

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	The First Identification of Lysine Malonylation Substrates and Its Regulatory Enzyme. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.012658.	3.8	598
2	Lysine Succinylation and Lysine Malonylation in Histones. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 100-107.	3.8	483
3	Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. <i>Nature</i> , 2011, 477, 471-476.	27.8	398
4	Probing Nucleosome Function: A Highly Versatile Library of Synthetic Histone H3 and H4 Mutants. <i>Cell</i> , 2008, 134, 1066-1078.	28.9	198
5	H3K36 methylation promotes longevity by enhancing transcriptional fidelity. <i>Genes and Development</i> , 2015, 29, 1362-1376.	5.9	196
6	Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. <i>Science</i> , 2017, 355, .	12.6	184
7	Bug mapping and fitness testing of chemically synthesized chromosome X. <i>Science</i> , 2017, 355, .	12.6	173
8	Engineering the ribosomal DNA in a megabase synthetic chromosome. <i>Science</i> , 2017, 355, .	12.6	169
9	Linear epitopes of SARS-CoV-2 spike protein elicit neutralizing antibodies in COVID-19 patients. <i>Cellular and Molecular Immunology</i> , 2020, 17, 1095-1097.	10.5	168
10	Critical roles of long noncoding RNAs in <i>Drosophila</i> spermatogenesis. <i>Genome Research</i> , 2016, 26, 1233-1244.	5.5	164
11	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. <i>Science</i> , 2017, 355, .	12.6	163
12	Oil accumulation mechanisms of the oleaginous microalga <i>Chlorella protothecoides</i> revealed through its genome, transcriptomes, and proteomes. <i>BMC Genomics</i> , 2014, 15, 582.	2.8	134
13	3D organization of synthetic and scrambled chromosomes. <i>Science</i> , 2017, 355, .	12.6	116
14	Controlling integration specificity of a yeast retrotransposon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5891-5895.	7.1	115
15	Rapid pathway prototyping and engineering using in vitro and in vivo synthetic genome SCRaMbLE-in methods. <i>Nature Communications</i> , 2018, 9, 1936.	12.8	101
16	Identifying and characterizing SCRaMbLEd synthetic yeast using ReSCuES. <i>Nature Communications</i> , 2018, 9, 1930.	12.8	95
17	YeastFab: the design and construction of standard biological parts for metabolic engineering in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2015, 43, e88-e88.	14.5	93
18	Landscape of the regulatory elements for lysine 2-hydroxyisobutyrylation pathway. <i>Cell Research</i> , 2018, 28, 111-125.	12.0	89

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19	Genome-Based Metabolic Mapping and ¹³ C Flux Analysis Reveal Systematic Properties of an Oleaginous Microalga <i>Chlorella protothecoides</i> . <i>Plant Physiology</i> , 2015, 167, 586-599.	4.8	82
20	MiYA, an efficient machine-learning workflow in conjunction with the YeastFab assembly strategy for combinatorial optimization of heterologous metabolic pathways in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 47, 294-302.	7.0	76
21	2-Hydroxyisobutyrylation on histone H4K8 is regulated by glucose homeostasis in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8782-8787.	7.1	74
22	Phosphorylation Regulates Integration of the Yeast Ty5 Retrotransposon into Heterochromatin. <i>Molecular Cell</i> , 2007, 27, 289-299.	9.7	72
23	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , 2020, 38, 1021-1024.	17.5	71
24	Heritable Genome Editing with CRISPR/Cas9 in the Silkworm, <i>Bombyx mori</i> . <i>PLoS ONE</i> , 2014, 9, e101210.	2.5	66
25	Efficient Gene Knock-out and Knock-in with Transgenic Cas9 in <i>Drosophila</i> . <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 925-929.	1.8	65
