

# Kenneth H Wolfe

## List of Publications by Year in descending order

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84  
papers

9,769  
citations

61984

43  
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62596

80  
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94  
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94  
docs citations

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times ranked

9065  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence data of the antagonistic soil-borne yeast <i>Cyberlindnera sargentensis</i> (SHA 17.2). Data in Brief, 2022, 40, 107799.	1.0	2
2	Mating-Type Switching in Budding Yeasts, from Flip/Flop Inversion to Cassette Mechanisms. Microbiology and Molecular Biology Reviews, 2022, 86, e0000721.	6.6	4
3	Giant <i>GAL</i> gene clusters for the melibiose-galactose pathway in <i>Torulaspora</i> . Yeast, 2021, 38, 117-126.	1.7	10
4	Into the wild—Exploring the life cycles of yeasts. Yeast, 2021, 38, 3-4.	1.7	0
5	Genomic diversity, chromosomal rearrangements, and interspecies hybridization in the <i>Ogataea polymorpha</i> species complex. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	2
6	Draft Genome Sequence of a Diploid and Hybrid <i>Candida</i> Strain, <i>Candida sanyaensis</i> UCD423, Isolated from Compost in Ireland. Microbiology Resource Announcements, 2021, 10, e0076121.	0.6	2
7	Draft Genome Sequence of the Yeast <i>Ogataea degrootiae</i> Strain UCD465, Isolated from Soil in Ireland. Microbiology Resource Announcements, 2021, 10, e0073621.	0.6	2
8	Carbon source requirements for mating and mating-type switching in the methylotrophic yeasts <i>Ogataea</i> ( <i>Hansenula</i> ) <i>polymorpha</i> and <i>Komagataella phaffii</i> ( <i>Pichia pastoris</i> ). Yeast, 2020, 37, 237-245.	1.7	5
9	Polymorphic centromere locations in the pathogenic yeast <i>Candida parapsilosis</i> . Genome Research, 2020, 30, 684-696.	5.5	22
10	The yeast mating-type switching endonuclease HO is a domesticated member of an unorthodox homing genetic element family. ELife, 2020, 9, .	6.0	15
11	The Methylotroph Gene Order Browser (MGOB) reveals conserved synteny and ancestral centromere locations in the yeast family Pichiaceae. FEMS Yeast Research, 2019, 19, .	2.3	8
12	Multiple Reinventions of Mating-type Switching during Budding Yeast Evolution. Current Biology, 2019, 29, 2555-2562.e8.	3.9	33
13	EvoChromo: towards a synthesis of chromatin biology and evolution. Development (Cambridge), 2019, 146, .	2.5	16
14	Coverage-Versus-Length Plots, a Simple Quality Control Step for <i>de Novo</i> Yeast Genome Sequence Assemblies. G3: Genes, Genomes, Genetics, 2019, 9, 879-887.	1.8	26
15	The CYPome of the model xenobiotic-biotransforming fungus <i>Cunninghamella elegans</i> . Scientific Reports, 2019, 9, 9240.	3.3	28
16	Draft Genome Sequence of the Birch Tree Fungal Pathogen <i>Taphrina betulina</i> UCD315. Microbiology Resource Announcements, 2019, 8, .	0.6	4
17	Origin of Lactose Fermentation in <i>Kluyveromyces lactis</i> by Interspecies Transfer of a Neo-functionalized Gene Cluster during Domestication. Current Biology, 2019, 29, 4284-4290.e2.	3.9	41
18	Genomic diversity and meiotic recombination among isolates of the biotech yeast <i>Komagataella phaffii</i> ( <i>Pichia pastoris</i> ). Microbial Cell Factories, 2019, 18, 211.	4.0	16

