

Edward J Louis

List of Publications by Year in descending order

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103
papers

14,070
citations

44069

48
h-index

32842

100
g-index

107
all docs

107
docs citations

107
times ranked

10584
citing authors

#	ARTICLE	IF	CITATIONS
1	The evolving species concepts used for yeasts: from phenotypes and genomes to speciation networks. <i>Fungal Diversity</i> , 2021, 109, 27-55.	12.3	37
2	Restoring fertility in yeast hybrids: Breeding and quantitative genetics of beneficial traits. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	21
3	Insights on life cycle and cell identity regulatory circuits for unlocking genetic improvement in <i>Zygosaccharomyces</i> and <i>Kluyveromyces</i> yeasts. <i>FEMS Yeast Research</i> , 2021, , .	2.3	4
4	Integrative Omics Analysis Reveals a Limited Transcriptional Shock After Yeast Interspecies Hybridization. <i>Frontiers in Genetics</i> , 2020, 11, 404.	2.3	22
5	A47â€¦Quantitative trait locus analysis in yeast: identifying candidate therapeutic targets for huntingtonâ€™s disease. , 2018, , .		0
6	PHENOS: a high-throughput and flexible tool for microorganism growth phenotyping on solid media. <i>BMC Microbiology</i> , 2018, 18, 9.	3.3	17
7	Genome Diversity and Evolution in the Budding Yeasts (<i>Saccharomycotina</i>). <i>Genetics</i> , 2017, 206, 717-750.	2.9	105
8	Meeting Report: Minutes from EMBO: Ten Years of Comparative Genomics of Eukaryotic Microorganisms. <i>Protist</i> , 2016, 167, 217-221.	1.5	0
9	Rif1 and Exo1 regulate the genomic instability following telomere losses. <i>Aging Cell</i> , 2016, 15, 553-562.	6.7	13
10	Telomere Dysfunction Triggers Palindrome Formation Independently of Double-Strand Break Repair Mechanisms. <i>Genetics</i> , 2016, 203, 1659-1668.	2.9	8
11	An ultra-dense library resource for rapid deconvolution of mutations that cause phenotypes in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, e41-e41.	14.5	14
12	Historical Evolution of Laboratory Strains of <i>Saccharomyces cerevisiae</i> . <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top077750.	0.3	7
13	A New Isolation and Evaluation Method for Marine-Derived Yeast spp. with Potential Applications in Industrial Biotechnology. <i>Journal of Microbiology and Biotechnology</i> , 2016, 26, 1891-1907.	2.1	28
14	Screening of Non- <i>Saccharomyces cerevisiae</i> Strains for Tolerance to Formic Acid in Bioethanol Fermentation. <i>PLoS ONE</i> , 2015, 10, e0135626.	2.5	12
15	The Genetic Basis of Variation in Clean Lineages of <i>Saccharomyces cerevisiae</i> in Response to Stresses Encountered during Bioethanol Fermentations. <i>PLoS ONE</i> , 2014, 9, e103233.	2.5	19
16	A High-Definition View of Functional Genetic Variation from Natural Yeast Genomes. <i>Molecular Biology and Evolution</i> , 2014, 31, 872-888.	8.9	328
17	Deletion of the <i>Saccharomyces cerevisiae</i> <i>ARO8</i> gene, encoding an aromatic amino acid transaminase, enhances phenylethanol production from glucose. <i>Yeast</i> , 2014, 32, n/a-n/a.	1.7	35
18	Phenotypic characterisation of <i>Saccharomyces</i> spp. yeast for tolerance to stresses encountered during fermentation of lignocellulosic residues to produce bioethanol. <i>Microbial Cell Factories</i> , 2014, 13, 47.	4.0	68

