

## List of Publications by Year in descending order

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310  
papers

88,157  
citations

1172

111  
h-index

329

287  
g-index

316  
all docs

316  
docs citations

316  
times ranked

76617  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	27.8	3,938
3	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
4	Functional Characterization of the <i>Saccharomyces cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. <i>Science</i> , 1999, 285, 901-906.	12.6	3,761
5	Fully integrated wearable sensor arrays for multiplexed in situ perspiration analysis. <i>Nature</i> , 2016, 529, 509-514.	27.8	3,508
6	Genomic responses in mouse models poorly mimic human inflammatory diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3507-3512.	7.1	2,518
7	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	9.7	1,927
8	Genome Sequence of an Obligate Intracellular Pathogen of Humans: <i>Chlamydia trachomatis</i> . <i>Science</i> , 1998, 282, 754-759.	12.6	1,449
9	A network-based analysis of systemic inflammation in humans. <i>Nature</i> , 2005, 437, 1032-1037.	27.8	1,419
10	[31] Electron microscope heteroduplex methods for mapping regions of base sequence homology in nucleic acids. <i>Methods in Enzymology</i> , 1971, 21, 413-428.	1.0	1,205
11	Sterile host yeasts (SHY): A eukaryotic system of biological containment for recombinant DNA experiments. <i>Gene</i> , 1979, 8, 17-24.	2.2	1,086
12	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , 2011, 208, 2581-2590.	8.5	1,040
13	Y chromosome sequence variation and the history of human populations. <i>Nature Genetics</i> , 2000, 26, 358-361.	21.4	935
14	Studies on the cleavage of bacteriophage lambda DNA with EcoRI restriction endonuclease. <i>Journal of Molecular Biology</i> , 1975, 91, 315-328.	4.2	910
15	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. <i>Science</i> , 2008, 320, 362-365.	12.6	892
16	Empirical Analysis of Transcriptional Activity in the <i>Arabidopsis</i> Genome. <i>Science</i> , 2003, 302, 842-846.	12.6	853
17	Gene Expression During the Life Cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 297, 2270-2275.	12.6	843
18	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003, 421, 63-66.	27.8	790

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19	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	21.4	765
20	Replication Dynamics of the Yeast Genome. <i>Science</i> , 2001, 294, 115-121.	12.6	736
21	The diploid genome sequence of <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7329-7334.	7.1	692
22	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	12.6	664
23	Comparative genomes of <i>Chlamydia pneumoniae</i> and <i>C. trachomatis</i> . <i>Nature Genetics</i> , 1999, 21, 385-389.	21.4	636
24	Evidence for transposition of dispersed repetitive DNA families in yeast. <i>Cell</i> , 1979, 16, 739-751.	28.9	619
25	Detection of Numerous Y Chromosome Biallelic Polymorphisms by Denaturing High-Performance Liquid Chromatography. <i>Genome Research</i> , 1997, 7, 996-1005.	5.5	617
26	A high-resolution map of transcription in the yeast genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5320-5325.	7.1	613
27	[49] Rapid DNA isolations for enzymatic and hybridization analysis. <i>Methods in Enzymology</i> , 1980, 65, 404-411.	1.0	610
28	Autonomous sweat extraction and analysis applied to cystic fibrosis and glucose monitoring using a fully integrated wearable platform. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4625-4630.	7.1	573
29	The poly(A) binding protein is required for poly(A) shortening and 60S ribosomal subunit-dependent translation initiation. <i>Cell</i> , 1989, 58, 857-867.	28.9	559
30	Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular bar-coding strategy. <i>Nature Genetics</i> , 1996, 14, 450-456.	21.4	545
31	Significance analysis of time course microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12837-12842.	7.1	534
32	Genomic profiling of drug sensitivities via induced haploinsufficiency. <i>Nature Genetics</i> , 1999, 21, 278-283.	21.4	533
33	Dissecting the architecture of a quantitative trait locus in yeast. <i>Nature</i> , 2002, 416, 326-330.	27.8	524
34	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002, 31, 400-404.	21.4	503
35	Multiplexed genotyping with sequence-tagged molecular inversion probes. <i>Nature Biotechnology</i> , 2003, 21, 673-678.	17.5	502
36	Identification of the SAAT Gene Involved in Strawberry Flavor Biogenesis by Use of DNA Microarrays. <i>Plant Cell</i> , 2000, 12, 647-661.	6.6	496

