

Michael Snyder

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201
papers

60,408
citations

98
h-index

206
g-index

206
ext. papers

68,550
ext. citations

15.9
avg, IF

7.42
L-index

#	Paper	IF	Citations
201	RNA-Seq: a revolutionary tool for transcriptomics. <i>Nature Reviews Genetics</i> , 2009 , 10, 57-63	30.1	8302
200	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
199	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002 , 418, 387-91	50.4	3278
198	Functional characterization of the <i>S. cerevisiae</i> genome by gene deletion and parallel analysis. <i>Science</i> , 1999 , 285, 901-6	33.3	3254
197	Global analysis of protein activities using proteome chips. <i>Science</i> , 2001 , 293, 2101-5	33.3	1899
196	The transcriptional landscape of the yeast genome defined by RNA sequencing. <i>Science</i> , 2008 , 320, 1344-9	33.3	1867
195	Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , 2012 , 22, 1790-7	9.7	1723
194	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012 , 22, 1813-31	9.7	1211
193	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012 , 489, 91-100	50.4	1104
192	High-quality binary protein interaction map of the yeast interactome network. <i>Science</i> , 2008 , 322, 104-10	33.3	1100
191	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007 , 4, 651-7	21.6	1077
190	A Bayesian networks approach for predicting protein-protein interactions from genomic data. <i>Science</i> , 2003 , 302, 449-53	33.3	1007
189	CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. <i>Genome Research</i> , 2011 , 21, 974-84	9.7	944
188	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001 , 409, 533-8	50.4	927
187	Personal omics profiling reveals dynamic molecular and medical phenotypes. <i>Cell</i> , 2012 , 148, 1293-307	56.2	921
186	Paired-end mapping reveals extensive structural variation in the human genome. <i>Science</i> , 2007 , 318, 420-6	33.3	895
185	Global identification of human transcribed sequences with genome tiling arrays. <i>Science</i> , 2004 , 306, 2242-6	33.3	868

184	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4	833
183	Global analysis of protein phosphorylation in yeast. <i>Nature</i> , 2005 , 438, 679-84	50.4	818
182	Protein chip technology. <i>Current Opinion in Chemical Biology</i> , 2003 , 7, 55-63	9.7	792
181	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004 , 431, 308-12	50.4	767
180	Integrative analysis of the <i>Caenorhabditis elegans</i> genome by the modENCODE project. <i>Science</i> , 2010 , 330, 1775-87	33.3	744
179	Analysis of yeast protein kinases using protein chips. <i>Nature Genetics</i> , 2000 , 26, 283-9	36.3	734
178	Unlocking the secrets of the genome. <i>Nature</i> , 2009 , 459, 927-30	50.4	620
177	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012 , 22, 1798-812	9.7	596
176	Subcellular localization of the yeast proteome. <i>Genes and Development</i> , 2002 , 16, 707-19	12.6	575
175	Protein analysis on a proteomic scale. <i>Nature</i> , 2003 , 422, 208-15	50.4	541
174	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , 2012 , 22, 1748-59	9.7	538
173	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. <i>Nature</i> , 1999 , 402, 413-8	50.4	470
172	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. <i>Nature Biotechnology</i> , 2009 , 27, 66-75	44.5	463
171	Variation in transcription factor binding among humans. <i>Science</i> , 2010 , 328, 232-5	33.3	447
170	What is a gene, post-ENCODE? History and updated definition. <i>Genome Research</i> , 2007 , 17, 669-81	9.7	417
169	A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , 2013 , 31, 1009-14	44.5	396
168	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , 2005 , 19, 2816-26	12.6	387
167	Getting connected: analysis and principles of biological networks. <i>Genes and Development</i> , 2007 , 21, 1010-24	12.6	380

