

Ronald W Davis, Ronald Davis, Ron W D

List of Publications by Year in descending order

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316
papers

88,457
citations

1163

111
h-index

339

285
g-index

323
all docs

323
docs citations

323
times ranked

76912
citing authors

#	ARTICLE	IF	CITATIONS
1	A touch-based multimodal and cryptographic bio-human-machine interface. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2201937119.	3.3	11
2	A Comprehensive Examination of Severely Ill ME/CFS Patients. Healthcare (Switzerland), 2021, 9, 1290.	1.0	12
3	Modeling Brownian Microparticle Trajectories in Lab-on-a-Chip Devices with Time Varying Dielectrophoretic or Optical Forces. Micromachines, 2021, 12, 1265.	1.4	9
4	Community members in activated sludge as determined by molecular probe technology. Water Research, 2020, 168, 115104.	5.3	4
5	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
6	Automated Motion Tracking and Data Extraction for Red Blood Cell Biomechanics. Current Protocols in Cytometry, 2020, 93, e75.	3.7	7
7	Microfluidic Point-of-Care Testing: Commercial Landscape and Future Directions. Frontiers in Bioengineering and Biotechnology, 2020, 8, 602659.	2.0	146
8	Meta-analysis of peptides to detect protein significance. Statistics and Its Interface, 2020, 13, 465-474.	0.2	0
9	A nanoelectronics-blood-based diagnostic biomarker for myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS). Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10250-10257.	3.3	64
10	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. Genetics in Medicine, 2019, 21, 896-903.	1.1	31
11	Red blood cell deformability is diminished in patients with Chronic Fatigue Syndrome. Clinical Hemorheology and Microcirculation, 2019, 71, 113-116.	0.9	36
12	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
13	HEx: A heterologous expression platform for the discovery of fungal natural products. Science Advances, 2018, 4, eaar5459.	4.7	167
14	Streamlined circular proximity ligation assay provides high stringency and compatibility with low-affinity antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E925-E933.	3.3	23
15	Template-Independent Enzymatic Oligonucleotide Synthesis (TIEOS): Its History, Prospects, and Challenges. Biochemistry, 2018, 57, 1821-1832.	1.2	50
16	Transplant Virus Detection Using Multiplex Targeted Sequencing. journal of applied laboratory medicine, The, 2018, 2, 757-769.	0.6	4
17	Multiplexed precision genome editing with trackable genomic barcodes in yeast. Nature Biotechnology, 2018, 36, 512-520.	9.4	138
18	Erythrocyte Deformability As a Potential Biomarker for Chronic Fatigue Syndrome. Blood, 2018, 132, 4874-4874.	0.6	8

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19	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
20	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
21	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
22	A method for high-throughput production of sequence-verified <i>scDNA</i> libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	3.2	41
23	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
24	A fully integrated electronic platform for multiplexed intermolecular force spectroscopy. , 2017, , .		0
25	A Wearable Electrochemical Platform for Noninvasive Simultaneous Monitoring of Ca^{2+} and pH. <i>ACS Nano</i> , 2016, 10, 7216-7224.	7.3	480
26	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
27	Detecting common genomic mechanism between diseases using paired sparse canonical correlation analysis. , 2016, , .		0
28	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
29	Systematic Mapping of Chemical-Genetic Interactions in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077701.	0.2	5
30	Application of 3D Printing for Smart Objects with Embedded Electronic Sensors and Systems. <i>Advanced Materials Technologies</i> , 2016, 1, 1600013.	3.0	167
31	Integrating Cell Phone Imaging with Magnetic Levitation (iLEV) for Label-Free Blood Analysis at the Point-of-Living. <i>Small</i> , 2016, 12, 1222-1229.	5.2	39
32	Fully integrated wearable sensor arrays for multiplexed in situ perspiration analysis. <i>Nature</i> , 2016, 529, 509-514.	13.7	3,508
33	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
34	Next-Generation Molecular Testing of Newborn Dried Blood Spots for Cystic Fibrosis. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 267-282.	1.2	26
35	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
36	Nucleotide-Specific Contrast for DNA Sequencing by Electron Spectroscopy. <i>PLoS ONE</i> , 2016, 11, e0154707.	1.1	10

