

The genes present in **UFmut\_mis** order by gene frequency

### ***F21C10.1*** (28.956522)

[https://wormbase.org/species/c\\_elegans/gene/WBGene00017652#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00017652#0-9f-10)

Predicted to be located in membrane. Predicted to be integral component of membrane.

### ***act-1*** (ACTin) (19.304348)

Sequence: T04C12.6

[https://wormbase.org/species/c\\_elegans/gene/WBGene00000063#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00000063#0-9f-10)

Predicted to be a structural constituent of cytoskeleton. Involved in cortical actin cytoskeleton organization; embryo development; and mitotic cytokinesis. Located in striated muscle thin filament. Expressed in body wall musculature and gonad. Human ortholog(s) of this gene implicated in Baraitser-Winter syndrome; autosomal dominant nonsyndromic deafness 20; and hand, foot and mouth disease. Is an ortholog of human ACTB (actin beta).

### ***F10E9.12*** [19.304348]

Sequence:

F10E9.12

[https://wormbase.org/species/c\\_elegans/gene/WBGene00017361#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00017361#0-9f-10)

Enriched in excretory cell; head mesodermal cell; intestine; and neurons based on tiling array; RNA-seq; and microarray studies. Is affected by several genes including [daf-16](#); [daf-2](#); and [skn-1](#) based on microarray and RNA-seq studies. Is affected by twenty-six chemicals including methylmercuric chloride; rotenone; and Tunicamycin based on microarray and RNA-seq studies.

### ***dhhc-7*** (DHHC-types zinc finger protein) [19.304348]

[https://wormbase.org/species/c\\_elegans/gene/WBGene00007637#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00007637#0-9f-10)

Sequence:

C17D12.1

Predicted to enable protein-cysteine S-palmitoyltransferase activity. Predicted to be involved in peptidyl-L-cysteine S-palmitoylation and protein targeting to membrane. Predicted to be located in Golgi apparatus and endoplasmic reticulum

### ***D1005.5*** [19.304348]

[https://wormbase.org/species/c\\_elegans/gene/WBGene00016999#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00016999#0-9f-10)

Is affected by several genes including [nhr-49](#); [lin-15B](#); and [hpl-2](#) based on microarray and RNA-seq studies. Is affected by nine chemicals including hydrogen sulfide; methylmercuric chloride; and Mercuric Chloride based on microarray and RNA-seq studies.

### ***sip-1*** (Stress Induced Protein) [19.304348]

Sequence:

F43D9.4

[https://wormbase.org/species/c\\_elegans/gene/WBGene00004798#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00004798#0-9f-10)

Predicted to enable protein folding chaperone. Involved in several processes, including determination of adult lifespan; embryo development; and response to heat. Located in cytosol. Expressed in body wall musculature and gonad.

### ***cllec-239*** (C-type LECTin) [19.304348]

Sequence:

Y102A5C.16

[https://wormbase.org/species/c\\_elegans/gene/WBGene00013621#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00013621#0-9f-10)

Predicted to enable carbohydrate binding activity.

### ***Y57G11B.6*** [14.478261]

[https://wormbase.org/species/c\\_elegans/gene/WBGene00013298#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00013298#0-9f-10)

Enriched in BAG; dopaminergic neurons; neurons; and sensory neurons based on tiling array and RNA-seq studies. Is affected by several genes including [prg-1](#); [mex-3](#); and [mex-1](#) based on RNA-seq and microarray studies. Is affected by Rifampin; allantoin; and Sirolimus based on RNA-seq studies.

### ***M03B6.4*** [14.478261]

[https://wormbase.org/species/c\\_elegans/gene/WBGene00010836#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00010836#0-9f-10)

Predicted to be located in membrane. Predicted to be integral component of membrane.

### ***R11A5.3*** [14.478261]

[https://wormbase.org/species/c\\_elegans/gene/WBGene00011231#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00011231#0-9f-10)

Expressed in Z1 and Z4.

## ***F48F7.5* [14.478261]**

[https://wormbase.org/species/c\\_elegans/gene/WBGene00009850#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00009850#0-9f-10)

Enriched in germline precursor cell; head mesodermal cell; hypodermis; muscle cell; and neurons based on tiling array; RNA-seq; and microarray studies. Is affected by several genes including [eat-2](#); [clk-1](#); and [sek-1](#) based on microarray; RNA-seq; tiling array; and proteomic studies. Is affected by nine chemicals including Zidovudine; metformin; and Sirolimus based on RNA-seq and microarray studies.