166	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012 , 13, 418	18.3	340
165	Protein arrays and microarrays. <i>Current Opinion in Chemical Biology</i> , 2001 , 5, 40-5	9.7	331
164	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010 , 11, 559-71	30.1	303
163	Proteomics. <i>Annual Review of Biochemistry</i> , 2003 , 72, 783-812	29.1	295
162	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. <i>Nature Genetics</i> , 2004 , 36, 1331-9	36.3	294
161	Divergence of transcription factor binding sites across related yeast species. <i>Science</i> , 2007 , 317, 815-9	33.3	286
160	The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 12031-6	11.5	280
159	Extensive variation in chromatin states across humans. <i>Science</i> , 2013 , 342, 750-2	33.3	276
158	Distribution of NF-kappaB-binding sites across human chromosome 22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 12247-52	11.5	276
157	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009 , 113, 2526-34	2.2	271
156	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. <i>Science Signaling</i> , 2010 , 3, ra12	8.8	262
155	Analyzing antibody specificity with whole proteome microarrays. <i>Nature Biotechnology</i> , 2003 , 21, 1509-12	14.5	248
154	Performance comparison of whole-genome sequencing platforms. <i>Nature Biotechnology</i> , 2011 , 30, 78-82	14.5	241
153	A genomic study of the bipolar bud site selection pattern in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2001 , 12, 2147-70	3.5	238
152	Protein microarray technology. <i>Mechanisms of Ageing and Development</i> , 2007 , 128, 161-7	5.6	237
151	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011 , 7, 522	12.2	228
150	Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 16594-9	11.5	208
149	Regulation of gene expression by a metabolic enzyme. <i>Science</i> , 2004 , 306, 482-4	33.3	206

148	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. <i>Genome Biology</i> , 2009 , 10, R23	18.3	201
147	Complex transcriptional circuitry at the G1/S transition in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2002 , 16, 3017-33	12.6	201
146	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. <i>Genome Biology</i> , 2012 , 13, R48	18.3	194
145	Recurrent somatic mutations in regulatory regions of human cancer genomes. <i>Nature Genetics</i> , 2015 , 47, 710-6	36.3	190
144	Promise of personalized omics to precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013 , 5, 73-82	6.6	188
143	TOS9 regulates white-opaque switching in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2006 , 5, 1674-87		179
142	RNA-Seq: a method for comprehensive transcriptome analysis. <i>Current Protocols in Molecular Biology</i> , 2010 , Chapter 4, Unit 4.11.1-13	2.9	168
141	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. <i>BMC Genomics</i> , 2010 , 11, 663	4.5	168
140	Comprehensive annotation of the transcriptome of the human fungal pathogen <i>Candida albicans</i> using RNA-seq. <i>Genome Research</i> , 2010 , 20, 1451-8	9.7	165
139	Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. <i>Genome Research</i> , 2007 , 17, 898-909	9.7	164
138	Mapping accessible chromatin regions using Sono-Seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 14926-31	11.5	163
137	Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. <i>Cell</i> , 2010 , 143, 639-50	56.2	162
136	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017 , 49, 1522-1528	36.3	158
135	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007 , 17, 839-51	9.7	158
134	Genome-wide occupancy of SREBP1 and its partners NFY and SP1 reveals novel functional roles and combinatorial regulation of distinct classes of genes. <i>PLoS Genetics</i> , 2008 , 4, e1000133	6	154
133	Molecular dissection of a yeast septin: distinct domains are required for septin interaction, localization, and function. <i>Molecular and Cellular Biology</i> , 2003 , 23, 2762-77	4.8	148
132	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008 , 18, 1906-17	9.7	147
131	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. <i>American Journal of Human Genetics</i> , 2013 , 93, 545-54	11	145