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37	A Hybrid Approach of Gene Sets and Single Genes for the Prediction of Survival Risks with Gene Expression Data. <i>PLoS ONE</i> , 2015, 10, e0122103.	1.1	3
38	The conserved histone deacetylase Rpd3 and its DNA binding subunit Ume6 control dynamic transcript architecture during mitotic growth and meiotic development. <i>Nucleic Acids Research</i> , 2015, 43, 115-128.	6.5	29
39	Robust Optimization of Biological Protocols. <i>Technometrics</i> , 2015, 57, 234-244.	1.3	5
40	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
41	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
42	Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 Td (States of America, 2015, 112, E4354-63.	3.3	56
43	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, 11917.	1.6	10
44	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
45	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
46	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
47	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
48	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
49	Computational identification and analysis of orphan assembly-line polyketide synthases. <i>Journal of Antibiotics</i> , 2014, 67, 89-97.	1.0	59
50	Detecting differential protein expression in large-scale population proteomics. <i>Bioinformatics</i> , 2014, 30, 2741-2746.	1.8	17
51	Label-free electronic detection of target cells. <i>Proceedings of SPIE</i> , 2014, , .	0.8	1
52	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	217
53	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. <i>Reproductive Sciences</i> , 2014, 21, 32-40.	1.1	259
54	The 50:50 method for PCR-based seamless genome editing in yeast. <i>Yeast</i> , 2014, 31, 103-112.	0.8	30

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55	IpO: plasmids and methods for simplified, PCR-based DNA transplant in yeast. <i>Yeast</i> , 2014, 31, 185-193.	0.8	1
56	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
57	Nanoelectronic impedance detection of target cells. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1161-1169.	1.7	21
58	Matrix independent label-free nanoelectronic biosensor. , 2014, , .		3
59	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
60	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
61	Scan statistics analysis for detection of introns in time-course tiling array data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 173-90.	0.2	3
62	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	1.2	30
63	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
64	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	3.9	39
65	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
66	Multiplex target capture with double-stranded DNA probes. <i>Genome Medicine</i> , 2013, 5, 50.	3.6	18
67	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. <i>Proteomics - Clinical Applications</i> , 2013, 7, 571-583.	0.8	17
68	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
69	Microneedle biosensor: A method for direct label-free real time protein detection. <i>Sensors and Actuators B: Chemical</i> , 2013, 177, 848-855.	4.0	60
70	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
71	Coded Corrugated Microfluidic Sidewalls for Code Division Multiplexing. <i>IEEE Sensors Journal</i> , 2013, 13, 1399-1400.	2.4	10
72	Thin Film Nanoelectronic Probe for Protein Detection. <i>Materials Research Society Symposia Proceedings</i> , 2013, 1572, 1.	0.1	5

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73	Rare variant detection using family-based sequencing analysis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3985-3990.	3.3	54
74	Label-free electronic probing of nucleic acids and proteins at the nanoscale using the nanoneedle biosensor. Biomicrofluidics, 2013, 7, 044114.	1.2	37
75	Reply to Osterburg et al.: To study human inflammatory diseases in humans. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3371-E3371.	3.3	6
76	Reply to Cauwels et al.: Of men, not mice, and inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E3151-E3151.	3.3	8
77	The Sequencing Bead Array (SBA), a Next-Generation Digital Suspension Array. PLoS ONE, 2013, 8, e76696.	1.1	8
78	Progress toward an aberration-corrected low energy electron microscope for DNA sequencing and surface analysis. Journal of Vacuum Science and Technology B:Nanotechnology and Microelectronics, 2012, 30, 6F402.	0.6	11
79	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
80	Benchmarking Outcomes in the Critically Injured Trauma Patient and the Effect of Implementing Standard Operating Procedures. Annals of Surgery, 2012, 255, 993-999.	2.1	92
81	Microfluidic Platform for Electrical Monitoring of Enzyme Activity. IEEE Sensors Journal, 2012, 12, 2733-2734.	2.4	3
82	High-throughput, high-fidelity HLA genotyping with deep sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8676-8681.	3.3	200
83	Microfluidic diagnostic tool for the developing world: contactless impedance flow cytometry. Lab on A Chip, 2012, 12, 4499.	3.1	59
84	Smart Surface for Elution of Protein-bound Particles: Nanonewton Dielectrophoretic Forces Using Atomic Layer Deposited Oxides. Analytical Chemistry, 2012, 84, 10793-10801.	3.2	15
85	Use of Negative Dielectrophoresis for Selective Elution of Protein-Bound Particles. Analytical Chemistry, 2012, 84, 1432-1438.	3.2	33
86	Electrochemical quantum tunneling for electronic detection and characterization of biological toxins. , 2012, , .		2
87	Cationic Amphiphilic Drugs Are Potent Inhibitors of Yeast Sporulation. PLoS ONE, 2012, 7, e42853.	1.1	8
88	Single Cell Profiling of Circulating Tumor Cells: Transcriptional Heterogeneity and Diversity from Breast Cancer Cell Lines. PLoS ONE, 2012, 7, e33788.	1.1	475
89	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. BioTechniques, 2012, 52, 386-8.	0.8	3
90	JETTA: junction and exon toolkits for transcriptome analysis. Bioinformatics, 2012, 28, 1274-1275.	1.8	20

