

Daisuke Watanabe

List of Publications by Year in descending order

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68
papers

1,605
citations

304368

22
h-index

329751

37
g-index

72
all docs

72
docs citations

72
times ranked

1604
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome Sequencing of Sake Yeast <i>Saccharomyces cerevisiae</i> Kyokai no. 7. <i>DNA Research</i> , 2011, 18, 423-434.	1.5	150
2	Dissection of Upstream Regulatory Components of the Rho1p Effector, 1,3- β -Glucan Synthase, in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2002, 162, 663-676.	1.2	112
3	SCMD: <i>Saccharomyces cerevisiae</i> Morphological Database. <i>Nucleic Acids Research</i> , 2004, 32, 319D-322.	6.5	84
4	Movement of yeast 1,3- β -glucan synthase is essential for uniform cell wall synthesis. <i>Genes To Cells</i> , 2002, 7, 1-9.	0.5	82
5	A Loss-of-Function Mutation in the PAS Kinase Rim15p Is Related to Defective Quiescence Entry and High Fermentation Rates of <i>Saccharomyces cerevisiae</i> Sake Yeast Strains. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4008-4016.	1.4	77
6	Overexpression of the yeast transcription activator Msn2 confers furfural resistance and increases the initial fermentation rate in ethanol production. <i>Journal of Bioscience and Bioengineering</i> , 2012, 113, 451-455.	1.1	73
7	Yeast Lrg1p acts as a specialized RhoGAP regulating 1,3- β -glucan synthesis. <i>Yeast</i> , 2001, 18, 943-951.	0.8	69
8	Enhancement of the Initial Rate of Ethanol Fermentation Due to Dysfunction of Yeast Stress Response Components Msn2p and/or Msn4p. <i>Applied and Environmental Microbiology</i> , 2011, 77, 934-941.	1.4	62
9	Comprehensive and quantitative analysis of yeast deletion mutants defective in apical and isotropic bud growth. <i>Current Genetics</i> , 2009, 55, 365-380.	0.8	50
10	Overexpression of MSN2 in a sake yeast strain promotes ethanol tolerance and increases ethanol production in sake brewing. <i>Journal of Bioscience and Bioengineering</i> , 2009, 107, 516-518.	1.1	48
11	An organic acid-tolerant HAA1-overexpression mutant of an industrial bioethanol strain of <i>Saccharomyces cerevisiae</i> and its application to the production of bioethanol from sugarcane molasses. <i>AMB Express</i> , 2013, 3, 74.	1.4	39
12	Accelerated Alcoholic Fermentation Caused by Defective Gene Expression Related to Glucose Derepression in <i>Saccharomyces cerevisiae</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2013, 77, 2255-2262.	0.6	34
13	Sake yeast strains have difficulty in entering a quiescent state after cell growth cessation. <i>Journal of Bioscience and Bioengineering</i> , 2011, 112, 44-48.	1.1	29
14	Association of Constitutive Hyperphosphorylation of Hsf1p with a Defective Ethanol Stress Response in <i>Saccharomyces cerevisiae</i> Sake Yeast Strains. <i>Applied and Environmental Microbiology</i> , 2012, 78, 385-392.	1.4	28
15	Inhibitory Role of Greatwall-Like Protein Kinase Rim15p in Alcoholic Fermentation via Upregulating the UDP-Glucose Synthesis Pathway in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2016, 82, 340-351.	1.4	28
16	Isolation of baker's yeast mutants with proline accumulation that showed enhanced tolerance to baking-associated stresses. <i>International Journal of Food Microbiology</i> , 2016, 238, 233-240.	2.1	27
17	Nitric oxide signaling and its role in oxidative stress response in <i>Schizosaccharomyces pombe</i> . <i>Nitric Oxide - Biology and Chemistry</i> , 2016, 52, 29-40.	1.2	27
18	High-level production of valine by expression of the feedback inhibition-insensitive acetohydroxyacid synthase in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 46, 60-67.	3.6	26