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19	Genomics of Subtelomeres: Technical Problems, Solutions and the Future. , 2014, , 259-271.		1
20	High quality de novo sequencing and assembly of the <i>Saccharomyces arboricolus</i> genome. <i>BMC Genomics</i> , 2013, 14, 69.	2.8	87
21	Thymineless death is inhibited by CsrA in <i>Escherichia coli</i> lacking the SOS response. <i>DNA Repair</i> , 2013, 12, 993-999.	2.8	4
22	High-Resolution Mapping of Complex Traits with a Four-Parent Advanced Intercross Yeast Population. <i>Genetics</i> , 2013, 195, 1141-1155.	2.9	164
23	Recurrent Rearrangement during Adaptive Evolution in an Interspecific Yeast Hybrid Suggests a Model for Rapid Introgression. <i>PLoS Genetics</i> , 2013, 9, e1003366.	3.5	102
24	Advances in Quantitative Trait Analysis in Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002912.	3.5	167
25	Telomere maintenance and telomerase activity are differentially regulated in asexual and sexual worms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4209-4214.	7.1	90
26	Life History Shapes Trait Heredity by Accumulation of Loss-of-Function Alleles in Yeast. <i>Molecular Biology and Evolution</i> , 2012, 29, 1781-1789.	8.9	76
27	New reservoirs of HLA alleles: pools of rare variants enhance immune defense. <i>Trends in Genetics</i> , 2012, 28, 480-486.	6.7	52
28	Apparent Ploidy Effects on Silencing Are Post-Transcriptional at HML and Telomeres in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e39044.	2.5	3
29	The Genetic Basis of Natural Variation in Oenological Traits in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e49640.	2.5	107
30	Population genomics and speciation in yeasts. <i>Fungal Biology Reviews</i> , 2011, 25, 136-142.	4.7	26
31	Assessing the complex architecture of polygenic traits in diverged yeast populations. <i>Molecular Ecology</i> , 2011, 20, 1401-1413.	3.9	194
32	Revealing the genetic structure of a trait by sequencing a population under selection. <i>Genome Research</i> , 2011, 21, 1131-1138.	5.5	263
33	<i>Saccharomyces cerevisiae</i> : Gene Annotation and Genome Variability, State of the Art Through Comparative Genomics. <i>Methods in Molecular Biology</i> , 2011, 759, 31-40.	0.9	7
34	Trait Variation in Yeast Is Defined by Population History. <i>PLoS Genetics</i> , 2011, 7, e1002111.	3.5	311
35	Cloning of the Repertoire of Individual <i>Plasmodium falciparum</i> var Genes Using Transformation Associated Recombination (TAR). <i>PLoS ONE</i> , 2011, 6, e17782.	2.5	14
36	Silenced yeast chromatin is maintained by Sir2 in preference to permitting histone acetylations for efficient NER. <i>Nucleic Acids Research</i> , 2010, 38, 4675-4686.	14.5	14

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37	In <i>Saccharomyces cerevisiae</i> , yKu and Subtelomeric Core X Sequences Repress Homologous Recombination Near Telomeres as Part of the Same Pathway. <i>Genetics</i> , 2009, 183, 441-451.	2.9	22
38	Segregating YKU80 and TLC1 Alleles Underlying Natural Variation in Telomere Properties in Wild Yeast. <i>PLoS Genetics</i> , 2009, 5, e1000659.	3.5	46
39	The Association of yKu With Subtelomeric Core X Sequences Prevents Recombination Involving Telomeric Sequences. <i>Genetics</i> , 2009, 183, 453-467.	2.9	28
40	Repressive and non-repressive chromatin at native telomeres in <i>Saccharomyces cerevisiae</i> . <i>Epigenetics and Chromatin</i> , 2009, 2, 18.	3.9	28
41	Population genomics of domestic and wild yeasts. <i>Nature</i> , 2009, 458, 337-341.	27.8	1,391
42	Origins of reproductive isolation. <i>Nature</i> , 2009, 457, 549-550.	27.8	15
43	Generation of a large set of genetically tractable haploid and diploid <i>Saccharomyces</i> strains. <i>FEMS Yeast Research</i> , 2009, 9, 1217-1225.	2.3	187
44	17-P036 How are the chromosome ends of immortal worms maintained?. <i>Mechanisms of Development</i> , 2009, 126, S281.	1.7	0
45	Isolation and analysis of the genetic diversity of repertoires of VSG expression site containing telomeres from <i>Trypanosoma brucei gambiense</i> , <i>T. b. brucei</i> and <i>T. equiperdum</i> . <i>BMC Genomics</i> , 2008, 9, 385.	2.8	39
46	Population genomics of domestic and wild yeasts. <i>Nature Precedings</i> , 2008, , .	0.1	1
47	Telomeric Expression Sites Are Highly Conserved in <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2008, 3, e3527.	2.5	254
48	Circadian Rhythm Gene Regulation in the Housefly <i>Musca domestica</i> . <i>Genetics</i> , 2007, 177, 1539-1551.	2.9	39
49	Metabolic footprinting as a tool for discriminating between brewing yeasts. <i>Yeast</i> , 2007, 24, 667-679.	1.7	103
50	Making the most of redundancy. <i>Nature</i> , 2007, 449, 673-674.	27.8	31
51	Localization of telomeres and telomere-associated proteins in telomerase-negative <i>Saccharomyces cerevisiae</i> . <i>Chromosome Research</i> , 2007, 15, 1033-50.	2.2	19
52	Sequence Diversity, Reproductive Isolation and Species Concepts in <i>Saccharomyces</i> . <i>Genetics</i> , 2006, 174, 839-850.	2.9	283
53	YEAST EVOLUTION AND COMPARATIVE GENOMICS. <i>Annual Review of Microbiology</i> , 2005, 59, 135-153.	7.3	113
54	Chromosome ends: different sequences may provide conserved functions. <i>BioEssays</i> , 2005, 27, 685-697.	2.5	58

