

# Michael Snyder

## List of Publications by Year in descending order

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204  
papers

72,859  
citations

1883

102  
h-index

2171

202  
g-index

206  
all docs

206  
docs citations

206  
times ranked

79002  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-Seq: a revolutionary tool for transcriptomics. <i>Nature Reviews Genetics</i> , 2009, 10, 57-63.	7.7	10,529
2	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
3	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	13.7	3,938
4	Functional Characterization of the <i>Saccharomyces cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. <i>Science</i> , 1999, 285, 901-906.	6.0	3,761
5	Annotation of functional variation in personal genomes using RegulomeDB. <i>Genome Research</i> , 2012, 22, 1790-1797.	2.4	2,335
6	The Transcriptional Landscape of the Yeast Genome Defined by RNA Sequencing. <i>Science</i> , 2008, 320, 1344-1349.	6.0	2,180
7	Global Analysis of Protein Activities Using Proteome Chips. <i>Science</i> , 2001, 293, 2101-2105.	6.0	2,082
8	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. <i>Genome Research</i> , 2012, 22, 1813-1831.	2.4	1,708
9	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.	2.4	1,387
10	Architecture of the human regulatory network derived from ENCODE data. <i>Nature</i> , 2012, 489, 91-100.	13.7	1,384
11	High-Quality Binary Protein Interaction Map of the Yeast Interactome Network. <i>Science</i> , 2008, 322, 104-110.	6.0	1,297
12	Genome-wide profiles of STAT1 DNA association using chromatin immunoprecipitation and massively parallel sequencing. <i>Nature Methods</i> , 2007, 4, 651-657.	9.0	1,254
13	A Bayesian Networks Approach for Predicting Protein-Protein Interactions from Genomic Data. <i>Science</i> , 2003, 302, 449-453.	6.0	1,183
14	Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes. <i>Cell</i> , 2012, 148, 1293-1307.	13.5	1,134
15	Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF. <i>Nature</i> , 2001, 409, 533-538.	13.7	1,030
16	Paired-End Mapping Reveals Extensive Structural Variation in the Human Genome. <i>Science</i> , 2007, 318, 420-426.	6.0	1,003
17	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011, 470, 59-65.	13.7	991
18	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. <i>Science</i> , 2004, 306, 2242-2246.	6.0	983

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19	Genomic analysis of regulatory network dynamics reveals large topological changes. <i>Nature</i> , 2004, 431, 308-312.	13.7	921
20	Global analysis of protein phosphorylation in yeast. <i>Nature</i> , 2005, 438, 679-684.	13.7	915
21	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	6.0	912
22	Protein chip technology. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 55-63.	2.8	861
23	Analysis of yeast protein kinases using protein chips. <i>Nature Genetics</i> , 2000, 26, 283-289.	9.4	810
24	Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. <i>Genome Research</i> , 2012, 22, 1798-1812.	2.4	762
25	Unlocking the secrets of the genome. <i>Nature</i> , 2009, 459, 927-930.	13.7	744
26	Subcellular localization of the yeast proteome. <i>Genes and Development</i> , 2002, 16, 707-719.	2.7	667
27	Linking disease associations with regulatory information in the human genome. <i>Genome Research</i> , 2012, 22, 1748-1759.	2.4	657
28	Protein analysis on a proteomic scale. <i>Nature</i> , 2003, 422, 208-215.	13.7	610
29	A single-molecule long-read survey of the human transcriptome. <i>Nature Biotechnology</i> , 2013, 31, 1009-1014.	9.4	600
30	What is a gene, post-ENCODE? History and updated definition. <i>Genome Research</i> , 2007, 17, 669-681.	2.4	530
31	Large-scale analysis of the yeast genome by transposon tagging and gene disruption. <i>Nature</i> , 1999, 402, 413-418.	13.7	521
32	Variation in Transcription Factor Binding Among Humans. <i>Science</i> , 2010, 328, 232-235.	6.0	521
33	PeakSeq enables systematic scoring of ChIP-seq experiments relative to controls. <i>Nature Biotechnology</i> , 2009, 27, 66-75.	9.4	514
34	Getting connected: analysis and principles of biological networks. <i>Genes and Development</i> , 2007, 21, 1010-1024.	2.7	477
35	Biochemical and genetic analysis of the yeast proteome with a movable ORF collection. <i>Genes and Development</i> , 2005, 19, 2816-2826.	2.7	443
36	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , 2012, 13, 418.	13.9	410