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91	Electrical Detection of Protein Biomarkers Using Nanoneedle Biosensors. Materials Research Society Symposia Proceedings, 2012, 1414, 7.	0.1	10
92	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
93	Whole-genome sequencing of the efficient industrial fuel-ethanol fermentative <i>Saccharomyces cerevisiae</i> strain CAT-1. Molecular Genetics and Genomics, 2012, 287, 485-494.	1.0	82
94	Improvement in cell capture throughput using parallel bioactivated microfluidic channels. Biomedical Microdevices, 2012, 14, 625-629.	1.4	9
95	Molecular probe technology detects bacteria without culture. BMC Microbiology, 2012, 12, 29.	1.3	10
96	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. Journal of Assisted Reproduction and Genetics, 2012, 29, 105-115.	1.2	124
97	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
98	A Rapid, Cost-Effective Method of Assembly and Purification of Synthetic DNA Probes >100 bp. PLoS ONE, 2012, 7, e34373.	1.1	2
99	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. PLoS ONE, 2011, 6, e20016.	1.1	10
100	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	4.2	1,040
101	Experimental demonstration and analysis of DNA passage in nanopore-based nanofluidic transistors. , 2011, , .		0
102	Execution of the meiotic noncoding RNA expression program and the onset of gametogenesis in yeast require the conserved exosome subunit Rrp6. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1058-1063.	3.3	124
103	A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance. G3: Genes, Genomes, Genetics, 2011, 1, 219-231.	0.8	25
104	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. Nucleic Acids Research, 2011, 39, 44-58.	6.5	37
105	Human transcriptome array for high-throughput clinical studies. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3707-3712.	3.3	122
106	High-quality DNA sequence capture of 524 disease candidate genes. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 6549-6554.	3.3	52
107	Evidence-Based Annotation of Gene Function in <i>Shewanella oneidensis</i> MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. PLoS Genetics, 2011, 7, e1002385.	1.5	119
108	The Automated Cell: Compound and Environment Screening System (ACCESS) for Chemogenomic Screening. Methods in Molecular Biology, 2011, 759, 239-269.	0.4	25

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109	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. BMC Bioinformatics, 2010, 11, S8.	1.2	12
110	A molecular inversion probe assay for detecting alternative splicing. BMC Genomics, 2010, 11, 712.	1.2	6
111	A direct comparison of the K&B, Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. BMC Research Notes, 2010, 3, 257.	0.6	9
112	Sensitive giant magnetoresistive-based immunoassay for multiplex mycotoxin detection. Biosensors and Bioelectronics, 2010, 25, 1635-1639.	5.3	108
113	Clinical microfluidics for neutrophil genomics and proteomics. Nature Medicine, 2010, 16, 1042-1047.	15.2	168
114	A universal TagModule collection for parallel genetic analysis of microorganisms. Nucleic Acids Research, 2010, 38, e146-e146.	6.5	54
115	Predicting Patient Survival from Longitudinal Gene Expression. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article41.	0.2	10
116	Gene Annotation and Drug Target Discovery in Candida albicans with a Tagged Transposon Mutant Collection. PLoS Pathogens, 2010, 6, e1001140.	2.1	85
117	Multiplex Identification of Microbes. Applied and Environmental Microbiology, 2010, 76, 3904-3910.	1.4	6
118	Gas-Phase Cleavage and Dephosphorylation of Universal Linker-Bound Oligodeoxynucleotides. Nucleosides, Nucleotides and Nucleic Acids, 2010, 29, 867-878.	0.4	6
119	Semi-Automated Library Preparation for High-Throughput DNA Sequencing Platforms. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-8.	3.0	31
120	Plasma Proteome Response to Severe Burn Injury Revealed by ¹⁸ O-Labeled α -Universal Reference-Based Quantitative Proteomics. Journal of Proteome Research, 2010, 9, 4779-4789.	1.8	54
121	Systematic analysis of genome-wide fitness data in yeast reveals novel gene function and drug action. Genome Biology, 2010, 11, R30.	13.9	94
122	DMSO and Betaine Greatly Improve Amplification of GC-Rich Constructs in De Novo Synthesis. PLoS ONE, 2010, 5, e11024.	1.1	108
123	Isolating highly enriched populations of circulating epithelial cells and other rare cells from blood using a magnetic sweeper device. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3970-3975.	3.3	448
124	High-throughput, high-accuracy array-based resequencing. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 6712-6717.	3.3	23
125	Label-free biosensing with functionalized nanopipette probes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 4611-4616.	3.3	152
126	Sequential Use of Transcriptional Profiling, Expression Quantitative Trait Mapping, and Gene Association Implicates MMP20 in Human Kidney Aging. PLoS Genetics, 2009, 5, e1000685.	1.5	50

