

## Supplementary Figure legends

### S1: NAC is an active component of the cellular proteostasis network

- A) The images depict the aggregation propensity of Q35-YFP in animals fed *E. coli* expressing  $\alpha+\beta$ NAC dsRNA or the empty RNAi vector L4440 on day 4, 6, 7 and 10. Shown here is the head region of the animals and aggregates are highlighted with white triangles. These images are a magnification of a subset of images also shown in (B).
- B) Representative images of the aggregation propensity of Q35-YFP in the head region of nematodes upon knockdown of  $\alpha$ NAC,  $\beta$ NAC,  $\alpha+\beta$ NAC and *hsp-1* as well as the control on day 4, 6, 7 and 10 of life.
- C) Whole animal images of (B).
- D) Quantification of the Q35-YFP aggregation propensity in the whole animal of (C). Error bars represent mean  $\pm$  SD of 50 animals.
- E) Representative images of the aggregation propensity of Q35-YFP in the head region of nematodes upon knockdown of the cytosolic *hsp70* genes: *hsp-1*, *F44E5.4*, *F11F1.1*, *C12C8.1* and *stc-1* as well as the control on day 4, 6, 7 and 10 of life.
- F) Whole animal images of (E).
- G) Quantification of the Q35-YFP aggregation propensity in the whole animal of (F). Error bars represent mean  $\pm$  SD of 50 animals.
- H) Representative images of the aggregation propensity of YFP (Q0) in animals fed *E. coli* expressing  $\alpha+\beta$ NAC dsRNA and as control, animals fed *E. coli* expressing the empty RNAi vector on days 4, 6, 7 and 10.

Magnifications of the head region are shown in the upper row and the respective images of the whole animal are shown below.

#### S2: Knockdown of NAC reduces the number of offspring

RNAi mediated knockdown of  $\beta$ NAC at the L1 stage reduces the number of laid eggs by 90% compared to the empty vector (L4440) control. RNAi of  $\alpha$ NAC had only a subtle effect and double RNAi resulted in an intermediate phenotype. Error bars represent mean  $\pm$  SD of ten biological replica of one adult animal per RNAi condition.

#### S3: The protein levels of NAC do not change in the course of aging

- A) Protein samples were harvested at the indicated time points and analyzed by SDS-PAGE and subsequent western blot using NAC antibodies. Antibodies against  $\alpha$ -tubulin were used as loading control.
- B) RNAi-mediated knockdown of  $\alpha+\beta$ NAC results in a reduction of about 80% of NAC protein levels (left side) and almost no signal was detected in the immunostaining analysis using the same experimental conditions as in Fig. 2C (right side). Animals were fed for three days with *E. coli* expressing  $\alpha+\beta$ NAC dsRNA prior to western blot analysis and immunostaining.

#### S4: NAC is present in all tissues and localizes to the nucleus and cytosol

- A) Immunohistochemistry of NAC in two different tissues of *C. elegans*. The upper panel shows the germ line and the lower panel represents cells of

the intestinal tissue. The signals for NAC are shown in red on the left. The co-stain of DAPI (blue, middle) and the merge of both channels (on the right) demonstrate a nuclear and cytosolic localization of NAC in both tissues.

- B) The biochemical fractionation of extracts of *C. elegans* confirms the cytosolic and nuclear localization of  $\alpha$  and  $\beta$ NAC. Histone H3 and  $\alpha$ -tubulin are used as organelle controls for the nucleus and cytosol, respectively.
- C) NAC does not localize to mitochondria. The image shows an overlay of Mitotracker (shown in green) and an immunostaining using NAC antibodies (detected using Alexa Fluor 546 as secondary antibody and is shown in red).

#### S5: Polysome association of $\alpha$ and $\beta$ NAC

- (A) Depicted are a polysome profile of day 2 old nematodes and the corresponding western blot of all fractions of the polysome profile. The antibody signals of  $\alpha$  and  $\beta$ NAC are indicated on the right. The assignment of the lanes to their ribosomal fraction (non-bound, 40S + 60S, 80S and polysomes) is indicated on top.
- (B) The interaction of NAC with the ribosome is sensitive to high salt. Total protein was isolated under low salt (75 mM KoAc) and high salt conditions (1 M KoAc) and separated into non-ribosomal fraction and ribosomal fraction. The fractions were then analyzed by SDS-PAGE and subsequent western blot using NAC, RPL-4, RPL-17 and RPL-25 antibodies.

#### S 6: Domain architecture of $\alpha$ and $\beta$ NAC in *C. elegans*

$\beta$ -NAC is encoded by the gene *icd-1* in *C. elegans*. It contains a conserved RRK-motif (pink) within its N-terminal region that is assumed to be involved in ribosome binding as well as a central NAC domain (green). Very recently, the gene encoding *C. elegans*  $\alpha$ -NAC has been named *icd-2*.  $\alpha$ NAC is characterized by a NAC domain (green) and a C-terminal UBA (ubiquitin associated) domain (purple). The two NAC subunits dimerize via their NAC domains to form a stable heterodimeric complex. The UBA domain in  $\alpha$ NAC is of unknown function.

#### S 7: Time series of polysomes sedimentation profiles

The polysome profiles of synchronized *C. elegans* populations from day 2 to day 14 are shown on the left and a representative image of *C. elegans* for each day is shown on the right.

#### S8: Knockdown of NAC does not lead to an upregulation of cytosolic heat shock genes

C12C8.1::GFP and Hsp-16.2::GFP expressing animals were placed on  $\beta$ NAC RNAi or control plates as L1s and analyzed on day 4 of life either with (1 hr 35°C + 4 h recovery at 20°C) or without heat shock. The exposure time for the imaging was kept constant at 400 ms.

#### S 9: Phosphorylation levels of eIF2 $\alpha$ are not affected by aging

The phosphorylation level eIF2 $\alpha$  was analyzed in extracts from day 4 to day 13 old nematodes at the indicated time points. The western blot shows the signals

for eIF2 $\alpha$  and eIF2 $\alpha$ -P in the upper and middle lane, respectively.  $\alpha$ -tubulin served as loading control for all samples (lower lane). As a positive control for the eIF2 $\alpha$  phosphorylation, a non-synchronized culture of nematodes was treated with tunicamycin (Tm; 10  $\mu$ g/ml for 24h).

S10: Gene ontology analysis of aggregated proteins during aging, upon heat shock or polyQ expression and upon knockdown of  $\beta$ NAC

Proteins identified by LC-MS/MS of the aggregated protein fraction in either 16 old nematodes (aging, black), day 4 old nematodes subjected to heat-shock for 1 h at 35°C (heat-shock, red), animals expressing Q35-YFP (Q35, blue) and day 4 old animals treated with RNAi as L1 against  $\beta$ NAC ( $\beta$ NAC RNAi, green) were analyzed using DAVID software.

Table S1: List of the identified insoluble proteins of day 16 old wt animals

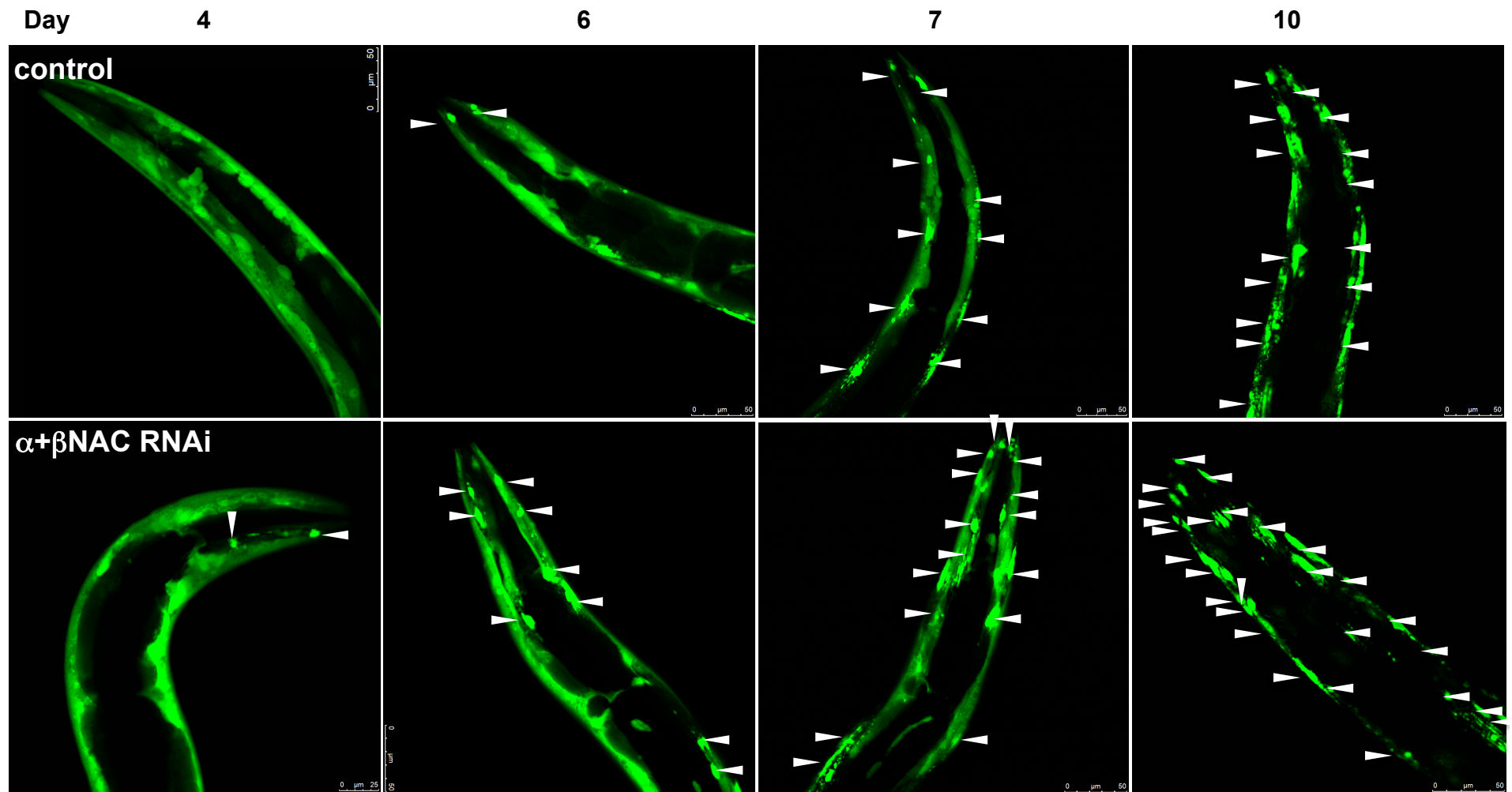
241 proteins could be identified, of which 178 (74%) are identical with previously identified aggregation-prone proteins (David et al., 2010). The identical proteins from both analyses are indicated.

Table S2: Aggregated proteins upon heat shock for 1 h at 35°C

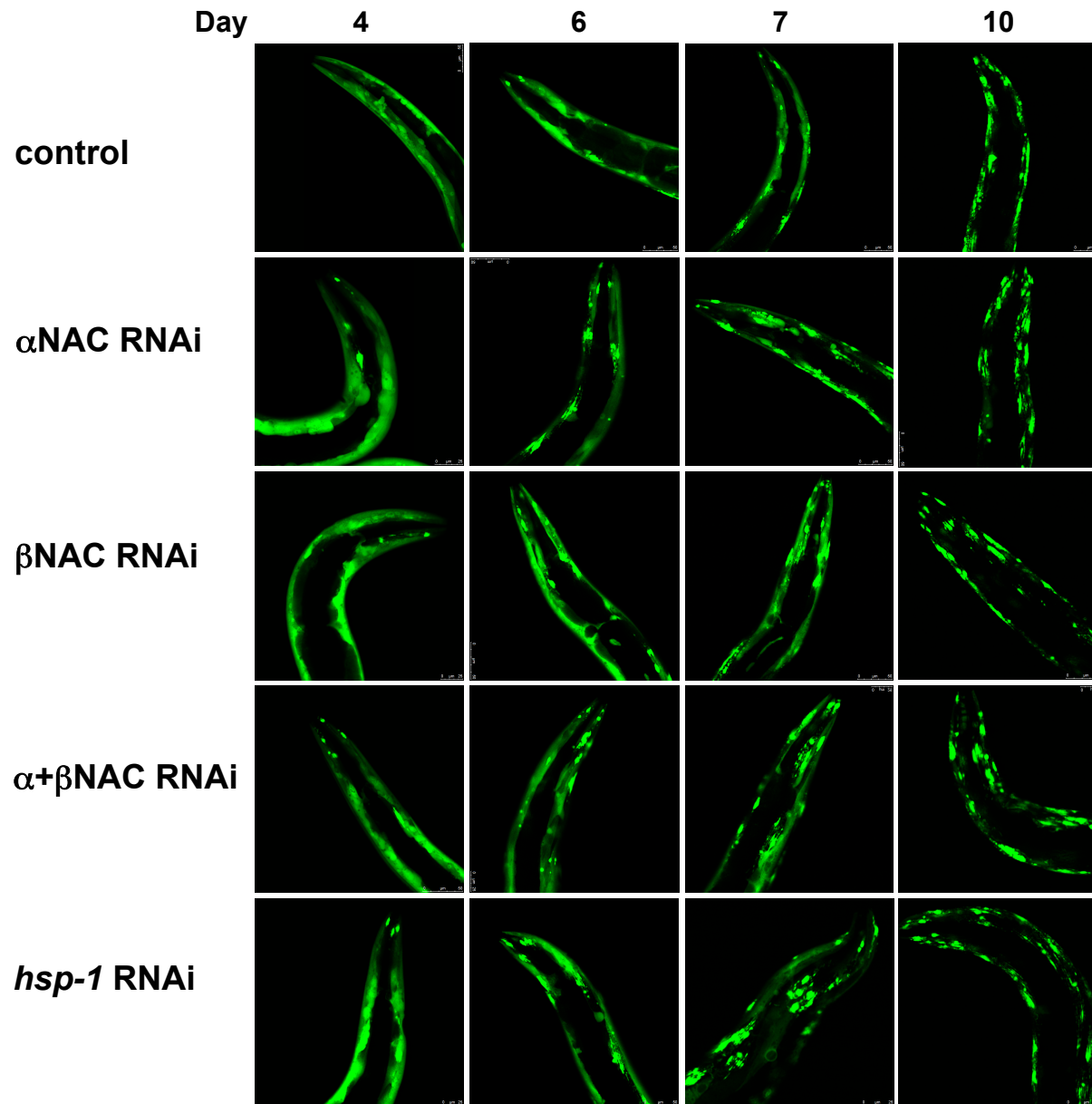
Table S3: Aggregated proteins in day 6 old animals expressing Q35

