

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	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	13.7	3,938
3	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
4	Functional Characterization of the <i>Saccharomyces cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. <i>Science</i> , 1999, 285, 901-906.	6.0	3,761
5	Fully integrated wearable sensor arrays for multiplexed in situ perspiration analysis. <i>Nature</i> , 2016, 529, 509-514.	13.7	3,508
6	Genomic responses in mouse models poorly mimic human inflammatory diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3507-3512.	3.3	2,518
7	A Genome-Wide Transcriptional Analysis of the Mitotic Cell Cycle. <i>Molecular Cell</i> , 1998, 2, 65-73.	4.5	1,927
8	Genome Sequence of an Obligate Intracellular Pathogen of Humans: <i>Chlamydia trachomatis</i> . , 1998, 282, 754-759.		1,449
9	A network-based analysis of systemic inflammation in humans. <i>Nature</i> , 2005, 437, 1032-1037.	13.7	1,419
10	[31] Electron microscope heteroduplex methods for mapping regions of base sequence homology in nucleic acids. <i>Methods in Enzymology</i> , 1971, 21, 413-428.	0.4	1,205
11	Sterile host yeasts (SHY): A eukaryotic system of biological containment for recombinant DNA experiments. <i>Gene</i> , 1979, 8, 17-24.	1.0	1,086
12	A genomic storm in critically injured humans. <i>Journal of Experimental Medicine</i> , 2011, 208, 2581-2590.	4.2	1,040
13	Y chromosome sequence variation and the history of human populations. <i>Nature Genetics</i> , 2000, 26, 358-361.	9.4	935
14	Studies on the cleavage of bacteriophage lambda DNA with EcoRI restriction endonuclease. <i>Journal of Molecular Biology</i> , 1975, 91, 315-328.	2.0	910
15	The Chemical Genomic Portrait of Yeast: Uncovering a Phenotype for All Genes. <i>Science</i> , 2008, 320, 362-365.	6.0	892
16	Empirical Analysis of Transcriptional Activity in the <i>Arabidopsis</i> Genome. <i>Science</i> , 2003, 302, 842-846.	6.0	853
17	Gene Expression During the Life Cycle of <i>Drosophila melanogaster</i> . <i>Science</i> , 2002, 297, 2270-2275.	6.0	843
18	Role of duplicate genes in genetic robustness against null mutations. <i>Nature</i> , 2003, 421, 63-66.	13.7	790

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19	A high-resolution atlas of nucleosome occupancy in yeast. <i>Nature Genetics</i> , 2007, 39, 1235-1244.	9.4	765
20	Replication Dynamics of the Yeast Genome. <i>Science</i> , 2001, 294, 115-121.	6.0	736
21	The diploid genome sequence of <i>Candida albicans</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7329-7334.	3.3	692
22	The Genome of the Basidiomycetous Yeast and Human Pathogen <i>Cryptococcus neoformans</i> . <i>Science</i> , 2005, 307, 1321-1324.	6.0	664
23	Comparative genomes of <i>Chlamydia pneumoniae</i> and <i>C. trachomatis</i> . <i>Nature Genetics</i> , 1999, 21, 385-389.	9.4	636
24	Evidence for transposition of dispersed repetitive DNA families in yeast. <i>Cell</i> , 1979, 16, 739-751.	13.5	619
25	Detection of Numerous Y Chromosome Biallelic Polymorphisms by Denaturing High-Performance Liquid Chromatography. <i>Genome Research</i> , 1997, 7, 996-1005.	2.4	617
26	A high-resolution map of transcription in the yeast genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 5320-5325.	3.3	613
27	[49] Rapid DNA isolations for enzymatic and hybridization analysis. <i>Methods in Enzymology</i> , 1980, 65, 404-411.	0.4	610
28	Autonomous sweat extraction and analysis applied to cystic fibrosis and glucose monitoring using a fully integrated wearable platform. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4625-4630.	3.3	573
29	The poly(A) binding protein is required for poly(A) shortening and 60S ribosomal subunit-dependent translation initiation. <i>Cell</i> , 1989, 58, 857-867.	13.5	559
30	Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular barcoding strategy. <i>Nature Genetics</i> , 1996, 14, 450-456.	9.4	545
31	Significance analysis of time course microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 12837-12842.	3.3	534
32	Genomic profiling of drug sensitivities via induced haploinsufficiency. <i>Nature Genetics</i> , 1999, 21, 278-283.	9.4	533
33	Dissecting the architecture of a quantitative trait locus in yeast. <i>Nature</i> , 2002, 416, 326-330.	13.7	524
34	Systematic screen for human disease genes in yeast. <i>Nature Genetics</i> , 2002, 31, 400-404.	9.4	503
35	Multiplexed genotyping with sequence-tagged molecular inversion probes. <i>Nature Biotechnology</i> , 2003, 21, 673-678.	9.4	502
36	Identification of the SAAT Gene Involved in Strawberry Flavor Biogenesis by Use of DNA Microarrays. <i>Plant Cell</i> , 2000, 12, 647-661.	3.1	496