26	The NuA4 Core Complex Acetylates Nucleosomal Histone H4 through a Double Recognition Mechanism. <i>Molecular Cell</i> , 2016, 63, 965-975.	9.7	64
27	Genome-wide landscape of position effects on heterogeneous gene expression in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 189.	6.2	53
28	HistoneHits: A database for histone mutations and their phenotypes. <i>Genome Research</i> , 2009, 19, 674-681.	5.5	47
29	CryoEM structure of yeast cytoplasmic exosome complex. <i>Cell Research</i> , 2016, 26, 822-837.	12.0	44
30	Autophagy-like processes are involved in lipid droplet degradation in <i>Auxenochlorella protothecoides</i> during the heterotrophy-autotrophy transition. <i>Frontiers in Plant Science</i> , 2014, 5, 400.	3.6	43
31	Analysis of Autophagy Genes in Microalgae: <i>Chlorella</i> as a Potential Model to Study Mechanism of Autophagy. <i>PLoS ONE</i> , 2012, 7, e41826.	2.5	36
32	Metabolic Flux Analysis of Lipid Biosynthesis in the Yeast <i>Yarrowia lipolytica</i> Using ¹³ C-Labeled Glucose and Gas Chromatography-Mass Spectrometry. <i>PLoS ONE</i> , 2016, 11, e0159187.	2.5	36
33	Synthetic genomics: a new venture to dissect genome fundamentals and engineer new functions. <i>Current Opinion in Chemical Biology</i> , 2018, 46, 56-62.	6.1	35
34	Title is missing!. <i>Journal of Applied Phycology</i> , 1999, 11, 137-142.	2.8	34
35	Photosynthetic Accumulation of Lutein in <i>Auxenochlorella protothecoides</i> after Heterotrophic Growth. <i>Marine Drugs</i> , 2018, 16, 283.	4.6	32
36	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

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37	Identification of Sporopollenin as the Outer Layer of Cell Wall in Microalga <i>Chlorella protothecoides</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 1047.	3.5	29
38	Compacting a synthetic yeast chromosome arm. <i>Genome Biology</i> , 2021, 22, 5.	8.8	28
39	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
40	Probing the Function of Metazoan Histones with a Systematic Library of H3 and H4 Mutants. <i>Developmental Cell</i> , 2019, 48, 406-419.e5.	7.0	27
41	Sc3.0: revamping and minimizing the yeast genome. <i>Genome Biology</i> , 2020, 21, 205.	8.8	26
42	Artificial Protein Scaffold System (AProSS): An efficient method to optimize exogenous metabolic pathways in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 49, 13-20.	7.0	24
43	Genetic interaction mapping informs integrative structure determination of protein complexes. <i>Science</i> , 2020, 370, .	12.6	24
44	Kinetochores Function and Chromosome Segregation Rely on Critical Residues in Histones H3 and H4 in Budding Yeast. <i>Genetics</i> , 2013, 195, 795-807.	2.9	23
45	Kinetic flux profiling dissects nitrogen utilization pathways in the oleaginous green alga <i>Chlorella protothecoides</i> . <i>Journal of Phycology</i> , 2016, 52, 116-124.	2.3	23
46	Coevolution of Eukaryote-like Vps4 and ESCRT-III Subunits in the Asgard Archaea. <i>MBio</i> , 2020, 11, .	4.1	23
47	Mammalian Synthetic Biology: Time for Big MACs. <i>ACS Synthetic Biology</i> , 2016, 5, 1040-1049.	3.8	22
48	Wicket: A Versatile Tool for the Integration and Optimization of Exogenous Pathways in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 782-788.	3.8	22
49	Design and chemical synthesis of eukaryotic chromosomes. <i>Chemical Society Reviews</i> , 2017, 46, 7191-7207.	38.1	21
50	<i>Auxenochlorella protothecoides</i> and <i>Prototheca wickerhamii</i> plastid genome sequences give insight into the origins of non-photosynthetic algae. <i>Scientific Reports</i> , 2015, 5, 14465.	3.3	20
51	Construction, characterization and application of a genome-wide promoter library in <i>Saccharomyces cerevisiae</i> . <i>Frontiers of Chemical Science and Engineering</i> , 2017, 11, 107-116.	4.4	20