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37	A Genome-Wide Study of Gene Activity Reveals Developmental Signaling Pathways in the Preimplantation Mouse Embryo. <i>Developmental Cell</i> , 2004, 6, 133-144.	7.0	481
38	A Wearable Electrochemical Platform for Noninvasive Simultaneous Monitoring of Ca <sup>2+</sup> and pH. <i>ACS Nano</i> , 2016, 10, 7216-7224.	14.6	480
39	Single Cell Profiling of Circulating Tumor Cells: Transcriptional Heterogeneity and Diversity from Breast Cancer Cell Lines. <i>PLoS ONE</i> , 2012, 7, e33788.	2.5	475
40	Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 793-798.	7.1	460
41	Mechanisms of Haploinsufficiency Revealed by Genome-Wide Profiling in Yeast. <i>Genetics</i> , 2005, 169, 1915-1925.	2.9	460
42	Isolating highly enriched populations of circulating epithelial cells and other rare cells from blood using a magnetic sweeper device. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3970-3975.	7.1	448
43	The core meiotic transcriptome in budding yeasts. <i>Nature Genetics</i> , 2000, 26, 415-423.	21.4	430
44	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001, 27, 48-54.	21.4	399
45	The organization and transcription of the galactose gene cluster of <i>Saccharomyces</i> . <i>Journal of Molecular Biology</i> , 1981, 152, 285-315.	4.2	378
46	Direct Allelic Variation Scanning of the Yeast Genome. , 1998, 281, 1194-1197.		368
47	Genes for the major protein antigens of the leprosy parasite <i>Mycobacterium leprae</i> . <i>Nature</i> , 1985, 316, 450-452.	27.8	365
48	Yeast centromere binding protein CBF1, of the helix-loop-helix protein family, is required for chromosome stability and methionine prototrophy. <i>Cell</i> , 1990, 61, 437-446.	28.9	360
49	Isolation of galactose-inducible DNA sequences from <i>Saccharomyces cerevisiae</i> by differential plaque filter hybridization. <i>Cell</i> , 1979, 16, 443-452.	28.9	338
50	Resolution of DNA molecules greater than 5 megabases by contour-clamped homogeneous electric fields. <i>Nucleic Acids Research</i> , 1987, 15, 7865-7876.	14.5	338
51	Transcriptional Profiling of Aging in Human Muscle Reveals a Common Aging Signature. <i>PLoS Genetics</i> , 2006, 2, e115.	3.5	331
52	Centromeric DNA from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1982, 158, 157-179.	4.2	317
53	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	21.4	294
54	Ultra-High-Efficiency Strong Cation Exchange LC/RPLC/MS/MS for High Dynamic Range Characterization of the Human Plasma Proteome. <i>Analytical Chemistry</i> , 2004, 76, 1134-1144.	6.5	290

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55	A Transcriptional Profile of Aging in the Human Kidney. <i>PLoS Biology</i> , 2004, 2, e427.	5.6	281
56	Microbes on the human vaginal epithelium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7952-7957.	7.1	281
57	Highly multiplexed molecular inversion probe genotyping: Over 10,000 targeted SNPs genotyped in a single tube assay. <i>Genome Research</i> , 2005, 15, 269-275.	5.5	276
58	Metabolic specialization associated with phenotypic switching in <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14907-14912.	7.1	271
59	Multiplex protein assays based on real-time magnetic nanotag sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20637-20640.	7.1	271
60	Functional selection and analysis of yeast centromeric DNA. <i>Cell</i> , 1985, 42, 913-921.	28.9	270
61	A study in evolution: the DNA base sequence homology between coliphages T7 and T3. <i>Journal of Molecular Biology</i> , 1971, 62, 287-301.	4.2	261
62	Genome-wide mapping with biallelic markers in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 1999, 23, 203-207.	21.4	260
63	Analysis of chromosomal integration and deletions of yeast plasmids. <i>Nucleic Acids Research</i> , 1977, 4, 1429-1448.	14.5	259
64	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. <i>Reproductive Sciences</i> , 2014, 21, 32-40.	2.5	259
65	A family of versatile centromeric vectors designed for use in the sectoring-shuffle mutagenesis assay in <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 1988, 70, 303-312.	2.2	253
66	Quantitative trait loci mapped to single-nucleotide resolution in yeast. <i>Nature Genetics</i> , 2005, 37, 1333-1340.	21.4	242
67	Regulatory networks affected by iron availability in <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 2004, 53, 1451-1469.	2.5	240
68	Genome sequencing and comparative analysis of <i>Saccharomyces cerevisiae</i> strain YJM789. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12825-12830.	7.1	240
69	Application of genome-wide expression analysis to human health and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4801-4806.	7.1	238
70	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	27.8	234
71	Transcriptional response of <i>Saccharomyces cerevisiae</i> to DNA-damaging agents does not identify the genes that protect against these agents. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8778-8783.	7.1	234
72	A physical study by electron microscopy of the terminally repetitious, circularly permuted DNA from the coliphage particles of <i>Escherichia coli</i> 15. <i>Journal of Molecular Biology</i> , 1970, 48, 1-22.	4.2	229

