

List of Publications by Year in descending order

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310
papers

88,157
citations

1163

111
h-index

339

285
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.	13.7	21,074
2	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	13.7	3,938
3	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	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.	6.0	3,761
5	Fully integrated wearable sensor arrays for multiplexed in situ perspiration analysis. <i>Nature</i> , 2016, 529, 509-514.	13.7	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.	3.3	2,518
7	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	4.5	1,927
8	Genome Sequence of an Obligate Intracellular Pathogen of Humans: <i>Chlamydia trachomatis</i> . , 1998, 282, 754-759.		1,449
9	A network-based analysis of systemic inflammation in humans. <i>Nature</i> , 2005, 437, 1032-1037.	13.7	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.	0.4	1,205
11	Sterile host yeasts (SHY): A eukaryotic system of biological containment for recombinant DNA experiments. <i>Gene</i> , 1979, 8, 17-24.	1.0	1,086
12	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , 2011, 208, 2581-2590.	4.2	1,040
13	Y chromosome sequence variation and the history of human populations. <i>Nature Genetics</i> , 2000, 26, 358-361.	9.4	935
14	Studies on the cleavage of bacteriophage lambda DNA with EcoRI restriction endonuclease. <i>Journal of Molecular Biology</i> , 1975, 91, 315-328.	2.0	910
15	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. <i>Science</i> , 2008, 320, 362-365.	6.0	892
16	Empirical Analysis of Transcriptional Activity in the <i>Arabidopsis</i> Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
17	Gene Expression During the Life Cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 297, 2270-2275.	6.0	843
18	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003, 421, 63-66.	13.7	790

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19	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	9.4	765
20	Replication Dynamics of the Yeast Genome. <i>Science</i> , 2001, 294, 115-121.	6.0	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.	3.3	692
22	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664
23	Comparative genomes of <i>Chlamydia pneumoniae</i> and <i>C. trachomatis</i> . <i>Nature Genetics</i> , 1999, 21, 385-389.	9.4	636
24	Evidence for transposition of dispersed repetitive DNA families in yeast. <i>Cell</i> , 1979, 16, 739-751.	13.5	619
25	Detection of Numerous Y Chromosome Biallelic Polymorphisms by Denaturing High-Performance Liquid Chromatography. <i>Genome Research</i> , 1997, 7, 996-1005.	2.4	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.	3.3	613
27	[49] Rapid DNA isolations for enzymatic and hybridization analysis. <i>Methods in Enzymology</i> , 1980, 65, 404-411.	0.4	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.	3.3	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.	13.5	559
30	Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular barcoding strategy. <i>Nature Genetics</i> , 1996, 14, 450-456.	9.4	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.	3.3	534
32	Genomic profiling of drug sensitivities via induced haploinsufficiency. <i>Nature Genetics</i> , 1999, 21, 278-283.	9.4	533
33	Dissecting the architecture of a quantitative trait locus in yeast. <i>Nature</i> , 2002, 416, 326-330.	13.7	524
34	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002, 31, 400-404.	9.4	503
35	Multiplexed genotyping with sequence-tagged molecular inversion probes. <i>Nature Biotechnology</i> , 2003, 21, 673-678.	9.4	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.	3.1	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.	3.1	481
38	A Wearable Electrochemical Platform for Noninvasive Simultaneous Monitoring of Ca ²⁺ and pH. <i>ACS Nano</i> , 2016, 10, 7216-7224.	7.3	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.	1.1	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.	3.3	460
41	Mechanisms of Haploinsufficiency Revealed by Genome-Wide Profiling in Yeast. <i>Genetics</i> , 2005, 169, 1915-1925.	1.2	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.	3.3	448
43	The core meiotic transcriptome in budding yeasts. <i>Nature Genetics</i> , 2000, 26, 415-423.	9.4	430
44	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001, 27, 48-54.	9.4	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.	2.0	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.	13.7	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.	13.5	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.	13.5	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.	6.5	338
51	Transcriptional Profiling of Aging in Human Muscle Reveals a Common Aging Signature. <i>PLoS Genetics</i> , 2006, 2, e115.	1.5	331
52	Centromeric DNA from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1982, 158, 157-179.	2.0	317
53	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	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.	3.2	290

