

Jef D Boeke

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

32,594
citations

14655

66
h-index

4548

171
g-index

220
all docs

220
docs citations

220
times ranked

23557
citing authors

#	ARTICLE	IF	CITATIONS
1	Sirt6 regulates lifespan in <i>Drosophila melanogaster</i> . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	29
2	LINE-1 expression in cancer correlates with p53 mutation, copy number alteration, and S phase checkpoint. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	36
3	Transcriptional neighborhoods regulate transcript isoform lengths and expression levels. Science, 2022, 375, 1000-1005.	12.6	23
4	Results of Two Cases of Pig-to-Human Kidney Xenotransplantation. New England Journal of Medicine, 2022, 386, 1889-1898.	27.0	166
5	A conditional counterselectable Piga knockout in mouse embryonic stem cells for advanced genome writing applications. Science, 2022, 25, 104438.	4.1	0
6	Synthetic regulatory reconstitution reveals principles of mammalian <i>Hox</i> cluster regulation. Science, 2022, 377, .	12.6	18
7	Regulation of the Dot1 histone H3K79 methyltransferase by histone H4K16 acetylation. Science, 2021, 371, .	12.6	70
8	Application of counter-selectable marker PIGA in engineering designer deletion cell lines and characterization of CRISPR deletion efficiency. Nucleic Acids Research, 2021, 49, 2642-2654.	14.5	7
9	RIP-seq reveals LINE-1 ORF1p association with p-body enriched mRNAs. Mobile DNA, 2021, 12, 5.	3.6	20
10	A versatile platform for locus-scale genome rewriting and verification. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
11	<i>De novo</i> assembly and delivery to mouse cells of a 101 kb functional human gene. Genetics, 2021, 218, .	2.9	23
12	Alternative splicing is a developmental switch for hTERT expression. Molecular Cell, 2021, 81, 2349-2360.e6.	9.7	19
13	Unbiased proteomic mapping of the LINE-1 promoter using CRISPR Cas9. Mobile DNA, 2021, 12, 21.	3.6	4
14	EUAdb: A resource for COVID-19 test development and comparison. PLoS ONE, 2021, 16, e0255417.	2.5	1
15	The role of retrotransposable elements in ageing and age-associated diseases. Nature, 2021, 596, 43-53.	27.8	156
16	Engineered dual selection for directed evolution of SpCas9 PAM specificity. Nature Communications, 2021, 12, 349.	12.8	10
17	Immune and Genome Engineering as the Future of Transplantable Tissue. New England Journal of Medicine, 2021, 385, 2451-2462.	27.0	28
18	SINGLE CELL TIPSEQ, A NEW METHOD TO MAP LINE-1 INSERTIONS, PROVIDES INFORMATION ABOUT SUB CHROMOSOMAL GENETIC VARIATION IN HUMAN EMBRYOS. Fertility and Sterility, 2020, 114, e524.	1.0	0

