CÃ©cile NeuvÃ©glise

List of Publications by Year
in descending order

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84	6,421	108046	78623
papers	citations	37 h-index	77 g-index

85	85	85	7000
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Development of a Vector Set for High or Inducible Gene Expression and Protein Secretion in the Yeast Genus Blastobotrys. Journal of Fungi (Basel, Switzerland), 2022, 8, 418.	1.5	0
2	A 37-amino acid loop in the Yarrowia lipolytica hexokinase impacts its activity and affinity and modulates gene expression. Scientific Reports, 2021, 11, 6412.	1.6	7
3	New Cytoplasmic Virus-Like Elements (VLEs) in the Yeast Debaryomyces hansenii. Toxins, 2021, 13, 615.	1.5	3
4	The native acyltransferase-coding genes DGA1 and DGA2 affect lipid accumulation in Blastobotrys raffinosifermentans differently when overexpressed. FEMS Yeast Research, 2020, 20, .	1.1	3
5	Developing Methods to Circumvent the Conundrum of Chromosomal Rearrangements Occurring in Multiplex Gene Edition. ACS Synthetic Biology, 2020, 9, 2562-2575.	1.9	4
6	Transforming Candida hispaniensis , a promising oleaginous and flavogenic yeast. Yeast, 2020, 37, 348-355.	0.8	8
7	Yarrowia lipolytica causes sporadic cases and local outbreaks of infections and colonisation. Mycoses, 2020, 63, 737-745.	1.8	12
8	High Complexity and Degree of Genetic Variation in Brettanomyces bruxellensis Population. Genome Biology and Evolution, 2020, 12, 795-807.	1.1	18
9	Blastobotrys adeninivorans and B. raffinosifermentans, two sibling yeast species which accumulate lipids at elevated temperatures and from diverse sugars. Biotechnology for Biofuels, 2019, 12, 154.	6.2	27
10	Identification of telomerase RNAs in species of the Yarrowia clade provides insights into the co-evolution of telomerase, telomeric repeats and telomere-binding proteins. Scientific Reports, 2019, 9, 13365.	1.6	27
11	Exon junction complex components Y14 and Mago still play a role in budding yeast. Scientific Reports, 2019, 9, 849.	1.6	3
12	Genome Sequence of the Oleaginous Yeast Yarrowia lipolytica H222. Microbiology Resource Announcements, 2019, 8, .	0.3	8
13	AndrÃ© Goffeau's imprinting on second generation yeast â€œgenomologistsâ€. Yeast, 2019, 36, 167-175.	0.8	1
14	Investigation of Genetic Relationships Between Hanseniaspora Species Found in Grape Musts Revealed Interspecific Hybrids With Dynamic Genome Structures. Frontiers in Microbiology, 2019, 10, 2960.	1.5	23
15	Genome Sequence of Torulaspora microellipsoides CLIB 830 ^T. Genome Announcements, 2018, 6, .	0.8	5
16	Multiple Parameters Drive the Efficiency of CRISPR/Cas9-Induced Gene Modifications in Yarrowia lipolytica. Journal of Molecular Biology, 2018, 430, 4293-4306.	2.0	19
17	Characterization of hexose transporters in Yarrowia lipolytica reveals new groups of Sugar Porters involved in yeast growth. Fungal Genetics and Biology, 2017, 100, 1-12.	0.9	31
18	EUF1 â€“ a newly identified gene involved in erythritol utilization in Yarrowia lipolytica. Scientific Reports, 2017, 7, 12507.	1.6	27