Table S4: Aggregated proteins upon knockdown of  $\beta$ NAC

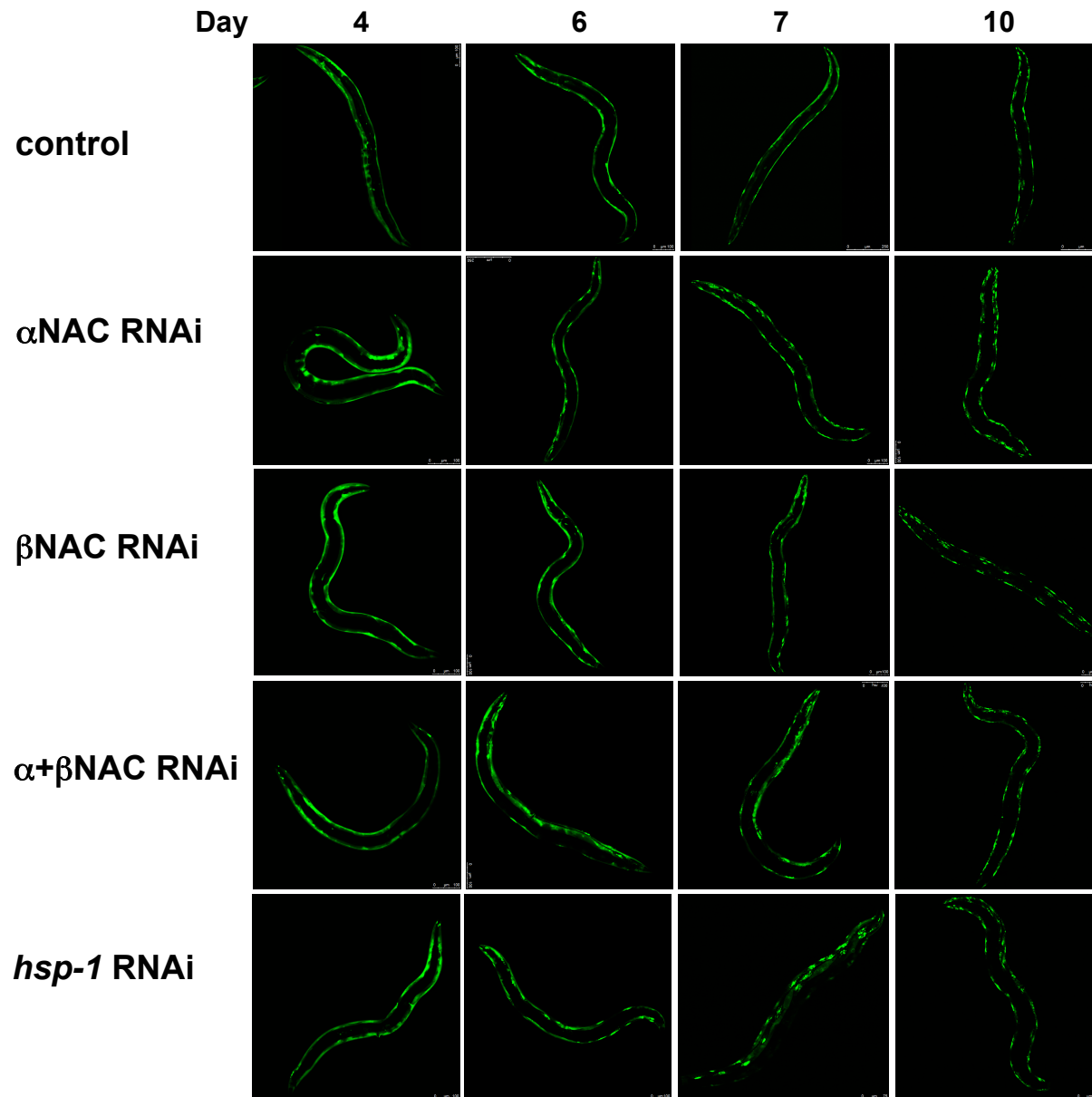
**Figure S 1A**



# S 1B

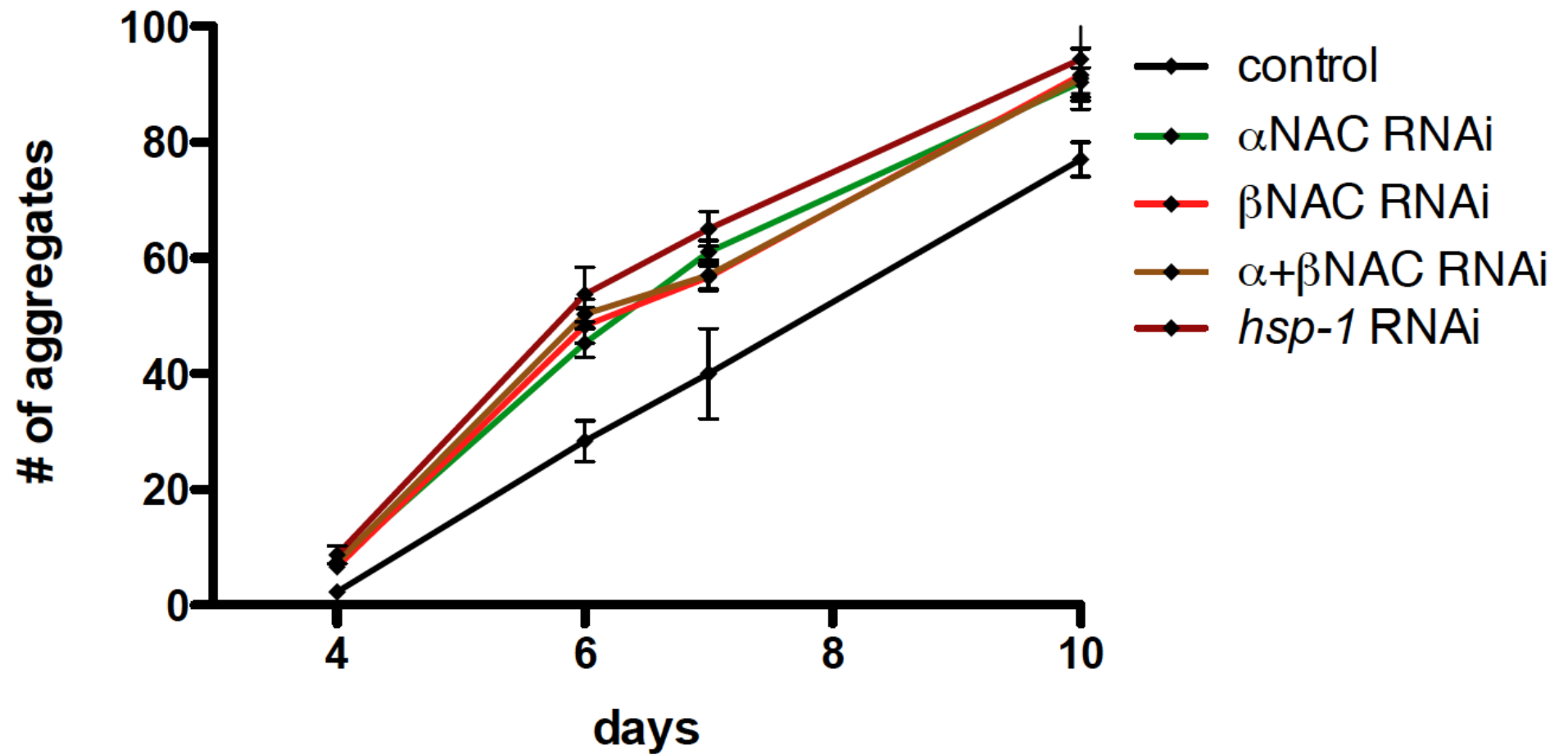


# S 1C

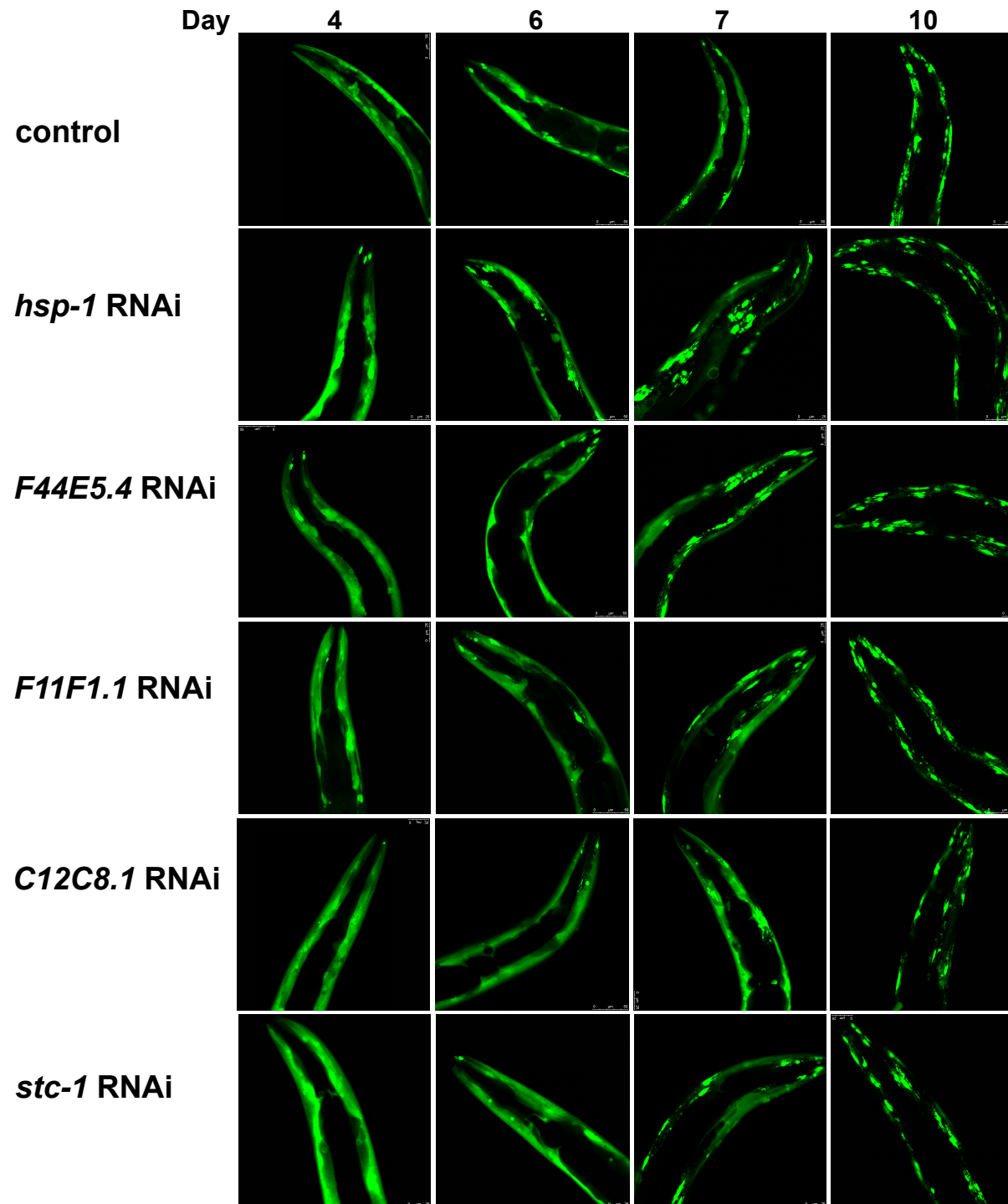




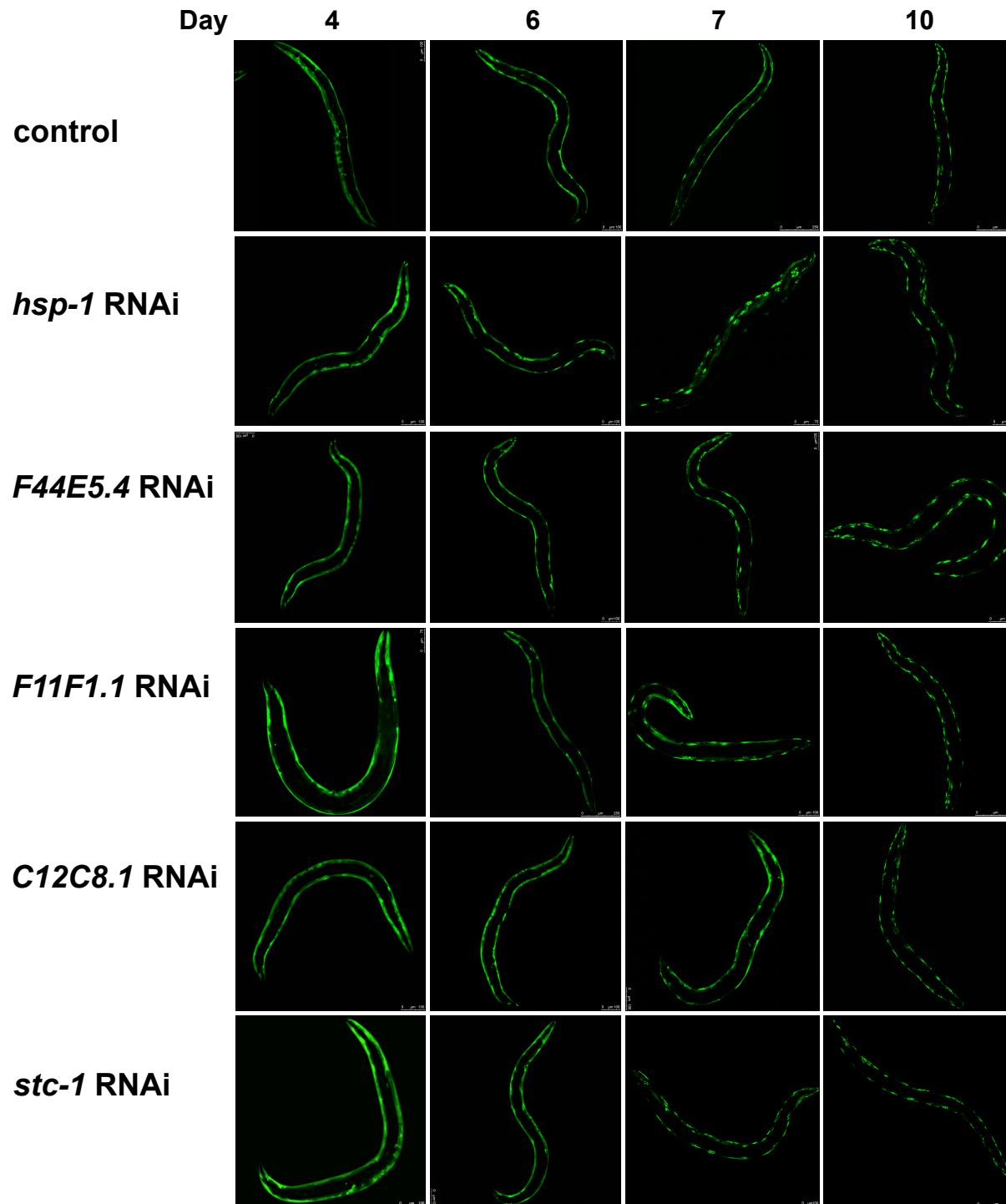
## Q35 aggregation propensity



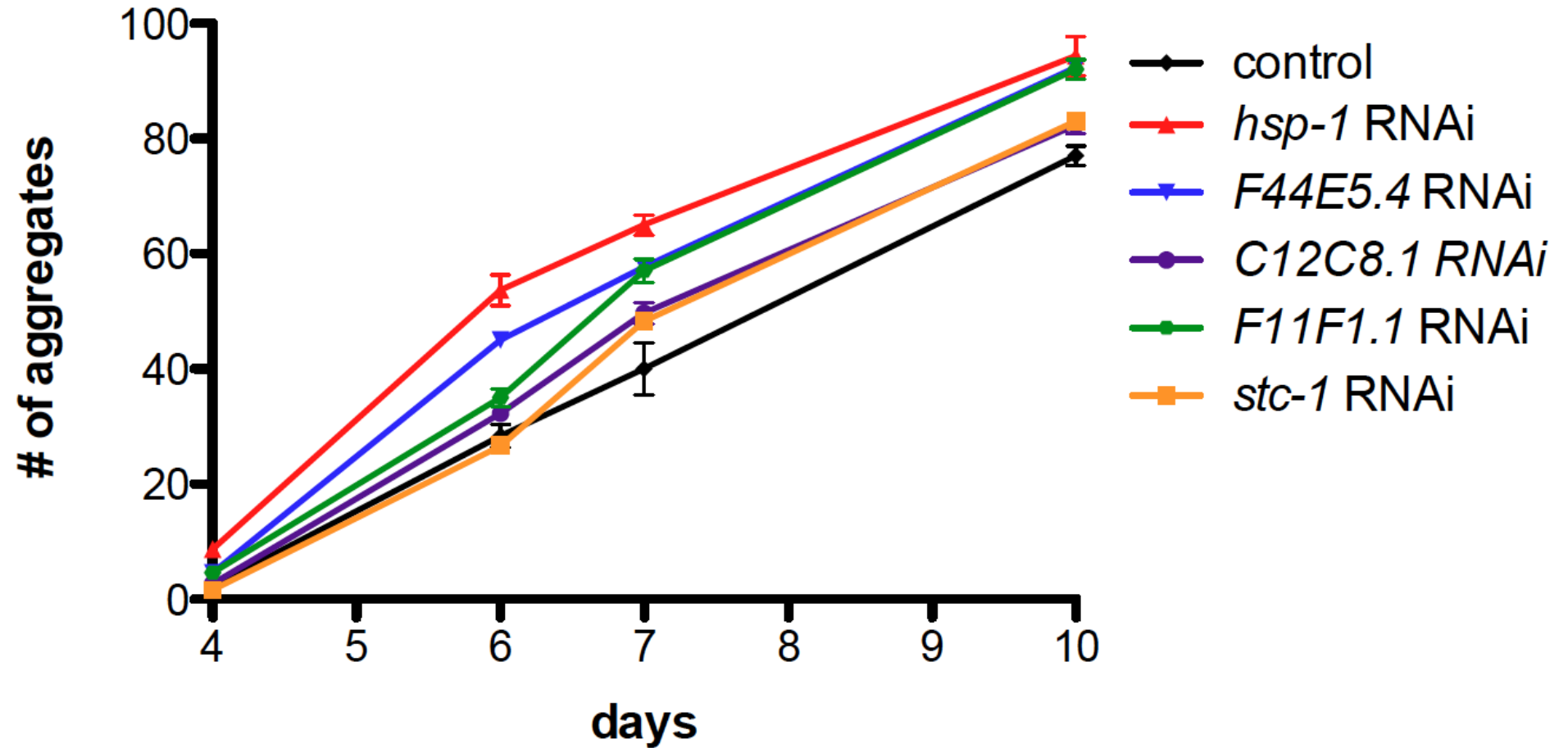
S 1E



S 1F

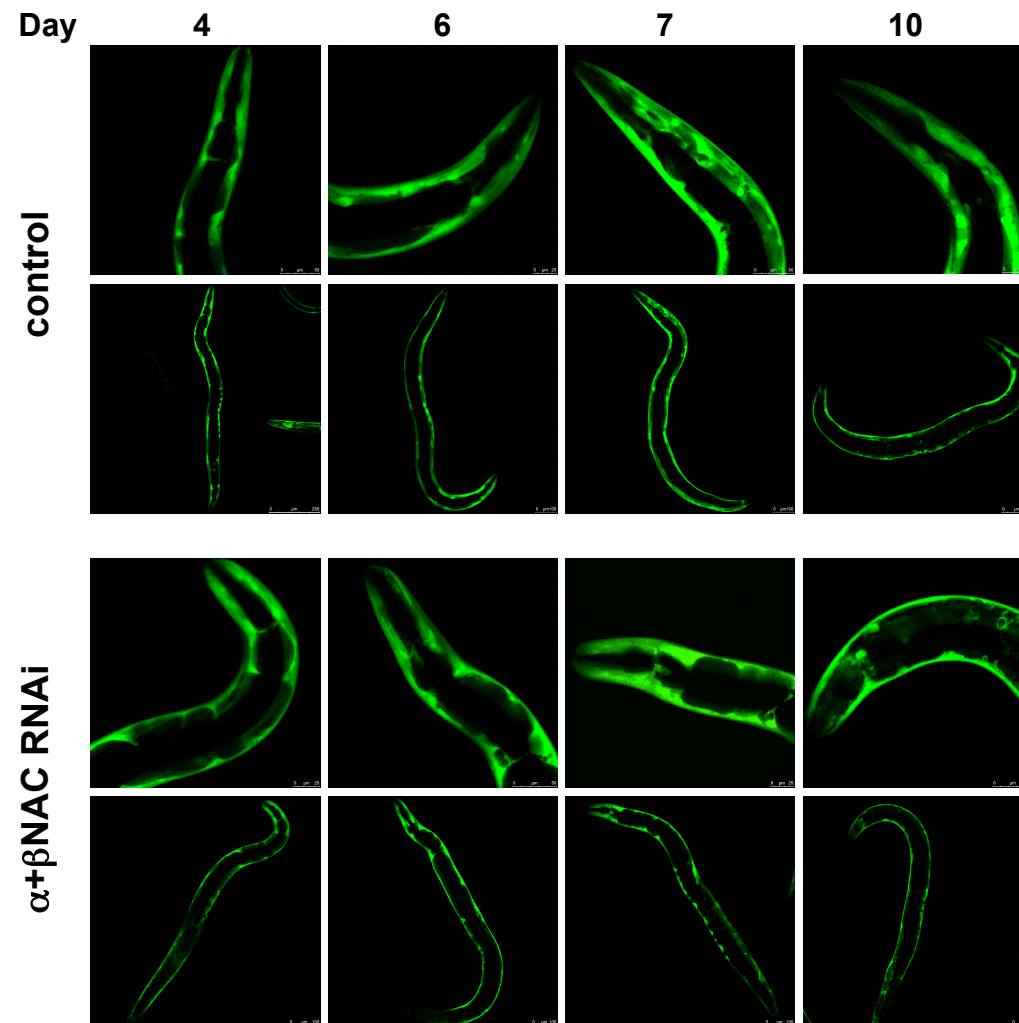


## Q35 aggregation propensity

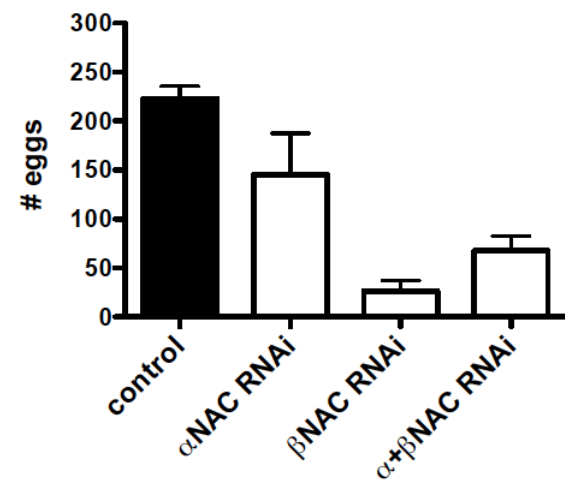


# S 1H

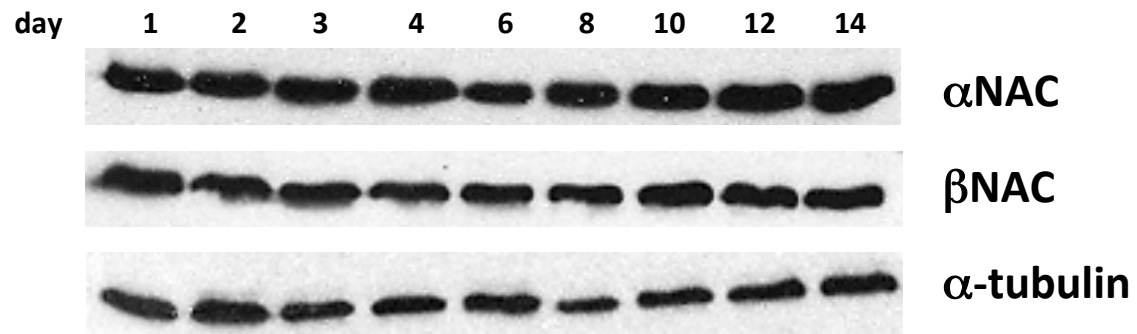
Q0



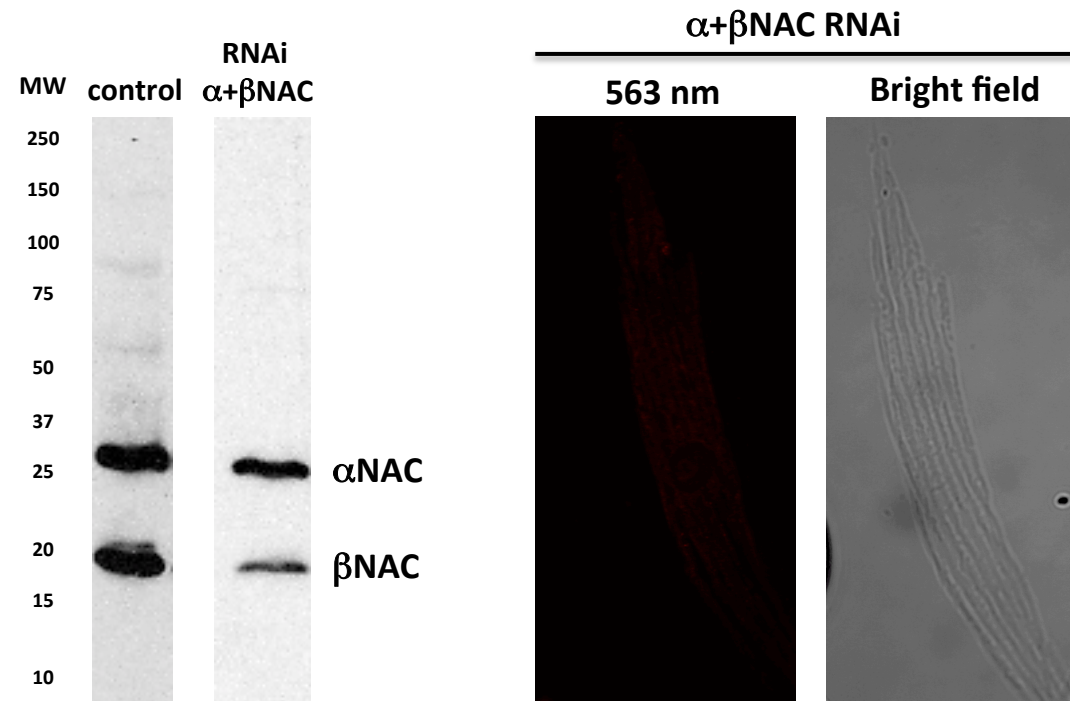
S 2



A

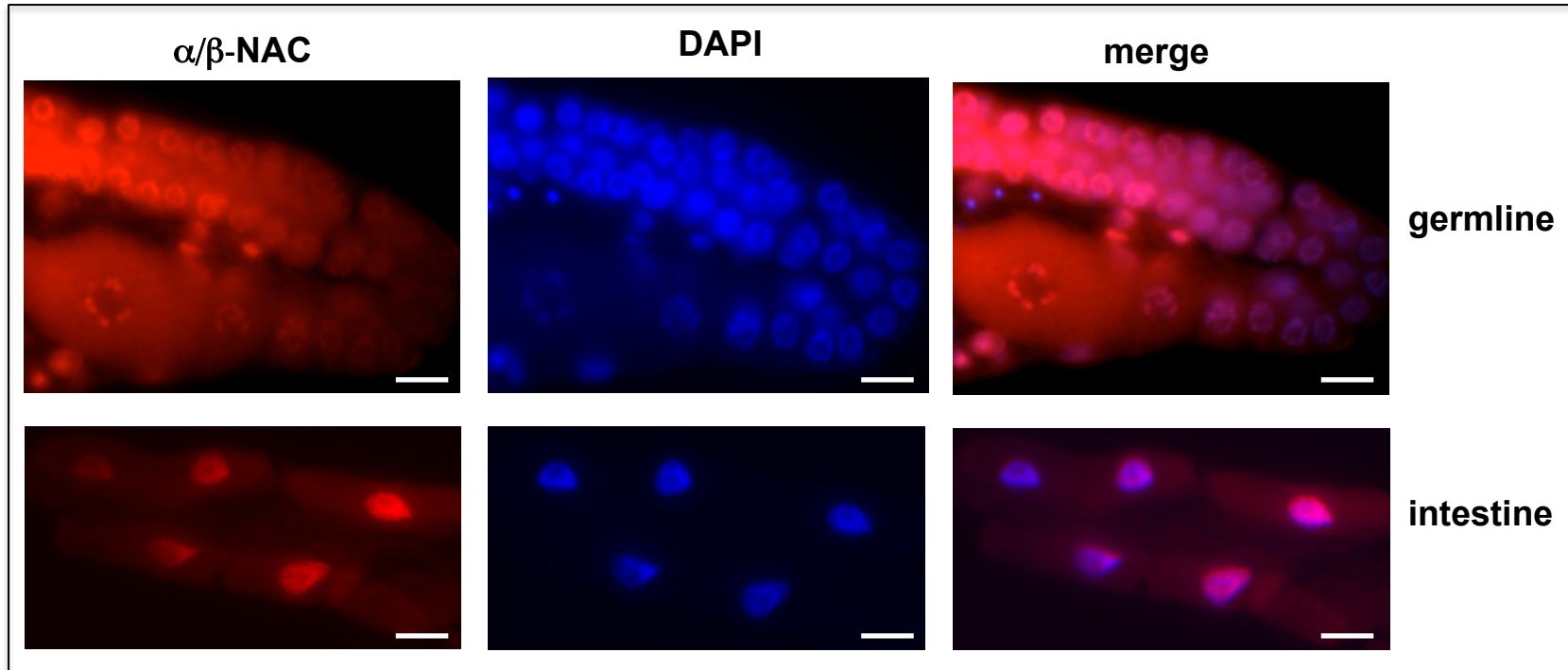


B

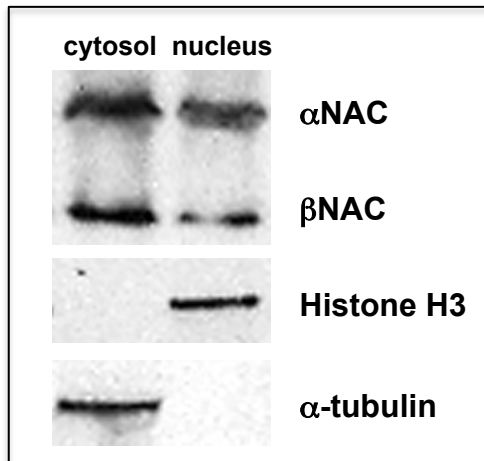


S 4

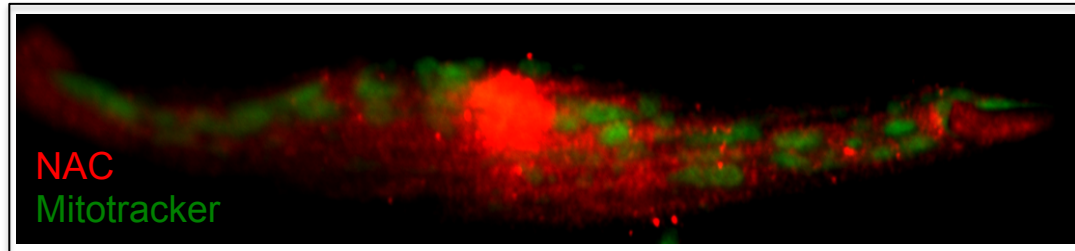
A



B



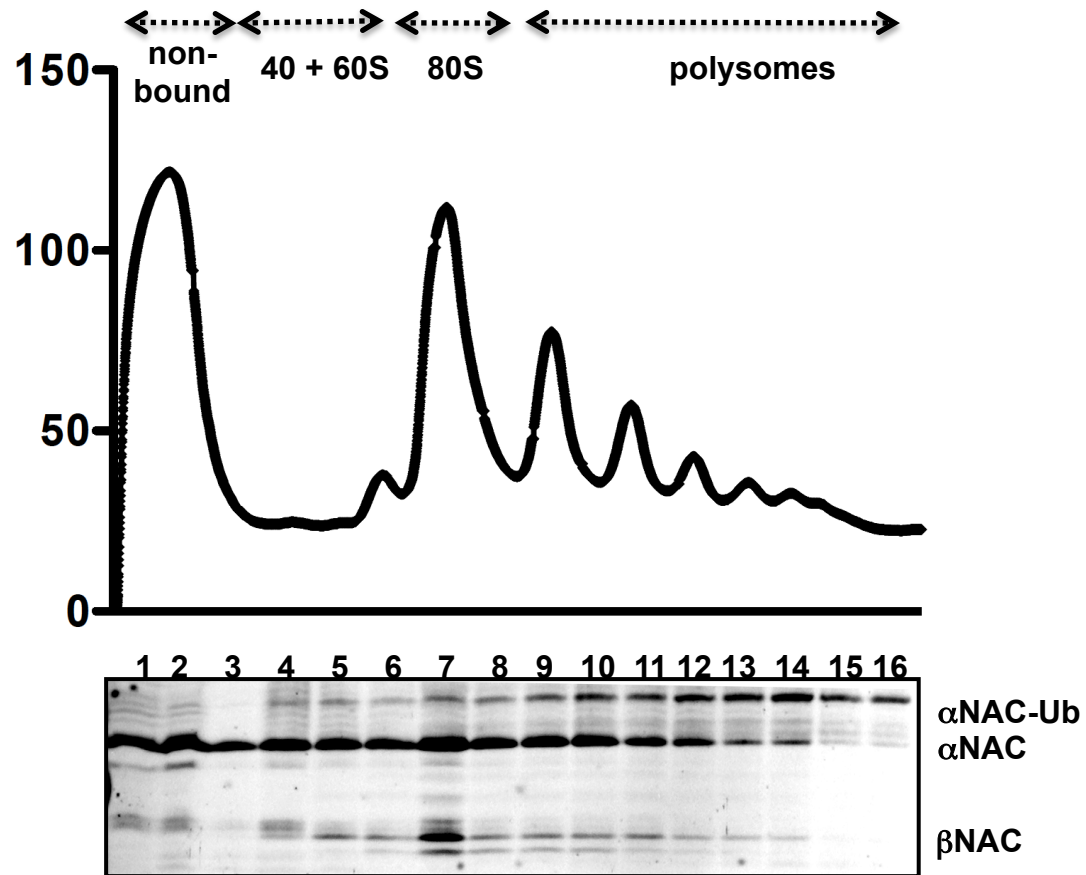
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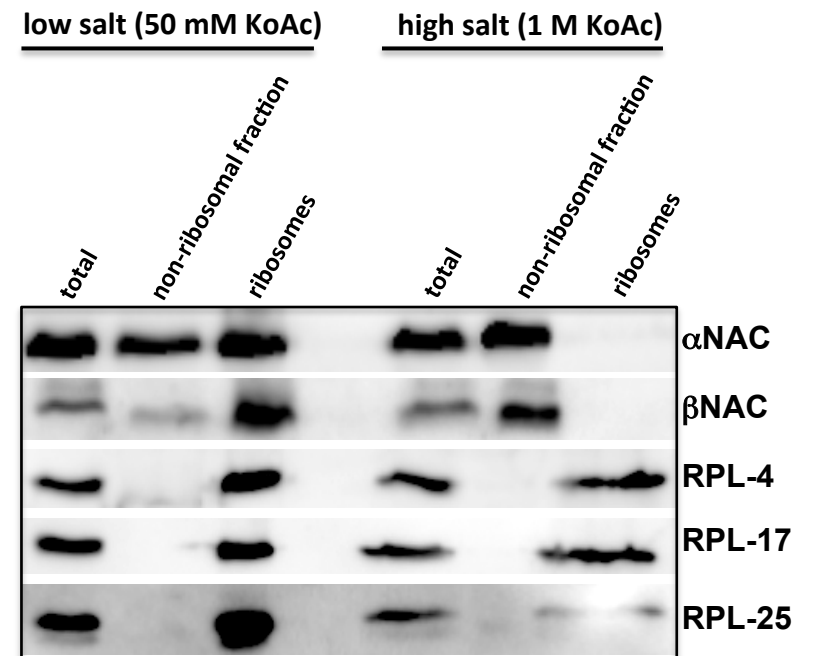


S 5

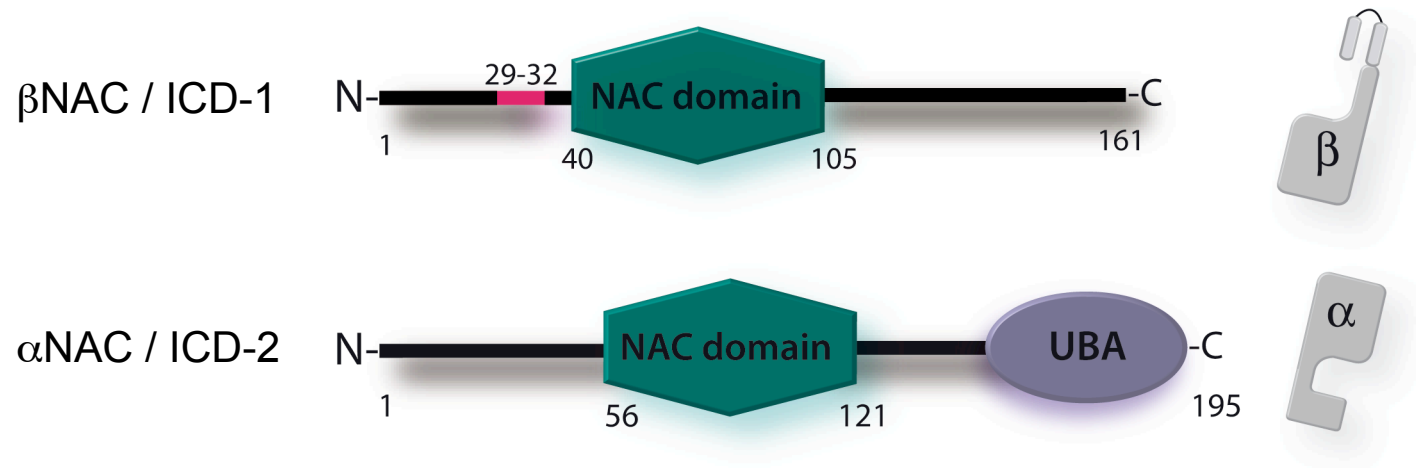
A



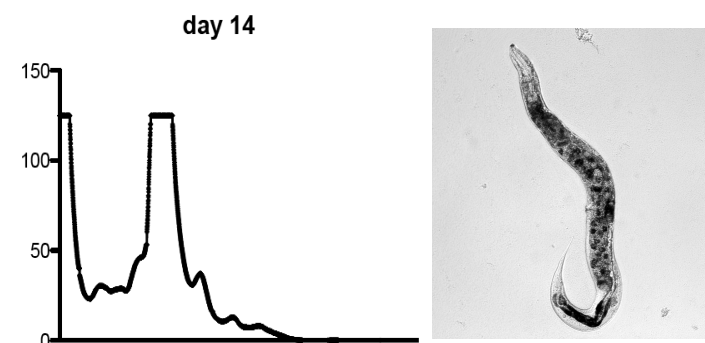
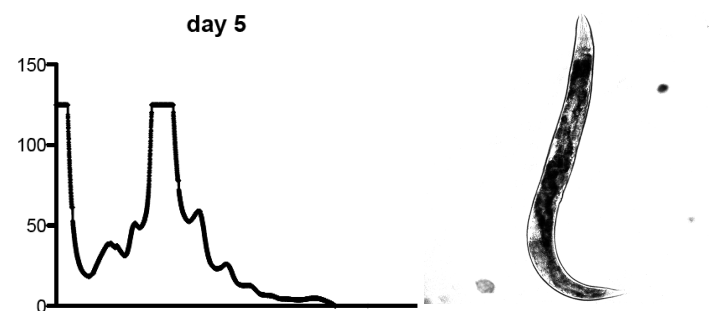
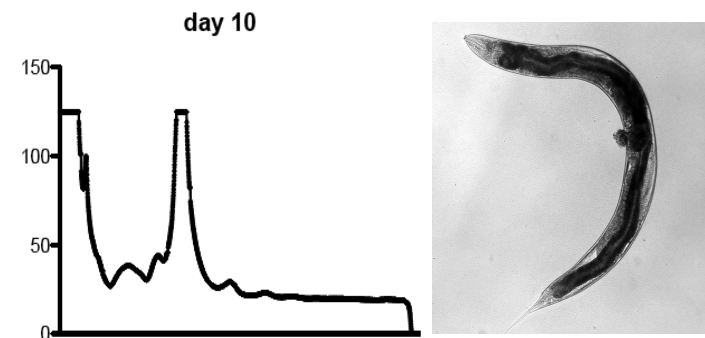
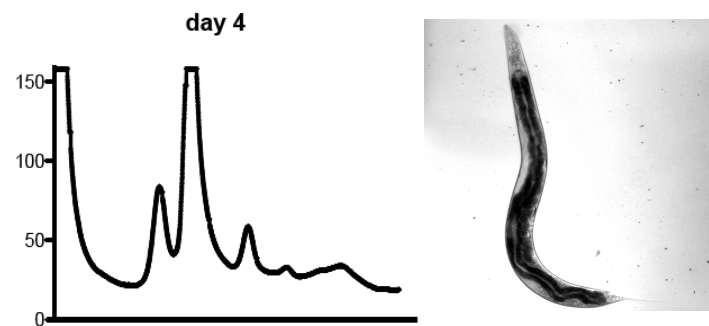
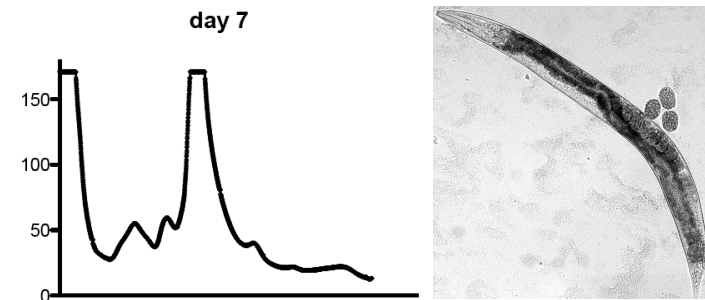
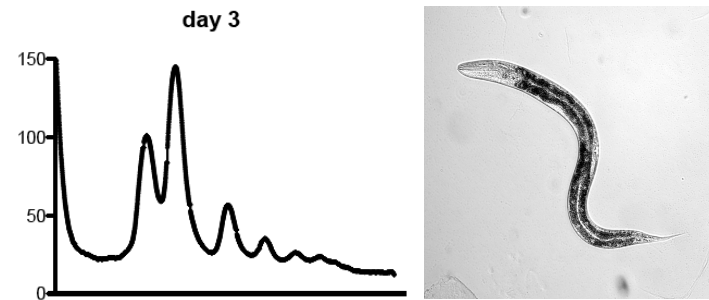
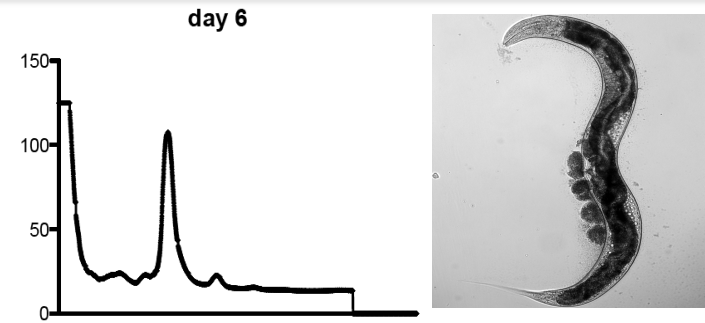
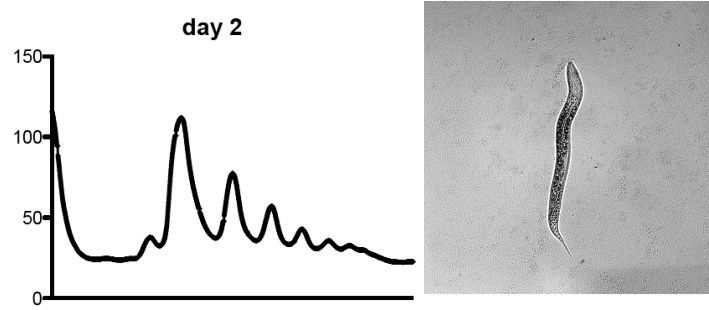
B

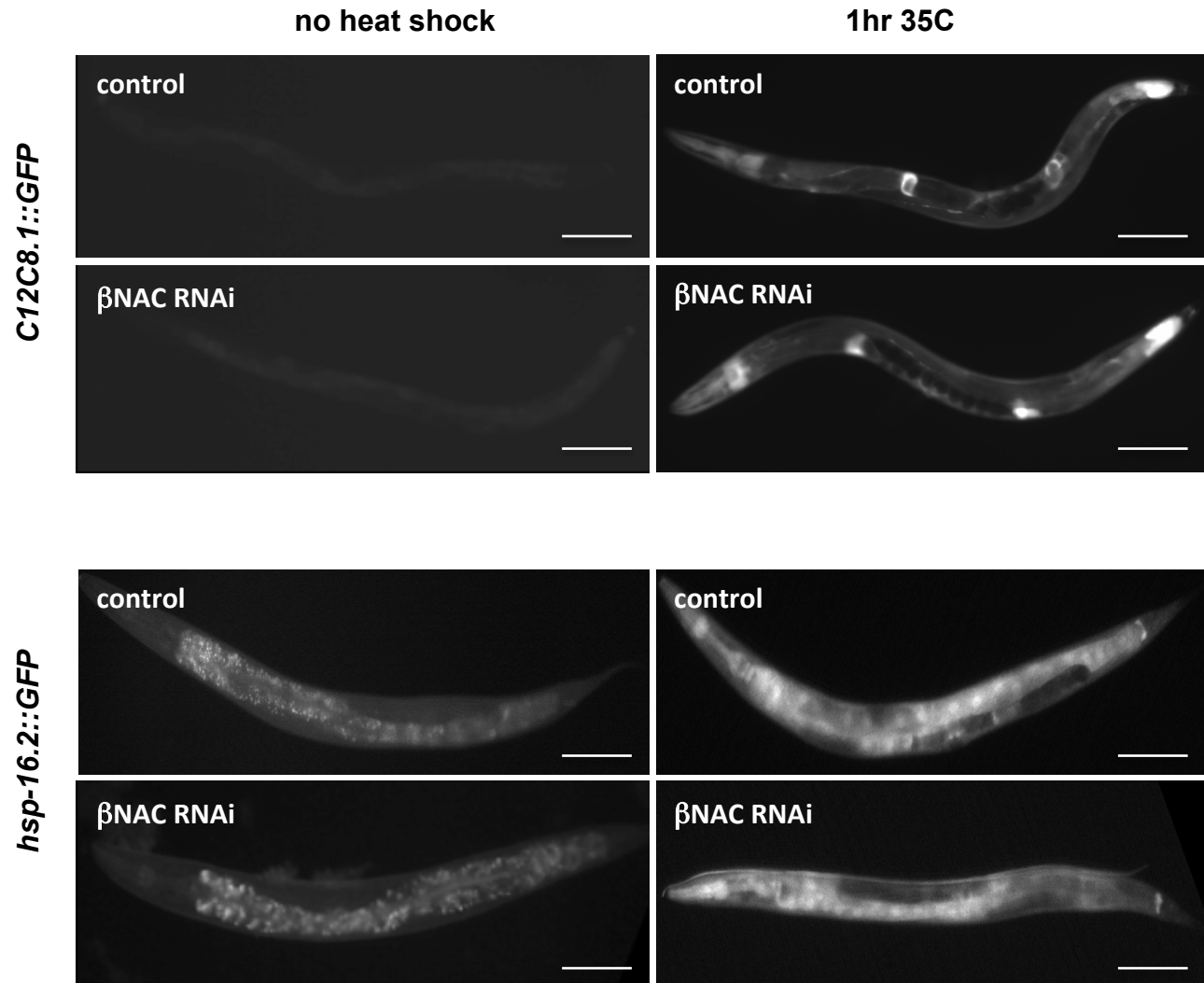


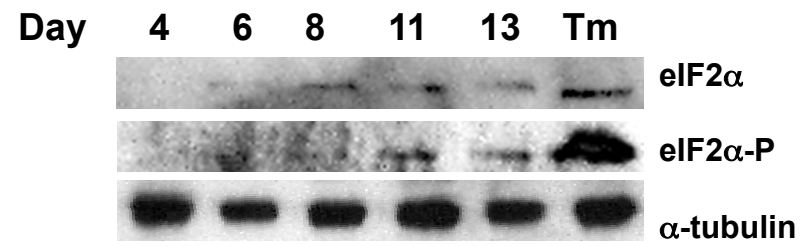
# S 6



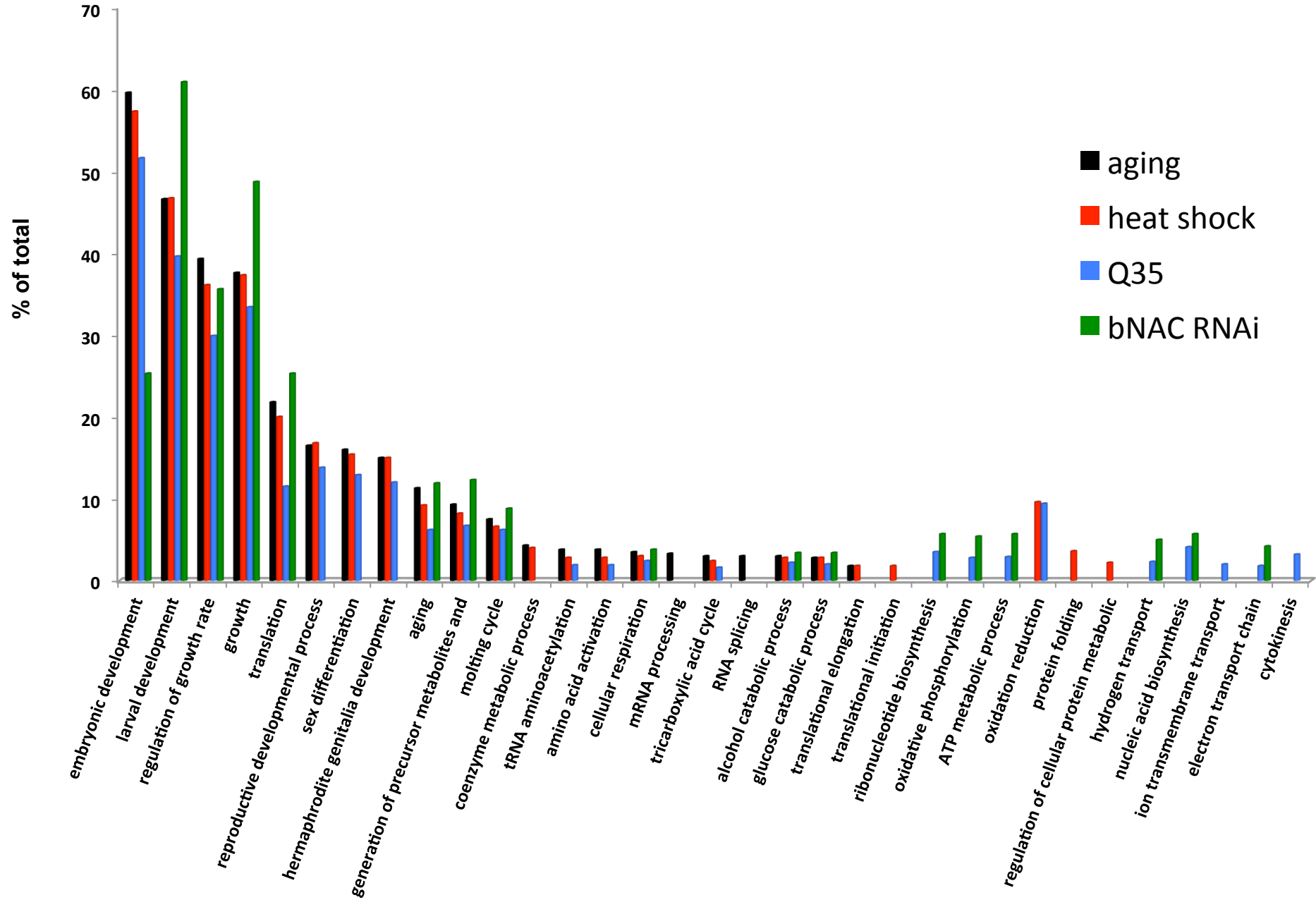
S 7







S 10



**Table S1**

Uniprot ID	Coverage [%]	Peptides	MW [kDA]	Score	Gene name	David (2010)	Description
P41932	31.05	8	28.17	984.6	par-5	X	14-3-3-like protein 1 OS=Caenorhabditis elegans GN=par-5 PE=1 SV=2 - [14331_CAEEL]
Q20655	31.05	7	28.05	618.1	ftt-2	X	14-3-3-like protein 2 OS=Caenorhabditis elegans GN=ftt-2 PE=1 SV=1 - [14332_CAEEL]
Q18787	11.72	4	48.58	435.4	rpt-1	X	26S protease regulatory subunit 7 OS=Caenorhabditis elegans GN=rpt-1 PE=1 SV=1 - [PRS7_CAEEL]
Q18115	2.28	2	105.94	215.3	rpn-2	X	26S proteasome non-ATPase regulatory subunit 1 OS=Caenorhabditis elegans GN=rpn-2 PE=2 SV=4 - [PSMD1_CAEEL]
Q04908	4.76	2	57.47	186.9	rpn-3	X	26S proteasome non-ATPase regulatory subunit 3 OS=Caenorhabditis elegans GN=rpn-3 PE=1 SV=1 - [PSMD3_CAEEL]
Q20585	2.44	1	47.55	46.0	rpn-7	X	26S proteasome non-ATPase regulatory subunit 6 OS=Caenorhabditis elegans GN=rpn-7 PE=2 SV=1 - [PSMD6_CAEEL]
P36573	16.85	3	31.79	258.7	lec-1		32 kDa beta-galactoside-binding lectin OS=Caenorhabditis elegans GN=lec-1 PE=1 SV=1 - [LEC1_CAEEL]
P49196	7.86	2	15.06	138.0	rps-12	X	40S ribosomal protein S12 OS=Caenorhabditis elegans GN=rps-12 PE=1 SV=2 - [RS12_CAEEL]
P51404	15.89	2	17.31	202.6	rps-13	X	40S ribosomal protein S13 OS=Caenorhabditis elegans GN=rps-13 PE=2 SV=2 - [RS13_CAEEL]
P48150	33.55	6	16.24	411.1	rps-14	X	40S ribosomal protein S14 OS=Caenorhabditis elegans GN=rps-14 PE=2 SV=1 - [RS14_CAEEL]
Q9XVP0	16.56	2	17.23	87.2	rps-15	X	40S ribosomal protein S15 OS=Caenorhabditis elegans GN=rps-15 PE=1 SV=3 - [RS15_CAEEL]
Q22054	47.92	7	16.31	594.5	rps-16	X	40S ribosomal protein S16 OS=Caenorhabditis elegans GN=rps-16 PE=1 SV=3 - [RS16_CAEEL]
O01692	37.69	3	14.93	189.0	rps-17	X	40S ribosomal protein S17 OS=Caenorhabditis elegans GN=rps-17 PE=2 SV=2 - [RS17_CAEEL]
O18650	26.03	3	16.31	197.2	rps-19	X	40S ribosomal protein S19 OS=Caenorhabditis elegans GN=rps-19 PE=2 SV=1 - [RS19_CAEEL]
P51403	38.24	9	28.94	520.5	rps-2	X	40S ribosomal protein S2 OS=Caenorhabditis elegans GN=rps-2 PE=2 SV=1 - [RS2_CAEEL]
Q19877	7.69	1	15.86	111.6	rps-23	X	40S ribosomal protein S23 OS=Caenorhabditis elegans GN=rps-23 PE=2 SV=1 - [RS23_CAEEL]
P52821	8.55	1	12.90	63.8	rps-25	X	40S ribosomal protein S25 OS=Caenorhabditis elegans GN=rps-25 PE=2 SV=1 - [RS25_CAEEL]
O45499	26.5	3	13.24	219.2	rps-26	X	40S ribosomal protein S26 OS=Caenorhabditis elegans GN=rps-26 PE=2 SV=1 - [RS26_CAEEL]
Q9TXP0	15.66	1	9.34	28.6	rps-27	X	40S ribosomal protein S27 OS=Caenorhabditis elegans GN=rps-27 PE=1 SV=3 - [RS27_CAEEL]
P48152	31.17	6	27.30	353.4	rps-3	X	40S ribosomal protein S3 OS=Caenorhabditis elegans GN=rps-3 PE=2 SV=1 - [RS3_CAEEL]
P48154	27.63	6	28.94	451.1	rps-1	X	40S ribosomal protein S3a OS=Caenorhabditis elegans GN=rps-1 PE=2 SV=2 - [RS3A_CAEEL]
Q9N3X2	38.22	10	29.03	920.2	rps-4	X	40S ribosomal protein S4 OS=Caenorhabditis elegans GN=rps-4 PE=1 SV=1 - [RS4_CAEEL]
P49041	27.14	7	23.14	938.0	rps-5	X	40S ribosomal protein S5 OS=Caenorhabditis elegans GN=rps-5 PE=2 SV=1 - [RS5_CAEEL]
Q9NEN6	10.98	2	28.12	195.4	rps-6	X	40S ribosomal protein S6 OS=Caenorhabditis elegans GN=rps-6 PE=1 SV=1 - [RS6_CAEEL]
Q23312	42.78	7	22.04	340.4	rps-7	X	40S ribosomal protein S7 OS=Caenorhabditis elegans GN=rps-7 PE=2 SV=1 - [RS7_CAEEL]
P48156	27.4	4	23.74	547.4	rps-8	X	40S ribosomal protein S8 OS=Caenorhabditis elegans GN=rps-8 PE=2 SV=1 - [RS8_CAEEL]
Q20228	39.68	9	21.94	575.2	rps-9	X	40S ribosomal protein S9 OS=Caenorhabditis elegans GN=rps-9 PE=2 SV=1 - [RS9_CAEEL]
P46769	30.07	6	30.68	830.3	rps-0	X	40S ribosomal protein SA OS=Caenorhabditis elegans GN=rps-0 PE=1 SV=3 - [RSSA_CAEEL]
Q95ZQ4	2.4	1	70.40	37.5	aak-2		5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Caenorhabditis elegans GN=aak-2 PE=1 SV=2 - [AAPK2_CAEEL]
Q17761	2.69	1	53.16	84.1	T25B9.9		6-phosphogluconate dehydrogenase, decarboxylating OS=Caenorhabditis elegans GN=T25B9.9 PE=2 SV=2 - [6PGD_CAEEL]

Q27274	19.91	11	72.80	781.2	rop-1	X	60 kDa SS-A/Ro ribonucleoprotein homolog OS=Caenorhabditis elegans GN=rop-1 PE=2 SV=1 - [RO60_CAEEL]
Q93572	35.9	9	33.75	973.7	rpa-0	X	60S acidic ribosomal protein P0 OS=Caenorhabditis elegans GN=rpa-0 PE=1 SV=3 - [RLA0_CAEEL]
P91913	53.15	3	11.28	291.3	rla-1	X	60S acidic ribosomal protein P1 OS=Caenorhabditis elegans GN=rla-1 PE=2 SV=2 - [RLA1_CAEEL]
O01504	30.84	2	10.81	124.2	rpa-2		60S acidic ribosomal protein P2 OS=Caenorhabditis elegans GN=rpa-2 PE=2 SV=2 - [RLA2_CAEEL]
Q09533	28.97	7	24.73	710.2	rpl-10		60S ribosomal protein L10 OS=Caenorhabditis elegans GN=rpl-10 PE=2 SV=1 - [RL10_CAEEL]
Q9N414	19.44	4	24.12	452.0	rpl-10a		60S ribosomal protein L10a OS=Caenorhabditis elegans GN=rpl-10a PE=2 SV=1 - [RL10A_CAEEL]
Q94300	11.22	2	22.70	287.8	rpl-11.1		60S ribosomal protein L11 OS=Caenorhabditis elegans GN=rpl-11.1 PE=2 SV=1 - [RL11_CAEEL]
P61866	16.97	2	17.82	117.3	rpl-12	X	60S ribosomal protein L12 OS=Caenorhabditis elegans GN=rpl-12 PE=2 SV=1 - [RL12_CAEEL]
P91128	10.63	2	23.74	96.1	rpl-13	X	60S ribosomal protein L13 OS=Caenorhabditis elegans GN=rpl-13 PE=2 SV=1 - [RL13_CAEEL]
Q27389	9.9	2	22.98	131.6	rpl-16	X	60S ribosomal protein L13a OS=Caenorhabditis elegans GN=rpl-16 PE=2 SV=1 - [RL13A_CAEEL]
Q9BL19	18.72	3	21.50	447.3	rpl-17	X	60S ribosomal protein L17 OS=Caenorhabditis elegans GN=rpl-17 PE=2 SV=1 - [RL17_CAEEL]
O45946	37.23	6	20.98	522.7	rpl-18	X	60S ribosomal protein L18 OS=Caenorhabditis elegans GN=rpl-18 PE=3 SV=1 - [RL18_CAEEL]
O44480	12.78	2	20.95	59.6	rpl-20	X	60S ribosomal protein L18a OS=Caenorhabditis elegans GN=rpl-20 PE=2 SV=2 - [RL18A_CAEEL]
O02639	22.22	5	23.64	442.3	rpl-19	X	60S ribosomal protein L19 OS=Caenorhabditis elegans GN=rpl-19 PE=2 SV=1 - [RL19_CAEEL]
P34334	16.15	2	18.30	72.4	rpl-21	X	60S ribosomal protein L21 OS=Caenorhabditis elegans GN=rpl-21 PE=1 SV=3 - [RL21_CAEEL]
P52819	23.85	3	14.94	119.5	rpl-22	X	60S ribosomal protein L22 OS=Caenorhabditis elegans GN=rpl-22 PE=1 SV=3 - [RL22_CAEEL]
P48158	25.71	3	14.94	224.3	rpl-23	X	60S ribosomal protein L23 OS=Caenorhabditis elegans GN=rpl-23 PE=2 SV=1 - [RL23_CAEEL]
Q20647	6.85	1	16.27	37.4	rpl-25.2	X	60S ribosomal protein L23a 2 OS=Caenorhabditis elegans GN=rpl-25.2 PE=2 SV=1 - [R23A2_CAEEL]
O01868	11.95	2	17.77	140.0	rpl-24.1	X	60S ribosomal protein L24 OS=Caenorhabditis elegans GN=rpl-24.1 PE=2 SV=1 - [RL24_CAEEL]
P91914	27.21	4	15.72	357.6	rpl-27	X	60S ribosomal protein L27 OS=Caenorhabditis elegans GN=rpl-27 PE=2 SV=1 - [RL27_CAEEL]
Q21930	7.94	1	13.72	91.2	rpl-28		60S ribosomal protein L28 OS=Caenorhabditis elegans GN=rpl-28 PE=1 SV=3 - [RL28_CAEEL]
P50880	3.74	1	45.63	29.7	rpl-3	X	60S ribosomal protein L3 OS=Caenorhabditis elegans GN=rpl-3 PE=2 SV=1 - [RL3_CAEEL]
P34662	8.13	1	14.19	55.4	rpl-35	X	60S ribosomal protein L35 OS=Caenorhabditis elegans GN=rpl-35 PE=2 SV=1 - [RL35_CAEEL]
P49180	9.68	1	13.76	59.4	rpl-33	X	60S ribosomal protein L35a OS=Caenorhabditis elegans GN=rpl-33 PE=1 SV=3 - [RL35A_CAEEL]
P49181	36.54	5	11.88	463.4	rpl-36		60S ribosomal protein L36 OS=Caenorhabditis elegans GN=rpl-36 PE=1 SV=3 - [RL36_CAEEL]
O02056	32.75	9	38.64	697.5	rpl-4	X	60S ribosomal protein L4 OS=Caenorhabditis elegans GN=rpl-4 PE=1 SV=3 - [RL4_CAEEL]
P49405	29.01	6	33.37	457.1	rpl-5	X	60S ribosomal protein L5 OS=Caenorhabditis elegans GN=rpl-5 PE=2 SV=1 - [RL5_CAEEL]
P47991	37.79	8	24.30	816.5	rpl-6	X	60S ribosomal protein L6 OS=Caenorhabditis elegans GN=rpl-6 PE=1 SV=1 - [RL6_CAEEL]
O01802	46.72	12	28.11	1132.5	rpl-7	X	60S ribosomal protein L7 OS=Caenorhabditis elegans GN=rpl-7 PE=1 SV=1 - [RL7_CAEEL]
Q966C6	23.77	6	30.16	566.5	rpl-7a	X	60S ribosomal protein L7a OS=Caenorhabditis elegans GN=rpl-7a PE=1 SV=3 - [RL7A_CAEEL]
Q9XVF7	14.62	3	28.19	293.3	rpl-8		60S ribosomal protein L8 OS=Caenorhabditis elegans GN=rpl-8 PE=1 SV=1 - [RL8_CAEEL]
Q95Y90	38.1	6	21.49	516.6	rpl-9	X	60S ribosomal protein L9 OS=Caenorhabditis elegans GN=rpl-9 PE=1 SV=1 - [RL9_CAEEL]



O01615	21.33	2	24.43	206.5	T19H12.2	X	Acidic leucine-rich nuclear phosphoprotein 32-related protein 2 OS=Caenorhabditis elegans GN=T19H12.2 [AN322_CAEEL]
P10984	50.27	15	41.75	3368.1	act-2		Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=2 SV=3 - [ACT2_CAEEL]
P53489	2.78	1	44.81	74.5	arx-2		Actin-related protein 2 OS=Caenorhabditis elegans GN=arx-2 PE=3 SV=1 - [ARP2_CAEEL]
Q9N4I0	2.59	1	48.06	92.9	arx-1		Actin-related protein 3 OS=Caenorhabditis elegans GN=arx-1 PE=2 SV=1 - [ARP3_CAEEL]
P91455	22.7	4	20.20	180.7	T19B4.3		Adenine phosphoribosyltransferase OS=Caenorhabditis elegans GN=T19B4.3 PE=2 SV=1 - [APT_CAEEL]
P27604	36.61	14	47.51	1934.2	ahcy-1		Adenosylhomocysteinase OS=Caenorhabditis elegans GN=ahcy-1 PE=1 SV=1 - [SAHH_CAEEL]
P91134	10.28	3	50.13	167.2	C37H5.6		Adenylosuccinate synthetase OS=Caenorhabditis elegans GN=C37H5.6 PE=2 SV=3 - [PURA_CAEEL]
O45379	3.8	1	20.76	58.5	arl-3		ADP-ribosylation factor-like protein 3 OS=Caenorhabditis elegans GN=arl-3 PE=1 SV=1 - [ARL3_CAEEL]
O01541	10.85	9	106.72	468.5	aars-2		Alanyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=aars-2 PE=2 SV=1 - [SYAC_CAEEL]
Q17334	35.82	9	37.67	790.4	sodh-1		Alcohol dehydrogenase 1 OS=Caenorhabditis elegans GN=sodh-1 PE=1 SV=2 - [ADH1_CAEEL]
P41847	2.94	1	25.53	42.0	T20B12.7		Anamorsin homolog OS=Caenorhabditis elegans GN=T20B12.7 PE=2 SV=1 - [DRE2_CAEEL]
P35603	2.04	1	50.27	57.7	dpy-23		AP-2 complex subunit mu OS=Caenorhabditis elegans GN=dpy-23 PE=2 SV=2 - [AP2M_CAEEL]
P34552	2.72	2	98.20	110.8	alx-1	X	Apoptosis-linked gene 2-interacting protein X 1 OS=Caenorhabditis elegans GN=alx-1 PE=1 SV=3 - [ALX1_CAEEL]
Q19722	7.34	3	61.15	339.3	nrs-1		Asparaginyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=nrs-1 PE=2 SV=1 - [SYNC_CAEEL]
Q03577	32.39	15	59.90	1157.7	drs-1	X	Aspartyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=drs-1 PE=2 SV=1 - [SYDC_CAEEL]
Q9XXK1	40.89	17	57.75	2528.7	H28O16.1		ATP synthase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=H28O16.1 PE=1 SV=1 - [ATPA_CAEEL]
P46561	30.67	11	57.49	1016.6	atp-2	X	ATP synthase subunit beta, mitochondrial OS=Caenorhabditis elegans GN=atp-2 PE=1 SV=2 - [ATPB_CAEEL]
Q95YF3	8.6	3	48.68	265.4	cgh-1	X	ATP-dependent RNA helicase cgh-1 OS=Caenorhabditis elegans GN=cgh-1 PE=1 SV=1 - [CGH1_CAEEL]
P34689	1.7	1	79.73	29.5	glh-1	X	ATP-dependent RNA helicase glh-1 OS=Caenorhabditis elegans GN=glh-1 PE=1 SV=3 - [GLH1_CAEEL]
O76743	0.95	1	120.57	58.5	glh-4	X	ATP-dependent RNA helicase glh-4 OS=Caenorhabditis elegans GN=glh-4 PE=2 SV=2 - [GLH4_CAEEL]
P30632	8.48	3	37.53	135.5	asna-1		ATPase asna-1 OS=Caenorhabditis elegans GN=asna-1 PE=1 SV=1 - [ASNA_CAEEL]
Q06561	1.78	5	368.82	278.9	unc-52		Basement membrane proteoglycan OS=Caenorhabditis elegans GN=unc-52 PE=1 SV=2 - [UNC52_CAEEL]
Q10663	24.17	20	108.56	2025.5	gei-7	X	Bifunctional glyoxylate cycle protein OS=Caenorhabditis elegans GN=gei-7 PE=1 SV=2 - [GCP_CAEEL]
O62305	1.81	1	79.88	76.6	unc-43		Calcium/calmodulin-dependent protein kinase type II OS=Caenorhabditis elegans GN=unc-43 PE=1 SV=2 - [KCC2D_CAEEL]
P27798	7.59	2	45.59	89.2	crt-1	X	Calreticulin OS=Caenorhabditis elegans GN=crt-1 PE=1 SV=1 - [CALR_CAEEL]
P42168	9.68	3	39.01	104.5	kin-19	X	Casein kinase I isoform alpha OS=Caenorhabditis elegans GN=kin-19 PE=2 SV=1 - [KC1A_CAEEL]
P18334	41.94	12	42.23	1537.1	kin-3	X	Casein kinase II subunit alpha OS=Caenorhabditis elegans GN=kin-3 PE=1 SV=1 - [CSK2A_CAEEL]
P28548	12.39	3	26.42	283.3	kin-10		Casein kinase II subunit beta OS=Caenorhabditis elegans GN=kin-10 PE=1 SV=2 - [CSK2B_CAEEL]
O61235	2.21	1	57.27	41.0	ctl-1	X	Catalase-2 OS=Caenorhabditis elegans GN=ctl-1 PE=2 SV=3 - [CATA2_CAEEL]
O76360	2.95	2	86.69	75.0	egl-4		cGMP-dependent protein kinase egl-4 OS=Caenorhabditis elegans GN=egl-4 PE=1 SV=2 - [EGL4_CAEEL]
P50140	2.99	1	60.06	47.3	hsp-60	X	Chaperonin homolog Hsp-60, mitochondrial OS=Caenorhabditis elegans GN=hsp-60 PE=1 SV=2 - [CH60_CAEEL]
Q18143	3.37	3	120.12	170.6	C25A8.4	X	Chitinase-like protein C25A8.4 OS=Caenorhabditis elegans GN=C25A8.4 PE=1 SV=3 - [CHITL_CAEEL]

