

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/12053712/publications.pdf>

Version: 2024-02-01

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	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	Modeling Brownian Microparticle Trajectories in Lab-on-a-Chip Devices with Time Varying Dielectrophoretic or Optical Forces. Micromachines, 2021, 12, 1265.	1.4	9
3	Community members in activated sludge as determined by molecular probe technology. Water Research, 2020, 168, 115104.	5.3	4
4	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
5	Automated Motion Tracking and Data Extraction for Red Blood Cell Biomechanics. Current Protocols in Cytometry, 2020, 93, e75.	3.7	7
6	Microfluidic Point-of-Care Testing: Commercial Landscape and Future Directions. Frontiers in Bioengineering and Biotechnology, 2020, 8, 602659.	2.0	146
7	Meta-analysis of peptides to detect protein significance. Statistics and Its Interface, 2020, 13, 465-474.	0.2	0
8	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. Genetics in Medicine, 2019, 21, 896-903.	1.1	31
9	Red blood cell deformability is diminished in patients with Chronic Fatigue Syndrome. Clinical Hemorheology and Microcirculation, 2019, 71, 113-116.	0.9	36
10	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
11	HEx: A heterologous expression platform for the discovery of fungal natural products. Science Advances, 2018, 4, eaar5459.	4.7	167
12	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
13	Template-Independent Enzymatic Oligonucleotide Synthesis (TiEOS): Its History, Prospects, and Challenges. Biochemistry, 2018, 57, 1821-1832.	1.2	50
14	Transplant Virus Detection Using Multiplex Targeted Sequencing. Journal of Applied Laboratory Medicine, 2018, 2, 757-769.	0.6	4
15	Multiplexed precision genome editing with trackable genomic barcodes in yeast. Nature Biotechnology, 2018, 36, 512-520.	9.4	138
16	Multifunctional, inexpensive, and reusable nanoparticle-printed biochip for cell manipulation and diagnosis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1306-E1315.	3.3	55
17	Heterologous expression of diverse propionyl-CoA carboxylases affects polyketide production in Escherichia coli. Journal of Antibiotics, 2017, 70, 859-863.	1.0	8
18	Autonomous sweat extraction and analysis applied to cystic fibrosis and glucose monitoring using a fully integrated wearable platform. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4625-4630.	3.3	573

#	ARTICLE	IF	CITATIONS
19	A method for high-throughput production of sequence-verified <sc>DNA</sc> libraries and strain collections. <i>Molecular Systems Biology</i> , 2017, 13, 913.	3.2	41
20	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	3.2	41
21	A fully integrated electronic platform for multiplexed intermolecular force spectroscopy. , 2017, , .		0
22	A Wearable Electrochemical Platform for Noninvasive Simultaneous Monitoring of Ca ²⁺ and pH. <i>ACS Nano</i> , 2016, 10, 7216-7224.	7.3	480
23	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
24	Detecting common genomic mechanism between diseases using paired sparse canonical correlation analysis. , 2016, , .		0
25	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
26	Systematic Mapping of Chemical-Genetic Interactions in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077701.	0.2	5
27	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
28	Fully integrated wearable sensor arrays for multiplexed in situ perspiration analysis. <i>Nature</i> , 2016, 529, 509-514.	13.7	3,508
29	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
30	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
31	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
32	Nucleotide-Specific Contrast for DNA Sequencing by Electron Spectroscopy. <i>PLoS ONE</i> , 2016, 11, e0154707.	1.1	10
33	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
34	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
35	Robust Optimization of Biological Protocols. <i>Technometrics</i> , 2015, 57, 234-244.	1.3	5
36	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