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55	Monomorphic subtelomeric DNA in the filamentous fungus, <i>Metarhizium anisopliae</i> , contains a RecQ helicase-like gene. <i>Molecular Genetics and Genomics</i> , 2005, 274, 79-90.	2.1	19
56	Telomeres: a diversity of solutions to the problem of chromosome ends. <i>Chromosome Research</i> , 2005, 13, 425-429.	2.2	2
57	Inferences of evolutionary relationships from a population survey of LTR-retrotransposons and telomeric-associated sequences in the <i>Saccharomyces sensu stricto</i> complex. <i>Yeast</i> , 2005, 22, 177-192.	1.7	148
58	Mapping of a Major Locus that Determines Telomere Length in Humans. <i>American Journal of Human Genetics</i> , 2005, 76, 147-151.	6.2	243
59	Isolation of the repertoire of VSG expression site containing telomeres of <i>Trypanosoma brucei</i> 427 using transformation-associated recombination in yeast. <i>Genome Research</i> , 2004, 14, 2319-2329.	5.5	63
60	Analysis of a Ty1-less variant of <i>Saccharomyces paradoxus</i> : the gain and loss of Ty1 elements. <i>Yeast</i> , 2004, 21, 649-660.	1.7	29
61	Developing methods and strains for genetic studies in the <i>Saccharomyces bayanus</i> var. <i>uvarum</i> species. <i>Yeast</i> , 2004, 21, 1195-1203.	1.7	13
62	Meiotic Recombination: Too Much of a Good Thing?. <i>Current Biology</i> , 2003, 13, R953-R955.	3.9	11
63	A role for the mismatch repair system during incipient speciation in <i>Saccharomyces</i> . <i>Journal of Evolutionary Biology</i> , 2003, 16, 429-437.	1.7	96
64	Engineering evolution to study speciation in yeasts. <i>Nature</i> , 2003, 422, 68-72.	27.8	232
65	NEJ1 Prevents NHEJ-Dependent Telomere Fusions in Yeast without Telomerase. <i>Molecular Cell</i> , 2003, 11, 1373-1378.	9.7	53
66	Hybrid Speciation in Experimental Populations of Yeast. <i>Science</i> , 2002, 298, 1773-1775.	12.6	155
67	Epistasis and hybrid sterility in <i>Saccharomyces</i> . <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 1167-1171.	2.6	95
68	Are <i>Drosophila</i> telomeres an exception or the rule?. <i>Genome Biology</i> , 2002, 3, reviews0007.1.	9.6	22
69	SGS1 is required for telomere elongation in the absence of telomerase. <i>Current Biology</i> , 2001, 11, 125-129.	3.9	178
70	Chromosomal evolution in <i>Saccharomyces</i> . <i>Nature</i> , 2000, 405, 451-454.	27.8	308
71	Exploring redundancy in the yeast genome: an improved strategy for use of the cre-loxP system. <i>Gene</i> , 2000, 252, 127-135.	2.2	120
72	Minisatellite Variants Generated in Yeast Meiosis Involve DNA Removal During Gene Conversion. <i>Genetics</i> , 2000, 156, 7-20.	2.9	18