O45405	4.2	1	27.51	39.6	exl-1		Chloride intracellular channel exl-1 OS=Caenorhabditis elegans GN=exl-1 PE=2 SV=2 - [EXL1_CAEEL]
P41877	0.79	1	116.60	27.7	isw-1		Chromatin-remodeling complex ATPase chain isw-1 OS=Caenorhabditis elegans GN=isw-1 PE=1 SV=2 - [ISW1_CAEEL]
Q9U2M8	1.89	1	85.45	150.0	Y37H9A.3		Coiled-coil and C2 domain-containing protein 1-like OS=Caenorhabditis elegans GN=Y37H9A.3 PE=1 SV=2 - [C2D1_CAEEL]
P17139	0.85	1	170.98	50.5	emb-9		Collagen alpha-1(IV) chain OS=Caenorhabditis elegans GN=emb-9 PE=1 SV=4 - [CO4A1_CAEEL]
P17140	1.48	2	167.65	201.4	let-2	X	Collagen alpha-2(IV) chain OS=Caenorhabditis elegans GN=let-2 PE=1 SV=2 - [CO4A2_CAEEL]
Q9GS00	1.5	1	68.36	26.4	csn-1		COP9 signalosome complex subunit 1 OS=Caenorhabditis elegans GN=csn-1 PE=1 SV=1 - [CSN1_CAEEL]
Q94261	3.08	1	44.06	50.3	cif-1	X	COP9/Signalosome and eIF3 complex-shared subunit 1 OS=Caenorhabditis elegans GN=cif-1 PE=1 SV=1 - [EIF3M_CAEEL]
P18833	6.03	1	28.13	229.4	col-8		Cuticle collagen 8 OS=Caenorhabditis elegans GN=col-8 PE=2 SV=2 - [COL8_CAEEL]
P34556	6.02	1	38.27	55.8	cdk-1		Cyclin-dependent kinase 1 OS=Caenorhabditis elegans GN=cdk-1 PE=1 SV=1 - [CDK1_CAEEL]
P98080	10.83	5	51.70	516.5	ucr-1		Cytochrome b-c1 complex subunit 1, mitochondrial OS=Caenorhabditis elegans GN=ucr-1 PE=2 SV=2 - [UCR1_CAEEL]
P19974	13.51	1	12.23	133.9	cyc-2.1		Cytochrome c 2.1 OS=Caenorhabditis elegans GN=cyc-2.1 PE=1 SV=2 - [CYC21_CAEEL]
P24894	4.76	1	26.53	56.6	cox-2		Cytochrome c oxidase subunit 2 OS=Caenorhabditis elegans GN=cox-2 PE=3 SV=2 - [COX2_CAEEL]
O44518	0.87	1	144.92	78.6	gex-2		Cytoplasmic FMR1-interacting protein homolog OS=Caenorhabditis elegans GN=gex-2 PE=1 SV=4 - [CYFIP_CAEEL]
Q93459	6.07	1	33.02	49.8	F10G8.6		Cytosolic Fe-S cluster assembly factor NUBP1 homolog OS=Caenorhabditis elegans GN=F10G8.6 PE=2 SV=2 - [NUBP1_CAEEL]
Q9U3C8	7.12	2	34.11	61.4	dcn-1		Defective in cullin neddylation protein 1 OS=Caenorhabditis elegans GN=dcn-1 PE=1 SV=2 - [DCN1_CAEEL]
Q19749	2.96	1	53.43	344.8	F23B12.5	X	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mito OS=Caenorhabditis elegans
Q18164	1.23	1	115.23	53.7	dpyd-1		Dihydropyrimidine dehydrogenase [NADP+] OS=Caenorhabditis elegans GN=dpyd-1 PE=2 SV=2 - [DPYD_CAEEL]
Q18066	3.59	2	71.80	217.3	dim-1	X	Disorganized muscle protein 1 OS=Caenorhabditis elegans GN=dim-1 PE=1 SV=3 - [DIM_CAEEL]
Q21554	0.71	1	125.64	48.6	ddb-1		DNA damage-binding protein 1 OS=Caenorhabditis elegans GN=ddb-1 PE=1 SV=2 - [DDB1_CAEEL]
Q27474	1.94	1	86.26	57.2	lig-1		DNA ligase 1 OS=Caenorhabditis elegans GN=lig-1 PE=2 SV=2 - [DNL1_CAEEL]
Q21902	11.59	8	84.88	517.4	mcm-5	X	DNA replication licensing factor mcm-5 OS=Caenorhabditis elegans GN=mcm-5 PE=2 SV=1 - [MCM5_CAEEL]
P34647	1.48	1	91.07	55.9	mcm-6	X	DNA replication licensing factor mcm-6 OS=Caenorhabditis elegans GN=mcm-6 PE=1 SV=1 - [MCM6_CAEEL]
P16356	0.59	1	203.85	32.5	ama-1		DNA-directed RNA polymerase II subunit RPB1 OS=Caenorhabditis elegans GN=ama-1 PE=1 SV=2 - [RPB1_CAEEL]
Q10578	2.26	3	134.82	115.6	rpb-2		DNA-directed RNA polymerase II subunit RPB2 OS=Caenorhabditis elegans GN=rpb-2 PE=2 SV=2 - [RPB2_CAEEL]
Q9N5K2	4.27	1	24.33	68.3	rpb-5		DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Caenorhabditis elegans GN=rpb-5 PE=2 SV=1 - [RPAB1_CAEEL]
P39055	3.25	2	93.35	75.8	dyn-1	X	Dynamin OS=Caenorhabditis elegans GN=dyn-1 PE=1 SV=3 - [DYN1_CAEEL]
Q95XR4	6.23	4	79.92	205.1	epg-2		Ectopic P granules protein 2 OS=Caenorhabditis elegans GN=epg-2 PE=2 SV=1 - [EPG2_CAEEL]
Q11190	3.35	1	65.29	74.9	let-721	X	Electron transfer flavoprotein-ubiquinone oxidoreductase, mito OS=Caenorhabditis elegans GN=let-721
P53013	41.04	16	50.64	6066.6	eft-3	X	Elongation factor 1-alpha OS=Caenorhabditis elegans GN=eft-3 PE=2 SV=1 - [EF1A_CAEEL]
P29691	31.92	24	94.74	2651.8	eef-2		Elongation factor 2 OS=Caenorhabditis elegans GN=eef-2 PE=1 SV=4 - [EF2_CAEEL]
Q9XV52	1.47	1	83.60	39.7	F29C12.4	X	Elongation factor G, mitochondrial OS=Caenorhabditis elegans GN=F29C12.4 PE=2 SV=1 - [EFGM_CAEEL]
P34529	0.49	1	210.79	39.3	dcr-1		Endoribonuclease dcr-1 OS=Caenorhabditis elegans GN=dcr-1 PE=1 SV=2 - [DCR1_CAEEL]

Q27527	17.97	6	46.59	428.7	enol-1	X	Enolase OS=Caenorhabditis elegans GN=enol-1 PE=1 SV=3 - [ENO_CAEEL]
P27639	24.38	9	45.38	583.3	inf-1	X	Eukaryotic initiation factor 4A OS=Caenorhabditis elegans GN=inf-1 PE=2 SV=1 - [IF4A_CAEEL]
O16520	6.8	3	62.13	268.2	erf-1		Eukaryotic peptide chain release factor subunit 1 OS=Caenorhabditis elegans GN=erf-1 PE=2 SV=2 - [ERF1_CAEEL]
Q21230	10.8	1	27.56	58.6	K04G2.1		Eukaryotic translation initiation factor 2 subunit 2 OS=Caenorhabditis elegans GN=K04G2.1 PE=3 SV=4 - [IF2B_CAEEL]
P34339	7.9	7	124.33	351.5	egl-45		Eukaryotic translation initiation factor 3 subunit A OS=Caenorhabditis elegans GN=egl-45 PE=2 SV=1 - [EIF3A_CAEEL]
O02328	5.12	4	103.78	127.6	eif-3.C	X	Eukaryotic translation initiation factor 3 subunit C OS=Caenorhabditis elegans GN=eif-3.C PE=2 SV=2 - [EIF3C_CAEEL]
P30642	2.81	1	64.25	157.6	eif-3.D		Eukaryotic translation initiation factor 3 subunit D OS=Caenorhabditis elegans GN=eif-3.D PE=1 SV=1 - [EIF3D_CAEEL]
Q18967	3.74	1	32.91	34.5	eif-3.F		Eukaryotic translation initiation factor 3 subunit F OS=Caenorhabditis elegans GN=eif-3.F PE=2 SV=1 - [EIF3F_CAEEL]
Q19706	10.94	2	29.27	126.3	eif-3.G	X	Eukaryotic translation initiation factor 3 subunit G OS=Caenorhabditis elegans GN=eif-3.G PE=2 SV=1 - [EIF3G_CAEEL]
Q965S8	7.65	2	36.85	317.1	eif-3.I		Eukaryotic translation initiation factor 3 subunit I OS=Caenorhabditis elegans GN=eif-3.I PE=2 SV=2 - [EIF3I_CAEEL]
O45551	6.13	1	24.30	49.6	ife-1		Eukaryotic translation initiation factor 4E-1 OS=Caenorhabditis elegans GN=ife-1 PE=1 SV=2 - [IF4E1_CAEEL]
Q21693	7.46	1	25.71	94.7	ife-2		Eukaryotic translation initiation factor 4E-2 OS=Caenorhabditis elegans GN=ife-2 PE=1 SV=1 - [IF4E2_CAEEL]
P34563	21.12	2	17.86	228.2	iff-1	X	Eukaryotic translation initiation factor 5A-1 OS=Caenorhabditis elegans GN=iff-1 PE=1 SV=1 - [IF5A1_CAEEL]
O62106	13.01	2	26.29	174.4	eif-6		Eukaryotic translation initiation factor 6 OS=Caenorhabditis elegans GN=eif-6 PE=2 SV=1 - [IF6_CAEEL]
Q20223	12.58	2	18.27	128.8	ibp-1		Fatty acid-binding protein homolog 1 OS=Caenorhabditis elegans GN=ibp-1 PE=1 SV=1 - [FABP1_CAEEL]
Q20224	11.8	2	18.83	142.9	ibp-2	X	Fatty acid-binding protein homolog 2 OS=Caenorhabditis elegans GN=ibp-2 PE=1 SV=1 - [FABP2_CAEEL]
O01812	9.63	1	15.63	134.3	ibp-6	X	Fatty acid-binding protein homolog 6 OS=Caenorhabditis elegans GN=ibp-6 PE=1 SV=1 - [FABP6_CAEEL]
P34383	12.64	2	20.02	71.0	far-2	X	Fatty-acid and retinol-binding protein 2 OS=Caenorhabditis elegans GN=far-2 PE=1 SV=1 - [FAR2_CAEEL]
P54216	3.01	1	39.22	114.0	aldo-1		Fructose-bisphosphate aldolase 1 OS=Caenorhabditis elegans GN=aldo-1 PE=1 SV=1 - [ALF1_CAEEL]
P46563	23.5	6	38.82	587.5	aldo-2		Fructose-bisphosphate aldolase 2 OS=Caenorhabditis elegans GN=aldo-2 PE=2 SV=1 - [ALF2_CAEEL]
P30627	6.92	1	18.49	80.4	glb-1		Globin-like protein OS=Caenorhabditis elegans GN=glb-1 PE=1 SV=2 - [GLBH_CAEEL]
P91406	1.43	1	85.45	33.0	R57.1		Glutamate carboxypeptidase 2 homolog OS=Caenorhabditis elegans GN=R57.1 PE=1 SV=2 - [GCP2_CAEEL]
Q20117	1.38	1	74.32	36.1	gcs-1		Glutamate--cysteine ligase OS=Caenorhabditis elegans GN=gcs-1 PE=1 SV=2 - [GSH1_CAEEL]
Q21355	18.84	4	23.88	238.2	gst-4		Glutathione S-transferase 4 OS=Caenorhabditis elegans GN=gst-4 PE=2 SV=1 - [GST4_CAEEL]
P10299	12.5	2	23.89	87.8	gst-1	X	Glutathione S-transferase P OS=Caenorhabditis elegans GN=gst-1 PE=1 SV=1 - [GSTP1_CAEEL]
P17329	41.94	10	36.43	2170.2	gpd-2	X	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Caenorhabditis elegans GN=gpd-2 PE=3 SV=2 - [G3P2_CAEEL]
O17915	22.79	4	24.24	249.8	ran-1	X	GTP-binding nuclear protein ran-1 OS=Caenorhabditis elegans GN=ran-1 PE=1 SV=1 - [RAN_CAEEL]
Q18905	3.1	2	67.73	70.7	cgp-1		GTP-binding protein cgp-1 OS=Caenorhabditis elegans GN=cgp-1 PE=2 SV=2 - [CGP1_CAEEL]
Q23445	24.35	3	21.70	220.4	ZK180.4		GTP-binding protein SAR1 OS=Caenorhabditis elegans GN=ZK180.4 PE=2 SV=1 - [SAR1_CAEEL]
P17343	4.12	1	37.38	117.2	gpb-1		Guanine nucleotide-binding protein subunit beta-1 OS=Caenorhabditis elegans GN=gpb-1 PE=2 SV=2 - [GBB1_CAEEL]
Q21215	26.15	8	35.81	507.4	rack-1	X	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Caenorhabditis elegans GN=rack-1 PE=1 SV=3 - [GBLP_CAEEL]
P09446	31.25	18	69.68	2261.2	hsp-1	X	Heat shock 70 kDa protein A OS=Caenorhabditis elegans GN=hsp-1 PE=1 SV=2 - [HSP7A_CAEEL]

P27420	8.47	5	72.98	710.1	hsp-3	X	Heat shock 70 kDa protein C OS=Caenorhabditis elegans GN=hsp-3 PE=1 SV=2 - [HSP7C_CAEEL]
P20163	8.98	5	72.24	649.1	hsp-4	X	Heat shock 70 kDa protein D OS=Caenorhabditis elegans GN=hsp-4 PE=1 SV=2 - [HSP7D_CAEEL]
P11141	9.74	5	70.80	216.7	hsp-6	X	Heat shock 70 kDa protein F, mitochondrial OS=Caenorhabditis elegans GN=hsp-6 PE=1 SV=2 - [HSP7F_CAEEL]
Q18688	28.35	19	80.23	2232.6	daf-21	X	Heat shock protein 90 OS=Caenorhabditis elegans GN=daf-21 PE=1 SV=1 - [HSP90_CAEEL]
P34696	56.55	5	16.24	454.5	hsp-16.1	X	Heat shock protein Hsp-16.1/Hsp-16.11 OS=Caenorhabditis elegans GN=hsp-16.1 PE=3 SV=1 - [HSP11_CAEEL]
P06582	44.83	4	16.23	405.3	hsp-16.2		Heat shock protein Hsp-16.2 OS=Caenorhabditis elegans GN=hsp-16.2 PE=2 SV=1 - [HSP12_CAEEL]
P02513	25.17	2	16.29	368.0	hsp-16.48	X	Heat shock protein Hsp-16.48/Hsp-16.49 OS=Caenorhabditis elegans GN=hsp-16.48 PE=2 SV=1 - [HSP17_CAEEL]
P53795	8.46	1	14.23	66.5	hint-1		Histidine triad nucleotide-binding protein 1 OS=Caenorhabditis elegans GN=hint-1 PE=2 SV=1 - [HINT_CAEEL]
P34183	4.03	2	58.52	82.9	hrs-1	X	Histidyl-tRNA synthetase OS=Caenorhabditis elegans GN=hrs-1 PE=2 SV=3 - [SYH_CAEEL]
O17695	1.95	1	52.10	56.4	had-1		Histone deacetylase 1 OS=Caenorhabditis elegans GN=hda-1 PE=1 SV=1 - [HDA1_CAEEL]
P10771	25	4	21.35	625.9	his-24		Histone H1.1 OS=Caenorhabditis elegans GN=his-24 PE=1 SV=4 - [H11_CAEEL]
P15796	6.81	1	19.77	70.7	hil-2		Histone H1.2 OS=Caenorhabditis elegans GN=hil-2 PE=1 SV=3 - [H12_CAEEL]
Q19743	6.25	1	21.69	87.4	hil-3		Histone H1.3 OS=Caenorhabditis elegans GN=hil-3 PE=2 SV=3 - [H13_CAEEL]
P09588	36.22	4	13.40	408.0	his-3		Histone H2A OS=Caenorhabditis elegans GN=his-3 PE=1 SV=2 - [H2A_CAEEL]
Q27511	61.43	7	14.66	598.9	htz-1		Histone H2A.V OS=Caenorhabditis elegans GN=htz-1 PE=2 SV=3 - [H2AV_CAEEL]
Q27532	13.24	2	15.34	104.3	his-74		Histone H3.3-like type 2 OS=Caenorhabditis elegans GN=his-74 PE=2 SV=3 - [H33L2_CAEEL]
P62784	41.75	5	11.36	546.9	his-1	X	Histone H4 OS=Caenorhabditis elegans GN=his-1 PE=1 SV=2 - [H4_CAEEL]
Q09599	4.09	1	41.46	69.4	cdl-1		Histone RNA hairpin-binding protein OS=Caenorhabditis elegans GN=cdl-1 PE=2 SV=1 - [SLBP_CAEEL]
P91276	2.45	1	59.14	30.3	ima-2	X	Importin subunit alpha-2 OS=Caenorhabditis elegans GN=ima-2 PE=1 SV=1 - [IMA2_CAEEL]
O02365	2.41	1	67.05	53.7	ifa-2		Intermediate filament protein ifa-2 OS=Caenorhabditis elegans GN=ifa-2 PE=1 SV=1 - [IFA2_CAEEL]
P90900	6.24	3	66.59	186.0	ifa-4	X	Intermediate filament protein ifa-4 OS=Caenorhabditis elegans GN=ifa-4 PE=1 SV=2 - [IFA4_CAEEL]
Q19289	14.77	8	67.11	620.5	ifb-1	X	Intermediate filament protein ifb-1 OS=Caenorhabditis elegans GN=ifb-1 PE=1 SV=1 - [IFB1_CAEEL]
Q19286	33.89	15	61.57	1449.6	ifb-2	X	Intermediate filament protein ifb-2 OS=Caenorhabditis elegans GN=ifb-2 PE=1 SV=1 - [IFB2_CAEEL]
Q21067	22.51	13	70.06	1025.9	ifc-2	X	Intermediate filament protein ifc-2 OS=Caenorhabditis elegans GN=ifc-2 PE=1 SV=3 - [IFC2_CAEEL]
Q19782	2.03	1	51.55	76.8	ifd-2	X	Intermediate filament protein ifd-2 OS=Caenorhabditis elegans GN=ifd-2 PE=2 SV=1 - [IFD2_CAEEL]
Q21926	5.08	5	129.93	232.7	irs-1	X	Isoleucyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=irs-1 PE=2 SV=1 - [SYIC_CAEEL]
P34540	4.42	3	91.84	187.9	unc-116	X	Kinesin heavy chain OS=Caenorhabditis elegans GN=unc-116 PE=2 SV=2 - [KINH_CAEEL]
P46822	1.85	1	60.19	37.6	klc-2		Kinesin light chain OS=Caenorhabditis elegans GN=klc-2 PE=2 SV=2 - [KLC_CAEEL]
Q27888	6.01	2	36.04	146.0	ldh-1		L-lactate dehydrogenase OS=Caenorhabditis elegans GN=ldh-1 PE=2 SV=1 - [LDH_CAEEL]
Q21313	0.98	3	403.97	183.5	epi-1		Laminin-like protein epi-1 OS=Caenorhabditis elegans GN=epi-1 PE=1 SV=1 - [EPI1_CAEEL]
Q18823	0.61	1	181.10	42.2	lam-2	X	Laminin-like protein lam-2 OS=Caenorhabditis elegans GN=lam-2 PE=1 SV=3 - [LAM2_CAEEL]
Q09996	1.85	2	134.43	151.5	lrs-1	X	Leucyl-tRNA synthetase OS=Caenorhabditis elegans GN=lrs-1 PE=2 SV=2 - [SYLC_CAEEL]

O01658	6.28	3	85.97	245.2	T28F2.4		Lysine-specific demethylase NO66 OS=Caenorhabditis elegans GN=T28F2.4 PE=2 SV=2 - [NO66_CAEEL]
Q22099	5.94	3	65.10	196.8	krs-1	x	Lysyl-tRNA synthetase OS=Caenorhabditis elegans GN=krs-1 PE=2 SV=1 - [SYK_CAEEL]
Q9N5A1	4.04	1	22.17	29.1	mdt-20		Mediator of RNA polymerase II transcription subunit 20 OS=Caenorhabditis elegans GN=mdt-20 PE=3 SV=2 - [MED20_CAEEL]
Q09165	0.38	2	1372.47	115.6	dig-1		Mesocentin OS=Caenorhabditis elegans GN=dig-1 PE=1 SV=2 - [DIG1_CAEEL]
Q20970	11.56	9	101.65	622.2	mrs-1	x	Methionyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=mrs-1 PE=2 SV=1 - [SYMC_CAEEL]
Q9BKU4	13.09	3	29.97	211.7	phb-1	x	Mitochondrial prohibitin complex protein 1 OS=Caenorhabditis elegans GN=phb-1 PE=1 SV=1 - [PHB1_CAEEL]
P50093	8.5	2	32.65	185.7	phb-2	x	Mitochondrial prohibitin complex protein 2 OS=Caenorhabditis elegans GN=phb-2 PE=1 SV=2 - [PHB2_CAEEL]
Q09591	0.72	1	140.25	34.7	mix-1	x	Mitotic chromosome and X-chromosome-associated protein mix-1 OS=Caenorhabditis elegans GN=mix-1
Q23223	2.83	2	116.30	144.3	mtr-4		mRNA transport homolog 4 OS=Caenorhabditis elegans GN=mtr-4 PE=2 SV=1 - [MTR4_CAEEL]
P34712	0.98	1	144.97	50.3	pgp-1		Multidrug resistance protein 1 OS=Caenorhabditis elegans GN=pgp-1 PE=2 SV=2 - [MDR1_CAEEL]
O01761	0.09	1	893.70	50.3	unc-89	x	Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89 PE=1 SV=3 - [UNC89_CAEEL]
P02567	22.86	42	223.19	3268.2	let-75	x	Myosin-1 OS=Caenorhabditis elegans GN=let-75 PE=2 SV=3 - [MYO1_CAEEL]
P12845	22.39	39	222.91	2946.9	myo-2	x	Myosin-2 OS=Caenorhabditis elegans GN=myo-2 PE=2 SV=2 - [MYO2_CAEEL]
P12844	10.06	17	225.37	1556.6	myo-3	x	Myosin-3 OS=Caenorhabditis elegans GN=myo-3 PE=2 SV=1 - [MYO3_CAEEL]
P02566	45.78	92	224.99	14347.6	unc-54	x	Myosin-4 OS=Caenorhabditis elegans GN=unc-54 PE=4 SV=1 - [MYO4_CAEEL]
P53014	7.19	1	17.13	88.3	mlc-3		Myosin, essential light chain OS=Caenorhabditis elegans GN=mlc-3 PE=1 SV=1 - [MLE_CAEEL]
Q21986	1.25	1	109.16	133.7	R13F6.10		N-terminal acetyltransferase B complex subunit NAA25 homolog OS=Caenorhabditis elegans GN=R13F6.10
Q86S66	7.11	1	22.06	60.5	Y65B4BR.5 / icd-2/ $\alpha$ NAC	x	Nascent polypeptide-associated complex subunit alpha OS=Caenorhabditis elegans GN=Y65B4BR.5 PE=1 SV=1 - [NACA_CAEEL]
Q9XVK5	8.89	1	21.09	129.1	ubc-12		NEDD8-conjugating enzyme ubc-12 OS=Caenorhabditis elegans GN=ubc-12 PE=2 SV=1 - [UBC12_CAEEL]
P46581	4.17	1	21.83	42.3	cnd-1		Neurogenic differentiation factor 1 OS=Caenorhabditis elegans GN=cnd-1 PE=2 SV=1 - [NDF1_CAEEL]
Q21568	17.19	1	13.99	48.0	M28.5	x	NHP2-like protein 1 homolog OS=Caenorhabditis elegans GN=M28.5 PE=2 SV=1 - [NH2L1_CAEEL]
Q9N4M4	20.91	24	955.90	1649.6	anc-1		Nuclear anchorage protein 1 OS=Caenorhabditis elegans GN=anc-1 PE=1 SV=3 - [ANC1_CAEEL]
Q22127	1.76	1	52.41	42.1	nhr-40		Nuclear hormone receptor family member nhr-40 OS=Caenorhabditis elegans GN=nhr-40 PE=2 SV=3 - [NHR40_CAEEL]
O76840	0.42	1	237.45	54.7	mig-6		Papilin OS=Caenorhabditis elegans GN=mig-6 PE=1 SV=1 - [PPN1_CAEEL]
P10567	33.45	27	101.89	2771.8	unc-15	x	Paramyosin OS=Caenorhabditis elegans GN=unc-15 PE=1 SV=1 - [MYSP_CAEEL]
P52018	7.65	1	20.18	86.0	cyn-11		Peptidyl-prolyl cis-trans isomerase 11 OS=Caenorhabditis elegans GN=cyn-11 PE=2 SV=1 - [CYP11_CAEEL]
Q19713	7.95	4	66.02	287.3	frs-2		Phenylalanyl-tRNA synthetase beta chain OS=Caenorhabditis elegans GN=frs-2 PE=1 SV=2 - [SYFB_CAEEL]
P40614	15.29	5	36.65	273.0	F01G4.6	x	Phosphate carrier protein, mitochondrial OS=Caenorhabditis elegans GN=F01G4.6 PE=2 SV=1 - [MPCP_CAEEL]
Q21109	15.64	4	35.47	279.4	K02A11.3		Poly(U)-specific endoribonuclease homolog OS=Caenorhabditis elegans GN=K02A11.3 PE=1 SV=1 - [ENDOU_CAEEL]
Q8ITY4	5.07	1	16.00	26.8	C50D2.5		Pre-mRNA branch site p14-like protein OS=Caenorhabditis elegans GN=C50D2.5 PE=2 SV=2 - [PM14_CAEEL]
Q10051	2.64	1	53.18	25.4	T10F2.4		Pre-mRNA-processing factor 19 homolog OS=Caenorhabditis elegans GN=T10F2.4 PE=2 SV=2 - [PRP19_CAEEL]
P34369	0.43	1	271.85	81.8	prp-8		Pre-mRNA-splicing factor 8 homolog OS=Caenorhabditis elegans GN=prp-8 PE=1 SV=1 - [PRP8_CAEEL]

O17071	10.1	3	45.83	173.5	rpt-4	X	Probable 26S protease regulatory subunit 10B OS=Caenorhabditis elegans GN=rpt-4 PE=1 SV=2 - [PRS10_CAEEL]
O16368	8.13	3	49.69	414.3	rpt-2	X	Probable 26S protease regulatory subunit 4 OS=Caenorhabditis elegans GN=rpt-2 PE=2 SV=1 - [PRS4_CAEEL]
P46502	4.35	1	46.33	35.2	rpt-3	X	Probable 26S protease regulatory subunit 6B OS=Caenorhabditis elegans GN=rpt-3 PE=2 SV=1 - [PRS6B_CAEEL]
Q9XWV5	9.62	1	17.85	88.1	Y37D8A.18		Probable 28S ribosomal protein S10, mitochondrial OS=Caenorhabditis elegans GN=Y37D8A.18 PE=2 SV=1 - [RT10_CAEEL]
Q21217	25.67	11	53.02	1144.9	gta-1	X	Probable 4-aminobutyrate aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=gta-1 PE=1 SV=1 - [GABT_CAEEL]
P34455	14.67	11	83.99	971.4	aco-2	X	Probable aconitate hydratase, mitochondrial OS=Caenorhabditis elegans GN=aco-2 PE=1 SV=2 - [ACON_CAEEL]
P58798	7.1	1	19.65	39.8	arx-6		Probable actin-related protein 2/3 complex subunit 4 OS=Caenorhabditis elegans GN=arx-6 PE=3 SV=1 - [ARPC4_CAEEL]
Q09527	5.49	1	21.01	38.9	E02H1.6		Probable adenylate kinase isoenzyme 6 OS=Caenorhabditis elegans GN=E02H1.6 PE=2 SV=2 - [KAD6_CAEEL]
Q20140	15.71	2	22.58	263.4	F38B2.4		Probable adenylate kinase isoenzyme F38B2.4 OS=Caenorhabditis elegans GN=F38B2.4 PE=2 SV=1 - [KAD1_CAEEL]
Q09629	7.66	1	24.89	37.9	ZK673.2		Probable adenylate kinase isoenzyme ZK673.2 OS=Caenorhabditis elegans GN=ZK673.2 PE=2 SV=1 - [KADY_CAEEL]
Q10454	40.66	14	44.14	2472.6	F46H5.3	X	Probable arginine kinase F46H5.3 OS=Caenorhabditis elegans GN=F46H5.3 PE=1 SV=2 - [KARG1_CAEEL]
Q27535	16.94	5	40.36	378.1	ZC434.8	X	Probable arginine kinase ZC434.8 OS=Caenorhabditis elegans GN=ZC434.8 PE=1 SV=1 - [KARG2_CAEEL]
Q19825	3.09	2	80.84	91.2	rrt-1		Probable arginyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=rrt-1 PE=2 SV=2 - [SYRC_CAEEL]
Q22067	5.64	2	45.46	212.3	T01C8.5		Probable aspartate aminotransferase, cytoplasmic OS=Caenorhabditis elegans GN=T01C8.5 PE=2 SV=1 - [AATC_CAEEL]
Q18803	18.32	2	14.82	89.1	asg-2		Probable ATP synthase subunit g 2, mitochondrial OS=Caenorhabditis elegans GN=asg-2 PE=2 SV=1 - [ATPL2_CAEEL]
P34640	4.15	2	65.79	126.5	ZK512.2		Probable ATP-dependent RNA helicase DDX55 homolog OS=Caenorhabditis elegans GN=ZK512.2 PE=2 SV=2 - [DDX55_CAEEL]
P34575	14.1	6	51.51	729.0	cts-1	X	Probable citrate synthase, mitochondrial OS=Caenorhabditis elegans GN=cts-1 PE=1 SV=1 - [CISY_CAEEL]
P34574	18.74	24	191.42	1655.0	chc-1	X	Probable clathrin heavy chain 1 OS=Caenorhabditis elegans GN=chc-1 PE=3 SV=1 - [CLH_CAEEL]
Q20168	1.8	2	111.04	90.8	F38E11.5		Probable coatomer subunit beta' OS=Caenorhabditis elegans GN=F38E11.5 PE=2 SV=3 - [COPB2_CAEEL]
Q22498	2.64	2	96.24	99.2	T14G10.5	X	Probable coatomer subunit gamma OS=Caenorhabditis elegans GN=T14G10.5 PE=2 SV=1 - [COPG_CAEEL]
Q23500	5.07	3	96.60	183.4	aco-1		Probable cytoplasmic aconitate hydratase OS=Caenorhabditis elegans GN=aco-1 PE=1 SV=1 - [ACOC_CAEEL]
P54889	1.13	1	86.47	38.4	alh-13		Probable delta-1-pyrroline-5-carboxylate synthase OS=Caenorhabditis elegans GN=alh-13 PE=2 SV=1 - [ALH13_CAEEL]
Q19366	2.44	1	50.37	20.5	F12F6.7		Probable DNA polymerase delta small subunit OS=Caenorhabditis elegans GN=F12F6.7 PE=2 SV=1 - [DPOD2_CAEEL]
Q23670	14.01	19	172.23	1312.5	K12D12.1	X	Probable DNA topoisomerase 2 OS=Caenorhabditis elegans GN=K12D12.1 PE=2 SV=2 - [TOP2_CAEEL]
Q93615	8.73	2	34.43	188.2	F27D4.1	X	Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F27D4.1
Q9U2H9	21.67	4	28.16	300.0	Y41E3.10	X	Probable elongation factor 1-beta/1-delta 2 OS=Caenorhabditis elegans GN=Y41E3.10 PE=1 SV=4 - [EF1B2_CAEEL]
P54412	21.86	8	44.36	487.0	F17C11.9	X	Probable elongation factor 1-gamma OS=Caenorhabditis elegans GN=F17C11.9 PE=2 SV=1 - [EF1G_CAEEL]
P34559	22.22	5	31.15	250.8	ech-6	X	Probable enoyl-CoA hydratase, mitochondrial OS=Caenorhabditis elegans GN=ech-6 PE=1 SV=1 - [ECHM_CAEEL]
Q22017	2.89	1	58.93	41.5	R53.1		Probable FAD synthase OS=Caenorhabditis elegans GN=R53.1 PE=2 SV=1 - [FLAD1_CAEEL]
O17214	2.4	1	53.61	39.3	fum-1	X	Probable fumarate hydratase, mitochondrial OS=Caenorhabditis elegans GN=fum-1 PE=1 SV=1 - [FUMH_CAEEL]
Q09610	15.56	2	20.43	284.6	lec-8		Probable galactin lec-8 OS=Caenorhabditis elegans GN=lec-8 PE=2 SV=2 - [LEC8_CAEEL]
P41992	2.99	1	37.20	110.1	ggbt-1		Probable geranylgeranyl transferase type-2 subunit beta OS=Caenorhabditis elegans GN=ggbt-1 PE=2 SV=2 - [GGTB2_CAEEL]

O62431	2.29	2	88.21	126.2	ers-1	X	Probable glutaminyl-tRNA synthetase OS=Caenorhabditis elegans GN=ers-1 PE=3 SV=1 - [SYQ_CAEEL]
O62327	29.45	5	18.14	249.4	R05H10.5		Probable glutathione peroxidase R05H10.5 OS=Caenorhabditis elegans GN=R05H10.5 PE=2 SV=1 - [GPX2_CAEEL]
Q09596	9.66	2	23.24	78.4	gst-5		Probable glutathione S-transferase 5 OS=Caenorhabditis elegans GN=gst-5 PE=1 SV=1 - [GST5_CAEEL]
P91253	27.67	5	23.07	322.6	gst-7	X	Probable glutathione S-transferase 7 OS=Caenorhabditis elegans GN=gst-7 PE=2 SV=1 - [GST7_CAEEL]
Q09607	35.24	7	23.86	315.6	gst-36		Probable glutathione S-transferase gst-36 OS=Caenorhabditis elegans GN=gst-36 PE=2 SV=2 - [GST36_CAEEL]
P34517	5.87	2	42.76	171.5	gpdh-2		Probable glycerol-3-phosphate dehydrogenase 2 OS=Caenorhabditis elegans GN=gpdh-2 PE=2 SV=2 - [GPDH2_CAEEL]
Q9U2D9	4.17	3	76.41	198.0	gsy-1	X	Probable glycogen [starch] synthase OS=Caenorhabditis elegans GN=gsy-1 PE=2 SV=1 - [GYS_CAEEL]
P46548	9.11	3	50.86	139.8	nmt-1		Probable glycylopeptide N-tetradecanoyltransferase OS=Caenorhabditis elegans GN=nmt-1 PE=2 SV=1 - [NMT_CAEEL]
P90916	7.91	3	47.14	155.6	lin-53	X	Probable histone-binding protein lin-53 OS=Caenorhabditis elegans GN=lin-53 PE=1 SV=2 - [LIN53_CAEEL]
Q9U2M4	2.8	1	50.47	55.0	Y38F1A.6	X	Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y38F1A.6 PE=2 SV=1
Q93714	22.35	6	38.44	268.0	F43G9.1	X	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F43G9.1
Q93353	4.75	2	41.53	102.7	C37E2.1	X	Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C37E2.1
Q21929	4.78	1	27.20	51.5	dhs-21		Probable L-xylulose reductase OS=Caenorhabditis elegans GN=dhs-21 PE=2 SV=2 - [DCXR_CAEEL]
O02640	43.4	9	35.10	1097.5	mdh-1	X	Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1 - [MDHM_CAEEL]
Q22347	15.59	5	44.79	488.8	acdh-10		Probable medium-chain specific acyl-CoA dehydrogenase 10, mitochondrial OS=Caenorhabditis elegans GN=acdh-10
Q17693	2.41	1	75.44	60.3	C06A8.1		Probable methylenetetrahydrofolate reductase OS=Caenorhabditis elegans GN=C06A8.1 PE=2 SV=2 - [MTHR_CAEEL]
P52713	4.4	2	56.43	110.3	alh-8	X	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Caenorhabditis elegans GN=alh-8
Q9N2W7	7.53	1	17.06	68.8	Y94H6A.8		Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Caenorhabditis elegans GN=Y94H6A.8
Q18359	19.33	3	17.32	137.7	C33A12.1	X	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Caenorhabditis elegans GN=C33A12.1
Q94360	5.03	1	21.90	84.5	nduf-7		Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Caenorhabditis elegans GN=nduf-7
O44411	1.32	1	78.44	38.0	T07A9.9		Probable nucleolar GTP-binding protein 1 OS=Caenorhabditis elegans GN=T07A9.9 PE=2 SV=1 - [NOG1_CAEEL]
Q18040	9.72	3	46.42	325.6	C16A3.10	X	Probable ornithine aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=3 - [OAT_CAEEL]
Q21824	22.12	5	24.92	248.1	prdx-3	X	Probable peroxiredoxin prdx-3 OS=Caenorhabditis elegans GN=prdx-3 PE=1 SV=1 - [TDX1_CAEEL]
P91427	10.31	3	44.09	253.5	pgk-1	X	Probable phosphoglycerate kinase OS=Caenorhabditis elegans GN=pgk-1 PE=1 SV=1 - [PGK_CAEEL]
O62515	3.21	1	35.70	39.9	ZK550.6		Probable phytyl-CoA dioxygenase OS=Caenorhabditis elegans GN=ZK550.6 PE=2 SV=2 - [PAHX_CAEEL]
Q11067	3.18	1	47.70	44.9	tag-320		Probable protein disulfide-isomerase A6 OS=Caenorhabditis elegans GN=tag-320 PE=2 SV=1 - [PDIA6_CAEEL]
P49595	6.31	3	53.11	139.4	F42G9.1	X	Probable protein phosphatase 2C F42G9.1 OS=Caenorhabditis elegans GN=F42G9.1 PE=2 SV=2 - [PP2C1_CAEEL]
Q19537	5.04	3	73.16	161.5	rpa-1	X	Probable replication factor A 73 kDa subunit OS=Caenorhabditis elegans GN=rpa-1 PE=1 SV=1 - [RFA1_CAEEL]
Q20496	6.28	1	21.91	73.9	rhi-1		Probable rho GDP-dissociation inhibitor OS=Caenorhabditis elegans GN=rhi-1 PE=2 SV=1 - [GDIR_CAEEL]
P91478	10.5	2	26.94	95.2	T20F5.3		Probable ribosome-recycling factor, mitochondrial OS=Caenorhabditis elegans GN=T20F5.3 PE=2 SV=2 - [RRFM_CAEEL]
O17680	28.78	9	43.55	495.0	sams-1		Probable S-adenosylmethionine synthase 1 OS=Caenorhabditis elegans GN=sams-1 PE=1 SV=1 - [METK1_CAEEL]
Q09543	12.2	6	66.11	358.7	paa-1	X	Probable serine/threonine-protein phosphatase PP2A regulatory subunit OS=Caenorhabditis elegans GN=paa-1

Q18678	4.31	2	55.19	71.1	srs-2	X	Probable seryl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=srs-2 PE=3 SV=1 - [SYSC_CAEEL]
P91918	9.38	2	16.73	61.2	snr-2		Probable small nuclear ribonucleoprotein-associated protein B OS=Caenorhabditis elegans GN=snr-2 PE=2 SV=1 - [RSMB_CAEEL]
Q23121	14.1	5	35.02	180.8	rsp-1	X	Probable splicing factor, arginine/serine-rich 1 OS=Caenorhabditis elegans GN=rsp-1 PE=2 SV=1 - [RSP1_CAEEL]
Q23120	4.27	1	32.40	96.4	rsp-2		Probable splicing factor, arginine/serine-rich 2 OS=Caenorhabditis elegans GN=rsp-2 PE=2 SV=1 - [RSP2_CAEEL]
Q9NEW6	25.58	6	28.66	401.2	rsp-3	X	Probable splicing factor, arginine/serine-rich 3 OS=Caenorhabditis elegans GN=rsp-3 PE=1 SV=2 - [RSP3_CAEEL]
Q09511	19.39	3	22.57	139.2	rsp-4		Probable splicing factor, arginine/serine-rich 4 OS=Caenorhabditis elegans GN=rsp-4 PE=2 SV=1 - [RSP4_CAEEL]
Q18409	19.55	2	20.47	202.2	rsp-6		Probable splicing factor, arginine/serine-rich 6 OS=Caenorhabditis elegans GN=rsp-6 PE=2 SV=1 - [RSP6_CAEEL]
P53588	12.64	5	47.39	453.6	F47B10.1	X	Probable succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=F47B10.1
P53596	15.22	4	33.78	298.7	C05G5.4	X	Probable succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=C05G5.4
Q09450	1.73	1	56.08	49.2	C05C10.3	X	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase, mitochondrial OS=Caenorhabditis elegans GN=C05C10.3 PE=2
Q09444	9.97	3	37.10	173.9	ubh-4		Probable ubiquitin carboxyl-terminal hydrolase ubh-4 OS=Caenorhabditis elegans GN=ubh-4 PE=2 SV=2 - [UBH4_CAEEL]
Q18493	2.27	1	53.46	112.0	C36A4.4		Probable UDP-N-acetylglucosamine pyrophosphorylase OS=Caenorhabditis elegans GN=C36A4.4 PE=2 SV=2 - [UAP1_CAEEL]
Q17413	5.24	1	28.37	33.4	B0001.4		Probable uridine-cytidine kinase OS=Caenorhabditis elegans GN=B0001.4 PE=2 SV=2 - [UCK_CAEEL]
Q19626	21.79	7	54.72	719.8	vha-12	X	Probable V-type proton ATPase subunit B OS=Caenorhabditis elegans GN=vha-12 PE=1 SV=1 - [VATB_CAEEL]
P91303	11.9	1	14.48	174.2	vha-10		Probable V-type proton ATPase subunit G OS=Caenorhabditis elegans GN=vha-10 PE=2 SV=1 - [VATG_CAEEL]
Q22494	2.13	1	54.18	35.0	vha-15	X	Probable V-type proton ATPase subunit H 2 OS=Caenorhabditis elegans GN=vha-15 PE=2 SV=1 - [VATH2_CAEEL]
Q21752	30.04	6	29.94	284.2	R05G6.7	X	Probable voltage-dependent anion-selective channel OS=Caenorhabditis elegans GN=R05G6.7 PE=2 SV=2 - [VDAC_CAEEL]
Q9XW16	11.36	1	14.25	81.6	pfn-1	X	Profilin-1 OS=Caenorhabditis elegans GN=pfn-1 PE=2 SV=1 - [PROF1_CAEEL]
Q20025	11.45	1	14.24	61.5	pfn-2		Profilin-2 OS=Caenorhabditis elegans GN=pfn-2 PE=2 SV=3 - [PROF2_CAEEL]
O02115	3.04	1	29.02	51.2	pcn-1	X	Proliferating cell nuclear antigen OS=Caenorhabditis elegans GN=pcn-1 PE=1 SV=3 - [PCNA_CAEEL]
Q20065	1.67	1	61.49	49.1	phy-2		Prolyl 4-hydroxylase subunit alpha-2 OS=Caenorhabditis elegans GN=phy-2 PE=1 SV=1 - [P4HA2_CAEEL]
Q19842	19.34	9	79.71	402.7	pcca-1	X	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Caenorhabditis elegans GN=pcca-1 PE=1 SV=1 - [PCCA_CAEEL]
O17586	5.28	1	27.03	49.7	pas-1	X	Proteasome subunit alpha type-6 OS=Caenorhabditis elegans GN=pas-1 PE=1 SV=1 - [PSA6_CAEEL]
Q95005	4.74	1	28.22	133.0	pas-4	X	Proteasome subunit alpha type-7 OS=Caenorhabditis elegans GN=pas-4 PE=1 SV=1 - [PSA7_CAEEL]
Q23237	13.73	2	22.68	224.0	pbs-3		Proteasome subunit beta type-3 OS=Caenorhabditis elegans GN=pbs-3 PE=1 SV=1 - [PSB3_CAEEL]
Q17967	7.84	3	53.40	213.9	pdi-1	X	Protein disulfide-isomerase 1 OS=Caenorhabditis elegans GN=pdi-1 PE=3 SV=1 - [PDI1_CAEEL]
Q17770	2.64	1	55.12	69.2	pdi-2	X	Protein disulfide-isomerase 2 OS=Caenorhabditis elegans GN=pdi-2 PE=1 SV=1 - [PDI2_CAEEL]
O44400	21.76	9	61.41	547.0	F37C4.5	X	Protein F37C4.5 OS=Caenorhabditis elegans GN=F37C4.5 PE=1 SV=3 - [F37C4_CAEEL]
P90947	1.19	1	103.93	74.0	hmp-1		Protein humpback-1 OS=Caenorhabditis elegans GN=hmp-1 PE=1 SV=2 - [HMP1_CAEEL]
Q23536	20	2	15.09	107.2	lgg-2		Protein lgg-2 OS=Caenorhabditis elegans GN=lgg-2 PE=1 SV=1 - [LGG2_CAEEL]
P37806	3.89	2	62.69	57.6	unc-87		Protein unc-87 OS=Caenorhabditis elegans GN=unc-87 PE=1 SV=3 - [UNC87_CAEEL]
P34511	1.78	1	71.28	50.3	vms-1		Protein vms-1 OS=Caenorhabditis elegans GN=vms-1 PE=2 SV=2 - [VMS1_CAEEL]