#	ARTICLE	IF	CITATIONS
37	Tunable control of antibody immobilization using electric field. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1995-1999.	3.3	39
38	Multitarget, quantitative nanoplasmonic electrical field-enhanced resonating device (NE Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 Td (States of America, 2015, 112, E4354-63.	3.3	56
39	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. Scientific Reports, 2015, 5, 11917.	1.6	10
40	Magnetic levitation of single cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3661-8.	3.3	192
41	A Rapid, High-Quality, Cost-Effective, Comprehensive and Expandable Targeted Next-Generation Sequencing Assay for Inherited Heart Diseases. Circulation Research, 2015, 117, 603-611.	2.0	34
42	Mice are not men. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E345.	3.3	102
43	A Simple Method for Encapsulating Single Cells in Alginate Microspheres Allows for Direct PCR and Whole Genome Amplification. PLoS ONE, 2015, 10, e0117738.	1.1	15
44	Functional Genomics with a Comprehensive Library of Transposon Mutants for the Sulfate-Reducing Bacterium Desulfovibrio alaskensis G20. MBio, 2014, 5, e01041-14.	1.8	56
45	Computational identification and analysis of orphan assembly-line polyketide synthases. Journal of Antibiotics, 2014, 67, 89-97.	1.0	59
46	Detecting differential protein expression in large-scale population proteomics. Bioinformatics, 2014, 30, 2741-2746.	1.8	17
47	Label-free electronic detection of target cells. Proceedings of SPIE, 2014, , .	0.8	1
48	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. Science, 2014, 344, 208-211.	6.0	217
49	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. Reproductive Sciences, 2014, 21, 32-40.	1.1	259
50	The 50:50 method for PCRâ€­based seamless genome editing in yeast. Yeast, 2014, 31, 103-112.	0.8	30
51	IpO: plasmids and methods for simplified, PCRâ€­based DNA transplant in yeast. Yeast, 2014, 31, 185-193.	0.8	1
52	Digital microfluidic assay for protein detection. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2110-2115.	3.3	115
53	Nanoelectronic impedance detection of target cells. Biotechnology and Bioengineering, 2014, 111, 1161-1169.	1.7	21
54	Matrix independent label-free nanoelectronic biosensor. , 2014, , .		3

#	ARTICLE	IF	CITATIONS
55	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
56	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
57	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
58	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	1.2	30
59	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
60	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	3.9	39
61	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
62	Multiplex target capture with double-stranded DNA probes. <i>Genome Medicine</i> , 2013, 5, 50.	3.6	18
63	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. <i>Proteomics - Clinical Applications</i> , 2013, 7, 571-583.	0.8	17
64	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
65	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
66	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
67	Coded Corrugated Microfluidic Sidewalls for Code Division Multiplexing. <i>IEEE Sensors Journal</i> , 2013, 13, 1399-1400.	2.4	10
68	Thin Film Nanoelectronic Probe for Protein Detection. <i>Materials Research Society Symposia Proceedings</i> , 2013, 1572, 1.	0.1	5
69	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
70	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
71	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
72	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

#	ARTICLE	IF	CITATIONS
73	The Sequencing Bead Array (SBA), a Next-Generation Digital Suspension Array. PLoS ONE, 2013, 8, e76696.	1.1	8
74	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
75	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
76	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
77	Microfluidic Platform for Electrical Monitoring of Enzyme Activity. IEEE Sensors Journal, 2012, 12, 2733-2734.	2.4	3
78	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
79	Microfluidic diagnostic tool for the developing world: contactless impedance flow cytometry. Lab on A Chip, 2012, 12, 4499.	3.1	59
80	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
81	Use of Negative Dielectrophoresis for Selective Elution of Protein-Bound Particles. Analytical Chemistry, 2012, 84, 1432-1438.	3.2	33
82	Electrochemical quantum tunneling for electronic detection and characterization of biological toxins. , 2012, , .		2
83	Cationic Amphiphilic Drugs Are Potent Inhibitors of Yeast Sporulation. PLoS ONE, 2012, 7, e42853.	1.1	8
84	Single Cell Profiling of Circulating Tumor Cells: Transcriptional Heterogeneity and Diversity from Breast Cancer Cell Lines. PLoS ONE, 2012, 7, e33788.	1.1	475
85	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. BioTechniques, 2012, 52, 386-8.	0.8	3
86	JETTA: junction and exon toolkits for transcriptome analysis. Bioinformatics, 2012, 28, 1274-1275.	1.8	20
87	Electrical Detection of Protein Biomarkers Using Nanoneedle Biosensors. Materials Research Society Symposia Proceedings, 2012, 1414, 7.	0.1	10
88	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
89	Whole-genome sequencing of the efficient industrial fuel-ethanol fermentative Saccharomyces cerevisiae strain CAT-1. Molecular Genetics and Genomics, 2012, 287, 485-494.	1.0	82
90	Improvement in cell capture throughput using parallel bioactivated microfluidic channels. Biomedical Microdevices, 2012, 14, 625-629.	1.4	9