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37	A Genome-Wide Study of Gene Activity Reveals Developmental Signaling Pathways in the Preimplantation Mouse Embryo. <i>Developmental Cell</i> , 2004, 6, 133-144.	3.1	481
38	A Wearable Electrochemical Platform for Noninvasive Simultaneous Monitoring of Ca ²⁺ and pH. <i>ACS Nano</i> , 2016, 10, 7216-7224.	7.3	480
39	Single Cell Profiling of Circulating Tumor Cells: Transcriptional Heterogeneity and Diversity from Breast Cancer Cell Lines. <i>PLoS ONE</i> , 2012, 7, e33788.	1.1	475
40	Chemogenomic profiling: Identifying the functional interactions of small molecules in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 793-798.	3.3	460
41	Mechanisms of Haploinsufficiency Revealed by Genome-Wide Profiling in Yeast. <i>Genetics</i> , 2005, 169, 1915-1925.	1.2	460
42	Isolating highly enriched populations of circulating epithelial cells and other rare cells from blood using a magnetic sweeper device. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3970-3975.	3.3	448
43	The core meiotic transcriptome in budding yeasts. <i>Nature Genetics</i> , 2000, 26, 415-423.	9.4	430
44	Transcriptional regulation and function during the human cell cycle. <i>Nature Genetics</i> , 2001, 27, 48-54.	9.4	399
45	The organization and transcription of the galactose gene cluster of <i>Saccharomyces</i> . <i>Journal of Molecular Biology</i> , 1981, 152, 285-315.	2.0	378
46	Direct Allelic Variation Scanning of the Yeast Genome. , 1998, 281, 1194-1197.		368
47	Genes for the major protein antigens of the leprosy parasite <i>Mycobacterium leprae</i> . <i>Nature</i> , 1985, 316, 450-452.	13.7	365
48	Yeast centromere binding protein CBF1, of the helix-loop-helix protein family, is required for chromosome stability and methionine prototrophy. <i>Cell</i> , 1990, 61, 437-446.	13.5	360
49	Isolation of galactose-inducible DNA sequences from <i>Saccharomyces cerevisiae</i> by differential plaque filter hybridization. <i>Cell</i> , 1979, 16, 443-452.	13.5	338
50	Resolution of DNA molecules greater than 5 megabases by contour-clamped homogeneous electric fields. <i>Nucleic Acids Research</i> , 1987, 15, 7865-7876.	6.5	338
51	Transcriptional Profiling of Aging in Human Muscle Reveals a Common Aging Signature. <i>PLoS Genetics</i> , 2006, 2, e115.	1.5	331
52	Centromeric DNA from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1982, 158, 157-179.	2.0	317
53	Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. <i>Nature Genetics</i> , 2007, 39, 199-206.	9.4	294
54	Ultra-High-Efficiency Strong Cation Exchange LC/RPLC/MS/MS for High Dynamic Range Characterization of the Human Plasma Proteome. <i>Analytical Chemistry</i> , 2004, 76, 1134-1144.	3.2	290