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127	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. PLoS Computational Biology, 2009, 5, e1000374.	1.5	74
128	A Genome-Wide Screen for Regulators of TORC1 in Response to Amino Acid Starvation Reveals a Conserved Npr2/3 Complex. PLoS Genetics, 2009, 5, e1000515.	1.5	134
129	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. Genome Research, 2009, 19, 757-769.	2.4	104
130	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. Genetics, 2009, 183, 185-194.	1.2	71
131	A dynamic network of transcription in LPS-treated human subjects. BMC Systems Biology, 2009, 3, 78.	3.0	36
132	Whole genome survey of coding SNPs reveals a reproducible pathway determinant of Parkinson disease. Human Mutation, 2009, 30, 228-238.	1.1	36
133	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ¹⁸ O-Labeled "Universal" Reference Sample. Journal of Proteome Research, 2009, 8, 290-299.	1.8	59
134	Electrical detection of protein biomarkers using bioactivated microfluidic channels. Lab on A Chip, 2009, 9, 1429.	3.1	36
135	Genome-wide transcriptome analysis of 150 cell samples. Integrative Biology (United Kingdom), 2009, 1, 99-107.	0.6	15
136	A Microfluidic Platform for Characterization of Protein-Protein Interactions. IEEE Sensors Journal, 2009, 9, 883-891.	2.4	11
137	Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways. Methods in Molecular Biology, 2009, 548, 115-143.	0.4	12
138	The Diversity of Nuclear Magnetic Resonance Spectroscopy. NATO Science for Peace and Security Series B: Physics and Biophysics, 2009, , 65-81.	0.2	0
139	Conformational flexibility of a model protein upon immobilization on self-assembled monolayers. Biotechnology and Bioengineering, 2008, 100, 19-27.	1.7	8
140	A system for multiplexed direct electrical detection of DNA synthesis. Sensors and Actuators B: Chemical, 2008, 129, 79-86.	4.0	10
141	An integrated platform of genomic assays reveals small-molecule bioactivities. Nature Chemical Biology, 2008, 4, 498-506.	3.9	178
142	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. Science, 2008, 320, 362-365.	6.0	892
143	Bisphenol A Induces a Profile of Tumor Aggressiveness in High-Risk Cells from Breast Cancer Patients. Cancer Research, 2008, 68, 2076-2080.	0.4	101
144	Microfluidic Leukocyte Isolation for Gene Expression Analysis in Critically Ill Hospitalized Patients. Clinical Chemistry, 2008, 54, 891-900.	1.5	26