#	ARTICLE	IF	CITATIONS
91	Molecular probe technology detects bacteria without culture. BMC Microbiology, 2012, 12, 29.	1.3	10
92	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
93	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	1.1	7
94	A Rapid, Cost-Effective Method of Assembly and Purification of Synthetic DNA Probes >100 bp. PLoS ONE, 2012, 7, e34373.	1.1	2
95	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. PLoS ONE, 2011, 6, e20016.	1.1	10
96	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	4.2	1,040
97	Experimental demonstration and analysis of DNA passage in nanopore-based nanofluidic transistors. , 2011, , .		0
98	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
99	A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance. G3: Genes, Genomes, Genetics, 2011, 1, 219-231.	0.8	25
100	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. Nucleic Acids Research, 2011, 39, 44-58.	6.5	37
101	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
102	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
103	Evidence-Based Annotation of Gene Function in Shewanella oneidensis MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. PLoS Genetics, 2011, 7, e1002385.	1.5	119
104	The Automated Cell: Compound and Environment Screening System (ACCESS) for Chemogenomic Screening. Methods in Molecular Biology, 2011, 759, 239-269.	0.4	25
105	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. BMC Bioinformatics, 2010, 11, S8.	1.2	12
106	A molecular inversion probe assay for detecting alternative splicing. BMC Genomics, 2010, 11, 712.	1.2	6
107	A direct comparison of the KBâ„¢ Basecaller and phred for identifying the bases from DNA sequencing using chain termination chemistry. BMC Research Notes, 2010, 3, 257.	0.6	9
108	Sensitive giant magnetoresistive-based immunoassay for multiplex mycotoxin detection. Biosensors and Bioelectronics, 2010, 25, 1635-1639.	5.3	108

#	ARTICLE	IF	CITATIONS
109	Clinical microfluidics for neutrophil genomics and proteomics. <i>Nature Medicine</i> , 2010, 16, 1042-1047.	15.2	168
110	A universal TagModule collection for parallel genetic analysis of microorganisms. <i>Nucleic Acids Research</i> , 2010, 38, e146-e146.	6.5	54
111	Predicting Patient Survival from Longitudinal Gene Expression. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article41.	0.2	10
112	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
113	Multiplex Identification of Microbes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3904-3910.	1.4	6
114	Gas-Phase Cleavage and Dephosphorylation of Universal Linker-Bound Oligodeoxynucleotides. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2010, 29, 867-878.	0.4	6
115	Semi-Automated Library Preparation for High-Throughput DNA Sequencing Platforms. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-8.	3.0	31
116	Plasma Proteome Response to Severe Burn Injury Revealed by ¹⁸ O-Labeled α -Universal Reference-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 4779-4789.	1.8	54
117	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
118	DMSO and Betaine Greatly Improve Amplification of GC-Rich Constructs in De Novo Synthesis. <i>PLoS ONE</i> , 2010, 5, e11024.	1.1	108
119	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
120	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
121	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
122	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
123	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. <i>PLoS Computational Biology</i> , 2009, 5, e1000374.	1.5	74
124	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
125	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. <i>Genome Research</i> , 2009, 19, 757-769.	2.4	104
126	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. <i>Genetics</i> , 2009, 183, 185-194.	1.2	71

