15, S11.	1.2	75
1350	Integrative Analysis of Multiple ChIP-X Data Sets Using Correlation Motifs. , 0, , 110-132.		0
1351	Fully automated high-throughput chromatin immunoprecipitation for ChIP-seq: Identifying ChIP-quality p300 monoclonal antibodies. Scientific Reports, 2014, 4, 5152.	1.6	34
1352	Sandcastle: software for revealing latent information in multiple experimental ChIP-chip datasets via a novel normalisation procedure. Scientific Reports, 2015, 5, 13395.	1.6	4
1353	Determination of the consensus sequence for FUS3-specific binding by protein binding microarray analysis. Journal of the Korean Society for Applied Biological Chemistry, 2015, 58, 723-728.	0.9	0
1354	Direct ChIP-Seq significance analysis improves target prediction. BMC Genomics, 2015, 16, S4.	1.2	8
1355	Identifying DNA-binding proteins by combining support vector machine and PSSM distance transformation. BMC Systems Biology, 2015, 9, S10.	3.0	85
1356	cChIP-seq: a robust small-scale method for investigation of histone modifications. BMC Genomics, 2015, 16, 1083.	1.2	14
1357	Genome-wide Snapshot of Chromatin Regulators and States in Xenopus Embryos by ChIP-Seq. Journal of Visualized Experiments, 2015, , .	0.2	13
1358	Choosing a suitable method for the identification of replication origins in microbial genomes. Frontiers in Microbiology, 2015, 6, 1049.	1.5	21
1359	MORPHEUS, a Webtool for Transcription Factor Binding Analysis Using Position Weight Matrices with Dependency. PLoS ONE, 2015, 10, e0135586.	1.1	16
1360	Reverse Engineering of Genome-wide Gene Regulatory Networks from Gene Expression Data. Current Genomics, 2015, 16, 3-22.	0.7	79
1361	Understanding Transcription Factor Regulation by Integrating Gene Expression and DNase I Hypersensitive Sites. BioMed Research International, 2015, 2015, 1-7.	0.9	13
1362	Introduction to Data Types in Epigenomics. Translational Bioinformatics, 2015, , 3-34.	0.0	2

#	ARTICLE	IF	CITATIONS
1363	Technologies for the Measurement and Mapping of Genomic 5-Methylcytosine and 5-Hydroxymethylcytosine. , 2015, , 19-38.		0
1364	Multiple levels of epigenetic control for bone biology and pathology. Bone, 2015, 81, 733-738.	1.4	18
1367	Application of Machine-Learning Methods to Understand Gene Expression Regulation. Genetic and Evolutionary Computation, 2015, , 1-15.	1.0	2
1368	Proteinâ€"DNA binding in high-resolution. Critical Reviews in Biochemistry and Molecular Biology, 2015, 50, 269-283.	2.3	41
1369	Probabilistic Inference on Multiple Normalized Signal Profiles from Next Generation Sequencing: Transcription Factor Binding Sites. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1416-1428.	1.9	4
1370	Using the ENCODE Resource for Functional Annotation of Genetic Variants. Cold Spring Harbor Protocols, 2015, 2015, pdb.top084988.	0.2	27
1371	Mapping Transcription Regulatory Networks with ChIP-seq and RNA-seq. Advances in Experimental Medicine and Biology, 2015, 883, 119-134.	0.8	20
1372	A Biophysical Approach to Predicting Proteinâ€"DNA Binding Energetics. Genetics, 2015, 200, 1349-1361.	1.2	5
1373	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. Bioinformatics, 2015, 31, 17-24.	1.8	39
1375	ChIP-seq and RNA-seq Methods to Study Circadian Control of Transcription in Mammals. Methods in Enzymology, 2015, 551, 285-321.	0.4	26
1376	Vision from next generation sequencing: Multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. Progress in Retinal and Eye Research, 2015, 46, 1-30.	7.3	50
1377	Bacterial Transcriptional Control. Methods in Molecular Biology, 2015, 1276, v.	0.4	1
1378	INTERACT-O-FINDER: A Tool for Prediction of DNA-Binding Proteins Using Sequence Features. International Journal of Peptide Research and Therapeutics, 2015, 21, 189-193.	0.9	0
1379	Elucidation of Sigma Factor-Associated Networks in Pseudomonas aeruginosa Reveals a Modular Architecture with Limited and Function-Specific Crosstalk. PLoS Pathogens, 2015, 11, e1004744.	2.1	134
1380	Nanopore sensing of individual transcription factors bound to DNA. Scientific Reports, 2015, 5, 11643.	1.6	64
1381	cDREM: Inferring Dynamic Combinatorial Gene Regulation. Journal of Computational Biology, 2015, 22, 324-333.	0.8	10
1382	Global identification of the genetic networks and<i>cis</i>-regulatory elements of the cold response in zebrafish. Nucleic Acids Research, 2015, 43, 9198-9213.	6.5	38
1383	Determinants of Receptor- and Tissue-Specific Actions in Androgen Signaling. Endocrine Reviews, 2015, 36, 357-384.	8.9	93

#	ARTICLE	IF	CITATIONS
1384	Intersecting transcription networks constrain gene regulatory evolution. Nature, 2015, 523, 361-365.	13.7	72
1385	A Post-Genomic View of the Ecophysiology, Catabolism and Biotechnological Relevance of Sulphate-Reducing Prokaryotes. Advances in Microbial Physiology, 2015, 66, 55-321.	1.0	238
1386	Effect of environmental stress on regulation of gene expression in the yeast. Physica A: Statistical Mechanics and Its Applications, 2015, 430, 224-235.	1.2	0
1387	Myogenesis in the Genomics Era. Journal of Molecular Biology, 2015, 427, 2023-2038.	2.0	10
1388	Epigenetics of the failing heart. Heart Failure Reviews, 2015, 20, 435-459.	1.7	16
1389	Systems biology approaches to defining transcription regulatory networks in halophilic archaea. Methods, 2015, 86, 102-114.	1.9	16
1390	An approach for determining and measuring network hierarchy applied to comparing the phosphorylome and the regulome. Genome Biology, 2015, 16, 63.	3.8	27
1391	The Ensembl Regulatory Build. Genome Biology, 2015, 16, 56.	3.8	382
1392	The Histone Chaperones FACT and Spt6 Restrict H2A.Z from Intragenic Locations. Molecular Cell, 2015, 58, 1113-1123.	4.5	108
1393	Making Sense of Transcription Networks. Cell, 2015, 161, 714-723.	13.5	133
1394	A new visible-light-driven photoelectrochemical biosensor for probing DNAâ€"protein interactions. Chemical Communications, 2015, 51, 8381-8384.	2.2	33
1395	Survey of proteinâ€"DNA interactions in Aspergillus oryzae on a genomic scale. Nucleic Acids Research, 2015, 43, 4429-4446.	6.5	9
1397	Formaldehyde Crosslinking: A Tool for the Study of Chromatin Complexes. Journal of Biological Chemistry, 2015, 290, 26404-26411.	1.6	290
1398	Precise Identification of DNA-Binding Proteins Genomic Location by Exonuclease Coupled Chromatin Immunoprecipitation (ChIP-exo). Methods in Molecular Biology, 2015, 1334, 173-193.	0.4	5
1399	A widespread role of the motif environment in transcription factor binding across diverse protein families. Genome Research, 2015, 25, 1268-1280.	2.4	134
1400	ChIP-Seq to Analyze the Binding of Replication Proteins to Chromatin. Methods in Molecular Biology, 2015, 1300, 155-168.	0.4	13
1401	Suppression subtractive hybridization and comparative expression of a pore-forming toxin and glycosyl hydrolase genes in Rhizoctonia solani during potato sprout infection. Molecular Genetics and Genomics, 2015, 290, 877-900.	1.0	10
1402	Promoter or enhancer, what's the difference? Deconstruction of established distinctions and presentation of a unifying model. BioEssays, 2015, 37, 314-323.	1.2	92