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19	Pathway engineering in yeast for synthesizing the complex polyketide bikaverin. <i>Nature Communications</i> , 2020, 11, 6197.	12.8	29
20	Sc3.0: revamping and minimizing the yeast genome. <i>Genome Biology</i> , 2020, 21, 205.	8.8	26
21	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	12.6	24
22	CRISPRa-Cas12a system in fission yeast for multiplex genomic editing and CRISPR interference. <i>Nucleic Acids Research</i> , 2020, 48, 5788-5798.	14.5	29
23	Synthetic Genomes. <i>Annual Review of Biochemistry</i> , 2020, 89, 77-101.	11.1	48
24	Human transposon insertion profiling by sequencing (TIPseq) to map LINE-1 insertions in single cells. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190335.	4.0	6
25	Cell fitness screens reveal a conflict between LINE-1 retrotransposition and DNA replication. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 168-178.	8.2	74
26	BRCA1 and S phase DNA repair pathways restrict LINE-1 retrotransposition in human cells. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 179-191.	8.2	60
27	Widespread Transcriptional Scanning in the Testis Modulates Gene Evolution Rates. <i>Cell</i> , 2020, 180, 248-262.e21.	28.9	111
28	Phylogenetic debugging of a complete human biosynthetic pathway transplanted into yeast. <i>Nucleic Acids Research</i> , 2020, 48, 486-499.	14.5	11
29	Structure and function of the Orc1 BAH-nucleosome complex. <i>Nature Communications</i> , 2019, 10, 2894.	12.8	31
30	Superloser: A Plasmid Shuffling Vector for <i>Saccharomyces cerevisiae</i> with Exceedingly Low Background. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2699-2707.	1.8	9
31	Transposon insertion profiling by sequencing (TIPseq) for mapping LINE-1 insertions in the human genome. <i>Mobile DNA</i> , 2019, 10, 8.	3.6	22
32	Big DNA as a tool to dissect an age-related macular degeneration-associated haplotype. <i>Precision Clinical Medicine</i> , 2019, 2, 1-7.	3.3	6
33	L1 drives IFN in senescent cells and promotes age-associated inflammation. <i>Nature</i> , 2019, 566, 73-78.	27.8	701
34	Comprehensive Scanning Mutagenesis of Human Retrotransposon LINE-1 Identifies Motifs Essential for Function. <i>Genetics</i> , 2019, 213, 1401-1414.	2.9	22
35	Inborn Errors of RNA Lariat Metabolism in Humans with Brainstem Viral Infection. <i>Cell</i> , 2018, 172, 952-965.e18.	28.9	92
36	Stress response factors drive regrowth of quiescent cells. <i>Current Genetics</i> , 2018, 64, 807-810.	1.7	8

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37	Dynamic motif occupancy (DynaMO) analysis identifies transcription factors and their binding sites driving dynamic biological processes. <i>Nucleic Acids Research</i> , 2018, 46, e2-e2.	14.5	11
38	Construction of Designer Selectable Marker Deletions with a CRISPR-Cas9 Toolbox in <i>Schizosaccharomyces pombe</i> and New Design of Common Entry Vectors. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 789-796.	1.8	12
39	A toolbox of immunoprecipitation-grade monoclonal antibodies to human transcription factors. <i>Nature Methods</i> , 2018, 15, 330-338.	19.0	58
40	Coupling Yeast Golden Gate and VEGAS for Efficient Assembly of the Violacein Pathway in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2018, 1671, 211-225.	0.9	8
41	Rapid and Efficient CRISPR/Cas9-Based Mating-Type Switching of <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 173-183.	1.8	39
42	A scalable peptide-GPCR language for engineering multicellular communication. <i>Nature Communications</i> , 2018, 9, 5057.	12.8	39
43	Transcription factor profiling reveals molecular choreography and key regulators of human retrotransposon expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E5526-E5535.	7.1	77
44	Precise control of SCRaMbLE in synthetic haploid and diploid yeast. <i>Nature Communications</i> , 2018, 9, 1933.	12.8	118
45	In vitro DNA SCRaMbLE. <i>Nature Communications</i> , 2018, 9, 1935.	12.8	81
46	Heterozygous diploid and interspecies SCRaMbLEing. <i>Nature Communications</i> , 2018, 9, 1934.	12.8	82
47	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018, 7, .	6.0	63
48	LINE-1 protein localization and functional dynamics during the cell cycle. <i>ELife</i> , 2018, 7, .	6.0	99
49	Karyotype engineering by chromosome fusion leads to reproductive isolation in yeast. <i>Nature</i> , 2018, 560, 392-396.	27.8	122
50	Meeting report: mobile genetic elements and genome plasticity 2018. <i>Mobile DNA</i> , 2018, 9, 21.	3.6	3
51	Gibson Deletion: a novel application of isothermal in vitro recombination. <i>Biological Procedures Online</i> , 2018, 20, 2.	2.9	4
52	Cycling to Maintain and Improve Fitness: Line-1 Modes of Nuclear Entrance and Retrotransposition. <i>SLAS Discovery</i> , 2018, 23, 491-494.	2.7	2
53	Human transposon insertion profiling: Analysis, visualization and identification of somatic LINE-1 insertions in ovarian cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E733-E740.	7.1	86
54	The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15.	6.2	29

