Michael Snyder

List of Publications by Year in Descending Order

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papers	citations	h-index	g-index
201	60,408	98	206

ext. papers	ext. citations	avg, IF	L-index
206	68,550	15.9	7.42

#	Paper	IF	Citations
201	Landscape of cohesin-mediated chromatin loops in the human genome. *Nature*, **2020**, 583, 737-743	50.4	37
200	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. *Frontiers in Genetics*, **2019**, 10, 834	4.5	22
199	Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. *FEMS Microbiology Letters*, **2018**, 365,	2.9	7
198	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. *Genome Research*, **2018**, 28, 231-242	9.7	38
197	Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. *Frontiers in Genetics*, **2018**, 9, 432	4.5	10
196	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. *Frontiers in Microbiology*, **2017**, 8, 2708	5.7	41
195	Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. *Scientific Reports*, **2017**, 7, 5557	4.9	7
194	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. *Nature Genetics*, **2017**, 49, 1522-1528	36.3	158
193	Long-Read Isoform Sequencing Reveals a Hidden Complexity of the Transcriptional Landscape of Herpes Simplex Virus Type 1. *Frontiers in Microbiology*, **2017**, 8, 1079	5.7	52
192	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. *Cell Metabolism*, **2016**, 24, 172-84	24.6	105
191	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. *PLoS ONE*, **2016**, 11, e0162868	3.7	53
190	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. *Scientific Reports*, **2016**, 6, 20104	4.9	46
189	Omics Profiling in Precision Oncology. *Molecular and Cellular Proteomics*, **2016**, 15, 2525-36	7.6	63
188	AGAPE (Automated Genome Analysis PipelinE) for pan-genome analysis of Saccharomyces cerevisiae. *PLoS ONE*, **2015**, 10, e0120671	3.7	41
187	Recurrent somatic mutations in regulatory regions of human cancer genomes. *Nature Genetics*, **2015**, 47, 710-6	36.3	190
186	Regulatory analysis of the C. elegans genome with spatiotemporal resolution. *Nature*, **2014**, 512, 400-5	50.4	81
185	Comparative analysis of regulatory information and circuits across distant species. *Nature*, **2014**, 512, 453-6	50.4	135

184	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	1.7	6
183	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. *Molecular Systems Biology*, **2014**, 10, 774	12.2	89
182	Coherent functional modules improve transcription factor target identification, cooperativity prediction, and disease association. *PLoS Genetics*, **2014**, 10, e1004122	6	26
181	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
180	Global analysis of transcription factor-binding sites in yeast using ChIP-Seq. *Methods in Molecular Biology*, **2014**, 1205, 231-55	1.4	3
179	Personal genomes, quantitative dynamic omics and personalized medicine. *Quantitative Biology*, **2013**, 1, 71-90	3.9	26
178	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. *American Journal of Human Genetics*, **2013**, 93, 545-54	11	145
177	Proteogenomic analysis of human colon carcinoma cell lines LIM1215, LIM1899, and LIM2405. *Journal of Proteome Research*, **2013**, 12, 1732-42	5.6	26
176	Dynamic trans-acting factor colocalization in human cells. *Cell*, **2013**, 155, 713-24	56.2	109
175	Extensive variation in chromatin states across humans. *Science*, **2013**, 342, 750-2	33.3	276
174	A single-molecule long-read survey of the human transcriptome. *Nature Biotechnology*, **2013**, 31, 1009-14	44.5	396
173	Systematic investigation of protein-small molecule interactions. *IUBMB Life*, **2013**, 65, 2-8	4.7	24
172	Promise of personalized omics to precision medicine. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2013**, 5, 73-82	6.6	188
171	Preparation of recombinant protein spotted arrays for proteome-wide identification of kinase targets. *Current Protocols in Protein Science*, **2013**, Chapter 27, Unit 27.4	3.1	3
170	Genome-wide profiling of human cap-independent translation-enhancing elements. *Nature Methods*, **2013**, 10, 747-50	21.6	22
169	iPOP goes the world: integrated personalized Omics profiling and the road toward improved health care. *Chemistry and Biology*, **2013**, 20, 660-6		57
168	Identification of genes critical for resistance to infection by West Nile virus using RNA-Seq analysis. *Viruses*, **2013**, 5, 1664-81	6.2	18
167	Comparative annotation of functional regions in the human genome using epigenomic data. *Nucleic Acids Research*, **2013**, 41, 4423-32	20.1	37

