

# Michael Snyder

## List of Publications by Year in descending order

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204  
papers

72,859  
citations

1893

102  
h-index

2178

202  
g-index

206  
all docs

206  
docs citations

206  
times ranked

79002  
citing authors

#	ARTICLE	IF	CITATIONS
1	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020, 583, 737-743.	27.8	134
2	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 834.	2.3	44
3	Multiplatform next-generation sequencing identifies novel RNA molecules and transcript isoforms of the endogenous retrovirus isolated from cultured cells. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	21
4	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , 2018, 28, 231-242.	5.5	64
5	Dual Platform Long-Read RNA-Sequencing Dataset of the Human Cytomegalovirus Lytic Transcriptome. <i>Frontiers in Genetics</i> , 2018, 9, 432.	2.3	14
6	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , 2018, 8, 2708.	3.5	64
7	Discovery of Novel Human Gene Regulatory Modules from Gene Co-expression and Promoter Motif Analysis. <i>Scientific Reports</i> , 2017, 7, 5557.	3.3	19
8	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528.	21.4	255
9	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.	3.5	97
10	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. <i>PLoS ONE</i> , 2016, 11, e0162868.	2.5	93
11	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. <i>Scientific Reports</i> , 2016, 6, 20104.	3.3	61
12	Omics Profiling in Precision Oncology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2525-2536.	3.8	84
13	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016, 24, 172-184.	16.2	133
14	AGAPE (Automated Genome Analysis PipelinE) for Pan-Genome Analysis of <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0120671.	2.5	73
15	Recurrent somatic mutations in regulatory regions of human cancer genomes. <i>Nature Genetics</i> , 2015, 47, 710-716.	21.4	225
16	Chromatin Immunoprecipitation and Multiplex Sequencing (ChIP-Seq) to Identify Global Transcription Factor Binding Sites in the Nematode <i>Caenorhabditis Elegans</i> . <i>Methods in Enzymology</i> , 2014, 539, 89-111.	1.0	7
17	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. <i>Molecular Systems Biology</i> , 2014, 10, 774.	7.2	138
18	Coherent Functional Modules Improve Transcription Factor Target Identification, Cooperativity Prediction, and Disease Association. <i>PLoS Genetics</i> , 2014, 10, e1004122.	3.5	29

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19	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, 349-360.	6.2	158
20	Regulatory analysis of the <i>C. elegans</i> genome with spatiotemporal resolution. <i>Nature</i> , 2014, 512, 400-405.	27.8	115
21	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	27.8	184
22	Global Analysis of Transcription Factor-Binding Sites in Yeast Using CHIP-Seq. <i>Methods in Molecular Biology</i> , 2014, 1205, 231-255.	0.9	4
23	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013, 1, 71-90.	0.5	29
24	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, 545-554.	6.2	189
25	Proteogenomic Analysis of Human Colon Carcinoma Cell Lines LIM1215, LIM1899, and LIM2405. <i>Journal of Proteome Research</i> , 2013, 12, 1732-1742.	3.7	30
26	Dynamic trans-Acting Factor Colocalization in Human Cells. <i>Cell</i> , 2013, 155, 713-724.	28.9	142
27	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	12.6	338
28	A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , 2013, 31, 1009-1014.	17.5	600
29	Systematic investigation of protein-small molecule interactions. <i>IUBMB Life</i> , 2013, 65, 2-8.	3.4	33
30	Promise of personalized omics to precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 73-82.	6.6	245
31	Preparation of Recombinant Protein Spotted Arrays for Proteome-Wide Identification of Kinase Targets. <i>Current Protocols in Protein Science</i> , 2013, 72, Unit 27.4.	2.8	4
32	Genome-wide profiling of human cap-independent translation-enhancing elements. <i>Nature Methods</i> , 2013, 10, 747-750.	19.0	29
33	iPOP Goes the World: Integrated Personalized Omics Profiling and the Road toward Improved Health Care. <i>Chemistry and Biology</i> , 2013, 20, 660-666.	6.0	67
34	Identification of Genes Critical for Resistance to Infection by West Nile Virus Using RNA-Seq Analysis. <i>Viruses</i> , 2013, 5, 1664-1681.	3.3	25
35	Comparative annotation of functional regions in the human genome using epigenomic data. <i>Nucleic Acids Research</i> , 2013, 41, 4423-4432.	14.5	50
36	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 387-397.	1.8	59