130	Close association of RNA polymerase II and many transcription factors with Pol III genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 3639-44	11.5	143
129	GATA-1 binding sites mapped in the beta-globin locus by using mammalian ChIP-chip analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 2924-9	11.5	143
128	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 5254-9	11.5	142
127	Advances in functional protein microarray technology. <i>FEBS Journal</i> , 2005 , 272, 5400-11	5.7	141
126	A question of size: the eukaryotic proteome and the problems in defining it. <i>Nucleic Acids Research</i> , 2002 , 30, 1083-90	20.1	141
125	Microarrays to characterize protein interactions on a whole-proteome scale. <i>Proteomics</i> , 2003 , 3, 2190-9	4.8	140
124	Target hub proteins serve as master regulators of development in yeast. <i>Genes and Development</i> , 2006 , 20, 435-48	12.6	138
123	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , 2010 , 28, 47-55	44.5	136
122	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014 , 512, 453-6	50.4	135
121	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
120	Genome-wide identification of binding sites defines distinct functions for Caenorhabditis elegans PHA-4/FOXA in development and environmental response. <i>PLoS Genetics</i> , 2010 , 6, e1000848	6	132
119	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. <i>American Journal of Human Genetics</i> , 2014 , 94, 349-60	11	131
118	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007 , 17, 852-64	9.7	131
117	ChIP-chip: a genomic approach for identifying transcription factor binding sites. <i>Methods in Enzymology</i> , 2002 , 350, 469-83	1.7	131
116	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010 , 464, 1187-91	50.4	130
115	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. <i>Genome Research</i> , 2012 , 22, 1735-47	9.7	129
114	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. <i>BMC Genomics</i> , 2009 , 10, 37	4.5	129
113	Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4011-6	11.5	118

112	Charging it up: global analysis of protein phosphorylation. <i>Trends in Genetics</i> , 2006 , 22, 545-54	8.5	116
111	Analysis of copy number variants and segmental duplications in the human genome: Evidence for a change in the process of formation in recent evolutionary history. <i>Genome Research</i> , 2008 , 18, 1865-74	9.7	114
110	High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 4534-9	11.5	112
109	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008 , 18, 393-403	9.7	111
108	Dynamic trans-acting factor colocalization in human cells. <i>Cell</i> , 2013 , 155, 713-24	56.2	109
107	DNA replication-timing analysis of human chromosome 22 at high resolution and different developmental states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 17771-6	11.5	107
106	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016 , 24, 172-84	24.6	105
105	Personal genome sequencing: current approaches and challenges. <i>Genes and Development</i> , 2010 , 24, 423-31	12.6	103
104	An integrated approach for finding overlooked genes in yeast. <i>Nature Biotechnology</i> , 2002 , 20, 58-63	44.5	97
103	Impact of chromatin structures on DNA processing for genomic analyses. <i>PLoS ONE</i> , 2009 , 4, e6700	3.7	95
102	Detecting and annotating genetic variations using the HugeSeq pipeline. <i>Nature Biotechnology</i> , 2012 , 30, 226-9	44.5	90
101	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. <i>Molecular Systems Biology</i> , 2014 , 10, 774	12.2	89
100	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. <i>Bioinformatics</i> , 2011 , 27, 281-3	7.2	89
99	Genomics. Defining genes in the genomics era. <i>Science</i> , 2003 , 300, 258-60	33.3	89
98	High-resolution copy-number variation map reflects human olfactory receptor diversity and evolution. <i>PLoS Genetics</i> , 2008 , 4, e1000249	6	87
97	Predicting essential genes in fungal genomes. <i>Genome Research</i> , 2006 , 16, 1126-35	9.7	84
96	Global changes in STAT target selection and transcription regulation upon interferon treatments. <i>Genes and Development</i> , 2005 , 19, 2953-68	12.6	83
95	Emerging technologies in yeast genomics. <i>Nature Reviews Genetics</i> , 2001 , 2, 302-12	30.1	82