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73	A Simple Procedure for the Analysis of Single Nucleotide Polymorphisms Facilitates Map-Based Cloning in Arabidopsis. <i>Plant Physiology</i> , 2000, 124, 1483-1492.	4.8	227
74	Bent DNA at a yeast autonomously replicating sequence. <i>Nature</i> , 1986, 324, 87-89.	27.8	218
75	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	12.6	217
76	Detection of single micron-sized magnetic bead and magnetic nanoparticles using spin valve sensors for biological applications. <i>Journal of Applied Physics</i> , 2003, 93, 7557-7559.	2.5	211
77	Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. <i>Nature Genetics</i> , 2007, 39, 1092-1099.	21.4	207
78	High-throughput, high-fidelity HLA genotyping with deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8676-8681.	7.1	200
79	The mouse mahogany locus encodes a transmembrane form of human attractin. <i>Nature</i> , 1999, 398, 152-156.	27.8	194
80	Unique arrangement of coding sequences for 5 S, 5.8 S, 18 S and 25 S ribosomal RNA in <i>Saccharomyces cerevisiae</i> as determined by R-loop and hybridization analysis. <i>Journal of Molecular Biology</i> , 1978, 123, 387-404.	4.2	193
81	Functional genomics of genes with small open reading frames (sORFs) in <i>S. cerevisiae</i> . <i>Genome Research</i> , 2006, 16, 365-373.	5.5	193
82	Magnetic levitation of single cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3661-8.	7.1	192
83	Current Rectification with Poly-L-Lysine-Coated Quartz Nanopipettes. <i>Nano Letters</i> , 2006, 6, 2486-2492.	9.1	188
84	Whole blood and leukocyte RNA isolation for gene expression analyses. <i>Physiological Genomics</i> , 2004, 19, 247-254.	2.3	186
85	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	5.6	181
86	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000113.	3.5	181
87	An integrated platform of genomic assays reveals small-molecule bioactivities. <i>Nature Chemical Biology</i> , 2008, 4, 498-506.	8.0	178
88	Deletion mutants of bacteriophage lambda. <i>Journal of Molecular Biology</i> , 1971, 56, 403-423.	4.2	174
89	Multiplexed protein detection by proximity ligation for cancer biomarker validation. <i>Nature Methods</i> , 2007, 4, 327-329.	19.0	169
90	Clinical microfluidics for neutrophil genomics and proteomics. <i>Nature Medicine</i> , 2010, 16, 1042-1047.	30.7	168

