

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

1172

111
h-index

322

288
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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.	7.1	11
2	A Comprehensive Examination of Severely Ill ME/CFS Patients. Healthcare (Switzerland), 2021, 9, 1290.	2.0	12
3	Modeling Brownian Microparticle Trajectories in Lab-on-a-Chip Devices with Time Varying Dielectrophoretic or Optical Forces. Micromachines, 2021, 12, 1265.	2.9	9
4	Community members in activated sludge as determined by molecular probe technology. Water Research, 2020, 168, 115104.	11.3	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.	7.1	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.	4.1	146
8	Meta-analysis of peptides to detect protein significance. Statistics and Its Interface, 2020, 13, 465-474.	0.3	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.	7.1	64
10	Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. Genetics in Medicine, 2019, 21, 896-903.	2.4	31
11	Red blood cell deformability is diminished in patients with Chronic Fatigue Syndrome. Clinical Hemorheology and Microcirculation, 2019, 71, 113-116.	1.7	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.	3.4	4
13	HEx: A heterologous expression platform for the discovery of fungal natural products. Science Advances, 2018, 4, eaar5459.	10.3	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.	7.1	23
15	Template-Independent Enzymatic Oligonucleotide Synthesis (TIEOS): Its History, Prospects, and Challenges. Biochemistry, 2018, 57, 1821-1832.	2.5	50
16	Transplant Virus Detection Using Multiplex Targeted Sequencing. journal of applied laboratory medicine, The, 2018, 2, 757-769.	1.3	4
17	Multiplexed precision genome editing with trackable genomic barcodes in yeast. Nature Biotechnology, 2018, 36, 512-520.	17.5	138
18	Erythrocyte Deformability As a Potential Biomarker for Chronic Fatigue Syndrome. Blood, 2018, 132, 4874-4874.	1.4	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.	7.1	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.	2.0	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.	7.1	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.	7.2	41
23	Quantitative analysis of protein interaction network dynamics in yeast. <i>Molecular Systems Biology</i> , 2017, 13, 934.	7.2	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.	14.6	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.	3.1	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.	0.3	4
29	Systematic Mapping of Chemical-Genetic Interactions in <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077701.	0.3	5
30	Application of 3D Printing for Smart Objects with Embedded Electronic Sensors and Systems. <i>Advanced Materials Technologies</i> , 2016, 1, 1600013.	5.8	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.	10.0	39
32	Fully integrated wearable sensor arrays for multiplexed in situ perspiration analysis. <i>Nature</i> , 2016, 529, 509-514.	27.8	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.	2.8	15
34	Next-Generation Molecular Testing of Newborn Dried Blood Spots for Cystic Fibrosis. <i>Journal of Molecular Diagnostics</i> , 2016, 18, 267-282.	2.8	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.	8.8	165
36	Nucleotide-Specific Contrast for DNA Sequencing by Electron Spectroscopy. <i>PLoS ONE</i> , 2016, 11, e0154707.	2.5	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.	2.5	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.	14.5	29
39	Robust Optimization of Biological Protocols. <i>Technometrics</i> , 2015, 57, 234-244.	1.9	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.	2.4	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.	7.1	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.	7.1	56
43	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <i>Scientific Reports</i> , 2015, 5, 11917.	3.3	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.	7.1	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.	4.5	34
46	Mice are not men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E345.	7.1	102
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.	2.5	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.	4.1	56
49	Computational identification and analysis of orphan assembly-line polyketide synthases. <i>Journal of Antibiotics</i> , 2014, 67, 89-97.	2.0	59
50	Detecting differential protein expression in large-scale population proteomics. <i>Bioinformatics</i> , 2014, 30, 2741-2746.	4.1	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.	12.6	217
53	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. <i>Reproductive Sciences</i> , 2014, 21, 32-40.	2.5	259
54	The 50:50 method for PCR-based seamless genome editing in yeast. <i>Yeast</i> , 2014, 31, 103-112.	1.7	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.	1.7	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.	7.1	115
57	Nanoelectronic impedance detection of target cells. <i>Biotechnology and Bioengineering</i> , 2014, 111, 1161-1169.	3.3	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.	2.6	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.	7.1	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.	0.6	3
62	A functional screen for copper homeostasis genes identifies a pharmacologically tractable cellular system. <i>BMC Genomics</i> , 2014, 15, 263.	2.8	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.	3.1	6
64	PITPs as targets for selectively interfering with phosphoinositide signaling in cells. <i>Nature Chemical Biology</i> , 2014, 10, 76-84.	8.0	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.	6.0	9
66	Multiplex target capture with double-stranded DNA probes. <i>Genome Medicine</i> , 2013, 5, 50.	8.2	18
67	Trauma-associated human neutrophil alterations revealed by comparative proteomics profiling. <i>Proteomics - Clinical Applications</i> , 2013, 7, 571-583.	1.6	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.	2.6	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.	7.8	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.	7.1	2,518
71	Coded Corrugated Microfluidic Sidewalls for Code Division Multiplexing. <i>IEEE Sensors Journal</i> , 2013, 13, 1399-1400.	4.7	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.	7.1	54
74	Label-free electronic probing of nucleic acids and proteins at the nanoscale using the nanoneedle biosensor. Biomicrofluidics, 2013, 7, 044114.	2.4	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.	7.1	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.	7.1	8
77	The Sequencing Bead Array (SBA), a Next-Generation Digital Suspension Array. PLoS ONE, 2013, 8, e76696.	2.5	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.	1.2	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.	14.5	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.	4.2	92
81	Microfluidic Platform for Electrical Monitoring of Enzyme Activity. IEEE Sensors Journal, 2012, 12, 2733-2734.	4.7	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.	7.1	200
83	Microfluidic diagnostic tool for the developing world: contactless impedance flow cytometry. Lab on A Chip, 2012, 12, 4499.	6.0	59
84	Smart Surface for Elution of Protein-bound Particles: Nanonewton Dielectrophoretic Forces Using Atomic Layer Deposited Oxides. Analytical Chemistry, 2012, 84, 10793-10801.	6.5	15
85	Use of Negative Dielectrophoresis for Selective Elution of Protein-Bound Particles. Analytical Chemistry, 2012, 84, 1432-1438.	6.5	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.	2.5	8
88	Single Cell Profiling of Circulating Tumor Cells: Transcriptional Heterogeneity and Diversity from Breast Cancer Cell Lines. PLoS ONE, 2012, 7, e33788.	2.5	475
89	Coding SNPs as intrinsic markers for sample tracking in large-scale transcriptome studies. BioTechniques, 2012, 52, 386-8.	1.8	3
90	JETTA: junction and exon toolkits for transcriptome analysis. Bioinformatics, 2012, 28, 1274-1275.	4.1	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.	7.1	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.	2.1	82
94	Improvement in cell capture throughput using parallel bioactivated microfluidic channels. Biomedical Microdevices, 2012, 14, 625-629.	2.8	9
95	Molecular probe technology detects bacteria without culture. BMC Microbiology, 2012, 12, 29.	3.3	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.	2.5	124
97	Knowledge-Based Reconstruction of mRNA Transcripts with Short Sequencing Reads for Transcriptome Research. PLoS ONE, 2012, 7, e31440.	2.5	7
98	A Rapid, Cost-Effective Method of Assembly and Purification of Synthetic DNA Probes >100 bp. PLoS ONE, 2012, 7, e34373.	2.5	2
99	Distinctive Responsiveness to Stromal Signaling Accompanies Histologic Grade Programming of Cancer Cells. PLoS ONE, 2011, 6, e20016.	2.5	10
100	A genomic storm in critically injured humans. Journal of Experimental Medicine, 2011, 208, 2581-2590.	8.5	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.	7.1	124
103	A Global Perspective of the Genetic Basis for Carbonyl Stress Resistance. G3: Genes, Genomes, Genetics, 2011, 1, 219-231.	1.8	25
104	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. Nucleic Acids Research, 2011, 39, 44-58.	14.5	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.	7.1	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.	7.1	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.	3.5	119
108	The Automated Cell: Compound and Environment Screening System (ACCESS) for Chemogenomic Screening. Methods in Molecular Biology, 2011, 759, 239-269.	0.9	25