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55	A Transcriptional Profile of Aging in the Human Kidney. PLoS Biology, 2004, 2, e427.	2.6	281
56	Microbes on the human vaginal epithelium. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7952-7957.	3.3	281
57	Highly multiplexed molecular inversion probe genotyping: Over 10,000 targeted SNPs genotyped in a single tube assay. Genome Research, 2005, 15, 269-275.	2.4	276
58	Metabolic specialization associated with phenotypic switching in <i>Candida albicans</i> . Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14907-14912.	3.3	271
59	Multiplex protein assays based on real-time magnetic nanotag sensing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20637-20640.	3.3	271
60	Functional selection and analysis of yeast centromeric DNA. Cell, 1985, 42, 913-921.	13.5	270
61	A study in evolution: the DNA base sequence homology between coliphages T7 and T3. Journal of Molecular Biology, 1971, 62, 287-301.	2.0	261
62	Genome-wide mapping with biallelic markers in <i>Arabidopsis thaliana</i> . Nature Genetics, 1999, 23, 203-207.	9.4	260
63	Analysis of chromosomal integration and deletions of yeast plasmids. Nucleic Acids Research, 1977, 4, 1429-1448.	6.5	259
64	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. Reproductive Sciences, 2014, 21, 32-40.	1.1	259
65	A family of versatile centromeric vectors designed for use in the sectoring-shuffle mutagenesis assay in <i>Saccharomyces cerevisiae</i> . Gene, 1988, 70, 303-312.	1.0	253
66	Quantitative trait loci mapped to single-nucleotide resolution in yeast. Nature Genetics, 2005, 37, 1333-1340.	9.4	242
67	Regulatory networks affected by iron availability in <i>Candida albicans</i> . Molecular Microbiology, 2004, 53, 1451-1469.	1.2	240
68	Genome sequencing and comparative analysis of <i>Saccharomyces cerevisiae</i> strain YJM789. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12825-12830.	3.3	240
69	Application of genome-wide expression analysis to human health and disease. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4801-4806.	3.3	238
70	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . Nature, 2000, 408, 816-820.	13.7	234
71	Transcriptional response of <i>Saccharomyces cerevisiae</i> to DNA-damaging agents does not identify the genes that protect against these agents. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8778-8783.	3.3	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. Journal of Molecular Biology, 1970, 48, 1-22.	2.0	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.	2.3	227
74	Bent DNA at a yeast autonomously replicating sequence. <i>Nature</i> , 1986, 324, 87-89.	13.7	218
75	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	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.	1.1	211
77	Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. <i>Nature Genetics</i> , 2007, 39, 1092-1099.	9.4	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.	3.3	200
79	The mouse mahogany locus encodes a transmembrane form of human attractin. <i>Nature</i> , 1999, 398, 152-156.	13.7	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.	2.0	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.	2.4	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.	3.3	192
83	Current Rectification with Poly-L-Lysine-Coated Quartz Nanopipettes. <i>Nano Letters</i> , 2006, 6, 2486-2492.	4.5	188
84	Whole blood and leukocyte RNA isolation for gene expression analyses. <i>Physiological Genomics</i> , 2004, 19, 247-254.	1.0	186
85	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	2.6	181
86	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000113.	1.5	181
87	An integrated platform of genomic assays reveals small-molecule bioactivities. <i>Nature Chemical Biology</i> , 2008, 4, 498-506.	3.9	178
88	Deletion mutants of bacteriophage lambda. <i>Journal of Molecular Biology</i> , 1971, 56, 403-423.	2.0	174
89	Multiplexed protein detection by proximity ligation for cancer biomarker validation. <i>Nature Methods</i> , 2007, 4, 327-329.	9.0	169
90	Clinical microfluidics for neutrophil genomics and proteomics. <i>Nature Medicine</i> , 2010, 16, 1042-1047.	15.2	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.	4.7	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.	3.8	165
93	[7] $\hat{\mu}$ gt 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	0.4	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.	3.3	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.	3.3	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.	2.5	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.	2.0	152
98	Single DNA Molecule Detection Using Nanopipettes and Nanoparticles. <i>Nano Letters</i> , 2005, 5, 403-407.	4.5	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.	3.3	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.	3.3	149
101	Microfluidic Point-of-Care Testing: Commercial Landscape and Future Directions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 602659.	2.0	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.	1.2	145
103	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
104	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
105	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	9.4	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.	2.0	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.	1.5	134
108	Sister-chromatid cohesion mediated by the alternative RF-CCtf18/Dcc1/Ctf8, the helicase Chl1 and the polymerase- α -associated protein Ctf4 is essential for chromatid disjunction during meiosis II. <i>Journal of Cell Science</i> , 2004, 117, 3547-3559.	1.2	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.	2.0	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.	1.3	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.	3.3	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.	1.2	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.	3.3	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.	1.5	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.	3.3	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.	3.3	115
117	Sensitive giant magnetoresistive-based immunoassay for multiplex mycotoxin detection. <i>Biosensors and Bioelectronics</i> , 2010, 25, 1635-1639.	5.3	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.	1.1	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.	3.3	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.	2.0	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.	3.3	106
122	A unique and universal molecular barcode array. <i>Nature Methods</i> , 2006, 3, 601-603.	9.0	105
123	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. <i>Genome Research</i> , 2009, 19, 757-769.	2.4	104
124	Mice are not men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E345.	3.3	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.	0.4	101
126	Introns Regulate RNA and Protein Abundance in Yeast. <i>Genetics</i> , 2006, 174, 511-518.	1.2	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.	13.9	94
128	Global Analysis of ATM Polymorphism Reveals Significant Functional Constraint. <i>American Journal of Human Genetics</i> , 2001, 69, 396-412.	2.6	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.	1.1	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.	2.1	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.	3.3	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.	3.3	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.	2.0	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.	2.1	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.	1.5	84
137	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004, 5, 190-201.	7.7	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.	1.6	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.	1.0	82
140	Reversion of a promoter deletion in yeast. <i>Nature</i> , 1982, 298, 815-819.	13.7	81
141	Allele quantification using molecular inversion probes (MIP). <i>Nucleic Acids Research</i> , 2005, 33, e183-e183.	6.5	81
142	Multiplex Pyrosequencing. <i>Nucleic Acids Research</i> , 2002, 30, 31e-31.	6.5	74
143	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. <i>PLoS Computational Biology</i> , 2009, 5, e1000374.	1.5	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.	13.5	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.	3.3	72
146	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. Genetics, 2009, 183, 185-194.	1.2	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.	3.3	71
148	Isolation of bacteriophage ϕ containing yeast ribosomal RNA genes: Screening by in situ RNA hybridization to plaques. Cell, 1976, 8, 227-232.	13.5	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.	3.3	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.	2.0	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.	3.3	62
152	Genomic and Proteomic Determinants of Outcome in Patients Undergoing Thoracoabdominal Aortic Aneurysm Repair. Journal of Immunology, 2004, 172, 7103-7109.	0.4	61
153	Microneedle biosensor: A method for direct label-free real time protein detection. Sensors and Actuators B: Chemical, 2013, 177, 848-855.	4.0	60
154	Cloning vectors for the synthesis of epitope-tagged, truncated and chimeric proteins in <i>Saccharomyces cerevisiae</i> . Gene, 1994, 144, 63-68.	1.0	59
155	Functional analysis of the yeast genome. Current Opinion in Genetics and Development, 1997, 7, 771-776.	1.5	59
156	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ^{18}O -Labeled α -Universal Reference Sample. Journal of Proteome Research, 2009, 8, 290-299.	1.8	59
157	Microfluidic diagnostic tool for the developing world: contactless impedance flow cytometry. Lab on A Chip, 2012, 12, 4499.	3.1	59
158	Computational identification and analysis of orphan assembly-line polyketide synthases. Journal of Antibiotics, 2014, 67, 89-97.	1.0	59
159	An electron microscopic method for studying and mapping the region of weak sequence homology between simian virus 40 and polyoma DNAs. Journal of Molecular Biology, 1975, 94, 135-149.	2.0	58
160	Sequence of Plasmodium falciparum chromosome 12. Nature, 2002, 419, 534-537.	13.7	58
161	Prediction of protein orientation upon immobilization on biological and nonbiological surfaces. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14773-14778.	3.3	56
162	Multiplex amplification of all coding sequences within 10 cancer genes by Gene-Collector. Nucleic Acids Research, 2007, 35, e47.	6.5	56