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73	Limitations of silencing at native yeast telomeres. <i>EMBO Journal</i> , 1999, 18, 2538-2550.	7.8	266
74	The topoisomerase II-associated protein, Pat1p, is required for maintenance of rDNA locus stability in <i>Saccharomyces cerevisiae</i> . <i>Molecular Genetics and Genomics</i> , 1999, 261, 831-840.	2.4	15
75	Mutation of yeast Ku genes disrupts the subnuclear organization of telomeres. <i>Current Biology</i> , 1998, 8, 653-657.	3.9	330
76	Minisatellite Origins in Yeast and Humans. <i>Genomics</i> , 1998, 48, 132-135.	2.9	38
77	The effect of sex on adaptation to high temperature in heterozygous and homozygous yeast. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1998, 265, 1017-1023.	2.6	65
78	2 Whole Chromosome Analysis. <i>Methods in Microbiology</i> , 1998, , 15-31.	0.8	15
79	Sequence comparison of human and yeast telomeres identifies structurally distinct subtelomeric domains. <i>Human Molecular Genetics</i> , 1997, 6, 1305-1313.	2.9	121
80	Chromosome ends: all the same under their caps. <i>Current Opinion in Genetics and Development</i> , 1997, 7, 822-828.	3.3	160
81	Life with 6000 Genes. <i>Science</i> , 1996, 274, 546-567.	12.6	3,548
82	<i>Pneumocystis carinii</i> telomere repeats are composed of TTAGGG and the subtelomeric sequence contains a gene encoding the major surface glycoprotein. <i>Molecular Microbiology</i> , 1996, 19, 273-281.	2.5	52
83	Pat1: a topoisomerase II-associated protein required for faithful chromosome transmission in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 1996, 24, 4791-4797.	14.5	54
84	<i>SGS1</i> , a Homologue of the Bloom's and Werner's Syndrome Genes, Is Required for Maintenance of Genome Stability in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1996, 144, 935-945.	2.9	368
85	A new genetically isolated population of the <i>Saccharomyces sensu stricto</i> complex from Brazil. <i>Antonie Van Leeuwenhoek</i> , 1995, 67, 351-355.	1.7	53
86	Sequence analysis of the right end of chromosome XV in <i>Saccharomyces cerevisiae</i> : An insight into the structural and functional significance of sub-telomeric repeat sequences. <i>Yeast</i> , 1995, 11, 371-382.	1.7	36
87	Genetic mapping of the α -galactosidase MEL gene family on right and left telomeres of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1995, 11, 481-483.	1.7	34
88	The chromosome ends of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1995, 11, 1553-1573.	1.7	233
89	The human SB1.8 gene (DXS423E) encodes a putative chromosome segregation protein conserved in lower eukaryotes and prokaryotes. <i>Human Molecular Genetics</i> , 1995, 4, 243-249.	2.9	25
90	Sgs1: A eukaryotic homolog of <i>E. coli</i> RecQ that interacts with topoisomerase II in vivo and is required for faithful chromosome segregation. <i>Cell</i> , 1995, 81, 253-260.	28.9	416

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91	Two new genetically isolated populations of the <i>Saccharomyces sensu stricto</i> complex from Japan.. <i>Journal of General and Applied Microbiology</i> , 1995, 41, 499-505.	0.7	46
92	Complete nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome VIII. <i>Science</i> , 1994, 265, 2077-2082.	12.6	303
93	III. Yeast sequencing reports. Corrected sequence for the right telomere of <i>Saccharomyces cerevisiae</i> chromosome III. <i>Yeast</i> , 1994, 10, 271-274.	1.7	16
94	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994, 369, 371-378.	27.8	382
95	Rescue of a single yeast artificial chromosome from a cotransformation event utilizing segregation at meiosis. <i>Genetic Analysis, Techniques and Applications</i> , 1993, 10, 123-127.	1.5	2
96	Genetic homology between <i>Saccharomyces cerevisiae</i> and its sibling species <i>S. paradoxus</i> and <i>S. bayanus</i> : Electrophoretic karyotypes. <i>Yeast</i> , 1992, 8, 599-612.	1.7	179
97	Evolutionarily recent transfer of a group I mitochondrial intron to telomere regions in <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 1991, 20, 411-415.	1.7	51
98	An Exact Test for Hardy-Weinberg and Multiple Alleles. <i>Biometrics</i> , 1987, 43, 805.	1.4	249
99	Three-allele synergistic mixed model for insulin-dependent diabetes mellitus. <i>Diabetes</i> , 1986, 35, 958-963.	0.6	10
100	Sickle Cell Anemia: "Interesting Pathology" and "Rarely Told Stories". <i>American Biology Teacher</i> , 1985, 47, 183-187.	0.2	1
101	The affected sib method. IV. Sib trios. <i>Annals of Human Genetics</i> , 1985, 49, 303-314.	0.8	51
102	Meiotic Gene Conversion Mediates Gene Amplification in Yeast. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 1984, 49, 55-65.	1.1	31
103	The affected sib method. II. The intermediate model. <i>Annals of Human Genetics</i> , 1983, 47, 225-243.	0.8	31