P46562	2.07	1	56.98	23.2	alh-9		Putative aldehyde dehydrogenase family 7 member A1 homolog OS=Caenorhabditis elegans GN=alh-9 PE=2 SV=2
O01739	4.7	1	42.48	89.6	F20H11.5		Putative D-amino-acid oxidase 1 OS=Caenorhabditis elegans GN=F20H11.5 PE=1 SV=1 - [OXDA1_CAEEL]
Q19264	9.24	2	33.07	209.9	F09E5.3		Putative deoxyribose-phosphate aldolase OS=Caenorhabditis elegans GN=F09E5.3 PE=2 SV=1 - [DEOC_CAEEL]
Q93341	9.52	2	21.59	105.5	dhfr-1		Putative dihydrofolate reductase OS=Caenorhabditis elegans GN=dhfr-1 PE=2 SV=1 - [DYR_CAEEL]
P91917	36.71	11	44.32	1183.3	tag-210		Putative GTP-binding protein tag-210 OS=Caenorhabditis elegans GN=tag-210 PE=2 SV=1 - [TG210_CAEEL]
O17919	4.27	2	50.18	103.8	K01G5.5		Putative H/ACA ribonucleoprotein complex subunit 4 OS=Caenorhabditis elegans GN=K01G5.5 PE=2 SV=1 - [DKC1_CAEEL]
Q9XWV2	11.21	6	65.40	288.9	Y37D8A.2		Putative phospholipase B-like 1 OS=Caenorhabditis elegans GN=Y37D8A.2 PE=1 SV=1 - [PLBL1_CAEEL]
Q20875	1.62	1	84.34	75.8	F56D2.6		Putative pre-mRNA-splicing factor ATP-dependent RNA helicase F56D2.6 OS=Caenorhabditis elegans GN=F56D2.6 PE=2 SV=1
Q21950	1.39	1	66.65	29.3	R11G10.2		Putative selenium-binding protein OS=Caenorhabditis elegans GN=R11G10.2 PE=2 SV=1 - [SBP_CAEEL]
Q09541	4.8	6	150.99	411.7	F21H12.6		Putative subtilase-type proteinase F21H12.6 OS=Caenorhabditis elegans GN=F21H12.6 PE=2 SV=1 - [YQS6_CAEEL]
P52652	3.25	1	34.85	117.0	T24H10.1		Putative transcription elongation factor S-II OS=Caenorhabditis elegans GN=T24H10.1 PE=3 SV=1 - [TFS2_CAEEL]
Q9U2G0	0.47	1	243.68	65.6	Y46G5A.4		Putative U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Caenorhabditis elegans GN=Y46G5A.4 PE=3 SV=1
O17732	18.38	19	129.20	1090.1	pyc-1		Pyruvate carboxylase 1 OS=Caenorhabditis elegans GN=pyc-1 PE=1 SV=1 - [PYC1_CAEEL]
O44451	5.4	2	38.12	102.7	C04C3.3		Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C04C3.3 PE=1
P34342	2.29	1	105.59	45.6	ran-2		Ran GTPase-activating protein 2 OS=Caenorhabditis elegans GN=ran-2 PE=2 SV=3 - [RGP2_CAEEL]
Q22038	5.73	1	21.62	34.9	rho-1	x	Ras-like GTP-binding protein rhoA OS=Caenorhabditis elegans GN=rho-1 PE=2 SV=1 - [RHO1_CAEEL]
Q8MXS1	5.42	1	22.61	83.0	rab-18		Ras-related protein Rab-18 OS=Caenorhabditis elegans GN=rab-18 PE=2 SV=1 - [RAB18_CAEEL]
Q94986	5.02	1	24.74	161.5	rab-3		Ras-related protein Rab-3 OS=Caenorhabditis elegans GN=rab-3 PE=2 SV=1 - [RAB3_CAEEL]
Q03604	3.81	3	88.91	208.1	rnr-1	x	Ribonucleoside-diphosphate reductase large subunit OS=Caenorhabditis elegans GN=rnr-1 PE=2 SV=1 - [RIR1_CAEEL]
P42170	5.51	2	44.26	72.4	rnr-2		Ribonucleoside-diphosphate reductase small chain OS=Caenorhabditis elegans GN=rnr-2 PE=2 SV=1 - [RIR2_CAEEL]
Q22053	32.67	11	36.36	1511.2	fib-1	x	rRNA 2'-O-methyltransferase fibrillar OS=Caenorhabditis elegans GN=fib-1 PE=2 SV=1 - [FBRL_CAEEL]
P50432	12.23	6	55.73	477.5	mel-32		Serine hydroxymethyltransferase OS=Caenorhabditis elegans GN=mel-32 PE=1 SV=2 - [GLYC_CAEEL]
Q9NB31	3.02	1	55.60	50.8	cst-1		Serine/threonine-protein kinase cst-1 OS=Caenorhabditis elegans GN=cst-1 PE=2 SV=1 - [CST1_CAEEL]
Q19848	2.13	2	67.31	128.4	vrk-1		Serine/threonine-protein kinase VRK1 OS=Caenorhabditis elegans GN=vrk-1 PE=1 SV=1 - [VRK1_CAEEL]
P48727	12.01	3	37.77	309.9	gsp-2		Serine/threonine-protein phosphatase PP1-beta OS=Caenorhabditis elegans GN=gsp-2 PE=2 SV=1 - [GLC7B_CAEEL]
O16927	12.93	1	13.19	84.8	F25G6.8		Signal recognition particle 14 kDa protein OS=Caenorhabditis elegans GN=F25G6.8 PE=2 SV=1 - [SRP14_CAEEL]
Q18212	16.71	6	48.46	383.0	hel-1	x	Spliceosome RNA helicase DDX39B homolog OS=Caenorhabditis elegans GN=hel-1 PE=2 SV=1 - [DX39B_CAEEL]
Q20363	80.5	9	17.83	1208.6	sip-1	x	Stress-induced protein 1 OS=Caenorhabditis elegans GN=sip-1 PE=1 SV=1 - [SIP1_CAEEL]
Q09508	3.72	2	70.35	124.5	sdha-1	x	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Caenorhabditis elegans GN=sdha-1
Q09545	12.42	3	32.87	85.9	sdhb-1	x	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Caenorhabditis elegans GN=sdhb-1
P31161	21.27	4	24.52	212.5	sod-2		Superoxide dismutase [Mn] 1, mitochondrial OS=Caenorhabditis elegans GN=sod-2 PE=1 SV=1 - [SODM1_CAEEL]
P34703	0.72	1	175.71	34.8	emb-5		Suppressor of Ty 6 homolog OS=Caenorhabditis elegans GN=emb-5 PE=1 SV=1 - [SPT6H_CAEEL]

P41988	4.01	3	58.77	161.9	cct-1	X	T-complex protein 1 subunit alpha OS=Caenorhabditis elegans GN=cct-1 PE=2 SV=2 - [TCPA_CAEEL]
P47207	4.54	2	56.94	100.2	cct-2		T-complex protein 1 subunit beta OS=Caenorhabditis elegans GN=cct-2 PE=1 SV=2 - [TCPB_CAEEL]
P47208	16.3	4	58.35	301.0	cct-4	X	T-complex protein 1 subunit delta OS=Caenorhabditis elegans GN=cct-4 PE=2 SV=1 - [TCPD_CAEEL]
P47209	2.21	1	59.37	119.3	cct-5	X	T-complex protein 1 subunit epsilon OS=Caenorhabditis elegans GN=cct-5 PE=1 SV=1 - [TCPE_CAEEL]
Q9N358	4.01	2	59.70	115.0	cct-8		T-complex protein 1 subunit theta OS=Caenorhabditis elegans GN=cct-8 PE=1 SV=3 - [TCPQ_CAEEL]
P46550	7.05	2	58.87	59.2	cct-6	X	T-complex protein 1 subunit zeta OS=Caenorhabditis elegans GN=cct-6 PE=1 SV=1 - [TCPZ_CAEEL]
Q95Q95	0.26	1	306.33	95.5	let-363		Target of rapamycin homolog OS=Caenorhabditis elegans GN=let-363 PE=2 SV=3 - [TOR_CAEEL]
Q20683	5.59	1	19.64	36.5	F52H3.5		Tetratricopeptide repeat protein 36 homolog OS=Caenorhabditis elegans GN=F52H3.5 PE=2 SV=1 - [TTC36_CAEEL]
P52709	4.28	3	84.36	171.7	trs-1	X	Threonyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=trs-1 PE=2 SV=1 - [SYTC_CAEEL]
Q18885	11.8	1	17.49	113.4	icd-1 / $\beta$ NAC		Transcription factor BTF3 homolog OS=Caenorhabditis elegans GN=icd-1 PE=1 SV=1 - [BTF3_CAEEL]
P34586	0.78	1	118.03	32.5	trp-1		Transient-receptor-potential-like protein OS=Caenorhabditis elegans GN=trp-1 PE=2 SV=3 - [TRPL_CAEEL]
P54812	7.53	4	89.58	359.1	cdc-48.2	X	Transitional endoplasmic reticulum ATPase homolog 2 OS=Caenorhabditis elegans GN=cdc-48.2 PE=1 SV=2 - [TERA2_CAEEL]
P34617	1.09	1	72.22	163.5	ZK1236.1		Translation factor GUF1 homolog, mitochondrial OS=Caenorhabditis elegans GN=ZK1236.1 PE=2 SV=2 - [GUF1_CAEEL]
Q93573	60.22	11	20.53	1169.8	tct-1	X	Translationally-controlled tumor protein homolog OS=Caenorhabditis elegans GN=tct-1 PE=1 SV=1 - [TCTP_CAEEL]
Q22288	6.15	1	14.49	77.4	ttr-15		Transthyretin-like protein 15 OS=Caenorhabditis elegans GN=ttr-15 PE=2 SV=1 - [TTR15_CAEEL]
P34500	30.41	5	15.69	258.8	ttr-2		Transthyretin-like protein 2 OS=Caenorhabditis elegans GN=ttr-2 PE=1 SV=1 - [TTR2_CAEEL]
Q10657	23.08	4	26.56	308.5	tpi-1		Triosephosphate isomerase OS=Caenorhabditis elegans GN=tpi-1 PE=1 SV=2 - [TPIS_CAEEL]
P34690	39.73	14	49.88	2509.5	tba-2	X	Tubulin alpha-2 chain OS=Caenorhabditis elegans GN=tba-2 PE=2 SV=1 - [TBA2_CAEEL]
P91910	9.33	3	50.08	284.1	mec-12		Tubulin alpha-3 chain OS=Caenorhabditis elegans GN=mec-12 PE=1 SV=1 - [TBA3_CAEEL]
P52275	68.67	25	50.31	5187.9	tbb-2	X	Tubulin beta-2 chain OS=Caenorhabditis elegans GN=tbb-2 PE=2 SV=1 - [TBB2_CAEEL]
Q23551	1.84	11	788.47	482.1	unc-22		Twitchin OS=Caenorhabditis elegans GN=unc-22 PE=1 SV=3 - [UNC22_CAEEL]
Q9XTQ6	2.22	1	66.71	142.8	tbh-1		Tyramine beta-hydroxylase OS=Caenorhabditis elegans GN=tbh-1 PE=1 SV=2 - [TBH1_CAEEL]
Q17361	2.86	1	55.84	152.3	usp-14	X	Ubiquitin carboxyl-terminal hydrolase 14 OS=Caenorhabditis elegans GN=usp-14 PE=2 SV=2 - [UBP14_CAEEL]
Q7JKC3	1.67	2	131.51	129.5	usp-7		Ubiquitin carboxyl-terminal hydrolase 7 OS=Caenorhabditis elegans GN=usp-7 PE=2 SV=1 - [UBP7_CAEEL]
Q09475	8.63	12	193.97	799.3	C28H8.3	X	Uncharacterized helicase C28H8.3 OS=Caenorhabditis elegans GN=C28H8.3 PE=2 SV=2 - [YP93_CAEEL]
Q21276	35.39	13	54.48	1317.9	K07C5.4	X	Uncharacterized NOP5 family protein K07C5.4 OS=Caenorhabditis elegans GN=K07C5.4 PE=2 SV=1 - [YZVL_CAEEL]
P34255	10.04	4	47.84	406.7	B0303.3	X	Uncharacterized protein B0303.3 OS=Caenorhabditis elegans GN=B0303.3 PE=2 SV=1 - [YKA3_CAEEL]
Q09216	1.12	1	102.06	251.1	B0495.7		Uncharacterized protein B0495.7 OS=Caenorhabditis elegans GN=B0495.7 PE=1 SV=2 - [YP67_CAEEL]
Q11108	2.69	1	35.03	86.8	C03B1.1		Uncharacterized protein C03B1.1 OS=Caenorhabditis elegans GN=C03B1.1 PE=4 SV=1 - [YX01_CAEEL]
Q18594	5.93	1	26.28	90.0	C44B7.5		Uncharacterized protein C44B7.5 OS=Caenorhabditis elegans GN=C44B7.5 PE=1 SV=1 - [YC4B5_CAEEL]
P34467	2.37	1	43.90	36.2	F55H2.7		Uncharacterized protein F55H2.7 OS=Caenorhabditis elegans GN=F55H2.7 PE=2 SV=3 - [YMF7_CAEEL]
P34518	4.39	1	25.87	27.6	K11H3.2		Uncharacterized protein K11H3.2 OS=Caenorhabditis elegans GN=K11H3.2 PE=2 SV=1 - [YM42_CAEEL]

Q22004	4	1	22.95	35.3	R166.3		Uncharacterized protein R166.3 OS=Caenorhabditis elegans GN=R166.3 PE=2 SV=1 - [AMERL_CAEEL]
Q23280	5.14	1	19.42	44.7	ZC395.10	X	Uncharacterized protein ZC395.10 OS=Caenorhabditis elegans GN=ZC395.10 PE=2 SV=1 - [YOCA_CAEEL]
P34748	9.02	1	15.38	35.6	ZK1098.7		Uncharacterized protein ZK1098.7 OS=Caenorhabditis elegans GN=ZK1098.7 PE=2 SV=1 - [YO67_CAEEL]
P34645	4.96	1	15.98	48.1	ZK512.7		Uncharacterized protein ZK512.7 OS=Caenorhabditis elegans GN=ZK512.7 PE=2 SV=1 - [YOQ7_CAEEL]
P30629	9.79	1	16.19	28.9	ZK637.2		Uncharacterized protein ZK637.2 OS=Caenorhabditis elegans GN=ZK637.2 PE=2 SV=2 - [YOU2_CAEEL]
P34546	7.45	1	16.40	81.2	vha-2		V-type proton ATPase 16 kDa proteolipid subunit 2/3 OS=Caenorhabditis elegans GN=vha-2 PE=2 SV=2 - [VATL2_CAEEL]
Q9XW92	9.24	5	66.42	239.1	vha-13		V-type proton ATPase catalytic subunit A OS=Caenorhabditis elegans GN=vha-13 PE=1 SV=3 - [VATA_CAEEL]
Q9XXU9	6.25	2	43.43	161.0	vha-11		V-type proton ATPase subunit C OS=Caenorhabditis elegans GN=vha-11 PE=2 SV=1 - [VATC_CAEEL]
Q9U1Q4	7.14	5	118.85	199.9	vrs-2	X	Valyl-tRNA synthetase OS=Caenorhabditis elegans GN=vrs-2 PE=1 SV=1 - [SYV_CAEEL]
Q94392	5.7	4	91.28	325.7	nsf-1		Vesicle-fusing ATPase OS=Caenorhabditis elegans GN=nsf-1 PE=2 SV=2 - [NSF_CAEEL]
P55155	39.29	69	187.95	11218.5	vit-1	X	Vitellogenin-1 OS=Caenorhabditis elegans GN=vit-1 PE=1 SV=2 - [VIT1_CAEEL]
P05690	64.97	99	187.60	20027.2	vit-2	X	Vitellogenin-2 OS=Caenorhabditis elegans GN=vit-2 PE=1 SV=5 - [VIT2_CAEEL]
Q9N4J2	36.62	58	186.41	6201.7	vit-3	X	Vitellogenin-3 OS=Caenorhabditis elegans GN=vit-3 PE=1 SV=1 - [VIT3_CAEEL]
P18947	34.68	56	186.19	6502.4	vit-4	X	Vitellogenin-4 OS=Caenorhabditis elegans GN=vit-4 PE=1 SV=3 - [VIT4_CAEEL]
P06125	43.54	69	186.32	8720.1	vit-5	X	Vitellogenin-5 OS=Caenorhabditis elegans GN=vit-5 PE=2 SV=2 - [VIT5_CAEEL]
P18948	65.35	98	193.20	20924.4	vit-6	X	Vitellogenin-6 OS=Caenorhabditis elegans GN=vit-6 PE=1 SV=5 - [VIT6_CAEEL]
O16999	2.64	1	50.90	71.0	W03F9.1		Zinc finger protein ZPR1 homolog OS=Caenorhabditis elegans GN=W03F9.1 PE=3 SV=2 - [ZPR1_CAEEL]
Q21059	1.98	1	66.22	37.7	hch-1		Zinc metalloproteinase nas-34 OS=Caenorhabditis elegans GN=hch-1 PE=1 SV=1 - [NAS34_CAEEL]
Q18206	1.78	1	69.42	61.4	nas-36		Zinc metalloproteinase nas-36 OS=Caenorhabditis elegans GN=nas-36 PE=1 SV=2 - [NAS36_CAEEL]

Table S2

Uniprot ID	Coverage [%]	# Peptides	MW [kDa]	Score	Gene name	Description
P41932	37.1	10	28.17	796.9	par-5	14-3-3-like protein 1 OS=Caenorhabditis elegans GN=par-5 PE=1 SV=2 - [14331_CAEEL]
Q20655	36.29	8	28.05	641.5	ftt-2	14-3-3-like protein 2 OS=Caenorhabditis elegans GN=ftt-2 PE=1 SV=1 - [14332_CAEEL]
O61199	5.93	4	115.59	150.6	T22B11.5	2-oxoglutarate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=T22B11.5 PE=1 SV=2 - [ODO1_CAEEL]
Q18787	19.77	7	48.58	474.5	rpt-1	26S protease regulatory subunit 7 OS=Caenorhabditis elegans GN=rpt-1 PE=1 SV=1 - [PRS7_CAEEL]
Q18115	9.33	9	105.94	361.6	rpn-2	26S proteasome non-ATPase regulatory subunit 1 OS=Caenorhabditis elegans GN=rpn-2 PE=2 SV=4 - [PSMD1_CAEEL]
Q04908	14.29	7	57.47	197.8	rpn-3	26S proteasome non-ATPase regulatory subunit 3 OS=Caenorhabditis elegans GN=rpn-3 PE=1 SV=1 - [PSMD3_CAEEL]
Q20585	17.07	6	47.55	172.7	rpn-7	26S proteasome non-ATPase regulatory subunit 6 OS=Caenorhabditis elegans GN=rpn-7 PE=2 SV=1 - [PSMD6_CAEEL]
Q23449	13.6	3	28.78	94.0	rpn-12	26S proteasome non-ATPase regulatory subunit 8 OS=Caenorhabditis elegans GN=rpn-12 PE=1 SV=1 - [PSMD8_CAEEL]
Q9NAP9	2.73	1	38.92	163.4	K07A12.7	28S ribosomal protein S15, mitochondrial OS=Caenorhabditis elegans GN=K07A12.7 PE=2 SV=1 - [RT15_CAEEL]
Q95Q11	4.95	1	25.64	66.8	Y57G11C.34	28S ribosomal protein S7, mitochondrial OS=Caenorhabditis elegans GN=Y57G11C.34 PE=3 SV=2 - [RT07_CAEEL]
P36573	10.39	3	31.79	45.7	lec-1	32 kDa beta-galactoside-binding lectin OS=Caenorhabditis elegans GN=lec-1 PE=1 SV=1 - [LEC1_CAEEL]
Q22633	3.05	1	44.36	79.7	hpd-1	4-hydroxyphenylpyruvate dioxygenase OS=Caenorhabditis elegans GN=hpd-1 PE=1 SV=1 - [HPPD_CAEEL]
P49196	7.86	2	15.06	149.5	rps-12	40S ribosomal protein S12 OS=Caenorhabditis elegans GN=rps-12 PE=1 SV=2 - [RS12_CAEEL]
P51404	32.45	6	17.31	380.2	rps-13	40S ribosomal protein S13 OS=Caenorhabditis elegans GN=rps-13 PE=2 SV=2 - [RS13_CAEEL]
P48150	33.55	6	16.24	534.7	rps-14	40S ribosomal protein S14 OS=Caenorhabditis elegans GN=rps-14 PE=2 SV=1 - [RS14_CAEEL]
Q9XVP0	40.4	7	17.23	688.6	rps-15	40S ribosomal protein S15 OS=Caenorhabditis elegans GN=rps-15 PE=1 SV=3 - [RS15_CAEEL]
Q22054	52.78	8	16.31	758.5	rps-16	40S ribosomal protein S16 OS=Caenorhabditis elegans GN=rps-16 PE=1 SV=3 - [RS16_CAEEL]
O01692	34.62	3	14.93	128.4	rps-17	40S ribosomal protein S17 OS=Caenorhabditis elegans GN=rps-17 PE=2 SV=2 - [RS17_CAEEL]
O18650	56.85	8	16.31	587.6	rps-19	40S ribosomal protein S19 OS=Caenorhabditis elegans GN=rps-19 PE=2 SV=1 - [RS19_CAEEL]
P51403	36.76	10	28.94	598.9	rps-2	40S ribosomal protein S2 OS=Caenorhabditis elegans GN=rps-2 PE=2 SV=1 - [RS2_CAEEL]
Q19877	15.38	2	15.86	138.3	rps-23	40S ribosomal protein S23 OS=Caenorhabditis elegans GN=rps-23 PE=2 SV=1 - [RS23_CAEEL]
P52821	16.24	2	12.90	87.1	rps-25	40S ribosomal protein S25 OS=Caenorhabditis elegans GN=rps-25 PE=2 SV=1 - [RS25_CAEEL]
O45499	26.5	3	13.24	182.2	rps-26	40S ribosomal protein S26 OS=Caenorhabditis elegans GN=rps-26 PE=2 SV=1 - [RS26_CAEEL]
Q9TXP0	15.66	1	9.34	130.6	rps-27	40S ribosomal protein S27 OS=Caenorhabditis elegans GN=rps-27 PE=1 SV=3 - [RS27_CAEEL]
P48152	43.32	11	27.30	911.0	rps-3	40S ribosomal protein S3 OS=Caenorhabditis elegans GN=rps-3 PE=2 SV=1 - [RS3_CAEEL]
P48154	37.74	11	28.94	787.9	rps-1	40S ribosomal protein S3a OS=Caenorhabditis elegans GN=rps-1 PE=2 SV=2 - [RS3A_CAEEL]
Q9N3X2	46.33	15	29.03	978.3	rps-4	40S ribosomal protein S4 OS=Caenorhabditis elegans GN=rps-4 PE=1 SV=1 - [RS4_CAEEL]
P49041	20.95	5	23.14	348.9	rps-5	40S ribosomal protein S5 OS=Caenorhabditis elegans GN=rps-5 PE=2 SV=1 - [RS5_CAEEL]
Q9NEN6	23.17	5	28.12	567.4	rps-6	40S ribosomal protein S6 OS=Caenorhabditis elegans GN=rps-6 PE=1 SV=1 - [RS6_CAEEL]
Q23312	32.99	7	22.04	242.4	rps-7	40S ribosomal protein S7 OS=Caenorhabditis elegans GN=rps-7 PE=2 SV=1 - [RS7_CAEEL]
P48156	40.87	6	23.74	587.8	rps-8	40S ribosomal protein S8 OS=Caenorhabditis elegans GN=rps-8 PE=2 SV=1 - [RS8_CAEEL]
Q20228	40.21	10	21.94	407.7	rps-9	40S ribosomal protein S9 OS=Caenorhabditis elegans GN=rps-9 PE=2 SV=1 - [RS9_CAEEL]
P46769	53.62	11	30.68	1059.6	rps-0	40S ribosomal protein SA OS=Caenorhabditis elegans GN=rps-0 PE=1 SV=3 - [RSSA_CAEEL]
Q95ZQ4	1.6	1	70.40	34.0	aak-2	5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Caenorhabditis elegans GN=aak-2 PE=1 SV=2 - [AAPK2_CAEEL]
Q17761	2.69	1	53.16	92.9	T25B9.9	6-phosphogluconate dehydrogenase, decarboxylating OS=Caenorhabditis elegans GN=T25B9.9 PE=2 SV=2 - [6PGD_CAEEL]
Q27274	5.44	3	72.80	152.0	rop-1	60 kDa SS-A/Ro ribonucleoprotein homolog OS=Caenorhabditis elegans GN=rop-1 PE=2 SV=1 - [RO60_CAEEL]
Q93572	48.4	11	33.75	1175.8	rpa-0	60S acidic ribosomal protein P0 OS=Caenorhabditis elegans GN=rpa-0 PE=1 SV=3 - [RLA0_CAEEL]
P91913	69.37	4	11.28	307.2	rla-1	60S acidic ribosomal protein P1 OS=Caenorhabditis elegans GN=rla-1 PE=2 SV=2 - [RLA1_CAEEL]
O01504	47.66	3	10.81	241.1	rpa-2	60S acidic ribosomal protein P2 OS=Caenorhabditis elegans GN=rpa-2 PE=2 SV=2 - [RLA2_CAEEL]
Q09533	33.18	10	24.73	744.7	rpl-10	60S ribosomal protein L10 OS=Caenorhabditis elegans GN=rpl-10 PE=2 SV=1 - [RL10_CAEEL]
Q9N414	27.78	6	24.12	607.5	rpl-10a	60S ribosomal protein L10a OS=Caenorhabditis elegans GN=rpl-10a PE=2 SV=1 - [RL10A_CAEEL]
Q94300	17.86	3	22.70	267.4	rpl-11.1	60S ribosomal protein L11 OS=Caenorhabditis elegans GN=rpl-11.1 PE=2 SV=1 - [RL11_CAEEL]
P61866	29.7	4	17.82	251.7	rpl-12	60S ribosomal protein L12 OS=Caenorhabditis elegans GN=rpl-12 PE=2 SV=1 - [RL12_CAEEL]
P91128	27.05	4	23.74	271.6	rpl-13	60S ribosomal protein L13 OS=Caenorhabditis elegans GN=rpl-13 PE=2 SV=1 - [RL13_CAEEL]
Q27389	7.43	1	22.98	41.2	rpl-16	60S ribosomal protein L13a OS=Caenorhabditis elegans GN=rpl-16 PE=2 SV=1 - [RL13A_CAEEL]
Q9BL19	21.39	3	21.50	413.1	rpl-17	60S ribosomal protein L17 OS=Caenorhabditis elegans GN=rpl-17 PE=2 SV=1 - [RL17_CAEEL]
O45946	34.04	6	20.98	277.0	rpl-18	60S ribosomal protein L18 OS=Caenorhabditis elegans GN=rpl-18 PE=3 SV=1 - [RL18_CAEEL]
O44480	6.11	1	20.95	26.4	rpl-20	60S ribosomal protein L18a OS=Caenorhabditis elegans GN=rpl-20 PE=2 SV=2 - [RL18A_CAEEL]
O02639	21.72	4	23.64	274.4	rpl-19	60S ribosomal protein L19 OS=Caenorhabditis elegans GN=rpl-19 PE=2 SV=1 - [RL19_CAEEL]
P34334	37.27	5	18.30	242.4	rpl-21	60S ribosomal protein L21 OS=Caenorhabditis elegans GN=rpl-21 PE=1 SV=3 - [RL21_CAEEL]
P52819	16.92	2	14.94	123.3	rpl-22	60S ribosomal protein L22 OS=Caenorhabditis elegans GN=rpl-22 PE=1 SV=3 - [RL22_CAEEL]
P48158	20.71	3	14.94	225.0	rpl-23	60S ribosomal protein L23 OS=Caenorhabditis elegans GN=rpl-23 PE=2 SV=1 - [RL23_CAEEL]

P48162	16.33	2	16.69	211.4	rpl-25.1	60S ribosomal protein L23a 1 OS=Caenorhabditis elegans GN=rpl-25.1 PE=2 SV=1 - [R23A1_CAEEL]
Q20647	23.29	3	16.27	219.7	rpl-25.2	60S ribosomal protein L23a 2 OS=Caenorhabditis elegans GN=rpl-25.2 PE=2 SV=1 - [R23A2_CAEEL]
O01868	8.18	1	17.77	67.3	rpl-24.1	60S ribosomal protein L24 OS=Caenorhabditis elegans GN=rpl-24.1 PE=2 SV=1 - [RL24_CAEEL]
Q19869	21.83	4	16.06	168.7	rpl-26	60S ribosomal protein L26 OS=Caenorhabditis elegans GN=rpl-26 PE=2 SV=1 - [RL26_CAEEL]
P91914	30.15	4	15.72	339.4	rpl-27	60S ribosomal protein L27 OS=Caenorhabditis elegans GN=rpl-27 PE=2 SV=1 - [RL27_CAEEL]
Q21930	23.02	3	13.72	143.1	rpl-28	60S ribosomal protein L28 OS=Caenorhabditis elegans GN=rpl-28 PE=1 SV=3 - [RL28_CAEEL]
P50880	17.46	8	45.63	748.5	rpl-3	60S ribosomal protein L3 OS=Caenorhabditis elegans GN=rpl-3 PE=2 SV=1 - [RL3_CAEEL]
Q9U332	7.38	1	14.25	77.1	rpl-31	60S ribosomal protein L31 OS=Caenorhabditis elegans GN=rpl-31 PE=2 SV=1 - [RL31_CAEEL]
P34662	16.26	3	14.19	120.8	rpl-35	60S ribosomal protein L35 OS=Caenorhabditis elegans GN=rpl-35 PE=2 SV=1 - [RL35_CAEEL]
P49180	27.42	4	13.76	237.4	rpl-33	60S ribosomal protein L35a OS=Caenorhabditis elegans GN=rpl-33 PE=1 SV=3 - [RL35A_CAEEL]
P49181	46.15	6	11.88	437.1	rpl-36	60S ribosomal protein L36 OS=Caenorhabditis elegans GN=rpl-36 PE=1 SV=3 - [RL36_CAEEL]
O02056	53.33	20	38.64	2710.7	rpl-4	60S ribosomal protein L4 OS=Caenorhabditis elegans GN=rpl-4 PE=1 SV=3 - [RL4_CAEEL]
P49405	45.05	9	33.37	1660.7	rpl-5	60S ribosomal protein L5 OS=Caenorhabditis elegans GN=rpl-5 PE=2 SV=1 - [RL5_CAEEL]
P47991	25.81	6	24.30	456.4	rpl-6	60S ribosomal protein L6 OS=Caenorhabditis elegans GN=rpl-6 PE=1 SV=1 - [RL6_CAEEL]
O01802	43.44	15	28.11	1157.9	rpl-7	60S ribosomal protein L7 OS=Caenorhabditis elegans GN=rpl-7 PE=1 SV=1 - [RL7_CAEEL]
Q966C6	36.23	11	30.16	664.7	rpl-7A	60S ribosomal protein L7a OS=Caenorhabditis elegans GN=rpl-7A PE=1 SV=3 - [RL7A_CAEEL]
Q9XVF7	23.08	7	28.19	738.1	rpl-8	60S ribosomal protein L8 OS=Caenorhabditis elegans GN=rpl-8 PE=1 SV=1 - [RL8_CAEEL]
Q95Y90	5.82	2	21.49	114.5	rpl-9	60S ribosomal protein L9 OS=Caenorhabditis elegans GN=rpl-9 PE=1 SV=1 - [RL9_CAEEL]
Q21166	2.29	1	78.29	28.4	sur-5	Acetoacetyl-CoA synthetase OS=Caenorhabditis elegans GN=sur-5 PE=2 SV=1 - [SUR5_CAEEL]
O01615	11.56	1	24.43	92.8	T19H12.2	Acidic leucine-rich nuclear phosphoprotein 32-related protein 2 OS=Caenorhabditis elegans GN=T19H12.2 PE=2 SV=1 - [AN322_CAEEL]
P10984	79.52	27	41.75	#####	act-2	Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=2 SV=3 - [ACT2_CAEEL]
Q07750	5.19	1	23.56	78.8	unc-60	Actin-depolymerizing factor 1, isoforms a/b OS=Caenorhabditis elegans GN=unc-60 PE=2 SV=2 - [ADF1_CAEEL]
P53489	11.39	3	44.81	106.4	arx-2	Actin-related protein 2 OS=Caenorhabditis elegans GN=arx-2 PE=3 SV=1 - [ARP2_CAEEL]
Q9N410	9.65	3	48.06	112.5	arx-1	Actin-related protein 3 OS=Caenorhabditis elegans GN=arx-1 PE=2 SV=1 - [ARP3_CAEEL]
P27604	30.21	13	47.51	1253.8	ahcy-1	Adenosylhomocysteinase OS=Caenorhabditis elegans GN=ahcy-1 PE=1 SV=1 - [SAHH_CAEEL]
P91408	2.14	1	51.61	41.1	T01B11.2	Alanine-glyoxylate aminotransferase 2-like OS=Caenorhabditis elegans GN=T01B11.2 PE=2 SV=1 - [AGT2L_CAEEL]
O01541	11.98	9	106.72	806.8	aars-2	Alanyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=aars-2 PE=2 SV=1 - [SYAC_CAEEL]
Q17334	51	18	37.67	3288.1	sodh-1	Alcohol dehydrogenase 1 OS=Caenorhabditis elegans GN=sodh-1 PE=1 SV=2 - [ADH1_CAEEL]
Q17335	11.98	4	41.27	332.2	H24K24.3	Alcohol dehydrogenase class-3 OS=Caenorhabditis elegans GN=H24K24.3 PE=2 SV=1 - [ADHX_CAEEL]
O45218	12.4	6	66.52	391.0	ads-1	Alkylidihydroxyacetonephosphate synthase OS=Caenorhabditis elegans GN=ads-1 PE=2 SV=1 - [ADAS_CAEEL]
O45380	0.9	1	139.82	44.1	tps-2	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 2 OS=Caenorhabditis elegans GN=tps-2 PE=2 SV=3 - [TPS2_CAEEL]
P41847	4.62	1	25.53	52.7	T20B12.7	Anamorfin homolog OS=Caenorhabditis elegans GN=T20B12.7 PE=2 SV=1 - [DRE2_CAEEL]
P35603	1.59	1	50.27	24.6	dpy-23	AP-2 complex subunit mu OS=Caenorhabditis elegans GN=dpy-23 PE=2 SV=2 - [AP2M_CAEEL]
P34552	7.71	6	98.20	325.6	alx-1	Apoptosis-linked gene 2-interacting protein X 1 OS=Caenorhabditis elegans GN=alx-1 PE=1 SV=3 - [ALX1_CAEEL]
Q19722	23.67	12	61.15	429.7	nrs-1	Asparaginyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=nrs-1 PE=2 SV=1 - [SYNC_CAEEL]
P55956	2.51	1	43.39	23.1	asp-3	Aspartic protease 3 OS=Caenorhabditis elegans GN=asp-3 PE=1 SV=2 - [ASP3_CAEEL]
O01530	6.43	1	41.49	38.5	asp-6	Aspartic protease 6 OS=Caenorhabditis elegans GN=asp-6 PE=2 SV=1 - [ASP6_CAEEL]
Q03577	25.99	12	59.90	709.5	drs-1	Aspartyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=drs-1 PE=2 SV=1 - [SYDC_CAEEL]
Q9XXK1	46.47	25	57.75	4734.7	H28O16.1	ATP synthase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=H28O16.1 PE=1 SV=1 - [ATPA_CAEEL]
P46561	42.01	15	57.49	1992.9	atp-2	ATP synthase subunit beta, mitochondrial OS=Caenorhabditis elegans GN=atp-2 PE=1 SV=2 - [ATPB_CAEEL]
Q09544	10.43	1	16.92	56.1	F58F12.1	ATP synthase subunit delta, mitochondrial OS=Caenorhabditis elegans GN=F58F12.1 PE=1 SV=1 - [ATPD_CAEEL]
Q95YF3	16.74	8	48.68	328.5	cgh-1	ATP-dependent RNA helicase cgh-1 OS=Caenorhabditis elegans GN=cgh-1 PE=1 SV=1 - [CGH1_CAEEL]
O01836	2.78	2	79.68	129.1	glh-3	ATP-dependent RNA helicase glh-3 OS=Caenorhabditis elegans GN=glh-3 PE=1 SV=1 - [GLH3_CAEEL]
O76743	2.68	3	120.57	130.0	glh-4	ATP-dependent RNA helicase glh-4 OS=Caenorhabditis elegans GN=glh-4 PE=2 SV=2 - [GLH4_CAEEL]
P30632	11.4	3	37.53	117.7	asna-1	ATPase asna-1 OS=Caenorhabditis elegans GN=asna-1 PE=1 SV=1 - [ASNA_CAEEL]
Q06561	0.77	2	368.82	66.4	unc-52	Basement membrane proteoglycan OS=Caenorhabditis elegans GN=unc-52 PE=1 SV=2 - [UNC52_CAEEL]
Q10663	46.38	39	108.56	6519.6	gei-7	Bifunctional glyoxylate cycle protein OS=Caenorhabditis elegans GN=gei-7 PE=1 SV=2 - [GCP_CAEEL]
O18017	0.71	1	110.59	31.7	him-6	Bloom syndrome protein homolog OS=Caenorhabditis elegans GN=him-6 PE=2 SV=2 - [BLM_CAEEL]
P30640	1.53	1	52.74	27.0	R08D7.1	BUD13 homolog OS=Caenorhabditis elegans GN=R08D7.1 PE=2 SV=1 - [BUD13_CAEEL]
Q86NG3	4.82	1	26.05	30.1	clec-88	C-type lectin domain-containing protein 88 OS=Caenorhabditis elegans GN=clec-88 PE=1 SV=1 - [CLC88_CAEEL]
O62305	2.64	1	79.88	37.0	unc-43	Calcium/calmodulin-dependent protein kinase type II OS=Caenorhabditis elegans GN=unc-43 PE=1 SV=2 - [KCC2D_CAEEL]
P27798	29.87	9	45.59	669.5	crt-1	Calreticulin OS=Caenorhabditis elegans GN=crt-1 PE=1 SV=1 - [CALR_CAEEL]
P30625	18.58	5	41.44	266.2	kin-2	cAMP-dependent protein kinase regulatory subunit OS=Caenorhabditis elegans GN=kin-2 PE=2 SV=3 - [KAPR_CAEEL]
P42168	6.45	2	39.01	113.1	kin-19	Casein kinase I isoform alpha OS=Caenorhabditis elegans GN=kin-19 PE=2 SV=1 - [KC1A_CAEEL]