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19	Genome sequence of the type strain CLIB 1764 T (= CBS 14374 T) of the yeast species Kazachstania saulgeensis isolated from French organic sourdough. Genomics Data, 2017, 13, 41-43.	1.3	21
20	Truncation of Gal4p explains the inactivation of theGAL/MELregulon in bothSaccharomyces bayanusand someSaccharomyces cerevisiaewine strains. FEMS Yeast Research, 2016, 16, fow070.	1.1	6
21	Sweet and sour potential of yeast from the Yarrowia clade. Biomass and Bioenergy, 2016, 92, 48-54.	2.9	31
22	Draft Genome Sequence of Yarrowia lipolytica Strain A-101 Isolated from Polluted Soil in Poland. Genome Announcements, 2016, 4, .	0.8	18
23	Reconstruction of ancestral chromosome architecture and gene repertoire reveals principles of genome evolution in a model yeast genus. Genome Research, 2016, 26, 918-932.	2.4	95
24	Whole-Genome Sequencing and Intraspecific Analysis of the Yeast SpeciesLachancea quebecensis. Genome Biology and Evolution, 2016, 8, 733-741.	1.1	12
25	Enhancing Structural Annotation of Yeast Genomes with RNA-Seq Data. Methods in Molecular Biology, 2016, 1361, 41-56.	0.4	1
26	Awakening the endogenous Leloir pathway for efficient galactose utilization by Yarrowia lipolytica. Biotechnology for Biofuels, 2015, 8, 185.	6.2	44
27	Comprehensive Analysis of a Yeast Lipase Family in the Yarrowia Clade. PLoS ONE, 2015, 10, e0143096.	1.1	33
28	Trends in IT Innovation to Build a Next Generation Bioinformatics Solution to Manage and Analyse Biological Big Data Produced by NGS Technologies. BioMed Research International, 2015, 2015, 1-15.	0.9	26
29	Evolutionary Dynamics of hAT DNA Transposon Families in Saccharomycetaceae. Genome Biology and Evolution, 2015, 7, 172-190.	1.1	20
30	Draft Genome Sequence of Lachancea lanzarotensis CBS 12615 ^T , an Ascomycetous Yeast Isolated from Grapes. Genome Announcements, 2015, 3, .	0.8	12
31	The evolution of Jen3 proteins and their role in dicarboxylic acid transport in Yarrowia. MicrobiologyOpen, 2015, 4, 100-120.	1.2	15
32	Hexokinaseâ€"A limiting factor in lipid production from fructose in Yarrowia lipolytica. Metabolic Engineering, 2014, 26, 89-99.	3.6	113
33	Genome Sequence of the Yeast Cyberlindnera fabianii (Hansenula fabianii). Genome Announcements, 2014, 2, .	0.8	31
34	Zinc Finger Transcription Factors Displaced SREBP Proteins as the Major Sterol Regulators during Saccharomycotina Evolution. PLoS Genetics, 2014, 10, e1004076.	1.5	63
35	Analysis of the Genome and Transcriptome of Cryptococcus neoformans var. grubii Reveals Complex RNA Expression and Microevolution Leading to Virulence Attenuation. PLoS Genetics, 2014, 10, e1004261.	1.5	336
36	Draft Genome Sequence of Rhodosporidium toruloides CECT1137, an Oleaginous Yeast of Biotechnological Interest. Genome Announcements, 2014, 2, .	0.8	24