52	Whole genome engineering by synthesis. <i>Science China Life Sciences</i> , 2018, 61, 1515-1527.	4.9	20
53	Relevance of the dietary glycemic index, glycemic load and genetic predisposition for the glucose homeostasis of Chinese adults without diabetes. <i>Scientific Reports</i> , 2017, 7, 400.	3.3	19
54	The Role of Y Chromosome Genes in Male Fertility in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2020, 215, 623-633.	2.9	19

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55	Biodegradation of aromatic pollutants meets synthetic biology. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 153-162.	3.7	17
56	Glutaredoxin Deletion Shortens Chronological Life Span in <i>Saccharomyces cerevisiae</i> via ROS-Mediated Ras/PKA Activation. <i>Journal of Proteome Research</i> , 2018, 17, 2318-2327.	3.7	16
57	Characterization of an ammonium transporter in the oleaginous alga <i>Chlorella protothecoides</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 919-928.	3.6	14
58	Yin and Yang of Histone H2B Roles in Silencing and Longevity: A Tale of Two Arginines. <i>Genetics</i> , 2010, 186, 813-828.	2.9	12
59	Industrial Fermentation of <i>Auxenochlorella protothecoides</i> for Production of Biodiesel and Its Application in Vehicle Diesel Engines. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 164.	4.1	12
60	Whole-Genome Regulation for Yeast Metabolic Engineering. <i>Small Methods</i> , 2020, 4, 1900640.	8.6	12
61	Identification of gene products that control lipid droplet size in yeast using a high-throughput quantitative image analysis. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2019, 1864, 113-127.	2.4	10
62	SCRaMble: A Study of Its Robustness and Challenges through Enhancement of Hygromycin B Resistance in a Semi-Synthetic Yeast. <i>Bioengineering</i> , 2021, 8, 42.	3.5	10
63	Microgrooved poly(3-hydroxybutyrate-co-3-hydroxyhexanoate) affects the phenotype of vascular smooth muscle cells through let-7a-involved regulation of actin dynamics. <i>Biotechnology Letters</i> , 2014, 36, 2125-2133.	2.2	9
64	EcoExpress™ Highly Efficient Construction and Expression of Multicomponent Protein Complexes in <i>Escherichia coli</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 1239-1246.	3.8	9
65	Construction of Comprehensive Dosage-Matching Core Histone Mutant Libraries for <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2017, 207, 1263-1273.	2.9	9
66	Engineering and functional analysis of yeast with a monotypic 40S ribosome subunit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	9
67	Efficient de novo assembly and modification of large DNA fragments. <i>Science China Life Sciences</i> , 2022, 65, 1445-1455.	4.9	9
68	Photosynthesis-fermentation hybrid system to produce lipid feedstock for algal biofuel. <i>Environmental Technology (United Kingdom)</i> , 2013, 34, 1869-1876.	2.2	8
69	YeastFab: High-Throughput Genetic Parts Construction, Measurement, and Pathway Engineering in Yeast. <i>Methods in Enzymology</i> , 2018, 608, 277-306.	1.0	8
70	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
71	Dissecting PCNA function with a systematically designed mutant library in yeast. <i>Journal of Genetics and Genomics</i> , 2019, 46, 301-313.	3.9	7
72	Multiplex Genome Engineering for Optimizing Bioproduction in <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2019, 58, 1492-1500.	2.5	7

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73	Synthetic yeast genomes for studying chromosomal features. <i>Current Opinion in Systems Biology</i> , 2020, 23, 1-7.	2.6	7