#	ARTICLE	IF	CITATIONS
127	A dynamic network of transcription in LPS-treated human subjects. <i>BMC Systems Biology</i> , 2009, 3, 78.	3.0	36
128	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
129	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ¹⁸ O-Labeled "Universal" Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	1.8	59
130	Electrical detection of protein biomarkers using bioactivated microfluidic channels. <i>Lab on A Chip</i> , 2009, 9, 1429.	3.1	36
131	Genome-wide transcriptome analysis of 150 cell samples. <i>Integrative Biology (United Kingdom)</i> , 2009, 1, 99-107.	0.6	15
132	A Microfluidic Platform for Characterization of Protein-Protein Interactions. <i>IEEE Sensors Journal</i> , 2009, 9, 883-891.	2.4	11
133	Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways. <i>Methods in Molecular Biology</i> , 2009, 548, 115-143.	0.4	12
134	The Diversity of Nuclear Magnetic Resonance Spectroscopy. <i>NATO Science for Peace and Security Series B: Physics and Biophysics</i> , 2009, , 65-81.	0.2	0
135	Conformational flexibility of a model protein upon immobilization on self-assembled monolayers. <i>Biotechnology and Bioengineering</i> , 2008, 100, 19-27.	1.7	8
136	A system for multiplexed direct electrical detection of DNA synthesis. <i>Sensors and Actuators B: Chemical</i> , 2008, 129, 79-86.	4.0	10
137	An integrated platform of genomic assays reveals small-molecule bioactivities. <i>Nature Chemical Biology</i> , 2008, 4, 498-506.	3.9	178
138	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. <i>Science</i> , 2008, 320, 362-365.	6.0	892
139	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
140	Microfluidic Leukocyte Isolation for Gene Expression Analysis in Critically Ill Hospitalized Patients. <i>Clinical Chemistry</i> , 2008, 54, 891-900.	1.5	26
141	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
142	Multiplex protein assays based on real-time magnetic nanotag sensing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20637-20640.	3.3	271
143	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
144	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000113.	1.5	181

#	ARTICLE	IF	CITATIONS
145	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
146	Structural optimization for heat detection of DNA thermosequencing platform using finite element analysis. <i>Biomicrofluidics</i> , 2008, 2, 24102.	1.2	7
147	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
148	High Throughput Automated Allele Frequency Estimation by Pyrosequencing. <i>PLoS ONE</i> , 2008, 3, e2693.	1.1	20
149	High-Resolution, In Vivo Magnetic Resonance Imaging of Drosophila at 18.8 Tesla. <i>PLoS ONE</i> , 2008, 3, e2817.	1.1	27
150	Analysis of Genomic Instability in Colorectal Carcinoma. <i>FASEB Journal</i> , 2008, 22, 798.4.	0.2	0
151	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
152	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
153	Multiplex amplification of all coding sequences within 10 cancer genes by Gene-Collector. <i>Nucleic Acids Research</i> , 2007, 35, e47.	6.5	56
154	Chemical Genomic Profiling for Identifying Intracellular Targets of Toxicants Producing Parkinson's Disease. <i>Toxicological Sciences</i> , 2007, 95, 182-187.	1.4	16
155	Targeted cell detection based on microchannel gating. <i>Biomicrofluidics</i> , 2007, 1, 44103.	1.2	24
156	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
157	Genome sequencing and comparative analysis of <i>Saccharomyces cerevisiae</i> strain YJM789. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12825-12830.	3.3	240
158	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
159	A Novel Catechol-Based Universal Support for Oligonucleotide Synthesis. <i>Journal of Organic Chemistry</i> , 2007, 72, 9875-9880.	1.7	12
160	Involvement of Skeletal Muscle Gene Regulatory Network in Susceptibility to Wound Infection Following Trauma. <i>PLoS ONE</i> , 2007, 2, e1356.	1.1	32
161	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	294
162	Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. <i>Nature Genetics</i> , 2007, 39, 1092-1099.	9.4	207

#	ARTICLE	IF	CITATIONS
163	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	9.4	765
164	Multiplexed protein detection by proximity ligation for cancer biomarker validation. <i>Nature Methods</i> , 2007, 4, 327-329.	9.0	169
165	PathogenMip Assay: A Multiplex Pathogen Detection Assay. <i>PLoS ONE</i> , 2007, 2, e223.	1.1	25
166	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
167	Current Rectification with Poly-L-Lysine-Coated Quartz Nanopipettes. <i>Nano Letters</i> , 2006, 6, 2486-2492.	4.5	188
168	Analysis of hybridization on the molecular barcode GeneChip microarray. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 689-696.	1.0	5
169	Data quality in genomics and microarrays. <i>Nature Biotechnology</i> , 2006, 24, 1112-1113.	9.4	48
170	A unique and universal molecular barcode array. <i>Nature Methods</i> , 2006, 3, 601-603.	9.0	105
171	PathogenMIPer: a tool for the design of molecular inversion probes to detect multiple pathogens. <i>BMC Bioinformatics</i> , 2006, 7, 500.	1.2	13
172	Transcriptional Profiling of Aging in Human Muscle Reveals a Common Aging Signature. <i>PLoS Genetics</i> , 2006, 2, e115.	1.5	331
173	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
174	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
175	Introns Regulate RNA and Protein Abundance in Yeast. <i>Genetics</i> , 2006, 174, 511-518.	1.2	99
176	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
177	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
178	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
179	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
180	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