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55	Engineering the ribosomal DNA in a megabase synthetic chromosome. <i>Science</i> , 2017, 355, .	12.6	169
56	Design of a synthetic yeast genome. <i>Science</i> , 2017, 355, 1040-1044.	12.6	464
57	3D organization of synthetic and scrambled chromosomes. <i>Science</i> , 2017, 355, .	12.6	116
58	â€œPerfectâ€ designer chromosome V and behavior of a ring derivative. <i>Science</i> , 2017, 355, .	12.6	185
59	Bug mapping and fitness testing of chemically synthesized chromosome X. <i>Science</i> , 2017, 355, .	12.6	173
60	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	12.6	163
61	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. <i>Science</i> , 2017, 355, .	12.6	184
62	Low escape-rate genome safeguards with minimal molecular perturbation of <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1470-E1479.	7.1	26
63	Structural variants caused by <i>Alu</i> insertions are associated with risks for many human diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3984-E3992.	7.1	113
64	Intact piRNA pathway prevents L1 mobilization in male meiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E5635-E5644.	7.1	81
65	Whole genome synthesis: from poliovirus to synthetic yeast. <i>Quantitative Biology</i> , 2017, 5, 105-109.	0.5	3
66	New Orthogonal Transcriptional Switches Derived from Tet Repressor Homologues for <i>Saccharomyces cerevisiae</i> Regulated by 2,4-Diacetylphloroglucinol and Other Ligands. <i>ACS Synthetic Biology</i> , 2017, 6, 497-506.	3.8	22
67	Dissecting Nucleosome Function with a Comprehensive Histone H2A and H2B Mutant Library. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3857-3866.	1.8	7
68	Resetting the Yeast Epigenome with Human Nucleosomes. <i>Cell</i> , 2017, 171, 1508-1519.e13.	28.9	53
69	Construction of Comprehensive Dosage-Matching Core Histone Mutant Libraries for <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 207, 1263-1273.	2.9	9
70	Dynamic silencing of somatic L1 retrotransposon insertions reflects the developmental and cellular contexts of their genomic integration. <i>Mobile DNA</i> , 2017, 8, 8.	3.6	12
71	The dynamic landscape of fission yeast meiosis alternative-splice isoforms. <i>Genome Research</i> , 2017, 27, 145-156.	5.5	40
72	A high throughput mutagenic analysis of yeast sumo structure and function. <i>PLoS Genetics</i> , 2017, 13, e1006612.	3.5	15