166	Accurate identification and analysis of human mRNA isoforms using deep long read sequencing. *G3: Genes, Genomes, Genetics*, **2013**, 3, 387-97	3.2	47
165	Extensive transcript diversity and novel upstream open reading frame regulation in yeast. *G3: Genes, Genomes, Genetics*, **2013**, 3, 343-52	3.2	44
164	Emerging Technologies to Study Long Non-coding RNAs **2013**, 163-195		
163	Investigating metabolite-protein interactions: an overview of available techniques. *Methods*, **2012**, 57, 459-66	4.6	33
162	Classification of human genomic regions based on experimentally determined binding sites of more than 100 transcription-related factors. *Genome Biology*, **2012**, 13, R48	18.3	194
161	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. *Genome Research*, **2012**, 22, 1813-31	9.7	1211
160	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. *Genome Research*, **2012**, 22, 1735-47	9.7	129
159	Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell*, **2012**, 148, 1293-307	56.2	921
158	Architecture of the human regulatory network derived from ENCODE data. *Nature*, **2012**, 489, 91-100	50.4	1104
157	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome Research*, **2012**, 22, 1658-67	9.7	133
156	Detecting and annotating genetic variations using the HugeSeq pipeline. *Nature Biotechnology*, **2012**, 30, 226-9	44.5	90
155	Characterization of enhancer function from genome-wide analyses. *Annual Review of Genomics and Human Genetics*, **2012**, 13, 29-57	9.7	80
154	Annotation of functional variation in personal genomes using RegulomeDB. *Genome Research*, **2012**, 22, 1790-7	9.7	1723
153	A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells. *Genome Research*, **2012**, 22, 1668-79	9.7	56
152	Linking disease associations with regulatory information in the human genome. *Genome Research*, **2012**, 22, 1748-59	9.7	538
151	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Genome Research*, **2012**, 22, 1798-812	9.7	596
150	An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biology*, **2012**, 13, 418	18.3	340
149	Performance comparison of whole-genome sequencing platforms. *Nature Biotechnology*, **2011**, 30, 78-82	44.5	241

148	Dissecting phosphorylation networks: lessons learned from yeast. *Expert Review of Proteomics*, **2011**, 8, 775-86	4.2	15
147	Regulatory variation within and between species. *Annual Review of Genomics and Human Genetics*, **2011**, 12, 327-46	9.7	52
146	Introduction and Historical Overview of DNA Sequencing. *Current Protocols in Molecular Biology*, **2011**, 96, 7.0.1	2.9	1
145	Deciphering DNA Sequence Information **2011**, 1-20		
144	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
143	Kinase substrate interactions. *Methods in Molecular Biology*, **2011**, 723, 201-12	1.4	2
142	Identification of genomic indels and structural variations using split reads. *BMC Genomics*, **2011**, 12, 375	4.5	52
141	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. *BioEssays*, **2011**, 33, 485-9	4.1	28
140	AlleleSeq: analysis of allele-specific expression and binding in a network framework. *Molecular Systems Biology*, **2011**, 7, 522	12.2	228
139	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. *Genes and Development*, **2011**, 25, 767-78	12.6	51
138	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. *Bioinformatics*, **2011**, 27, 281-3	7.2	89
137	CNVnator: an approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. *Genome Research*, **2011**, 21, 974-84	9.7	944
136	Cooperative transcription factor associations discovered using regulatory variation. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 13353-8	11.5	38
135	Analyzing In Vivo Metabolite-Protein Interactions By Large-Scale Systematic Analyses. *Current Protocols in Chemical Biology*, **2011**, 3, 181-196	1.8	5
134	Construction and analysis of an integrated regulatory network derived from high-throughput sequencing data. *PLoS Computational Biology*, **2011**, 7, e1002190	5	69
133	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. *PLoS ONE*, **2011**, 6, e27859	3.7	51
132	RNA sequencing. *Methods in Molecular Biology*, **2011**, 759, 125-32	1.4	12
131	Genetic analysis of variation in transcription factor binding in yeast. *Nature*, **2010**, 464, 1187-91	50.4	130