#	ARTICLE	IF	CITATIONS
181	Quantitative trait loci mapped to single-nucleotide resolution in yeast. <i>Nature Genetics</i> , 2005, 37, 1333-1340.	9.4	242
182	A network-based analysis of systemic inflammation in humans. <i>Nature</i> , 2005, 437, 1032-1037.	13.7	1,419
183	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
184	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
185	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
186	Mechanisms of Haploinsufficiency Revealed by Genome-Wide Profiling in Yeast. <i>Genetics</i> , 2005, 169, 1915-1925.	1.2	460
187	Allele quantification using molecular inversion probes (MIP). <i>Nucleic Acids Research</i> , 2005, 33, e183-e183.	6.5	81
188	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
189	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
190	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
191	Quantitative Proteome Analysis of Human Plasma following <i>In Vivo</i> Lipopolysaccharide Administration Using ¹⁶ O/ ¹⁸ O Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	2.5	156
192	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
193	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
194	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664
195	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
196	Single DNA Molecule Detection Using Nanopipettes and Nanoparticles. <i>Nano Letters</i> , 2005, 5, 403-407.	4.5	152
197	A Novel Method for STR-based DNA Profiling Using Microarrays. <i>Journal of Forensic Sciences</i> , 2005, 50, 1-5.	0.9	12
198	A novel method for STR-based DNA profiling using microarrays. <i>Journal of Forensic Sciences</i> , 2005, 50, 1109-13.	0.9	7

#	ARTICLE	IF	CITATIONS
199	Sister-chromatid cohesion mediated by the alternative RF-CCtf18/Dcc1/Ctf8, the helicase Chl1 and the polymerase- δ -associated protein Ctf4 is essential for chromatid disjunction during meiosis II. <i>Journal of Cell Science</i> , 2004, 117, 3547-3559.	1.2	130
200	SNP Discovery in Pooled Samples With Mismatch Repair Detection. <i>Genome Research</i> , 2004, 14, 1404-1412.	2.4	25
201	A multi-enzyme model for pyrosequencing. <i>Nucleic Acids Research</i> , 2004, 32, e166-e166.	6.5	47
202	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
203	To Give or Not to Give? That Is the Question: Figure 1.. <i>Plant Physiology</i> , 2004, 135, 4-9.	2.3	8
204	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
205	Whole blood and leukocyte RNA isolation for gene expression analyses. <i>Physiological Genomics</i> , 2004, 19, 247-254.	1.0	186
206	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
207	A Transcriptional Profile of Aging in the Human Kidney. <i>PLoS Biology</i> , 2004, 2, e427.	2.6	281
208	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	2.6	181
209	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004, 5, 190-201.	7.7	83
210	Regulatory networks affected by iron availability in <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 2004, 53, 1451-1469.	1.2	240
211	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
212	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
213	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
214	Determination of hepatitis C virus genotype by Pyrosequencing. <i>Journal of Virological Methods</i> , 2003, 109, 171-176.	1.0	45
215	Genotyping African haplotypes in ATM using a co-spotted single-base extension assay. <i>Human Mutation</i> , 2003, 22, 214-221.	1.1	4
216	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003, 421, 63-66.	13.7	790

