Jun-biao Dai

List of Publications by Year
in descending order

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97 papers	5,277 citations	126907 33 h-index	95266 68 g-index
104 all docs	104 docs citations	104 times ranked	7219 citing authors

#	Article	IF	Citations
1	Engineering and functional analysis of yeast with a monotypic 40S ribosome subunit. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	9
2	Efficient de novo assembly and modification of large DNA fragments. Science China Life Sciences, 2022, 65, 1445-1455.	4.9	9
3	Studying bona fide SARS-CoV-2 biology in a BSL-2 biosafety environment using a split-virus-genome system. Science China Life Sciences, 2022, 65, 1894-1897.	4.9	2
4	Compacting a synthetic yeast chromosome arm. Genome Biology, 2021, 22, 5.	8.8	28
5	SCRaMbLE: A Study of Its Robustness and Challenges through Enhancement of Hygromycin B Resistance in a Semi-Synthetic Yeast. Bioengineering, 2021, 8, 42.	3.5	10
6	Coevolution of ribosomal RNA expansion segment 7L and assembly factor Noc2p specializes the ribosome biogenesis pathway between <i>Saccharomyces cerevisiae</i> and <i>Candida albicans</i>. Nucleic Acids Research, 2021, 49, 4655-4667.	14.5	4
7	Reconstruction of Secondary Metabolic Pathway to Synthesize Novel Metabolite in Saccharopolyspora erythraea. Frontiers in Bioengineering and Biotechnology, 2021, 9, 628569.	4.1	1
8	Biodegradation of aromatic pollutants meets synthetic biology. Synthetic and Systems Biotechnology, 2021, 6, 153-162.	3.7	17
9	Chromosomal Rearrangements of Synthetic Yeast by SCRaMbLE. Methods in Molecular Biology, 2021, 2196, 153-165.	0.9	2
10	Use YeastFab to Construct Genetic Parts and Multicomponent Pathways for Metabolic Engineering. Methods in Molecular Biology, 2021, 2196, 167-180.	0.9	1
11	Wholeâ€Genome Regulation for Yeast Metabolic Engineering. Small Methods, 2020, 4, 1900640.	8.6	12
12	Sc3.0: revamping and minimizing the yeast genome. Genome Biology, 2020, 21, 205.	8.8	26
13	Linear epitopes of SARS-CoV-2 spike protein elicit neutralizing antibodies in COVID-19 patients. Cellular and Molecular Immunology, 2020, 17, 1095-1097.	10.5	168
14	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	17.5	71
15	Genetic interaction mapping informs integrative structure determination of protein complexes. Science, 2020, 370, .	12.6	24
16	Synthetic yeast genomes for studying chromosomal features. Current Opinion in Systems Biology, 2020, 23, 1-7.	2.6	7
17	Coevolution of Eukaryote-like Vps4 and ESCRT-III Subunits in the Asgard Archaea. MBio, 2020, 11, .	4.1	23
18	The Role of Y Chromosome Genes in Male Fertility in<i>Drosophila melanogaster</i>. Genetics, 2020, 215, 623-633.	2.9	19