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37	Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 343-352.	1.8	59
38	Emerging Technologies to Study Long Non-coding RNAs. , 2013, , 163-195.		0
39	Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , 2012, 22, 1790-1797.	5.5	2,335
40	A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells. <i>Genome Research</i> , 2012, 22, 1668-1679.	5.5	75
41	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , 2012, 22, 1748-1759.	5.5	657
42	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012, 22, 1798-1812.	5.5	762
43	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	9.6	410
44	Investigating metabolite-protein interactions: An overview of available techniques. <i>Methods</i> , 2012, 57, 459-466.	3.8	40
45	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.	9.6	233
46	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	5.5	1,708
47	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. <i>Genome Research</i> , 2012, 22, 1735-1747.	5.5	168
48	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	28.9	1,134
49	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	27.8	1,384
50	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	5.5	166
51	Detecting and annotating genetic variations using the HugerSeq pipeline. <i>Nature Biotechnology</i> , 2012, 30, 226-229.	17.5	104
52	Performance comparison of whole-genome sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 78-82.	17.5	281
53	Characterization of Enhancer Function from Genome-Wide Analyses. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 29-57.	6.2	86
54	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011, 7, 522.	7.2	284

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55	Dissecting phosphorylation networks: lessons learned from yeast. <i>Expert Review of Proteomics</i> , 2011, 8, 775-786.	3.0	15
56	Regulatory Variation Within and Between Species. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 327-346.	6.2	70
57	Introduction and Historical Overview of DNA Sequencing. <i>Current Protocols in Molecular Biology</i> , 2011, 96, 7.0.1.	2.9	1
58	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	27.8	991
59	Kinase Substrate Interactions. <i>Methods in Molecular Biology</i> , 2011, 723, 201-212.	0.9	3
60	Identification of genomic indels and structural variations using split reads. <i>BMC Genomics</i> , 2011, 12, 375.	2.8	57
61	Metabolites as global regulators: A new view of protein regulation. <i>BioEssays</i> , 2011, 33, 485-489.	2.5	36
62	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. <i>Genes and Development</i> , 2011, 25, 767-778.	5.9	60
63	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. <i>Bioinformatics</i> , 2011, 27, 281-283.	4.1	93
64	CNVnator: An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing. <i>Genome Research</i> , 2011, 21, 974-984.	5.5	1,387
65	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, 13353-13358.	7.1	53
66	Analyzing In Vivo Metabolite-Protein Interactions by Large-Scale Systematic Analyses. <i>Current Protocols in Chemical Biology</i> , 2011, 3, 181-196.	1.7	5
67	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002190.	3.2	92
68	RNA Sequencing. <i>Methods in Molecular Biology</i> , 2011, 759, 125-132.	0.9	14
69	Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms. <i>PLoS ONE</i> , 2011, 6, e27859.	2.5	59
70	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. <i>Science Signaling</i> , 2010, 3, ra12.	3.6	341
71	MOTIPS: Automated Motif Analysis for Predicting Targets of Modular Protein Domains. <i>BMC Bioinformatics</i> , 2010, 11, 243.	2.6	28
72	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. <i>BMC Genomics</i> , 2010, 11, 663.	2.8	201

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73	Yeast proteomics and protein microarrays. <i>Journal of Proteomics</i> , 2010, 73, 2147-2157.	2.4	31
74	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010, 464, 1187-1191.	27.8	162
75	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , 2010, 28, 47-55.	17.5	158
76	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010, 11, 559-571.	16.3	398
77	Systems Biology Approaches to Disease Marker Discovery. <i>Disease Markers</i> , 2010, 28, 209-224.	1.3	18
78	Personal genome sequencing: current approaches and challenges. <i>Genes and Development</i> , 2010, 24, 423-431.	5.9	119
79	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, 3704-3709.	7.1	44
80	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, 5254-5259.	7.1	168
81	Genome-Wide Identification of Binding Sites Defines Distinct Functions for <i>Caenorhabditis elegans</i> PHA-4/FOXA in Development and Environmental Response. <i>PLoS Genetics</i> , 2010, 6, e1000848.	3.5	165
82	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, 3639-3644.	7.1	167
83	Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235.	12.6	521
84	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
85	RNA-Seq: A Method for Comprehensive Transcriptome Analysis. <i>Current Protocols in Molecular Biology</i> , 2010, 89, Unit 4.11.1-13.	2.9	218
86	ChIP-Seq: A Method for Global Identification of Regulatory Elements in the Genome. <i>Current Protocols in Molecular Biology</i> , 2010, 91, Unit 21.19.1-14.	2.9	49
87	ChIP-Seq. <i>Methods in Enzymology</i> , 2010, 470, 77-104.	1.0	23
88	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. <i>Cell</i> , 2010, 143, 639-650.	28.9	200
89	Global Analysis of Phosphoregulatory Networks. , 2010, , 645-655.		1
90	Comprehensive annotation of the transcriptome of the human fungal pathogen <i>Candida albicans</i> using RNA-seq. <i>Genome Research</i> , 2010, 20, 1451-1458.	5.5	191