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145	Superoxide anions regulate TORC1 and its ability to bind Fpr1:rapamycin complex. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15166-15171.	3.3	48
146	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
147	Multiplexed Proximity Ligation Assays to Profile Putative Plasma Biomarkers Relevant to Pancreatic and Ovarian Cancer. Clinical Chemistry, 2008, 54, 582-589.	1.5	84
148	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. PLoS Genetics, 2008, 4, e1000113.	1.5	181
149	Sequential Elimination of Major-Effect Contributors Identifies Additional Quantitative Trait Loci Conditioning High-Temperature Growth in Yeast. Genetics, 2008, 180, 1661-1670.	1.2	145
150	Picocalorimetric method for DNA sequencing. Journal of Vacuum Science & Technology B, 2008, 26, 661-665.	1.3	6
151	Structural optimization for heat detection of DNA thermosequencing platform using finite element analysis. Biomicrofluidics, 2008, 2, 24102.	1.2	7
152	High-Throughput Creation of a Whole-Genome Collection of Yeast Knockout Strains. Methods in Molecular Biology, 2008, 416, 205-220.	0.4	20
153	High Throughput Automated Allele Frequency Estimation by Pyrosequencing. PLoS ONE, 2008, 3, e2693.	1.1	20
154	High-Resolution, In Vivo Magnetic Resonance Imaging of Drosophila at 18.8 Tesla. PLoS ONE, 2008, 3, e2817.	1.1	27
155	Analysis of Genomic Instability in Colorectal Carcinoma. FASEB Journal, 2008, 22, 798.4.	0.2	0
156	Branch migration displacement assay with automated heuristic analysis for discrete DNA length measurement using DNA microarrays. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6146-6151.	3.3	12
157	Multigene amplification and massively parallel sequencing for cancer mutation discovery. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9387-9392.	3.3	159
158	Multiplex amplification of all coding sequences within 10 cancer genes by Gene-Collector. Nucleic Acids Research, 2007, 35, e47.	6.5	56
159	Chemical Genomic Profiling for Identifying Intracellular Targets of Toxicants Producing Parkinson's Disease. Toxicological Sciences, 2007, 95, 182-187.	1.4	16
160	Targeted cell detection based on microchannel gating. Biomicrofluidics, 2007, 1, 44103.	1.2	24
161	High-density yeast-tiling array reveals previously undiscovered introns and extensive regulation of meiotic splicing. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1522-1527.	3.3	116
162	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

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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	A Novel Catechol-Based Universal Support for Oligonucleotide Synthesis. <i>Journal of Organic Chemistry</i> , 2007, 72, 9875-9880.	1.7	12
165	Involvement of Skeletal Muscle Gene Regulatory Network in Susceptibility to Wound Infection Following Trauma. <i>PLoS ONE</i> , 2007, 2, e1356.	1.1	32
166	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	294
167	Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. <i>Nature Genetics</i> , 2007, 39, 1092-1099.	9.4	207
168	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	9.4	765
169	Multiplexed protein detection by proximity ligation for cancer biomarker validation. <i>Nature Methods</i> , 2007, 4, 327-329.	9.0	169
170	PathogenMip Assay: A Multiplex Pathogen Detection Assay. <i>PLoS ONE</i> , 2007, 2, e223.	1.1	25
171	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
172	Current Rectification with Poly-L-Lysine-Coated Quartz Nanopipettes. <i>Nano Letters</i> , 2006, 6, 2486-2492.	4.5	188
173	Analysis of hybridization on the molecular barcode GeneChip microarray. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 689-696.	1.0	5
174	Data quality in genomics and microarrays. <i>Nature Biotechnology</i> , 2006, 24, 1112-1113.	9.4	48
175	A unique and universal molecular barcode array. <i>Nature Methods</i> , 2006, 3, 601-603.	9.0	105
176	PathogenMIPer: a tool for the design of molecular inversion probes to detect multiple pathogens. <i>BMC Bioinformatics</i> , 2006, 7, 500.	1.2	13
177	Transcriptional Profiling of Aging in Human Muscle Reveals a Common Aging Signature. <i>PLoS Genetics</i> , 2006, 2, e115.	1.5	331
178	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
179	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
180	Introns Regulate RNA and Protein Abundance in Yeast. <i>Genetics</i> , 2006, 174, 511-518.	1.2	99

