

Jef D Boeke

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/154192/publications.pdf>

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	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. <i>Nature</i> , 2002, 418, 387-391.	27.8	3,938
2	Functional Characterization of the <i>S. cerevisiae</i> Genome by Gene Deletion and Parallel Analysis. <i>Science</i> , 1999, 285, 901-906.	12.6	3,761
3	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
4	A positive selection for mutants lacking orotidine-5-phosphate decarboxylase activity in yeast: 5-fluoro-orotic acid resistance. <i>Molecular Genetics and Genomics</i> , 1984, 197, 345-346.	2.4	2,469
5	[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
6	Human L1 Retrotransposon Encodes a Conserved Endonuclease Required for Retrotransposition. <i>Cell</i> , 1996, 87, 905-916.	28.9	1,048
7	High Frequency Retrotransposition in Cultured Mammalian Cells. <i>Cell</i> , 1996, 87, 917-927.	28.9	950
8	L1 drives IFN in senescent cells and promotes age-associated inflammation. <i>Nature</i> , 2019, 566, 73-78.	27.8	701
9	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
10	[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
11	A DNA Integrity Network in the Yeast <i>Saccharomyces cerevisiae</i> . <i>Cell</i> , 2006, 124, 1069-1081.	28.9	490
12	Total Synthesis of a Functional Designer Eukaryotic Chromosome. <i>Science</i> , 2014, 344, 55-58.	12.6	486
13	Design of a synthetic yeast genome. <i>Science</i> , 2017, 355, 1040-1044.	12.6	464
14	Transcriptional disruption by the L1 retrotransposon and implications for mammalian transcriptomes. <i>Nature</i> , 2004, 429, 268-274.	27.8	453
15	Human L1 element target-primed reverse transcription in vitro. <i>EMBO Journal</i> , 2002, 21, 5899-5910.	7.8	448
16	Human L1 Retrotransposition Is Associated with Genetic Instability In Vivo. <i>Cell</i> , 2002, 110, 327-338.	28.9	435
17	Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. <i>Nature</i> , 2011, 477, 471-476.	27.8	398
18	Active Transposition in Genomes. <i>Annual Review of Genetics</i> , 2012, 46, 651-675.	7.6	347

#	ARTICLE	IF	CITATIONS
19	Regulated nucleosome mobility and the histone code. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1037-1043.	8.2	336
20	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
21	Human Transposon Tectonics. <i>Cell</i> , 2012, 149, 740-752.	28.9	258
22	LINEs and Alus â€” the polyA connection. <i>Nature Genetics</i> , 1997, 16, 6-7.	21.4	257
23	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
24	Frequent Human Genomic DNA Transduction Driven by LINE-1 Retrotransposition. <i>Genome Research</i> , 2000, 10, 411-415.	5.5	247
25	Mobile Interspersed Repeats Are Major Structural Variants in the Human Genome. <i>Cell</i> , 2010, 141, 1171-1182.	28.9	242
26	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
27	Probing Nucleosome Function: A Highly Versatile Library of Synthetic Histone H3 and H4 Mutants. <i>Cell</i> , 2008, 134, 1066-1078.	28.9	198
28	H3K36 methylation promotes longevity by enhancing transcriptional fidelity. <i>Genes and Development</i> , 2015, 29, 1362-1376.	5.9	196
29	The Genome Project-Write. <i>Science</i> , 2016, 353, 126-127.	12.6	194
30	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
31	Affinity Proteomics Reveals Human Host Factors Implicated in Discrete Stages of LINE-1 Retrotransposition. <i>Cell</i> , 2013, 155, 1034-1048.	28.9	190
32	â€œPerfectâ€• designer chromosome V and behavior of a ring derivative. <i>Science</i> , 2017, 355, .	12.6	185
33	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. <i>Science</i> , 2017, 355, .	12.6	184
34	Molecular archeology of L1 insertions in the human genome. <i>Genome Biology</i> , 2002, 3, research0052.1.	9.6	180
35	Bug mapping and fitness testing of chemically synthesized chromosome X. <i>Science</i> , 2017, 355, .	12.6	173
36	A highly active synthetic mammalian retrotransposon. <i>Nature</i> , 2004, 429, 314-318.	27.8	170