#	ARTICLE	IF	CITATIONS
163	Accelerating the Discovery of Biologically Active Small Molecules Using a High-Throughput Yeast Halo Assay. <i>Journal of Natural Products</i> , 2007, 70, 383-390.	1.5	56
164	Functional Genomics with a Comprehensive Library of Transposon Mutants for the Sulfate-Reducing Bacterium <i>Desulfovibrio alaskensis</i> G20. <i>MBio</i> , 2014, 5, e01041-14.	1.8	56
165	Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 States of America, 2015, 112, E4354-63.	3.3	56
166	Multifunctional, inexpensive, and reusable nanoparticle-printed biochip for cell manipulation and diagnosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1306-E1315.	3.3	55
167	A universal TagModule collection for parallel genetic analysis of microorganisms. <i>Nucleic Acids Research</i> , 2010, 38, e146-e146.	6.5	54
168	Plasma Proteome Response to Severe Burn Injury Revealed by ¹⁸ O-Labeled ϵ -Universal Reference-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 4779-4789.	1.8	54
169	Rare variant detection using family-based sequencing analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3985-3990.	3.3	54
170	High-quality DNA sequence capture of 524 disease candidate genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6549-6554.	3.3	52
171	Sequential Use of Transcriptional Profiling, Expression Quantitative Trait Mapping, and Gene Association Implicates MMP20 in Human Kidney Aging. <i>PLoS Genetics</i> , 2009, 5, e1000685.	1.5	50
172	Template-Independent Enzymatic Oligonucleotide Synthesis (TiEOS): Its History, Prospects, and Challenges. <i>Biochemistry</i> , 2018, 57, 1821-1832.	1.2	50
173	Data quality in genomics and microarrays. <i>Nature Biotechnology</i> , 2006, 24, 1112-1113.	9.4	48
174	Superoxide anions regulate TORC1 and its ability to bind Fpr1:rapamycin complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15166-15171.	3.3	48
175	A multi-enzyme model for pyrosequencing. <i>Nucleic Acids Research</i> , 2004, 32, e166-e166.	6.5	47
176	Promoter mutants of the yeast his3 gene. <i>Journal of Molecular Biology</i> , 1981, 152, 553-568.	2.0	46
177	Divergent transcription in the yeast ribosomal RNA coding region as shown by hybridization to separated strands and sequence analysis of cloned DNA. <i>Journal of Molecular Biology</i> , 1978, 123, 405-416.	2.0	45
178	Identification and preliminary characterization of mouse Adam33. <i>BMC Genetics</i> , 2002, 3, 2.	2.7	45
179	Determination of hepatitis C virus genotype by Pyrosequencing. <i>Journal of Virological Methods</i> , 2003, 109, 171-176.	1.0	45
180	On the in vivo function of the RecA ATPase 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 1999, 286, 437-445.	2.0	43