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91	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. <i>Genome Research</i> , 2009, 19, 106-117.	5.5	33
92	Personal phenotypes to go with personal genomes. <i>Molecular Systems Biology</i> , 2009, 5, 273.	7.2	41
93	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.	7.2	79
94	Integrating Sequencing Technologies in Personal Genomics: Optimal Low Cost Reconstruction of Structural Variants. <i>PLoS Computational Biology</i> , 2009, 5, e1000432.	3.2	14
95	Efficient yeast ChIP-Seq using multiplex short-read DNA sequencing. <i>BMC Genomics</i> , 2009, 10, 37.	2.8	137
96	Systems biology from a yeast omics perspective. <i>FEBS Letters</i> , 2009, 583, 3895-3899.	2.8	46
97	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. <i>Nature Biotechnology</i> , 2009, 27, 66-75.	17.5	514
98	Unlocking the secrets of the genome. <i>Nature</i> , 2009, 459, 927-930.	27.8	744
99	RNA-Seq: a revolutionary tool for transcriptomics. <i>Nature Reviews Genetics</i> , 2009, 10, 57-63.	16.3	10,529
100	Mapping accessible chromatin regions using Sono-Seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14926-14931.	7.1	186
101	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, 12031-12036.	7.1	342
102	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.	9.6	223
103	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009, 113, 2526-2534.	1.4	330
104	Protein Microarrays. <i>Methods in Molecular Biology</i> , 2009, 548, 209-222.	0.9	18
105	Impact of Chromatin Structures on DNA Processing for Genomic Analyses. <i>PLoS ONE</i> , 2009, 4, e6700.	2.5	115
106	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, 366-374.	5.7	92
107	The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. <i>Science</i> , 2008, 320, 1344-1349.	12.6	2,180
108	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	12.6	1,297

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109	RNA polymerase II stalling: loading at the start prepares genes for a sprint. <i>Genome Biology</i> , 2008, 9, 220.	9.6	38
110	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.	9.6	53
111	A genomic analysis of RNA polymerase II modification and chromatin architecture related to 3' end RNA polyadenylation. <i>Genome Research</i> , 2008, 18, 1224-1237.	5.5	50
112	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, 1865-1874.	5.5	126
113	The Development of Protein Microarrays and Their Applications in DNA-Protein and Protein-Protein Interaction Analyses of Arabidopsis Transcription Factors. <i>Molecular Plant</i> , 2008, 1, 27-41.	8.3	78
114	Modeling ChIP Sequencing In Silico with Applications. <i>PLoS Computational Biology</i> , 2008, 4, e1000158.	3.2	70
115	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000249.	3.5	99
116	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.	3.5	191
117	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	5.5	117
118	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008, 18, 1906-1917.	5.5	163
119	Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE). <i>Genome Research</i> , 2007, 17, 910-916.	5.5	61
120	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, 10110-10115.	7.1	78
121	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. <i>Genome Research</i> , 2007, 17, 787-797.	5.5	56
122	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.	5.5	181
123	Assessing the performance of different high-density tiling microarray strategies for mapping transcribed regions of the human genome. <i>Genome Research</i> , 2007, 17, 886-897.	5.5	25
124	The DART classification of unannotated transcription within the ENCODE regions: Associating transcription with known and novel loci. <i>Genome Research</i> , 2007, 17, 732-745.	5.5	25
125	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	5.5	150
126	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. <i>Science</i> , 2007, 317, 815-819.	12.6	320