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37	Annotating non-coding regions of the genome. <i>Nature Reviews Genetics</i> , 2010, 11, 559-571.	7.7	398
38	Protein arrays and microarrays. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 40-45.	2.8	376
39	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.	3.3	342
40	Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. <i>Nature Genetics</i> , 2004, 36, 1331-1339.	9.4	341
41	Deciphering Protein Kinase Specificity Through Large-Scale Analysis of Yeast Phosphorylation Site Motifs. <i>Science Signaling</i> , 2010, 3, ra12.	1.6	341
42	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	6.0	338
43	Proteomics. <i>Annual Review of Biochemistry</i> , 2003, 72, 783-812.	5.0	332
44	A myelopoiesis-associated regulatory intergenic noncoding RNA transcript within the human HOXA cluster. <i>Blood</i> , 2009, 113, 2526-2534.	0.6	330
45	Divergence of Transcription Factor Binding Sites Across Related Yeast Species. <i>Science</i> , 2007, 317, 815-819.	6.0	320
46	Distribution of NF- $\kappa$ B-binding sites across human chromosome 22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12247-12252.	3.3	298
47	AlleleSeq: analysis of allele-specific expression and binding in a network framework. <i>Molecular Systems Biology</i> , 2011, 7, 522.	3.2	284
48	Performance comparison of whole-genome sequencing platforms. <i>Nature Biotechnology</i> , 2012, 30, 78-82.	9.4	281
49	Analyzing antibody specificity with whole proteome microarrays. <i>Nature Biotechnology</i> , 2003, 21, 1509-1512.	9.4	270
50	Protein microarray technology. <i>Mechanisms of Ageing and Development</i> , 2007, 128, 161-167.	2.2	268
51	A Genomic Study of the Bipolar Bud Site Selection Pattern in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2001, 12, 2147-2170.	0.9	266
52	Lineage-specific dynamic and pre-established enhancer-promoter contacts cooperate in terminal differentiation. <i>Nature Genetics</i> , 2017, 49, 1522-1528.	9.4	255
53	Promise of personalized omics to precision medicine. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 73-82.	6.6	245
54	Complex transcriptional circuitry at the G1/S transition in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2002, 16, 3017-3033.	2.7	236

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55	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.	13.9	233
56	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.	3.3	225
57	Recurrent somatic mutations in regulatory regions of human cancer genomes. <i>Nature Genetics</i> , 2015, 47, 710-716.	9.4	225
58	Regulation of Gene Expression by a Metabolic Enzyme. <i>Science</i> , 2004, 306, 482-484.	6.0	223
59	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.	13.9	223
60	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
61	TOS9 Regulates White-Opaque Switching in <i>Candida albicans</i> . <i>Eukaryotic Cell</i> , 2006, 5, 1674-1687.	3.4	207
62	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. <i>BMC Genomics</i> , 2010, 11, 663.	1.2	201
63	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. <i>Cell</i> , 2010, 143, 639-650.	13.5	200
64	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. <i>Genome Research</i> , 2007, 17, 839-851.	2.4	191
65	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.	1.5	191
66	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.	2.4	191
67	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.	2.6	189
68	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.	3.3	186
69	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	13.7	184
70	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.	2.4	181
71	A question of size: the eukaryotic proteome and the problems in defining it. <i>Nucleic Acids Research</i> , 2002, 30, 1083-1090.	6.5	172
72	Molecular Dissection of a Yeast Septin: Distinct Domains Are Required for Septin Interaction, Localization, and Function. <i>Molecular and Cellular Biology</i> , 2003, 23, 2762-2777.	1.1	170