#	ARTICLE	IF	CITATIONS
181	Simulation and fabrication of a new novel 3D injectable biosensor for high throughput genomics and proteomics in a lab-on-a-chip device. <i>Nanotechnology</i> , 2013, 24, 465301.	1.3	43
182	Cloning of the yeast tyrosine transfer RNA genes in bacteriophage lambda. <i>Journal of Molecular Biology</i> , 1979, 127, 285-295.	2.0	42
183	A method for high-throughput production of sequence-verified <scp>DNA</scp> libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	3.2	41
184	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
185	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	3.9	39
186	Tunable control of antibody immobilization using electric field. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1995-1999.	3.3	39
187	Integrating Cell Phone Imaging with Magnetic Levitation (iâ€LEV) for Labelâ€Free Blood Analysis at the Pointâ€ofâ€Living. <i>Small</i> , 2016, 12, 1222-1229.	5.2	39
188	Toxic mutations in the recA gene of E. coli prevent proper chromosome segregation 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 1999, 286, 417-435.	2.0	38
189	Connector Inversion Probe Technology: A Powerful One-Primer Multiplex DNA Amplification System for Numerous Scientific Applications. <i>PLoS ONE</i> , 2007, 2, e915.	1.1	38
190	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. <i>Nucleic Acids Research</i> , 2011, 39, 44-58.	6.5	37
191	Label-free electronic probing of nucleic acids and proteins at the nanoscale using the nanoneedle biosensor. <i>Biomicrofluidics</i> , 2013, 7, 044114.	1.2	37
192	Chemical Composition and Ultrastructure of Suberin from Hollow Heart Tissue of Potato Tubers (<i>Solanum tuberosum</i>). <i>Plant Physiology</i> , 1977, 59, 1008-1010.	2.3	36
193	A dynamic network of transcription in LPS-treated human subjects. <i>BMC Systems Biology</i> , 2009, 3, 78.	3.0	36
194	Whole genome survey of coding SNPs reveals a reproducible pathway determinant of Parkinson disease. <i>Human Mutation</i> , 2009, 30, 228-238.	1.1	36
195	Electrical detection of protein biomarkers using bioactivated microfluidic channels. <i>Lab on A Chip</i> , 2009, 9, 1429.	3.1	36
196	Red blood cell deformability is diminished in patients with Chronic Fatigue Syndrome. <i>Clinical Hemorheology and Microcirculation</i> , 2019, 71, 113-116.	0.9	36
197	A Rapid, High-Quality, Cost-Effective, Comprehensive and Expandable Targeted Next-Generation Sequencing Assay for Inherited Heart Diseases. <i>Circulation Research</i> , 2015, 117, 603-611.	2.0	34
198	Use of Negative Dielectrophoresis for Selective Elution of Protein-Bound Particles. <i>Analytical Chemistry</i> , 2012, 84, 1432-1438.	3.2	33