94	Regulatory analysis of the <i>C. elegans</i> genome with spatiotemporal resolution. <i>Nature</i> , 2014 , 512, 400-5	50.4	81
93	Characterization of enhancer function from genome-wide analyses. <i>Annual Review of Genomics and Human Genetics</i> , 2012 , 13, 29-57	9.7	80
92	The current excitement about copy-number variation: how it relates to gene duplications and protein families. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 366-74	8.1	78
91	Global analysis of the glycoproteome in <i>Saccharomyces cerevisiae</i> reveals new roles for protein glycosylation in eukaryotes. <i>Molecular Systems Biology</i> , 2009 , 5, 308	12.2	71
90	The development of protein microarrays and their applications in DNA-protein and protein-protein interaction analyses of <i>Arabidopsis</i> transcription factors. <i>Molecular Plant</i> , 2008 , 1, 27-41	14.4	70
89	Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 10110-5	11.5	70
88	Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. <i>PLoS Computational Biology</i> , 2011 , 7, e1002190	5	69
87	Global analysis of gene expression in yeast. <i>Functional and Integrative Genomics</i> , 2002 , 2, 171-80	3.8	65
86	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. <i>Genes and Development</i> , 2003 , 17, 2698-708	12.6	63
85	Omic Profiling in Precision Oncology. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2525-36	7.6	63
84	Modeling CHIP sequencing in silico with applications. <i>PLoS Computational Biology</i> , 2008 , 4, e1000158	5	62
83	Proteome chips for whole-organism assays. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 617-22	48.7	61
82	"Omic" approaches for unraveling signaling networks. <i>Current Opinion in Cell Biology</i> , 2002 , 14, 173-9	9	60
81	Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. <i>Chromosome Research</i> , 2005 , 13, 259-74	4.4	58
80	iPOP goes the world: integrated personalized Omics profiling and the road toward improved health care. <i>Chemistry and Biology</i> , 2013 , 20, 660-6		57
79	Linking DNA-binding proteins to their recognition sequences by using protein microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 9940-5	11.5	57
78	A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells. <i>Genome Research</i> , 2012 , 22, 1668-79	9.7	56
77	Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE). <i>Genome Research</i> , 2007 , 17, 910-6	9.7	54

76	A novel mitochondrial protein, Tar1p, is encoded on the antisense strand of the nuclear 25S rDNA. <i>Genes and Development</i> , 2002 , 16, 2755-60	12.6	53
75	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. <i>PLoS ONE</i> , 2016 , 11, e0162868	3.7	53
74	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. <i>Frontiers in Microbiology</i> , 2017 , 8, 1079	5.7	52
73	Regulatory variation within and between species. <i>Annual Review of Genomics and Human Genetics</i> , 2011 , 12, 327-46	9.7	52
72	Identification of genomic indels and structural variations using split reads. <i>BMC Genomics</i> , 2011 , 12, 375	4.5	52
71	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. <i>Genes and Development</i> , 2011 , 25, 767-78	12.6	51
70	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. <i>PLoS ONE</i> , 2011 , 6, e27859	3.7	51
69	Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. <i>Genome Biology</i> , 2008 , 9, R3	18.3	48
68	Accurate identification and analysis of human mRNA isoforms using deep long read sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 387-97	3.2	47
67	A genomic analysis of RNA polymerase II modification and chromatin architecture related to 3Rend RNA polyadenylation. <i>Genome Research</i> , 2008 , 18, 1224-37	9.7	47
66	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. <i>Genome Research</i> , 2007 , 17, 787-97	9.7	47
65	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. <i>Scientific Reports</i> , 2016 , 6, 20104	4.9	46
64	Extensive transcript diversity and novel upstream open reading frame regulation in yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 343-52	3.2	44
63	ProCAT: a data analysis approach for protein microarrays. <i>Genome Biology</i> , 2006 , 7, R110	18.3	43
62	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , 2017 , 8, 2708	5.7	41
61	AGAPE (Automated Genome Analysis PipelinE) for pan-genome analysis of <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015 , 10, e0120671	3.7	41
60	Design optimization methods for genomic DNA tiling arrays. <i>Genome Research</i> , 2006 , 16, 271-81	9.7	41
59	ChIP-Seq: a method for global identification of regulatory elements in the genome. <i>Current Protocols in Molecular Biology</i> , 2010 , Chapter 21, Unit 21.19.1-14	2.9	39