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19	Probing eukaryotic genome functions with synthetic chromosomes. Experimental Cell Research, 2020, 390, 111936.	2.6	5
20	SCRaMbLE-in: A Fast and Efficient Method to Diversify and Improve the Yields of Heterologous Pathways in Synthetic Yeast. Methods in Molecular Biology, 2020, 2205, 305-327.	0.9	0
21	Dissecting PCNA function with a systematically designed mutant library in yeast. Journal of Genetics and Genomics, 2019, 46, 301-313.	3.9	7
22	Improving Chromosome Synthesis with a Semiquantitative Phenotypic Assay and Refined Assembly Strategy. ACS Synthetic Biology, 2019, 8, 2203-2211.	3.8	5
23	Investigating loss of heterozygosity in a SCRaMbLEd yeast genome. Science China Life Sciences, 2019, 62, 868-869.	4.9	0
24	Multiplex Genome Engineering for Optimizing Bioproduction in <i>Saccharomyces cerevisiae</i>. Biochemistry, 2019, 58, 1492-1500.	2.5	7
25	Probing the Function of Metazoan Histones with a Systematic Library of H3 and H4 Mutants. Developmental Cell, 2019, 48, 406-419.e5.	7.0	27
26	Identification of gene products that control lipid droplet size in yeast using a high-throughput quantitative image analysis. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2019, 1864, 113-127.	2.4	10
27	Inevitability or contingency: how many chromosomes do we really need?. Science China Life Sciences, 2019, 62, 140-143.	4.9	5
28	PyMut: A Web Tool for Overlapping Gene Loss-of-Function Mutation Design. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1107-1110.	3.0	2
29	Wicket: A Versatile Tool for the Integration and Optimization of Exogenous Pathways in <i>Saccharomyces cerevisiae</i>. ACS Synthetic Biology, 2018, 7, 782-788.	3.8	22
30	MiYA, an efficient machine-learning workflow in conjunction with the YeastFab assembly strategy for combinatorial optimization of heterologous metabolic pathways in Saccharomyces cerevisiae. Metabolic Engineering, 2018, 47, 294-302.	7.0	76
31	Landscape of the regulatory elements for lysine 2-hydroxyisobutyrylation pathway. Cell Research, 2018, 28, 111-125.	12.0	89
32	Whole genome engineering by synthesis. Science China Life Sciences, 2018, 61, 1515-1527.	4.9	20
33	YeastFab: High-Throughput Genetic Parts Construction, Measurement, and Pathway Engineering in Yeast. Methods in Enzymology, 2018, 608, 277-306.	1.0	8
34	Identifying and characterizing SCRaMbLEd synthetic yeast using ReSCuES. Nature Communications, 2018, 9, 1930.	12.8	95
35	Rapid pathway prototyping and engineering using in vitro and in vivo synthetic genome SCRaMbLE-in methods. Nature Communications, 2018, 9, 1936.	12.8	101
36	Glutaredoxin Deletion Shortens Chronological Life Span in <i>Saccharomyces cerevisiae</i> via ROS-Mediated Ras/PKA Activation. Journal of Proteome Research, 2018, 17, 2318-2327.	3.7	16

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37	Artificial Protein Scaffold System (AProSS): An efficient method to optimize exogenous metabolic pathways in Saccharomyces cerevisiae. Metabolic Engineering, 2018, 49, 13-20.	7.0	24
38	Synthetic genomics: a new venture to dissect genome fundamentals and engineer new functions. Current Opinion in Chemical Biology, 2018, 46, 56-62.	6.1	35
39	Photosynthetic Accumulation of Lutein in Auxenochlorella protothecoides after Heterotrophic Growth. Marine Drugs, 2018, 16, 283.	4.6	32
40	Cell Lysate Microarray for Mapping the Network of Genetic Regulators for Histone Marks. Molecular and Cellular Proteomics, 2018, 17, 1720-1736.	3.8	1
41	Engineering the ribosomal DNA in a megabase synthetic chromosome. Science, 2017, 355, .	12.6	169
42	3D organization of synthetic and scrambled chromosomes. Science, 2017, 355, .	12.6	116
43	Bug mapping and fitness testing of chemically synthesized chromosome X. Science, 2017, 355, .	12.6	173
44	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. Science, 2017, 355, .	12.6	163
45	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. Science, 2017, 355, .	12.6	184
46	Whole genome synthesis: from poliovirus to synthetic yeast. Quantitative Biology, 2017, 5, 105-109.	0.5	3
47	Construction, characterization and application of a genome-wide promoter library in Saccharomyces cerevisiae. Frontiers of Chemical Science and Engineering, 2017, 11, 107-116.	4.4	20
48	Relevance of the dietary glycemic index, glycemic load and genetic predisposition for the glucose homeostasis of Chinese adults without diabetes. Scientific Reports, 2017, 7, 400.	3.3	19
49	Methods to Synthesize Large DNA Fragments for a Synthetic Yeast Genome. Cold Spring Harbor Protocols, 2017, 2017, pdb.prot080978.	0.3	0
50	Design and chemical synthesis of eukaryotic chromosomes. Chemical Society Reviews, 2017, 46, 7191-7207.	38.1	21
51	Dissecting Nucleosome Function with a Comprehensive Histone H2A and H2B Mutant Library. G3: Genes, Genomes, Genetics, 2017, 7, 3857-3866.	1.8	7
52	2-Hydroxyisobutyrylation on histone H4K8 is regulated by glucose homeostasis in <i>Saccharomyces cerevisiae</i>. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8782-8787.	7.1	74
53	Construction of Comprehensive Dosage-Matching Core Histone Mutant Libraries for <i>Saccharomyces cerevisiae</i>. Genetics, 2017, 207, 1263-1273.	2.9	9
54	Genome-wide landscape of position effects on heterogeneous gene expression in Saccharomyces cerevisiae. Biotechnology for Biofuels, 2017, 10, 189.	6.2	53