#	ARTICLE	IF	CITATIONS
199	Involvement of Skeletal Muscle Gene Regulatory Network in Susceptibility to Wound Infection Following Trauma. PLoS ONE, 2007, 2, e1356.	1.1	32
200	Semi-Automated Library Preparation for High-Throughput DNA Sequencing Platforms. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-8.	3.0	31
201	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. Genetics in Medicine, 2019, 21, 896-903.	1.1	31
202	Polymerase chain reaction mapping of yeast GAL7 mRNA polyadenylation sites demonstrates that 3' end processing invitro faithfully reproduces the 3' ends observed in vivo. Nucleic Acids Research, 1991, 19, 3683-3688.	6.5	30
203	Molecular Inversion Probe Analysis of Gene Copy Alterations Reveals Distinct Categories of Colorectal Carcinoma. Cancer Research, 2006, 66, 7910-7919.	0.4	30
204	The 50:50 method for PCR-based seamless genome editing in yeast. Yeast, 2014, 31, 103-112.	0.8	30
205	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. BMC Genomics, 2014, 15, 263.	1.2	30
206	DNA SEQUENCES THAT ALLOW THE REPLICATION AND SEGREGATION OF YEAST CHROMOSOMES. , 1981, , 473-488.		30
207	The conserved histone deacetylase Rpd3 and its DNA binding subunit Ume6 control dynamic transcript architecture during mitotic growth and meiotic development. Nucleic Acids Research, 2015, 43, 115-128.	6.5	29
208	High-Resolution, In Vivo Magnetic Resonance Imaging of Drosophila at 18.8 Tesla. PLoS ONE, 2008, 3, e2817.	1.1	27
209	A physiological study of functional expression in Escherichia coli of the cloned yeast imidazoleglycerolphosphate dehydratase gene. Journal of Molecular Biology, 1980, 136, 291-307.	2.0	26
210	Microfluidic Leukocyte Isolation for Gene Expression Analysis in Critically Ill Hospitalized Patients. Clinical Chemistry, 2008, 54, 891-900.	1.5	26
211	Next-Generation Molecular Testing of Newborn Dried Blood Spots for Cystic Fibrosis. Journal of Molecular Diagnostics, 2016, 18, 267-282.	1.2	26
212	<i>CDP1</i> , a Novel <i>Saccharomyces cerevisiae</i> Gene Required for Proper Nuclear Division and Chromosome Segregation. Genetics, 1996, 144, 1387-1397.	1.2	26
213	SNP Discovery in Pooled Samples With Mismatch Repair Detection. Genome Research, 2004, 14, 1404-1412.	2.4	25
214	Multiplexed variation scanning for 1,000 amplicons in hundreds of patients using mismatch repair detection (MRD) on tag arrays. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14717-14722.	3.3	25
215	A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance. G3: Genes, Genomes, Genetics, 2011, 1, 219-231.	0.8	25
216	The Automated Cell: Compound and Environment Screening System (ACCESS) for Chemogenomic Screening. Methods in Molecular Biology, 2011, 759, 239-269.	0.4	25