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55	A Transcriptional Profile of Aging in the Human Kidney. PLoS Biology, 2004, 2, e427.	2.6	281
56	Microbes on the human vaginal epithelium. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7952-7957.	3.3	281
57	Highly multiplexed molecular inversion probe genotyping: Over 10,000 targeted SNPs genotyped in a single tube assay. Genome Research, 2005, 15, 269-275.	2.4	276
58	Metabolic specialization associated with phenotypic switching in <i>Candida albicans</i> . Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14907-14912.	3.3	271
59	Multiplex protein assays based on real-time magnetic nanotag sensing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20637-20640.	3.3	271
60	Functional selection and analysis of yeast centromeric DNA. Cell, 1985, 42, 913-921.	13.5	270
61	A study in evolution: the DNA base sequence homology between coliphages T7 and T3. Journal of Molecular Biology, 1971, 62, 287-301.	2.0	261
62	Genome-wide mapping with biallelic markers in <i>Arabidopsis thaliana</i> . Nature Genetics, 1999, 23, 203-207.	9.4	260
63	Analysis of chromosomal integration and deletions of yeast plasmids. Nucleic Acids Research, 1977, 4, 1429-1448.	6.5	259
64	Diversity of the Vaginal Microbiome Correlates With Preterm Birth. Reproductive Sciences, 2014, 21, 32-40.	1.1	259
65	A family of versatile centromeric vectors designed for use in the sectoring-shuffle mutagenesis assay in <i>Saccharomyces cerevisiae</i> . Gene, 1988, 70, 303-312.	1.0	253
66	Quantitative trait loci mapped to single-nucleotide resolution in yeast. Nature Genetics, 2005, 37, 1333-1340.	9.4	242
67	Regulatory networks affected by iron availability in <i>Candida albicans</i> . Molecular Microbiology, 2004, 53, 1451-1469.	1.2	240
68	Genome sequencing and comparative analysis of <i>Saccharomyces cerevisiae</i> strain YJM789. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12825-12830.	3.3	240
69	Application of genome-wide expression analysis to human health and disease. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4801-4806.	3.3	238
70	Sequence and analysis of chromosome 1 of the plant <i>Arabidopsis thaliana</i> . Nature, 2000, 408, 816-820.	13.7	234
71	Transcriptional response of <i>Saccharomyces cerevisiae</i> to DNA-damaging agents does not identify the genes that protect against these agents. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8778-8783.	3.3	234
72	A physical study by electron microscopy of the terminally repetitious, circularly permuted DNA from the coliphage particles of <i>Escherichia coli</i> 15. Journal of Molecular Biology, 1970, 48, 1-22.	2.0	229