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19	The reported point centromeres of <i>Scheffersomyces stipitis</i> are retrotransposon long terminal repeats. <i>Yeast</i> , 2019, 36, 275-283.	1.7	7
20	Draft Genome Sequences of Two Isolates of the Yeast <i>Kazachstania servazzii</i> Recovered from Soil in Ireland. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
21	Draft Genome Sequence of a Red Basidiomycete Yeast, <i>Symmetrospora coprosmae</i> Strain UCD350, Isolated from Soil in Ireland. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
22	Transcriptional Response to Lactic Acid Stress in the Hybrid Yeast <i>Zygosaccharomyces parabailii</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	18
23	Draft Genome Sequences of Two Natural Isolates of the Yeast <i>Barnettozyma californica</i> from Ireland, UCD09 and UCD89. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
24	Draft Genome Sequence of the Yeast <i>Nadsonia starkeyi-henricii</i> UCD142, Isolated from Forest Soil in Ireland. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
25	Genome Sequence of <i>Torulaspota microellipsoides</i> CLIB 830 <sup>T</sup> . <i>Genome Announcements</i> , 2018, 6, .	0.8	5
26	Evolutionary instability of CUG-Leu in the genetic code of budding yeasts. <i>Nature Communications</i> , 2018, 9, 1887.	12.8	70
27	<i>Zygosaccharomyces pseudobailii</i> , another yeast interspecies hybrid that regained fertility by damaging one of its MAT loci. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	39
28	Ploidy Variation in <i>Kluyveromyces marxianus</i> Separates Dairy and Non-dairy Isolates. <i>Frontiers in Genetics</i> , 2018, 9, 94.	2.3	71
29	Draft Genome Sequence of a Highly Heterozygous Yeast Strain from the <i>Metschnikowia pulcherrima</i> Subclade, UCD127. <i>Genome Announcements</i> , 2018, 6, .	0.8	14
30	TPP riboswitch-dependent regulation of an ancient thiamin transporter in <i>Candida</i> . <i>PLoS Genetics</i> , 2018, 14, e1007429.	3.5	29
31	Population genomics shows no distinction between pathogenic <i>Candida krusei</i> and environmental <i>Pichia kudriavzevii</i> : One species, four names. <i>PLoS Pathogens</i> , 2018, 14, e1007138.	4.7	144
32	An Evolutionary Perspective on Yeast Mating-Type Switching. <i>Genetics</i> , 2017, 206, 9-32.	2.9	72
33	Evolution of Mating in the Saccharomycotina. <i>Annual Review of Microbiology</i> , 2017, 71, 197-214.	7.3	22
34	Flip/flop mating-type switching in the methylotrophic yeast <i>Ogataea polymorpha</i> is regulated by an Efg1-Rme1-Ste12 pathway. <i>PLoS Genetics</i> , 2017, 13, e1007092.	3.5	13
35	Evolutionary restoration of fertility in an interspecies hybrid yeast, by whole-genome duplication after a failed mating-type switch. <i>PLoS Biology</i> , 2017, 15, e2002128.	5.6	84
36	Multiple Origins of the Pathogenic Yeast <i>Candida orthopsilosis</i> by Separate Hybridizations between Two Parental Species. <i>PLoS Genetics</i> , 2016, 12, e1006404.	3.5	125

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37	Comparative genomics of biotechnologically important yeasts. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9882-9887.	7.1	302
38	Centromeres of the Yeast <i>Komagataella phaffii</i> ( <i>Pichia pastoris</i> ) Have a Simple Inverted-Repeat Structure. Genome Biology and Evolution, 2016, 8, 2482-2492.	2.5	36
39	Origin of the Yeast Whole-Genome Duplication. PLoS Biology, 2015, 13, e1002221.	5.6	123
40	Discovery of an Unconventional Centromere in Budding Yeast Redefines Evolution of Point Centromeres. Current Biology, 2015, 25, 2026-2033.	3.9	45
41	Clade- and species-specific features of genome evolution in the Saccharomycetaceae. FEMS Yeast Research, 2015, 15, fov035.	2.3	58
42	Loss of lager specific genes and subtelomeric regions define two different <i>Saccharomyces cerevisiae</i> lineages for <i>Saccharomyces pastorianus</i> Group I and II strains. FEMS Yeast Research, 2015, 15, .	2.3	41
43	The Genomic Aftermath of Hybridization in the Opportunistic Pathogen <i>Candida metapsilosis</i> . PLoS Genetics, 2015, 11, e1005626.	3.5	139
44	Zinc Finger Transcription Factors Displaced SREBP Proteins as the Major Sterol Regulators during <i>Saccharomycotina</i> Evolution. PLoS Genetics, 2014, 10, e1004076.	3.5	63
45	Mating-type switching by chromosomal inversion in methylotrophic yeasts suggests an origin for the three-locus <i>Saccharomyces cerevisiae</i> system. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4851-8.	7.1	76
46	Comparative Genome Analysis and Gene Finding in <i>Candida</i> Species Using CGOB. Molecular Biology and Evolution, 2013, 30, 1281-1291.	8.9	115
47	A pipeline for automated annotation of yeast genome sequences by a conserved-synteny approach. BMC Bioinformatics, 2012, 13, 237.	2.6	86
48	Sequence and Analysis of the Genome of the Pathogenic Yeast <i>Candida orthopsilosis</i> . PLoS ONE, 2012, 7, e35750.	2.5	69
49	Genome Sequences of <i>Saccharomycotina</i> . , 2011, , 145-157.		5
50	Systematic discovery of unannotated genes in 11 yeast species using a database of orthologous genomic segments. BMC Genomics, 2011, 12, 377.	2.8	17
51	Evolutionary erosion of yeast sex chromosomes by mating-type switching accidents. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20024-20029.	7.1	137
52	Mechanisms of Chromosome Number Evolution in Yeast. PLoS Genetics, 2011, 7, e1002190.	3.5	114
53	Chromosomal G + C Content Evolution in Yeasts: Systematic Interspecies Differences, and GC-Poor Troughs at Centromeres. Genome Biology and Evolution, 2010, 2, 572-583.	2.5	62
54	Additions, Losses, and Rearrangements on the Evolutionary Route from a Reconstructed Ancestor to the Modern <i>Saccharomyces cerevisiae</i> Genome. PLoS Genetics, 2009, 5, e1000485.	3.5	213