#	Article	IF	Citations
1403	Network motifs that recur across species, including gene regulatory and proteinâ€"protein interaction networks. Archives of Toxicology, 2015, 89, 489-499.	1.9	5
1404	Parasite Genomics Protocols. Methods in Molecular Biology, 2015, 1201, v-vi.	0.4	2
1405	Multiplexed electrochemical coding of DNAâ€"protein bindings. Biosensors and Bioelectronics, 2015, 64, 429-433.	5.3	7
1406	Analysis of PBase Binding Profile Indicates an Insertion Target Selection Mechanism Dependent on TTAA, But Not Transcriptional Activity. International Journal of Biological Sciences, 2016, 12, 1074-1082.	2.6	2
1407	Modeling proteinâ€"DNA binding via high-throughput<i>in vitro</i>technologies. Briefings in Functional Genomics, 2017, 16, elw030.	1.3	14
1408	Genomics Era for Plants and Crop Species â€" Advances Made and Needed Tasks Ahead. , 0, , .		11
1409	A basic domain in the histone H2B N-terminal tail is important for nucleosome assembly by FACT. Nucleic Acids Research, 2016, 44, gkw588.	6.5	14
1410	Genome-Wide Mapping of Binding Sites Reveals Multiple Biological Functions of the Transcription Factor Cst6p in Saccharomyces cerevisiae. MBio, 2016, 7, .	1.8	22
1411	Ensembl regulation resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav119.	1.4	45
1412	- Protein-Protein Functional Linkage Predictions: Bringing Regulation to Context. , 2016, , 172-191.		0
1413	Gene-Centered Yeast One-Hybrid Assays. Cold Spring Harbor Protocols, 2016, 2016, pdb.top077669.	0.2	12
1414	Label-free electrochemiluminescent detection of transcription factors with hybridization chain reaction amplification. RSC Advances, 2016, 6, 37681-37688.	1.7	14
1415	Fast training on large genomics data using distributed Support Vector Machines. , 2016, , .		3
1416	Rlm1 mediates a positive autoregulatory transcriptional feedback essential for Slt2 MAPK dependent gene expression. Journal of Cell Science, 2016, 129, 1649-60.	1.2	33
1417	Unsupervised Learning in Genome Informatics. , 2016, , 405-448.		4
1418	Unsupervised Learning Algorithms. , 2016, , .		115
1419	Disruption of promoter memory by synthesis of a long noncoding RNA. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9575-9580.	3.3	21
1420	FootprintDB: Analysis of Plant Cis-Regulatory Elements, Transcription Factors, and Binding Interfaces. Methods in Molecular Biology, 2016, 1482, 259-277.	0.4	20

#	Article	IF	Citations
1421	Plant Synthetic Promoters. Methods in Molecular Biology, 2016, , .	0.4	3
1422	Genome-Wide Techniques for the Study of Clinical Epigenetic Biomarkers. , 2016, , 119-135.		0
1423	Profiling of Transcription Factor Binding Events by Chromatin Immunoprecipitation Sequencing (ChIPâ€seq). Current Protocols in Plant Biology, 2016, 1, 293-306.	2.8	24
1424	Evaluating tools for transcription factor binding site prediction. BMC Bioinformatics, 2016, 17, 547.	1.2	80
1425	Transcription Factorâ€"DNA Binding Motifs in Saccharomyces cerevisiae: Tools and Resources. Cold Spring Harbor Protocols, 2016, 2016, pdb.top080622.	0.2	2
1426	Investigation of Viral and Host Chromatin by ChIPâ€PCR or ChIPâ€Seq Analysis. Current Protocols in Microbiology, 2016, 40, 1E.10.1-1E.10.21.	6.5	9
1427	Mapping Proteinâ€"DNA Interactions Using ChIP-exo and Illumina-Based Sequencing. Methods in Molecular Biology, 2016, 1443, 119-137.	0.4	4
1428	ChIP-seq in studying epigenetic mechanisms of disease and promoting precision medicine: progresses and future directions. Epigenomics, 2016, 8, 1239-1258.	1.0	22
1429	Review of Methods to Study Gene Expression Regulation Applied to Asthma. Methods in Molecular Biology, 2016, 1434, 71-89.	0.4	1
1430	16 Sexual Development in Fungi. , 2016, , 407-455.		12
1431	Dam it's good! DamID profiling of protein-DNA interactions. Wiley Interdisciplinary Reviews: Developmental Biology, 2016, 5, 25-37.	5.9	48
1432	FabR regulates Salmonella biofilm formation via its direct target FabB. BMC Genomics, 2016, 17, 253.	1.2	9
1433	Decoding the nonâ€coding genome: elucidating genetic risk outside the coding genome. Genes, Brain and Behavior, 2016, 15, 187-204.	1.1	32
1434	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. Nucleic Acids Research, 2016, 44, e51-e51.	6.5	18
1435	Mit1 Transcription Factor Mediates Methanol Signaling and Regulates the Alcohol Oxidase 1 (AOX1) Promoter in Pichia pastoris. Journal of Biological Chemistry, 2016, 291, 6245-6261.	1.6	82
1436	A duplex DNAâ€"gold nanoparticle probe composed as a colorimetric biosensor for sequence-specific DNA-binding proteins. Analyst, The, 2016, 141, 2040-2045.	1.7	15
1437	Genome-wide targets identification of â€œcoreâ€• pluripotency transcription factors with integrated features in human embryonic stem cells. Molecular BioSystems, 2016, 12, 1324-1332.	2.9	3
1438	Amplified detection of nuclear factor-kappa B activity and inhibition based on exonuclease III assisted cleavage-induced DNAzyme releasing strategy. Sensors and Actuators B: Chemical, 2016, 228, 605-611.	4.0	13