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55	Meeting report on Synthetic Biology Young Scholar Forum. Quantitative Biology, 2016, 3, 206-211.	0.5	0
56	Identification of Sporopollenin as the Outer Layer of Cell Wall in Microalga Chlorella protothecoides. Frontiers in Microbiology, 2016, 7, 1047.	3.5	29
57	CryoEM structure of yeast cytoplasmic exosome complex. Cell Research, 2016, 26, 822-837.	12.0	44
58	Mammalian Synthetic Biology: Time for Big MACs. ACS Synthetic Biology, 2016, 5, 1040-1049.	3.8	22
59	The NuA4 Core Complex Acetylates Nucleosomal Histone H4 through a Double Recognition Mechanism. Molecular Cell, 2016, 63, 965-975.	9.7	64
60	Critical roles of long noncoding RNAs in <i>Drosophila</i> spermatogenesis. Genome Research, 2016, 26, 1233-1244.	5.5	164
61	Kinetic flux profiling dissects nitrogen utilization pathways in the oleaginous green alga <i>Chlorella protothecoides</i>. Journal of Phycology, 2016, 52, 116-124.	2.3	23
62	EcoExpressâ€”Highly Efficient Construction and Expression of Multicomponent Protein Complexes in <i>Escherichia coli</i>. ACS Synthetic Biology, 2016, 5, 1239-1246.	3.8	9
63	Metabolic Flux Analysis of Lipid Biosynthesis in the Yeast Yarrowia lipolytica Using 13C-Labled Glucose and Gas Chromatography-Mass Spectrometry. PLoS ONE, 2016, 11, e0159187.	2.5	36
64	Auxenochlorella protothecoides and Prototheca wickerhamii plastid genome sequences give insight into the origins of non-photosynthetic algae. Scientific Reports, 2015, 5, 14465.	3.3	20
65	Industrial Fermentation of Auxenochlorella protothecoides for Production of Biodiesel and Its Application in Vehicle Diesel Engines. Frontiers in Bioengineering and Biotechnology, 2015, 3, 164.	4.1	12
66	Interplay Between Histone H3 Lysine 56 Deacetylation and Chromatin Modifiers in Response to DNA Damage. Genetics, 2015, 200, 185-205.	2.9	29
67	H3K36 methylation promotes longevity by enhancing transcriptional fidelity. Genes and Development, 2015, 29, 1362-1376.	5.9	196
68	YeastFab: the design and construction of standard biological parts for metabolic engineering in<i>Saccharomyces cerevisiae</i>. Nucleic Acids Research, 2015, 43, e88-e88.	14.5	93
69	Genome-Based Metabolic Mapping and 13C Flux Analysis Reveal Systematic Properties of an Oleaginous Microalga <i>Chlorella protothecoides</i> Â Â. Plant Physiology, 2015, 167, 586-599.	4.8	82
70	Autophagy-like processes are involved in lipid droplet degradation in Auxenochlorella protothecoides during the heterotrophy-autotrophy transition. Frontiers in Plant Science, 2014, 5, 400.	3.6	43
71	Engineered TAL Effector modulators for the large-scale gain-of-function screening. Nucleic Acids Research, 2014, 42, e114-e114.	14.5	6
72	Efficient Gene Knock-out and Knock-in with Transgenic Cas9 in <i>Drosophila</i>. G3: Genes, Genomes, Genetics, 2014, 4, 925-929.	1.8	65