130	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. *Nature Biotechnology*, **2010**, 28, 47-55	44.5	136
129	Annotating non-coding regions of the genome. *Nature Reviews Genetics*, **2010**, 11, 559-71	30.1	303
128	Systems Biology Approaches to Disease Marker Discovery. *Disease Markers*, **2010**, 28, 209-224	3.2	17
127	Personal genome sequencing: current approaches and challenges. *Genes and Development*, **2010**, 24, 423-31	12.6	103
126	X chromosome-wide analyses of genomic DNA methylation states and gene expression in male and female neutrophils. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 3704-9	11.5	29
125	Dynamic transcriptomes during neural differentiation of human embryonic stem cells revealed by short, long, and paired-end sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 5254-9	11.5	142
124	Genome-wide identification of binding sites defines distinct functions for Caenorhabditis elegans PHA-4/FOXA in development and environmental response. *PLoS Genetics*, **2010**, 6, e1000848	6	132
123	Close association of RNA polymerase II and many transcription factors with Pol III genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 3639-44	11.5	143
122	Variation in transcription factor binding among humans. *Science*, **2010**, 328, 232-5	33.3	447
121	Integrative analysis of the Caenorhabditis elegans genome by the modENCODE project. *Science*, **2010**, 330, 1775-87	33.3	744
120	RNA-Seq: a method for comprehensive transcriptome analysis. *Current Protocols in Molecular Biology*, **2010**, Chapter 4, Unit 4.11.1-13	2.9	168
119	ChIP-Seq: a method for global identification of regulatory elements in the genome. *Current Protocols in Molecular Biology*, **2010**, Chapter 21, Unit 21.19.1-14	2.9	39
118	ChIP-Seq using high-throughput DNA sequencing for genome-wide identification of transcription factor binding sites. *Methods in Enzymology*, **2010**, 470, 77-104	1.7	21
117	Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analyses. *Cell*, **2010**, 143, 639-50	56.2	162
116	Global Analysis of Phosphoregulatory Networks **2010**, 645-655		
115	Comprehensive annotation of the transcriptome of the human fungal pathogen Candida albicans using RNA-seq. *Genome Research*, **2010**, 20, 1451-8	9.7	165
114	Deciphering protein kinase specificity through large-scale analysis of yeast phosphorylation site motifs. *Science Signaling*, **2010**, 3, ra12	8.8	262
113	MOTIPS: automated motif analysis for predicting targets of modular protein domains. *BMC Bioinformatics*, **2010**, 11, 243	3.6	25

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112	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. *BMC Genomics*, **2010**, 11, 663	4.5	168
111	Yeast proteomics and protein microarrays. *Journal of Proteomics*, **2010**, 73, 2147-57	3.9	28
110	Global analysis of the glycoproteome in Saccharomyces cerevisiae reveals new roles for protein glycosylation in eukaryotes. *Molecular Systems Biology*, **2009**, 5, 308	12.2	71
109	Integrating sequencing technologies in personal genomics: optimal low cost reconstruction of structural variants. *PLoS Computational Biology*, **2009**, 5, e1000432	5	13
108	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. *BMC Genomics*, **2009**, 10, 37	4.5	129
107	Systems biology from a yeast omics perspective. *FEBS Letters*, **2009**, 583, 3895-9	3.8	39
106	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. *Nature Biotechnology*, **2009**, 27, 66-75	44.5	463
105	Unlocking the secrets of the genome. *Nature*, **2009**, 459, 927-30	50.4	620
104	RNA-Seq: a revolutionary tool for transcriptomics. *Nature Reviews Genetics*, **2009**, 10, 57-63	30.1	8302
103	Mapping accessible chromatin regions using Sono-Seq. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 14926-31	11.5	163
102	The genetic architecture of Down syndrome phenotypes revealed by high-resolution analysis of human segmental trisomies. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 12031-6	11.5	280
101	PEMer: a computational framework with simulation-based error models for inferring genomic structural variants from massive paired-end sequencing data. *Genome Biology*, **2009**, 10, R23	18.3	201
100	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. *Blood*, **2009**, 113, 2526-34	2.2	271
99	MSB: a mean-shift-based approach for the analysis of structural variation in the genome. *Genome Research*, **2009**, 19, 106-17	9.7	29
98	Impact of chromatin structures on DNA processing for genomic analyses. *PLoS ONE*, **2009**, 4, e6700	3.7	95
97	Protein microarrays. *Methods in Molecular Biology*, **2009**, 548, 209-22	1.4	17
96	The current excitement about copy-number variation: how it relates to gene duplications and protein families. *Current Opinion in Structural Biology*, **2008**, 18, 366-74	8.1	78
95	The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science*, **2008**, 320, 1344-9	33.3	1867