#	Article	IF	Citations
1439	Protein Binding Bends the Gold Nanoparticle Capped DNA Sequence: Toward Novel Energy-Transfer-Based Photoelectrochemical Protein Detection. Analytical Chemistry, 2016, 88, 3864-3871.	3.2	67
1440	Create, activate, destroy, repeat: Cdk1 controls proliferation by limiting transcription factor activity. Current Genetics, 2016, 62, 271-276.	0.8	22
1442	Genome-Wide Chromatin Immunoprecipitation in Candida albicans and Other Yeasts. Methods in Molecular Biology, 2016, 1361, 161-184.	0.4	4
1444	Label-free and enzyme-free detection of transcription factors with graphene oxide fluorescence switch-based multifunctional G-quadruplex-hairpin probe. Biosensors and Bioelectronics, 2016, 75, 155-160.	5.3	32
1445	Sensitive detection of transcription factors in cell nuclear extracts by using a molecular beacons based amplification strategy. Biosensors and Bioelectronics, 2016, 77, 264-269.	5.3	26
1446	Association analysis between the distributions of histone modifications and gene expression in the human embryonic stem cell. Gene, 2016, 575, 90-100.	1.0	10
1447	A Comparison Study for DNA Motif Modeling on Protein Binding Microarray. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 261-271.	1.9	16
1448	Methods to Study Transcription Factor Structure and Function. , 2016, , 13-33.		4
1449	Control of Hormone Gene Expression. , 2016, , 16-29.e2.		0
1450	Probabilistic Inference on Multiple Normalized Genome-Wide Signal Profiles With Model Regularization. IEEE Transactions on Nanobioscience, 2017, 16, 43-50.	2.2	0
1451	Systematic dissection of genomic features determining transcription factor binding and enhancer function. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1291-E1300.	3.3	150
1452	RNA-Seq-based transcriptomic and metabolomic analysis reveal stress responses and programmed cell death induced by acetic acid in Saccharomyces cerevisiae. Scientific Reports, 2017, 7, 42659.	1.6	72
1455	Mocap: large-scale inference of transcription factor binding sites from chromatin accessibility. Nucleic Acids Research, 2017, 45, 4315-4329.	6.5	30
1456	Genome-wide identification of grain filling genes regulated by the OsSMF1 transcription factor in rice. Rice, 2017, 10, 16.	1.7	23
1457	Modeling gene regulation from paired expression and chromatin accessibility data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4914-E4923.	3.3	167
1458	Conjugated-Polymer-Amplified Sensing, Imaging, and Therapy. CheM, 2017, 2, 760-790.	5.8	139
1459	ChIP-seq for the Identification of Functional Elements in the Human Genome. Methods in Molecular Biology, 2017, 1543, 3-18.	0.4	9
1460	Quantitative Genome-Wide Measurements of Meiotic DNA Double-Strand Breaks and Protein Binding in S. pombe. Methods in Molecular Biology, 2017, 1471, 25-49.	0.4	0

#	Article	IF	Citations
1461	Genome-wide analysis of chromatin structures in Trypanosoma brucei using high-resolution MNase-ChIP-seq. Experimental Parasitology, 2017, 180, 2-12.	0.5	10
1462	Genome-wide discovery of active regulatory elements and transcription factor footprints in <i>Caenorhabditis elegans</i> using DNase-seq. Genome Research, 2017, 27, 2108-2119.	2.4	15
1463	Methods for monitoring and measurement of protein translation in time and space. Molecular BioSystems, 2017, 13, 2477-2488.	2.9	28
1464	Enzymatic methods for genome-wide profiling of protein binding sites. Briefings in Functional Genomics, 2018, 17, 138-145.	1.3	11
1465	Mathematical Modeling of Avidity Distribution and Estimating General Binding Properties of Transcription Factors from Genome-Wide Binding Profiles. Methods in Molecular Biology, 2017, 1613, 193-276.	0.4	4
1466	How transcription circuits explore alternative architectures while maintaining overall circuit output. Genes and Development, 2017, 31, 1397-1405.	2.7	29
1467	ChIP-Seq Analysis for Identifying Genome-Wide Histone Modifications Associated with Stress-Responsive Genes in Plants. Methods in Molecular Biology, 2017, 1631, 139-149.	0.4	2
1469	Application of Bioinformatics and System Biology in Medicinal Plant Studies. , 2017, , 375-393.		6
1470	A fast, efficient chromatin immunoprecipitation method for studying protein-DNA binding in Arabidopsis mesophyll protoplasts. Plant Methods, 2017, 13, 42.	1.9	66
1471	Eukaryotic Transcriptional and Post-Transcriptional Gene Expression Regulation. Methods in Molecular Biology, 2017, , .	0.4	3
1472	Efficient Preparation of High-Complexity ChIP-Seq Profiles from Early Xenopus Embryos. Methods in Molecular Biology, 2017, 1507, 23-42.	0.4	6
1473	A new method for sensitive detection of microphthalmia-associated transcription factor based on â€œOFF-stateâ€•and â€œON-stateâ€•equilibrium of a well-designed probe and duplex-specific nuclease signal amplification. Biosensors and Bioelectronics, 2017, 87, 299-304.	5.3	14
1474	UVâ€Induced DNA Damage and Mutagenesis in Chromatin. Photochemistry and Photobiology, 2017, 93, 216-228.	1.3	58
1475	Programming sites of meiotic crossovers using Spo11 fusion proteins. Nucleic Acids Research, 2017, 45, e164-e164.	6.5	44
1477	Big Cellular Mechanisms in the Cell Cycle by System Identification and Big Data Mining. , 2017, , 39-86.		0
1478	Analyses of Genome-Wide Histone Modifications in the Mammalian Genome. , 2017, , 135-152.		1
1479	GTRD: a database of transcription factor binding sites identified by ChIP-seq experiments. Nucleic Acids Research, 2017, 45, D61-D67.	6.5	206
1480	Big Mechanisms of Information Flow in Cellular Systems in Response to Environmental Stress Signals via System Identification and Data Mining. , 2017, , 155-248.		0

#	Article	IF	Citations
1481	Excitonâ€“Plasmon Interaction between AuNPs/Graphene Nanohybrids and CdS Quantum Dots/TiO₂ for Photoelectrochemical Aptasensing of Prostate-Specific Antigen. ACS Sensors, 2018, 3, 632-639.	4.0	277
1482	ChIP-ping the branches of the tree: functional genomics and the evolution of eukaryotic gene regulation. Briefings in Functional Genomics, 2018, 17, 116-137.	1.3	5
1483	A semi-synthetic regulon enables rapid growth of yeast on xylose. Nature Communications, 2018, 9, 1233.	5.8	26
1484	Chromatin Immunoprecipitation-Polymerase Chain Reaction (ChIP-PCR) Detects Methylation, Acetylation, and Ubiquitylation in S. pombe. Methods in Molecular Biology, 2018, 1721, 25-34.	0.4	8
1485	Insights from resolving proteinâ€“DNA interactions at near base-pair resolution. Briefings in Functional Genomics, 2018, 17, 80-88.	1.3	12
1486	Chromatin Immunoprecipitation (ChIP) Analysis of Proteinâ€“DNA Interactions. Cold Spring Harbor Protocols, 2018, 2018, pdb.top082586.	0.2	3
1487	An improved method for rapid analysis of promoters using modified sonication-assisted transient assay. 3 Biotech, 2018, 8, 198.	1.1	1
1488	A decade of ChIP-seq. Briefings in Functional Genomics, 2018, 17, 77-79.	1.3	8
1489	RNA cytosine methylation and methyltransferases mediate chromatin organization and 5-azacytidine response and resistance in leukaemia. Nature Communications, 2018, 9, 1163.	5.8	132
1490	Chromatin Immunoprecipitation and High-Throughput Sequencing (ChIP-Seq): Tips and Tricks Regarding the Laboratory Protocol and Initial Downstream Data Analysis. Methods in Molecular Biology, 2018, 1767, 271-288.	0.4	2
1491	How low can you go? Pushing the limits of low-input ChIP-seq. Briefings in Functional Genomics, 2018, 17, 89-95.	1.3	15
1492	The Gut Microbiome and Mental Health: Implications for Anxiety- and Trauma-Related Disorders. OMICS A Journal of Integrative Biology, 2018, 22, 90-107.	1.0	110
1495	Population Epigenomics: Advancing Understanding of Phenotypic Plasticity, Acclimation, Adaptation and Diseases. Population Genomics, 2018, , 179-260.	0.2	18
1496	DNA Surface Technology: From Gene Sensors to Integrated Systems for Life and Materials Sciences. Angewandte Chemie, 2018, 130, 17204-17212.	1.6	10
1497	DNA Surface Technology: From Gene Sensors to Integrated Systems for Life and Materials Sciences. Angewandte Chemie - International Edition, 2018, 57, 16959-16967.	7.2	44
1498	A Chromatin Immunoprecipitation Assay to Identify Novel NFAT2 Target Genes in Chronic Lymphocytic Leukemia. Journal of Visualized Experiments, 2018, , .	0.2	8
1499	Emerging Concepts and Techniques. , 2018, , 729-743.		0
1500	Insect Transcription Factors: A Landscape of Their Structures and Biological Functions in Drosophila and beyond. International Journal of Molecular Sciences, 2018, 19, 3691.	1.8	37