#	ARTICLE	IF	CITATIONS
217	Multiplexed genotyping with sequence-tagged molecular inversion probes. <i>Nature Biotechnology</i> , 2003, 21, 673-678.	9.4	502
218	Empirical Analysis of Transcriptional Activity in the Arabidopsis Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
219	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
220	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
221	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
222	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
223	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
224	Gene Expression During the Life Cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 297, 2270-2275.	6.0	843
225	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002, 31, 400-404.	9.4	503
226	Multiplex Pyrosequencing. <i>Nucleic Acids Research</i> , 2002, 30, 31e-31.	6.5	74
227	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
228	Identification and preliminary characterization of mouse Adam33. <i>BMC Genetics</i> , 2002, 3, 2.	2.7	45
229	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	13.7	3,938
230	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
231	Sequence of <i>Plasmodium falciparum</i> chromosome 12. <i>Nature</i> , 2002, 419, 534-537.	13.7	58
232	Dissecting the architecture of a quantitative trait locus in yeast. <i>Nature</i> , 2002, 416, 326-330.	13.7	524
233	Replication Dynamics of the Yeast Genome. <i>Science</i> , 2001, 294, 115-121.	6.0	736
234	Global Analysis of ATM Polymorphism Reveals Significant Functional Constraint. <i>American Journal of Human Genetics</i> , 2001, 69, 396-412.	2.6	93

#	ARTICLE	IF	CITATIONS
235	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001, 27, 48-54.	9.4	399
236	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
237	Y chromosome sequence variation and the history of human populations. <i>Nature Genetics</i> , 2000, 26, 358-361.	9.4	935
238	The core meiotic transcriptome in budding yeasts. <i>Nature Genetics</i> , 2000, 26, 415-423.	9.4	430
239	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 816-820.	13.7	234
240	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
241	A Simple Procedure for the Analysis of Single Nucleotide Polymorphisms Facilitates Map-Based Cloning in <i>Arabidopsis</i> . <i>Plant Physiology</i> , 2000, 124, 1483-1492.	2.3	227
242	High-Density Arrays and Insights into Genome function. <i>Biotechnology and Genetic Engineering Reviews</i> , 2000, 17, 109-146.	2.4	11
243	Parallel analysis with biological chips. , 1999, , 445-II.		1
244	The mouse mahogany locus encodes a transmembrane form of human attractin. <i>Nature</i> , 1999, 398, 152-156.	13.7	194
245	Genome-wide mapping with biallelic markers in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , 1999, 23, 203-207.	9.4	260
246	Genomic profiling of drug sensitivities via induced haploinsufficiency. <i>Nature Genetics</i> , 1999, 21, 278-283.	9.4	533
247	Comparative genomes of <i>Chlamydia pneumoniae</i> and <i>C. trachomatis</i> . <i>Nature Genetics</i> , 1999, 21, 385-389.	9.4	636
248	Functional Characterization of the <i>S.&nbsp;cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. <i>Science</i> , 1999, 285, 901-906.	6.0	3,761
249	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
250	On the in vivo function of the <i>RecA</i> ATPase 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 1999, 286, 437-445.	2.0	43
251	An Automated Sample Preparation System for Large-Scale DNA Sequencing. <i>Genome Research</i> , 1999, 9, 457-462.	2.4	21
252	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	4.5	1,927

#	ARTICLE	IF	CITATIONS
253	Direct Allelic Variation Scanning of the Yeast Genome. , 1998, 281, 1194-1197.		368
254	Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis. , 1998, 282, 754-759.		1,449
255	Detection of Numerous Y Chromosome Biallelic Polymorphisms by Denaturing High-Performance Liquid Chromatography. Genome Research, 1997, 7, 996-1005.	2.4	617
256	Functional analysis of the yeast genome. Current Opinion in Genetics and Development, 1997, 7, 771-776.	1.5	59
257	Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular bar coding strategy. Nature Genetics, 1996, 14, 450-456.	9.4	545
258	<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
259	Functional expression of the yeast FLP/FRT site-specific recombination system in <i>Nicotiana tabacum</i> . Molecular Genetics and Genomics, 1994, 242, 653-657.	2.4	86
260	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
261	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
262	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
263	The <i>Saccharomyces cerevisiae</i> RPB4 gene is tightly linked to the TIF2 gene. Nucleic Acids Research, 1991, 19, 2781-2781.	6.5	9
264	Yeast centromere binding protein CBF1, of the helix-loop-helix protein family, is required for chromosome stability and methionine prototrophy. Cell, 1990, 61, 437-446.	13.5	360
265	The poly(A) binding protein is required for poly(A) shortening and 60S ribosomal subunit-dependent translation initiation. Cell, 1989, 58, 857-867.	13.5	559
266	Strategies for Genetic Modification of Parasites. Annals of the New York Academy of Sciences, 1989, 569, 104-117.	1.8	1
267	Genomic organization of two families of highly repeated nuclear DNA sequences of maize selected for autonomous replicating activity in yeast. Plant Molecular Biology, 1988, 11, 161-172.	2.0	5
268	Sequence analysis of three fragments of maize nuclear DNA which replicate autonomously in yeast. Plant Molecular Biology, 1988, 11, 173-182.	2.0	7
269	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
270	SPA1: A gene important for chromosome segregation and other mitotic functions in <i>S. cerevisiae</i> . Cell, 1988, 54, 743-754.	13.5	72