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19	Phenotypic Diagnosis of Lineage and Differentiation During Sake Yeast Breeding. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2807-2820.	0.8	25
20	Involvement of methionine salvage pathway genes of <i>Saccharomyces cerevisiae</i> in the production of precursor compounds of dimethyl trisulfide (DMTS). <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 475-479.	1.1	23
21	Regulatory mechanism of the flavoprotein Tah18-dependent nitric oxide synthesis and cell death in yeast. <i>Nitric Oxide - Biology and Chemistry</i> , 2016, 57, 85-91.	1.2	23
22	Metabolic switching of sake yeast by kimoto lactic acid bacteria through the [GAR] non-genetic element. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 624-629.	1.1	23
23	Automatic measurement of sake fermentation kinetics using a multi-channel gas monitor system. <i>Journal of Bioscience and Bioengineering</i> , 2011, 112, 54-57.	1.1	20
24	Ethanol fermentation driven by elevated expression of the G1 cyclin gene CLN3 in sake yeast. <i>Journal of Bioscience and Bioengineering</i> , 2011, 112, 577-582.	1.1	20
25	Finding of thiosulfate pathway for synthesis of organic sulfur compounds in <i>Saccharomyces cerevisiae</i> and improvement of ethanol production. <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 666-669.	1.1	19
26	Sake yeast YHR032W/ERC1 haplotype contributes to high S-adenosylmethionine accumulation in sake yeast strains. <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 8-14.	1.1	18
27	Exogenous addition of histidine reduces copper availability in the yeast <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell</i> , 2014, 1, 241-246.	1.4	18
28	Valine biosynthesis in <i>Saccharomyces cerevisiae</i> is regulated by the mitochondrial branched-chain amino acid aminotransferase Bat1. <i>Microbial Cell</i> , 2018, 5, 293-299.	1.4	18
29	Proline metabolism regulates replicative lifespan in the yeast <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell</i> , 2019, 6, 482-490.	1.4	18
30	Vacuolar amino acid transporters upregulated by exogenous proline and involved in cellular localization of proline in <i>Saccharomyces cerevisiae</i> . <i>Journal of General and Applied Microbiology</i> , 2016, 62, 132-139.	0.4	17
31	Promoter engineering of the <i>Saccharomyces cerevisiae</i> RIM15 gene for improvement of alcoholic fermentation rates under stress conditions. <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 183-189.	1.1	17
32	Genome Editing to Generate Sake Yeast Strains with Eight Mutations That Confer Excellent Brewing Characteristics. <i>Cells</i> , 2021, 10, 1299.	1.8	17
33	Rim15p-mediated regulation of sucrose utilization during molasses fermentation using <i>Saccharomyces cerevisiae</i> strain PE-2. <i>Journal of Bioscience and Bioengineering</i> , 2013, 116, 591-594.	1.1	16
34	Nutrient Signaling via the TORC1-Greatwall-PP2A Pathway Is Responsible for the High Initial Rates of Alcoholic Fermentation in Sake Yeast Strains of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	16
35	Quality Control of Plasma Membrane Proteins by <i>Saccharomyces cerevisiae</i> Nedd4-Like Ubiquitin Ligase Rsp5p under Environmental Stress Conditions. <i>Eukaryotic Cell</i> , 2014, 13, 1191-1199.	3.4	15
36	Isolation and functional analysis of yeast ubiquitin ligase Rsp5 variants that alleviate the toxicity of human α -synuclein. <i>Journal of Biochemistry</i> , 2015, 157, 251-260.	0.9	15

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37	Defective quiescence entry promotes the fermentation performance of bottom-fermenting brewer's yeast. <i>Journal of Bioscience and Bioengineering</i> , 2016, 122, 577-582.	1.1	15
38	Characterization of a New <i>Saccharomyces cerevisiae</i> Isolated From Hibiscus Flower and Its Mutant With L-Leucine Accumulation for Awamori Brewing. <i>Frontiers in Genetics</i> , 2019, 10, 490.	1.1	15
39	Cell shape and growth of budding yeast cells in restrictive microenvironments. <i>Yeast</i> , 2004, 21, 983-989.	0.8	14
40	Isolation and characterization of awamori yeast mutants with l-leucine accumulation that overproduce isoamyl alcohol. <i>Journal of Bioscience and Bioengineering</i> , 2015, 119, 140-147.	1.1	14
41	Accumulation of intracellular S-adenosylmethionine increases the fermentation rate of bottom-fermenting brewer's yeast during high-gravity brewing. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 736-741.	1.1	13
42	Pleiotropic functions of the yeast Greatwall-family protein kinase Rim15p: a novel target for the control of alcoholic fermentation. <i>Bioscience, Biotechnology and Biochemistry</i> , 2017, 81, 1061-1068.	0.6	11
43	Involvement of the stress-responsive transcription factor gene MSN2 in the control of amino acid uptake in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	11
44	Meiotic chromosomal recombination defect in sake yeasts. <i>Journal of Bioscience and Bioengineering</i> , 2019, 127, 190-196.	1.1	11
45	Bacterial inducible expression of plant cell wall-binding protein YesO through conflict between <i>Glycine max</i> and saprophytic <i>Bacillus subtilis</i> . <i>Scientific Reports</i> , 2020, 10, 18691.	1.6	10
46	Putative mitochondrial α -ketoglutarate-dependent dioxygenase Fmp12 controls utilization of proline as an energy source in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell</i> , 2016, 3, 522-528.	1.4	10
47	Cooperative and selective roles of the WW domains of the yeast Nedd4-like ubiquitin ligase Rsp5 in the recognition of the arrestin-like adaptors Bul1 and Bul2. <i>Biochemical and Biophysical Research Communications</i> , 2015, 463, 76-81.	1.0	9
48	α -Glutamyl kinase is involved in selective autophagy of ribosomes in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2016, 590, 2906-2914.	1.3	9
49	Enhanced sodium acetate tolerance in <i>Saccharomyces cerevisiae</i> by the Thr255Ala mutation of the ubiquitin ligase Rsp5. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	9
50	Sodium Acetate Responses in <i>Saccharomyces cerevisiae</i> and the Ubiquitin Ligase Rsp5. <i>Frontiers in Microbiology</i> , 2018, 9, 2495.	1.5	9
51	Calcineurin inhibitors suppress the high-temperature stress sensitivity of the yeast ubiquitin ligase Rsp5 mutant: a new method of screening for calcineurin inhibitors. <i>FEMS Yeast Research</i> , 2014, 14, 567-574.	1.1	8
52	Yeast prion-based metabolic reprogramming induced by bacteria in fermented foods. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	8
53	Screening of High-Level 4-Hydroxy-2 (or 5)-Ethyl-5 (or 2)-Methyl-3(2-H)-Furanone-Producing Strains from a Collection of Gene Deletion Mutants of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 453-460.	1.4	7
54	Awa1p on the cell surface of sake yeast inhibits biofilm formation and the co-aggregation between sake yeasts and <i>Lactobacillus plantarum</i> ML11-11. <i>Journal of Bioscience and Bioengineering</i> , 2015, 119, 532-537.	1.1	6