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73	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.	3.3	168
74	Ubiquitous heterogeneity and asymmetry of the chromatin environment at regulatory elements. <i>Genome Research</i> , 2012, 22, 1735-1747.	2.4	168
75	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.	3.3	167
76	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012, 22, 1658-1667.	2.4	166
77	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.	1.5	165
78	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008, 18, 1906-1917.	2.4	163
79	Genetic analysis of variation in transcription factor binding in yeast. <i>Nature</i> , 2010, 464, 1187-1191.	13.7	162
80	Protein complexes take the bait. <i>Nature</i> , 2002, 415, 123-124.	13.7	161
81	Advances in functional protein microarray technology. <i>FEBS Journal</i> , 2005, 272, 5400-5411.	2.2	160
82	Nucleotide-resolution analysis of structural variants using BreakSeq and a breakpoint library. <i>Nature Biotechnology</i> , 2010, 28, 47-55.	9.4	158
83	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.	2.6	158
84	Microarrays to characterize protein interactions on a whole-proteome scale. <i>Proteomics</i> , 2003, 3, 2190-2199.	1.3	155
85	Target hub proteins serve as master regulators of development in yeast. <i>Genes and Development</i> , 2006, 20, 435-448.	2.7	153
86	ChIP-chip: A genomic approach for identifying transcription factor binding sites. <i>Methods in Enzymology</i> , 2002, 350, 469-483.	0.4	151
87	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
88	GATA-1 binding sites mapped in the $\hat{\text{A}}$ -globin locus by using mammalian chlp-chip analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2924-2929.	3.3	149
89	Dynamic trans-Acting Factor Colocalization in Human Cells. <i>Cell</i> , 2013, 155, 713-724.	13.5	142
90	Integrated systems analysis reveals a molecular network underlying autism spectrum disorders. <i>Molecular Systems Biology</i> , 2014, 10, 774.	3.2	138

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91	Efficient yeast CHIP-Seq using multiplex short-read DNA sequencing. <i>BMC Genomics</i> , 2009, 10, 37.	1.2	137
92	Landscape of cohesin-mediated chromatin loops in the human genome. <i>Nature</i> , 2020, 583, 737-743.	13.7	134
93	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016, 24, 172-184.	7.2	133
94	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.	3.3	131
95	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.	2.4	126
96	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.	3.3	125
97	Charging it up: global analysis of protein phosphorylation. <i>Trends in Genetics</i> , 2006, 22, 545-554.	2.9	123
98	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.	3.3	121
99	Personal genome sequencing: current approaches and challenges. <i>Genes and Development</i> , 2010, 24, 423-431.	2.7	119
100	Systematic evaluation of variability in ChIP-chip experiments using predefined DNA targets. <i>Genome Research</i> , 2008, 18, 393-403.	2.4	117
101	Regulatory analysis of the <i>C. elegans</i> genome with spatiotemporal resolution. <i>Nature</i> , 2014, 512, 400-405.	13.7	115
102	Impact of Chromatin Structures on DNA Processing for Genomic Analyses. <i>PLoS ONE</i> , 2009, 4, e6700.	1.1	115
103	GENOMICS: Defining Genes in the Genomics Era. <i>Science</i> , 2003, 300, 258-260.	6.0	114
104	An integrated approach for finding overlooked genes in yeast. <i>Nature Biotechnology</i> , 2002, 20, 58-63.	9.4	112
105	Predicting essential genes in fungal genomes. <i>Genome Research</i> , 2006, 16, 1126-1135.	2.4	109
106	Detecting and annotating genetic variations using the HugeSeq pipeline. <i>Nature Biotechnology</i> , 2012, 30, 226-229.	9.4	104
107	High-Resolution Copy-Number Variation Map Reflects Human Olfactory Receptor Diversity and Evolution. <i>PLoS Genetics</i> , 2008, 4, e1000249.	1.5	99
108	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.	1.5	97