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55	Elaboration, Diversification and Regulation of the Sir1 Family of Silencing Proteins in <i>Saccharomyces</i> . <i>Genetics</i> , 2009, 181, 1477-1491.	2.9	20
56	Evolutionary Capture of Viral and Plasmid DNA by Yeast Nuclear Chromosomes. <i>Eukaryotic Cell</i> , 2009, 8, 1521-1531.	3.4	64
57	RNAi in Budding Yeast. <i>Science</i> , 2009, 326, 544-550.	12.6	480
58	Recent allopolyploid origin of <i>Zygosaccharomyces rouxii</i> strain ATCC 42981. <i>Yeast</i> , 2008, 25, 449-456.	1.7	89
59	Independent sorting-out of thousands of duplicated gene pairs in two yeast species descended from a whole-genome duplication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8397-8402.	7.1	210
60	Consequences of genome duplication. <i>Current Opinion in Genetics and Development</i> , 2007, 17, 505-512.	3.3	384
61	Yeast genome evolution—the origin of the species. <i>Yeast</i> , 2007, 24, 929-942.	1.7	114
62	Multiple rounds of speciation associated with reciprocal gene loss in polyploid yeasts. <i>Nature</i> , 2006, 440, 341-345.	27.8	411
63	Visualizing syntenic relationships among the hemiascomycetes with the Yeast Gene Order Browser. <i>Nucleic Acids Research</i> , 2006, 34, D452-D455.	14.5	60
64	Complete DNA sequences of the mitochondrial genomes of the pathogenic yeasts <i>Candida orthopsilosis</i> and <i>Candida metapsilosis</i> : insight into the evolution of linear DNA genomes from mitochondrial telomere mutants. <i>Nucleic Acids Research</i> , 2006, 34, 2472-2481.	14.5	62
65	Comparative genomics and genome evolution in yeasts. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006, 361, 403-412.	4.0	60
66	Birth of a metabolic gene cluster in yeast by adaptive gene relocation. <i>Nature Genetics</i> , 2005, 37, 777-782.	21.4	202
67	The Yeast Gene Order Browser: Combining curated homology and syntenic context reveals gene fate in polyploid species. <i>Genome Research</i> , 2005, 15, 1456-1461.	5.5	633
68	A Genome Sequence Survey Shows that the Pathogenic Yeast <i>Candida parapsilosis</i> Has a Defective MTL a 1 Allele at Its Mating Type Locus. <i>Eukaryotic Cell</i> , 2005, 4, 1009-1017.	3.4	64
69	Function and Evolution of HO and VDE Endonucleases in Fungi. , 2005, , 161-175.		12
70	Evolution of the MAT locus and its Ho endonuclease in yeast species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 1632-1637.	7.1	217
71	The 2R hypothesis and the human genome sequence. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 95-110.	1.2	59
72	Molecular evolution meets the genomics revolution. <i>Nature Genetics</i> , 2003, 33, 255-265.	21.4	120

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73	Yesterday's polyploids and the mystery of diploidization. <i>Nature Reviews Genetics</i> , 2001, 2, 333-341.	16.3	658
74	Many Parallel Losses of <i>infA</i> from Chloroplast DNA during Angiosperm Evolution with Multiple Independent Transfers to the Nucleus. <i>Plant Cell</i> , 2001, 13, 645-658.	6.6	415
75	Relationship of codon bias to mRNA concentration and protein length in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2000, 16, 1131-1145.	1.7	246
76	Evidence for a High Frequency of Simultaneous Double-Nucleotide Substitutions. <i>Science</i> , 2000, 287, 1283-1286.	12.6	111
77	Proteome composition and codon usage in spirochaetes: species-specific and DNA strand-specific mutational biases. <i>Nucleic Acids Research</i> , 1999, 27, 1642-1649.	14.5	130
78	Gene Duplication and Gene Conversion in the <i>Caenorhabditis elegans</i> Genome. <i>Journal of Molecular Evolution</i> , 1999, 48, 555-564.	1.8	127
79	Evolution of gene order and chromosome number in <i>Saccharomyces</i> , <i>Kluyveromyces</i> and related fungi. <i>Yeast</i> , 1998, 14, 443-457.		101
80	Base Composition Skews, Replication Orientation, and Gene Orientation in 12 Prokaryote Genomes. <i>Journal of Molecular Evolution</i> , 1998, 47, 691-696.	1.8	262
81	A Subset of Conserved tRNA Genes in Plastid DNA of Nongreen Plants. <i>Genetics</i> , 1998, 150, 425-433.	2.9	45
82	Molecular evidence for an ancient duplication of the entire yeast genome. <i>Nature</i> , 1997, 387, 708-713.	27.8	1,702
83	Sequence of 29 kb around the <i>PDR10</i> locus on the right arm of <i>Saccharomyces cerevisiae</i> chromosome XV: Similarity to part of chromosome I. <i>Yeast</i> , 1996, 12, 999-1004.	1.7	10
84	II. Yeast sequencing reports. Sequence around the centromere of <i>Saccharomyces cerevisiae</i> chromosome II: Similarity of <i>CEN2</i> to <i>CEN4</i> . <i>Yeast</i> , 1994, 10, S41-S46.	1.7	29