58	Systems biology from a yeast omics perspective. <i>FEBS Letters</i> , 2009 , 583, 3895-9	3.8	39
57	Cooperative transcription factor associations discovered using regulatory variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 13353-8	11.5	38
56	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , 2018 , 28, 231-242	9.7	38
55	Comparative annotation of functional regions in the human genome using epigenomic data. <i>Nucleic Acids Research</i> , 2013 , 41, 4423-32	20.1	37
54	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020 , 583, 737-743	50.4	37
53	Proteomic approaches for the global analysis of proteins. <i>BioTechniques</i> , 2002 , 33, 1308-16	2.5	35
52	ExpressYourself: A modular platform for processing and visualizing microarray data. <i>Nucleic Acids Research</i> , 2003 , 31, 3477-82	20.1	34
51	Global analysis of protein function using protein microarrays. <i>Mechanisms of Ageing and Development</i> , 2005 , 126, 171-5	5.6	34
50	Investigating metabolite-protein interactions: an overview of available techniques. <i>Methods</i> , 2012 , 57, 459-66	4.6	33
49	RNA polymerase II stalling: loading at the start prepares genes for a sprint. <i>Genome Biology</i> , 2008 , 9, 220	18.3	33
48	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007 , 17, 720-31	9.7	31
47	A supervised hidden markov model framework for efficiently segmenting tiling array data in transcriptional and chip-chip experiments: systematically incorporating validated biological knowledge. <i>Bioinformatics</i> , 2006 , 22, 3016-24	7.2	31
46	Large-scale mutagenesis: yeast genetics in the genome era. <i>Current Opinion in Biotechnology</i> , 2001 , 12, 28-34	11.4	30
45	X chromosome-wide analyses of genomic DNA methylation states and gene expression in male and female neutrophils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 3704-9	11.5	29
44	MSB: a mean-shift-based approach for the analysis of structural variation in the genome. <i>Genome Research</i> , 2009 , 19, 106-17	9.7	29
43	Metabolites as global regulators: a new view of protein regulation: systematic investigation of metabolite-protein interactions may help bridge the gap between genome-wide association studies and small molecule screening studies. <i>BioEssays</i> , 2011 , 33, 485-9	4.1	28
42	Yeast proteomics and protein microarrays. <i>Journal of Proteomics</i> , 2010 , 73, 2147-57	3.9	28
41	Yeast as a model for human disease. <i>Current Protocols in Human Genetics</i> , 2006 , Chapter 15, Unit 15.6	3.2	27

40	Large-scale identification of genes important for apical growth in <i>Saccharomyces cerevisiae</i> by directed allele replacement technology (DART) screening. <i>Functional and Integrative Genomics</i> , 2002 , 1, 345-56	3.8	27
39	High-throughput methods for the large-scale analysis of gene function by transposon tagging. <i>Methods in Enzymology</i> , 2000 , 328, 550-74	1.7	27
38	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013 , 1, 71-90	3.9	26
37	Proteogenomic analysis of human colon carcinoma cell lines LIM1215, LIM1899, and LIM2405. <i>Journal of Proteome Research</i> , 2013 , 12, 1732-42	5.6	26
36	Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association. <i>PLoS Genetics</i> , 2014 , 10, e1004122	6	26
35	MOTIPS: automated motif analysis for predicting targets of modular protein domains. <i>BMC Bioinformatics</i> , 2010 , 11, 243	3.6	25
34	Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome. <i>Genome Research</i> , 2007 , 17, 886-97	9.7	25
33	Systematic investigation of protein-small molecule interactions. <i>IUBMB Life</i> , 2013 , 65, 2-8	4.7	24
32	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019 , 10, 834	4.5	22
31	Genome-wide profiling of human cap-independent translation-enhancing elements. <i>Nature Methods</i> , 2013 , 10, 747-50	21.6	22
30	ChIP-Seq using high-throughput DNA sequencing for genome-wide identification of transcription factor binding sites. <i>Methods in Enzymology</i> , 2010 , 470, 77-104	1.7	21
29	The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci. <i>Genome Research</i> , 2007 , 17, 732-45	9.7	21
28	Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms. <i>Functional and Integrative Genomics</i> , 2007 , 7, 335-45	2.8	19
27	Identification of genes critical for resistance to infection by West Nile virus using RNA-Seq analysis. <i>Viruses</i> , 2013 , 5, 1664-81	6.2	18
26	Systems Biology Approaches to Disease Marker Discovery. <i>Disease Markers</i> , 2010 , 28, 209-224	3.2	17
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