74	Engineered TAL Effector modulators for the large-scale gain-of-function screening. <i>Nucleic Acids Research</i> , 2014, 42, e114-e114.	14.5	6
75	A quantitative analysis of histone methylation and acetylation isoforms from their deuterioacetylated derivatives: application to a series of knockout mutants. <i>Journal of Mass Spectrometry</i> , 2013, 48, 608-615.	1.6	5
76	Improving Chromosome Synthesis with a Semiquantitative Phenotypic Assay and Refined Assembly Strategy. <i>ACS Synthetic Biology</i> , 2019, 8, 2203-2211.	3.8	5
77	Inevitability or contingency: how many chromosomes do we really need?. <i>Science China Life Sciences</i> , 2019, 62, 140-143.	4.9	5
78	Probing eukaryotic genome functions with synthetic chromosomes. <i>Experimental Cell Research</i> , 2020, 390, 111936.	2.6	5
79	Identification of long chain isoprenoid hydrocarbons from pyrolytic product of <i>Dunaliella</i> . <i>Science Bulletin</i> , 1999, 44, 1700-1705.	1.7	4
80	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> . <i>Nucleic Acids Research</i> , 2021, 49, 4655-4667.	14.5	4
81	Whole genome synthesis: from poliovirus to synthetic yeast. <i>Quantitative Biology</i> , 2017, 5, 105-109.	0.5	3
82	PyMut: A Web Tool for Overlapping Gene Loss-of-Function Mutation Design. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1107-1110.	3.0	2
83	Chromosomal Rearrangements of Synthetic Yeast by SCRaMbLE. <i>Methods in Molecular Biology</i> , 2021, 2196, 153-165.	0.9	2
84	Strain Construction and Screening Methods for a Yeast Histone H3/H4 Mutant Library. <i>Methods in Molecular Biology</i> , 2012, 833, 1-14.	0.9	2
85	Probing the Function of Metazoan Histones with a Systematic Library of H3 and H4 Mutants. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
86	Studying bona fide SARS-CoV-2 biology in a BSL-2 biosafety environment using a split-virus-genome system. <i>Science China Life Sciences</i> , 2022, 65, 1894-1897.	4.9	2
87	Hydrocarbons pyrolysed from nannoplanktonic algae: An experimental organism system for study on the origin of petroleum and natural gas. <i>Science Bulletin</i> , 1999, 44, 767-768.	1.7	1
88	Molecular source of biomarkers by genetic engineering techniques. <i>Science Bulletin</i> , 2000, 45, 1025-1030.	1.7	1
89	Cell Lysate Microarray for Mapping the Network of Genetic Regulators for Histone Marks. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1720-1736.	3.8	1
90	Reconstruction of Secondary Metabolic Pathway to Synthesize Novel Metabolite in <i>Saccharopolyspora erythraea</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 628569.	4.1	1

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91	Use YeastFab to Construct Genetic Parts and Multicomponent Pathways for Metabolic Engineering. <i>Methods in Molecular Biology</i> , 2021, 2196, 167-180.	0.9	1
92	Carbon isotopic values of individual n-alkanes in pyrolysates of algae. <i>Diqiu Huaxue</i> , 2000, 19, 181-185.	0.5	0
93	Meeting report on Synthetic Biology Young Scholar Forum. <i>Quantitative Biology</i> , 2016, 3, 206-211.	0.5	0
94	Methods to Synthesize Large DNA Fragments for a Synthetic Yeast Genome. <i>Cold Spring Harbor Protocols</i> , 2017, 2017, pdb.prot080978.	0.3	0
95	Investigating loss of heterozygosity in a SCRaMbLEd yeast genome. <i>Science China Life Sciences</i> , 2019, 62, 868-869.	4.9	0
96	Association of Histone Modification Patterns With Transcription Factor Binding Revealed by Systematic Analysis. <i>Acta Agronomica Sinica(China)</i> , 2013, 40, 177.	0.3	0
97	SCRaMbLE-in: A Fast and Efficient Method to Diversify and Improve the Yields of Heterologous Pathways in Synthetic Yeast. <i>Methods in Molecular Biology</i> , 2020, 2205, 305-327.	0.9	0