#	ARTICLE	IF	CITATIONS
1501	Refining cellular pathway models using an ensemble of heterogeneous data sources. Annals of Applied Statistics, 2018, 12, .	0.5	1
1502	The Emerging Role of Epigenetics. Translational Bioinformatics, 2018, , 65-101.	0.0	1
1503	Real-Time Genetic Compensation Defines the Dynamic Demands of Feedback Control. Cell, 2018, 175, 877-886.e10.	13.5	67
1504	In Silico Prediction and Validation of Novel RNA Binding Proteins and Residues in the Human Proteome. Proteomics, 2018, 18, e1800064.	1.3	19
1505	Repeated Cis-Regulatory Tuning of a Metabolic Bottleneck Gene during Evolution. Molecular Biology and Evolution, 2018, 35, 1968-1981.	3.5	30
1506	Two-Hybrid Systems. Methods in Molecular Biology, 2018, , .	0.4	1
1508	Integrating ChIP-seq with other functional genomics data. Briefings in Functional Genomics, 2018, 17, 104-115.	1.3	63
1509	Molecular Toxicity of Metal Oxide Nanoparticles in <i>Danio rerio</i>. Environmental Science & Technology, 2018, 52, 7996-8004.	4.6	55
1510	Function of TFIIIC, RNA polymerase III initiation factor, in activation and repression of tRNA gene transcription. Nucleic Acids Research, 2018, 46, 9444-9455.	6.5	19
1512	How to Tackle Challenging ChIP-Seq, with Long-Range Cross-Linking, Using ATRX as an Example. Methods in Molecular Biology, 2018, 1832, 105-130.	0.4	7
1513	Fengycins, Cyclic Lipopeptides from Marine Bacillus subtilis Strains, Kill the Plant-Pathogenic Fungus Magnaporthe grisea by Inducing Reactive Oxygen Species Production and Chromatin Condensation. Applied and Environmental Microbiology, 2018, 84, .	1.4	138
1514	Rpd3L HDAC links H3K4me3 to transcriptional repression memory. Nucleic Acids Research, 2018, 46, 8261-8274.	6.5	41
1515	Protein binding protection in combination with DNA masking for sensitive and reliable transcription factor detection. Talanta, 2018, 186, 293-298.	2.9	8
1516	RNA-Based dCas9â€"VP64 System Improves the Viability of Cryopreserved Mammalian Cells. Nano LIFE, 2018, 08, 1850004.	0.6	1
1517	Chromatin Immunoprecipitation for Identification of Proteinâ€"DNA Interactions in Human Cells. Methods in Molecular Biology, 2018, 1794, 335-352.	0.4	2
1518	CAPTURE: <i>In Situ</i> Analysis of Chromatin Composition of Endogenous Genomic Loci by Biotinylated dCas9. Current Protocols in Molecular Biology, 2018, 123, e64.	2.9	14
1519	Cell Modeling and Simulation. , 2019, , 864-873.		1
1520	PropaNet: Time-Varying Condition-Specific Transcriptional Network Construction by Network Propagation. Frontiers in Plant Science, 2019, 10, 698.	1.7	6

#	Article	IF	Citations
1521	Histone Recycling by FACT and Spt6 during Transcription Prevents the Scrambling of Histone Modifications. Cell Reports, 2019, 28, 1206-1218.e8.	2.9	81
1522	Isolation and identification of a TetR family protein that regulates the biodesulfurization operon. AMB Express, 2019, 9, 71.	1.4	21
1523	TCF7L2 regulates pancreatic Î²-cell function through PI3K/AKT signal pathway. Diabetology and Metabolic Syndrome, 2019, 11, 55.	1.2	14
1524	Cross-Cell-Type Prediction of TF-Binding Site by Integrating Convolutional Neural Network and Adversarial Network. International Journal of Molecular Sciences, 2019, 20, 3425.	1.8	18
1525	Target-induced steric hindrance protection of DNAzyme junctions for completely enzyme-free and amplified sensing of transcription factors. Sensors and Actuators B: Chemical, 2019, 298, 126865.	4.0	11
1526	Going low to reach high: Smallâ€scale ChIPâ€seq maps new terrain. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2020, 12, e1465.	6.6	8
1527	Essentials of Bioinformatics, Volume III. , 2019, , .		0
1528	Pinpointing the Genomic Localizations of Chromatinâ€Associated Proteins: The Yesterday, Today, and Tomorrow of ChIPâ€seq. Current Protocols in Cell Biology, 2019, 84, e89.	2.3	10
1529	MTTFsite: cross-cell type TF binding site prediction by using multi-task learning. Bioinformatics, 2019, 35, 5067-5077.	1.8	24
1530	Nucleic Acid Platform Technologies. Cold Spring Harbor Protocols, 2019, 2019, pdb.top096388.	0.2	3
1531	Continuous in vivo Metabolism by NMR. Frontiers in Molecular Biosciences, 2019, 6, 26.	1.6	41
1532	Cyclic enzymatic amplification method for highly sensitive detection of nuclear factor-kappa B. Analytica Chimica Acta, 2019, 1068, 80-86.	2.6	8
1533	A Comprehensive Drosophila melanogaster Transcription Factor Interactome. Cell Reports, 2019, 27, 955-970.e7.	2.9	66
1534	Proteins as Nanosized Components of Biosensors. , 2019, , 229-255.		0
1535	Atheroprotective Flow Upregulates ITPR3 (Inositol 1,4,5-Trisphosphate Receptor 3) in Vascular Endothelium via KLF4 (KrÃ¼ppel-Like Factor 4)-Mediated Histone Modifications. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 902-914.	1.1	45
1536	Identification and characterization of dwarf mistletoe responding genes in Ziarat juniper tree (Juniperus excelsa M.Bieb) through suppression subtractive hybridization and deep sequencing. Trees - Structure and Function, 2019, 33, 1027-1039.	0.9	1
1537	Sugar Sensing and Signaling in Candida albicans and Candida glabrata. Frontiers in Microbiology, 2019, 10, 99.	1.5	63
1538	Microbial Genomics in Sustainable Agroecosystems. , 2019, , .		5