#	ARTICLE	IF	CITATIONS
271	[7] 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	0.4	161
272	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
273	Bent DNA at a yeast autonomously replicating sequence. <i>Nature</i> , 1986, 324, 87-89.	13.7	218
274	Genes for the major protein antigens of the leprosy parasite <i>Mycobacterium leprae</i> . <i>Nature</i> , 1985, 316, 450-452.	13.7	365
275	Functional selection and analysis of yeast centromeric DNA. <i>Cell</i> , 1985, 42, 913-921.	13.5	270
276	Immunoscreening Recombinant DNA Expression Libraries. , 1985, , 29-41.		17
277	Centromeric DNA from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1982, 158, 157-179.	2.0	317
278	Reversion of a promoter deletion in yeast. <i>Nature</i> , 1982, 298, 815-819.	13.7	81
279	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
280	Deletion analysis of the <i>Saccharomyces GAL</i> gene cluster. <i>Journal of Molecular Biology</i> , 1981, 152, 317-334.	2.0	85
281	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
282	Promoter mutants of the yeast <i>his3</i> gene. <i>Journal of Molecular Biology</i> , 1981, 152, 553-568.	2.0	46
283	DNA SEQUENCES THAT ALLOW THE REPLICATION AND SEGREGATION OF YEAST CHROMOSOMES. , 1981, , 473-488.		30
284	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
285	[49] Rapid DNA isolations for enzymatic and hybridization analysis. <i>Methods in Enzymology</i> , 1980, 65, 404-411.	0.4	610
286	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
287	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
288	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

#	ARTICLE	IF	CITATIONS
289	Suppression of a yeast amber mutation in <i>Escherichia coli</i> . <i>Nature</i> , 1979, 279, 78-79.	13.7	5
290	Evidence for transposition of dispersed repetitive DNA families in yeast. <i>Cell</i> , 1979, 16, 739-751.	13.5	619
291	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
292	Cloning of the yeast tyrosine transfer RNA genes in bacteriophage lambda. <i>Journal of Molecular Biology</i> , 1979, 127, 285-295.	2.0	42
293	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
294	Cloning of the yeast ribosomal DNA repeat unit in SstI and HindIII lambda vectors using genetic and physical size selections. <i>Journal of Molecular Biology</i> , 1978, 123, 371-386.	2.0	136
295	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
296	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
297	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
298	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
299	Analysis of chromosomal integration and deletions of yeast plasmids. <i>Nucleic Acids Research</i> , 1977, 4, 1429-1448.	6.5	259
300	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
301	Determination of DNA concentration by electron microscopy. <i>Analytical Biochemistry</i> , 1976, 72, 460-467.	1.1	12
302	KINETIC STUDIES ON THE HYBRIDIZATION OF RNA TO DOUBLE STRANDED DNA. , 1976, , 427-444.		0
303	An electron microscopic method for studying and mapping the region of weak sequence homology between simian virus 40 and polyoma DNAs. <i>Journal of Molecular Biology</i> , 1975, 94, 135-149.	2.0	58
304	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
305	A study in evolution: the DNA base sequence homology between coliphages T7 and T3. <i>Journal of Molecular Biology</i> , 1971, 62, 287-301.	2.0	261
306	A physical map of the left arm of the lambda chromosome. <i>Journal of Molecular Biology</i> , 1971, 56, 425-428.	2.0	24

#	ARTICLE	IF	CITATIONS
307	Deletion mutants of bacteriophage lambda. Journal of Molecular Biology, 1971, 56, 403-423.	2.0	174
308	[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
309	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
310	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