#	ARTICLE	IF	CITATIONS
181	Molecular Inversion Probe Analysis of Gene Copy Alterations Reveals Distinct Categories of Colorectal Carcinoma. <i>Cancer Research</i> , 2006, 66, 7910-7919.	0.4	30
182	Prediction of protein orientation upon immobilization on biological and nonbiological surfaces. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14773-14778.	3.3	56
183	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
184	Direct electrical detection of DNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6466-6470.	3.3	72
185	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
186	Quantitative trait loci mapped to single-nucleotide resolution in yeast. <i>Nature Genetics</i> , 2005, 37, 1333-1340.	9.4	242
187	A network-based analysis of systemic inflammation in humans. <i>Nature</i> , 2005, 437, 1032-1037.	13.7	1,419
188	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
189	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
190	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.	3.3	238
191	Mechanisms of Haploinsufficiency Revealed by Genome-Wide Profiling in Yeast. <i>Genetics</i> , 2005, 169, 1915-1925.	1.2	460
192	Allele quantification using molecular inversion probes (MIP). <i>Nucleic Acids Research</i> , 2005, 33, e183-e183.	6.5	81
193	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
194	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
195	Multiplexed variation scanning for 1,000 amplicons in hundreds of patients using mismatch repair detection (MRD) on tag arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14717-14722.	3.3	25
196	Quantitative Proteome Analysis of Human Plasma following <i>In Vivo</i> Lipopolysaccharide Administration Using 16O/18O Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	2.5	156
197	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
198	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.	3.3	281

#	ARTICLE	IF	CITATIONS
199	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664
200	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.	2.4	276
201	Single DNA Molecule Detection Using Nanopipettes and Nanoparticles. <i>Nano Letters</i> , 2005, 5, 403-407.	4.5	152
202	A Novel Method for STR-based DNA Profiling Using Microarrays. <i>Journal of Forensic Sciences</i> , 2005, 50, 1-5.	0.9	12
203	A novel method for STR-based DNA profiling using microarrays. <i>Journal of Forensic Sciences</i> , 2005, 50, 1109-13.	0.9	7
204	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
205	SNP Discovery in Pooled Samples With Mismatch Repair Detection. <i>Genome Research</i> , 2004, 14, 1404-1412.	2.4	25
206	A multi-enzyme model for pyrosequencing. <i>Nucleic Acids Research</i> , 2004, 32, e166-e166.	6.5	47
207	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
208	To Give or Not to Give? That Is the Question: Figure 1.. <i>Plant Physiology</i> , 2004, 135, 4-9.	2.3	8
209	Genomic and Proteomic Determinants of Outcome in Patients Undergoing Thoracoabdominal Aortic Aneurysm Repair. <i>Journal of Immunology</i> , 2004, 172, 7103-7109.	0.4	61
210	Whole blood and leukocyte RNA isolation for gene expression analyses. <i>Physiological Genomics</i> , 2004, 19, 247-254.	1.0	186
211	Characterization of synthetic DNA bar codes in <i>Saccharomyces cerevisiae</i> gene-deletion strains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11046-11051.	3.3	69
212	A Transcriptional Profile of Aging in the Human Kidney. <i>PLoS Biology</i> , 2004, 2, e427.	2.6	281
213	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	2.6	181
214	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004, 5, 190-201.	7.7	83
215	Regulatory networks affected by iron availability in <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 2004, 53, 1451-1469.	1.2	240
216	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

#	ARTICLE	IF	CITATIONS
217	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
218	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
219	Determination of hepatitis C virus genotype by Pyrosequencing. <i>Journal of Virological Methods</i> , 2003, 109, 171-176.	1.0	45
220	Genotyping African haplotypes in ATM using a co-spotted single-base extension assay. <i>Human Mutation</i> , 2003, 22, 214-221.	1.1	4
221	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003, 421, 63-66.	13.7	790
222	Multiplexed genotyping with sequence-tagged molecular inversion probes. <i>Nature Biotechnology</i> , 2003, 21, 673-678.	9.4	502
223	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
224	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
225	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
226	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.	3.3	271
227	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.	3.3	234
228	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
229	Gene Expression During the Life Cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 297, 2270-2275.	6.0	843
230	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002, 31, 400-404.	9.4	503
231	Multiplex Pyrosequencing. <i>Nucleic Acids Research</i> , 2002, 30, 31e-31.	6.5	74
232	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
233	Identification and preliminary characterization of mouse Adam33. <i>BMC Genetics</i> , 2002, 3, 2.	2.7	45
234	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	13.7	3,938