#	ARTICLE	IF	CITATIONS
1539	Pentose Metabolism in <i>Saccharomyces cerevisiae</i>: The Need to Engineer Global Regulatory Systems. Biotechnology Journal, 2019, 14, e1800364.	1.8	28
1540	Integrative Approaches for Inference of Genome-Scale Gene Regulatory Networks. Methods in Molecular Biology, 2019, 1883, 161-194.	0.4	3
1541	A Blueprint for Systems Biology. Clinical Chemistry, 2019, 65, 342-344.	1.5	6
1542	RNA Polymerase II CTD Tyrosine 1 Is Required for Efficient Termination by the Nrd1-Nab3-Sen1 Pathway. Molecular Cell, 2019, 73, 655-669.e7.	4.5	33
1543	Repression of yeast RNA polymerase III by stress leads to ubiquitylation and proteasomal degradation of its largest subunit, C160. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2019, 1862, 25-34.	0.9	10
1544	DNA mapping and kinetic modeling of the HrdB regulon in<i>Streptomyces coelicolor</i>. Nucleic Acids Research, 2019, 47, 621-633.	6.5	35
1545	Gene Regulatory Networks. Methods in Molecular Biology, 2019, , .	0.4	41
1547	Assaying epigenome functions of PRMTs and their substrates. Methods, 2020, 175, 53-65.	1.9	16
1548	Nut1/Hos1 and Sas2/Rpd3 control the H3 acetylation of two different sets of osmotic stress-induced genes. Epigenetics, 2020, 15, 251-271.	1.3	9
1549	Genomic methods in profiling DNA accessibility and factor localization. Chromosome Research, 2020, 28, 69-85.	1.0	71
1550	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
1551	BENIN: Biologically enhanced network inference. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040007.	0.3	6
1552	Homogenous cathodic photoelectrochemistry for DNA binding protein analysis. Sensors and Actuators B: Chemical, 2020, 324, 128660.	4.0	13
1553	Seven myths of how transcription factors read the cis-regulatory code. Current Opinion in Systems Biology, 2020, 23, 22-31.	1.3	68
1554	A Review About Transcription Factor Binding Sites Prediction Based on Deep Learning. IEEE Access, 2020, 8, 219256-219274.	2.6	16
1555	Profiling chromatin regulatory landscape: insights into the development of ChIP-seq and ATAC-seq. Molecular Biomedicine, 2020, 1, 9.	1.7	34
1556	Functional Annotation and Curation of Hypothetical Proteins Present in A Newly Emerged Serotype 1c of Shigella flexneri: Emphasis on Selecting Targets for Virulence and Vaccine Design Studies. Genes, 2020, 11, 340.	1.0	18
1557	ChIPSummitDB: a ChIP-seq-based database of human transcription factor binding sites and the topological arrangements of the proteins bound to them. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	22

#	ARTICLE	IF	CITATIONS
1558	Identification of Highest-Affinity Binding Sites of Yeast Transcription Factor Families. Journal of Chemical Information and Modeling, 2020, 60, 1876-1883.	2.5	26
1559	Genomic Profiling by ALaP-Seq Reveals Transcriptional Regulation by PML Bodies through DNMT3A Exclusion. Molecular Cell, 2020, 78, 493-505.e8.	4.5	31
1560	StackPDB: Predicting DNA-binding proteins based on XGB-RFE feature optimization and stacked ensemble classifier. Applied Soft Computing Journal, 2021, 99, 106921.	4.1	37
1561	Super enhancersâ€"Functional cores under the 3D genome. Cell Proliferation, 2021, 54, e12970.	2.4	17
1562	A One-Pot CRISPR/Cas9-Typing PCR for DNA Detection and Genotyping. Journal of Molecular Diagnostics, 2021, 23, 46-60.	1.2	16
1563	Transcriptional enhancers: from prediction to functional assessment on a genome-wide scale. Genome, 2021, 64, 426-448.	0.9	12
1564	Profiling Proteinâ€"DNA Interactions by Chromatin Immunoprecipitation in Arabidopsis. Methods in Molecular Biology, 2021, 2261, 345-356.	0.4	4
1565	Oxidative and Other Stress Research atÂthe Cellular Level. , 2021, , 29-56.		0
1566	A personal journey on cracking the genomic codes. Quantitative Biology, 2021, 9, 8-22.	0.3	1
1567	DNA affinity purification sequencing and transcriptional profiling reveal new aspects of nitrogen regulation in a filamentous fungus. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
1570	Genome-wide binding analysis of 195 DNA binding proteins reveals â€œreservoirâ€• promoters and human specific SVA-repeat family regulation. PLoS ONE, 2021, 16, e0237055.	1.1	2
1571	Filtering of Data-Driven Gene Regulatory Networks Using Drosophila melanogaster as a Case Study. Frontiers in Genetics, 2021, 12, 649764.	1.1	2
1572	Quantifying Intensities of Transcription Factor-DNA Binding by Learning From an Ensemble of Protein Binding Microarrays. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 2811-2819.	3.9	2
1573	DNAâ€"protein interaction studies: a historical and comparative analysis. Plant Methods, 2021, 17, 82.	1.9	23
1575	Emerging Single-Cell Technological Approaches to Investigate Chromatin Dynamics and Centromere Regulation in Human Health and Disease. International Journal of Molecular Sciences, 2021, 22, 8809.	1.8	7
1577	FACT is recruited to theÂ+1 nucleosome of transcribed genes and spreads in a Chd1-dependent manner. Molecular Cell, 2021, 81, 3542-3559.e11.	4.5	33
1578	Rice protein-binding microarrays: a tool to detect cis-acting elements near promoter regions in rice. Planta, 2021, 253, 40.	1.6	1
1579	Computational biology approaches for mapping transcriptional regulatory networks. Computational and Structural Biotechnology Journal, 2021, 19, 4884-4895.	1.9	14

#	ARTICLE	IF	CITATIONS
1580	Prokaryotic Systems Biology. Cell Engineering, 2007, , 395-423.	0.4	1
1581	Conditional Random Fields for Predicting and Analyzing Histone Occupancy, Acetylation and Methylation Areas in DNA Sequences. Lecture Notes in Computer Science, 2006, , 221-230.	1.0	2
1582	The Genomics of Stress Response in Fission Yeast. , 2006, , 97-111.		1
1583	Yeast functional genomics and metabolic engineering: past, present and future. Topics in Current Genetics, 2003, , 331-360.	0.7	2
1584	High-Density GeneChip Oligonucleotide Probe Arrays. Advances in Biochemical Engineering/Biotechnology, 2002, 77, 21-42.	0.6	26
1585	Cancer Development and Progression. , 2007, 593, 117-133.		13
1586	Epigenetic Profiling of Histone Variants. , 2009, , 101-118.		2
1587	Statistical Models for Biological Sequence Motif Discovery. Lecture Notes in Statistics, 2002, , 3-32.	0.1	5
1588	Novel Approaches to Controlling Transcription. , 2002, 24, 137-178.		4
1589	Chromatin Immunoprecipitation for ChIP-chip and ChIP-seq. Methods in Molecular Biology, 2014, 1149, 591-605.	0.4	16
1590	Cell Cycle-Regulated Transcription: Effectively Using a Genomics Toolbox. Methods in Molecular Biology, 2014, 1170, 3-27.	0.4	7
1591	Omic Data, Information Derivable and Computational Needs. , 2014, , 41-63.		1
1592	Techniques to Study Epigenetic Control and the Epigenome in Parasites. Methods in Molecular Biology, 2015, 1201, 177-191.	0.4	6
1593	Purification of Specific Chromatin Loci for Proteomic Analysis. Methods in Molecular Biology, 2015, 1228, 83-92.	0.4	9
1594	ChIP-Seq for Genome-Scale Analysis of Bacterial DNA-Binding Proteins. Methods in Molecular Biology, 2015, 1276, 327-340.	0.4	19
1595	Chromatin Immunoprecipitation (ChIP) Assay in Candida albicans. Methods in Molecular Biology, 2016, 1356, 43-57.	0.4	6
1596	Chromatin Immunoprecipitation Assays: Application of ChIP-on-Chip for Defining Dynamic Transcriptional Mechanisms in Bone Cells. Methods in Molecular Biology, 2008, 455, 165-176.	0.4	5
1597	Identification of Transcription Factor Target Genes by ChIP Display. Methods in Molecular Biology, 2008, 455, 177-190.	0.4	4