#	ARTICLE	IF	CITATIONS
37	Engineering the ribosomal DNA in a megabase synthetic chromosome. <i>Science</i> , 2017, 355, .	12.6	169
38	Results of Two Cases of Pig-to-Human Kidney Xenotransplantation. <i>New England Journal of Medicine</i> , 2022, 386, 1889-1898.	27.0	166
39	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	12.6	163
40	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
41	The role of retrotransposable elements in ageing and age-associated diseases. <i>Nature</i> , 2021, 596, 43-53.	27.8	156
42	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
43	How retrotransposons shape genome regulation. <i>Current Opinion in Genetics and Development</i> , 2016, 37, 90-100.	3.3	139
44	A general method for the chromosomal amplification of genes in yeast. <i>Science</i> , 1988, 239, 280-282.	12.6	128
45	Retrotransposon insertions in the clonal evolution of pancreatic ductal adenocarcinoma. <i>Nature Medicine</i> , 2015, 21, 1060-1064.	30.7	127
46	GeneDesign: Rapid, automated design of multikilobase synthetic genes. <i>Genome Research</i> , 2006, 16, 550-556.	5.5	125
47	SCRaMbLE generates designed combinatorial stochastic diversity in synthetic chromosomes. <i>Genome Research</i> , 2016, 26, 36-49.	5.5	124
48	Karyotype engineering by chromosome fusion leads to reproductive isolation in yeast. <i>Nature</i> , 2018, 560, 392-396.	27.8	122
49	Precise control of SCRaMbLE in synthetic haploid and diploid yeast. <i>Nature Communications</i> , 2018, 9, 1933.	12.8	118
50	3D organization of synthetic and scrambled chromosomes. <i>Science</i> , 2017, 355, .	12.6	116
51	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
52	Widespread Transcriptional Scanning in the Testis Modulates Gene Evolution Rates. <i>Cell</i> , 2020, 180, 248-262.e21.	28.9	111
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	Effect of reverse transcriptase inhibitors on LINE-1 and Ty1 reverse transcriptase activities and on LINE-1 retrotransposition. BMC Biochemistry, 2011, 12, 18.	4.4	104
56	LINE-1 protein localization and functional dynamics during the cell cycle. ELife, 2018, 7, .	6.0	99
57	Versatile genetic assembly system (VEGAS) to assemble pathways for expression in <i>S. cerevisiae</i> . Nucleic Acids Research, 2015, 43, 6620-6630.	14.5	96
58	Inborn Errors of RNA Lariat Metabolism in Humans with Brainstem Viral Infection. Cell, 2018, 172, 952-965.e18.	28.9	92
59	Characterization of L1 retrotransposition with high-throughput dual-luciferase assays. Nucleic Acids Research, 2011, 39, e16-e16.	14.5	88
60	Human transposon insertion profiling: Analysis, visualization and identification of somatic LINE-1 insertions in ovarian cancer. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E733-E740.	7.1	86
61	Yeast retrotransposon revealed. Nature, 1992, 358, 717-717.	27.8	82
62	Heterozygous diploid and interspecies SCRaMbLEing. Nature Communications, 2018, 9, 1934.	12.8	82
63	tRNA genes rapidly change in evolution to meet novel translational demands. ELife, 2013, 2, e01339.	6.0	81
64	Intact piRNA pathway prevents L1 mobilization in male meiosis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5635-E5644.	7.1	81
65	In vitro DNA SCRaMbLE. Nature Communications, 2018, 9, 1935.	12.8	81
66	New antiviral strategy using capsid-nuclease fusion proteins. Nature, 1991, 352, 632-635.	27.8	78
67	Transcription factor profiling reveals molecular choreography and key regulators of human retrotransposon expression. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E5526-E5535.	7.1	77
68	A useful colony colour phenotype associated with the yeast selectable/counter-selectable marker MET15. Yeast, 1996, 12, 939-941.	1.7	76
69	Yeast Golden Gate (yGC) for the Efficient Assembly of <i>S. cerevisiae</i> Transcription Units. ACS Synthetic Biology, 2015, 4, 853-859.	3.8	75
70	Histone H3 K56 Hyperacetylation Perturbs Replisomes and Causes DNA Damage. Genetics, 2008, 179, 1769-1784.	2.9	74
71	Cell fitness screens reveal a conflict between LINE-1 retrotransposition and DNA replication. Nature Structural and Molecular Biology, 2020, 27, 168-178.	8.2	74
72	High-temporal-resolution view of transcription and chromatin states across distinct metabolic states in budding yeast. Nature Structural and Molecular Biology, 2014, 21, 854-863.	8.2	70