#	ARTICLE	IF	CITATIONS
235	Genome sequence of the human malaria parasite Plasmodium falciparum. Nature, 2002, 419, 498-511.	13.7	3,881
236	Sequence of Plasmodium falciparum chromosome 12. Nature, 2002, 419, 534-537.	13.7	58
237	Dissecting the architecture of a quantitative trait locus in yeast. Nature, 2002, 416, 326-330.	13.7	524
238	Replication Dynamics of the Yeast Genome. Science, 2001, 294, 115-121.	6.0	736
239	Global Analysis of ATM Polymorphism Reveals Significant Functional Constraint. American Journal of Human Genetics, 2001, 69, 396-412.	2.6	93
240	Transcriptional regulation and function during the human cell cycle. Nature Genetics, 2001, 27, 48-54.	9.4	399
241	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	13.7	21,074
242	Y chromosome sequence variation and the history of human populations. Nature Genetics, 2000, 26, 358-361.	9.4	935
243	The core meiotic transcriptome in budding yeasts. Nature Genetics, 2000, 26, 415-423.	9.4	430
244	Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana. Nature, 2000, 408, 816-820.	13.7	234
245	Identification of the SAAT Gene Involved in Strawberry Flavor Biogenesis by Use of DNA Microarrays. Plant Cell, 2000, 12, 647-661.	3.1	496
246	A Simple Procedure for the Analysis of Single Nucleotide Polymorphisms Facilitates Map-Based Cloning in Arabidopsis. Plant Physiology, 2000, 124, 1483-1492.	2.3	227
247	High-Density Arrays and Insights into Genome function. Biotechnology and Genetic Engineering Reviews, 2000, 17, 109-146.	2.4	11
248	Parallel analysis with biological chips. , 1999, , 445-II.		1
249	The mouse mahogany locus encodes a transmembrane form of human attractin. Nature, 1999, 398, 152-156.	13.7	194
250	Genome-wide mapping with biallelic markers in Arabidopsis thaliana. Nature Genetics, 1999, 23, 203-207.	9.4	260
251	Genomic profiling of drug sensitivities via induced haploinsufficiency. Nature Genetics, 1999, 21, 278-283.	9.4	533
252	Comparative genomes of Chlamydia pneumoniae and C. trachomatis. Nature Genetics, 1999, 21, 385-389.	9.4	636

#	ARTICLE	IF	CITATIONS
253	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
254	Toxic mutations in the <i>recA</i> gene of <i>E. coli</i> prevent proper chromosome segregation 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 1999, 286, 417-435.	2.0	38
255	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
256	An Automated Sample Preparation System for Large-Scale DNA Sequencing. <i>Genome Research</i> , 1999, 9, 457-462.	2.4	21
257	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	4.5	1,927
258	Direct Allelic Variation Scanning of the Yeast Genome. , 1998, 281, 1194-1197.		368
259	Genome Sequence of an Obligate Intracellular Pathogen of Humans: <i>Chlamydia trachomatis</i> . , 1998, 282, 754-759.		1,449
260	Detection of Numerous Y Chromosome Biallelic Polymorphisms by Denaturing High-Performance Liquid Chromatography. <i>Genome Research</i> , 1997, 7, 996-1005.	2.4	617
261	Functional analysis of the yeast genome. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 771-776.	1.5	59
262	Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular bar coding strategy. <i>Nature Genetics</i> , 1996, 14, 450-456.	9.4	545
263	<i>CDP1</i> , a Novel <i>Saccharomyces cerevisiae</i> Gene Required for Proper Nuclear Division and Chromosome Segregation. <i>Genetics</i> , 1996, 144, 1387-1397.	1.2	26
264	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
265	Cloning vectors for the synthesis of epitope-tagged, truncated and chimeric proteins in <i>Saccharomyces cerevisiae</i> . <i>Gene</i> , 1994, 144, 63-68.	1.0	59
266	ATP hydrolysis and the displaced strand are two factors that determine the polarity of RecA-promoted DNA strand exchange. <i>Journal of Molecular Biology</i> , 1992, 227, 38-53.	2.0	62
267	Polymerase chain reaction mapping of yeast GAL7 mRNA polyadenylation sites demonstrates that 3' end processing invitro faithfully reproduces the 3' ends observed in vivo. <i>Nucleic Acids Research</i> , 1991, 19, 3683-3688.	6.5	30
268	The use of proline as a nitrogen source causes hypersensitivity to, and allows more economical use of 5FOA in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1991, 7, 607-608.	0.8	42
269	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
270	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