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109	Knowledge-based analysis of microarrays for the discovery of transcriptional regulation relationships. BMC Bioinformatics, 2010, 11, S8.	2.6	12
110	A molecular inversion probe assay for detecting alternative splicing. BMC Genomics, 2010, 11, 712.	2.8	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.	1.4	9
112	Sensitive giant magnetoresistive-based immunoassay for multiplex mycotoxin detection. Biosensors and Bioelectronics, 2010, 25, 1635-1639.	10.1	108
113	Clinical microfluidics for neutrophil genomics and proteomics. Nature Medicine, 2010, 16, 1042-1047.	30.7	168
114	A universal TagModule collection for parallel genetic analysis of microorganisms. Nucleic Acids Research, 2010, 38, e146-e146.	14.5	54
115	Predicting Patient Survival from Longitudinal Gene Expression. Statistical Applications in Genetics and Molecular Biology, 2010, 9, Article41.	0.6	10
116	Gene Annotation and Drug Target Discovery in Candida albicans with a Tagged Transposon Mutant Collection. PLoS Pathogens, 2010, 6, e1001140.	4.7	85
117	Multiplex Identification of Microbes. Applied and Environmental Microbiology, 2010, 76, 3904-3910.	3.1	6
118	Gas-Phase Cleavage and Dephosphorylation of Universal Linker-Bound Oligodeoxynucleotides. Nucleosides, Nucleotides and Nucleic Acids, 2010, 29, 867-878.	1.1	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.	3.7	54
121	Systematic analysis of genome-wide fitness data in yeast reveals novel gene function and drug action. Genome Biology, 2010, 11, R30.	9.6	94
122	DMSO and Betaine Greatly Improve Amplification of GC-Rich Constructs in De Novo Synthesis. PLoS ONE, 2010, 5, e11024.	2.5	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.	7.1	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.	7.1	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.	7.1	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.	3.5	50