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55	Structure-based molecular design for thermostabilization of N-acetyltransferase Mpr1 involved in a novel pathway of L-arginine synthesis in yeast. <i>Journal of Biochemistry</i> , 2016, 159, 271-277.	0.9	5
56	Effect of the deubiquitination enzyme gene UBP6 on the stress-responsive transcription factor Msn2-mediated control of the amino acid permease Gnp1 in yeast. <i>Journal of Bioscience and Bioengineering</i> , 2020, 129, 423-427.	1.1	5
57	Importance of Proteasome Gene Expression during Model Dough Fermentation after Preservation of Baker's Yeast Cells by Freezing. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	4
58	Stable N-acetyltransferase Mpr1 improves ethanol productivity in the sake yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019, 46, 1039-1045.	1.4	4
59	Loss of Rim15p in shochu yeast alters carbon utilization during barley shochu fermentation. <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1594-1597.	0.6	3
60	The sake yeast YHR032W/ERC1 allele contributes to the regulation of the tetrahydrofolate content in the folate synthetic pathway in sake yeast strains. <i>Bioscience, Biotechnology and Biochemistry</i> , 2020, 84, 1073-1076.	0.6	2
61	Polysaturated fatty acids-enriched lipid from reduced sugar alcohol mannitol by marine yeast <i>Rhodospiridiobolus fluvialis</i> Y2. <i>Biochemical and Biophysical Research Communications</i> , 2020, 526, 1138-1142.	1.0	2
62	Mechanism of High Alcoholic Fermentation Ability of Sake Yeast. , 2015, , 59-75.		2
63	The C2 domain of the ubiquitin ligase Rsp5 is required for ubiquitination of the endocytic protein Rvs167 upon change of nitrogen source. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	2
64	How Has Sake Yeast Acquired High Alcohol Fermentation Ability ?. <i>Kagaku To Seibutsu</i> , 2012, 50, 723-729.	0.0	0
65	Screening of High-level 4-Hydroxy-2(or 5)-Ethyl-5(or 2)-Methyl-3(2H)-Furanone-Producing Strains from a Collection of Gene Deletion Mutants of <i>Saccharomyces cerevisiae</i> . <i>Journal of the Brewing Society of Japan</i> , 2015, 110, 840-848.	0.1	0
66	RIM15, a Kyokai Sake Yeast-specific Mutated Gene Associated with the High Alcoholic Fermentation Performance. <i>Journal of the Brewing Society of Japan</i> , 2016, 111, 638-647.	0.1	0
67	Characterization and Potential Application of Substrate-Specific Recognition by the Yeast Ubiquitin Ligase Rsp5: To Prevent Ubiquitin "Missending". <i>Kagaku To Seibutsu</i> , 2018, 57, 36-42.	0.0	0
68	Crystal structures of EfeB and EfeO in a bacterial siderophore-independent iron transport system. <i>Biochemical and Biophysical Research Communications</i> , 2022, 594, 124-130.	1.0	0