Resource Summary Report

Generated by dkNET on Aug 23, 2026

PD1074

RRID:WB-STRAIN:WBStrain00030553
Type: Organism

Proper Citation

RRID:WB-STRAIN:WBStrain00030553

Organism Information

URL: http://www.wormbase.org/db/get?name=WBStrain00030553

Proper Citation: RRID:WB-STRAIN:WBStrain00030553

Description: Caenorhabditis elegans with name EMPTY from WB.

Species: Caenorhabditis elegans

Synonyms: EMPTY

Notes: A defined and recently cloned population of animals derived from the original Bristol variant of C. elegans originally obtained by Brenner from E. Dougherty with no known history of mutagenesis. Brenners original population, called N2, was used as the basis for the vast majority of laboratory strains in use currently. No early frozen stock of the unmutagenized N2 population currently exists, but later stocks were available from several laboratories. PD1074 is a clonal population founded by picking a single worm of one such stock, VC3510. VC3510 in turn derives from a subpopulation of N2 described in the literature as VC2010. PD1074 is intended to be used as a wild type reference strain with the closely matched genome assembly of Yoshimura et al (ref) available on Wormbase as VC2010-1.0. (ENA study accession PRJEB28388; assembly accession GCA_900538205). We note that PD1074 is expected to be largely similar to most lab N2 strains, but that as a clonal isolate derived from N2, there will be some loci that will vary compared to any other particular N2 isolate. One such example is a partial deletion of the alh-2 locus in PD1074. Additional loci that were found to vary between the prior N2 reference genome (WormBase release WS264) and the VC2010-1.0 assembly are detailed in supplemental table 8 in Yoshimura et al (ref).|"A defined and recently cloned population of animals derived from the original Bristol variant of C. elegans originally obtained by Brenner from E. Dougherty with no known history of mutagenesis. Brenners original population, called N2, was used as the basis for the vast majority of laboratory strains in use currently. No early frozen stock of the unmutagenized N2 population currently exists, but later stocks were available from several laboratories. PD1074 is a clonal population founded by picking a single worm of one such stock, VC3510. VC3510 in

turn derives from a subpopulation of N2 described in the literature as VC2010. PD1074 is intended to be used as a wild type reference strain with the closely matched genome assembly of Yoshimura, et al. (Genome Res. 2019 Jun;29(6):1009-1022) available on Wormbase as VC2010-1.0. (ENA study accession PRJEB28388; assembly accession GCA_900538205). We note that PD1074 is expected to be largely similar to most lab N2 strains, but that as a clonal isolate derived from N2, there will be some loci that will vary compared to any other particular N2 isolate. One such example is a partial deletion of the alh-2 locus in PD1074. Additional loci that were found to vary between the prior N2 reference genome (WormBase release WS264) and the VC2010-1.0 assembly are detailed in supplemental table 8 in Yoshimura, et al, (2019)."|"Added Wild_Isolate tag as genotype info suggesting that they were sampled from the wild."|"Made_by: Karen Artiles & Mark Edgley"|"no longer available from the CGC."|"Supplementary_genotype"|"WBStrain provided so WBPaper00061243 paper added based on AFP_Strain data."|"WBStrain provided so WBPaper00061573 paper added based on AFP_Strain data."

Catalog Number: WB-STRAIN:WBStrain00030553

Database: WormBase (WB)

Database Abbreviation: WB

Availability: unknown

Source References: PMID:33313486, PMID:33458604, PMID:33693840, PMID:34156835, PMID:37008729, PMID:36595469, PMID:37170380, PMID:37590248, PMID:37777524, PMID:38596360, PMID:38488606, PMID:38771761, PMID:39712935

Alternate IDs: WB-STRAIN:PD1074

Organism Name: PD1074

Record Creation Time: 20230227T013609+0000

Record Last Update: 20260815T163121+0000

Ratings and Alerts

No rating or validation information has been found for PD1074.

No alerts have been found for PD1074.

Data and Source Information

Source: Integrated Animals

Source Database: WormBase (WB)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Link AC, et al. (2025) A novel, fig-associated microbe promotes reproductive success via variable life history mechanisms in C. elegans and C. inopinata. bioRxiv : the preprint server for biology.

Ichikawa K, et al. (2025) CGC1, a new reference genome for Caenorhabditis elegans. Genome research, 35(8), 1902.

Ichikawa K, et al. (2024) CGC1, a new reference genome for Caenorhabditis elegans. bioRxiv : the preprint server for biology.

Asif MZ, et al. (2024) Role of UDP-Glycosyltransferase (ugt) Genes in Detoxification and Glycosylation of 1-Hydroxyphenazine (1-HP) in Caenorhabditis elegans. Chemical research in toxicology, 37(4), 590.

Lopez JS, et al. (2024) Pavement ant extract is a chemotaxis repellent for C. elegans. microPublication biology, 2024.

Shaver AO, et al. (2023) Variation in anthelmintic responses are driven by genetic differences among diverse C. elegans wild strains. PLoS pathogens, 19(4), e1011285.

Scheer E, et al. (2023) Sensory neurons couple arousal and foraging decisions in Caenorhabditis elegans. eLife, 12.

Chrystal PW, et al. (2022) The inner junction protein CFAP20 functions in motile and non-motile cilia and is critical for vision. Nature communications, 13(1), 6595.

Lee BY, et al. (2022) Intraspecific de novo gene birth revealed??by presence-absence variant genes in Caenorhabditis elegans. NAR genomics and bioinformatics, 4(2), lqac031.

Hammerschmith EW, et al. (2022) Opposing directions of stage-specific body shape change in a close relative of C. elegans. BMC zoology, 7(1), 38.

Kim E, et al. (2021) Long-read sequencing and de novo genome assemblies reveal complex chromosome end structures caused by telomere dysfunction at the single nucleotide level. Nucleic acids research, 49(6), 3338.