## ***ech-5* (Enoyl-CoA Hydratase) [14.478261]**

Sequence:

F56B3.5

[https://wormbase.org/species/c\\_elegans/gene/WBGene00001154#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00001154#0-9f-10)

Predicted to enable enoyl-CoA hydratase activity. Predicted to be involved in fatty acid beta-oxidation. Predicted to be located in mitochondrion. Human ortholog(s) of this gene implicated in 3-methylglutaconic aciduria type 1 and renal tubular transport disease. Is an ortholog of human AUH (AU RNA binding methylglutaconyl-CoA hydratase) and ECHDC2 (enoyl-CoA hydratase domain containing 2).

## ***dod-18* (Downstream Of DAF-16 (regulated by DAF-16)) [14.478261]**

Sequence:

C54G4.6

[https://wormbase.org/species/c\\_elegans/gene/WBGene00008316#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00008316#0-9f-10)

Predicted to enable nucleoside-triphosphate diphosphatase activity. Is an ortholog of human ASMTL (acetylserotonin O-methyltransferase like).

## ***F54D12.11* pseudogene [14.478261]**

Sequence:

F54D12.11

[https://wormbase.org/species/c\\_elegans/gene/WBGene00044425#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00044425#0-9f-10)

Is affected by [rsr-2](#) based on tiling array studies.

### ***ztf-1*** (Zinc finger putative Transcription Factor family [12.409938])

Sequence:

F54F2.5

[https://wormbase.org/species/c\\_elegans/gene/WBGene00018833#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00018833#0-9f-10)

Predicted to enable DNA-binding transcription factor activity, RNA polymerase II-specific and sequence-specific DNA binding activity. Predicted to be involved in regulation of transcription by RNA polymerase II. Predicted to be located in nucleus. Expressed in intestine and pharyngeal neurons.

### ***flp-28*** (FMRF-Like Peptide) [11.582609]

Sequence:

W07E11.4

[https://wormbase.org/species/c\\_elegans/gene/WBGene00044686#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00044686#0-9f-10)

Enriched in neurons based on RNA-seq; single-cell RNA-seq; and microarray studies. Is affected by several genes including [daf-2](#); [glp-1](#); and [skn-1](#) based on tiling array; microarray; and RNA-seq studies. Is affected by nine chemicals including rotenone; Psoralens; and allantoin based on RNA-seq and microarray studies.

### ***bir-1*** (BIR (baculovirus inhibitory repeat) family) [11.582609]

Sequence:

T27F2.3

[https://wormbase.org/species/c\\_elegans/gene/WBGene00000249#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00000249#0-9f-10)

Predicted to enable metal ion binding activity. Involved in several processes, including chromosome organization; inductive cell migration; and oviposition. Located in condensed chromosome and spindle midzone. Expressed in egg-laying apparatus; hypodermis; pharynx; rectal muscle; and somatic nervous system. Human ortholog(s) of this gene implicated in several diseases, including ductal carcinoma in situ; endometrial hyperplasia; and urinary system cancer (multiple). Is an ortholog of human BIRC5 (baculoviral IAP repeat containing 5).

### ***icap-1*** (Integrin Cytoplasmic domain-Associated Protein homolog) [11.582609]

Sequence:

Y45F10D.10

[https://wormbase.org/species/c\\_elegans/gene/WBGene00012889#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00012889#0-9f-10)

Predicted to be involved in integrin-mediated signaling pathway. Is an ortholog of human ITGB1BP1 (integrin subunit beta 1 binding protein 1).

### **syx-5 (SYntaXin)**

[https://wormbase.org/species/c\\_elegans/gene/WBGene00006373#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00006373#0-9f-10)

Sequence:

F55A11.2

Predicted to enable SNAP receptor activity and SNARE binding activity. Predicted to be involved in intracellular protein transport and vesicle-mediated transport. Predicted to be located in Golgi membrane. Predicted to be integral component of membrane. Predicted to be part of SNARE complex. Is an ortholog of human STX5 (syntaxin 5).

### **K01A2.5 [11.582609]**

[https://wormbase.org/species/c\\_elegans/gene/WBGene00019280#0-9f-10](https://wormbase.org/species/c_elegans/gene/WBGene00019280#0-9f-10)

Predicted to enable hydrolase activity. Expressed in hypodermis. Is an ortholog of human BPHL (biphenyl hydrolase like).