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127	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	5.5	191
128	14 Yeast Protein Microarrays. <i>Methods in Microbiology</i> , 2007, 36, 303-705.	0.8	1
129	Getting connected: analysis and principles of biological networks. <i>Genes and Development</i> , 2007, 21, 1010-1024.	5.9	477
130	What is a gene, post-ENCODE? History and updated definition. <i>Genome Research</i> , 2007, 17, 669-681.	5.5	530
131	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007, 17, 720-731.	5.5	31
132	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007, 4, 651-657.	19.0	1,254
133	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
134	Protein microarray technology. <i>Mechanisms of Ageing and Development</i> , 2007, 128, 161-167.	4.6	268
135	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. <i>Science</i> , 2007, 318, 420-426.	12.6	1,003
136	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, 335-345.	3.5	22
137	BoCaTFBS: a boosted cascade learner to refine the binding sites suggested by ChIP-chip experiments. <i>Genome Biology</i> , 2006, 7, R102.	9.6	1
138	ProCAT: a data analysis approach for protein microarrays. <i>Genome Biology</i> , 2006, 7, R110.	9.6	46
139	Yeast as a Model for Human Disease. <i>Current Protocols in Human Genetics</i> , 2006, 48, Unit 15.6.	3.5	36
140	Proteome chips for whole-organism assays. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 617-622.	37.0	69
141	Charging it up: global analysis of protein phosphorylation. <i>Trends in Genetics</i> , 2006, 22, 545-554.	6.7	123
142	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, 3016-3024.	4.1	32
143	Positional artifacts in microarrays: experimental verification and construction of COP, an automated detection tool. <i>Nucleic Acids Research</i> , 2006, 35, e8-e8.	14.5	12
144	Predicting essential genes in fungal genomes. <i>Genome Research</i> , 2006, 16, 1126-1135.	5.5	109

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145	[15] Extrapolating Traditional DNA Microarray Statistics to Tiling and Protein Microarray Technologies. <i>Methods in Enzymology</i> , 2006, 411, 282-311.	1.0	23
146	Target hub proteins serve as master regulators of development in yeast. <i>Genes and Development</i> , 2006, 20, 435-448.	5.9	153
147	TOS9 Regulates White-Opaque Switching in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2006, 5, 1674-1687.	3.4	207
148	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, 9940-9945.	7.1	63
149	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, 4534-4539.	7.1	125
150	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, 4011-4016.	7.1	131
151	Global analysis of protein phosphorylation in yeast. <i>Nature</i> , 2005, 438, 679-684.	27.8	915
152	Advances in functional protein microarray technology. <i>FEBS Journal</i> , 2005, 272, 5400-5411.	4.7	160
153	Global analysis of protein function using protein microarrays. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 171-175.	4.6	35
154	Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. <i>Chromosome Research</i> , 2005, 13, 259-274.	2.2	72
155	A Pilot Study of Transcription Unit Analysis in Rice Using Oligonucleotide Tiling-path Microarray. <i>Plant Molecular Biology</i> , 2005, 59, 137-149.	3.9	17
156	Design optimization methods for genomic DNA tiling arrays. <i>Genome Research</i> , 2005, 16, 271-281.	5.5	46
157	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , 2005, 19, 2816-2826.	5.9	443
158	Prospects and Challenges in Proteomics. <i>Plant Physiology</i> , 2005, 138, 560-562.	4.8	19
159	Global changes in STAT target selection and transcription regulation upon interferon treatments. <i>Genes and Development</i> , 2005, 19, 2953-2968.	5.9	95
160	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, 16594-16599.	7.1	225
161	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, 17771-17776.	7.1	121
162	Fast Optimal Genome Tiling with Applications to Microarray Design and Homology Search. <i>Journal of Computational Biology</i> , 2004, 11, 766-785.	1.6	11

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163	A plethora of sites. <i>Nature Genetics</i> , 2004, 36, 325-326.	21.4	16
164	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. <i>Nature Genetics</i> , 2004, 36, 1331-1339.	21.4	341
165	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	27.8	921
166	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. <i>Science</i> , 2004, 306, 2242-2246.	12.6	983
167	Regulation of Gene Expression by a Metabolic Enzyme. <i>Science</i> , 2004, 306, 482-484.	12.6	223
168	Protein chip technology. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 55-63.	6.1	861
169	Microarrays to characterize protein interactions on a whole-proteome scale. <i>Proteomics</i> , 2003, 3, 2190-2199.	2.2	155
170	Protein analysis on a proteomic scale. <i>Nature</i> , 2003, 422, 208-215.	27.8	610
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