94	High-quality binary protein interaction map of the yeast interactome network. *Science*, **2008**, 322, 104-10	33.3	1100
93	RNA polymerase II stalling: loading at the start prepares genes for a sprint. *Genome Biology*, **2008**, 9, 220	18.3	33
92	Systematic analysis of transcribed loci in ENCODE regions using RACE sequencing reveals extensive transcription in the human genome. *Genome Biology*, **2008**, 9, R3	18.3	48
91	A genomic analysis of RNA polymerase II modification and chromatin architecture related to 3Rend RNA polyadenylation. *Genome Research*, **2008**, 18, 1224-37	9.7	47
90	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. *Genome Research*, **2008**, 18, 1865-74	9.7	114
89	The development of protein microarrays and their applications in DNA-protein and protein-protein interaction analyses of Arabidopsis transcription factors. *Molecular Plant*, **2008**, 1, 27-41	14.4	70
88	Modeling ChIP sequencing in silico with applications. *PLoS Computational Biology*, **2008**, 4, e1000158	5	62
87	High-resolution copy-number variation map reflects human olfactory receptor diversity and evolution. *PLoS Genetics*, **2008**, 4, e1000249	6	87
86	Genome-wide occupancy of SREBP1 and its partners NFY and SP1 reveals novel functional roles and combinatorial regulation of distinct classes of genes. *PLoS Genetics*, **2008**, 4, e1000133	6	154
85	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. *Genome Research*, **2008**, 18, 393-403	9.7	111
84	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. *Genome Research*, **2008**, 18, 1906-17	9.7	147
83	What is a gene, post-ENCODE? History and updated definition. *Genome Research*, **2007**, 17, 669-81	9.7	417
82	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. *Genome Research*, **2007**, 17, 720-31	9.7	31
81	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. *Nature Methods*, **2007**, 4, 651-7	21.6	1077
80	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
79	Protein microarray technology. *Mechanisms of Ageing and Development*, **2007**, 128, 161-7	5.6	237
78	Paired-end mapping reveals extensive structural variation in the human genome. *Science*, **2007**, 318, 420-6	33.3	895
77	Transcription factor binding site identification in yeast: a comparison of high-density oligonucleotide and PCR-based microarray platforms. *Functional and Integrative Genomics*, **2007**, 7, 335-45	3.8	19

76	Positional artifacts in microarrays: experimental verification and construction of COP, an automated detection tool. *Nucleic Acids Research*, **2007**, 35, e8	20.1	9
75	Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE). *Genome Research*, **2007**, 17, 910-6	9.7	54
74	Systematic prediction and validation of breakpoints associated with copy-number variants in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 10110-5	11.5	70
73	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. *Genome Research*, **2007**, 17, 787-97	9.7	47
72	Mapping of transcription factor binding regions in mammalian cells by ChIP: comparison of array- and sequencing-based technologies. *Genome Research*, **2007**, 17, 898-909	9.7	164
71	Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome. *Genome Research*, **2007**, 17, 886-97	9.7	25
70	The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci. *Genome Research*, **2007**, 17, 732-45	9.7	21
69	Structured RNAs in the ENCODE selected regions of the human genome. *Genome Research*, **2007**, 17, 852-64	9.7	131
68	Divergence of transcription factor binding sites across related yeast species. *Science*, **2007**, 317, 815-9	33.3	286
67	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. *Genome Research*, **2007**, 17, 839-51	9.7	158
66	14 Yeast Protein Microarrays. *Methods in Microbiology*, **2007**, 36, 303-705	2.8	1
65	Getting connected: analysis and principles of biological networks. *Genes and Development*, **2007**, 21, 1010-24	12.6	380
64	Charging it up: global analysis of protein phosphorylation. *Trends in Genetics*, **2006**, 22, 545-54	8.5	116
63	A supervised hidden markov model framework for efficiently segmenting tiling array data in transcriptional and chIP-chip experiments: systematically incorporating validated biological knowledge. *Bioinformatics*, **2006**, 22, 3016-24	7.2	31
62	Predicting essential genes in fungal genomes. *Genome Research*, **2006**, 16, 1126-35	9.7	84
61	Extrapolating traditional DNA microarray statistics to tiling and protein microarray technologies. *Methods in Enzymology*, **2006**, 411, 282-311	1.7	12
60	Target hub proteins serve as master regulators of development in yeast. *Genes and Development*, **2006**, 20, 435-48	12.6	138
59	TOS9 regulates white-opaque switching in Candida albicans. *Eukaryotic Cell*, **2006**, 5, 1674-87		179