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109	Emerging technologies in yeast genomics. <i>Nature Reviews Genetics</i> , 2001, 2, 302-312.	7.7	96
110	Global changes in STAT target selection and transcription regulation upon interferon treatments. <i>Genes and Development</i> , 2005, 19, 2953-2968.	2.7	95
111	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. <i>Bioinformatics</i> , 2011, 27, 281-283.	1.8	93
112	Full-Length Isoform Sequencing Reveals Novel Transcripts and Substantial Transcriptional Overlaps in a Herpesvirus. <i>PLoS ONE</i> , 2016, 11, e0162868.	1.1	93
113	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.	2.6	92
114	Construction and Analysis of an Integrated Regulatory Network Derived from High-Throughput Sequencing Data. <i>PLoS Computational Biology</i> , 2011, 7, e1002190.	1.5	92
115	Characterization of Enhancer Function from Genome-Wide Analyses. <i>Annual Review of Genomics and Human Genetics</i> , 2012, 13, 29-57.	2.5	86
116	Omics Profiling in Precision Oncology. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2525-2536.	2.5	84
117	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.	3.2	79
118	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.	3.3	78
119	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.	3.9	78
120	A highly integrated and complex PPARGC1A transcription factor binding network in HepG2 cells. <i>Genome Research</i> , 2012, 22, 1668-1679.	2.4	75
121	Global analysis of gene expression in yeast. <i>Functional and Integrative Genomics</i> , 2002, 2, 171-180.	1.4	74
122	Negative regulation of calcineurin signaling by Hrr25p, a yeast homolog of casein kinase I. <i>Genes and Development</i> , 2003, 17, 2698-2708.	2.7	74
123	Omics™ approaches for unraveling signaling networks. <i>Current Opinion in Cell Biology</i> , 2002, 14, 173-179.	2.6	73
124	AGAPE (Automated Genome Analysis Pipeline) for Pan-Genome Analysis of <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2015, 10, e0120671.	1.1	73
125	Applications of DNA tiling arrays to experimental genome annotation and regulatory pathway discovery. <i>Chromosome Research</i> , 2005, 13, 259-274.	1.0	72
126	Modeling CHIP Sequencing In Silico with Applications. <i>PLoS Computational Biology</i> , 2008, 4, e1000158.	1.5	70



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127	Regulatory Variation Within and Between Species. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 327-346.	2.5	70
128	Proteome chips for whole-organism assays. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 617-622.	16.1	69
129	A novel mitochondrial protein, Tar1p, is encoded on the antisense strand of the nuclear 25S rDNA. <i>Genes and Development</i> , 2002, 16, 2755-2760.	2.7	67
130	iPOP Goes the World: Integrated Personalized Omics Profiling and the Road toward Improved Health Care. <i>Chemistry and Biology</i> , 2013, 20, 660-666.	6.2	67
131	Microfluidic isoform sequencing shows widespread splicing coordination in the human transcriptome. <i>Genome Research</i> , 2018, 28, 231-242.	2.4	64
132	Multi-Platform Sequencing Approach Reveals a Novel Transcriptome Profile in Pseudorabies Virus. <i>Frontiers in Microbiology</i> , 2018, 8, 2708.	1.5	64
133	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.	3.3	63
134	Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE). <i>Genome Research</i> , 2007, 17, 910-916.	2.4	61
135	Proteome-wide survey of the autoimmune target repertoire in autoimmune polyendocrine syndrome type 1. <i>Scientific Reports</i> , 2016, 6, 20104.	1.6	61
136	Diverse protein kinase interactions identified by protein microarrays reveal novel connections between cellular processes. <i>Genes and Development</i> , 2011, 25, 767-778.	2.7	60
137	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 387-397.	0.8	59
138	Extensive Transcript Diversity and Novel Upstream Open Reading Frame Regulation in Yeast. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 343-352.	0.8	59
139	Genome-Wide Mapping of Copy Number Variation in Humans: Comparative Analysis of High Resolution Array Platforms. <i>PLoS ONE</i> , 2011, 6, e27859.	1.1	59
140	Identification of genomic indels and structural variations using split reads. <i>BMC Genomics</i> , 2011, 12, 375.	1.2	57
141	Statistical analysis of the genomic distribution and correlation of regulatory elements in the ENCODE regions. <i>Genome Research</i> , 2007, 17, 787-797.	2.4	56
142	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.	13.9	53
143	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.	3.3	53
144	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.	2.4	50