#	ARTICLE	IF	CITATIONS
1598	Genomewide Identification of Protein Binding Locations Using Chromatin Immunoprecipitation Coupled with Microarray. Methods in Molecular Biology, 2008, 439, 131-145.	0.4	10
1599	Methods for the Inference of Biological Pathways and Networks. Methods in Molecular Biology, 2009, 541, 225-245.	0.4	18
1600	Structure-Based Ab Initio Prediction of Transcription Factorâ€"Binding Sites. Methods in Molecular Biology, 2009, 541, 23-41.	0.4	9
1601	Promoter Analysis: Gene Regulatory Motif Identification with A-GLAM. Methods in Molecular Biology, 2009, 537, 263-276.	0.4	7
1602	Incorporation of Gene Ontology Annotations to Enhance Microarray Data Analysis. Methods in Molecular Biology, 2007, 377, 243-254.	0.4	17
1603	Determining DNA Sequence Specificity of Natural and Artificial Transcription Factors by Cognate Site Identifier Analysis. Methods in Molecular Biology, 2009, 544, 637-653.	0.4	6
1604	Identification of Transcription Factorâ€"DNA Interactions Using Chromatin Immunoprecipitation Assays. Methods in Molecular Biology, 2009, 493, 311-322.	0.4	7
1605	Association Analysis for Large-Scale Gene Set Data. Methods in Molecular Biology, 2007, 408, 19-33.	0.4	9
1606	ChIP-Chip: Algorithms for Calling Binding Sites. Methods in Molecular Biology, 2009, 556, 165-175.	0.4	2
1607	Relative Avidity, Specificity, and Sensitivity of Transcription Factorâ€"DNA Binding in Genome-Scale Experiments. Methods in Molecular Biology, 2009, 563, 15-50.	0.4	5
1608	Genome-Wide Mapping of Protein-DNA Interaction by Chromatin Immunoprecipitation and DNA Microarray Hybridization (ChIP-chip). Part A: ChIP-chip Molecular Methods. Methods in Molecular Biology, 2010, 631, 139-160.	0.4	29
1609	An Overview of the Computational Analyses and Discovery of Transcription Factor Binding Sites. Methods in Molecular Biology, 2010, 674, 1-22.	0.4	11
1610	Sequence Analysis of Chromatin Immunoprecipitation Data for Transcription Factors. Methods in Molecular Biology, 2010, 674, 179-193.	0.4	6
1611	Statistical Analysis of Dynamic Transcriptional Regulatory Network Structure. Methods in Molecular Biology, 2011, 781, 337-352.	0.4	2
1612	Genome-Wide Profiling of DNA-Binding Proteins Using Barcode-Based Multiplex Solexa Sequencing. Methods in Molecular Biology, 2012, 786, 247-262.	0.4	6
1613	Genome-Wide In Vivo Cross-linking of Sequence-Specific Transcription Factors. Methods in Molecular Biology, 2012, 809, 3-26.	0.4	6
1614	Using ChIPMotifs for De Novo Motif Discovery of OCT4 and ZNF263 Based on ChIP-Based High-Throughput Experiments. Methods in Molecular Biology, 2012, 802, 323-334.	0.4	4
1615	Knowledge Integration: Its Meaning and Measurement. Springer Handbooks, 2019, , 69-94.	0.3	18

#	ARTICLE	IF	CITATIONS
1616	Bioinformatics and Medicinal Plant Research: Current Scenario. , 2019, , 141-157.		1
1617	Transcriptome Analysis by Macroarrays. , 2003, , 145-156.		1
1618	Learning and Validating Bayesian Network Models of Gene Networks. Studies in Fuzziness and Soft Computing, 2007, , 359-375.	0.6	3
1619	A Streamlined and Generalized Analysis of Chromatin ImmunoPrecipitation Paired-End diTag Data. Lecture Notes in Computer Science, 2008, , 130-139.	1.0	2
1620	Mechanisms of Transcriptional Activation in Eukaryotes. Handbook of Experimental Pharmacology, 2004, , 3-31.	0.9	2
1621	Regulatory Motif Identification in Biological Sequences: An Overview of Computational Methodologies. , 2013, , 111-124.		3
1622	The Epigenomics of Cancer. , 2010, , 51-67.		3
1623	DNA microarrays for functional plant genomics. , 2001, , 99-118.		7
1624	Single-stranded DNA-binding protein facilitates gel-free analysis of polymerase chain reaction products in capillary electrophoresis. Journal of Chromatography A, 2004, 1051, 171-175.	1.8	6
1625	Reverse engineering of gene regulatory networks. IET Systems Biology, 2007, 1, 149-163.	0.8	100
1626	Complex impact of DNA methylation on transcriptional dysregulation across 22 human cancer types. Nucleic Acids Research, 2020, 48, 2287-2302.	6.5	35
1633	Systems Approaches Applied to the Study of Saccharomyces cerevisiae and Halobacterium sp.. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 345-358.	2.0	12
1634	Harvesting the Genome's Bounty: Integrative Genomics. Cold Spring Harbor Symposia on Quantitative Biology, 2003, 68, 431-444.	2.0	9
1635	MSL Complex Associates with Clusters of Actively Transcribed Genes along the Drosophila Male X Chromosome. Cold Spring Harbor Symposia on Quantitative Biology, 2006, 71, 385-394.	2.0	7
1636	Modeling dependencies in protein-DNA binding sites. , 2003, , .		106
1637	Alterations in an IRE1-RNA complex in the mammalian unfolded protein response. Journal of Cell Science, 2001, 114, 3207-3212.	1.2	21
1638	A ChIP on the shoulder? Chromatin immunoprecipitation and validation strategies for ChIP antibodies. F1000Research, 2015, 4, 235.	0.8	17
1639	A Discriminative Approach for Unsupervised Clustering of DNA Sequence Motifs. PLoS Computational Biology, 2013, 9, e1002958.	1.5	12

#	ARTICLE	IF	CITATIONS
1640	Control of Signaling in a MAP-kinase Pathway by an RNA-Binding Protein. PLoS ONE, 2007, 2, e249.	1.1	19
1641	Modeling Transcriptome Based on Transcript-Sampling Data. PLoS ONE, 2008, 3, e1659.	1.1	20
1642	Global Identification of Myc Target Genes Reveals Its Direct Role in Mitochondrial Biogenesis and Its E-Box Usage In Vivo. PLoS ONE, 2008, 3, e1798.	1.1	197
1643	Probabilistic Inference of Transcription Factor Binding from Multiple Data Sources. PLoS ONE, 2008, 3, e1820.	1.1	42
1644	An Integrated Approach to Identifying Cis-Regulatory Modules in the Human Genome. PLoS ONE, 2009, 4, e5501.	1.1	17
1645	ChIP-Chip Designs to Interrogate the Genome of Xenopus Embryos for Transcription Factor Binding and Epigenetic Regulation. PLoS ONE, 2010, 5, e8820.	1.1	10
1646	Genomic Approaches Uncover Increasing Complexities in the Regulatory Landscape at the Human SCL (TAL1) Locus. PLoS ONE, 2010, 5, e9059.	1.1	15
1647	Identification of SOX9 Interaction Sites in the Genome of Chondrocytes. PLoS ONE, 2010, 5, e10113.	1.1	81
1648	A Linear Model for Transcription Factor Binding Affinity Prediction in Protein Binding Microarrays. PLoS ONE, 2011, 6, e20059.	1.1	40
1649	Systems Biology of the qa Gene Cluster in Neurospora crassa. PLoS ONE, 2011, 6, e20671.	1.1	24
1650	The Peptidyl Prolyl Isomerase Rrd1 Regulates the Elongation of RNA Polymerase II during Transcriptional Stresses. PLoS ONE, 2011, 6, e23159.	1.1	20
1651	Transcription Factor Binding Sites Prediction Based on Modified Nucleosomes. PLoS ONE, 2014, 9, e89226.	1.1	12
1652	A Force-Based, Parallel Assay for the Quantification of Protein-DNA Interactions. PLoS ONE, 2014, 9, e89626.	1.1	13
1653	Low RNA Polymerase III activity results in up regulation of HXT2 glucose transporter independently of glucose signaling and despite changing environment. PLoS ONE, 2017, 12, e0185516.	1.1	4
1654	Genome Wide Approaches to Identify Protein-DNA Interactions. Current Medicinal Chemistry, 2020, 26, 7641-7654.	1.2	7
1655	The HaloTag: Improving Soluble Expression and Applications in Protein Functional Analysis. Current Chemical Genomics, 2013, 6, 8-17.	2.0	35
1660	Construction and Application of a Microarray for Profiling Mouse Transcription Factor Activities*. Progress in Biochemistry and Biophysics, 2009, 2009, 244-253.	0.3	1
1661	Prioritize Transcription Factor Binding Sites for Multiple Co-Expressed Gene Sets Based on Lasso Multinomial Regression Models. Advances in Medical Technologies and Clinical Practice Book Series, 0, , 280-315.	0.3	1