58	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, 9940-5	11.5	57
57	High-resolution mapping of DNA copy alterations in human chromosome 22 using high-density tiling oligonucleotide arrays. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 4534-9	11.5	112
56	Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 4011-6	11.5	118
55	BoCaTFBS: a boosted cascade learner to refine the binding sites suggested by ChIP-chip experiments. *Genome Biology*, **2006**, 7, R102	18.3	1
54	ProCAT: a data analysis approach for protein microarrays. *Genome Biology*, **2006**, 7, R110	18.3	43
53	Yeast as a model for human disease. *Current Protocols in Human Genetics*, **2006**, Chapter 15, Unit 15.6	3.2	27
52	Proteome chips for whole-organism assays. *Nature Reviews Molecular Cell Biology*, **2006**, 7, 617-22	48.7	61
51	Design optimization methods for genomic DNA tiling arrays. *Genome Research*, **2006**, 16, 271-81	9.7	41
50	Global analysis of protein phosphorylation in yeast. *Nature*, **2005**, 438, 679-84	50.4	818
49	Advances in functional protein microarray technology. *FEBS Journal*, **2005**, 272, 5400-11	5.7	141
48	Global analysis of protein function using protein microarrays. *Mechanisms of Ageing and Development*, **2005**, 126, 171-5	5.6	34
47	Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. *Chromosome Research*, **2005**, 13, 259-74	4.4	58
46	A pilot study of transcription unit analysis in rice using oligonucleotide tiling-path microarray. *Plant Molecular Biology*, **2005**, 59, 137-49	4.6	17
45	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. *Genes and Development*, **2005**, 19, 2816-26	12.6	387
44	Prospects and challenges in proteomics. *Plant Physiology*, **2005**, 138, 560-2	6.6	17
43	Global changes in STAT target selection and transcription regulation upon interferon treatments. *Genes and Development*, **2005**, 19, 2953-68	12.6	83
42	Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 16594-9	11.5	208
41	DNA replication-timing analysis of human chromosome 22 at high resolution and different developmental states. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 17771-6	11.5	107