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73	A Simple Procedure for the Analysis of Single Nucleotide Polymorphisms Facilitates Map-Based Cloning in Arabidopsis. <i>Plant Physiology</i> , 2000, 124, 1483-1492.	2.3	227
74	Bent DNA at a yeast autonomously replicating sequence. <i>Nature</i> , 1986, 324, 87-89.	13.7	218
75	Mapping the Cellular Response to Small Molecules Using Chemogenomic Fitness Signatures. <i>Science</i> , 2014, 344, 208-211.	6.0	217
76	Detection of single micron-sized magnetic bead and magnetic nanoparticles using spin valve sensors for biological applications. <i>Journal of Applied Physics</i> , 2003, 93, 7557-7559.	1.1	211
77	Unusual selection on the KIR3DL1/S1 natural killer cell receptor in Africans. <i>Nature Genetics</i> , 2007, 39, 1092-1099.	9.4	207
78	High-throughput, high-fidelity HLA genotyping with deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 8676-8681.	3.3	200
79	The mouse mahogany locus encodes a transmembrane form of human attractin. <i>Nature</i> , 1999, 398, 152-156.	13.7	194
80	Unique arrangement of coding sequences for 5 S, 5.8 S, 18 S and 25 S ribosomal RNA in <i>Saccharomyces cerevisiae</i> as determined by R-loop and hybridization analysis. <i>Journal of Molecular Biology</i> , 1978, 123, 387-404.	2.0	193
81	Functional genomics of genes with small open reading frames (sORFs) in <i>S. cerevisiae</i> . <i>Genome Research</i> , 2006, 16, 365-373.	2.4	193
82	Magnetic levitation of single cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3661-8.	3.3	192
83	Current Rectification with Poly-L-Lysine-Coated Quartz Nanopipettes. <i>Nano Letters</i> , 2006, 6, 2486-2492.	4.5	188
84	Whole blood and leukocyte RNA isolation for gene expression analyses. <i>Physiological Genomics</i> , 2004, 19, 247-254.	1.0	186
85	Integrative Analysis of the Mitochondrial Proteome in Yeast. <i>PLoS Biology</i> , 2004, 2, e160.	2.6	181
86	Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000113.	1.5	181
87	An integrated platform of genomic assays reveals small-molecule bioactivities. <i>Nature Chemical Biology</i> , 2008, 4, 498-506.	3.9	178
88	Deletion mutants of bacteriophage lambda. <i>Journal of Molecular Biology</i> , 1971, 56, 403-423.	2.0	174
89	Multiplexed protein detection by proximity ligation for cancer biomarker validation. <i>Nature Methods</i> , 2007, 4, 327-329.	9.0	169
90	Clinical microfluidics for neutrophil genomics and proteomics. <i>Nature Medicine</i> , 2010, 16, 1042-1047.	15.2	168

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91	Application of 3D Printing for Smart Objects with Embedded Electronic Sensors and Systems. <i>Advanced Materials Technologies</i> , 2016, 1, 1600013.	3.0	167
92	HEx: A heterologous expression platform for the discovery of fungal natural products. <i>Science Advances</i> , 2018, 4, eaar5459.	4.7	167
93	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
94	[7] λ gt 11: Gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987, 154, 107-128.	0.4	161
95	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
96	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
97	Quantitative Proteome Analysis of Human Plasma following in Vivo Lipopolysaccharide Administration Using $^{16}\text{O}/^{18}\text{O}$ Labeling and the Accurate Mass and Time Tag Approach. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 700-709.	2.5	156
98	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
99	Single DNA Molecule Detection Using Nanopipettes and Nanoparticles. <i>Nano Letters</i> , 2005, 5, 403-407.	4.5	152
100	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
101	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
102	Microfluidic Point-of-Care Testing: Commercial Landscape and Future Directions. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 602659.	2.0	146
103	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
104	Genome-Wide Requirements for Resistance to Functionally Distinct DNA-Damaging Agents. <i>PLoS Genetics</i> , 2005, 1, e24.	1.5	144
105	High Dynamic Range Characterization of the Trauma Patient Plasma Proteome. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1899-1913.	2.5	142
106	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	9.4	138
107	Cloning of the yeast ribosomal DNA repeat unit in <i>Sst</i> I and <i>Hind</i> III λ vectors using genetic and physical size selections. <i>Journal of Molecular Biology</i> , 1978, 123, 371-386.	2.0	136
108	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