P18334	30.83	8	42.23	471.8	kin-3	Casein kinase II subunit alpha OS=Caenorhabditis elegans GN=kin-3 PE=1 SV=1 - [CSK2A_CAEEL]
O61235	2.01	1	57.27	25.3	ctl-1	Catalase-2 OS=Caenorhabditis elegans GN=ctl-1 PE=2 SV=3 - [CATA2_CAEEL]
Q9U2Y2	10.02	4	55.70	209.4	Y113G7B.16	CDK5RAP3-like protein OS=Caenorhabditis elegans GN=Y113G7B.16 PE=2 SV=1 - [CK5P3_CAEEL]
O76360	17.18	11	86.69	550.0	egl-4	cGMP-dependent protein kinase egl-4 OS=Caenorhabditis elegans GN=egl-4 PE=1 SV=2 - [EGL4_CAEEL]
P50140	27.46	12	60.06	749.1	hsp-60	Chaperonin homolog Hsp-60, mitochondrial OS=Caenorhabditis elegans GN=hsp-60 PE=1 SV=2 - [CH60_CAEEL]
P46559	4.61	1	42.24	30.3	ckb-2	Choline kinase B2 OS=Caenorhabditis elegans GN=ckb-2 PE=1 SV=2 - [KICB2_CAEEL]
O62246	10.96	2	32.78	43.6	F45G2.4	Coatomer subunit epsilon OS=Caenorhabditis elegans GN=F45G2.4 PE=2 SV=1 - [COPE_CAEEL]
Q9GS00	1.5	1	68.36	48.5	csn-1	COP9 signalosome complex subunit 1 OS=Caenorhabditis elegans GN=csn-1 PE=1 SV=1 - [CSN1_CAEEL]
Q9N359	2.67	1	46.10	72.5	csn-4	COP9 signalosome complex subunit 4 OS=Caenorhabditis elegans GN=csn-4 PE=1 SV=1 - [CSN4_CAEEL]
Q94261	15.64	6	44.06	257.1	cif-1	COP9/Signalosome and eIF3 complex-shared subunit 1 OS=Caenorhabditis elegans GN=cif-1 PE=1 SV=1 - [EIF3M_CAEEL]
Q09221	0.09	1	857.57	25.5	cpna-2	Copine family protein 2 OS=Caenorhabditis elegans GN=cpna-2 PE=2 SV=4 - [CPNA2_CAEEL]
Q17389	1.28	1	89.47	39.0	cul-1	Cullin-1 OS=Caenorhabditis elegans GN=cul-1 PE=1 SV=1 - [CUL1_CAEEL]
Q17391	1.93	1	90.18	38.3	cul-3	Cullin-3 OS=Caenorhabditis elegans GN=cul-3 PE=1 SV=2 - [CUL3_CAEEL]
Q23639	1.57	1	88.85	47.0	cul-5	Cullin-5 OS=Caenorhabditis elegans GN=cul-5 PE=1 SV=2 - [CUL5_CAEEL]
P18833	6.03	1	28.13	180.9	col-8	Cuticle collagen 8 OS=Caenorhabditis elegans GN=col-8 PE=2 SV=2 - [COL8_CAEEL]
P98080	22.08	9	51.70	848.9	ucr-1	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Caenorhabditis elegans GN=ucr-1 PE=2 SV=2 - [UCR1_CAEEL]
P19974	13.51	1	12.23	53.4	cyc-2.1	Cytochrome c 2.1 OS=Caenorhabditis elegans GN=cyc-2.1 PE=1 SV=2 - [CYC21_CAEEL]
P24894	4.76	1	26.53	78.1	cox-2	Cytochrome c oxidase subunit 2 OS=Caenorhabditis elegans GN=cox-2 PE=3 SV=2 - [COX2_CAEEL]
P55954	17.82	3	20.10	145.8	cco-2	Cytochrome c oxidase subunit 5A, mitochondrial OS=Caenorhabditis elegans GN=cco-2 PE=1 SV=2 - [COX5A_CAEEL]
O76365	4.56	1	41.31	32.0	tut-1	Cytoplasmic tRNA 2-thiolation protein 1 OS=Caenorhabditis elegans GN=tut-1 PE=1 SV=1 - [CTU1_CAEEL]
Q9U3C8	3.05	1	34.11	41.5	dcn-1	Defective in cullin neddylation protein 1 OS=Caenorhabditis elegans GN=dcn-1 PE=1 SV=2 - [DCN1_CAEEL]
Q19749	23.87	8	53.43	1489.7	F23B12.5	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial
Q18164	15.58	14	115.23	690.5	dpyd-1	Dihydropyrimidine dehydrogenase [NADP+] OS=Caenorhabditis elegans GN=dpyd-1 PE=2 SV=2 - [DPYD_CAEEL]
Q18066	18.44	10	71.80	600.9	dim-1	Disorganized muscle protein 1 OS=Caenorhabditis elegans GN=dim-1 PE=1 SV=3 - [DIM_CAEEL]
P34409	2.98	1	57.27	23.6	polk-1	DNA polymerase kappa OS=Caenorhabditis elegans GN=polk-1 PE=2 SV=2 - [POLK_CAEEL]
Q21902	1.58	1	84.88	43.4	mcm-5	DNA replication licensing factor mcm-5 OS=Caenorhabditis elegans GN=mcm-5 PE=2 SV=1 - [MCM5_CAEEL]
P16356	2.27	3	203.85	131.3	ama-1	DNA-directed RNA polymerase II subunit RPB1 OS=Caenorhabditis elegans GN=ama-1 PE=1 SV=2 - [RPB1_CAEEL]
Q9N5K2	4.74	1	24.33	50.8	rpb-5	DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Caenorhabditis elegans GN=rpb-5 PE=2 SV=1 - [RPAB1_CAEEL]
Q8MPX3	2.54	1	39.84	43.3	dnoj-20	DnaJ homolog dnoj-20 OS=Caenorhabditis elegans GN=dnoj-20 PE=2 SV=2 - [DNJ20_CAEEL]
P39055	9.52	7	93.35	372.7	dyn-1	Dynamin OS=Caenorhabditis elegans GN=dyn-1 PE=1 SV=3 - [DYN1_CAEEL]
Q19020	1.07	5	521.25	170.4	dhc-1	Dynein heavy chain, cytoplasmic OS=Caenorhabditis elegans GN=dhc-1 PE=2 SV=1 - [DYHC_CAEEL]
Q65XX2	0.69	1	165.30	30.2	Y54E10A.11	E3 ubiquitin-protein ligase listerin OS=Caenorhabditis elegans GN=Y54E10A.11 PE=2 SV=1 - [LTN1_CAEEL]
Q11190	10.22	4	65.29	270.5	let-721	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Caenorhabditis elegans GN=let-721 PE=1
P53013	43.63	17	50.64	6625.8	eft-3	Elongation factor 1-alpha OS=Caenorhabditis elegans GN=eft-3 PE=2 SV=1 - [EF1A_CAEEL]
P29691	30.16	24	94.74	2476.7	eef-2	Elongation factor 2 OS=Caenorhabditis elegans GN=eef-2 PE=1 SV=4 - [EF2_CAEEL]
Q9XV52	9.87	6	83.60	367.1	F29C12.4	Elongation factor G, mitochondrial OS=Caenorhabditis elegans GN=F29C12.4 PE=2 SV=1 - [EFGM_CAEEL]
Q20819	14.56	3	34.07	203.2	tsfm-1	Elongation factor Ts, mitochondrial OS=Caenorhabditis elegans GN=tsfm-1 PE=2 SV=1 - [EFTS_CAEEL]
Q95NM6	2.92	1	34.49	27.6	cps-6	Endonuclease G, mitochondrial OS=Caenorhabditis elegans GN=cps-6 PE=1 SV=1 - [NUCG_CAEEL]
P34529	0.87	2	210.79	46.2	dcr-1	Endoribonuclease dcr-1 OS=Caenorhabditis elegans GN=dcr-1 PE=1 SV=2 - [DCR1_CAEEL]
Q27527	39.86	11	46.59	687.7	enol-1	Enolase OS=Caenorhabditis elegans GN=enol-1 SV=3 - [ENO_CAEEL]
Q07085	1.97	1	62.48	42.1	F13H6.3	Esterase CM06B1 OS=Caenorhabditis elegans GN=F13H6.3 PE=2 SV=2 - [EST2_CAEEL]
P27639	31.34	13	45.38	1148.4	inf-1	Eukaryotic initiation factor 4A OS=Caenorhabditis elegans GN=inf-1 PE=2 SV=1 - [IF4A_CAEEL]
O16520	12.34	6	62.13	395.4	erf-1	Eukaryotic peptide chain release factor subunit 1 OS=Caenorhabditis elegans GN=erf-1 PE=2 SV=2 - [ERF1_CAEEL]
Q21230	4	1	27.56	42.0	K04G2.1	Eukaryotic translation initiation factor 2 subunit 2 OS=Caenorhabditis elegans GN=K04G2.1 PE=3 SV=4 - [IF2B_CAEEL]
P34339	21.84	22	124.33	1087.7	egl-45	Eukaryotic translation initiation factor 3 subunit A OS=Caenorhabditis elegans GN=egl-45 PE=2 SV=1 - [EIF3A_CAEEL]
Q9XW16	11.31	8	83.10	586.4	eif-3.B	Eukaryotic translation initiation factor 3 subunit B OS=Caenorhabditis elegans GN=eif-3.B PE=2 SV=1 - [EIF3B_CAEEL]
O02328	13.59	10	103.78	412.9	eif-3.C	Eukaryotic translation initiation factor 3 subunit C OS=Caenorhabditis elegans GN=eif-3.C PE=2 SV=2 - [EIF3C_CAEEL]
P30642	13.68	6	64.25	272.1	eif-3.D	Eukaryotic translation initiation factor 3 subunit D OS=Caenorhabditis elegans GN=eif-3.D PE=1 SV=1 - [EIF3D_CAEEL]
O61820	16.67	5	50.69	252.8	eif-3.E	Eukaryotic translation initiation factor 3 subunit E OS=Caenorhabditis elegans GN=eif-3.E PE=2 SV=1 - [EIF3E_CAEEL]
Q18967	3.74	1	32.91	81.8	eif-3.F	Eukaryotic translation initiation factor 3 subunit F OS=Caenorhabditis elegans GN=eif-3.F PE=2 SV=1 - [EIF3F_CAEEL]
Q19706	12.5	2	29.27	102.6	eif-3.G	Eukaryotic translation initiation factor 3 subunit G OS=Caenorhabditis elegans GN=eif-3.G PE=2 SV=1 - [EIF3G_CAEEL]
O01974	3.01	1	40.94	32.0	eif-3.H	Eukaryotic translation initiation factor 3 subunit H OS=Caenorhabditis elegans GN=eif-3.H PE=1 SV=2 - [EIF3H_CAEEL]
Q965S8	10.7	3	36.85	258.5	eif-3.I	Eukaryotic translation initiation factor 3 subunit I OS=Caenorhabditis elegans GN=eif-3.I PE=2 SV=2 - [EIF3I_CAEEL]
Q9XUP3	4.58	1	27.01	75.4	eif-3.K	Eukaryotic translation initiation factor 3 subunit K OS=Caenorhabditis elegans GN=eif-3.K PE=2 SV=1 - [EIF3K_CAEEL]
Q95QW0	4.66	2	62.44	88.4	eif-3.L	Eukaryotic translation initiation factor 3 subunit L OS=Caenorhabditis elegans GN=eif-3.L PE=1 SV=1 - [EIF3L_CAEEL]

O45551	6.13	1	24.30	32.1	ife-1	Eukaryotic translation initiation factor 4E-1 OS=Caenorhabditis elegans GN=ife-1 PE=1 SV=2 - [IF4E1_CAEEL]
Q21693	22.37	3	25.71	271.9	ife-2	Eukaryotic translation initiation factor 4E-2 OS=Caenorhabditis elegans GN=ife-2 PE=1 SV=1 - [IF4E2_CAEEL]
O61955	8.06	2	27.79	43.1	ife-3	Eukaryotic translation initiation factor 4E-3 OS=Caenorhabditis elegans GN=ife-3 PE=1 SV=1 - [IF4E3_CAEEL]
Q22888	5.19	1	24.57	27.6	ife-4	Eukaryotic translation initiation factor 4E-4 OS=Caenorhabditis elegans GN=ife-4 PE=2 SV=1 - [IF4E4_CAEEL]
P34563	21.12	2	17.86	191.1	iff-1	Eukaryotic translation initiation factor 5A-1 OS=Caenorhabditis elegans GN=iff-1 PE=1 SV=1 - [IF5A1_CAEEL]
Q20751	45.34	4	17.94	238.7	iff-2	Eukaryotic translation initiation factor 5A-2 OS=Caenorhabditis elegans GN=iff-2 PE=2 SV=1 - [IF5A2_CAEEL]
O62106	6.1	1	26.29	70.7	eif-6	Eukaryotic translation initiation factor 6 OS=Caenorhabditis elegans GN=eif-6 PE=2 SV=1 - [IF6_CAEEL]
P34685	30.5	7	32.16	302.8	cap-1	F-actin-capping protein subunit alpha OS=Caenorhabditis elegans GN=cap-1 PE=2 SV=1 - [CAPZA_CAEEL]
P34686	11.85	2	30.77	258.1	cap-2	F-actin-capping protein subunit beta OS=Caenorhabditis elegans GN=cap-2 PE=2 SV=1 - [CAPZB_CAEEL]
O16299	2.02	1	66.15	45.1	figl-1	Fidgetin-like protein 1 OS=Caenorhabditis elegans GN=figl-1 PE=1 SV=1 - [FIGL1_CAEEL]
P54216	44.81	13	39.22	933.5	aldo-1	Fructose-bisphosphate aldolase 1 OS=Caenorhabditis elegans GN=aldo-1 PE=1 SV=1 - [ALF1_CAEEL]
P46563	48.09	13	38.82	1039.3	aldo-2	Fructose-bisphosphate aldolase 2 OS=Caenorhabditis elegans GN=aldo-2 PE=2 SV=1 - [ALF2_CAEEL]
Q21253	34.95	15	54.56	1378.0	gsnl-1	Gelsolin-like protein 1 OS=Caenorhabditis elegans GN=gsnl-1 PE=1 SV=1 - [GELS1_CAEEL]
P30627	13.21	2	18.49	111.1	glb-1	Globin-like protein OS=Caenorhabditis elegans GN=glb-1 PE=1 SV=2 - [GLBH_CAEEL]
Q17427	13.33	1	18.45	48.1	gna-1	Glucosamine 6-phosphate N-acetyltransferase OS=Caenorhabditis elegans GN=gna-1 PE=2 SV=1 - [GNA1_CAEEL]
Q27464	1.92	1	60.18	31.6	gspd-1	Glucose-6-phosphate 1-dehydrogenase OS=Caenorhabditis elegans GN=gspd-1 PE=2 SV=1 - [G6PD_CAEEL]
P91406	1.43	1	85.45	25.4	R57.1	Glutamate carboxypeptidase 2 homolog OS=Caenorhabditis elegans GN=R57.1 PE=1 SV=2 - [GCP2_CAEEL]
Q20117	7.19	4	74.32	178.5	gcs-1	Glutamate--cysteine ligase OS=Caenorhabditis elegans GN=gcs-1 PE=1 SV=2 - [GSH1_CAEEL]
P10299	6.73	1	23.89	139.9	gst-1	Glutathione S-transferase P OS=Caenorhabditis elegans GN=gst-1 PE=1 SV=1 - [GSTP1_CAEEL]
O17915	16.74	3	24.24	117.4	ran-1	GTP-binding nuclear protein ran-1 OS=Caenorhabditis elegans GN=ran-1 PE=1 SV=1 - [RAN_CAEEL]
Q9XTB2	3.16	1	40.04	37.7	gpa-13	Guanine nucleotide-binding protein alpha-13 subunit OS=Caenorhabditis elegans GN=gpa-13 PE=2 SV=2 - [GPA13_CAEEL]
P51875	12.15	4	40.43	159.0	goa-1	Guanine nucleotide-binding protein G(o) subunit alpha OS=Caenorhabditis elegans GN=goa-1 PE=1 SV=3 - [GNAO_CAEEL]
P17343	9.71	2	37.38	172.8	gpb-1	Guanine nucleotide-binding protein subunit beta-1 OS=Caenorhabditis elegans GN=gpb-1 PE=2 SV=2 - [GBB1_CAEEL]
Q21215	33.54	9	35.81	1048.6	rack-1	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Caenorhabditis elegans GN=rack-1 PE=1 SV=3 - [GBLP_CAEEL]
Q21086	3.24	2	62.30	27.2	nst-1	Guanine nucleotide-binding protein-like 3 homolog OS=Caenorhabditis elegans GN=nst-1 PE=2 SV=1 - [GNL3_CAEEL]
P09446	31.87	18	69.68	1631.1	hsp-1	Heat shock 70 kDa protein A OS=Caenorhabditis elegans GN=hsp-1 PE=1 SV=2 - [HSP7A_CAEEL]
P27420	18.46	11	72.98	805.9	hsp-3	Heat shock 70 kDa protein C OS=Caenorhabditis elegans GN=hsp-3 PE=1 SV=2 - [HSP7C_CAEEL]
P20163	11.87	7	72.24	626.3	hsp-4	Heat shock 70 kDa protein D OS=Caenorhabditis elegans GN=hsp-4 PE=1 SV=2 - [HSP7D_CAEEL]
P11141	20.4	10	70.80	930.4	hsp-6	Heat shock 70 kDa protein F, mitochondrial OS=Caenorhabditis elegans GN=hsp-6 PE=1 SV=2 - [HSP7F_CAEEL]
Q18688	48.29	36	80.23	4670.9	daf-21	Heat shock protein 90 OS=Caenorhabditis elegans GN=daf-21 PE=1 SV=1 - [HSP90_CAEEL]
Q22037	2.02	1	36.32	24.5	hrp-1	Heterogeneous nuclear ribonucleoprotein A1 OS=Caenorhabditis elegans GN=hrp-1 PE=1 SV=1 - [ROA1_CAEEL]
P34183	27.64	10	58.52	615.1	hrs-1	Histidyl-tRNA synthetase OS=Caenorhabditis elegans GN=hrs-1 PE=2 SV=3 - [SYH_CAEEL]
O17695	3.9	2	52.10	142.2	hda-1	Histone deacetylase 1 OS=Caenorhabditis elegans GN=hda-1 PE=1 SV=1 - [HDA1_CAEEL]
P10771	6.25	1	21.35	334.3	his-24	Histone H1.1 OS=Caenorhabditis elegans GN=his-24 PE=1 SV=4 - [H11_CAEEL]
P09588	36.22	3	13.40	121.1	his-3	Histone H2A OS=Caenorhabditis elegans GN=his-3 PE=1 SV=2 - [H2A_CAEEL]
Q27511	18.57	3	14.66	187.0	htz-1	Histone H2A.V OS=Caenorhabditis elegans GN=htz-1 PE=2 SV=3 - [H2AV_CAEEL]
P62784	19.42	2	11.36	97.9	his-1	Histone H4 OS=Caenorhabditis elegans GN=his-1 PE=1 SV=2 - [H4_CAEEL]
P91276	1.88	1	59.14	90.2	ima-2	Importin subunit alpha-2 OS=Caenorhabditis elegans GN=ima-2 PE=1 SV=1 - [IMA2_CAEEL]
Q19969	11.09	3	56.13	229.8	ima-3	Importin subunit alpha-3 OS=Caenorhabditis elegans GN=ima-3 PE=1 SV=2 - [IMA3_CAEEL]
Q19420	3.16	1	30.96	33.5	txx-7	Inositol monophosphatase txx-7 OS=Caenorhabditis elegans GN=txx-7 PE=1 SV=2 - [IMPA1_CAEEL]
P90901	12.87	7	66.49	262.8	ifa-1	Intermediate filament protein ifa-1 OS=Caenorhabditis elegans GN=ifa-1 PE=1 SV=2 - [IFA1_CAEEL]
O02365	5.34	3	67.05	115.8	ifa-2	Intermediate filament protein ifa-2 OS=Caenorhabditis elegans GN=ifa-2 PE=1 SV=1 - [IFA2_CAEEL]
P90900	11.09	6	66.59	385.8	ifa-4	Intermediate filament protein ifa-4 OS=Caenorhabditis elegans GN=ifa-4 PE=1 SV=2 - [IFA4_CAEEL]
Q19289	30.22	19	67.11	1574.3	ifb-1	Intermediate filament protein ifb-1 OS=Caenorhabditis elegans GN=ifb-1 PE=1 SV=1 - [IFB1_CAEEL]
Q19286	37.75	18	61.57	2219.8	ifb-2	Intermediate filament protein ifb-2 OS=Caenorhabditis elegans GN=ifb-2 PE=1 SV=1 - [IFB2_CAEEL]
O45168	9.4	5	55.83	144.9	ifc-1	Intermediate filament protein ifc-1 OS=Caenorhabditis elegans GN=ifc-1 PE=2 SV=2 - [IFC1_CAEEL]
Q21067	26.37	16	70.06	930.6	ifc-2	Intermediate filament protein ifc-2 OS=Caenorhabditis elegans GN=ifc-2 PE=1 SV=3 - [IFC2_CAEEL]
Q86DC6	3.83	2	66.66	44.5	ifd-1	Intermediate filament protein ifd-1 OS=Caenorhabditis elegans GN=ifd-1 PE=2 SV=2 - [IFD1_CAEEL]
Q09501	1.93	1	89.00	78.5	ifp-1	Intermediate filament protein ifp-1 OS=Caenorhabditis elegans GN=ifp-1 PE=2 SV=1 - [IFP1_CAEEL]
Q21926	7.01	7	129.93	387.5	irs-1	Isoleucyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=irs-1 PE=2 SV=1 - [SYIC_CAEEL]
P34540	6.13	4	91.84	111.9	unc-116	Kinesin heavy chain OS=Caenorhabditis elegans GN=unc-116 PE=2 SV=2 - [KINH_CAEEL]
P46822	2.04	1	60.19	24.2	klc-2	Kinesin light chain OS=Caenorhabditis elegans GN=klc-2 PE=2 SV=2 - [KLC_CAEEL]
P34341	0.97	1	94.43	26.8	kle-2	Kleisin, abnormal closure, protein 2 OS=Caenorhabditis elegans GN=kle-2 PE=2 SV=2 - [KLE2_CAEEL]
Q9N4Z0	2.54	1	47.87	33.5	Y45G12B.3	L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y45G12B.3 PE=2 SV=2 - [L2HDAH_CAEEL]
Q27888	9.01	3	36.04	105.1	ldh-1	L-lactate dehydrogenase OS=Caenorhabditis elegans GN=ldh-1 PE=2 SV=1 - [LDH_CAEEL]

Q21443	15.55	7	64.05	294.8	lmn-1	Lamin-1 OS=Caenorhabditis elegans GN=lmn-1 PE=1 SV=2 - [LMN1_CAEEL]
Q22875	5.01	2	62.44	95.5	soc-2	Leucine-rich repeat protein soc-2 OS=Caenorhabditis elegans GN=soc-2 PE=1 SV=3 - [SHOC2_CAEEL]
Q09996	12.48	11	134.43	706.4	lrs-1	Leucyl-tRNA synthetase OS=Caenorhabditis elegans GN=lrs-1 PE=2 SV=2 - [SYLC_CAEEL]
O44952	0.93	1	108.14	34.3	C34B2.6	Lon protease homolog, mitochondrial OS=Caenorhabditis elegans GN=C34B2.6 PE=2 SV=1 - [LONM_CAEEL]
Q22099	15.38	8	65.10	456.8	krs-1	Lysyl-tRNA synthetase OS=Caenorhabditis elegans GN=krs-1 PE=2 SV=1 - [SYK_CAEEL]
Q18788	1.86	1	66.91	42.8	C52E4.5	Mannosyl-oligosaccharide 1,2-alpha-mannosidase C52E4.5 OS=Caenorhabditis elegans GN=C52E4.5 PE=1 SV=1 - [MAN12_CAEEL]
Q20970	13.3	10	101.65	900.8	mrs-1	Methionyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=mrs-1 PE=2 SV=1 - [SYMC_CAEEL]
Q22111	9.77	3	44.19	220.7	mmaa-1	Methylmalonic aciduria type A homolog, mitochondrial OS=Caenorhabditis elegans GN=mmaa-1 PE=2 SV=2 - [MMAA1_CAEEL]
Q09357	1.88	1	53.77	22.4	mett-10	Methyltransferase-like protein 16 homolog OS=Caenorhabditis elegans GN=mett-10 PE=1 SV=2 - [MET16_CAEEL]
Q9BKU4	13.45	3	29.97	217.7	phb-1	Mitochondrial prohibitin complex protein 1 OS=Caenorhabditis elegans GN=phb-1 PE=1 SV=1 - [PHB1_CAEEL]
P50093	15.99	4	32.65	161.1	phb-2	Mitochondrial prohibitin complex protein 2 OS=Caenorhabditis elegans GN=phb-2 PE=1 SV=2 - [PHB2_CAEEL]
P34496	8.24	1	19.17	38.4	mtss-1	Mitochondrial single stranded DNA binding protein 1 OS=Caenorhabditis elegans GN=mtss-1 PE=1 SV=2 - [MTSS1_CAEEL]
P39745	4.28	1	50.63	71.9	mpk-1	Mitogen-activated protein kinase mpk-1 OS=Caenorhabditis elegans GN=mpk-1 PE=1 SV=2 - [SUR1_CAEEL]
O18211	2.66	1	39.41	74.0	mop-25.2	MO25-like protein 2 OS=Caenorhabditis elegans GN=mop-25.2 PE=2 SV=1 - [MO25M_CAEEL]
Q23223	1.66	1	116.30	85.4	mtr-4	mRNA transport homolog 4 OS=Caenorhabditis elegans GN=mtr-4 PE=2 SV=1 - [MTR4_CAEEL]
Q19272	0.73	1	153.04	21.2	msh-5	MutS protein homolog 5 OS=Caenorhabditis elegans GN=msh-5 PE=2 SV=2 - [MSH5_CAEEL]
P19625	87.06	19	18.61	2087.3	mhc-1	Myosin regulatory light chain 1 OS=Caenorhabditis elegans GN=mhc-1 PE=2 SV=1 - [MLR1_CAEEL]
P19626	87.06	19	18.59	2345.0	mhc-2	Myosin regulatory light chain 2 OS=Caenorhabditis elegans GN=mhc-2 PE=1 SV=1 - [MLR2_CAEEL]
P02567	39.53	70	223.19	6451.2	let-75	Myosin-1 OS=Caenorhabditis elegans GN=let-75 PE=2 SV=3 - [MYO1_CAEEL]
P12845	43.04	74	222.91	#####	myo-2	Myosin-2 OS=Caenorhabditis elegans GN=myo-2 PE=2 SV=2 - [MYO2_CAEEL]
P12844	40.38	77	225.37	7947.1	myo-3	Myosin-3 OS=Caenorhabditis elegans GN=myo-3 PE=2 SV=1 - [MYO3_CAEEL]
P02566	65.62	168	224.99	#####	unc-54	Myosin-4 OS=Caenorhabditis elegans GN=unc-54 PE=4 SV=1 - [MYO4_CAEEL]
P53014	87.58	18	17.13	2480.1	mhc-3	Myosin, essential light chain OS=Caenorhabditis elegans GN=mhc-3 PE=1 SV=1 - [MLE_CAEEL]
Q9BKR0	5.45	1	23.31	23.5	Y67D2.5	N-acetyltransferase 9-like protein OS=Caenorhabditis elegans GN=Y67D2.5 PE=3 SV=2 - [NAT9_CAEEL]
Q21986	2.4	2	109.16	281.5	R13F6.10	N-terminal acetyltransferase B complex subunit NAA25 homolog OS=Caenorhabditis elegans GN=R13F6.10
Q86S66	15.23	3	22.06	252.3	Y65B4BR.5 / icd-2 / $\alpha$	Nascent polypeptide-associated complex subunit alpha OS=Caenorhabditis elegans GN=Y65B4BR.5 PE=1 SV=1 - [NACA_CAEEL]
Q19360	2.79	1	47.99	34.3	uba-3	NEDD8-activating enzyme E1 catalytic subunit OS=Caenorhabditis elegans GN=uba-3 PE=2 SV=2 - [UBA3_CAEEL]
Q18217	2.22	1	60.74	27.0	ula-1	NEDD8-activating enzyme E1 regulatory subunit OS=Caenorhabditis elegans GN=ula-1 PE=2 SV=2 - [ULA1_CAEEL]
Q9N4M4	0.14	1	955.90	46.7	anc-1	Nuclear anchorage protein 1 OS=Caenorhabditis elegans GN=anc-1 PE=1 SV=3 - [ANC1_CAEEL]
O01763	5.64	4	92.47	207.7	ncbp-1	Nuclear cap-binding protein subunit 1 OS=Caenorhabditis elegans GN=ncbp-1 PE=2 SV=3 - [NCBP1_CAEEL]
Q94407	1.1	1	90.65	36.1	nhr-48	Nuclear hormone receptor family member nhr-48 OS=Caenorhabditis elegans GN=nhr-48 PE=2 SV=3 - [NHR48_CAEEL]
O16962	1.65	1	49.21	32.6	nhr-55	Nuclear hormone receptor family member nhr-55 OS=Caenorhabditis elegans GN=nhr-55 PE=2 SV=2 - [NHR55_CAEEL]
Q9XVS7	2.39	1	70.92	48.5	nxf-1	Nuclear RNA export factor 1 OS=Caenorhabditis elegans GN=nxf-1 PE=1 SV=1 - [NXF1_CAEEL]
Q9TZQ3	2.47	2	78.41	49.5	ppl-1	P granule abnormality protein 1 OS=Caenorhabditis elegans GN=ppl-1 PE=1 SV=1 - [PGL1_CAEEL]
O16785	3.47	1	42.97	78.5	pat-6	Paralyzed arrest at two-fold protein 6 OS=Caenorhabditis elegans GN=pat-6 PE=1 SV=1 - [PARV_CAEEL]
P10567	41.95	34	101.89	2921.2	unc-15	Paramyosin OS=Caenorhabditis elegans GN=unc-15 PE=1 SV=1 - [MYSP_CAEEL]
Q95QU0	2.18	1	47.13	82.9	C27F2.10	PCI domain-containing protein 2 homolog OS=Caenorhabditis elegans GN=C27F2.10 PE=3 SV=1 - [PCID2_CAEEL]
P52009	13.54	2	20.70	273.7	cyn-1	Peptidyl-prolyl cis-trans isomerase 1 OS=Caenorhabditis elegans GN=cyn-1 PE=2 SV=1 - [CYP1_CAEEL]
P52018	7.65	1	20.18	73.0	cyn-11	Peptidyl-prolyl cis-trans isomerase 11 OS=Caenorhabditis elegans GN=cyn-11 PE=2 SV=1 - [CYP11_CAEEL]
P52011	32.95	7	18.54	460.6	cyn-3	Peptidyl-prolyl cis-trans isomerase 3 OS=Caenorhabditis elegans GN=cyn-3 PE=1 SV=1 - [CYP3_CAEEL]
P52013	3.92	1	21.91	33.9	cyn-5	Peptidyl-prolyl cis-trans isomerase 5 OS=Caenorhabditis elegans GN=cyn-5 PE=1 SV=2 - [CYP5_CAEEL]
P52015	42.11	8	18.39	732.4	cyn-7	Peptidyl-prolyl cis-trans isomerase 7 OS=Caenorhabditis elegans GN=cyn-7 PE=1 SV=2 - [CYP7_CAEEL]
Q27487	2.4	1	57.43	24.4	ctl-2	Peroxisomal catalase 1 OS=Caenorhabditis elegans GN=ctl-2 PE=2 SV=3 - [CATA1_CAEEL]
Q19713	19.12	9	66.02	830.1	frs-2	Phenylalanyl-tRNA synthetase beta chain OS=Caenorhabditis elegans GN=frs-2 PE=1 SV=2 - [SYFB_CAEEL]
P40614	22.35	8	36.65	519.7	F01G4.6	Phosphate carrier protein, mitochondrial OS=Caenorhabditis elegans GN=F01G4.6 PE=2 SV=1 - [MPCP_CAEEL]
Q9TXQ1	0.35	1	254.42	20.4	pme-5	Poly(ADP-ribose) polymerase pme-5 OS=Caenorhabditis elegans GN=pme-5 PE=2 SV=1 - [PME5_CAEEL]
Q10051	10.37	4	53.18	146.0	T10F2.4	Pre-mRNA-processing factor 19 homolog OS=Caenorhabditis elegans GN=T10F2.4 PE=2 SV=2 - [PRP19_CAEEL]
P34369	1.55	4	271.85	184.4	prp-8	Pre-mRNA-splicing factor 8 homolog OS=Caenorhabditis elegans GN=prp-8 PE=1 SV=1 - [PRP8_CAEEL]
Q19329	4.33	3	89.16	84.6	tag-151	Pre-rRNA-processing protein TSR1 homolog OS=Caenorhabditis elegans GN=tag-151 PE=3 SV=1 - [TSR1_CAEEL]
Q02332	4.49	1	45.25	37.4	pdhk-2	Probable [pyruvate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Caenorhabditis elegans GN=pdhk-2
Q23629	2.63	2	102.67	91.2	ZK836.2	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial OS=Caenorhabditis elegans GN=ZK836.2
O17071	17.49	6	45.83	409.1	rpt-4	Probable 26S protease regulatory subunit 10B OS=Caenorhabditis elegans GN=rpt-4 PE=1 SV=2 - [PRS10_CAEEL]
O16368	20.09	7	49.69	428.4	rpt-2	Probable 26S protease regulatory subunit 4 OS=Caenorhabditis elegans GN=rpt-2 PE=2 SV=1 - [PRS4_CAEEL]
P46502	15.22	4	46.33	139.0	rpt-3	Probable 26S protease regulatory subunit 6B OS=Caenorhabditis elegans GN=rpt-3 PE=2 SV=1 - [PRS6B_CAEEL]
Q20938	14.38	5	49.06	273.6	rpn-6.1	Probable 26S proteasome regulatory subunit rpn-6.1 OS=Caenorhabditis elegans GN=rpn-6.1 PE=2 SV=2 - [PS11A_CAEEL]



Q10129	11.56	1	16.30	199.8	F56D1.3	Probable 28S ribosomal protein S16, mitochondrial OS=Caenorhabditis elegans GN=F56D1.3 PE=3 SV=2 - [RT16_CAEEL]
P41938	3.56	1	33.36	31.8	B0272.3	Probable 3-hydroxyacyl-CoA dehydrogenase B0272.3 OS=Caenorhabditis elegans GN=B0272.3 PE=1 SV=1 - [HCDH2_CAEEL]
Q9XTI0	13.71	3	31.20	160.2	B0250.5	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=B0250.5 PE=2 SV=1 - [3HIDH_CAEEL]
Q95Y71	3.08	1	41.29	67.1	Y119D3B.16	Probable 39S ribosomal protein L45, mitochondrial OS=Caenorhabditis elegans GN=Y119D3B.16 PE=2 SV=3 - [RM45_CAEEL]
Q21217	40.58	16	53.02	2288.0	gta-1	Probable 4-aminobutyrate aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=gta-1 PE=1 SV=1 - [GABT_CAEEL]
P34388	2.55	1	43.67	117.6	F09G8.3	Probable 40S ribosomal protein S9, mitochondrial OS=Caenorhabditis elegans GN=F09G8.3 PE=2 SV=2 - [RT09_CAEEL]
P34455	26.51	14	83.99	1955.9	aco-2	Probable aconitate hydratase, mitochondrial OS=Caenorhabditis elegans GN=aco-2 PE=1 SV=2 - [ACON_CAEEL]
Q8WTM6	2.99	1	34.46	56.7	arx-4	Probable actin-related protein 2/3 complex subunit 2 OS=Caenorhabditis elegans GN=arx-4 PE=2 SV=1 - [ARPC2_CAEEL]
Q20140	29.52	4	22.58	314.0	F38B2.4	Probable adenylate kinase isoenzyme F38B2.4 OS=Caenorhabditis elegans GN=F38B2.4 PE=2 SV=1 - [KAD1_CAEEL]
Q09629	13.51	3	24.89	93.9	ZK673.2	Probable adenylate kinase isoenzyme ZK673.2 OS=Caenorhabditis elegans GN=ZK673.2 PE=2 SV=1 - [KADY_CAEEL]
Q10454	56.06	22	44.14	5353.2	F46H5.3	Probable arginine kinase F46H5.3 OS=Caenorhabditis elegans GN=F46H5.3 PE=1 SV=2 - [KARG1_CAEEL]
Q27535	20	6	40.36	448.9	ZC434.8	Probable arginine kinase ZC434.8 OS=Caenorhabditis elegans GN=ZC434.8 PE=1 SV=1 - [KARG2_CAEEL]
Q19825	13.6	9	80.84	562.8	rrt-1	Probable arginyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=rrt-1 PE=2 SV=2 - [SYRC_CAEEL]
Q22067	13.24	4	45.46	413.3	T01C8.5	Probable aspartate aminotransferase, cytoplasmic OS=Caenorhabditis elegans GN=T01C8.5 PE=2 SV=1 - [AATC_CAEEL]
Q18803	18.32	2	14.82	118.6	asg-2	Probable ATP synthase subunit g 2, mitochondrial OS=Caenorhabditis elegans GN=asg-2 PE=2 SV=1 - [ATPL2_CAEEL]
P53585	8.41	6	121.54	258.0	D1005.1	Probable ATP-citrate synthase OS=Caenorhabditis elegans GN=D1005.1 PE=2 SV=1 - [ACLY_CAEEL]
P34640	4.5	2	65.79	149.0	ZK512.2	Probable ATP-dependent RNA helicase DDX55 homolog OS=Caenorhabditis elegans GN=ZK512.2 PE=2 SV=2 - [DDX55_CAEEL]
P34575	23.08	10	51.51	1267.0	cts-1	Probable citrate synthase, mitochondrial OS=Caenorhabditis elegans GN=cts-1 PE=1 SV=1 - [CISY_CAEEL]
P34574	22.31	33	191.42	2780.4	chc-1	Probable clathrin heavy chain 1 OS=Caenorhabditis elegans GN=chc-1 PE=3 SV=1 - [CLH_CAEEL]
Q20168	8.8	7	111.04	385.2	F38E11.5	Probable coatamer subunit beta' OS=Caenorhabditis elegans GN=F38E11.5 PE=2 SV=3 - [COPB2_CAEEL]
Q09236	4.47	2	56.61	118.9	C13B9.3	Probable coatamer subunit delta OS=Caenorhabditis elegans GN=C13B9.3 PE=2 SV=1 - [COPD_CAEEL]
Q22498	4.25	3	96.24	244.2	T14G10.5	Probable coatamer subunit gamma OS=Caenorhabditis elegans GN=T14G10.5 PE=2 SV=1 - [COPG_CAEEL]
Q23500	17.7	14	96.60	730.8	aco-1	Probable cytoplasmic aconitate hydratase OS=Caenorhabditis elegans GN=aco-1 PE=1 SV=1 - [ACOC_CAEEL]
P54889	16.88	11	86.47	841.7	alh-13	Probable delta-1-pyrroline-5-carboxylate synthase OS=Caenorhabditis elegans GN=alh-13 PE=2 SV=1 - [ALH13_CAEEL]
Q23670	3.16	4	172.23	200.1	K12D12.1	Probable DNA topoisomerase 2 OS=Caenorhabditis elegans GN=K12D12.1 PE=2 SV=2 - [TOP2_CAEEL]
P45971	2.02	1	48.73	37.4	T09A5.11	Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Caenorhabditis elegans GN=T09A5.11
Q93615	27.41	7	34.43	435.2	F27D4.1	Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F27D4.1
P34460	46.01	9	22.69	570.1	F54H12.6	Probable elongation factor 1-beta/1-delta 1 OS=Caenorhabditis elegans GN=F54H12.6 PE=1 SV=1 - [EF1B1_CAEEL]
Q9U2H9	42.59	9	28.16	701.3	Y41E3.10	Probable elongation factor 1-beta/1-delta 2 OS=Caenorhabditis elegans GN=Y41E3.10 PE=1 SV=4 - [EF1B2_CAEEL]
P54412	37.44	14	44.36	1325.2	F17C11.9	Probable elongation factor 1-gamma OS=Caenorhabditis elegans GN=F17C11.9 PE=2 SV=1 - [EF1G_CAEEL]
P34559	25.35	7	31.15	684.7	ech-6	Probable enoyl-CoA hydratase, mitochondrial OS=Caenorhabditis elegans GN=ech-6 PE=1 SV=1 - [ECHM_CAEEL]
Q17632	1.14	1	108.72	41.3	dis-3	Probable exosome complex exonuclease RRP44 OS=Caenorhabditis elegans GN=dis-3 PE=2 SV=2 - [RRP44_CAEEL]
Q22017	5.2	2	58.93	41.5	R53.1	Probable FAD synthase OS=Caenorhabditis elegans GN=R53.1 PE=2 SV=1 - [FLAD1_CAEEL]
O17214	2.4	1	53.61	90.1	fum-1	Probable fumarate hydratase, mitochondrial OS=Caenorhabditis elegans GN=fum-1 PE=1 SV=1 - [FUMH_CAEEL]
O62431	11.83	9	88.21	447.9	ers-1	Probable glutaminyl-tRNA synthetase OS=Caenorhabditis elegans GN=ers-1 PE=3 SV=1 - [SYQ_CAEEL]
O62327	25.15	4	18.14	210.0	R05H10.5	Probable glutathione peroxidase R05H10.5 OS=Caenorhabditis elegans GN=R05H10.5 PE=2 SV=1 - [GPX2_CAEEL]
Q09596	10.14	2	23.24	62.5	gst-5	Probable glutathione S-transferase 5 OS=Caenorhabditis elegans GN=gst-5 PE=1 SV=1 - [GST5_CAEEL]
P91253	9.71	2	23.07	122.7	gst-7	Probable glutathione S-transferase 7 OS=Caenorhabditis elegans GN=gst-7 PE=2 SV=1 - [GST7_CAEEL]
Q09607	4.29	1	23.86	38.5	gst-36	Probable glutathione S-transferase gst-36 OS=Caenorhabditis elegans GN=gst-36 PE=2 SV=2 - [GST36_CAEEL]
Q9U2D9	12.95	8	76.41	441.6	gsy-1	Probable glycogen [starch] synthase OS=Caenorhabditis elegans GN=gsy-1 PE=2 SV=1 - [GYS_CAEEL]
P46548	11.56	4	50.86	176.8	nmt-1	Probable glycopeptide N-tetradecanoyltransferase OS=Caenorhabditis elegans GN=nmt-1 PE=2 SV=1 - [NMT_CAEEL]
Q09580	1.39	1	88.02	42.2	M106.4	Probable GMP synthase [glutamine-hydrolyzing] OS=Caenorhabditis elegans GN=M106.4 PE=1 SV=2 - [GUAA_CAEEL]
Q9TYK1	16.8	3	24.61	244.9	Y66H1A.4	Probable H/ACA ribonucleoprotein complex subunit 1-like protein OS=Caenorhabditis elegans GN=Y66H1A.4
P90916	6.24	3	47.14	130.5	lin-53	Probable histone-binding protein lin-53 OS=Caenorhabditis elegans GN=lin-53 PE=1 SV=2 - [LIN53_CAEEL]
Q9U2M4	10.11	3	50.47	157.8	Y38F1A.6	Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y38F1A.6 PE=2 SV=1 - [HOT_CAEEL]
Q93714	53.35	14	38.44	1791.8	F43G9.1	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F43G9.1
Q93353	27.44	8	41.53	347.2	C37E2.1	Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C37E2.1
P46554	3.6	1	37.79	121.7	B0285.4	Probable leucine carboxyl methyltransferase 1 OS=Caenorhabditis elegans GN=B0285.4 PE=2 SV=1 - [LCMT1_CAEEL]
O02640	68.62	19	35.10	3083.3	mdh-1	Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1 - [MDHM_CAEEL]
P34650	12.26	4	46.35	233.2	ZK632.4	Probable mannose-6-phosphate isomerase OS=Caenorhabditis elegans GN=ZK632.4 PE=2 SV=3 - [MPI_CAEEL]
Q22347	23.5	8	44.79	799.2	acdh-10	Probable medium-chain specific acyl-CoA dehydrogenase 10, mitochondrial OS=Caenorhabditis elegans GN=acdh-10
Q09582	1.12	1	138.81	47.5	nos-1	Probable methionine synthase OS=Caenorhabditis elegans GN=nos-1 PE=1 SV=1 - [METH_CAEEL]
P34385	11.84	6	66.48	253.8	F02A9.4	Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Caenorhabditis elegans GN=F02A9.4
Q17693	13.73	6	75.44	667.5	C06A8.1	Probable methylenetetrahydrofolate reductase OS=Caenorhabditis elegans GN=C06A8.1 PE=2 SV=2 - [MTHR_CAEEL]