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73	Msn2/4 regulate expression of glycolytic enzymes and control transition from quiescence to growth. <i>ELife</i> , 2017, 6, .	6.0	51
74	Somatic retrotransposition is infrequent in glioblastomas. <i>Mobile DNA</i> , 2016, 7, 22.	3.6	17
75	BioPartsBuilder: a synthetic biology tool for combinatorial assembly of biological parts. <i>Bioinformatics</i> , 2016, 32, 937-939.	4.1	15
76	Barcode Sequencing Screen Identifies <i>SUB1</i> as a Regulator of Yeast Pheromone Inducible Genes. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 881-892.	1.8	9
77	Meeting Report: The Role of the Mobilome in Cancer. <i>Cancer Research</i> , 2016, 76, 4316-4319.	0.9	3
78	URI Regulates KAP1 Phosphorylation and Transcriptional Repression via PP2A Phosphatase in Prostate Cancer Cells. <i>Journal of Biological Chemistry</i> , 2016, 291, 25516-25528.	3.4	20
79	BioPartsDB: a synthetic biology workflow web-application for education and research. <i>Bioinformatics</i> , 2016, 32, 3519-3521.	4.1	5
80	Fluorescence ImmunoPrecipitation (FLIP): a Novel Assay for High-Throughput IP. <i>Biological Procedures Online</i> , 2016, 18, 16.	2.9	6
81	The Genome Project-Write. <i>Science</i> , 2016, 353, 126-127.	12.6	194
82	SCRaMBLE generates designed combinatorial stochastic diversity in synthetic chromosomes. <i>Genome Research</i> , 2016, 26, 36-49.	5.5	124
83	How retrotransposons shape genome regulation. <i>Current Opinion in Genetics and Development</i> , 2016, 37, 90-100.	3.3	139
84	Characterization of L1-Ribonucleoprotein Particles. <i>Methods in Molecular Biology</i> , 2016, 1400, 311-338.	0.9	19
85	qPCRTag Analysis - A High Throughput, Real Time PCR Assay for Sc2.0 Genotyping. <i>Journal of Visualized Experiments</i> , 2015, , e52941.	0.3	6
86	Development of a Tightly Controlled Off Switch for <i>Saccharomyces cerevisiae</i> Regulated by Camphor, a Low-Cost Natural Product. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1983-1990.	1.8	27
87	Interplay Between Histone H3 Lysine 56 Deacetylation and Chromatin Modifiers in Response to DNA Damage. <i>Genetics</i> , 2015, 200, 185-205.	2.9	29
88	RADOM, an Efficient <i>In Vivo</i> Method for Assembling Designed DNA Fragments up to 10 kb Long in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2015, 4, 213-220.	3.8	36
89	Intrinsic biocontainment: Multiplex genome safeguards combine transcriptional and recombinational control of essential yeast genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1803-1808.	7.1	61
90	Mechanistic analysis of ghrelin-O-acyltransferase using substrate analogs. <i>Bioorganic Chemistry</i> , 2015, 62, 64-73.	4.1	17

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91	H3K36 methylation promotes longevity by enhancing transcriptional fidelity. <i>Genes and Development</i> , 2015, 29, 1362-1376.	5.9	196
92	Versatile genetic assembly system (VEGAS) to assemble pathways for expression in <i>S. cerevisiae</i> . <i>Nucleic Acids Research</i> , 2015, 43, 6620-6630.	14.5	96
93	Yeast Golden Gate (yGG) for the Efficient Assembly of <i>S. cerevisiae</i> Transcription Units. <i>ACS Synthetic Biology</i> , 2015, 4, 853-859.	3.8	75
94	Freedom and Responsibility in Synthetic Genomics: The Synthetic Yeast Project. <i>Genetics</i> , 2015, 200, 1021-1028.	2.9	29
95	Much Ado about Zero. <i>Cell</i> , 2015, 163, 534-535.	28.9	3
96	Retrotransposon insertions in the clonal evolution of pancreatic ductal adenocarcinoma. <i>Nature Medicine</i> , 2015, 21, 1060-1064.	30.7	127
97	Sleeping dogs of the genome. <i>Science</i> , 2014, 346, 1187-1188.	12.6	54
98	Circular permutation of a synthetic eukaryotic chromosome with the telomerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17003-17010.	7.1	31
99	Expression and detection of LINE-1 ORF-encoded proteins. <i>Mobile Genetic Elements</i> , 2014, 4, e29319.	1.8	35
100	Total Synthesis of a Functional Designer Eukaryotic Chromosome. <i>Science</i> , 2014, 344, 55-58.	12.6	486
101	Long Interspersed Element-1 Protein Expression Is a Hallmark of Many Human Cancers. <i>American Journal of Pathology</i> , 2014, 184, 1280-1286.	3.8	250
102	High-temporal-resolution view of transcription and chromatin states across distinct metabolic states in budding yeast. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 854-863.	8.2	70
103	Characterisation of cytoplasmic DNA complementary to non-retroviral RNA viruses in human cells. <i>Scientific Reports</i> , 2014, 4, 5074.	3.3	40
104	Affinity Proteomics Reveals Human Host Factors Implicated in Discrete Stages of LINE-1 Retrotransposition. <i>Cell</i> , 2013, 155, 1034-1048.	28.9	190
105	TE-array—a high throughput tool to study transposon transcription. <i>BMC Genomics</i> , 2013, 14, 869.	2.8	12
106	Multichange Isothermal Mutagenesis: A New Strategy for Multiple Site-Directed Mutations in Plasmid DNA. <i>ACS Synthetic Biology</i> , 2013, 2, 473-477.	3.8	49
107	Controlled insertional mutagenesis using a LINE-1 (<i>ORFeus</i>) gene-trap mouse model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2706-13.	7.1	22
108	tRNA genes rapidly change in evolution to meet novel translational demands. <i>ELife</i> , 2013, 2, e01339.	6.0	81