40	Fast optimal genome tiling with applications to microarray design and homology search. *Journal of Computational Biology*, **2004**, 11, 766-85	1.7	10
39	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. *Nature Genetics*, **2004**, 36, 1331-9	36.3	294
38	Genomic analysis of regulatory network dynamics reveals large topological changes. *Nature*, **2004**, 431, 308-12	50.4	767
37	Global identification of human transcribed sequences with genome tiling arrays. *Science*, **2004**, 306, 2242-6	33.3	868
36	Regulation of gene expression by a metabolic enzyme. *Science*, **2004**, 306, 482-4	33.3	206
35	Genomics. Defining genes in the genomics era. *Science*, **2003**, 300, 258-60	33.3	89
34	Distribution of NF-kappaB-binding sites across human chromosome 22. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 12247-52	11.5	276
33	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. *Genes and Development*, **2003**, 17, 2698-708	12.6	63
32	Protein chip technology. *Current Opinion in Chemical Biology*, **2003**, 7, 55-63	9.7	792
31	Microarrays to characterize protein interactions on a whole-proteome scale. *Proteomics*, **2003**, 3, 2190-9	4.8	140
30	Protein analysis on a proteomic scale. *Nature*, **2003**, 422, 208-15	50.4	541
29	Analyzing antibody specificity with whole proteome microarrays. *Nature Biotechnology*, **2003**, 21, 1509-12	44.5	248
28	Proteomics. *Annual Review of Biochemistry*, **2003**, 72, 783-812	29.1	295
27	A Bayesian networks approach for predicting protein-protein interactions from genomic data. *Science*, **2003**, 302, 449-53	33.3	1007
26	ExpressYourself: A modular platform for processing and visualizing microarray data. *Nucleic Acids Research*, **2003**, 31, 3477-82	20.1	34
25	Molecular dissection of a yeast septin: distinct domains are required for septin interaction, localization, and function. *Molecular and Cellular Biology*, **2003**, 23, 2762-77	4.8	148
24	Proteomic approaches for the global analysis of proteins. *BioTechniques*, **2002**, 33, 1308-16	2.5	35
23	"Omic" approaches for unraveling signaling networks. *Current Opinion in Cell Biology*, **2002**, 14, 173-9	9	60

22	Large-scale identification of genes important for apical growth in Saccharomyces cerevisiae by directed allele replacement technology (DART) screening. *Functional and Integrative Genomics*, **2002**, 1, 345-56	3.8	27
21	Global analysis of gene expression in yeast. *Functional and Integrative Genomics*, **2002**, 2, 171-80	3.8	65
20	Carbohydrate analysis prepares to enter the "Omics" era. *Chemistry and Biology*, **2002**, 9, 400-1		8
19	Functional profiling of the Saccharomyces cerevisiae genome. *Nature*, **2002**, 418, 387-91	50.4	3278
18	An integrated approach for finding overlooked genes in yeast. *Nature Biotechnology*, **2002**, 20, 58-63	44.5	97
17	A novel mitochondrial protein, Tar1p, is encoded on the antisense strand of the nuclear 25S rDNA. *Genes and Development*, **2002**, 16, 2755-60	12.6	53
16	Complex transcriptional circuitry at the G1/S transition in Saccharomyces cerevisiae. *Genes and Development*, **2002**, 16, 3017-33	12.6	201
15	GATA-1 binding sites mapped in the beta-globin locus by using mammalian chIp-chip analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 2924-9	11.5	143
14	A question of size: the eukaryotic proteome and the problems in defining it. *Nucleic Acids Research*, **2002**, 30, 1083-90	20.1	141
13	Subcellular localization of the yeast proteome. *Genes and Development*, **2002**, 16, 707-19	12.6	575
12	ChIP-chip: a genomic approach for identifying transcription factor binding sites. *Methods in Enzymology*, **2002**, 350, 469-83	1.7	131
11	Fast Optimal Genome Tiling with Applications to Microarray Design and Homology Search. *Lecture Notes in Computer Science*, **2002**, 419-433	0.9	1
10	Large-scale mutagenesis: yeast genetics in the genome era. *Current Opinion in Biotechnology*, **2001**, 12, 28-34	11.4	30
9	Protein arrays and microarrays. *Current Opinion in Chemical Biology*, **2001**, 5, 40-5	9.7	331
8	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. *Nature*, **2001**, 409, 533-8	50.4	927
7	Emerging technologies in yeast genomics. *Nature Reviews Genetics*, **2001**, 2, 302-12	30.1	82
6	A genomic study of the bipolar bud site selection pattern in Saccharomyces cerevisiae. *Molecular Biology of the Cell*, **2001**, 12, 2147-70	3.5	238
5	Global analysis of protein activities using proteome chips. *Science*, **2001**, 293, 2101-5	33.3	1899

4	Analysis of yeast protein kinases using protein chips. *Nature Genetics*, **2000**, 26, 283-9	36.3	734
3	High-throughput methods for the large-scale analysis of gene function by transposon tagging. *Methods in Enzymology*, **2000**, 328, 550-74	1.7	27
2	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. *Nature*, **1999**, 402, 413-8	50.4	470
1	Functional characterization of the S. cerevisiae genome by gene deletion and parallel analysis. *Science*, **1999**, 285, 901-6	33.3	3254