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73	Oil accumulation mechanisms of the oleaginous microalga Chlorella protothecoides revealed through its genome, transcriptomes, and proteomes. BMC Genomics, 2014, 15, 582.	2.8	134
74	Microgrooved poly(3-hydroxybutyrate-co-3-hydroxyhexanoate) affects the phenotype of vascular smooth muscle cells through let-7a-involved regulation of actin dynamics. Biotechnology Letters, 2014, 36, 2125-2133.	2.2	9
75	Heritable Genome Editing with CRISPR/Cas9 in the Silkworm, Bombyx mori. PLoS ONE, 2014, 9, e101210.	2.5	66
76	Characterization of an ammonium transporter in the oleaginous alga Chlorella protothecoides. Applied Microbiology and Biotechnology, 2013, 97, 919-928.	3.6	14
77	Kinetochore Function and Chromosome Segregation Rely on Critical Residues in Histones H3 and H4 in Budding Yeast. Genetics, 2013, 195, 795-807.	2.9	23
78	Photosynthesis-fermentation hybrid system to produce lipid feedstock for algal biofuel. Environmental Technology (United Kingdom), 2013, 34, 1869-1876.	2.2	8
79	A quantitative analysis of histone methylation and acetylation isoforms from their deuteroacetylated derivatives: application to a series of knockout mutants. Journal of Mass Spectrometry, 2013, 48, 608-615.	1.6	5
80	Association of Histone Modification Patterns With Transcription Factor Binding Revealed by Systematic Analysis. Acta Agronomica Sinica(China), 2013, 40, 177.	0.3	0
81	Lysine Succinylation and Lysine Malonylation in Histones. Molecular and Cellular Proteomics, 2012, 11, 100-107.	3.8	483
82	Analysis of Autophagy Genes in Microalgae: Chlorella as a Potential Model to Study Mechanism of Autophagy. PLoS ONE, 2012, 7, e41826.	2.5	36
83	Strain Construction and Screening Methods for a Yeast Histone H3/H4 Mutant Library. Methods in Molecular Biology, 2012, 833, 1-14.	0.9	2
84	The First Identification of Lysine Malonylation Substrates and Its Regulatory Enzyme. Molecular and Cellular Proteomics, 2011, 10, M111.012658.	3.8	598
85	Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. Nature, 2011, 477, 471-476.	27.8	398
86	An evolutionarily â€˜youngâ€™ lysine residue in histone H3 attenuates transcriptional output in <i>Saccharomyces cerevisiae</i>. Genes and Development, 2011, 25, 1306-1319.	5.9	27
87	Yin and Yang of Histone H2B Roles in Silencing and Longevity: A Tale of Two Arginines. Genetics, 2010, 186, 813-828.	2.9	12
88	HistoneHits: A database for histone mutations and their phenotypes. Genome Research, 2009, 19, 674-681.	5.5	47
89	Probing Nucleosome Function: A Highly Versatile Library of Synthetic Histone H3 and H4 Mutants. Cell, 2008, 134, 1066-1078.	28.9	198
90	Phosphorylation Regulates Integration of the Yeast Ty5 Retrotransposon into Heterochromatin. Molecular Cell, 2007, 27, 289-299.	9.7	72

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91	Controlling integration specificity of a yeast retrotransposon. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5891-5895.	7.1	115
92	Carbon isotopic values of individual n-alkanes in pyrolysates of algae. Diqiu Huaxue, 2000, 19, 181-185.	0.5	0
93	Molecular source of biomarkers by genetic engineering techniques. Science Bulletin, 2000, 45, 1025-1030.	1.7	1
94	Title is missing!. Journal of Applied Phycology, 1999, 11, 137-142.	2.8	34
95	Identification of long chain isoprenoid hydrocarbons from pyrolytic product ofDunaliella. Science Bulletin, 1999, 44, 1700-1705.	1.7	4
96	Hydrocarbons pyrolysed from nannoplanktonic algae: An experimental organism system for study on the origin of petroleum and natural gas. Science Bulletin, 1999, 44, 767-768.	1.7	1
97	Probing the Function of Metazoan Histones with a Systematic Library of H3 and H4 Mutants. SSRN Electronic Journal, 0, , .	0.4	2