#	ARTICLE	IF	CITATIONS
217	PathogenMip Assay: A Multiplex Pathogen Detection Assay. <i>PLoS ONE</i> , 2007, 2, e223.	1.1	25
218	A physical map of the left arm of the lambda chromosome. <i>Journal of Molecular Biology</i> , 1971, 56, 425-428.	2.0	24
219	Targeted cell detection based on microchannel gating. <i>Biomicrofluidics</i> , 2007, 1, 44103.	1.2	24
220	High-throughput, high-accuracy array-based resequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6712-6717.	3.3	23
221	Streamlined circular proximity ligation assay provides high stringency and compatibility with low-affinity antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E925-E933.	3.3	23
222	Yeast tRNA as Carrier in the Isolation of Microscale RNA for Global Amplification and Expression Profiling. <i>BioTechniques</i> , 2002, 33, 788-796.	0.8	21
223	Nanoelectronic impedance detection of target cells. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1161-1169.	1.7	21
224	An Automated Sample Preparation System for Large-Scale DNA Sequencing. <i>Genome Research</i> , 1999, 9, 457-462.	2.4	21
225	JETTA: junction and exon toolkits for transcriptome analysis. <i>Bioinformatics</i> , 2012, 28, 1274-1275.	1.8	20
226	High-Throughput Creation of a Whole-Genome Collection of Yeast Knockout Strains. <i>Methods in Molecular Biology</i> , 2008, 416, 205-220.	0.4	20
227	High Throughput Automated Allele Frequency Estimation by Pyrosequencing. <i>PLoS ONE</i> , 2008, 3, e2693.	1.1	20
228	Multiplex target capture with double-stranded DNA probes. <i>Genome Medicine</i> , 2013, 5, 50.	3.6	18
229	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. <i>Proteomics - Clinical Applications</i> , 2013, 7, 571-583.	0.8	17
230	Detecting differential protein expression in large-scale population proteomics. <i>Bioinformatics</i> , 2014, 30, 2741-2746.	1.8	17
231	Immunoscreening of Recombinant DNA Expression Libraries. , 1985, , 29-41.		17
232	Chemical Genomic Profiling for Identifying Intracellular Targets of Toxicants Producing Parkinson's Disease. <i>Toxicological Sciences</i> , 2007, 95, 182-187.	1.4	16
233	Genome-wide transcriptome analysis of 150 cell samples. <i>Integrative Biology (United Kingdom)</i> , 2009, 1, 99-107.	0.6	15
234	Smart Surface for Elution of Protein-Bound Particles: Nanonewton Dielectrophoretic Forces Using Atomic Layer Deposited Oxides. <i>Analytical Chemistry</i> , 2012, 84, 10793-10801.	3.2	15

#	ARTICLE	IF	CITATIONS
235	Nanoelectronic three-dimensional (3D) nanotip sensing array for real-time, sensitive, label-free sequence specific detection of nucleic acids. <i>Biomedical Microdevices</i> , 2016, 18, 7.	1.4	15
236	A Simple Method for Encapsulating Single Cells in Alginate Microspheres Allows for Direct PCR and Whole Genome Amplification. <i>PLoS ONE</i> , 2015, 10, e0117738.	1.1	15
237	A new electron microscopic technique for establishing the positions of genes: an analysis of the yeast ribosomal RNA coding region. <i>Journal of Molecular Biology</i> , 1978, 123, 417-430.	2.0	14
238	PathogenMIPer: a tool for the design of molecular inversion probes to detect multiple pathogens. <i>BMC Bioinformatics</i> , 2006, 7, 500.	1.2	13
239	Determination of DNA concentration by electron microscopy. <i>Analytical Biochemistry</i> , 1976, 72, 460-467.	1.1	12
240	Branch migration displacement assay with automated heuristic analysis for discrete DNA length measurement using DNA microarrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6146-6151.	3.3	12
241	A Novel Catechol-Based Universal Support for Oligonucleotide Synthesis. <i>Journal of Organic Chemistry</i> , 2007, 72, 9875-9880.	1.7	12
242	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. <i>BMC Bioinformatics</i> , 2010, 11, S8.	1.2	12
243	Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways. <i>Methods in Molecular Biology</i> , 2009, 548, 115-143.	0.4	12
244	A Novel Method for STR-based DNA Profiling Using Microarrays. <i>Journal of Forensic Sciences</i> , 2005, 50, 1-5.	0.9	12
245	High-Density Arrays and Insights into Genome function. <i>Biotechnology and Genetic Engineering Reviews</i> , 2000, 17, 109-146.	2.4	11
246	A Microfluidic Platform for Characterization of Protein-Protein Interactions. <i>IEEE Sensors Journal</i> , 2009, 9, 883-891.	2.4	11
247	Progress toward an aberration-corrected low energy electron microscope for DNA sequencing and surface analysis. <i>Journal of Vacuum Science and Technology B: Nanotechnology and Microelectronics</i> , 2012, 30, 6F402.	0.6	11
248	A touch-based multimodal and cryptographic bio-human-machine interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2201937119.	3.3	11
249	A system for multiplexed direct electrical detection of DNA synthesis. <i>Sensors and Actuators B: Chemical</i> , 2008, 129, 79-86.	4.0	10
250	Predicting Patient Survival from Longitudinal Gene Expression. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article41.	0.2	10
251	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. <i>PLoS ONE</i> , 2011, 6, e20016.	1.1	10
252	Electrical Detection of Protein Biomarkers Using Nanoneedle Biosensors. <i>Materials Research Society Symposia Proceedings</i> , 2012, 1414, 7.	0.1	10