P52713	13.77	6	56.43	362.2	alh-8	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Caenorhabditis elegans GN=alh-8
Q23381	15.73	12	81.63	839.1	mmcm-1	Probable methylmalonyl-CoA mutase, mitochondrial OS=Caenorhabditis elegans GN=mmcm-1 PE=2 SV=2 - [MUTA_CAEEL]
Q10457	4.73	1	46.95	66.8	B0286.3	Probable multifunctional protein ADE2 OS=Caenorhabditis elegans GN=B0286.3 PE=1 SV=1 - [PUR6_CAEEL]
Q09510	6.4	1	19.93	45.1	mlc-4	Probable myosin regulatory light chain OS=Caenorhabditis elegans GN=mlc-4 PE=2 SV=1 - [MLRH_CAEEL]
Q9N2W7	7.53	1	17.06	70.7	Y94H6A.8	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Caenorhabditis elegans GN=Y94H6A.8
Q18359	26	4	17.32	149.5	C33A12.1	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Caenorhabditis elegans GN=C33A12.1
Q20719	20.08	4	26.22	180.9	F53F4.10	Probable NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Caenorhabditis elegans GN=F53F4.10
Q93873	10.17	4	54.53	227.4	gas-1	Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Caenorhabditis elegans GN=gas-1
Q94360	12.56	2	21.90	191.2	nduf-7	Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Caenorhabditis elegans GN=nduf-7
Q18040	35.55	12	46.42	1341.6	C16A3.10	Probable ornithine aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=3 - [OAT_CAEEL]
Q21824	5.31	1	24.92	39.7	prdx-3	Probable peroxiredoxin prdx-3 OS=Caenorhabditis elegans GN=prdx-3 PE=1 SV=1 - [TDX1_CAEEL]
P34355	2.28	1	74.67	61.6	C48B4.1	Probable peroxisomal acyl-coenzyme A oxidase OS=Caenorhabditis elegans GN=C48B4.1 PE=3 SV=1 - [ACOX_CAEEL]
P91427	36.45	11	44.09	1044.5	pgk-1	Probable phosphoglycerate kinase OS=Caenorhabditis elegans GN=pgk-1 PE=1 SV=1 - [PGK_CAEEL]
Q9XUE6	5.51	1	28.82	97.4	F52B11.2	Probable phosphomannomutase OS=Caenorhabditis elegans GN=F52B11.2 PE=3 SV=2 - [PMM_CAEEL]
O62515	7.69	2	35.70	134.2	ZK550.6	Probable phytanoyl-CoA dioxygenase OS=Caenorhabditis elegans GN=ZK550.6 PE=2 SV=2 - [PAHX_CAEEL]
O45244	1.19	1	114.22	37.1	mog-4	Probable pre-mRNA-splicing factor ATP-dependent RNA helicase mog-4 OS=Caenorhabditis elegans GN=mog-4
O18054	5.95	1	20.87	103.1	pfd-3	Probable prefoldin subunit 3 OS=Caenorhabditis elegans GN=pfd-3 PE=2 SV=1 - [PFD3_CAEEL]
Q21993	11.18	1	17.14	55.1	pfd-5	Probable prefoldin subunit 5 OS=Caenorhabditis elegans GN=pfd-5 PE=2 SV=1 - [PFD5_CAEEL]
P34329	2.1	1	69.75	260.7	C14B9.2	Probable protein disulfide-isomerase A4 OS=Caenorhabditis elegans GN=C14B9.2 PE=2 SV=2 - [PDIA4_CAEEL]
Q11067	22.5	6	47.70	484.7	tag-320	Probable protein disulfide-isomerase A6 OS=Caenorhabditis elegans GN=tag-320 PE=2 SV=1 - [PDIA6_CAEEL]
P49595	3.87	2	53.11	67.2	F42G9.1	Probable protein phosphatase 2C F42G9.1 OS=Caenorhabditis elegans GN=F42G9.1 PE=2 SV=2 - [PP2C1_CAEEL]
P49596	15.17	4	39.04	176.8	T23F11.1	Probable protein phosphatase 2C T23F11.1 OS=Caenorhabditis elegans GN=T23F11.1 PE=2 SV=2 - [PP2C2_CAEEL]
P52899	20.15	6	43.76	449.4	T05H10.6	Probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=T05H10.6
O17680	34.24	14	43.55	1790.5	sams-1	Probable S-adenosylmethionine synthase 1 OS=Caenorhabditis elegans GN=sams-1 PE=1 SV=1 - [METK1_CAEEL]
Q09543	20.85	11	66.11	571.8	paa-1	Probable serine/threonine-protein phosphatase PP2A regulatory subunit OS=Caenorhabditis elegans GN=paa-1
Q23120	2.49	1	32.40	38.0	rsp-2	Probable splicing factor, arginine/serine-rich 2 OS=Caenorhabditis elegans GN=rsp-2 PE=2 SV=1 - [RSP2_CAEEL]
Q9NEW6	7.75	2	28.66	68.1	rsp-3	Probable splicing factor, arginine/serine-rich 3 OS=Caenorhabditis elegans GN=rsp-3 PE=1 SV=2 - [RSP3_CAEEL]
P53588	33.56	12	47.39	1210.7	F47B10.1	Probable succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=F47B10.1
P53596	29.19	10	33.78	720.0	C05G5.4	Probable succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=C05G5.4
Q09450	18.81	8	56.08	614.5	C05C10.3	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase, mitochondrial OS=Caenorhabditis elegans GN=C05C10.3
O45903	2.62	1	38.17	77.5	W09H1.5	Probable trans-2-enoyl-CoA reductase 1, mitochondrial OS=Caenorhabditis elegans GN=W09H1.5 PE=2 SV=1 - [MECR1_CAEEL]
Q9BLB6	20.55	3	28.85	272.3	sap-1	Probable U2 small nuclear ribonucleoprotein A' OS=Caenorhabditis elegans GN=sap-1 PE=1 SV=1 - [RU2A_CAEEL]
Q09444	8.41	2	37.10	57.5	ubh-4	Probable ubiquitin carboxyl-terminal hydrolase ubh-4 OS=Caenorhabditis elegans GN=ubh-4 PE=2 SV=2 - [UBH4_CAEEL]
Q09349	1.53	1	113.16	49.7	ufd-2	Probable ubiquitin conjugation factor E4 OS=Caenorhabditis elegans GN=ufd-2 PE=2 SV=1 - [UBE4_CAEEL]
Q18493	23.76	8	53.46	832.5	C36A4.4	Probable UDP-N-acetylglucosamine pyrophosphorylase OS=Caenorhabditis elegans GN=C36A4.4 PE=2 SV=2 - [UAP1_CAEEL]
Q19626	22.2	8	54.72	814.0	vha-12	Probable V-type proton ATPase subunit B OS=Caenorhabditis elegans GN=vha-12 PE=1 SV=1 - [VATB_CAEEL]
P91303	11.9	1	14.48	139.0	vha-10	Probable V-type proton ATPase subunit G OS=Caenorhabditis elegans GN=vha-10 PE=2 SV=1 - [VATG_CAEEL]
Q22494	14.89	6	54.18	208.4	vha-15	Probable V-type proton ATPase subunit H 2 OS=Caenorhabditis elegans GN=vha-15 PE=2 SV=1 - [VATH2_CAEEL]
Q21752	42.05	11	29.94	524.8	R05G6.7	Probable voltage-dependent anion-selective channel OS=Caenorhabditis elegans GN=R05G6.7 PE=2 SV=2 - [VDAC_CAEEL]
P52057	3.69	1	27.18	26.9	F09E5.8	Proline synthase co-transcribed bacterial homolog protein OS=Caenorhabditis elegans GN=F09E5.8 PE=2 SV=1 - [PROSC_CAEEL]
Q10576	16.46	8	63.89	447.4	dpy-18	Prolyl 4-hydroxylase subunit alpha-1 OS=Caenorhabditis elegans GN=dpy-18 PE=1 SV=2 - [P4HA1_CAEEL]
Q20065	7.24	3	61.49	125.9	phy-2	Prolyl 4-hydroxylase subunit alpha-2 OS=Caenorhabditis elegans GN=phy-2 PE=1 SV=1 - [P4HA2_CAEEL]
Q19842	25.83	14	79.71	591.9	pcca-1	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Caenorhabditis elegans GN=pcca-1 PE=1 SV=1 - [PCCA_CAEEL]
O44156	3.85	1	28.29	74.5	pas-6	Proteasome subunit alpha type-1 OS=Caenorhabditis elegans GN=pas-6 PE=1 SV=1 - [PSA1_CAEEL]
Q95008	10.89	2	27.19	166.9	pas-5	Proteasome subunit alpha type-5 OS=Caenorhabditis elegans GN=pas-5 PE=1 SV=1 - [PSA5_CAEEL]
Q95005	4.74	1	28.22	125.8	pas-4	Proteasome subunit alpha type-7 OS=Caenorhabditis elegans GN=pas-4 PE=1 SV=1 - [PSA7_CAEEL]
Q27257	2.88	1	33.11	37.0	dif-1	Protein dif-1 OS=Caenorhabditis elegans GN=dif-1 PE=2 SV=1 - [DIF1_CAEEL]
Q17967	38.14	16	53.40	1441.2	pdi-1	Protein disulfide-isomerase 1 OS=Caenorhabditis elegans GN=pdi-1 PE=3 SV=1 - [PDI1_CAEEL]
Q17770	9.53	5	55.12	239.5	pdi-2	Protein disulfide-isomerase 2 OS=Caenorhabditis elegans GN=pdi-2 PE=1 SV=1 - [PDI2_CAEEL]
O44400	23.92	11	61.41	839.7	F37C4.5	Protein F37C4.5 OS=Caenorhabditis elegans GN=F37C4.5 PE=1 SV=3 - [F37C4_CAEEL]
Q18691	3.37	2	37.88	80.4	C47E8.4	Protein FAM50 homolog OS=Caenorhabditis elegans GN=C47E8.4 PE=1 SV=3 - [FAM50_CAEEL]
O01839	2	1	78.72	22.7	B0414.8	Protein fat-free homolog OS=Caenorhabditis elegans GN=B0414.8 PE=1 SV=2 - [FFR_CAEEL]
P34466	11.55	13	139.83	877.6	clu-1	Protein KIAA0664 homolog OS=Caenorhabditis elegans GN=clu-1 PE=2 SV=1 - [K0664_CAEEL]
P49029	28.95	4	17.63	166.3	mag-1	Protein mago nashi homolog OS=Caenorhabditis elegans GN=mag-1 PE=1 SV=2 - [MGN_CAEEL]
Q09564	0.68	1	117.75	41.8	F43C1.1	Protein phosphatase PHLPP-like protein OS=Caenorhabditis elegans GN=F43C1.1 PE=2 SV=2 - [PHLPP_CAEEL]

Q9N4A7	7.99	2	34.67	116.0	npp-20	Protein SEC13 homolog OS=Caenorhabditis elegans GN=npp-20 PE=1 SV=1 - [SEC13_CAEEL]
Q18685	1.81	1	82.30	38.5	unc-112	Protein unc-112 OS=Caenorhabditis elegans GN=unc-112 PE=1 SV=1 - [UN112_CAEEL]
Q01630	2.22	1	90.76	35.6	unc-33	Protein unc-33 OS=Caenorhabditis elegans GN=unc-33 PE=2 SV=1 - [UNC33_CAEEL]
Q9XV66	0.31	1	362.51	30.1	unc-80	Protein unc-80 OS=Caenorhabditis elegans GN=unc-80 PE=2 SV=3 - [UNC80_CAEEL]
P37806	36.11	19	62.69	2477.0	unc-87	Protein unc-87 OS=Caenorhabditis elegans GN=unc-87 PE=1 SV=3 - [UNC87_CAEEL]
P34815	1.78	1	76.68	39.2	unc-18	Putative acetylcholine regulator unc-18 OS=Caenorhabditis elegans GN=unc-18 PE=2 SV=3 - [UNC18_CAEEL]
P46562	2.07	1	56.98	24.1	alh-9	Putative aldehyde dehydrogenase family 7 member A1 homolog OS=Caenorhabditis elegans GN=alh-9 PE=2 SV=2 - [AL7A1_CAEEL]
Q27245	2.49	1	56.05	68.6	W07G4.4	Putative aminopeptidase W07G4.4 OS=Caenorhabditis elegans GN=W07G4.4 PE=1 SV=1 - [YH24_CAEEL]
Q22021	5.23	1	18.74	49.2	R53.4	Putative ATP synthase subunit f, mitochondrial OS=Caenorhabditis elegans GN=R53.4 PE=2 SV=1 - [ATPK_CAEEL]
Q19264	35.97	8	33.07	492.2	F09E5.3	Putative deoxyribose-phosphate aldolase OS=Caenorhabditis elegans GN=F09E5.3 PE=2 SV=1 - [DEOC_CAEEL]
Q09509	1.57	1	56.40	57.0	F25B5.6	Putative polyglutamate synthase OS=Caenorhabditis elegans GN=F25B5.6 PE=2 SV=1 - [FOLC_CAEEL]
P91917	34.94	11	44.32	1231.4	tag-210	Putative GTP-binding protein tag-210 OS=Caenorhabditis elegans GN=tag-210 PE=2 SV=1 - [TG210_CAEEL]
Q9XXD4	6.13	1	18.08	94.8	Y48A6B.3	Putative H/ACA ribonucleoprotein complex subunit 2-like protein OS=Caenorhabditis elegans GN=Y48A6B.3
O17919	13.26	5	50.18	399.6	K01G5.5	Putative H/ACA ribonucleoprotein complex subunit 4 OS=Caenorhabditis elegans GN=K01G5.5 PE=2 SV=1 - [DKC1_CAEEL]
Q17574	9.09	5	76.79	225.3	tag-165	Putative methionine synthase reductase OS=Caenorhabditis elegans GN=tag-165 PE=2 SV=1 - [MTRR_CAEEL]
P91148	3.73	1	33.48	39.7	ndx-7	Putative nudix hydrolase 7 OS=Caenorhabditis elegans GN=ndx-7 PE=2 SV=2 - [NDX7_CAEEL]
Q9XWV2	1.58	1	65.40	24.5	Y37D8A.2	Putative phospholipase B-like 1 OS=Caenorhabditis elegans GN=Y37D8A.2 PE=1 SV=1 - [PLBL1_CAEEL]
Q18846	1.17	1	87.01	36.3	rskn-2	Putative ribosomal protein S6 kinase alpha-2 OS=Caenorhabditis elegans GN=rskn-2 PE=2 SV=2 - [KS6A2_CAEEL]
P90761	0.53	1	189.73	33.1	unc-41	Putative stoned B-like protein OS=Caenorhabditis elegans GN=unc-41 PE=2 SV=2 - [STNB_CAEEL]
Q09541	7.28	8	150.99	644.8	F21H12.6	Putative subtilase-type proteinase F21H12.6 OS=Caenorhabditis elegans GN=F21H12.6 PE=2 SV=1 - [YQS6_CAEEL]
O17730	6.1	2	36.92	131.9	D2023.5	Putative thiosulfate sulfurtransferase D2023.5 OS=Caenorhabditis elegans GN=D2023.5 PE=2 SV=1 - [THT2_CAEEL]
Q9U2G0	1.72	3	243.68	165.1	Y46G5A.4	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Caenorhabditis elegans GN=Y46G5A.4 PE=3 SV=1 - [U520_CAEEL]
Q22295	1.72	1	60.25	34.8	ugt-50	Putative UDP-glucuronosyltransferase ugt-50 OS=Caenorhabditis elegans GN=ugt-50 PE=1 SV=2 - [UGT50_CAEEL]
Q10040	1.05	1	98.20	30.2	C28F5.4	Putative zinc protease C28F5.4 OS=Caenorhabditis elegans GN=C28F5.4 PE=2 SV=2 - [YQA4_CAEEL]
O17732	31.06	26	129.20	1868.1	pyc-1	Pyruvate carboxylase 1 OS=Caenorhabditis elegans GN=pyc-1 PE=1 SV=1 - [PYC1_CAEEL]
O44451	16.48	4	38.12	198.7	C04C3.3	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C04C3.3
Q94986	5.02	1	24.74	32.4	rab-3	Ras-related protein Rab-3 OS=Caenorhabditis elegans GN=rab-3 PE=2 SV=1 - [RAB3_CAEEL]
Q18211	8.44	3	61.45	396.8	ran-3	Regulator of chromosome condensation OS=Caenorhabditis elegans GN=ran-3 PE=2 SV=1 - [RCC1_CAEEL]
P34560	3.75	1	33.69	53.6	rmd-1	Regulator of microtubule dynamics protein 1 OS=Caenorhabditis elegans GN=rmd-1 PE=2 SV=1 - [RMD1_CAEEL]
Q93575	0.7	1	112.87	39.3	rtel-1	Regulator of telomere elongation helicase 1 homolog OS=Caenorhabditis elegans GN=rtel-1 PE=2 SV=3 - [RTEL1_CAEEL]
P92199	0.77	1	135.69	29.4	let-502	Rho-associated protein kinase let-502 OS=Caenorhabditis elegans GN=let-502 PE=1 SV=1 - [ROCK_CAEEL]
Q03604	2.79	2	88.91	106.5	mr-1	Ribonucleoside-diphosphate reductase large subunit OS=Caenorhabditis elegans GN=mr-1 PE=2 SV=1 - [RIR1_CAEEL]
Q23314	2.59	1	31.20	51.1	ZC434.4	Ribosomal RNA-processing protein 7 homolog OS=Caenorhabditis elegans GN=ZC434.4 PE=2 SV=3 - [RRP7_CAEEL]
Q22053	42.61	12	36.36	1543.4	fib-1	rRNA 2'-O-methyltransferase fibrillarlin OS=Caenorhabditis elegans GN=fib-1 PE=2 SV=1 - [FBRL_CAEEL]
P50432	38.66	18	55.73	1997.0	mel-32	Serine hydroxymethyltransferase OS=Caenorhabditis elegans GN=mel-32 PE=1 SV=2 - [GLYC_CAEEL]
Q17941	3.7	2	62.16	94.2	akt-1	Serine/threonine-protein kinase akt-1 OS=Caenorhabditis elegans GN=akt-1 PE=1 SV=2 - [AKT1_CAEEL]
Q9XTG7	2.08	1	61.02	57.3	akt-2	Serine/threonine-protein kinase akt-2 OS=Caenorhabditis elegans GN=akt-2 PE=1 SV=1 - [AKT2_CAEEL]
Q09422	3.87	1	32.47	42.9	pgam-5	Serine/threonine-protein phosphatase Pgam5, mitochondrial OS=Caenorhabditis elegans GN=pgam-5 PE=2 SV=2 - [PGAM5_CAEEL]
Q27497	4.26	1	37.18	42.9	gsp-1	Serine/threonine-protein phosphatase PP1-alpha OS=Caenorhabditis elegans GN=gsp-1 PE=2 SV=2 - [GLC7A_CAEEL]
P48727	11.41	4	37.77	191.0	gsp-2	Serine/threonine-protein phosphatase PP1-beta OS=Caenorhabditis elegans GN=gsp-2 PE=2 SV=1 - [GLC7B_CAEEL]
O17819	4.31	1	37.26	27.5	srg-16	Serpentine receptor class gamma-16 OS=Caenorhabditis elegans GN=srg-16 PE=2 SV=2 - [SRG16_CAEEL]
Q966L5	0.98	1	80.75	30.4	E01A2.2	Serrate RNA effector molecule homolog OS=Caenorhabditis elegans GN=E01A2.2 PE=2 SV=1 - [SRRT_CAEEL]
O16927	12.93	1	13.19	54.0	F25G6.8	Signal recognition particle 14 kDa protein OS=Caenorhabditis elegans GN=F25G6.8 PE=2 SV=1 - [SRP14_CAEEL]
P91240	3.31	2	71.37	48.2	F08D12.1	Signal recognition particle 72 kDa protein homolog OS=Caenorhabditis elegans GN=F08D12.1 PE=3 SV=2 - [SRP72_CAEEL]
Q93235	3.75	1	36.65	66.5	nkb-1	Sodium/potassium-transporting ATPase subunit beta-1 OS=Caenorhabditis elegans GN=nkb-1 PE=1 SV=1 - [AT1B1_CAEEL]
Q18212	21.41	8	48.46	733.5	hel-1	Spliceosome RNA helicase DDX39B homolog OS=Caenorhabditis elegans GN=hel-1 PE=2 SV=1 - [DX39B_CAEEL]
Q20363	72.96	8	17.83	657.4	sip-1	Stress-induced protein 1 OS=Caenorhabditis elegans GN=sip-1 PE=1 SV=1 - [SIP1_CAEEL]
Q20060	0.52	1	176.46	40.8	smc-4	Structural maintenance of chromosomes protein 4 OS=Caenorhabditis elegans GN=smc-4 PE=1 SV=1 - [SMC4_CAEEL]
Q09508	8.98	5	70.35	368.2	sdha-1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Caenorhabditis elegans GN=sdha-1
Q09545	10.4	2	32.87	134.0	sdhb-1	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Caenorhabditis elegans GN=sdhb-1
Q17820	3.21	1	38.71	30.4	aos-1	SUMO-activating enzyme subunit aos-1 OS=Caenorhabditis elegans GN=aos-1 PE=2 SV=1 - [SAE1_CAEEL]
Q95017	4.82	1	19.10	41.1	ubc-9	SUMO-conjugating enzyme UBC9 OS=Caenorhabditis elegans GN=ubc-9 PE=1 SV=1 - [UBC9_CAEEL]
Q18240	2.88	1	35.85	38.1	spr-2	Suppressor of presenilin-2 OS=Caenorhabditis elegans GN=spr-2 PE=2 SV=2 - [SPR2_CAEEL]
P34703	1.38	2	175.71	112.4	emb-5	Suppressor of Ty 6 homolog OS=Caenorhabditis elegans GN=emb-5 PE=1 SV=1 - [SPT6H_CAEEL]
P41988	19.31	9	58.77	536.4	cct-1	T-complex protein 1 subunit alpha OS=Caenorhabditis elegans GN=cct-1 PE=2 SV=2 - [TCPA_CAEEL]

P47207	24.57	10	56.94	557.8	cct-2	T-complex protein 1 subunit beta OS=Caenorhabditis elegans GN=cct-2 PE=1 SV=2 - [TCPB_CAEEL]
P47208	18.15	6	58.35	326.8	cct-4	T-complex protein 1 subunit delta OS=Caenorhabditis elegans GN=cct-4 PE=2 SV=1 - [TCPD_CAEEL]
P47209	7.93	4	59.37	226.3	cct-5	T-complex protein 1 subunit epsilon OS=Caenorhabditis elegans GN=cct-5 PE=1 SV=1 - [TCPE_CAEEL]
Q9N358	8.03	4	59.70	275.8	cct-8	T-complex protein 1 subunit theta OS=Caenorhabditis elegans GN=cct-8 PE=1 SV=3 - [TCPQ_CAEEL]
P46550	10.95	4	58.87	250.5	cct-6	T-complex protein 1 subunit zeta OS=Caenorhabditis elegans GN=cct-6 PE=1 SV=1 - [TCPZ_CAEEL]
P54816	0.46	1	146.33	37.6	lex-1	Tat-binding homolog 7 OS=Caenorhabditis elegans GN=lex-1 PE=1 SV=3 - [TBP7_CAEEL]
Q17688	6.05	2	47.17	79.7	C06A6.5	Thioredoxin domain-containing protein C06A6.5 OS=Caenorhabditis elegans GN=C06A6.5 PE=1 SV=2 - [TXNDL_CAEEL]
Q17745	1.2	1	74.22	30.9	trxr-1	Thioredoxin reductase 1 OS=Caenorhabditis elegans GN=trxr-1 PE=2 SV=3 - [TRXR1_CAEEL]
P52709	7.17	5	84.36	229.2	trs-1	Threonyl-tRNA synthetase, cytoplasmic OS=Caenorhabditis elegans GN=trs-1 PE=2 SV=1 - [SYTC_CAEEL]
Q11069	0.75	1	135.97	24.5	B0416.1	TMC family membrane protein B0416.1 OS=Caenorhabditis elegans GN=B0416.1 PE=1 SV=2 - [YT41_CAEEL]
P41842	1.3	1	87.92	23.4	T20B12.1	TPR repeat-containing protein T20B12.1 OS=Caenorhabditis elegans GN=T20B12.1 PE=2 SV=2 - [YO91_CAEEL]
Q02335	1.93	1	64.83	24.2	ZK370.8	TPR repeat-containing protein ZK370.8 OS=Caenorhabditis elegans GN=ZK370.8 PE=2 SV=3 - [YOL8_CAEEL]
Q18885	11.8	1	17.49	76.2	icd-1 / $\beta$ NAC	Transcription factor BTF3 homolog OS=Caenorhabditis elegans GN=icd-1 PE=1 SV=1 - [BTF3_CAEEL]
Q20646	2.02	1	74.52	40.3	cep-1	Transcription factor cep-1 OS=Caenorhabditis elegans GN=cep-1 PE=1 SV=2 - [CEP1_CAEEL]
P54811	16.69	9	89.73	503.2	cdc-48.1	Transitional endoplasmic reticulum ATPase homolog 1 OS=Caenorhabditis elegans GN=cdc-48.1 PE=1 SV=1 - [TERA1_CAEEL]
P34617	1.09	1	72.22	254.1	ZK1236.1	Translation factor GUF1 homolog, mitochondrial OS=Caenorhabditis elegans GN=ZK1236.1 PE=2 SV=2 - [GUF1_CAEEL]
Q93573	54.7	9	20.53	585.6	tct-1	Translationally-controlled tumor protein homolog OS=Caenorhabditis elegans GN=tct-1 PE=1 SV=1 - [TCTP_CAEEL]
Q10657	25.91	4	26.56	508.2	tpi-1	Triosephosphate isomerase OS=Caenorhabditis elegans GN=tpi-1 PE=1 SV=2 - [TPIS_CAEEL]
Q01479	11.99	3	44.37	109.9	unc-94	Tropomodulin OS=Caenorhabditis elegans GN=unc-94 PE=1 SV=2 - [TMOD_CAEEL]
Q22866	83.45	43	32.98	7149.3	lev-11	Tropomyosin isoforms a/b/d/f OS=Caenorhabditis elegans GN=lev-11 PE=1 SV=1 - [TPM1_CAEEL]
Q27249	80.08	33	29.61	4125.3	lev-11	Tropomyosin isoforms c/e OS=Caenorhabditis elegans GN=lev-11 PE=1 SV=1 - [TPM3_CAEEL]
Q9GYF1	45.87	12	27.54	799.8	unc-27	Troponin I 2 OS=Caenorhabditis elegans GN=unc-27 PE=2 SV=2 - [TNNI2_CAEEL]
Q9XUN9	29.62	8	29.82	657.0	tni-3	Troponin I 3 OS=Caenorhabditis elegans GN=tni-3 PE=2 SV=1 - [TNNI3_CAEEL]
O44572	17.53	4	23.05	173.0	tni-4	Troponin I 4 OS=Caenorhabditis elegans GN=tni-4 PE=2 SV=2 - [TNNI4_CAEEL]
Q27371	49.38	30	47.01	4647.2	mup-2	Troponin T OS=Caenorhabditis elegans GN=mup-2 PE=2 SV=1 - [TNNT_CAEEL]
Q09306	1.64	1	48.42	60.8	tub-1	Tubby protein homolog 1 OS=Caenorhabditis elegans GN=tub-1 PE=1 SV=3 - [TUB1_CAEEL]
P34690	47.32	16	49.88	2867.8	tba-2	Tubulin alpha-2 chain OS=Caenorhabditis elegans GN=tba-2 PE=2 SV=1 - [TBA2_CAEEL]
P91910	16.89	7	50.08	376.5	mec-12	Tubulin alpha-3 chain OS=Caenorhabditis elegans GN=mec-12 PE=1 SV=1 - [TBA3_CAEEL]
P12456	14.06	8	49.23	1276.4	mec-7	Tubulin beta-1 chain OS=Caenorhabditis elegans GN=mec-7 PE=2 SV=1 - [TBB1_CAEEL]
P52275	68.22	25	50.31	7221.2	tbb-2	Tubulin beta-2 chain OS=Caenorhabditis elegans GN=tbb-2 PE=2 SV=1 - [TBB2_CAEEL]
Q23551	1.03	7	788.47	286.4	unc-22	Twitchin OS=Caenorhabditis elegans GN=unc-22 PE=1 SV=3 - [UNC22_CAEEL]
Q17361	13.7	4	55.84	245.1	usp-14	Ubiquitin carboxyl-terminal hydrolase 14 OS=Caenorhabditis elegans GN=usp-14 PE=2 SV=2 - [UBP14_CAEEL]
Q7JKC3	9.6	8	131.51	420.4	usp-7	Ubiquitin carboxyl-terminal hydrolase 7 OS=Caenorhabditis elegans GN=usp-7 PE=2 SV=1 - [UBP7_CAEEL]
Q9XVR6	4.23	1	32.27	40.0	otub-1	Ubiquitin thioesterase otubain-like OS=Caenorhabditis elegans GN=otub-1 PE=2 SV=1 - [OTUBL_CAEEL]
P91430	4.06	1	46.48	61.8	T03F1.1	Ubiquitin-like modifier-activating enzyme 5 OS=Caenorhabditis elegans GN=T03F1.1 PE=3 SV=1 - [UBA5_CAEEL]
Q19905	12.47	5	52.72	276.5	sqv-4	UDP-glucose 6-dehydrogenase OS=Caenorhabditis elegans GN=sqv-4 PE=1 SV=1 - [UGDH_CAEEL]
Q09475	11.03	15	193.97	1012.1	C28H8.3	Uncharacterized helicase C28H8.3 OS=Caenorhabditis elegans GN=C28H8.3 PE=2 SV=2 - [YP93_CAEEL]
Q21276	34.16	12	54.48	1133.6	K07C5.4 ]	Uncharacterized NOP5 family protein K07C5.4 OS=Caenorhabditis elegans GN=K07C5.4 PE=2 SV=1 - [YZVL_CAEEL]
Q22230	4.21	1	33.08	92.5	T05C12.3	Uncharacterized oxidoreductase T05C12.3 OS=Caenorhabditis elegans GN=T05C12.3 PE=2 SV=1 - [YVX3_CAEEL]
P34255	14.29	6	47.84	336.0	B0303.3	Uncharacterized protein B0303.3 OS=Caenorhabditis elegans GN=B0303.3 PE=2 SV=1 - [YKA3_CAEEL]
Q09217	3.83	1	36.95	25.1	B0495.8	Uncharacterized protein B0495.8 OS=Caenorhabditis elegans GN=B0495.8 PE=2 SV=1 - [YP68_CAEEL]
P48053	0.9	1	111.18	49.8	C05D11.1	Uncharacterized protein C05D11.1 OS=Caenorhabditis elegans GN=C05D11.1 PE=1 SV=2 - [YPD1_CAEEL]
Q11189	6.88	1	18.38	43.0	C05D11.10	Uncharacterized protein C05D11.10 OS=Caenorhabditis elegans GN=C05D11.10 PE=2 SV=2 - [YPDA_CAEEL]
Q05036	26.42	18	86.84	891.0	C30C11.4	Uncharacterized protein C30C11.4 OS=Caenorhabditis elegans GN=C30C11.4 PE=1 SV=1 - [YLA4_CAEEL]
P34384	7.87	3	44.35	179.2	F02A9.4b	Uncharacterized protein F02A9.4b OS=Caenorhabditis elegans GN=F02A9.4 PE=2 SV=3 - [YLPD_CAEEL]
P34452	7.64	1	17.18	31.1	F54F2.7	Uncharacterized protein F54F2.7 OS=Caenorhabditis elegans GN=F54F2.7 PE=2 SV=2 - [YMA7_CAEEL]
P34542	2.63	1	72.59	64.1	R05D3.9	Uncharacterized protein R05D3.9 OS=Caenorhabditis elegans GN=R05D3.9/R05D3.10 PE=2 SV=3 - [YNC9_CAEEL]
Q09347	8.86	1	18.36	42.9	T05H10.3	Uncharacterized protein T05H10.3 OS=Caenorhabditis elegans GN=T05H10.3 PE=1 SV=1 - [YRS3_CAEEL]
P34583	2.88	1	38.98	27.9	T26G10.4	Uncharacterized protein T26G10.4 OS=Caenorhabditis elegans GN=T26G10.4 PE=2 SV=1 - [YN24_CAEEL]
Q09359	7.89	2	31.15	42.3	ZK1307.1	Uncharacterized protein ZK1307.1 OS=Caenorhabditis elegans GN=ZK1307.1 PE=2 SV=1 - [YS11_CAEEL]
P34643	0.97	1	134.84	30.3	ZK512.5	Uncharacterized protein ZK512.5 OS=Caenorhabditis elegans GN=ZK512.5 PE=1 SV=1 - [YOQ5_CAEEL]
P34669	3.02	1	37.66	25.3	ZK686.3	Uncharacterized protein ZK686.3 OS=Caenorhabditis elegans GN=ZK686.3 PE=2 SV=1 - [YO13_CAEEL]
P52717	2.35	1	53.61	37.7	F41C3.5	Uncharacterized serine carboxypeptidase F41C3.5 OS=Caenorhabditis elegans GN=F41C3.5 PE=1 SV=1 - [YUW5_CAEEL]
Q10122	0.9	1	153.66	25.4	F52C9.1	Uncharacterized WD repeat-containing protein F52C9.1 OS=Caenorhabditis elegans GN=F52C9.1 PE=4 SV=2 - [YSM1_CAEEL]

Q23256	2.4	1	54.44	25.8	ZC302.2	Uncharacterized WD repeat-containing protein ZC302.2 OS=Caenorhabditis elegans GN=ZC302.2 PE=2 SV=1 - [YH92_CAEEL]
O17606	5.88	2	38.44	74.1	C27H6.8	UPF0160 protein C27H6.8 OS=Caenorhabditis elegans GN=C27H6.8 PE=2 SV=2 - [YK4P_CAEEL]
Q9XW92	25.74	12	66.42	595.9	vha-13	V-type proton ATPase catalytic subunit A OS=Caenorhabditis elegans GN=vha-13 PE=1 SV=3 - [VATA_CAEEL]
Q9XXU9	42.45	16	43.43	882.8	vha-11	V-type proton ATPase subunit C OS=Caenorhabditis elegans GN=vha-11 PE=2 SV=1 - [VATC_CAEEL]
Q9U1Q4	24.1	21	118.85	1403.4	vrs-2	Valyl-tRNA synthetase OS=Caenorhabditis elegans GN=vrs-2 PE=1 SV=1 - [SYV_CAEEL]
Q94392	4.25	3	91.28	227.2	nsf-1	Vesicle-fusing ATPase OS=Caenorhabditis elegans GN=nsf-1 PE=2 SV=2 - [NSF_CAEEL]
P19826	9.5	8	111.85	330.7	deb-1	Vinculin OS=Caenorhabditis elegans GN=deb-1 PE=2 SV=1 - [VINC_CAEEL]
P55155	37.07	59	187.95	4001.1	vit-1	Vitellogenin-1 OS=Caenorhabditis elegans GN=vit-1 PE=1 SV=2 - [VIT1_CAEEL]
P05690	51.15	77	187.60	6580.4	vit-2	Vitellogenin-2 OS=Caenorhabditis elegans GN=vit-2 PE=1 SV=5 - [VIT2_CAEEL]
Q9N4J2	33	51	186.41	3068.7	vit-3	Vitellogenin-3 OS=Caenorhabditis elegans GN=vit-3 PE=1 SV=1 - [VIT3_CAEEL]
P18947	29.07	48	186.19	2850.4	vit-4	Vitellogenin-4 OS=Caenorhabditis elegans GN=vit-4 PE=1 SV=3 - [VIT4_CAEEL]
P06125	33.5	54	186.32	3273.3	vit-5	Vitellogenin-5 OS=Caenorhabditis elegans GN=vit-5 PE=2 SV=2 - [VIT5_CAEEL]
P18948	51.79	76	193.20	8314.9	vit-6	Vitellogenin-6 OS=Caenorhabditis elegans GN=vit-6 PE=1 SV=5 - [VIT6_CAEEL]
O16999	4.4	2	50.90	124.6	W03F9.1	Zinc finger protein ZPR1 homolog OS=Caenorhabditis elegans GN=W03F9.1 PE=3 SV=2 - [ZPR1_CAEEL]
Q21432	2.07	1	64.99	47.4	nas-11	Zinc metalloproteinase nas-11 OS=Caenorhabditis elegans GN=nas-11 PE=1 SV=2 - [NAS11_CAEEL]
Q22396	3.17	1	43.35	112.8	nas-20	Zinc metalloproteinase nas-20 OS=Caenorhabditis elegans GN=nas-20 PE=1 SV=2 - [NAS20_CAEEL]

**Table S3**

Uniprot ID	Coverage [%]	# Peptides	MW [kDa]	Score	Gene name	Description
P41932	11.69	3	28.17	118.9	par-5	14-3-3-like protein 1 OS=Caenorhabditis elegans GN=par-5 PE=1 SV=2 - [14331_CAEEL]
Q20655	47.98	12	28.05	975.5	ftt-2	14-3-3-like protein 2 OS=Caenorhabditis elegans GN=ftt-2 PE=1 SV=1 - [14332_CAEEL]
O61199	8.36	5	115.59	288.1	T22B11.5	2-oxoglutarate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=T22B11.5 PE=1 SV=2 - [ODO1_CAEEL]
Q18787	6.21	2	48.58	218.9	rpt-1	26S protease regulatory subunit 7 OS=Caenorhabditis elegans GN=rpt-1 PE=1 SV=1 - [PRRS7_CAEEL]
Q18115	4.77	2	105.94	166.7	rpn-2	26S proteasome non-ATPase regulatory subunit 1 OS=Caenorhabditis elegans GN=rpn-2 PE=2 SV=4 - [PSMD1_CAEEL]
O76577	16.67	3	34.57	146.1	rpn-11	26S proteasome non-ATPase regulatory subunit 14 OS=Caenorhabditis elegans GN=rpn-11 PE=1 SV=1 - [PSDE_CAEEL]
Q04908	5.56	2	57.47	170.3	rpn-3	26S proteasome non-ATPase regulatory subunit 3 OS=Caenorhabditis elegans GN=rpn-3 PE=1 SV=1 - [PSMD3_CAEEL]
Q20585	21.71	7	47.55	561.2	rpn-7	26S proteasome non-ATPase regulatory subunit 6 OS=Caenorhabditis elegans GN=rpn-7 PE=2 SV=1 - [PSMD6_CAEEL]
Q9NAP9	6.97	2	38.92	136.2	K07A12.7	28S ribosomal protein S15, mitochondrial OS=Caenorhabditis elegans GN=K07A12.7 PE=2 SV=1 - [RT15_CAEEL]
Q95Q11	18.47	3	25.64	163.4	Y57G11C.34	28S ribosomal protein S7, mitochondrial OS=Caenorhabditis elegans GN=Y57G11C.34 PE=3 SV=2 - [RT07_CAEEL]
G5EC67	15.57	3	28.69	160.6	2O16	2O16 OS=Caenorhabditis elegans GN=2O16 PE=2 SV=1 - [G5EC67_CAEEL]
P36573	50.18	15	31.79	1557.1	lec-1	32 kDa beta-galactoside-binding lectin OS=Caenorhabditis elegans GN=lec-1 PE=1 SV=1 - [LEC1_CAEEL]
Q22633	12.47	3	44.36	107.1	hpd-1	4-hydroxyphenylpyruvate dioxygenase OS=Caenorhabditis elegans GN=hpd-1 PE=1 SV=1 - [HPPD_CAEEL]
P49196	7.86	1	15.06	108.5	rps-12	40S ribosomal protein S12 OS=Caenorhabditis elegans GN=rps-12 PE=1 SV=2 - [RS12_CAEEL]
P51404	20.53	5	17.31	490.3	rps-13	40S ribosomal protein S13 OS=Caenorhabditis elegans GN=rps-13 PE=2 SV=2 - [RS13_CAEEL]
P48150	50	9	16.24	837.7	rps-14	40S ribosomal protein S14 OS=Caenorhabditis elegans GN=rps-14 PE=2 SV=1 - [RS14_CAEEL]
Q9XVP0	28.48	3	17.23	427.6	rps-15	40S ribosomal protein S15 OS=Caenorhabditis elegans GN=rps-15 PE=1 SV=3 - [RS15_CAEEL]
Q22054	37.5	6	16.31	563.5	rps-16	40S ribosomal protein S16 OS=Caenorhabditis elegans GN=rps-16 PE=1 SV=3 - [RS16_CAEEL]
O01692	53.85	6	14.93	344.5	rps-17	40S ribosomal protein S17 OS=Caenorhabditis elegans GN=rps-17 PE=2 SV=2 - [RS17_CAEEL]
O18650	39.73	6	16.31	598.4	rps-19	40S ribosomal protein S19 OS=Caenorhabditis elegans GN=rps-19 PE=2 SV=1 - [RS19_CAEEL]
P51403	17.65	4	28.94	217.9	rps-2	40S ribosomal protein S2 OS=Caenorhabditis elegans GN=rps-2 PE=2 SV=1 - [RS2_CAEEL]
Q19877	7.69	1	15.86	277.7	rps-23	40S ribosomal protein S23 OS=Caenorhabditis elegans GN=rps-23 PE=2 SV=1 - [RS23_CAEEL]
P52821	24.79	5	12.90	423.4	rps-25	40S ribosomal protein S25 OS=Caenorhabditis elegans GN=rps-25 PE=2 SV=1 - [RS25_CAEEL]
O45499	23.08	2	13.24	132.6	rps-26	40S ribosomal protein S26 OS=Caenorhabditis elegans GN=rps-26 PE=2 SV=1 - [RS26_CAEEL]
Q9TXP0	15.66	1	9.34	177.6	rps-27	40S ribosomal protein S27 OS=Caenorhabditis elegans GN=rps-27 PE=1 SV=3 - [RS27_CAEEL]
P48152	64.37	15	27.30	1189.5	rps-3	40S ribosomal protein S3 OS=Caenorhabditis elegans GN=rps-3 PE=2 SV=1 - [RS3_CAEEL]
P48154	34.24	9	28.94	809.3	rps-1	40S ribosomal protein S3a OS=Caenorhabditis elegans GN=rps-1 PE=2 SV=2 - [RS3A_CAEEL]
Q9N3X2	52.12	14	29.03	1168.9	rps-4	40S ribosomal protein S4 OS=Caenorhabditis elegans GN=rps-4 PE=1 SV=1 - [RS4_CAEEL]
P49041	16.67	3	23.14	331.2	rps-5	40S ribosomal protein S5 OS=Caenorhabditis elegans GN=rps-5 PE=2 SV=1 - [RS5_CAEEL]
Q9NEN6	24.39	6	28.12	694.6	rps-6	40S ribosomal protein S6 OS=Caenorhabditis elegans GN=rps-6 PE=1 SV=1 - [RS6_CAEEL]
Q23312	47.42	8	22.04	321.6	rps-7	40S ribosomal protein S7 OS=Caenorhabditis elegans GN=rps-7 PE=2 SV=1 - [RS7_CAEEL]
P48156	51.92	8	23.74	582.6	rps-8	40S ribosomal protein S8 OS=Caenorhabditis elegans GN=rps-8 PE=2 SV=1 - [RS8_CAEEL]
Q20228	25.93	6	21.94	329.5	rps-9	40S ribosomal protein S9 OS=Caenorhabditis elegans GN=rps-9 PE=2 SV=1 - [RS9_CAEEL]
P46769	23.19	5	30.68	222.6	rps-0	40S ribosomal protein SA OS=Caenorhabditis elegans GN=rps-0 PE=1 SV=3 - [RSSA_CAEEL]
G5EBI0	6.1	1	23.99	123.0	4D656	4D656 OS=Caenorhabditis elegans GN=4D656 PE=2 SV=1 - [G5EBI0_CAEEL]
Q9TZL8	5.04	3	89.68	206.8	Y71H10A.1	6-phosphofructokinase OS=Caenorhabditis elegans GN=Y71H10A.1 PE=2 SV=2 - [Q9TZL8_CAEEL]
Q17761	4.96	2	53.16	161.4	T25B9.9	6-phosphogluconate dehydrogenase, decarboxylating OS=Caenorhabditis elegans GN=T25B9.9 PE=2 SV=2 - [6PGD_CAEEL]
Q27274	19.13	10	72.80	844.4	rop-1	60 kDa SS-A/Ro ribonucleoprotein homolog OS=Caenorhabditis elegans GN=rop-1 PE=2 SV=1 - [RO60_CAEEL]
Q93572	50.64	12	33.75	1588.5	rpa-0	60S acidic ribosomal protein P0 OS=Caenorhabditis elegans GN=rpa-0 PE=1 SV=3 - [RLA0_CAEEL]
O01504	21.5	1	10.81	111.2	rpa-2	60S acidic ribosomal protein P2 OS=Caenorhabditis elegans GN=rpa-2 PE=2 SV=2 - [RLA2_CAEEL]
Q09533	16.36	4	24.73	522.5	rpl-10	60S ribosomal protein L10 OS=Caenorhabditis elegans GN=rpl-10 PE=2 SV=1 - [RL10_CAEEL]
Q9N414	32.41	5	24.12	633.6	rpl-10a	60S ribosomal protein L10a OS=Caenorhabditis elegans GN=rpl-10a PE=2 SV=1 - [RL10A_CAEEL]
P61866	24.24	3	17.82	246.7	rpl-12	60S ribosomal protein L12 OS=Caenorhabditis elegans GN=rpl-12 PE=2 SV=1 - [RL12_CAEEL]
P91128	23.19	4	23.74	281.1	rpl-13	60S ribosomal protein L13 OS=Caenorhabditis elegans GN=rpl-13 PE=2 SV=1 - [RL13_CAEEL]
P91374	12.75	2	24.11	126.1	rpl-15	60S ribosomal protein L15 OS=Caenorhabditis elegans GN=rpl-15 PE=2 SV=1 - [RL15_CAEEL]
Q9BL19	13.9	2	21.50	273.3	rpl-17	60S ribosomal protein L17 OS=Caenorhabditis elegans GN=rpl-17 PE=2 SV=1 - [RL17_CAEEL]
O45946	44.15	7	20.98	958.0	rpl-18	60S ribosomal protein L18 OS=Caenorhabditis elegans GN=rpl-18 PE=3 SV=1 - [RL18_CAEEL]
O44480	35.56	6	20.95	623.1	rpl-20	60S ribosomal protein L18a OS=Caenorhabditis elegans GN=rpl-20 PE=2 SV=2 - [RL18A_CAEEL]