#	ARTICLE	IF	CITATIONS
271	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
272	Strategies for Genetic Modification of Parasites. <i>Annals of the New York Academy of Sciences</i> , 1989, 569, 104-117.	1.8	1
273	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
274	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
275	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.	1.0	253
276	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
277	[7] $\hat{\gg}$ 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	0.4	161
278	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
279	Bent DNA at a yeast autonomously replicating sequence. <i>Nature</i> , 1986, 324, 87-89.	13.7	218
280	Genes for the major protein antigens of the leprosy parasite <i>Mycobacterium leprae</i> . <i>Nature</i> , 1985, 316, 450-452.	13.7	365
281	Functional selection and analysis of yeast centromeric DNA. <i>Cell</i> , 1985, 42, 913-921.	13.5	270
282	Immunoscreening $\hat{\gg}$ Recombinant DNA Expression Libraries. , 1985, , 29-41.		17
283	Centromeric DNA from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1982, 158, 157-179.	2.0	317
284	Reversion of a promoter deletion in yeast. <i>Nature</i> , 1982, 298, 815-819.	13.7	81
285	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
286	Deletion analysis of the <i>Saccharomyces</i> GAL gene cluster. <i>Journal of Molecular Biology</i> , 1981, 152, 317-334.	2.0	85
287	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
288	Promoter mutants of the yeast <i>his3</i> gene. <i>Journal of Molecular Biology</i> , 1981, 152, 553-568.	2.0	46

#	ARTICLE	IF	CITATIONS
289	DNA SEQUENCES THAT ALLOW THE REPLICATION AND SEGREGATION OF YEAST CHROMOSOMES. , 1981, , 473-488.		30
290	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
291	[49] Rapid DNA isolations for enzymatic and hybridization analysis. <i>Methods in Enzymology</i> , 1980, 65, 404-411.	0.4	610
292	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
293	A physiological study of functional expression in <i>Escherichia coli</i> of the cloned yeast imidazoleglycerolphosphate dehydratase gene. <i>Journal of Molecular Biology</i> , 1980, 136, 291-307.	2.0	26
294	A physical, genetic and transcriptional map of the cloned <i>his3</i> gene region of <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1980, 136, 309-332.	2.0	128
295	Suppression of a yeast amber mutation in <i>Escherichia coli</i> . <i>Nature</i> , 1979, 279, 78-79.	13.7	5
296	Evidence for transposition of dispersed repetitive DNA families in yeast. <i>Cell</i> , 1979, 16, 739-751.	13.5	619
297	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
298	Cloning of the yeast tyrosine transfer RNA genes in bacteriophage lambda. <i>Journal of Molecular Biology</i> , 1979, 127, 285-295.	2.0	42
299	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
300	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
301	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
302	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
303	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
304	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
305	Analysis of chromosomal integration and deletions of yeast plasmids. <i>Nucleic Acids Research</i> , 1977, 4, 1429-1448.	6.5	259
306	Isolation of bacteriophage λ containing yeast ribosomal RNA genes: Screening by in situ RNA hybridization to plaques. <i>Cell</i> , 1976, 8, 227-232.	13.5	70

#	ARTICLE	IF	CITATIONS
307	Determination of DNA concentration by electron microscopy. Analytical Biochemistry, 1976, 72, 460-467.	1.1	12
308	KINETIC STUDIES ON THE HYBRIDIZATION OF RNA TO DOUBLE STRANDED DNA. , 1976, , 427-444.		0
309	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
310	Studies on the cleavage of bacteriophage lambda DNA with EcoRI restriction endonuclease. Journal of Molecular Biology, 1975, 91, 315-328.	2.0	910
311	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
312	A physical map of the left arm of the lambda chromosome. Journal of Molecular Biology, 1971, 56, 425-428.	2.0	24
313	Deletion mutants of bacteriophage lambda. Journal of Molecular Biology, 1971, 56, 403-423.	2.0	174
314	[31] Electron microscope heteroduplex methods for mapping regions of base sequence homology in nucleic acids. Methods in Enzymology, 1971, 21, 413-428.	0.4	1,205
315	A physical study by electron microscopy of the terminally repetitious, circularly permuted DNA from the coliphage particles of Escherichia coli 15. Journal of Molecular Biology, 1970, 48, 1-22.	2.0	229
316	Homology and structural relationships between the dimeric and monomeric circular forms of mitochondrial DNA from human leukemic leukocytes. Journal of Molecular Biology, 1970, 47, 137-153.	2.0	106