#	ARTICLE	IF	CITATIONS
253	Molecular probe technology detects bacteria without culture. <i>BMC Microbiology</i> , 2012, 12, 29.	1.3	10
254	Coded Corrugated Microfluidic Sidewalls for Code Division Multiplexing. <i>IEEE Sensors Journal</i> , 2013, 13, 1399-1400.	2.4	10
255	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, 11917.	1.6	10
256	Nucleotide-Specific Contrast for DNA Sequencing by Electron Spectroscopy. <i>PLoS ONE</i> , 2016, 11, e0154707.	1.1	10
257	The <i>Saccharomyces cerevisiae</i> RPB4 gene is tightly linked to the TIF2 gene. <i>Nucleic Acids Research</i> , 1991, 19, 2781-2781.	6.5	9
258	A direct comparison of the KBâ„¢ Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. <i>BMC Research Notes</i> , 2010, 3, 257.	0.6	9
259	Improvement in cell capture throughput using parallel bioactivated microfluidic channels. <i>Biomedical Microdevices</i> , 2012, 14, 625-629.	1.4	9
260	Multiplexed actuation using ultra dielectrophoresis for proteomics applications: a comprehensive electrical and electrothermal design methodology. <i>Lab on A Chip</i> , 2014, 14, 2105-2114.	3.1	9
261	Ndt80 activates the meiotic ORC1 transcript isoform and SMA2 via a bi-directional middle sporulation element in <i>Saccharomyces cerevisiae</i> . <i>RNA Biology</i> , 2016, 13, 772-782.	1.5	9
262	Modeling Brownian Microparticle Trajectories in Lab-on-a-Chip Devices with Time Varying Dielectrophoretic or Optical Forces. <i>Micromachines</i> , 2021, 12, 1265.	1.4	9
263	To Give or Not to Give? That Is the Question: Figure 1.. <i>Plant Physiology</i> , 2004, 135, 4-9.	2.3	8
264	Conformational flexibility of a model protein upon immobilization on selfâ€ assembled monolayers. <i>Biotechnology and Bioengineering</i> , 2008, 100, 19-27.	1.7	8
265	Cationic Amphiphilic Drugs Are Potent Inhibitors of Yeast Sporulation. <i>PLoS ONE</i> , 2012, 7, e42853.	1.1	8
266	Reply to Cauwels et al.: Of men, not mice, and inflammation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3151-E3151.	3.3	8
267	The Sequencing Bead Array (SBA), a Next-Generation Digital Suspension Array. <i>PLoS ONE</i> , 2013, 8, e76696.	1.1	8
268	Heterologous expression of diverse propionyl-CoA carboxylases affects polyketide production in <i>Escherichia coli</i> . <i>Journal of Antibiotics</i> , 2017, 70, 859-863.	1.0	8
269	Conservation and DNA sequence arrangement of the DNA polymerase I gene region from <i>Klebsiella aerogenes</i> , <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> . <i>Journal of Molecular Biology</i> , 1980, 141, 343-368.	2.0	7
270	Sequence analysis of three fragments of maize nuclear DNA which replicate autonomously in yeast. <i>Plant Molecular Biology</i> , 1988, 11, 173-182.	2.0	7