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91	HEx: A heterologous expression platform for the discovery of fungal natural products. <i>Science Advances</i> , 2018, 4, eaar5459.	10.3	167
92	Quantitative CRISPR interference screens in yeast identify chemical-genetic interactions and new rules for guide RNA design. <i>Genome Biology</i> , 2016, 17, 45.	8.8	165
93	[7] $\hat{\mu}$ gt 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	1.0	161
94	Multigene amplification and massively parallel sequencing for cancer mutation discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9387-9392.	7.1	159
95	Nonlinear partial differential equations and applications: Parallel phenotypic analysis of sporulation and postgermination growth in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15530-15535.	7.1	157
96	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using $^{16}\text{O}/^{18}\text{O}$ Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	3.8	156
97	Transcription of the <i>his3</i> gene region in <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1981, 152, 535-552.	4.2	152
98	Single DNA Molecule Detection Using Nanopipettes and Nanoparticles. <i>Nano Letters</i> , 2005, 5, 403-407.	9.1	152
99	Label-free biosensing with functionalized nanopipette probes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4611-4616.	7.1	152
100	Profiling early infection responses: <i>Pseudomonas aeruginosa</i> eludes host defenses by suppressing antimicrobial peptide gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2573-2578.	7.1	149
101	Microfluidic Point-of-Care Testing: Commercial Landscape and Future Directions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 602659.	4.1	146
102	Sequential Elimination of Major-Effect Contributors Identifies Additional Quantitative Trait Loci Conditioning High-Temperature Growth in Yeast. <i>Genetics</i> , 2008, 180, 1661-1670.	2.9	145
103	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	3.5	144
104	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	3.8	142
105	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	17.5	138
106	Cloning of the yeast ribosomal DNA repeat unit in <i>Sst</i> I and <i>Hind</i> III lambda vectors using genetic and physical size selections. <i>Journal of Molecular Biology</i> , 1978, 123, 371-386.	4.2	136
107	A Genome-Wide Screen for Regulators of TORC1 in Response to Amino Acid Starvation Reveals a Conserved Npr2/3 Complex. <i>PLoS Genetics</i> , 2009, 5, e1000515.	3.5	134
108	Sister-chromatid cohesion mediated by the alternative RF-CCtf18/Dcc1/Ctf8, the helicase Chl1 and the polymerase- $\alpha$ -associated protein Ctf4 is essential for chromatid disjunction during meiosis II. <i>Journal of Cell Science</i> , 2004, 117, 3547-3559.	2.0	130

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109	A physical, genetic and transcriptional map of the cloned his3 gene region of <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1980, 136, 309-332.	4.2	128
110	Comparative proteome analyses of human plasma following <i>in vivo</i> lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. <i>Proteomics</i> , 2005, 5, 572-584.	2.2	125
111	Execution of the meiotic noncoding RNA expression program and the onset of gametogenesis in yeast require the conserved exosome subunit Rrp6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1058-1063.	7.1	124
112	The dynamics of the vaginal microbiome during infertility therapy with <i>in vitro</i> fertilization-embryo transfer. <i>Journal of Assisted Reproduction and Genetics</i> , 2012, 29, 105-115.	2.5	124
113	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	7.1	122
114	Evidence-Based Annotation of Gene Function in <i>Shewanella oneidensis</i> MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. <i>PLoS Genetics</i> , 2011, 7, e1002385.	3.5	119
115	High-density yeast-tiling array reveals previously undiscovered introns and extensive regulation of meiotic splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 1522-1527.	7.1	116
116	Digital microfluidic assay for protein detection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2110-2115.	7.1	115
117	Sensitive giant magnetoresistive-based immunoassay for multiplex mycotoxin detection. <i>Biosensors and Bioelectronics</i> , 2010, 25, 1635-1639.	10.1	108
118	DMSO and Betaine Greatly Improve Amplification of GC-Rich Constructs in <i>De Novo</i> Synthesis. <i>PLoS ONE</i> , 2010, 5, e11024.	2.5	108
119	The Ume6 regulon coordinates metabolic and meiotic gene expression in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13431-13436.	7.1	107
120	Homology and structural relationships between the dimeric and monomeric circular forms of mitochondrial DNA from human leukemic leukocytes. <i>Journal of Molecular Biology</i> , 1970, 47, 137-153.	4.2	106
121	Cell-specific expression and pathway analyses reveal alterations in trauma-related human T cell and monocyte pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 15564-15569.	7.1	106
122	A unique and universal molecular barcode array. <i>Nature Methods</i> , 2006, 3, 601-603.	19.0	105
123	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. <i>Genome Research</i> , 2009, 19, 757-769.	5.5	104
124	Mice are not men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E345.	7.1	102
125	Bisphenol A Induces a Profile of Tumor Aggressiveness in High-Risk Cells from Breast Cancer Patients. <i>Cancer Research</i> , 2008, 68, 2076-2080.	0.9	101
126	Introns Regulate RNA and Protein Abundance in Yeast. <i>Genetics</i> , 2006, 174, 511-518.	2.9	99