#	Article	IF	Citations
1662	Transcriptomics to Metabolomics. Advances in Bioinformatics and Biomedical Engineering Book Series, 2018, , 188-206.	0.2	5
1663	Transcriptomics to Metabolomics. , 2019, , 361-379.		1
1664	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 2011, , 187-201.		2
1665	Epigenetic memory in gene regulation and immune response. BMB Reports, 2019, 52, 127-132.	1.1	9
1666	Ongoing resolution of duplicate gene functions shapes the diversification of a metabolic network. ELife, 2016, 5, .	2.8	29
1667	The deubiquitylase Ubp15 couples transcription to mRNA export. ELife, 2020, 9, .	2.8	1
1668	A machine learning framework for the prediction of chromatin folding in<i>Drosophila</i>using epigenetic features. PeerJ Computer Science, 2020, 6, e307.	2.7	11
1669	Inferring primase-DNA specific recognition using a data driven approach. Nucleic Acids Research, 2021, 49, 11447-11458.	6.5	1
1670	greenCUT&RUN: Efficient Genomic Profiling of GFPâ€Tagged Transcription Factors and Chromatin Regulators. Current Protocols, 2021, 1, e266.	1.3	14
1672	Functional Genomics and Proteomics: Basics, Opportunities and Challenges. , 2003, , 39-66.		1
1673	Modeling transcription programs. , 2003, , .		2
1674	Genomic Approaches to the Study of Transcription Factors. Handbook of Experimental Pharmacology, 2004, , 69-93.	0.9	0
1675	Functional Genomics in Fungi. , 2004, , 115-128.		0
1676	Gene Regulation in Yeast. , 2004, , 129-145.		0
1678	Improving the Nutritional Value of Cereal Grains Using a Genomic Approach. Nutrition and Disease Prevention, 2004, , 317-329.	0.1	0
1680	Qualitative Determination of 5-Methylcytosine and Other Components of the DNA Methylation Machinery. , 2004, , 121-136.		0
1684	Transcriptional Responses to DNA Damage: Systems-Level Delineation by Functional Genomics. , 2006, , 116-131.		0
1685	Systems biology and its impact on anti-infective drug development. , 2007, 64, 1-20.		3

#	ARTICLE	IF	CITATIONS
1687	Web-Based Resources for Clinical Bioinformatics. Methods in Molecular Medicine, 2008, 141, 309-329.	0.8	0
1688	Paradigmatic Role of Galactose Switch. , 2008, , 175-214.		0
1689	6. Ã‰pigÃ©nomique et morphodynamique. , 2008, , 113-125.		0
1692	Integrative Systems Approaches to Study Innate Immunity. , 2009, , 1-13.		0
1693	An Integrative Approach for Analyzing the Interplay of Genetic and Epigenetic Changes in Tumors. Archives of Pathology and Laboratory Medicine, 2008, 132, 1557-1561.	1.2	0
1694	Analyzing Origin Activation Patterns by Copy Number Change Experiments. Methods in Molecular Biology, 2009, 521, 279-294.	0.4	0
1695	Stem Cell Epigenetics. , 2009, , 235-246.		1
1696	Stem Cell Chromatin Patterns and DNA Hypermethylation. , 2009, , 85-97.		0
1697	Bioinformatic and Computational Analysis for Genomic Medicine. , 2009, , 206-225.		0
1698	DNA Microarrays. , 2009, , 911-935.		0
1699	Systems Microbiology: Gaining Insights in Transcriptional Networks. , 2010, , 93-122.		0
1700	Reverse Engineering a Signaling Network Using Alternative Inputs. PLoS ONE, 2009, 4, e7622.	1.1	0
1701	Mapping Transcription Factors on Extended DNA: A Single Molecule Approach. Springer Series in Chemical Physics, 2010, , 203-216.	0.2	0
1702	Control of Hormone Gene Expression. , 2010, , 13-25.		0
1703	Long-Range Chromatin Interactions in Cells. Biological and Medical Physics Series, 2010, , 325-339.	0.3	0
1704	Transcription Factor Binding Site Identification by Phylogenetic Footprinting. Computational Biology, 2010, , 113-131.	0.1	1
1705	Emerging Concepts and Techniques. , 2010, , 731-741.		0
1706	False Positive Control for Genome-Wide ChIP-Chip Tiling Arrays. Computational Biology, 2010, , 371-381.	0.1	0

#	ARTICLE	IF	CITATIONS
1707	Cis regulatory module discovery in immune cell development. , 2010, , .		0
1709	GLOBE: Analysis of DNAâ€"Protein Interaction Analysis. Methods in Molecular Biology, 2011, 687, 307-317.	0.4	0
1710	The Non-coding Landscape of the Genome of Arabidopsis thaliana. , 2011, , 67-121.		0
1711	Regulation of the Transcription of G Protein-Coupled Receptor Genes. Neuromethods, 2011, , 49-69.	0.2	0
1713	Computational Analysis of ChIP-chip Data. , 2011, , 257-282.		1
1714	Broader Considerations of Medical and Dental Data Integration. Computers in Health Care, 2012, , 167-298.	0.2	0
1715	JAMIE: A Software Tool for Jointly Analyzing Multiple ChIP-chip Experiments. Methods in Molecular Biology, 2012, 802, 363-375.	0.4	1
1716	Genome Mapping and Genomics in Drosophila. , 2012, , 31-86.		1
1718	Untersuchung der Funktion von DNA-Sequenzen. , 2013, , 211-268.		0
1719	Genome-Wide Analysis of Transcription Factor-Binding Sites in Skeletal Muscle Cells Using ChIP-Seq. Methods in Molecular Biology, 2013, 1067, 51-64.	0.4	0
1720	Learning Protein-DNA Interaction Landscapes by Integrating Experimental Data through Computational Models. Lecture Notes in Computer Science, 2014, , 433-447.	1.0	0
1721	Molecular Networks â€" Representation and Analysis. , 2014, , 399-418.		0
1722	Architecture and Dynamics of Transcriptional Networks. , 0, , 17-30.		0
1723	Principles and Practice of DNA Microarray Technology. , 0, , 978-994.		0
1724	Global Approaches to the Bacterial Cell as an Integrated System. , 0, , 53-64.		0
1725	Genome-Wide Approaches to Studying Prokaryotic Biology. , 0, , 489-515.		0
1726	Systematic Determination of Transcription Factor DNA-Binding Specificities in Yeast. Methods in Molecular Biology, 2016, 1361, 203-225.	0.4	0
1727	Neurospora: A Gateway to Biology. , 2016, , 207-226.		0