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37	Genes encoding DNA polymerases on linear dsDNA plasmids of Debaryomyces hansenii yeasts share very high homology. New Biotechnology, 2014, 31, S219.	2.4	0
38	The complete genome of Blastobotrys (Arxula) adeninivorans LS3 - a yeast of biotechnological interest. Biotechnology for Biofuels, 2014, 7, 66.	6.2	57
39	Yarrowia lipolytica: Safety assessment of an oleaginous yeast with a great industrial potential. Critical Reviews in Microbiology, 2014, 40, 187-206.	2.7	369
40	Comparative genomics of emerging pathogens in the Candida glabrata clade. BMC Genomics, 2013, 14, 623.	1.2	174
41	Genome Sequence of the Food Spoilage Yeast Zygosaccharomyces bailii CLIB 213 T. Genome Announcements, 2013, 1, .	0.8	39
42	The Complex Evolutionary Dynamics of Hsp70s: A Genomic and Functional Perspective. Genome Biology and Evolution, 2013, 5, 2460-2477.	1.1	44
43	Comparative Physiology of Oleaginous Species from the Yarrowia Clade. PLoS ONE, 2013, 8, e63356.	1.1	41
44	Comparative Genomics of Yarrowia lipolytica. Microbiology Monographs, 2013, , 1-30.	0.3	4
45	Noncoding RNA Genes Transcribed by RNA Polymerase III in Yarrowia lipolytica. Microbiology Monographs, 2013, , 79-109.	0.3	0
46	Alternative Splicing Regulates Targeting of Malate Dehydrogenase in Yarrowia lipolytica. DNA Research, 2012, 19, 231-244.	1.5	48
47	Pichia sorbitophila, an Interspecies Yeast Hybrid, Reveals Early Steps of Genome Resolution After Polyploidization. G3: Genes, Genomes, Genetics, 2012, 2, 299-311.	0.8	113
48	Comparative Mitochondrial Genomics within and among Yeast Species of the Lachancea Genus. PLoS ONE, 2012, 7, e47834.	1.1	45
49	Mitochondrial genomes of yeasts of the Yarrowia clade. FEMS Yeast Research, 2012, 12, 317-331.	1.1	28
50	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS Genetics, 2011, 7, e1002230.	1.5	902
51	The intronome of budding yeasts. Comptes Rendus - Biologies, 2011, 334, 662-670.	0.1	64
52	Transposable elements in yeasts. Comptes Rendus - Biologies, 2011, 334, 679-686.	0.1	44
53	Deciphering the Hybridisation History Leading to the Lager Lineage Based on the Mosaic Genomes of Saccharomyces bayanus Strains NBRC1948 and CBS380T. PLoS ONE, 2011, 6, e25821.	1.1	93
54	Engineering polyhydroxyalkanoate content and monomer composition in the oleaginous yeast Yarrowia lipolytica by modifying the ÃŸ-oxidation multifunctional protein. Applied Microbiology and Biotechnology, 2011, 91, 1327-1340.	1.7	58

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55	SOAgenes encode proteins controlling lipase expression in response to triacylglycerol utilization in the yeastYarrowia lipolytica. FEMS Yeast Research, 2010, 10, 93-103.	1.1	23
56	Roles of multiple acyl-CoA oxidases in the routing of carbon flow towards Î²-oxidation and polyhydroxyalkanoate biosynthesis in Yarrowia lipolytica. FEMS Yeast Research, 2010, 10, 917-927.	1.1	55
57	Detection and analysis of alternative splicing in Yarrowia lipolytica reveal structural constraints facilitating nonsense-mediated decay of intron-retaining transcripts. Genome Biology, 2010, 11, R65.	13.9	63
58	Unusual composition of a yeast chromosome arm is associated with its delayed replication. Genome Research, 2009, 19, 1710-1721.	2.4	43
59	Comparative genomics of protoploid Saccharomycetaceae. Genome Research, 2009, 19, 1696-1709.	2.4	207
60	Differentiation ofDebaryomyces hanseniiandCandida famataby rRNA gene intergenic spacer fingerprinting and reassessment of phylogenetic relationships amongD. hansenii, C. famata, D. fabryi, C. flareri(=D. subglobosus) andD. prosopidis: description ofD. vietnamensissp. nov. closely related toD. nepalensis. FEMS Yeast Research, 2009, 9, 641-662.	1.1	55
61	Important genetic diversity revealed by inter-LTR PCR fingerprinting ofKluyveromyces marxianusandDebaryomyces hanseniistrains from French traditional cheeses. Dairy Science and Technology, 2009, 89, 569-581.	2.2	18
62	Insertion of Horizontally Transferred Genes within Conserved Syntenic Regions of Yeast Genomes. PLoS ONE, 2009, 4, e6515.	1.1	57
63	Dicistronic tRNAâ€“5S rRNA genes in Yarrowia lipolytica: an alternative TFIIIA-independent way for expression of 5S rRNA genes. Nucleic Acids Research, 2008, 36, 5832-5844.	6.5	23
64	l-Methionine Degradation Pathway in Kluyveromyces lactis: Identification and Functional Analysis of the Genes Encoding l-Methionine Aminotransferase. Applied and Environmental Microbiology, 2006, 72, 3330-3335.	1.4	27
65	Triplicate genes for mitochondrial ADP/ATP carriers in the aerobic yeast Yarrowia lipolytica are regulated differentially in the absence of oxygen. Molecular Genetics and Genomics, 2005, 273, 84-91.	1.0	8
66	Mutator -Like Element in the Yeast Yarrowia lipolytica Displays Multiple Alternative Splicings. Eukaryotic Cell, 2005, 4, 615-624.	3.4	41
67	Genome evolution in yeasts. Nature, 2004, 430, 35-44.	13.7	1,498
68	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. Nucleic Acids Research, 2003, 31, 1121-1135.	6.5	118
69	Genomic Evolution of the Long Terminal Repeat Retrotransposons in Hemiascomycetous Yeasts. Genome Research, 2002, 12, 930-943.	2.4	96
70	Ylli, a Nonâ€“LTR Retrotransposon L1 Family in the Dimorphic Yeast Yarrowia lipolytica. Molecular Biology and Evolution, 2002, 19, 664-677.	3.5	33
71	Evolution of Gene Order in the Genomes of Two Related Yeast Species. Genome Research, 2001, 11, 2009-2019.	2.4	84
72	Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of yeast species for molecular evolution studies1. FEBS Letters, 2000, 487, 3-12.	1.3	186