#	ARTICLE	IF	CITATIONS
73	Regulation of the Dot1 histone H3K79 methyltransferase by histone H4K16 acetylation. <i>Science</i> , 2021, 371, .	12.6	70
74	The <i>Saccharomyces cerevisiae</i> SCRaMbLE system and genome minimization. <i>Bioengineered</i> , 2012, 3, 170-173.	3.2	69
75	The <i>Schizosaccharomyces pombe</i> hst4 ⁺ Gene Is a SIR2 Homologue with Silencing and Centromeric Functions. <i>Molecular Biology of the Cell</i> , 1999, 10, 3171-3186.	2.1	68
76	Target DNA chromatinization modulates nicking by L1 endonuclease. <i>Nucleic Acids Research</i> , 2001, 29, 573-577.	14.5	66
77	dSLAM analysis of genome-wide genetic interactions in <i>Saccharomyces cerevisiae</i> . <i>Methods</i> , 2007, 41, 206-221.	3.8	63
78	Dissection of affinity captured LINE-1 macromolecular complexes. <i>ELife</i> , 2018, 7, .	6.0	63
79	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
80	Characterization of a synthetic human LINE-1 retrotransposon ORFeus-Hs. <i>Mobile DNA</i> , 2011, 2, 2.	3.6	60
81	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
82	GeneDesign 3.0 is an updated synthetic biology toolkit. <i>Nucleic Acids Research</i> , 2010, 38, 2603-2606.	14.5	59
83	A toolbox of immunoprecipitation-grade monoclonal antibodies to human transcription factors. <i>Nature Methods</i> , 2018, 15, 330-338.	19.0	58
84	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
85	Teaching Synthetic Biology, Bioinformatics and Engineering to Undergraduates: The Interdisciplinary Build-a-Genome Course. <i>Genetics</i> , 2009, 181, 13-21.	2.9	55
86	Sleeping dogs of the genome. <i>Science</i> , 2014, 346, 1187-1188.	12.6	54
87	Resetting the Yeast Epigenome with Human Nucleosomes. <i>Cell</i> , 2017, 171, 1508-1519.e13.	28.9	53
88	The Unusual Phylogenetic Distribution of Retrotransposons: A Hypothesis. <i>Genome Research</i> , 2003, 13, 1975-1983.	5.5	51
89	Msn2/4 regulate expression of glycolytic enzymes and control transition from quiescence to growth. <i>ELife</i> , 2017, 6, .	6.0	51
90	Silent information regulator 3: the Goldilocks of the silencing complex. <i>Genes and Development</i> , 2010, 24, 115-122.	5.9	49

#	ARTICLE	IF	CITATIONS
91	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
92	Synthetic Genomes. <i>Annual Review of Biochemistry</i> , 2020, 89, 77-101.	11.1	48
93	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
94	Characterisation of cytoplasmic DNA complementary to non-retroviral RNA viruses in human cells. <i>Scientific Reports</i> , 2014, 4, 5074.	3.3	40
95	The dynamic landscape of fission yeast meiosis alternative-splice isoforms. <i>Genome Research</i> , 2017, 27, 145-156.	5.5	40
96	A hotspot for the <i>Drosophila</i> gypsy retroelement in the ovo locus. <i>Nucleic Acids Research</i> , 1998, 26, 4019-4025.	14.5	39
97	Compensatory Interactions between Sir3p and the Nucleosomal LRS Surface Imply Their Direct Interaction. <i>PLoS Genetics</i> , 2008, 4, e1000301.	3.5	39
98	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
99	A scalable peptide-GPCR language for engineering multicellular communication. <i>Nature Communications</i> , 2018, 9, 5057.	12.8	39
100	A versatile platform for locus-scale genome rewriting and verification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	37
101	RANDOM, 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
102	LINE-1 expression in cancer correlates with p53 mutation, copy number alteration, and S phase checkpoint. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	36
103	Expression and detection of LINE-1 ORF-encoded proteins. <i>Mobile Genetic Elements</i> , 2014, 4, e29319.	1.8	35
104	Retroshuffling the genomic deck. <i>Nature</i> , 1999, 398, 109-111.	27.8	34
105	Assembling Large DNA Segments in Yeast. <i>Methods in Molecular Biology</i> , 2012, 852, 133-150.	0.9	34
106	Conditional activation of a single-copy L1 transgene in mice by Cre. <i>Genesis</i> , 2008, 46, 373-383.	1.6	32
107	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
108	Structure and function of the Orc1 BAH-nucleosome complex. <i>Nature Communications</i> , 2019, 10, 2894.	12.8	31