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109	The <i>Saccharomyces cerevisiae</i> SCRaMble system and genome minimization. <i>Bioengineered</i> , 2012, 3, 170-173.	3.2	69
110	Novel Transcript Truncating Function of Rap1p Revealed by Synthetic Codon-Optimized Ty1 Retrotransposon. <i>Genetics</i> , 2012, 190, 523-535.	2.9	13
111	Active Transposition in Genomes. <i>Annual Review of Genetics</i> , 2012, 46, 651-675.	7.6	347
112	Poly(A) Binding Protein C1 Is Essential for Efficient L1 Retrotransposition and Affects L1 RNP Formation. <i>Molecular and Cellular Biology</i> , 2012, 32, 4323-4336.	2.3	56
113	Human Transposon Tectonics. <i>Cell</i> , 2012, 149, 740-752.	28.9	258
114	Assembling Large DNA Segments in Yeast. <i>Methods in Molecular Biology</i> , 2012, 852, 133-150.	0.9	34
115	Design-A-Gene with GeneDesign. <i>Methods in Molecular Biology</i> , 2012, 852, 235-247.	0.9	9
116	Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. <i>Nature</i> , 2011, 477, 471-476.	27.8	398
117	Characterization of a synthetic human LINE-1 retrotransposon ORFeus-Hs. <i>Mobile DNA</i> , 2011, 2, 2.	3.6	60
118	Effect of reverse transcriptase inhibitors on LINE-1 and Ty1 reverse transcriptase activities and on LINE-1 retrotransposition. <i>BMC Biochemistry</i> , 2011, 12, 18.	4.4	104
119	Characterization of L1 retrotransposition with high-throughput dual-luciferase assays. <i>Nucleic Acids Research</i> , 2011, 39, e16-e16.	14.5	88
120	An evolutionarily "young" lysine residue in histone H3 attenuates transcriptional output in <i>Saccharomyces cerevisiae</i> . <i>Genes and Development</i> , 2011, 25, 1306-1319.	5.9	27
121	Real-time imaging and quantification of p300/CBP acetyltransferase inhibition using a FRET-based reporter in living mammalian cells. <i>FASEB Journal</i> , 2011, 25, 896.3.	0.5	0
122	GeneDesign 3.0 is an updated synthetic biology toolkit. <i>Nucleic Acids Research</i> , 2010, 38, 2603-2606.	14.5	59
123	Silent information regulator 3: the Goldilocks of the silencing complex. <i>Genes and Development</i> , 2010, 24, 115-122.	5.9	49
124	Mobile Interspersed Repeats Are Major Structural Variants in the Human Genome. <i>Cell</i> , 2010, 141, 1171-1182.	28.9	242
125	Automated Design of Assemblable, Modular, Synthetic Chromosomes. <i>Lecture Notes in Computer Science</i> , 2010, , 280-289.	1.3	3
126	Teaching Synthetic Biology, Bioinformatics and Engineering to Undergraduates: The Interdisciplinary Build-a-Genome Course. <i>Genetics</i> , 2009, 181, 13-21.	2.9	55