O02639	23.23	7	23.64	356.3	rpl-19	60S ribosomal protein L19 OS=Caenorhabditis elegans GN=rpl-19 PE=2 SV=1 - [RL19_CAEEEL]
P34334	25.47	4	18.30	287.7	rpl-21	60S ribosomal protein L21 OS=Caenorhabditis elegans GN=rpl-21 PE=1 SV=3 - [RL21_CAEEEL]
P52819	29.23	4	14.94	338.2	rpl-22	60S ribosomal protein L22 OS=Caenorhabditis elegans GN=rpl-22 PE=1 SV=3 - [RL22_CAEEEL]
P48158	25	2	14.94	201.3	rpl-23	60S ribosomal protein L23 OS=Caenorhabditis elegans GN=rpl-23 PE=2 SV=1 - [RL23_CAEEEL]
Q20647	23.29	3	16.27	244.4	rpl-25.2	60S ribosomal protein L23a 2 OS=Caenorhabditis elegans GN=rpl-25.2 PE=2 SV=1 - [R23A2_CAEEEL]
O01868	20.13	4	17.77	436.0	rpl-24.1	60S ribosomal protein L24 OS=Caenorhabditis elegans GN=rpl-24.1 PE=2 SV=1 - [RL24_CAEEEL]
P91914	31.62	5	15.72	382.3	rpl-27	60S ribosomal protein L27 OS=Caenorhabditis elegans GN=rpl-27 PE=2 SV=1 - [RL27_CAEEEL]
Q21930	15.87	2	13.72	326.0	rpl-28	60S ribosomal protein L28 OS=Caenorhabditis elegans GN=rpl-28 PE=1 SV=3 - [RL28_CAEEEL]
P34662	11.38	1	14.19	128.7	rpl-35	60S ribosomal protein L35 OS=Caenorhabditis elegans GN=rpl-35 PE=2 SV=1 - [RL35_CAEEEL]
P49181	46.15	6	11.88	455.2	rpl-36	60S ribosomal protein L36 OS=Caenorhabditis elegans GN=rpl-36 PE=1 SV=3 - [RL36_CAEEEL]
O02056	49.28	19	38.64	1660.0	rpl-4	60S ribosomal protein L4 OS=Caenorhabditis elegans GN=rpl-4 PE=1 SV=3 - [RL4_CAEEEL]
P49405	41.64	9	33.37	2753.2	rpl-5	60S ribosomal protein L5 OS=Caenorhabditis elegans GN=rpl-5 PE=2 SV=1 - [RL5_CAEEEL]
P47991	38.71	9	24.30	784.4	rpl-6	60S ribosomal protein L6 OS=Caenorhabditis elegans GN=rpl-6 PE=1 SV=1 - [RL6_CAEEEL]
O01802	40.98	10	28.11	878.1	rpl-7	60S ribosomal protein L7 OS=Caenorhabditis elegans GN=rpl-7 PE=1 SV=1 - [RL7_CAEEEL]
Q966C6	26.04	8	30.16	580.3	rpl-7A	60S ribosomal protein L7a OS=Caenorhabditis elegans GN=rpl-7A PE=1 SV=3 - [RL7A_CAEEEL]
Q9XVF7	24.23	5	28.19	237.2	rpl-8	60S ribosomal protein L8 OS=Caenorhabditis elegans GN=rpl-8 PE=1 SV=1 - [RL8_CAEEEL]
Q95Y90	24.87	4	21.49	553.2	rpl-9	60S ribosomal protein L9 OS=Caenorhabditis elegans GN=rpl-9 PE=1 SV=1 - [RL9_CAEEEL]
P91154	8.33	1	20.12	111.2	C43E11.9	60S ribosome subunit biogenesis protein NIP7 homolog OS=Caenorhabditis elegans GN=C43E11.9
O01615	15.56	2	24.43	101.9	T19H12.2	Acidic leucine-rich nuclear phosphoprotein 32-related protein 2 OS=Caenorhabditis elegans GN=T19H12.2
P10984	42.02	12	41.75	1806.1	act-2	Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=2 SV=3 - [ACT2_CAEEEL]
Q07750	15.57	3	23.56	270.5	unc-60	Actin-depolymerizing factor 1, isoforms a/b OS=Caenorhabditis elegans GN=unc-60 PE=2 SV=2 - [ADF1_CAEEEL]
P53489	11.39	3	44.81	237.3	arx-2	Actin-related protein 2 OS=Caenorhabditis elegans GN=arx-2 PE=3 SV=1 - [ARP2_CAEEEL]
P27604	29.06	9	47.51	904.7	ahcy-1	Adenosylhomocysteinase OS=Caenorhabditis elegans GN=ahcy-1 PE=1 SV=1 - [SAHH_CAEEEL]
P34346	38.25	8	27.91	620.0	let-754	Adenylate kinase 2, mitochondrial OS=Caenorhabditis elegans GN=let-754 PE=2 SV=2 - [KAD2_CAEEEL]
Q21774	2.72	1	53.53	147.0	R06C7.5	Adenylosuccinate lyase OS=Caenorhabditis elegans GN=R06C7.5 PE=1 SV=1 - [PUR8_CAEEEL]
P91134	10.5	4	50.13	273.7	C37H5.6	Adenylosuccinate synthetase OS=Caenorhabditis elegans GN=C37H5.6 PE=2 SV=3 - [PURA_CAEEEL]
H2L023	9.9	4	52.98	327.4	cas-1	Adenylyl cyclase-associated protein OS=Caenorhabditis elegans GN=cas-1 PE=3 SV=1 - [H2L023_CAEEEL]
Q10943	19.34	3	20.51	127.9	arf-1.2	ADP-ribosylation factor 1-like 2 OS=Caenorhabditis elegans GN=arf-1.2 PE=2 SV=2 - [ARF12_CAEEEL]
G5EFK4	19.44	3	20.58	141.6	arf-3	ADP-ribosylation factor related (20.5 kD) (Arf-3) OS=Caenorhabditis elegans GN=arf-3 PE=2 SV=1 - [G5EFK4_CAEEEL]
O01541	8.57	5	106.72	258.2	aars-2	Alanine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=aars-2 PE=2 SV=1 - [SYAC_CAEEEL]
Q17334	44.13	13	37.67	813.7	sodh-1	Alcohol dehydrogenase 1 OS=Caenorhabditis elegans GN=sodh-1 PE=1 SV=2 - [ADH1_CAEEEL]
Q17335	10.16	3	41.27	239.3	H24K24.3	Alcohol dehydrogenase class-3 OS=Caenorhabditis elegans GN=H24K24.3 PE=2 SV=1 - [ADHX_CAEEEL]
O16518	5.68	2	55.53	147.6	alh-4	Aldehyde dehydrogenase OS=Caenorhabditis elegans GN=alh-4 PE=2 SV=2 - [O16518_CAEEEL]
O45218	7.04	3	66.52	232.6	ads-1	Alkylidihydroxyacetonephosphate synthase OS=Caenorhabditis elegans GN=ads-1 PE=2 SV=1 - [ADAS_CAEEEL]
Q22968	17.66	6	43.89	400.7	F25B4.1	Aminomethyltransferase OS=Caenorhabditis elegans GN=F25B4.1 PE=2 SV=1 - [Q22968_CAEEEL]
P41847	4.62	1	25.53	108.8	T20B12.7	Anamorsin homolog OS=Caenorhabditis elegans GN=T20B12.7 PE=2 SV=1 - [DRE2_CAEEEL]
G5EEA8	54.66	14	35.67	1543.0	nex-1	Annexin OS=Caenorhabditis elegans GN=nex-1 PE=2 SV=1 - [G5EEA8_CAEEEL]
Q7JMT5	7.03	2	49.41	158.4	nex-2	Annexin OS=Caenorhabditis elegans GN=nex-2 PE=2 SV=1 - [Q7JMT5_CAEEEL]
Q27473	18.3	5	36.07	305.7	nex-3	Annexin OS=Caenorhabditis elegans GN=nex-3 PE=2 SV=1 - [Q27473_CAEEEL]
Q19722	10.83	5	61.15	323.1	nrs-1	Asparagine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=nrs-1 PE=2 SV=1 - [SYNC_CAEEEL]
O01804	5.97	2	46.59	116.9	got-2.1	Aspartate aminotransferase OS=Caenorhabditis elegans GN=got-2.1 PE=2 SV=3 - [O01804_CAEEEL]
Q17994	39.13	16	45.59	1041.2	got-2.2	Aspartate aminotransferase OS=Caenorhabditis elegans GN=got-2.2 PE=2 SV=1 - [Q17994_CAEEEL]
Q03577	11.68	5	59.90	436.8	drs-1	Aspartate--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=drs-1 PE=2 SV=1 - [SYDC_CAEEEL]
O01530	16.2	3	41.49	304.5	asp-6	Aspartic protease 6 OS=Caenorhabditis elegans GN=asp-6 PE=2 SV=1 - [ASP6_CAEEEL]
Q94123	4.38	2	41.22	283.3	Ceasp1	Aspartic protease OS=Caenorhabditis elegans GN=Ceasp1 PE=2 SV=1 - [Q94123_CAEEEL]
Q95XJ0	44.82	12	32.36	1991.7	Y69A2AR.18	ATP synthase gamma chain OS=Caenorhabditis elegans GN=Y69A2AR.18 PE=2 SV=1 - [Q95XJ0_CAEEEL]
Q9XXK1	49.26	21	57.75	4220.4	H28O16.1	ATP synthase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=H28O16.1 PE=1 SV=1 - [ATPA_CAEEEL]
P46561	55.76	20	57.49	2780.2	atp-2	ATP synthase subunit beta, mitochondrial OS=Caenorhabditis elegans GN=atp-2 PE=1 SV=2 - [ATPB_CAEEEL]
Q95YF3	17.44	6	48.68	442.0	cgh-1	ATP-dependent RNA helicase cgh-1 OS=Caenorhabditis elegans GN=cgh-1 PE=1 SV=1 - [CGH1_CAEEEL]
P34689	10.75	5	79.73	300.5	glh-1	ATP-dependent RNA helicase glh-1 OS=Caenorhabditis elegans GN=glh-1 PE=1 SV=3 - [GLH1_CAEEEL]
P54813	3.32	3	79.78	159.3	ymel-1	ATP-dependent zinc metalloprotease YME1 homolog OS=Caenorhabditis elegans GN=ymel-1 PE=2 SV=2 - [YME1_CAEEEL]

P30632	16.37	4	37.53	318.8	asna-1	ATPase asna-1 OS=Caenorhabditis elegans GN=asna-1 PE=1 SV=1 - [ASNA_CAEEL]
O01427	16.07	3	34.73	235.9	air-2	Aurora/PL1-related protein kinase 2 OS=Caenorhabditis elegans GN=air-2 PE=1 SV=2 - [AIR2_CAEEL]
Q10663	28.72	16	108.56	1154.0	gei-7	Bifunctional glyoxylate cycle protein OS=Caenorhabditis elegans GN=gei-7 PE=1 SV=2 - [GCP_CAEEL]
P54688	8.19	3	47.31	151.4	bcat-1	Branched-chain-amino-acid aminotransferase, cytosolic OS=Caenorhabditis elegans GN=bcat-1 PE=2 SV=2 - [BCAT_CAEEL]
O62518	5.48	1	33.93	147.8	ZK795.3	Brix domain-containing protein ZK795.3 OS=Caenorhabditis elegans GN=ZK795.3 PE=2 SV=1 - [YHPK_CAEEL]
G5ECX9	14.39	3	32.25	177.8	cdr-2	Cadmium-inducible lysosomal protein CDR-2 OS=Caenorhabditis elegans GN=cdr-2 PE=2 SV=1 - [G5ECX9_CAEEL]
G5EDZ7	14.08	3	32.01	312.2	cdr-4	Cadmium-inducible lysosomal protein CDR-4 OS=Caenorhabditis elegans GN=cdr-4 PE=2 SV=1 - [G5EDZ7_CAEEL]
G5EET3	20.58	4	31.63	169.6	cdr-6	Cadmium-inducible lysosomal protein CDR-6 OS=Caenorhabditis elegans GN=cdr-6 PE=2 SV=1 - [G5EET3_CAEEL]
O76833	2.42	2	126.84	143.7	mca-2	Calcium ATPase OS=Caenorhabditis elegans GN=mca-2 PE=2 SV=1 - [O76833_CAEEL]
P27798	9.87	2	45.59	129.6	crt-1	Calreticulin OS=Caenorhabditis elegans GN=crt-1 PE=1 SV=1 - [CALR_CAEEL]
Q20203	17.51	4	48.30	238.3	csq-1	Calsequestrin OS=Caenorhabditis elegans GN=csq-1 PE=2 SV=1 - [Q20203_CAEEL]
P42168	31.38	10	39.01	457.9	kin-19	Casein kinase I isoform alpha OS=Caenorhabditis elegans GN=kin-19 PE=2 SV=1 - [KC1A_CAEEL]
P18334	33.89	9	42.23	619.2	kin-3	Casein kinase II subunit alpha OS=Caenorhabditis elegans GN=kin-3 PE=1 SV=1 - [CSK2A_CAEEL]
O61235	12.88	4	57.27	186.3	ctl-1	Catalase-2 OS=Caenorhabditis elegans GN=ctl-1 PE=2 SV=3 - [CATA2_CAEEL]
Q94051	13.19	3	26.27	310.8	cav-1	Caveolin-1 OS=Caenorhabditis elegans GN=cav-1 PE=2 SV=1 - [CAV1_CAEEL]
G5ED07	28.28	12	54.89	1005.2	pdi-3	CeERP57 OS=Caenorhabditis elegans GN=pdi-3 PE=2 SV=1 - [G5ED07_CAEEL]
G5EG18	11.19	2	31.71	201.7	crn-2	Cell death-related nuclease 2 OS=Caenorhabditis elegans GN=crn-2 PE=2 SV=1 - [G5EG18_CAEEL]
P50140	29.58	17	60.06	1459.0	hsp-60	Chaperonin homolog Hsp-60, mitochondrial OS=Caenorhabditis elegans GN=hsp-60 PE=1 SV=2 - [CH60_CAEEL]
Q18143	10.78	9	120.12	440.0	C25A8.4	Chitinase-like protein C25A8.4 OS=Caenorhabditis elegans GN=C25A8.4 PE=1 SV=3 - [CHITL_CAEEL]
O45405	10.92	2	27.51	117.8	exl-1	Chloride intracellular channel exl-1 OS=Caenorhabditis elegans GN=exl-1 PE=2 SV=2 - [EXL1_CAEEL]
Q9TYL9	2.16	2	107.46	124.9	Y25C1A.5	Coatomer subunit beta OS=Caenorhabditis elegans GN=Y25C1A.5 PE=2 SV=1 - [Q9TYL9_CAEEL]
O62246	8.9	2	32.78	132.7	F45G2.4	Coatomer subunit epsilon OS=Caenorhabditis elegans GN=F45G2.4 PE=2 SV=1 - [COPE_CAEEL]
Q9N359	3.64	1	46.10	147.5	csn-4	COP9 signalosome complex subunit 4 OS=Caenorhabditis elegans GN=csn-4 PE=1 SV=1 - [CSN4_CAEEL]
Q94261	11.03	4	44.06	156.8	cif-1	COP9/Signalosome and eIF3 complex-shared subunit 1 OS=Caenorhabditis elegans GN=cif-1 SV=1 - [EIF3M_CAEEL]
P34556	20.18	4	38.27	269.4	cdk-1	Cyclin-dependent kinase 1 OS=Caenorhabditis elegans GN=cdk-1 PE=1 SV=1 - [CDK1_CAEEL]
G5EDZ9	20.86	2	15.08	182.6	cpi-1	Cystatin OS=Caenorhabditis elegans GN=cpi-1 PE=2 SV=1 - [G5EDZ9_CAEEL]
Q93244	4.69	1	35.88	104.5	cysl-1	Cysteine synthase OS=Caenorhabditis elegans GN=cysl-1 PE=2 SV=2 - [Q93244_CAEEL]
O45679	18.69	3	36.13	194.9	cysl-2	Cysteine synthase OS=Caenorhabditis elegans GN=cysl-2 PE=2 SV=1 - [O45679_CAEEL]
P98080	37.58	14	51.70	1362.5	ucr-1	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Caenorhabditis elegans GN=ucr-1 PE=2 SV=2 - [UCR1_CAEEL]
P19974	10.81	2	12.23	131.4	cyc-2.1	Cytochrome c 2.1 OS=Caenorhabditis elegans GN=cyc-2.1 PE=1 SV=2 - [CYC21_CAEEL]
P24894	4.76	1	26.53	112.6	cox-2	Cytochrome c oxidase subunit 2 OS=Caenorhabditis elegans GN=cox-2 PE=3 SV=2 - [COX2_CAEEL]
P55954	12.07	3	20.10	125.9	cco-2	Cytochrome c oxidase subunit 5A, mitochondrial OS=Caenorhabditis elegans GN=cco-2 PE=1 SV=2 - [COX5A_CAEEL]
Q19564	14.07	4	37.58	192.7	F18E3.7	D-aspartate oxidase 1 OS=Caenorhabditis elegans GN=F18E3.7 PE=1 SV=1 - [OXDD1_CAEEL]
Q9U3C8	3.05	1	34.11	117.6	dcn-1	Defective in cullin neddylation protein 1 OS=Caenorhabditis elegans GN=dcn-1 PE=1 SV=2 - [DCN1_CAEEL]
O17953	16.97	5	52.60	444.0	dld-1	Dihydrolipoyl dehydrogenase OS=Caenorhabditis elegans GN=dld-1 PE=3 SV=2 - [O17953_CAEEL]
Q19749	16.37	4	53.43	460.4	F23B12.5	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial
Q18066	10.47	5	71.80	524.0	dim-1	Disorganized muscle protein 1 OS=Caenorhabditis elegans GN=dim-1 PE=1 SV=3 - [DIM_CAEEL]
Q27474	2.59	1	86.26	109.1	lig-1	DNA ligase 1 OS=Caenorhabditis elegans GN=lig-1 PE=2 SV=2 - [DNL11_CAEEL]
Q21902	4.08	2	84.88	130.0	mcm-5	DNA replication licensing factor mcm-5 OS=Caenorhabditis elegans GN=mcm-5 PE=2 SV=1 - [MCM5_CAEEL]
P16356	1.78	2	204.40	112.8	ama-1	DNA-directed RNA polymerase II subunit RPB1 OS=Caenorhabditis elegans GN=ama-1 PE=1 SV=3 - [RPB1_CAEEL]
Q17433	8.31	2	39.97	182.7	dnj-2	DnaJ homolog dnj-2 OS=Caenorhabditis elegans GN=dnj-2 PE=1 SV=1 - [DNJ2_CAEEL]
P39055	10.48	6	93.35	337.1	dyn-1	Dynamin OS=Caenorhabditis elegans GN=dyn-1 PE=1 SV=3 - [DYN1_CAEEL]
G5EDY8	4.96	2	79.22	143.9	drp-1	Dynamin-related protein OS=Caenorhabditis elegans GN=drp-1 PE=2 SV=1 - [G5EDY8_CAEEL]
Q19020	1.82	6	521.25	214.4	dhc-1	Dynein heavy chain, cytoplasmic OS=Caenorhabditis elegans GN=dhc-1 PE=2 SV=1 - [DYHC_CAEEL]
Q19070	5.54	4	96.17	235.7	eft-1	Eft-1 protein OS=Caenorhabditis elegans GN=eft-1 PE=2 SV=1 - [Q19070_CAEEL]
P53013	42.98	14	50.64	7956.8	eft-3	Elongation factor 1-alpha OS=Caenorhabditis elegans GN=eft-3 PE=2 SV=1 - [EF1A_CAEEL]
P29691	37.09	29	94.74	5475.0	eef-2	Elongation factor 2 OS=Caenorhabditis elegans GN=eef-2 PE=1 SV=4 - [EF2_CAEEL]
Q20819	12.97	3	34.07	319.2	tsfm-1	Elongation factor Ts, mitochondrial OS=Caenorhabditis elegans GN=tsfm-1 PE=2 SV=1 - [EFTS_CAEEL]
O01971	15.66	2	18.11	119.6	emr-1	Emerin homolog 1 OS=Caenorhabditis elegans GN=emr-1 PE=1 SV=1 - [EMR1_CAEEL]
Q27527	45.39	12	46.59	1084.1	enol-1	Enolase OS=Caenorhabditis elegans GN=enol-1 PE=1 SV=3 - [ENO_CAEEL]
G5EES2	12.61	7	65.96	365.1	erm-1	ERM-1A OS=Caenorhabditis elegans GN=erm-1 PE=2 SV=1 - [G5EES2_CAEEL]



P27639	20.9	7	45.38	431.7	inf-1	Eukaryotic initiation factor 4A OS=Caenorhabditis elegans GN=inf-1 PE=2 SV=1 - [IF4A_CAEEL]
O16520	13.6	5	62.13	261.4	erf-1	Eukaryotic peptide chain release factor subunit 1 OS=Caenorhabditis elegans GN=erf-1 PE=2 SV=2 - [ERF1_CAEEL]
P34339	8.74	9	124.33	491.7	egl-45	Eukaryotic translation initiation factor 3 subunit A OS=Caenorhabditis elegans GN=egl-45 PE=2 SV=1 - [EIF3A_CAEEL]
Q9XW16	5.24	3	83.10	145.0	eif-3.B	Eukaryotic translation initiation factor 3 subunit B OS=Caenorhabditis elegans GN=eif-3.B PE=2 SV=1 - [EIF3B_CAEEL]
O02328	11.02	7	103.78	380.4	eif-3.C	Eukaryotic translation initiation factor 3 subunit C OS=Caenorhabditis elegans GN=eif-3.C PE=2 SV=2 - [EIF3C_CAEEL]
Q18967	15.99	3	32.91	239.8	eif-3.F	Eukaryotic translation initiation factor 3 subunit F OS=Caenorhabditis elegans GN=eif-3.F PE=2 SV=1 - [EIF3F_CAEEL]
Q19706	14.84	2	29.27	105.4	eif-3.G	Eukaryotic translation initiation factor 3 subunit G OS=Caenorhabditis elegans GN=eif-3.G PE=2 SV=1 - [EIF3G_CAEEL]
O01974	10.96	3	40.94	144.3	eif-3.H	Eukaryotic translation initiation factor 3 subunit H OS=Caenorhabditis elegans GN=eif-3.H PE=1 SV=2 - [EIF3H_CAEEL]
Q965S8	7.65	3	36.85	303.9	eif-3.I	Eukaryotic translation initiation factor 3 subunit I OS=Caenorhabditis elegans GN=eif-3.I PE=2 SV=2 - [EIF3I_CAEEL]
Q95QW0	9.87	4	62.44	402.4	eif-3.L	Eukaryotic translation initiation factor 3 subunit L OS=Caenorhabditis elegans GN=eif-3.L PE=1 SV=1 - [EIF3L_CAEEL]
O45551	12.26	2	24.30	107.3	ife-1	Eukaryotic translation initiation factor 4E-1 OS=Caenorhabditis elegans GN=ife-1 PE=1 SV=2 - [IF4E1_CAEEL]
Q21693	20.18	3	25.71	153.7	ife-2	Eukaryotic translation initiation factor 4E-2 OS=Caenorhabditis elegans GN=ife-2 PE=1 SV=1 - [IF4E2_CAEEL]
P34563	39.75	4	17.86	840.8	iff-1	Eukaryotic translation initiation factor 5A-1 OS=Caenorhabditis elegans GN=iff-1 PE=1 SV=1 - [IF5A1_CAEEL]
Q20751	42.24	5	17.94	415.5	iff-2	Eukaryotic translation initiation factor 5A-2 OS=Caenorhabditis elegans GN=iff-2 PE=2 SV=1 - [IF5A2_CAEEL]
O62106	17.48	3	26.29	208.4	eif-6	Eukaryotic translation initiation factor 6 OS=Caenorhabditis elegans GN=eif-6 PE=2 SV=1 - [IF6_CAEEL]
G5EGT7	3.26	2	120.34	172.7	iffb-1	Eukaryotic translation initiation factor eIF5B OS=Caenorhabditis elegans GN=iffb-1 PE=2 SV=1 - [G5EGT7_CAEEL]
Q10901	2.58	1	54.64	180.2	glt-1	Excitatory amino acid transporter OS=Caenorhabditis elegans GN=glt-1 PE=1 SV=2 - [EAA1_CAEEL]
Q9N5R9	7.28	5	116.79	331.5	spt-16	FACT complex subunit spt-16 OS=Caenorhabditis elegans GN=spt-16 PE=2 SV=1 - [SPT16_CAEEL]
Q20224	31.68	8	18.83	250.5	lbp-2	Fatty acid-binding protein homolog 2 OS=Caenorhabditis elegans GN=lbp-2 PE=1 SV=1 - [FABP2_CAEEL]
O01814	29.41	3	15.52	232.3	lbp-5	Fatty acid-binding protein homolog 5 OS=Caenorhabditis elegans GN=lbp-5 PE=2 SV=1 - [FABP5_CAEEL]
O01812	34.07	5	15.63	359.7	lbp-6	Fatty acid-binding protein homolog 6 OS=Caenorhabditis elegans GN=lbp-6 PE=1 SV=1 - [FABP6_CAEEL]
O02323	20.44	2	16.16	155.2	lbp-7	Fatty acid-binding protein homolog 7 OS=Caenorhabditis elegans GN=lbp-7 PE=1 SV=1 - [FABP7_CAEEL]
Q17339	11.66	4	50.55	151.7	gld-1	Female germline-specific tumor suppressor gld-1 OS=Caenorhabditis elegans GN=gld-1 PE=1 SV=1 - [GLD1_CAEEL]
Q9TYS3	43.53	5	19.58	340.0	ftn-2	Ferritin OS=Caenorhabditis elegans GN=ftn-2 PE=1 SV=1 - [Q9TYS3_CAEEL]
G5EBJ7	19.65	5	37.16	506.3	fbp-1	Fructose-1,6-bisphosphatase OS=Caenorhabditis elegans GN=fbp-1 PE=2 SV=1 - [G5EBJ7_CAEEL]
P54216	18.58	4	39.22	330.9	aldo-1	Fructose-bisphosphate aldolase 1 OS=Caenorhabditis elegans GN=aldo-1 PE=1 SV=1 - [ALF1_CAEEL]
P46563	46.17	14	38.82	1321.6	aldo-2	Fructose-bisphosphate aldolase 2 OS=Caenorhabditis elegans GN=aldo-2 PE=2 SV=1 - [ALF2_CAEEL]
G5EGB1	50.72	16	31.28	1043.2	lec-2	Galectin LEC-2 OS=Caenorhabditis elegans GN=lec-2 PE=2 SV=1 - [G5EGB1_CAEEL]
G5EFI4	34.71	10	35.42	953.0	lec-5	Galectin LEC-5 OS=Caenorhabditis elegans GN=lec-5 PE=2 SV=1 - [G5EFI4_CAEEL]
G5EC10	27.14	3	15.55	237.1	lec-9	Galectin LEC-9 OS=Caenorhabditis elegans GN=lec-9 PE=2 SV=1 - [G5EC10_CAEEL]
Q9U1Q2	8.89	4	61.08	302.1	gpi-1	Glucose-6-phosphate isomerase OS=Caenorhabditis elegans GN=gpi-1 PE=2 SV=1 - [Q9U1Q2_CAEEL]
Q23621	45.71	21	58.76	2051.4	gdh-1	Glutamate dehydrogenase OS=Caenorhabditis elegans GN=gdh-1 PE=2 SV=1 - [Q23621_CAEEL]
Q9XTU9	23.24	3	15.76	251.2	glrx-5	Glutaredoxin OS=Caenorhabditis elegans GN=glrx-5 PE=3 SV=1 - [Q9XTU9_CAEEL]
Q21355	31.88	4	23.88	153.9	gst-4	Glutathione S-transferase 4 OS=Caenorhabditis elegans GN=gst-4 PE=2 SV=1 - [GST4_CAEEL]
Q09652	11.95	2	26.46	118.4	gstk-1	Glutathione S-transferase kappa 1 OS=Caenorhabditis elegans GN=gstk-1 PE=3 SV=1 - [GSTK1_CAEEL]
Q9N4X8	15.71	3	24.78	156.7	gst-10	Glutathione S-transferase P 10 OS=Caenorhabditis elegans GN=gst-10 PE=1 SV=3 - [GSTP10_CAEEL]
P10299	22.12	4	23.89	455.4	gst-1	Glutathione S-transferase P OS=Caenorhabditis elegans GN=gst-1 PE=1 SV=1 - [GSTP1_CAEEL]
P04970	22.87	7	36.36	1278.5	gpd-1	Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Caenorhabditis elegans GN=gpd-1 PE=1 SV=1 - [G3P1_CAEEL]
P17329	40.47	11	36.43	2637.1	gpd-2	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Caenorhabditis elegans GN=gpd-2 PE=3 SV=2 - [G3P2_CAEEL]
G5EGA7	8.53	1	24.02	125.2	ras-2	GTP binding protein OS=Caenorhabditis elegans GN=ras-2 PE=2 SV=1 - [G5EGA7_CAEEL]
Q18905	10.11	4	67.73	218.0	cgp-1	GTP-binding protein cgp-1 OS=Caenorhabditis elegans GN=cgp-1 PE=2 SV=2 - [CGP1_CAEEL]
P17343	13.24	4	37.38	458.4	gpb-1	Guanine nucleotide-binding protein subunit beta-1 OS=Caenorhabditis elegans GN=gpb-1 PE=2 SV=2 - [GGB1_CAEEL]
Q21215	62.46	14	35.81	3964.8	rack-1	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Caenorhabditis elegans GN=rack-1 PE=1 SV=3 - [GBLP_CAEEL]
Q23495	1.15	1	185.11	104.9	toe-1	HEAT repeat-containing protein 1 homolog OS=Caenorhabditis elegans GN=toe-1 PE=2 SV=1 - [HEAT1_CAEEL]
P09446	40.16	21	69.68	1886.8	hsp-1	Heat shock 70 kDa protein A OS=Caenorhabditis elegans GN=hsp-1 PE=1 SV=2 - [HSP7A_CAEEL]
P27420	22.54	13	72.98	1399.1	hsp-3	Heat shock 70 kDa protein C OS=Caenorhabditis elegans GN=hsp-3 PE=1 SV=2 - [HSP7C_CAEEL]
P20163	15.37	10	72.24	1053.9	hsp-4	Heat shock 70 kDa protein D OS=Caenorhabditis elegans GN=hsp-4 PE=1 SV=2 - [HSP7D_CAEEL]
P11141	22.22	12	70.80	1080.6	hsp-6	Heat shock 70 kDa protein F, mitochondrial OS=Caenorhabditis elegans GN=hsp-6 PE=1 SV=2 - [HSP7F_CAEEL]
Q18688	25.93	13	80.23	1077.7	daf-21	Heat shock protein 90 OS=Caenorhabditis elegans GN=daf-21 PE=1 SV=1 - [HSP90_CAEEL]
Q22037	13.58	4	36.32	228.7	hrp-1	Heterogeneous nuclear ribonucleoprotein A1 OS=Caenorhabditis elegans GN=hrp-1 PE=1 SV=1 - [ROA1_CAEEL]
P53795	31.54	2	14.23	104.2	hint-1	Histidine triad nucleotide-binding protein 1 OS=Caenorhabditis elegans GN=hint-1 PE=2 SV=1 - [HINT_CAEEL]

P34183	8.64	3	58.52	262.9	hrs-1	Histidine--tRNA ligase OS=Caenorhabditis elegans GN=hrs-1 PE=2 SV=3 - [SYH_CAEEL]
P10771	12.5	2	21.35	126.6	his-24	Histone H1.1 OS=Caenorhabditis elegans GN=his-24 PE=1 SV=4 - [H11_CAEEL]
P09588	12.6	2	13.40	190.8	his-3	Histone H2A OS=Caenorhabditis elegans GN=his-3 PE=1 SV=2 - [H2A_CAEEL]
Q27511	23.57	3	14.66	243.1	htz-1	Histone H2A.V OS=Caenorhabditis elegans GN=htz-1 PE=2 SV=3 - [H2AV_CAEEL]
P04255	27.87	3	13.49	676.8	his-11	Histone H2B.1 OS=Caenorhabditis elegans GN=his-11 PE=1 SV=4 - [H2B1_CAEEL]
P62784	45.63	7	11.36	618.6	his-1	Histone H4 OS=Caenorhabditis elegans GN=his-1 PE=1 SV=2 - [H4_CAEEL]
P91276	2.82	1	59.14	150.7	ima-2	Importin subunit alpha-2 OS=Caenorhabditis elegans GN=ima-2 PE=1 SV=1 - [IMA2_CAEEL]
Q23593	3.93	2	44.51	144.8	inx-8	Innexin-8 OS=Caenorhabditis elegans GN=inx-8 PE=2 SV=2 - [INX8_CAEEL]
Q19420	12.28	2	30.96	231.3	ttx-7	Inositol monophosphatase ttx-7 OS=Caenorhabditis elegans GN=ttx-7 PE=1 SV=2 - [IMPA1_CAEEL]
P90901	5.22	2	66.49	113.6	ifa-1	Intermediate filament protein ifa-1 OS=Caenorhabditis elegans GN=ifa-1 PE=1 SV=2 - [IFA1_CAEEL]
O02365	10.5	4	67.05	123.3	ifa-2	Intermediate filament protein ifa-2 OS=Caenorhabditis elegans GN=ifa-2 PE=1 SV=1 - [IFA2_CAEEL]
P90900	21.49	7	66.59	478.4	ifa-4	Intermediate filament protein ifa-4 OS=Caenorhabditis elegans GN=ifa-4 PE=1 SV=2 - [IFA4_CAEEL]
Q19289	14.77	6	67.11	578.3	ifb-1	Intermediate filament protein ifb-1 OS=Caenorhabditis elegans GN=ifb-1 PE=1 SV=1 - [IFB1_CAEEL]
Q19286	43.09	17	61.57	1599.1	ifb-2	Intermediate filament protein ifb-2 OS=Caenorhabditis elegans GN=ifb-2 PE=1 SV=1 - [IFB2_CAEEL]
Q21067	13.18	8	70.06	567.6	ifc-2	Intermediate filament protein ifc-2 OS=Caenorhabditis elegans GN=ifc-2 PE=1 SV=3 - [IFC2_CAEEL]
Q09501	1.93	1	89.00	164.3	ifp-1	Intermediate filament protein ifp-1 OS=Caenorhabditis elegans GN=ifp-1 PE=2 SV=1 - [IFP1_CAEEL]
P49049	7.48	3	52.76	149.9	imp-2	Intramembrane protease 2 OS=Caenorhabditis elegans GN=imp-2 PE=1 SV=1 - [IMP2_CAEEL]
Q21032	35.68	11	45.93	867.8	idh-1	Isocitrate dehydrogenase [NADP] OS=Caenorhabditis elegans GN=idh-1 PE=2 SV=1 - [Q21032_CAEEL]
O17643	14.94	5	49.01	311.5	idh-2	Isocitrate dehydrogenase [NADP] OS=Caenorhabditis elegans GN=idh-2 PE=2 SV=1 - [O17643_CAEEL]
Q21926	7.1	6	129.93	446.1	irs-1	Isoleucine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=irs-1 PE=2 SV=1 - [SYIC_CAEEL]
G5EEH6	21.24	5	45.61	290.5	ivd-1	Isovaleryl-CoA dehydrogenase OS=Caenorhabditis elegans GN=ivd-1 PE=2 SV=1 - [G5EEH6_CAEEL]
P34540	3.31	2	91.84	235.7	unc-116	Kinesin heavy chain OS=Caenorhabditis elegans GN=unc-116 PE=2 SV=2 - [KIN1_CAEEL]
G5EC43	11.14	5	87.38	355.8	zen-4	Kinesin-like protein ZEN-4b OS=Caenorhabditis elegans GN=zen-4 PE=2 SV=1 - [G5EC43_CAEEL]
Q18026	11.3	4	54.01	233.1	C15H9.7	Kynureninase OS=Caenorhabditis elegans GN=C15H9.7 PE=2 SV=1 - [KYNU_CAEEL]
Q21443	36.57	15	64.05	739.8	lmn-1	Lamin-1 OS=Caenorhabditis elegans GN=lmn-1 PE=1 SV=2 - [LMN1_CAEEL]
Q11117	16.03	3	25.78	364.4	imp-1	LAMP family protein Imp-1 OS=Caenorhabditis elegans GN=imp-1 PE=2 SV=1 - [LMP1_CAEEL]
Q9XTB5	7.4	2	55.12	125.7	lem-2	LEM protein 2 OS=Caenorhabditis elegans GN=lem-2 PE=1 SV=1 - [LEM2_CAEEL]
G5EBZ4	0.44	1	209.02	114.4	let-418	LET-418 OS=Caenorhabditis elegans GN=let-418 PE=1 SV=1 - [G5EBZ4_CAEEL]
P34629	18.94	5	52.42	274.6	lap-1	Leucine aminopeptidase 1 OS=Caenorhabditis elegans GN=lap-1 PE=1 SV=1 - [AMPL_CAEEL]
Q09996	9.11	8	134.43	523.8	irs-1	Leucine--tRNA ligase OS=Caenorhabditis elegans GN=irs-1 PE=2 SV=2 - [SYLC_CAEEL]
O01658	7.35	4	85.97	181.9	T28F2.4	Lysine-specific demethylase NO66 OS=Caenorhabditis elegans GN=T28F2.4 PE=2 SV=2 - [NO66_CAEEL]
Q2XN16	17.12	5	58.55	470.2	kars-1	Lysyl-tRNA synthetase OS=Caenorhabditis elegans GN=kars-1 PE=2 SV=1 - [Q2XN16_CAEEL]
G5ECY0	3.62	2	106.93	180.2	dlg-1	MAGUK protein DLG-1 OS=Caenorhabditis elegans GN=dlg-1 PE=2 SV=1 - [G5ECY0_CAEEL]
P05634	23.62	2	14.23	140.3	msp-10	Major sperm protein 10/36/56/76 OS=Caenorhabditis elegans GN=msp-10 PE=2 SV=4 - [MSP10_CAEEL]
Q44782	33.06	5	26.83	528.7	vpr-1	Major sperm protein OS=Caenorhabditis elegans GN=vpr-1 PE=1 SV=1 - [O44782_CAEEL]
Q9UAV5	39.29	9	35.78	631.2	mdh-1	Malate dehydrogenase OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1 - [Q9UAV5_CAEEL]
Q9U296	13.87	5	69.49	296.1	men-1	Malic enzyme OS=Caenorhabditis elegans GN=men-1 PE=2 SV=1 - [Q9U296_CAEEL]
Q09293	14.71	4	41.08	225.3	mel-47	Maternal effect lethal protein 47 OS=Caenorhabditis elegans GN=mel-47 PE=2 SV=2 - [MEL47_CAEEL]
Q20970	9.49	6	101.65	592.1	mrs-1	Methionine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=mrs-1 PE=2 SV=1 - [SYMC_CAEEL]
Q22111	10.28	3	44.19	237.8	mmaa-1	Methylmalonic aciduria type A homolog, mitochondrial OS=Caenorhabditis elegans GN=mmaa-1 PE=2 SV=2 - [MMAA1_CAEEL]
O62252	8.75	1	18.15	171.6	F45G2.10	MIP18 family protein F45G2.10 OS=Caenorhabditis elegans GN=F45G2.10 PE=1 SV=1 - [J195_CAEEL]
Q22647	16.15	4	51.35	345.5	scpl-4	Mitochondrial import inner membrane translocase subunit TIM50 OS=Caenorhabditis elegans GN=scpl-4
Q18090	27.91	7	32.37	769.0	C18E9.6	Mitochondrial import receptor subunit TOM40 homolog OS=Caenorhabditis elegans GN=C18E9.6 PE=2 SV=1 - [TOM40_CAEEL]
Q9N4K0	21.9	4	11.13	267.7	F54A3.5	Mitochondrial inner membrane organizing system protein F54A3.5 OS=Caenorhabditis elegans GN=F54A3.5
G5EEG4	19.75	4	17.55	244.7	mce-1	Mitochondrial methylmalonyl-CoA epimerase OS=Caenorhabditis elegans GN=mce-1 PE=2 SV=1 - [G5EEG4_CAEEL]
Q9BKU4	44	10	29.97	1448.9	phb-1	Mitochondrial prohibitin complex protein 1 OS=Caenorhabditis elegans GN=phb-1 PE=1 SV=1 - [PHB1_CAEEL]
P50093	32.99	9	32.65	1633.2	phb-2	Mitochondrial prohibitin complex protein 2 OS=Caenorhabditis elegans GN=phb-2 PE=1 SV=2 - [PHB2_CAEEL]
P54815	5.26	2	37.64	105.6	mspn-1	Mitochondrial sorting homolog OS=Caenorhabditis elegans GN=mspn-1 PE=2 SV=2 - [MSP1_CAEEL]
Q9N4G7	15.89	4	36.93	187.3	Y71F9B.2	Mitochondrial translocator assembly and maintenance protein 41 homolog OS=Caenorhabditis elegans GN=Y71F9B.2
P34713	2.68	2	140.20	125.9	pgp-3	Multidrug resistance protein pgp-3 OS=Caenorhabditis elegans GN=pgp-3 PE=2 SV=2 - [PGP3_CAEEL]
P19625	51.18	5	18.61	328.3	mlc-1	Myosin regulatory light chain 1 OS=Caenorhabditis elegans GN=mlc-1 PE=2 SV=1 - [MLR1_CAEEL]