#	Article	IF	Citations
1728	Chapter 1 The Role of General Methods and Mathematical Models on Microbial Evolution, Ecological Interactions, and Population Dynamics. , 2016, , 1-16.		0
1730	Current Status and Future Prospects of Omics Tools in Climate Change Research. , 2019, , 197-214.		0
1731	Annotation of Biological Network of Fungus Saccharomyces cerevisiae Using Cytoscape in Systems Biology. , 2019, , 111-129.		0
1732	Prioritize Transcription Factor Binding Sites for Multiple Co-Expressed Gene Sets Based on Lasso Multinomial Regression Models. , 2019, , 940-968.		0
1736	Genome-wide Identification of DNA-protein Interaction to Reconstruct Bacterial Transcription Regulatory Network. Biotechnology and Bioprocess Engineering, 2020, 25, 944-954.	1.4	6
1737	Transcription for Protein Biosynthesis. Biological and Medical Physics Series, 2020, , 477-508.	0.3	0
1738	Meeting a Challenge: A View on Studying Transcriptional Control of Genes Involved in Plant Biomass Degradation in Aspergillus niger. Grand Challenges in Biology and Biotechnology, 2020, , 211-235.	2.4	1
1739	Prediction of Epigenetic Target Sites by Using Genomic DNA Sequence. , 0, , 498-512.		0
1740	Monitoring the Trascriptome. Advances in Digital Crime, Forensics, and Cyber Terrorism, 0, , 89-107.	0.4	0
1742	Inferring Genetic Regulatory Networks from Microarray Experiments with Bayesian Networks. , 2005, , 239-267.		1
1743	Regulators of Candida glabrata Pathogenicity. , 2006, , 205-219.		0
1746	DBRF-MEGN Method: An Algorithm for Inferring Gene Regulatory Networks from Large-Scale Gene Expression Profiles. , 2007, , 435-448.		0
1747	Dissecting Transcriptional Control Networks. , 2007, , 106-123.		0
1748	An Efficient Algorithm for Deciphering Regulatory Motifs. , 2007, , 249-269.		0
1749	A Bayesian Approach for Integrating Transcription Regulation and Gene Expression: Application to Saccharomyces Cerevisiae Cell Cycle Data. , 2005, , 178-187.		0
1751	GSE: a comprehensive database system for the representation, retrieval, and analysis of microarray data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 539-50.	0.7	6
1754	Epigenetics and tissue immunityâ€"Translating environmental cues into functional adaptations*. Immunological Reviews, 2022, 305, 111-136.	2.8	6
1756	D-Xylose Sensing in Saccharomyces cerevisiae: Insights from D-Glucose Signaling and Native D-Xylose Utilizers. International Journal of Molecular Sciences, 2021, 22, 12410.	1.8	17

#	Article	IF	Citations
1757	Fine mapping with epigenetic information and 3D structure. Seminars in Immunopathology, 2022, 44, 115-125.	2.8	8
1758	Single-Cell Factor Localization on Chromatin using Ultra-Low Input Cleavage Under Targets and Release using Nuclease. Journal of Visualized Experiments, 2022, , .	0.2	0
1759	Ensemble Methods for Identifying RNA Operons and Regulons in the Clock Network of Neurospora Crassa. IEEE Access, 2022, 10, 32510-32524.	2.6	3
1760	Applications of microbial omics in healthcare. , 2022, , 227-248.		0
1761	Integration with systems biology approaches and -omics data to characterize risk variation. , 2022, , 289-315.		4
1762	Applications of cell- and tissue-specific â€˜omics to improve plant productivity. Emerging Topics in Life Sciences, 2022, 6, 163-173.	1.1	6
1763	Epigenomic alterations in cancer: mechanisms and therapeutic potential. Clinical Science, 2022, 136, 473-492.	1.8	4
1764	Systems biology approaches bring new insights in the understanding of global gene regulatory mechanisms and their deregulation in cancer. , 0, , 56-69.		0
1778	Understanding of the various aspects of gene regulatory networks related to crop improvement. Gene, 2022, 833, 146556.	1.0	1
1779	Studying Epigenetics of Cardiovascular Diseases on Chip Guide. Neurology International, 2022, 12, 218-234.	0.2	0
1781	Deciphering the molecular basis of tissue-specific gene expression in plants: Can synthetic biology help?. Current Opinion in Plant Biology, 2022, 68, 102241.	3.5	16
1783	Chromatin Dynamics in Digestive System Cancer: Commander and Regulator. Frontiers in Oncology, 0, 12, .	1.3	1
1784	TFLink: an integrated gateway to access transcription factorâ€“target gene interactions for multiple species. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	22
1786	Public goodâ€driven release of heterogeneous resources leads to genotypic diversification of an isogenic yeast population. Evolution; International Journal of Organic Evolution, 0, , .	1.1	1
1794	Dissecting Locus-Specific Chromatin Interactions by CRISPR CAPTURE. Methods in Molecular Biology, 2023, , 69-97.	0.4	1
1795	Epigenetic Regulation of Fungal Genes Involved in Plant Colonization. , 2023, , 255-281.		0
1796	Genome-wide analysis of the TCP gene family and their expression pattern in Cymbidium goeringii. Frontiers in Plant Science, 0, 13, .	1.7	6
1797	Damage mapping techniques and the light they have shed on canonical and atypical UV photoproducts. Frontiers in Genetics, 0, 13, .	1.1	2

#	Article	IF	Citations
1798	Using Restriction Endonuclease, Protection, Selection, and Amplification to Identify Preferred DNA-Binding Sequences of Microbial Transcription Factors. Microbiology Spectrum, 2023, 11, .	1.2	1
1799	Advances in sequencing technologies for amyotrophic lateral sclerosis research. Molecular Neurodegeneration, 2023, 18, .	4.4	4
1801	Evolution of genome wide approaches to unveil transcriptional networks. , 2024, , 36-45.		0
1802	peaksat: an R package for ChIP-seq peak saturation analysis. BMC Genomics, 2023, 24, .	1.2	0
1803	Analysis of genomesâ€"II. , 2023, , 65-87.		0
1804	Mediterranean exposotype: Genomic architecture and plant-based dietary metabolites. Clinical Nutrition ESPEN, 2023, 55, 1-9.	0.5	1
1805	Kinetic networks identify TWIST2 as a key regulatory node in adipogenesis. Genome Research, 2023, 33, 314-331.	2.4	4
1806	CHIP-seq: The evolution of genome-wide approaches to unveil the transcriptional network. , 2023, , .		0
1807	GeoBind: segmentation of nucleic acid binding interface on protein surface with geometric deep learning. Nucleic Acids Research, 2023, 51, e60-e60.	6.5	4
1812	Oxidativer Stress und andere AnsÃtze der Stressforschung auf Zellebene. , 2023, , 33-63.		0
1816	Photoelectrochemical DNA analysis. , 2023, , 71-97.		0
1818	Epigenetic regulation: Histone modifying enzymes as targets for novel therapeutics. , 2024, , 430-452.		0
1819	Prediction and Analysis of Transcription Factor Binding Sites: Practical Examples and Case Studies Using R Programming. Methods in Molecular Biology, 2024, , 199-225.	0.4	0
1823	Machine learning applications in cancer genomics. , 2024, , 41-72.		0