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145	Comparative annotation of functional regions in the human genome using epigenomic data. <i>Nucleic Acids Research</i> , 2013, 41, 4423-4432.	6.5	50
146	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
147	Design optimization methods for genomic DNA tiling arrays. <i>Genome Research</i> , 2005, 16, 271-281.	2.4	46
148	ProCAT: a data analysis approach for protein microarrays. <i>Genome Biology</i> , 2006, 7, R110.	13.9	46
149	Systems biology from a yeast omics perspective. <i>FEBS Letters</i> , 2009, 583, 3895-3899.	1.3	46
150	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.	3.3	44
151	Multiple Long-Read Sequencing Survey of Herpes Simplex Virus Dynamic Transcriptome. <i>Frontiers in Genetics</i> , 2019, 10, 834.	1.1	44
152	Personal phenotypes to go with personal genomes. <i>Molecular Systems Biology</i> , 2009, 5, 273.	3.2	41
153	Proteomic Approaches for the Global Analysis of Proteins. <i>BioTechniques</i> , 2002, 33, 1308-1316.	0.8	40
154	Investigating metabolite-protein interactions: An overview of available techniques. <i>Methods</i> , 2012, 57, 459-466.	1.9	40
155	ExpressYourself: a modular platform for processing and visualizing microarray data. <i>Nucleic Acids Research</i> , 2003, 31, 3477-3482.	6.5	38
156	RNA polymerase II stalling: loading at the start prepares genes for a sprint. <i>Genome Biology</i> , 2008, 9, 220.	13.9	38
157	Yeast as a Model for Human Disease. <i>Current Protocols in Human Genetics</i> , 2006, 48, Unit 15.6.	3.5	36
158	Metabolites as global regulators: A new view of protein regulation. <i>BioEssays</i> , 2011, 33, 485-489.	1.2	36
159	Global analysis of protein function using protein microarrays. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 171-175.	2.2	35
160	[33] High-throughput methods for the large-scale analysis of gene function by transposon tagging. <i>Methods in Enzymology</i> , 2000, 328, 550-574.	0.4	34
161	Large-scale mutagenesis: yeast genetics in the genome era. <i>Current Opinion in Biotechnology</i> , 2001, 12, 28-34.	3.3	34
162	MSB: A mean-shift-based approach for the analysis of structural variation in the genome. <i>Genome Research</i> , 2009, 19, 106-117.	2.4	33

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163	Systematic investigation of protein–small molecule interactions. <i>IUBMB Life</i> , 2013, 65, 2-8.	1.5	33
164	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.	1.8	32
165	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, 345-356.	1.4	31
166	Integrated analysis of experimental data sets reveals many novel promoters in 1% of the human genome. <i>Genome Research</i> , 2007, 17, 720-731.	2.4	31
167	Yeast proteomics and protein microarrays. <i>Journal of Proteomics</i> , 2010, 73, 2147-2157.	1.2	31
168	Proteogenomic Analysis of Human Colon Carcinoma Cell Lines LIM1215, LIM1899, and LIM2405. <i>Journal of Proteome Research</i> , 2013, 12, 1732-1742.	1.8	30
169	Personal genomes, quantitative dynamic omics and personalized medicine. <i>Quantitative Biology</i> , 2013, 1, 71-90.	0.3	29
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