#	ARTICLE	IF	CITATIONS
109	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
110	Freedom and Responsibility in Synthetic Genomics: The Synthetic Yeast Project. <i>Genetics</i> , 2015, 200, 1021-1028.	2.9	29
111	The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15.	6.2	29
112	Pathway engineering in yeast for synthesizing the complex polyketide bikaverin. <i>Nature Communications</i> , 2020, 11, 6197.	12.8	29
113	CRISPR-Cas12a system in fission yeast for multiplex genomic editing and CRISPR interference. <i>Nucleic Acids Research</i> , 2020, 48, 5788-5798.	14.5	29
114	Sirt6 regulates lifespan in <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	29
115	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
116	Immune and Genome Engineering as the Future of Transplantable Tissue. <i>New England Journal of Medicine</i> , 2021, 385, 2451-2462.	27.0	28
117	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
118	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
119	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
120	Sc3.0: revamping and minimizing the yeast genome. <i>Genome Biology</i> , 2020, 21, 205.	8.8	26
121	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	12.6	24
122	<i>De novo</i> assembly and delivery to mouse cells of a 101 kb functional human gene. <i>Genetics</i> , 2021, 218, .	2.9	23
123	Transcriptional neighborhoods regulate transcript isoform lengths and expression levels. <i>Science</i> , 2022, 375, 1000-1005.	12.6	23
124	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
125	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
126	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

#	ARTICLE	IF	CITATIONS
127	Comprehensive Scanning Mutagenesis of Human Retrotransposon LINE-1 Identifies Motifs Essential for Function. <i>Genetics</i> , 2019, 213, 1401-1414.	2.9	22
128	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
129	RIP-seq reveals LINE-1 ORF1p association with p-body enriched mRNAs. <i>Mobile DNA</i> , 2021, 12, 5.	3.6	20
130	Characterization of L1-Ribonucleoprotein Particles. <i>Methods in Molecular Biology</i> , 2016, 1400, 311-338.	0.9	19
131	Alternative splicing is a developmental switch for hTERT expression. <i>Molecular Cell</i> , 2021, 81, 2349-2360.e6.	9.7	19
132	Synthetic regulatory reconstitution reveals principles of mammalian <i>Hox</i> cluster regulation. <i>Science</i> , 2022, 377, .	12.6	18
133	Alu sequences in RMSA-1 protein?. <i>Nature</i> , 1994, 370, 106-106.	27.8	17
134	Mechanistic analysis of ghrelin-O-acyltransferase using substrate analogs. <i>Bioorganic Chemistry</i> , 2015, 62, 64-73.	4.1	17
135	Somatic retrotransposition is infrequent in glioblastomas. <i>Mobile DNA</i> , 2016, 7, 22.	3.6	17
136	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
137	BioPartsBuilder: a synthetic biology tool for combinatorial assembly of biological parts. <i>Bioinformatics</i> , 2016, 32, 937-939.	4.1	15
138	A high throughput mutagenic analysis of yeast sumo structure and function. <i>PLoS Genetics</i> , 2017, 13, e1006612.	3.5	15
139	Novel Transcript Truncating Function of Rap1p Revealed by Synthetic Codon-Optimized Ty1 Retrotransposon. <i>Genetics</i> , 2012, 190, 523-535.	2.9	13
140	TRANSCRIPTION: Is S Phase Important for Transcriptional Silencing?. <i>Science</i> , 2001, 291, 608-609.	12.6	12
141	TE-array—a high throughput tool to study transposon transcription. <i>BMC Genomics</i> , 2013, 14, 869.	2.8	12
142	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
143	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
144	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