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73	Genomic Exploration of the Hemiascomycetous Yeasts: 3. Methods and strategies used for sequence analysis and annotation. FEBS Letters, 2000, 487, 17-30.	1.3	37
74	Genomic Exploration of the Hemiascomycetous Yeasts: 4. The genome ofSaccharomyces cerevisiaerevisited. FEBS Letters, 2000, 487, 31-36.	1.3	75
75	Genomic Exploration of the Hemiascomycetous Yeasts: 5.Saccharomyces bayanusvar.uvarum. FEBS Letters, 2000, 487, 37-41.	1.3	40
76	Genomic Exploration of the Hemiascomycetous Yeasts: 6. Saccharomyces exiguus. FEBS Letters, 2000, 487, 42-46.	1.3	17
77	Genomic Exploration of the Hemiascomycetous Yeasts: 7.Saccharomyces servazzii. FEBS Letters, 2000, 487, 47-51.	1.3	13
78	Genomic Exploration of the Hemiascomycetous Yeasts: 9.Saccharomyces kluyveri. FEBS Letters, 2000, 487, 56-60.	1.3	18
79	Genomic Exploration of the Hemiascomycetous Yeasts: 14.Debaryomyces hanseniivar.hansenii. FEBS Letters, 2000, 487, 82-86.	1.3	56
80	Genomic Exploration of the Hemiascomycetous Yeasts: 17. Yarrowia lipolytica. FEBS Letters, 2000, 487, 95-100.	1.3	88
81	Genomic Exploration of the Hemiascomycetous Yeasts: 18. Comparative analysis of chromosome maps and synteny withSaccharomyces cerevisiae. FEBS Letters, 2000, 487, 101-112.	1.3	71
82	Genomic Exploration of the Hemiascomycetous Yeasts: 19. Ascomycetes-specific genes. FEBS Letters, 2000, 487, 113-121.	1.3	47
83	Genomic Exploration of the Hemiascomycetous Yeasts: 20. Evolution of gene redundancy compared to Saccharomyces cerevisiae. FEBS Letters, 2000, 487, 122-133.	1.3	49
84	Genomic Exploration of the Hemiascomycetous Yeasts: 21. Comparative functional classification of genes. FEBS Letters, 2000, 487, 134-149.	1.3	23