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127	Conditional activation of a single-copy L1 transgene in mice by Cre. <i>Genesis</i> , 2008, 46, 373-383.	1.6	32
128	Probing Nucleosome Function: A Highly Versatile Library of Synthetic Histone H3 and H4 Mutants. <i>Cell</i> , 2008, 134, 1066-1078.	28.9	198
129	Orientation-Dependent Regulation of Integrated HIV-1 Expression by Host Gene Transcriptional Readthrough. <i>Cell Host and Microbe</i> , 2008, 4, 134-146.	11.0	190
130	Histone H3 K56 Hyperacetylation Perturbs Replisomes and Causes DNA Damage. <i>Genetics</i> , 2008, 179, 1769-1784.	2.9	74
131	Compensatory Interactions between Sir3p and the Nucleosomal LRS Surface Imply Their Direct Interaction. <i>PLoS Genetics</i> , 2008, 4, e1000301.	3.5	39
132	dSLAM analysis of genome-wide genetic interactions in <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2007, 41, 206-221.	3.8	63
133	A DNA Integrity Network in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2006, 124, 1069-1081.	28.9	490
134	The Sirtuins Hst3 and Hst4p Preserve Genome Integrity by Controlling Histone H3 Lysine 56 Deacetylation. <i>Current Biology</i> , 2006, 16, 1280-1289.	3.9	280
135	Active retrotransposition by a synthetic L1 element in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 18662-18667.	7.1	108
136	GeneDesign: Rapid, automated design of multikilobase synthetic genes. <i>Genome Research</i> , 2006, 16, 550-556.	5.5	125
137	Transposon insertion site profiling chip (TIP-chip). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17632-17637.	7.1	43
138	Insights into the Role of Histone H3 and Histone H4 Core Modifiable Residues in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2005, 25, 10060-10070.	2.3	215
139	Regulated nucleosome mobility and the histone code. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1037-1043.	8.2	336
140	A highly active synthetic mammalian retrotransposon. <i>Nature</i> , 2004, 429, 314-318.	27.8	170
141	Transcriptional disruption by the L1 retrotransposon and implications for mammalian transcriptomes. <i>Nature</i> , 2004, 429, 268-274.	27.8	453
142	The Unusual Phylogenetic Distribution of Retrotransposons: A Hypothesis. <i>Genome Research</i> , 2003, 13, 1975-1983.	5.5	51
143	Molecular archeology of L1 insertions in the human genome. <i>Genome Biology</i> , 2002, 3, research0052.1.	9.6	180
144	Human L1 Retrotransposition Is Associated with Genetic Instability In Vivo. <i>Cell</i> , 2002, 110, 327-338.	28.9	435