#	ARTICLE	IF	CITATIONS
145	Phylogenetic debugging of a complete human biosynthetic pathway transplanted into yeast. <i>Nucleic Acids Research</i> , 2020, 48, 486-499.	14.5	11
146	Engineered dual selection for directed evolution of SpCas9 PAM specificity. <i>Nature Communications</i> , 2021, 12, 349.	12.8	10
147	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
148	Construction of Comprehensive Dosage-Matching Core Histone Mutant Libraries for <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 207, 1263-1273.	2.9	9
149	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
150	Design-A-Gene with GeneDesign. <i>Methods in Molecular Biology</i> , 2012, 852, 235-247.	0.9	9
151	Stress response factors drive regrowth of quiescent cells. <i>Current Genetics</i> , 2018, 64, 807-810.	1.7	8
152	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
153	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
154	Application of counter-selectable marker PIGA in engineering designer deletion cell lines and characterization of CRISPR deletion efficiency. <i>Nucleic Acids Research</i> , 2021, 49, 2642-2654.	14.5	7
155	A little help for my ends. <i>Nature</i> , 1996, 383, 579-581.	27.8	6
156	qPCRTag Analysis - A High Throughput, Real Time PCR Assay for Sc2.0 Genotyping. <i>Journal of Visualized Experiments</i> , 2015, , e52941.	0.3	6
157	Fluorescence ImmunoPrecipitation (FLIP): a Novel Assay for High-Throughput IP. <i>Biological Procedures Online</i> , 2016, 18, 16.	2.9	6
158	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
159	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
160	BioPartsDB: a synthetic biology workflow web-application for education and research. <i>Bioinformatics</i> , 2016, 32, 3519-3521.	4.1	5
161	Gibson Deletion: a novel application of isothermal in vitro recombination. <i>Biological Procedures Online</i> , 2018, 20, 2.	2.9	4
162	Unbiased proteomic mapping of the LINE-1 promoter using CRISPR Cas9. <i>Mobile DNA</i> , 2021, 12, 21.	3.6	4

#	ARTICLE	IF	CITATIONS
163	Transposition of copia elements in Drosophila. Nature, 1988, 332, 21-21.	27.8	3
164	Much Ado about Zero. Cell, 2015, 163, 534-535.	28.9	3
165	Meeting Report: The Role of the Mobilome in Cancer. Cancer Research, 2016, 76, 4316-4319.	0.9	3
166	Whole genome synthesis: from poliovirus to synthetic yeast. Quantitative Biology, 2017, 5, 105-109.	0.5	3
167	Meeting report: mobile genetic elements and genome plasticity 2018. Mobile DNA, 2018, 9, 21.	3.6	3
168	Automated Design of Assemblable, Modular, Synthetic Chromosomes. Lecture Notes in Computer Science, 2010, , 280-289.	1.3	3
169	Cycling to Maintain and Improve Fitness: Line-1 Modes of Nuclear Entrance and Retrotransposition. SLAS Discovery, 2018, 23, 491-494.	2.7	2
170	Optical fibers as tetrad dissection needles. Yeast, 1990, 6, 139-139.	1.7	1
171	Overview: Fusion proteins: Fundamental and therapeutic applications. Expert Opinion on Therapeutic Patents, 1994, 4, 1037-1051.	5.0	1
172	EUAdb: A resource for COVID-19 test development and comparison. PLoS ONE, 2021, 16, e0255417.	2.5	1
173	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
174	Real-time imaging and quantification of p300/CBP acetyltransferase inhibition using a FRET-based reporter in living mammalian cells. FASEB Journal, 2011, 25, 896.3.	0.5	0
175	A conditional counterselectable Piga knockout in mouse embryonic stem cells for advanced genome writing applications. iScience, 2022, 25, 104438.	4.1	0