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127	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. PLoS Computational Biology, 2009, 5, e1000374.	3.2	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.	3.5	134
129	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. Genome Research, 2009, 19, 757-769.	5.5	104
130	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. Genetics, 2009, 183, 185-194.	2.9	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.	2.5	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.	3.7	59
134	Electrical detection of protein biomarkers using bioactivated microfluidic channels. Lab on A Chip, 2009, 9, 1429.	6.0	36
135	Genome-wide transcriptome analysis of 150 cell samples. Integrative Biology (United Kingdom), 2009, 1, 99-107.	1.3	15
136	A Microfluidic Platform for Characterization of Protein-Protein Interactions. IEEE Sensors Journal, 2009, 9, 883-891.	4.7	11
137	Chemogenomic Approaches to Elucidation of Gene Function and Genetic Pathways. Methods in Molecular Biology, 2009, 548, 115-143.	0.9	12
138	The Diversity of Nuclear Magnetic Resonance Spectroscopy. NATO Science for Peace and Security Series B: Physics and Biophysics, 2009, , 65-81.	0.3	0
139	Conformational flexibility of a model protein upon immobilization on self-assembled monolayers. Biotechnology and Bioengineering, 2008, 100, 19-27.	3.3	8
140	A system for multiplexed direct electrical detection of DNA synthesis. Sensors and Actuators B: Chemical, 2008, 129, 79-86.	7.8	10
141	An integrated platform of genomic assays reveals small-molecule bioactivities. Nature Chemical Biology, 2008, 4, 498-506.	8.0	178
142	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. Science, 2008, 320, 362-365.	12.6	892
143	Bisphenol A Induces a Profile of Tumor Aggressiveness in High-Risk Cells from Breast Cancer Patients. Cancer Research, 2008, 68, 2076-2080.	0.9	101
144	Microfluidic Leukocyte Isolation for Gene Expression Analysis in Critically Ill Hospitalized Patients. Clinical Chemistry, 2008, 54, 891-900.	3.2	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.	7.1	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.	7.1	271
147	Multiplexed Proximity Ligation Assays to Profile Putative Plasma Biomarkers Relevant to Pancreatic and Ovarian Cancer. Clinical Chemistry, 2008, 54, 582-589.	3.2	84
148	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. PLoS Genetics, 2008, 4, e1000113.	3.5	181
149	Sequential Elimination of Major-Effect Contributors Identifies Additional Quantitative Trait Loci Conditioning High-Temperature Growth in Yeast. Genetics, 2008, 180, 1661-1670.	2.9	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.	2.4	7
152	High-Throughput Creation of a Whole-Genome Collection of Yeast Knockout Strains. Methods in Molecular Biology, 2008, 416, 205-220.	0.9	20
153	High Throughput Automated Allele Frequency Estimation by Pyrosequencing. PLoS ONE, 2008, 3, e2693.	2.5	20
154	High-Resolution, In Vivo Magnetic Resonance Imaging of Drosophila at 18.8 Tesla. PLoS ONE, 2008, 3, e2817.	2.5	27
155	Analysis of Genomic Instability in Colorectal Carcinoma. FASEB Journal, 2008, 22, 798.4.	0.5	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.	7.1	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.	7.1	159
158	Multiplex amplification of all coding sequences within 10 cancer genes by Gene-Collector. Nucleic Acids Research, 2007, 35, e47.	14.5	56
159	Chemical Genomic Profiling for Identifying Intracellular Targets of Toxicants Producing Parkinson's Disease. Toxicological Sciences, 2007, 95, 182-187.	3.1	16
160	Targeted cell detection based on microchannel gating. Biomicrofluidics, 2007, 1, 44103.	2.4	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.	7.1	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.	7.1	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.	3.0	56
164	A Novel Catechol-Based Universal Support for Oligonucleotide Synthesis. <i>Journal of Organic Chemistry</i> , 2007, 72, 9875-9880.	3.2	12
165	Involvement of Skeletal Muscle Gene Regulatory Network in Susceptibility to Wound Infection Following Trauma. <i>PLoS ONE</i> , 2007, 2, e1356.	2.5	32
166	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	21.4	294
167	Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. <i>Nature Genetics</i> , 2007, 39, 1092-1099.	21.4	207
168	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	21.4	765
169	Multiplexed protein detection by proximity ligation for cancer biomarker validation. <i>Nature Methods</i> , 2007, 4, 327-329.	19.0	169
170	PathogenMip Assay: A Multiplex Pathogen Detection Assay. <i>PLoS ONE</i> , 2007, 2, e223.	2.5	25
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