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109	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
110	A physical, genetic and transcriptional map of the cloned his3 gene region of <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 1980, 136, 309-332.	2.0	128
111	Comparative proteome analyses of human plasma following in vivo lipopolysaccharide administration using multidimensional separations coupled with tandem mass spectrometry. <i>Proteomics</i> , 2005, 5, 572-584.	1.3	125
112	Execution of the meiotic noncoding RNA expression program and the onset of gametogenesis in yeast require the conserved exosome subunit Rrp6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1058-1063.	3.3	124
113	The dynamics of the vaginal microbiome during infertility therapy with in vitro fertilization-embryo transfer. <i>Journal of Assisted Reproduction and Genetics</i> , 2012, 29, 105-115.	1.2	124
114	Human transcriptome array for high-throughput clinical studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 3707-3712.	3.3	122
115	Evidence-Based Annotation of Gene Function in <i>Shewanella oneidensis</i> MR-1 Using Genome-Wide Fitness Profiling across 121 Conditions. <i>PLoS Genetics</i> , 2011, 7, e1002385.	1.5	119
116	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
117	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
118	Sensitive giant magnetoresistive-based immunoassay for multiplex mycotoxin detection. <i>Biosensors and Bioelectronics</i> , 2010, 25, 1635-1639.	5.3	108
119	DMSO and Betaine Greatly Improve Amplification of GC-Rich Constructs in De Novo Synthesis. <i>PLoS ONE</i> , 2010, 5, e11024.	1.1	108
120	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
121	Homology and structural relationships between the dimeric and monomeric circular forms of mitochondrial DNA from human leukemic leukocytes. <i>Journal of Molecular Biology</i> , 1970, 47, 137-153.	2.0	106
122	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
123	A unique and universal molecular barcode array. <i>Nature Methods</i> , 2006, 3, 601-603.	9.0	105
124	Meiotic recombination generates rich diversity in NK cell receptor genes, alleles, and haplotypes. <i>Genome Research</i> , 2009, 19, 757-769.	2.4	104
125	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
126	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

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127	Introns Regulate RNA and Protein Abundance in Yeast. <i>Genetics</i> , 2006, 174, 511-518.	1.2	99
128	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
129	Global Analysis of ATM Polymorphism Reveals Significant Functional Constraint. <i>American Journal of Human Genetics</i> , 2001, 69, 396-412.	2.6	93
130	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
131	Benchmarking Outcomes in the Critically Injured Trauma Patient and the Effect of Implementing Standard Operating Procedures. <i>Annals of Surgery</i> , 2012, 255, 993-999.	2.1	92
132	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
133	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
134	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
135	Deletion analysis of the <i>Saccharomyces GAL</i> gene cluster. <i>Journal of Molecular Biology</i> , 1981, 152, 317-334.	2.0	85
136	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
137	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
138	Maximizing the potential of functional genomics. <i>Nature Reviews Genetics</i> , 2004, 5, 190-201.	7.7	83
139	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
140	Whole-genome sequencing of the efficient industrial fuel-ethanol fermentative <i>Saccharomyces cerevisiae</i> strain CAT-1. <i>Molecular Genetics and Genomics</i> , 2012, 287, 485-494.	1.0	82
141	Reversion of a promoter deletion in yeast. <i>Nature</i> , 1982, 298, 815-819.	13.7	81
142	Allele quantification using molecular inversion probes (MIP). <i>Nucleic Acids Research</i> , 2005, 33, e183-e183.	6.5	81
143	Multiplex Pyrosequencing. <i>Nucleic Acids Research</i> , 2002, 30, 31e-31.	6.5	74
144	Mapping Gene Associations in Human Mitochondria using Clinical Disease Phenotypes. <i>PLoS Computational Biology</i> , 2009, 5, e1000374.	1.5	74

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145	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
146	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
147	Alternative Splicing of PTC7 in <i>Saccharomyces cerevisiae</i> Determines Protein Localization. <i>Genetics</i> , 2009, 183, 185-194.	1.2	71
148	Noninvasive wearable electroactive pharmaceutical monitoring for personalized therapeutics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 19017-19025.	3.3	71
149	Isolation of bacteriophage ϕ containing yeast ribosomal RNA genes: Screening by in situ RNA hybridization to plaques. <i>Cell</i> , 1976, 8, 227-232.	13.5	70
150	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
151	A nanoelectronics-blood-based diagnostic biomarker for myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10250-10257.	3.3	64
152	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
153	Multiplex assay for condition-dependent changes in protein-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9213-9218.	3.3	62
154	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
155	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
156	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
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158	Large-Scale Multiplexed Quantitative Discovery Proteomics Enabled by the Use of an ^{18}O -Labeled α -Universal Reference Sample. <i>Journal of Proteome Research</i> , 2009, 8, 290-299.	1.8	59
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