#	ARTICLE	IF	CITATIONS
271	Structural optimization for heat detection of DNA thermosequencing platform using finite element analysis. <i>Biomicrofluidics</i> , 2008, 2, 24102.	1.2	7
272	Automated Motion Tracking and Data Extraction for Red Blood Cell Biomechanics. <i>Current Protocols in Cytometry</i> , 2020, 93, e75.	3.7	7
273	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. <i>PLoS ONE</i> , 2012, 7, e31440.	1.1	7
274	A novel method for STR-based DNA profiling using microarrays. <i>Journal of Forensic Sciences</i> , 2005, 50, 1109-13.	0.9	7
275	A molecular inversion probe assay for detecting alternative splicing. <i>BMC Genomics</i> , 2010, 11, 712.	1.2	6
276	Multiplex Identification of Microbes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3904-3910.	1.4	6
277	Gas-Phase Cleavage and Dephosphorylation of Universal Linker-Bound Oligodeoxynucleotides. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2010, 29, 867-878.	0.4	6
278	Reply to Osterburg et al.: To study human inflammatory diseases in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E3371-E3371.	3.3	6
279	Targeted and Highly Multiplexed Detection of Microorganisms by Employing an Ensemble of Molecular Probes. <i>Applied and Environmental Microbiology</i> , 2014, 80, 4153-4161.	1.4	6
280	Suppression of a yeast amber mutation in <i>Escherichia coli</i> . <i>Nature</i> , 1979, 279, 78-79.	13.7	5
281	Genomic organization of two families of highly repeated nuclear DNA sequences of maize selected for autonomous replicating activity in yeast. <i>Plant Molecular Biology</i> , 1988, 11, 161-172.	2.0	5
282	Analysis of hybridization on the molecular barcode GeneChip microarray. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 689-696.	1.0	5
283	Thin Film Nanoelectronic Probe for Protein Detection. <i>Materials Research Society Symposia Proceedings</i> , 2013, 1572, 1.	0.1	5
284	Robust Optimization of Biological Protocols. <i>Technometrics</i> , 2015, 57, 234-244.	1.3	5
285	Integrated RNA- and protein profiling of fermentation and respiration in diploid budding yeast provides insight into nutrient control of cell growth and development. <i>Journal of Proteomics</i> , 2015, 119, 30-44.	1.2	5
286	Systematic Mapping of Chemical-Genetic Interactions in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077701.	0.2	5
287	Genotyping African haplotypes in ATM using a co-spotted single-base extension assay. <i>Human Mutation</i> , 2003, 22, 214-221.	1.1	4
288	Identification of Chemical-Genetic Interactions via Parallel Analysis of Barcoded Yeast Strains. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot088054.	0.2	4

#	ARTICLE	IF	CITATIONS
289	Transplant Virus Detection Using Multiplex Targeted Sequencing. journal of applied laboratory medicine, The, 2018, 2, 757-769.	0.6	4
290	A biosensor-based approach reveals links between efflux pump expression and cell cycle regulation in pleiotropic drug resistance of yeast. Journal of Biological Chemistry, 2019, 294, 1257-1266.	1.6	4
291	Community members in activated sludge as determined by molecular probe technology. Water Research, 2020, 168, 115104.	5.3	4
292	The Human OligoGenome Resource: a database of oligonucleotide capture probes for resequencing target regions across the human genome. Nucleic Acids Research, 2012, 40, D1137-D1143.	6.5	3
293	Microfluidic Platform for Electrical Monitoring of Enzyme Activity. IEEE Sensors Journal, 2012, 12, 2733-2734.	2.4	3
294	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. BioTechniques, 2012, 52, 386-8.	0.8	3
295	Matrix independent label-free nanoelectronic biosensor. , 2014, , .		3
296	Scan statistics analysis for detection of introns in time-course tiling array data. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 173-90.	0.2	3
297	A Hybrid Approach of Gene Sets and Single Genes for the Prediction of Survival Risks with Gene Expression Data. PLoS ONE, 2015, 10, e0122103.	1.1	3
298	Electrochemical quantum tunneling for electronic detection and characterization of biological toxins. , 2012, , .		2
299	A Rapid, Cost-Effective Method of Assembly and Purification of Synthetic DNA Probes >100 bp. PLoS ONE, 2012, 7, e34373.	1.1	2
300	Strategies for Genetic Modification of Parasites. Annals of the New York Academy of Sciences, 1989, 569, 104-117.	1.8	1
301	Parallel analysis with biological chips. , 1999, , 445-II.		1
302	Label-free electronic detection of target cells. Proceedings of SPIE, 2014, , .	0.8	1
303	IpO: plasmids and methods for simplified, PCRâ€based DNA transplant in yeast. Yeast, 2014, 31, 185-193.	0.8	1
304	Experimental demonstration and analysis of DNA passage in nanopore-based nanofluidic transistors. , 2011, , .		0
305	Detecting common genomic mechanism between diseases using paired sparse canonical correlation analysis. , 2016, , .		0
306	A fully integrated electronic platform for multiplexed intermolecular force spectroscopy. , 2017, , .		0

#	ARTICLE	IF	CITATIONS
307	Analysis of Genomic Instability in Colorectal Carcinoma. FASEB Journal, 2008, 22, 798.4.	0.2	0
308	The Diversity of Nuclear Magnetic Resonance Spectroscopy. NATO Science for Peace and Security Series B: Physics and Biophysics, 2009, , 65-81.	0.2	0
309	KINETIC STUDIES ON THE HYBRIDIZATION OF RNA TO DOUBLE STRANDED DNA. , 1976, , 427-444.		0
310	Meta-analysis of peptides to detect protein significance. Statistics and Its Interface, 2020, 13, 465-474.	0.2	0