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127	Systematic analysis of genome-wide fitness data in yeast reveals novel gene function and drug action. <i>Genome Biology</i> , 2010, 11, R30.	9.6	94
128	Global Analysis of ATM Polymorphism Reveals Significant Functional Constraint. <i>American Journal of Human Genetics</i> , 2001, 69, 396-412.	6.2	93
129	Single cell mutational analysis of PIK3CA in circulating tumor cells and metastases in breast cancer reveals heterogeneity, discordance, and mutation persistence in cultured disseminated tumor cells from bone marrow. <i>BMC Cancer</i> , 2014, 14, 456.	2.6	93
130	Benchmarking Outcomes in the Critically Injured Trauma Patient and the Effect of Implementing Standard Operating Procedures. <i>Annals of Surgery</i> , 2012, 255, 993-999.	4.2	92
131	Elevated evolutionary rates in the laboratory strain of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1092-1097.	7.1	90
132	Molecular indexing enables quantitative targeted RNA sequencing and reveals poor efficiencies in standard library preparations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1891-1896.	7.1	90
133	Functional expression of the yeast FLP/FRT site-specific recombination system in <i>Nicotiana tabacum</i> . <i>Molecular Genetics and Genomics</i> , 1994, 242, 653-657.	2.4	86
134	Deletion analysis of the <i>Saccharomyces GAL</i> gene cluster. <i>Journal of Molecular Biology</i> , 1981, 152, 317-334.	4.2	85
135	Gene Annotation and Drug Target Discovery in <i>Candida albicans</i> with a Tagged Transposon Mutant Collection. <i>PLoS Pathogens</i> , 2010, 6, e1001140.	4.7	85
136	Multiplexed Proximity Ligation Assays to Profile Putative Plasma Biomarkers Relevant to Pancreatic and Ovarian Cancer. <i>Clinical Chemistry</i> , 2008, 54, 582-589.	3.2	84
137	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004, 5, 190-201.	16.3	83
138	Composition, ultrastructure and function of the cutin- and suberin-containing layers in the leaf, fruit peel, juice-sac and inner seed coat of grapefruit ( <i>Citrus paradisi</i> Macfed.). <i>Planta</i> , 1980, 149, 498-511.	3.2	82
139	Whole-genome sequencing of the efficient industrial fuel-ethanol fermentative <i>Saccharomyces cerevisiae</i> strain CAT-1. <i>Molecular Genetics and Genomics</i> , 2012, 287, 485-494.	2.1	82
140	Reversion of a promoter deletion in yeast. <i>Nature</i> , 1982, 298, 815-819.	27.8	81
141	Allele quantification using molecular inversion probes (MIP). <i>Nucleic Acids Research</i> , 2005, 33, e183-e183.	14.5	81
142	Multiplex Pyrosequencing. <i>Nucleic Acids Research</i> , 2002, 30, 31e-31.	14.5	74
143	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. <i>PLoS Computational Biology</i> , 2009, 5, e1000374.	3.2	74
144	SPA1: A gene important for chromosome segregation and other mitotic functions in <i>S. cerevisiae</i> . <i>Cell</i> , 1988, 54, 743-754.	28.9	72

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145	Direct electrical detection of DNA synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6466-6470.	7.1	72
146	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. Genetics, 2009, 183, 185-194.	2.9	71
147	Noninvasive wearable electroactive pharmaceutical monitoring for personalized therapeutics. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19017-19025.	7.1	71
148	Isolation of bacteriophage $\phi$ containing yeast ribosomal RNA genes: Screening by in situ RNA hybridization to plaques. Cell, 1976, 8, 227-232.	28.9	70
149	Characterization of synthetic DNA bar codes in <i>Saccharomyces cerevisiae</i> gene-deletion strains. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11046-11051.	7.1	69
150	ATP hydrolysis and the displaced strand are two factors that determine the polarity of RecA-promoted DNA strand exchange. Journal of Molecular Biology, 1992, 227, 38-53.	4.2	62
151	Multiplex assay for condition-dependent changes in protein-protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9213-9218.	7.1	62
152	Genomic and Proteomic Determinants of Outcome in Patients Undergoing Thoracoabdominal Aortic Aneurysm Repair. Journal of Immunology, 2004, 172, 7103-7109.	0.8	61
153	Microneedle biosensor: A method for direct label-free real time protein detection. Sensors and Actuators B: Chemical, 2013, 177, 848-855.	7.8	60
154	Cloning vectors for the synthesis of epitope-tagged, truncated and chimeric proteins in <i>Saccharomyces cerevisiae</i> . Gene, 1994, 144, 63-68.	2.2	59
155	Functional analysis of the yeast genome. Current Opinion in Genetics and Development, 1997, 7, 771-776.	3.3	59
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