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145	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	27.8	3,938
146	Human L1 element target-primed reverse transcription in vitro. <i>EMBO Journal</i> , 2002, 21, 5899-5910.	7.8	448
147	TRANSCRIPTION: Is S Phase Important for Transcriptional Silencing?. <i>Science</i> , 2001, 291, 608-609.	12.6	12
148	Human L1 Retrotransposition: <i>cis</i> Preference versus <i>trans</i> Complementation. <i>Molecular and Cellular Biology</i> , 2001, 21, 1429-1439.	2.3	587
149	Target DNA chromatinization modulates nicking by L1 endonuclease. <i>Nucleic Acids Research</i> , 2001, 29, 573-577.	14.5	66
150	A DNA Microarray-Based Genetic Screen for Nonhomologous End-Joining Mutants in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2001, 294, 2552-2556.	12.6	150
151	Frequent Human Genomic DNA Transduction Driven by LINE-1 Retrotransposition. <i>Genome Research</i> , 2000, 10, 411-415.	5.5	247
152	The yeast retrotransposon Ty5 uses the anticodon stem-loop of the initiator methionine tRNA as a primer for reverse transcription. <i>Rna</i> , 1999, 5, 929-938.	3.5	28
153	The <i>Schizosaccharomyces pombe</i> <i>hst4</i> ⁺ Gene Is a <i>SIR2</i> Homologue with Silencing and Centromeric Functions. <i>Molecular Biology of the Cell</i> , 1999, 10, 3171-3186.	2.1	68
154	Retroshuffling the genomic deck. <i>Nature</i> , 1999, 398, 109-111.	27.8	34
155	Functional Characterization of the <i>Saccharomyces cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. <i>Science</i> , 1999, 285, 901-906.	12.6	3,761
156	Designer deletion strains derived from <i>Saccharomyces cerevisiae</i> S288C: A useful set of strains and plasmids for PCR-mediated gene disruption and other applications. <i>Yeast</i> , 1998, 14, 115-132.	1.7	3,028
157	A hotspot for the <i>Drosophila</i> gypsy retroelement in the <i>ovo</i> locus. <i>Nucleic Acids Research</i> , 1998, 26, 4019-4025.	14.5	39
158	Intronic snoRNA biosynthesis in <i>Saccharomyces cerevisiae</i> depends on the lariat-debranching enzyme: Intron length effects and activity of a precursor snoRNA. <i>Rna</i> , 1998, 4, 1096-1110.	3.5	105
159	Designer deletion strains derived from <i>Saccharomyces cerevisiae</i> S288C: A useful set of strains and plasmids for PCR-mediated gene disruption and other applications. , 1998, 14, 115.		17
160	Distribution of a Limited Sir2 Protein Pool Regulates the Strength of Yeast rDNA Silencing and Is Modulated by Sir4p. <i>Genetics</i> , 1998, 149, 1205-1219.	2.9	157
161	LINEs and Alus â€” the polyA connection. <i>Nature Genetics</i> , 1997, 16, 6-7.	21.4	257
162	Human L1 Retrotransposon Encodes a Conserved Endonuclease Required for Retrotransposition. <i>Cell</i> , 1996, 87, 905-916.	28.9	1,048

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163	High Frequency Retrotransposition in Cultured Mammalian Cells. <i>Cell</i> , 1996, 87, 917-927.	28.9	950
164	A useful colony colour phenotype associated with the yeast selectable/counter-selectable marker MET15. <i>Yeast</i> , 1996, 12, 939-941.	1.7	76
165	A little help for my ends. <i>Nature</i> , 1996, 383, 579-581.	27.8	6
166	Overview: Fusion proteins: Fundamental and therapeutic applications. <i>Expert Opinion on Therapeutic Patents</i> , 1994, 4, 1037-1051.	5.0	1
167	Alu sequences in RMSA-1 protein?. <i>Nature</i> , 1994, 370, 106-106.	27.8	17
168	Yeast retrotransposon revealed. <i>Nature</i> , 1992, 358, 717-717.	27.8	82
169	[20] In vitro mutagenesis and plasmid shuffling: From cloned gene to mutant yeast. <i>Methods in Enzymology</i> , 1991, 194, 302-318.	1.0	585
170	New antiviral strategy using capsid-nuclease fusion proteins. <i>Nature</i> , 1991, 352, 632-635.	27.8	78
171	Optical fibers as tetrad dissection needles. <i>Yeast</i> , 1990, 6, 139-139.	1.7	1
172	Transposition of copia elements in <i>Drosophila</i> . <i>Nature</i> , 1988, 332, 21-21.	27.8	3
173	A general method for the chromosomal amplification of genes in yeast. <i>Science</i> , 1988, 239, 280-282.	12.6	128
174	[10] 5-Fluoroorotic acid as a selective agent in yeast molecular genetics. <i>Methods in Enzymology</i> , 1987, 154, 164-175.	1.0	1,384
175	A positive selection for mutants lacking orotidine-5- ϵ -phosphate decarboxylase activity in yeast: 5-fluoro-orotic acid resistance. <i>Molecular Genetics and Genomics</i> , 1984, 197, 345-346.	2.4	2,469