P02567	2.17	3	223.19	184.0	let-75	Myosin-1 OS=Caenorhabditis elegans GN=let-75 PE=2 SV=3 - [MYO1_CAEEL]
P12844	5.79	8	225.37	553.5	myo-3	Myosin-3 OS=Caenorhabditis elegans GN=myo-3 PE=2 SV=1 - [MYO3_CAEEL]
P02566	26.7	39	224.99	4203.4	unc-54	Myosin-4 OS=Caenorhabditis elegans GN=unc-54 PE=4 SV=1 - [MYO4_CAEEL]
Q9UB28	2.92	6	497.15	198.2	let-805	Myotactin form B OS=Caenorhabditis elegans GN=let-805 PE=2 SV=1 - [Q9UB28_CAEEL]
P90789	46.34	4	14.40	303.4	D2030.4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Caenorhabditis elegans GN=D2030.4
Q86S66	35.53	6	22.06	421.2	Y65B4BR.5 / icd-2 / $\alpha$ NAC	Nascent polypeptide-associated complex subunit alpha OS=Caenorhabditis elegans GN=Y65B4BR.5
G5EFS2	10.63	2	35.48	109.2	msi-1	Neural RNA-binding protein MSI-1 OS=Caenorhabditis elegans GN=msi-1 PE=2 SV=1 - [G5EFS2_CAEEL]
Q21568	35.94	3	13.99	350.7	M28.5	NHP2-like protein 1 homolog OS=Caenorhabditis elegans GN=M28.5 PE=2 SV=1 - [NH2L1_CAEEL]
Q23655	18.64	2	13.12	128.2	nlt-1	Non-specific lipid-transfer protein-like OS=Caenorhabditis elegans GN=nlt-1 PE=2 SV=1 - [NLT1_CAEEL]
Q93576	26.14	3	17.11	554.4	ndk-1	Nucleoside diphosphate kinase OS=Caenorhabditis elegans GN=ndk-1 PE=1 SV=1 - [Q93576_CAEEL]
G5EE74	4.06	1	36.40	104.4	nud-1	NUD-1 OS=Caenorhabditis elegans GN=nud-1 PE=2 SV=1 - [G5EE74_CAEEL]
G5EE96	14.14	4	32.00	110.5	K11G12.5	Oxoglutarate/malate carrier protein OS=Caenorhabditis elegans GN=K11G12.5 PE=2 SV=1 - [G5EE96_CAEEL]
Q9TZQ3	9.18	5	78.41	286.6	pgl-1	P granule abnormality protein 1 OS=Caenorhabditis elegans GN=pgl-1 PE=1 SV=1 - [PGL1_CAEEL]
P10567	7.26	4	101.89	207.7	unc-15	Paramyosin OS=Caenorhabditis elegans GN=unc-15 PE=1 SV=1 - [MYSP_CAEEL]
P52009	19.79	3	20.70	466.4	cyn-1	Peptidyl-prolyl cis-trans isomerase 1 OS=Caenorhabditis elegans GN=cyn-1 PE=2 SV=1 - [CYP1_CAEEL]
P52017	31.68	3	17.95	151.2	cyn-10	Peptidyl-prolyl cis-trans isomerase 10 OS=Caenorhabditis elegans GN=cyn-10 PE=2 SV=2 - [CYP10_CAEEL]
P52011	50.87	6	18.54	505.5	cyn-3	Peptidyl-prolyl cis-trans isomerase 3 OS=Caenorhabditis elegans GN=cyn-3 PE=1 SV=1 - [CYP3_CAEEL]
P52013	22.55	4	21.91	267.3	cyn-5	Peptidyl-prolyl cis-trans isomerase 5 OS=Caenorhabditis elegans GN=cyn-5 PE=1 SV=2 - [CYP5_CAEEL]
P52015	72.51	9	18.39	1065.8	cyn-7	Peptidyl-prolyl cis-trans isomerase 7 OS=Caenorhabditis elegans GN=cyn-7 PE=1 SV=2 - [CYP7_CAEEL]
Q18445	21.3	2	18.51	198.2	cyn-12	Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=cyn-12 PE=1 SV=1 - [Q18445_CAEEL]
Q27462	20.37	3	11.62	194.3	FKBP-2	Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=FKBP-2 PE=2 SV=1 - [Q27462_CAEEL]
Q95Y89	9.79	4	61.59	102.3	lpd-7	Pescadillo homolog OS=Caenorhabditis elegans GN=lpd-7 PE=2 SV=1 - [PESC_CAEEL]
Q19713	9.81	5	66.02	251.1	frs-2	Phenylalanine--tRNA ligase beta subunit OS=Caenorhabditis elegans GN=frs-2 PE=1 SV=2 - [SYFB_CAEEL]
P40614	32.65	11	36.65	1159.4	F01G4.6	Phosphate carrier protein, mitochondrial OS=Caenorhabditis elegans GN=F01G4.6 PE=2 SV=1 - [MPCC_CAEEL]
Q10949	14.85	3	42.46	304.8	psd-1	Phosphatidylserine decarboxylase proenzyme OS=Caenorhabditis elegans GN=psd-1 PE=2 SV=2 - [PISD_CAEEL]
Q9N5U1	25.62	16	101.55	1292.3	T22F3.3	Phosphorylase OS=Caenorhabditis elegans GN=T22F3.3 PE=2 SV=1 - [Q9N5U1_CAEEL]
G5EF02	3.7	1	39.19	100.3	spn-4	PIP-1 OS=Caenorhabditis elegans GN=spn-4 PE=2 SV=1 - [G5EF02_CAEEL]
P0CG71	32.82	2	93.93	528.4	ubq-1	Polyubiquitin-A OS=Caenorhabditis elegans GN=ubq-1 PE=3 SV=1 - [UBIQ1_CAEEL]
P34369	2.49	3	271.85	152.8	prp-8	Pre-mRNA-splicing factor 8 homolog OS=Caenorhabditis elegans GN=prp-8 PE=1 SV=1 - [PRP8_CAEEL]
Q17336	3.57	2	104.21	109.5	let-858	Pre-mRNA-splicing factor CWC22 homolog OS=Caenorhabditis elegans GN=let-858 PE=2 SV=1 - [CWC22_CAEEL]
Q02332	8.98	2	45.25	118.0	pdhk-2	Probable [pyruvate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Caenorhabditis elegans GN=pdhk-2
O17071	29.31	9	45.83	541.1	rpt-4	Probable 26S protease regulatory subunit 10B OS=Caenorhabditis elegans GN=rpt-4 PE=1 SV=2 - [PRS10_CAEEL]
O16368	13.54	4	49.69	458.0	rpt-2	Probable 26S protease regulatory subunit 4 OS=Caenorhabditis elegans GN=rpt-2 PE=2 SV=1 - [PRS4_CAEEL]
P46502	14.98	3	46.33	104.1	rpt-3	Probable 26S protease regulatory subunit 6B OS=Caenorhabditis elegans GN=rpt-3 PE=2 SV=1 - [PRS6B_CAEEL]
Q20938	7.08	2	49.06	116.2	rpn-6.1	Probable 26S proteasome regulatory subunit rpn-6.1 OS=Caenorhabditis elegans GN=rpn-6.1 PE=2 SV=2 - [PS11A_CAEEL]
P41938	24.27	5	33.36	443.5	B0272.3	Probable 3-hydroxyacyl-CoA dehydrogenase B0272.3 OS=Caenorhabditis elegans GN=B0272.3 PE=1 SV=1 - [HCDH2_CAEEL]
Q9XTI0	35.45	7	31.20	327.4	B0250.5	Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=B0250.5
Q9GYS9	12.58	2	19.08	115.8	T08B2.8	Probable 39S ribosomal protein L23, mitochondrial OS=Caenorhabditis elegans GN=T08B2.8 PE=2 SV=1 - [RM23_CAEEL]
Q95Y71	5.88	2	41.29	137.9	Y119D3B.16	Probable 39S ribosomal protein L45, mitochondrial OS=Caenorhabditis elegans GN=Y119D3B.16 PE=2 SV=3 - [RM45_CAEEL]
Q21939	18.18	3	21.76	144.0	R11D1.9	Probable 39S ribosomal protein L49, mitochondrial OS=Caenorhabditis elegans GN=R11D1.9 PE=2 SV=2 - [RM49_CAEEL]
Q21217	26.92	9	53.02	768.9	gta-1	Probable 4-aminobutyrate aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=gta-1 PE=1 SV=1 - [GABT_CAEEL]
P34388	5.36	2	43.67	190.8	F09G8.3	Probable 40S ribosomal protein S9, mitochondrial OS=Caenorhabditis elegans GN=F09G8.3 PE=2 SV=2 - [RT09_CAEEL]
P34455	13.77	7	83.99	585.3	aco-2	Probable aconitate hydratase, mitochondrial OS=Caenorhabditis elegans GN=aco-2 PE=1 SV=2 - [ACON_CAEEL]
Q8WTM6	10.3	3	34.46	154.6	arx-4	Probable actin-related protein 2/3 complex subunit 2 OS=Caenorhabditis elegans GN=arx-4 PE=2 SV=1 - [ARPC2_CAEEL]
P58798	23.08	5	19.65	337.6	arx-6	Probable actin-related protein 2/3 complex subunit 4 OS=Caenorhabditis elegans GN=arx-6 PE=3 SV=1 - [ARPC4_CAEEL]
Q20140	32.38	4	22.58	359.2	F38B2.4	Probable adenylate kinase isoenzyme F38B2.4 OS=Caenorhabditis elegans GN=F38B2.4 PE=2 SV=1 - [KAD1_CAEEL]
Q10454	37.88	11	44.14	1647.7	F46H5.3	Probable arginine kinase F46H5.3 OS=Caenorhabditis elegans GN=F46H5.3 PE=1 SV=2 - [KARG1_CAEEL]
Q27535	20.28	5	40.36	479.6	ZC434.8	Probable arginine kinase ZC434.8 OS=Caenorhabditis elegans GN=ZC434.8 PE=1 SV=1 - [KARG2_CAEEL]
Q22067	14.95	4	45.46	202.2	T01C8.5	Probable aspartate aminotransferase, cytoplasmic OS=Caenorhabditis elegans GN=T01C8.5 PE=2 SV=1 - [AATC_CAEEL]
P90921	18.32	2	14.91	205.4	asg-1	Probable ATP synthase subunit g 1, mitochondrial OS=Caenorhabditis elegans GN=asg-1 PE=2 SV=1 - [ATPL1_CAEEL]
Q18803	36.64	4	14.82	347.7	asg-2	Probable ATP synthase subunit g 2, mitochondrial OS=Caenorhabditis elegans GN=asg-2 PE=2 SV=1 - [ATPL2_CAEEL]

P53585	8.5	6	121.54	364.8	D1005.1	Probable ATP-citrate synthase OS=Caenorhabditis elegans GN=D1005.1 PE=2 SV=1 - [ACLY_CAEEL]
P34640	4.5	2	65.79	146.6	ZK512.2	Probable ATP-dependent RNA helicase DDX55 homolog OS=Caenorhabditis elegans GN=ZK512.2
Q21153	6.08	4	78.62	189.6	K02F3.2	Probable calcium-binding mitochondrial carrier K02F3.2 OS=Caenorhabditis elegans GN=K02F3.2 PE=2 SV=2 - [CMC1_CAEEL]
P34575	22.01	6	51.51	622.8	cts-1	Probable citrate synthase, mitochondrial OS=Caenorhabditis elegans GN=cts-1 PE=1 SV=1 - [CISY_CAEEL]
P34574	11.36	13	191.42	1038.8	chc-1	Probable clathrin heavy chain 1 OS=Caenorhabditis elegans GN=chc-1 PE=3 SV=1 - [CLH_CAEEL]
Q20168	4.9	3	111.04	157.4	F38E11.5	Probable coatomer subunit beta' OS=Caenorhabditis elegans GN=F38E11.5 PE=2 SV=3 - [COPB2_CAEEL]
Q09236	10.49	2	56.61	152.3	C13B9.3	Probable coatomer subunit delta OS=Caenorhabditis elegans GN=C13B9.3 PE=2 SV=1 - [COPD_CAEEL]
Q22498	4.6	2	96.24	111.1	T14G10.5	Probable coatomer subunit gamma OS=Caenorhabditis elegans GN=T14G10.5 PE=2 SV=1 - [COPG_CAEEL]
Q20779	44.53	6	14.73	442.5	tag-174	Probable cytochrome c oxidase subunit 6A, mitochondrial OS=Caenorhabditis elegans GN=tag-174
Q23500	9.7	5	96.60	238.1	aco-1	Probable cytoplasmic aconitate hydratase OS=Caenorhabditis elegans GN=aco-1 PE=1 SV=1 - [ACOC_CAEEL]
Q23670	11.64	12	172.23	688.4	K12D12.1	Probable DNA topoisomerase 2 OS=Caenorhabditis elegans GN=K12D12.1 PE=2 SV=2 - [TOP2_CAEEL]
Q9XVH6	26.23	2	13.69	138.4	rpb-11	Probable DNA-directed RNA polymerase II subunit RPB11 OS=Caenorhabditis elegans GN=rpb-11
Q93615	43.37	11	34.43	1020.6	F27D4.1	Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F27D4.1
P34559	28.47	7	31.15	626.3	ech-6	Probable enoyl-CoA hydratase, mitochondrial OS=Caenorhabditis elegans GN=ech-6 PE=1 SV=1 - [ECHM_CAEEL]
O17214	28.54	7	53.61	404.8	fum-1	Probable fumarate hydratase, mitochondrial OS=Caenorhabditis elegans GN=fum-1 PE=1 SV=1 - [FUMH_CAEEL]
Q09610	15.56	2	20.43	385.0	lec-8	Probable galactin lec-8 OS=Caenorhabditis elegans GN=lec-8 PE=2 SV=2 - [LEC8_CAEEL]
P41992	2.99	1	37.20	109.3	ggtb-1	Probable geranylgeranyl transferase type-2 subunit beta OS=Caenorhabditis elegans GN=ggtb-1 PE=2 SV=2 - [GGTB2_CAEEL]
Q9XVJ2	4.49	1	29.89	110.8	T03F6.3	Probable glucosamine-6-phosphate isomerase OS=Caenorhabditis elegans GN=T03F6.3 PE=1 SV=1 - [GNPI_CAEEL]
O62431	18.96	9	88.21	432.3	ers-1	Probable glutamine-tRNA ligase OS=Caenorhabditis elegans GN=ers-1 PE=3 SV=1 - [SYQ_CAEEL]
P91253	25.73	4	23.07	185.0	gst-7	Probable glutathione S-transferase 7 OS=Caenorhabditis elegans GN=gst-7 PE=2 SV=1 - [GST7_CAEEL]
Q09607	49.52	7	23.86	281.1	gst-36	Probable glutathione S-transferase gst-36 OS=Caenorhabditis elegans GN=gst-36 PE=2 SV=2 - [GST36_CAEEL]
P90795	20.5	10	80.76	730.9	T25G3.4	Probable glycerol-3-phosphate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=T25G3.4
O16294	20.11	5	38.78	246.0	F32D1.5	Probable GMP reductase OS=Caenorhabditis elegans GN=F32D1.5 PE=2 SV=1 - [GMPR_CAEEL]
Q9TYK1	11.07	2	24.61	151.1	Y66H1A.4	Probable HIACA ribonucleoprotein complex subunit 1-like protein OS=Caenorhabditis elegans GN=Y66H1A.4
Q09250	19.88	3	18.96	201.6	C16C10.4	Probable histone deacetylase complex subunit SAP18 OS=Caenorhabditis elegans GN=C16C10.4
P90916	10.31	3	47.14	247.8	lin-53	Probable histone-binding protein lin-53 OS=Caenorhabditis elegans GN=lin-53 PE=1 SV=2 - [LIN53_CAEEL]
Q9U2M4	15.91	3	50.47	213.8	Y38F1A.6	Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y38F1A.6
Q18680	9.34	3	44.13	184.5	pyp-1	Probable inorganic pyrophosphatase 1 OS=Caenorhabditis elegans GN=pyp-1 PE=2 SV=3 - [IPYR_CAEEL]
Q93714	31.28	7	38.44	778.5	F43G9.1	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F43G9.1
Q93353	22.43	7	41.53	564.1	C37E2.1	Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C37E2.1
O02640	66.86	16	35.10	1480.1	mdh-1	Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1 - [MDHM_CAEEL]
Q18938	11.68	2	23.64	109.3	gst-42	Probable maleylacetoacetate isomerase OS=Caenorhabditis elegans GN=gst-42 PE=1 SV=1 - [MAAI_CAEEL]
P34650	6.49	2	46.35	146.5	ZK632.4	Probable mannose-6-phosphate isomerase OS=Caenorhabditis elegans GN=ZK632.4 PE=2 SV=3 - [MPI_CAEEL]
Q22347	19.18	6	44.79	433.9	acdH-10	Probable medium-chain specific acyl-CoA dehydrogenase 10, mitochondrial OS=Caenorhabditis elegans GN=acdH-10
P52713	15.49	5	56.43	462.2	alh-8	Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Caenorhabditis elegans GN=alh-8
Q23381	4.97	3	81.63	120.0	mmcm-1	Probable methylmalonyl-CoA mutase, mitochondrial OS=Caenorhabditis elegans GN=mmcm-1 PE=2 SV=2 - [MUTA_CAEEL]
Q10457	12.29	3	46.95	215.8	B0286.3	Probable multifunctional protein ADE2 OS=Caenorhabditis elegans GN=B0286.3 PE=1 SV=1 - [PUR6_CAEEL]
Q9N2W7	26.71	4	17.06	218.0	Y94H6A.8	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Caenorhabditis elegans GN=Y94H6A.8
Q18359	39.33	5	17.32	452.0	C33A12.1	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Caenorhabditis elegans GN=C33A12.1
Q20412	20.63	3	18.47	180.5	F44G4.2	Probable NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial OS=Caenorhabditis elegans
Q20719	30.13	8	26.22	471.3	F53F4.10	Probable NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Caenorhabditis elegans GN=F53F4.10
Q93873	4.98	2	54.53	149.3	gas-1	Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Caenorhabditis elegans GN=gas-1
Q94360	12.56	2	21.90	222.4	nduf-7	Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Caenorhabditis elegans GN=nduf-7
Q18040	39.81	11	46.42	975.5	C16A3.10	Probable ornithine aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=3 - [OAT_CAEEL]
Q21824	21.24	5	24.92	394.4	prdx-3	Probable peroxiredoxin prdx-3 OS=Caenorhabditis elegans GN=prdx-3 PE=1 SV=1 - [TDX1_CAEEL]
P91427	29.26	8	44.09	600.1	pgk-1	Probable phosphoglycerate kinase OS=Caenorhabditis elegans GN=pgk-1 PE=1 SV=1 - [PGK_CAEEL]
O62515	5.45	1	35.70	136.3	ZK550.6	Probable phytanoyl-CoA dioxygenase OS=Caenorhabditis elegans GN=ZK550.6 PE=2 SV=2 - [PAHX_CAEEL]
Q21993	17.76	2	17.14	144.2	pdf-5	Probable prefoldin subunit 5 OS=Caenorhabditis elegans GN=pdf-5 PE=2 SV=1 - [PFD5_CAEEL]
P34329	2.1	1	69.75	147.3	C14B9.2	Probable protein disulfide-isomerase A4 OS=Caenorhabditis elegans GN=C14B9.2 PE=2 SV=2 - [PDIA4_CAEEL]
Q11067	19.32	6	47.70	826.5	tag-320	Probable protein disulfide-isomerase A6 OS=Caenorhabditis elegans GN=tag-320 PE=2 SV=1 - [PDIA6_CAEEL]
P52899	22.67	5	43.76	397.3	T05H10.6	Probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Caenorhabditis elegans

Q19537	11.76	4	73.16	168.1	rpa-1	Probable replication factor A 73 kDa subunit OS=Caenorhabditis elegans GN=rpa-1 PE=1 SV=1 - [RFA1_CAEEL]
P34429	14.95	4	41.15	179.0	F44B9.8	Probable replication factor C subunit 5 OS=Caenorhabditis elegans GN=F44B9.8 PE=3 SV=3 - [RFC5_CAEEL]
Q20496	28.27	3	21.91	181.2	rhi-1	Probable rho GDP-dissociation inhibitor OS=Caenorhabditis elegans GN=rhi-1 PE=2 SV=1 - [GDIR_CAEEL]
Q17606	9.26	2	18.79	377.7	rpl-24.2	Probable ribosome biogenesis protein RLP24 OS=Caenorhabditis elegans GN=rpl-24.2 PE=2 SV=1 - [RLP24_CAEEL]
O17680	9.93	3	43.55	325.2	sams-1	Probable S-adenosylmethionine synthase 1 OS=Caenorhabditis elegans GN=sams-1 PE=1 SV=1 - [METK1_CAEEL]
Q18678	12.32	4	55.19	419.2	srs-2	Probable serine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=srs-2 PE=3 SV=1 - [SYSC_CAEEL]
Q09543	12.71	6	66.11	459.9	paa-1	Probable serine/threonine-protein phosphatase PP2A regulatory subunit OS=Caenorhabditis elegans GN=paa-1
P34525	20.56	3	20.67	192.1	K12H4.4	Probable signal peptidase complex subunit 3 OS=Caenorhabditis elegans GN=K12H4.4 PE=1 SV=1 - [SPCS3_CAEEL]
Q20822	9.16	4	70.53	295.5	F55C5.8	Probable signal recognition particle 68 kDa protein OS=Caenorhabditis elegans GN=F55C5.8 PE=2 SV=2 - [SRP68_CAEEL]
P91918	33.13	3	16.73	138.5	snr-2	Probable small nuclear ribonucleoprotein-associated protein B OS=Caenorhabditis elegans GN=snr-2
Q9XUY5	28.39	7	35.73	357.0	nkb-3	Probable sodium/potassium-transporting ATPase subunit beta-3 OS=Caenorhabditis elegans GN=nkb-3
Q23121	10.9	4	35.02	401.4	rsp-1	Probable splicing factor, arginine/serine-rich 1 OS=Caenorhabditis elegans GN=rsp-1 PE=2 SV=1 - [RSP1_CAEEL]
Q23120	12.1	3	32.40	257.5	rsp-2	Probable splicing factor, arginine/serine-rich 2 OS=Caenorhabditis elegans GN=rsp-2 PE=2 SV=1 - [RSP2_CAEEL]
Q9NEW6	15.89	4	28.66	162.2	rsp-3	Probable splicing factor, arginine/serine-rich 3 OS=Caenorhabditis elegans GN=rsp-3 PE=1 SV=2 - [RSP3_CAEEL]
P53588	11.72	5	47.39	422.7	F47B10.1	Probable succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=F47B10.1
P53596	25.47	8	33.78	573.1	C05G5.4	Probable succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=C05G5.4
P53589	6.27	2	45.06	130.5	C50F7.4	Probable succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C50F7.4
Q09450	11.9	3	56.08	216.6	C05C10.3	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase, mitochondrial OS=Caenorhabditis elegans
P34604	16.39	3	34.10	126.3	ZK1098.4	Probable translation initiation factor eIF-2B subunit alpha OS=Caenorhabditis elegans GN=ZK1098.4
Q9BLB6	5.53	1	28.85	130.6	sap-1	Probable U2 small nuclear ribonucleoprotein A' OS=Caenorhabditis elegans GN=sap-1 PE=1 SV=1 - [RU2A_CAEEL]
Q09444	7.48	2	37.10	104.3	ubh-4	Probable ubiquitin carboxyl-terminal hydrolase ubh-4 OS=Caenorhabditis elegans GN=ubh-4 PE=2 SV=2 - [UBH4_CAEEL]
Q18493	6.2	2	53.46	170.3	C36A4.4	Probable UDP-N-acetylglucosamine pyrophosphorylase OS=Caenorhabditis elegans GN=C36A4.4 PE=2 SV=2 - [UAP1_CAEEL]
Q94218	8.66	4	66.54	192.3	F38A5.1	Probable Ufm1-specific protease OS=Caenorhabditis elegans GN=F38A5.1 PE=2 SV=1 - [JFSP_CAEEL]
P30628	1.66	1	103.33	157.1	unc-32	Probable V-type proton ATPase 116 kDa subunit a OS=Caenorhabditis elegans GN=unc-32 PE=2 SV=3 - [VPP1_CAEEL]
Q19626	31.77	9	54.72	873.4	vha-12	Probable V-type proton ATPase subunit B OS=Caenorhabditis elegans GN=vha-12 PE=1 SV=1 - [VATB_CAEEL]
P91303	25.4	3	14.48	319.1	vha-10	Probable V-type proton ATPase subunit G OS=Caenorhabditis elegans GN=vha-10 PE=2 SV=1 - [VATG_CAEEL]
Q22494	12.13	4	54.18	301.3	vha-15	Probable V-type proton ATPase subunit H 2 OS=Caenorhabditis elegans GN=vha-15 PE=2 SV=1 - [VATH2_CAEEL]
Q21752	92.93	25	29.94	8151.0	R05G6.7	Probable voltage-dependent anion-selective channel OS=Caenorhabditis elegans GN=R05G6.7 PE=2 SV=2 - [VDAC_CAEEL]
Q9XW16	60.61	6	14.25	328.0	pfn-1	Profilin-1 OS=Caenorhabditis elegans GN=pfn-1 PE=2 SV=1 - [PROF1_CAEEL]
Q20025	30.53	2	14.24	104.3	pfn-2	Profilin-2 OS=Caenorhabditis elegans GN=pfn-2 PE=2 SV=3 - [PROF2_CAEEL]
Q10576	9.84	4	63.89	219.6	dpy-18	Prolyl 4-hydroxylase subunit alpha-1 OS=Caenorhabditis elegans GN=dpy-18 PE=1 SV=2 - [P4HA1_CAEEL]
P34676	3.35	1	56.90	100.6	pcp-5	Prolyl carboxy peptidase like protein 5 OS=Caenorhabditis elegans GN=pcp-5 PE=1 SV=1 - [PCP5_CAEEL]
Q19842	22.24	9	79.71	786.5	pcca-1	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Caenorhabditis elegans GN=pcca-1 PE=1 SV=1 - [PCCA_CAEEL]
O44156	32.69	6	28.29	594.5	pas-6	Proteasome subunit alpha type-1 OS=Caenorhabditis elegans GN=pas-6 PE=1 SV=1 - [PSA1_CAEEL]
Q27488	18.18	3	25.32	247.0	pas-2	Proteasome subunit alpha type-2 OS=Caenorhabditis elegans GN=pas-2 PE=1 SV=1 - [PSA2_CAEEL]
Q09583	16.4	3	27.73	293.8	pas-7	Proteasome subunit alpha type-3 OS=Caenorhabditis elegans GN=pas-7 PE=1 SV=3 - [PSA3_CAEEL]
Q95008	24.19	4	27.19	199.7	pas-5	Proteasome subunit alpha type-5 OS=Caenorhabditis elegans GN=pas-5 PE=1 SV=1 - [PSA5_CAEEL]
O17586	26.42	5	27.03	537.8	pas-1	Proteasome subunit alpha type-6 OS=Caenorhabditis elegans GN=pas-1 PE=1 SV=1 - [PSA6_CAEEL]
Q95005	26.88	4	28.22	407.0	pas-4	Proteasome subunit alpha type-7 OS=Caenorhabditis elegans GN=pas-4 PE=1 SV=1 - [PSA7_CAEEL]
O62102	5.05	1	29.84	106.4	pbs-2	Proteasome subunit beta type OS=Caenorhabditis elegans GN=pbs-2 PE=1 SV=1 - [O62102_CAEEL]
Q9XUV0	17.25	4	31.21	341.5	pbs-5	Proteasome subunit beta type OS=Caenorhabditis elegans GN=pbs-5 PE=3 SV=1 - [Q9XUV0_CAEEL]
P34286	12.4	2	28.91	238.9	pbs-6	Proteasome subunit beta type-1 OS=Caenorhabditis elegans GN=pbs-6 PE=1 SV=2 - [PSB1_CAEEL]
Q23237	29.41	4	22.68	251.4	pbs-3	Proteasome subunit beta type-3 OS=Caenorhabditis elegans GN=pbs-3 PE=1 SV=1 - [PSB3_CAEEL]
Q9U3F8	2.97	2	103.67	148.5	aagr-3	Protein AAGR-3, isoform b OS=Caenorhabditis elegans GN=aagr-3 PE=2 SV=1 - [Q9U3F8_CAEEL]
Q9U2K8	7.05	3	68.95	170.5	abce-1	Protein ABCE-1 OS=Caenorhabditis elegans GN=abce-1 PE=3 SV=1 - [Q9U2K8_CAEEL]
G5EFG4	8.36	4	70.33	155.6	abcf-2	Protein ABCF-2 OS=Caenorhabditis elegans GN=abcf-2 PE=3 SV=1 - [G5EFG4_CAEEL]
Q20306	1.83	1	80.24	104.7	abcf-3	Protein ABCF-3 OS=Caenorhabditis elegans GN=abcf-3 PE=2 SV=1 - [Q20306_CAEEL]
Q3T978	3.45	2	67.21	178.2	acdh-11	Protein ACDH-11, isoform b OS=Caenorhabditis elegans GN=acdh-11 PE=2 SV=1 - [Q3T978_CAEEL]
Q19057	6.2	2	66.13	242.3	acdh-12	Protein ACDH-12, isoform a OS=Caenorhabditis elegans GN=acdh-12 PE=2 SV=1 - [Q19057_CAEEL]
O44549	14.56	5	45.75	480.4	acdh-3	Protein ACDH-3 OS=Caenorhabditis elegans GN=acdh-3 PE=2 SV=1 - [O44549_CAEEL]
Q22781	20.87	6	44.59	385.3	acdh-7	Protein ACDH-7 OS=Caenorhabditis elegans GN=acdh-7 PE=2 SV=2 - [Q22781_CAEEL]

P90731	6.82	5	120.52	403.9	acly-2	Protein ACly-2 OS=Caenorhabditis elegans GN=acly-2 PE=2 SV=1 - [P90731_CAEEEL]
Q9GUF2	33.6	11	43.00	684.7	acp-6	Protein ACP-6 OS=Caenorhabditis elegans GN=acp-6 PE=2 SV=2 - [Q9GUF2_CAEEEL]
Q9N302	6.54	3	78.97	264.1	acs-13	Protein ACS-13 OS=Caenorhabditis elegans GN=acs-13 PE=2 SV=1 - [Q9N302_CAEEEL]
Q20121	13.95	7	81.20	409.2	acs-4	Protein ACS-4 OS=Caenorhabditis elegans GN=acs-4 PE=2 SV=2 - [Q20121_CAEEEL]
Q9XWD1	5.24	3	75.71	280.0	acs-5	Protein ACS-5 OS=Caenorhabditis elegans GN=acs-5 PE=2 SV=1 - [Q9XWD1_CAEEEL]
Q95ZL1	32.23	7	37.25	453.1	act-4	Protein ACT-4, isoform b OS=Caenorhabditis elegans GN=act-4 PE=2 SV=1 - [Q95ZL1_CAEEEL]
Q6A8K1	43.65	12	40.40	1925.3	act-4	Protein ACT-4, isoform c OS=Caenorhabditis elegans GN=act-4 PE=2 SV=1 - [Q6A8K1_CAEEEL]
O45815	38.13	9	41.85	899.5	act-5	Protein ACT-5 OS=Caenorhabditis elegans GN=act-5 PE=2 SV=1 - [O45815_CAEEEL]
O62334	2.04	2	165.82	141.0	agl-1	Protein AGL-1 OS=Caenorhabditis elegans GN=agl-1 PE=2 SV=1 - [O62334_CAEEEL]
Q86B39	2.92	2	99.46	106.6	alg-2	Protein ALG-2, isoform b OS=Caenorhabditis elegans GN=alg-2 PE=2 SV=1 - [Q86B39_CAEEEL]
Q8IG19	21.09	7	45.56	475.9	alh-1	Protein ALH-1, isoform b OS=Caenorhabditis elegans GN=alh-1 PE=2 SV=1 - [Q8IG19_CAEEEL]
G4RZC3	8.04	2	45.97	178.1	alh-6	Protein ALH-6, isoform d OS=Caenorhabditis elegans GN=alh-6 PE=4 SV=1 - [G4RZC3_CAEEEL]
O45865	43.33	18	33.02	8121.6	ant-1.1	Protein ANT-1.1, isoform a OS=Caenorhabditis elegans GN=ant-1.1 PE=2 SV=1 - [O45865_CAEEEL]
Q22601	1.95	1	104.11	130.5	apa-2	Protein APA-2 OS=Caenorhabditis elegans GN=apa-2 PE=1 SV=2 - [Q22601_CAEEEL]
Q19202	14.08	4	40.29	255.6	apy-1	Protein APY-1 OS=Caenorhabditis elegans GN=apy-1 PE=1 SV=2 - [Q19202_CAEEEL]
Q7JMQ6	5.61	1	30.85	129.3	aqp-2	Protein AQP-2, isoform b OS=Caenorhabditis elegans GN=aqp-2 PE=2 SV=1 - [Q7JMQ6_CAEEEL]
Q19102	35.27	6	27.13	361.4	ard-1	Protein ARD-1 OS=Caenorhabditis elegans GN=ard-1 PE=2 SV=1 - [Q19102_CAEEEL]
Q9NA98	16.04	4	42.04	355.7	arp-1	Protein ARP-1 OS=Caenorhabditis elegans GN=arp-1 PE=2 SV=2 - [Q9NA98_CAEEEL]
Q9U1R7	4.35	1	41.06	130.9	arx-3	Protein ARX-3 OS=Caenorhabditis elegans GN=arx-3 PE=2 SV=1 - [Q9U1R7_CAEEEL]
Q20053	42.86	12	34.35	732.2	asb-1	Protein ASB-1 OS=Caenorhabditis elegans GN=asb-1 PE=2 SV=1 - [Q20053_CAEEEL]
Q19126	43.28	12	34.92	665.8	asb-2	Protein ASB-2 OS=Caenorhabditis elegans GN=asb-2 PE=2 SV=1 - [Q19126_CAEEEL]
Q21966	16.22	6	49.25	583.1	asp-4	Protein ASP-4 OS=Caenorhabditis elegans GN=asp-4 PE=2 SV=1 - [Q21966_CAEEEL]
Q20748	21.68	9	67.11	700.0	atad-3	Protein ATAD-3 OS=Caenorhabditis elegans GN=atad-3 PE=2 SV=2 - [Q20748_CAEEEL]
H2L2C8	4.01	3	95.55	104.2	atn-1	Protein ATN-1, isoform d OS=Caenorhabditis elegans GN=atn-1 PE=4 SV=1 - [H2L2C8_CAEEEL]
P91283	41.55	11	22.38	1083.8	atp-3	Protein ATP-3, isoform a OS=Caenorhabditis elegans GN=atp-3 PE=2 SV=1 - [P91283_CAEEEL]
Q17763	40.31	6	21.78	355.7	atp-5	Protein ATP-5 OS=Caenorhabditis elegans GN=atp-5 PE=2 SV=2 - [Q17763_CAEEEL]
Q17432	12.32	2	22.10	255.8	B0035.3	Protein B0035.3 OS=Caenorhabditis elegans GN=B0035.3 PE=2 SV=1 - [Q17432_CAEEEL]
O61741	7.28	2	45.30	123.0	B0205.6	Protein B0205.6 OS=Caenorhabditis elegans GN=B0205.6 PE=2 SV=2 - [O61741_CAEEEL]
O16486	11.87	2	31.88	126.2	B0238.10	Protein B0238.10 OS=Caenorhabditis elegans GN=B0238.10 PE=2 SV=1 - [O16486_CAEEEL]
O16487	5.36	1	36.48	186.2	B0238.11	Protein B0238.11 OS=Caenorhabditis elegans GN=B0238.11 PE=2 SV=1 - [O16487_CAEEEL]
Q17475	14.92	5	61.09	274.3	B0334.3	Protein B0334.3, isoform b OS=Caenorhabditis elegans GN=B0334.3 PE=3 SV=2 - [Q17475_CAEEEL]
Q17512	49.24	12	36.41	1057.8	B0491.5	Protein B0491.5 OS=Caenorhabditis elegans GN=B0491.5 PE=2 SV=1 - [Q17512_CAEEEL]
O61815	10.29	4	61.24	255.6	B0511.6	Protein B0511.6 OS=Caenorhabditis elegans GN=B0511.6 PE=2 SV=2 - [O61815_CAEEEL]
Q18817	31.98	10	49.41	1184.8	ben-1	Protein BEN-1 OS=Caenorhabditis elegans GN=ben-1 PE=2 SV=3 - [Q18817_CAEEEL]
Q9U1S2	16.67	6	63.26	347.4	brp-1	Protein BRP-1, isoform a OS=Caenorhabditis elegans GN=brp-1 PE=2 SV=1 - [Q9U1S2_CAEEEL]
Q9XWH0	22.16	4	38.10	213.1	bub-3	Protein BUB-3 OS=Caenorhabditis elegans GN=bub-3 PE=1 SV=1 - [Q9XWH0_CAEEEL]
O02207	4.64	1	40.48	103.0	C01A2.3	Protein C01A2.3 OS=Caenorhabditis elegans GN=C01A2.3 PE=2 SV=2 - [O02207_CAEEEL]
Q93168	28.07	6	38.54	623.7	C01G10.8	Protein C01G10.8 OS=Caenorhabditis elegans GN=C01G10.8 PE=2 SV=1 - [Q93168_CAEEEL]
Q17572	10.59	3	44.85	152.2	C01G6.3	Protein C01G6.3 OS=Caenorhabditis elegans GN=C01G6.3 PE=2 SV=2 - [Q17572_CAEEEL]
O44444	15.17	2	23.23	103.2	C02B10.4	Protein C02B10.4 OS=Caenorhabditis elegans GN=C02B10.4 PE=2 SV=1 - [O44444_CAEEEL]
A6PVA5	7.04	1	22.63	102.6	C05C8.1	Protein C05C8.1, isoform b OS=Caenorhabditis elegans GN=C05C8.1 PE=4 SV=1 - [A6PVA5_CAEEEL]
Q17686	6.8	2	45.44	165.8	C06A6.4	Protein C06A6.4, isoform a OS=Caenorhabditis elegans GN=C06A6.4 PE=2 SV=3 - [Q17686_CAEEEL]
P91020	34.38	7	35.17	727.3	C07D8.6	Protein C07D8.6 OS=Caenorhabditis elegans GN=C07D8.6 PE=1 SV=1 - [P91020_CAEEEL]
G5EFJ3	21.53	3	24.36	221.6	C08E8.4	Protein C08E8.4 OS=Caenorhabditis elegans GN=C08E8.4 PE=4 SV=1 - [G5EFJ3_CAEEEL]
Q17832	18.36	17	134.26	1243.3	C08H9.2	Protein C08H9.2, isoform a OS=Caenorhabditis elegans GN=C08H9.2 PE=2 SV=2 - [Q17832_CAEEEL]
Q8MXH7	22.16	3	20.76	237.2	C11D2.7	Protein C11D2.7 OS=Caenorhabditis elegans GN=C11D2.7 PE=2 SV=1 - [Q8MXH7_CAEEEL]
Q5TYL8	18.14	3	25.56	145.5	C16A3.10	Protein C16A3.10, isoform c OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=1 - [Q5TYL8_CAEEEL]
Q18036	52.15	6	19.35	392.5	C16A3.5	Protein C16A3.5 OS=Caenorhabditis elegans GN=C16A3.5 PE=2 SV=1 - [Q18036_CAEEEL]
Q18074	33.47	5	26.62	404.7	C18B2.3	Protein C18B2.3 OS=Caenorhabditis elegans GN=C18B2.3 PE=2 SV=2 - [Q18074_CAEEEL]
Q18076	5.2	2	74.76	192.9	C18B2.5	Protein C18B2.5, isoform a OS=Caenorhabditis elegans GN=C18B2.5 PE=2 SV=1 - [Q18076_CAEEEL]
Q18095	32.04	4	12.08	189.6	C18E9.4	Protein C18E9.4 OS=Caenorhabditis elegans GN=C18E9.4 PE=2 SV=1 - [Q18095_CAEEEL]

O44133	16.77	2	18.02	135.9	C24D10.6	Protein C24D10.6 OS=Caenorhabditis elegans GN=C24D10.6 PE=2 SV=1 - [O44133_CAEEL]
Q8MQC1	10.91	2	31.57	127.2	C25H3.7	Protein C25H3.7 OS=Caenorhabditis elegans GN=C25H3.7 PE=2 SV=1 - [Q8MQC1_CAEEL]
D7SFJ4	8.74	1	21.73	106.5	C25H3.9	Protein C25H3.9, isoform b OS=Caenorhabditis elegans GN=C25H3.9 PE=4 SV=1 - [D7SFJ4_CAEEL]
O17622	16.23	2	21.19	189.4	C29F7.3	Protein C29F7.3 OS=Caenorhabditis elegans GN=C29F7.3 PE=2 SV=1 - [O17622_CAEEL]
Q09486	12.08	2	29.26	510.0	C30G12.2	Protein C30G12.2 OS=Caenorhabditis elegans GN=C30G12.2 PE=2 SV=2 - [Q09486_CAEEL]
O45279	6.23	2	36.39	129.6	C30H6.7	Protein C30H6.7, isoform a OS=Caenorhabditis elegans GN=C30H6.7 PE=2 SV=1 - [O45279_CAEEL]
G5EFF8	6.36	2	44.79	140.8	C30H7.2	Protein C30H7.2, isoform a OS=Caenorhabditis elegans GN=C30H7.2 PE=4 SV=1 - [G5EFF8_CAEEL]
O17626	42.24	9	34.67	811.2	C31C9.2	Protein C31C9.2 OS=Caenorhabditis elegans GN=C31C9.2 PE=2 SV=1 - [O17626_CAEEL]
Q09489	30.71	3	15.66	261.2	C32D5.8	Protein C32D5.8, isoform a OS=Caenorhabditis elegans GN=C32D5.8 PE=2 SV=1 - [Q09489_CAEEL]
O44955	36.84	5	20.09	231.8	C34B2.8	Protein C34B2.8 OS=Caenorhabditis elegans GN=C34B2.8 PE=2 SV=1 - [O44955_CAEEL]
G5ECE7	14.11	3	26.91	145.4	C34E7.4	Protein C34E7.4 OS=Caenorhabditis elegans GN=C34E7.4 PE=4 SV=1 - [G5ECE7_CAEEL]
O45060	22.52	3	16.95	201.1	C35B1.5	Protein C35B1.5 OS=Caenorhabditis elegans GN=C35B1.5 PE=2 SV=1 - [O45060_CAEEL]
Q18494	4.81	3	91.94	224.6	C36A4.5	Protein C36A4.5 OS=Caenorhabditis elegans GN=C36A4.5 PE=4 SV=2 - [Q18494_CAEEL]
A3RMS7	43.43	2	11.27	147.5	C37H5.13	Protein C37H5.13, isoform c OS=Caenorhabditis elegans GN=C37H5.13 PE=4 SV=1 - [A3RMS7_CAEEL]
Q18599	39.07	11	50.72	835.5	C44B7.10	Protein C44B7.10 OS=Caenorhabditis elegans GN=C44B7.10 PE=2 SV=3 - [Q18599_CAEEL]
O01806	11.87	3	43.60	202.3	C44E4.4	Protein C44E4.4 OS=Caenorhabditis elegans GN=C44E4.4 PE=2 SV=1 - [O01806_CAEEL]
Q9U3M0	6.28	1	24.98	124.6	C46C2.5	Protein C46C2.5 OS=Caenorhabditis elegans GN=C46C2.5 PE=2 SV=2 - [Q9U3M0_CAEEL]
Q95QQ4	7.24	3	64.75	119.0	C55F2.1	Protein C55F2.1, isoform b OS=Caenorhabditis elegans GN=C55F2.1 PE=2 SV=3 - [Q95QQ4_CAEEL]
G5ED41	9.5	7	141.64	282.3	cand-1	Protein CAND-1 OS=Caenorhabditis elegans GN=cand-1 PE=4 SV=1 - [G5ED41_CAEEL]
Q9XW17	31.47	7	37.59	611.0	car-1	Protein CAR-1 OS=Caenorhabditis elegans GN=car-1 PE=2 SV=1 - [Q9XW17_CAEEL]
Q96516	5.51	4	105.15	126.0	cars-1	Protein CARS-1, isoform b OS=Caenorhabditis elegans GN=cars-1 PE=2 SV=1 - [Q96516_CAEEL]
O45599	3.11	3	144.10	319.0	cbd-1	Protein CBD-1 OS=Caenorhabditis elegans GN=cbd-1 PE=2 SV=2 - [O45599_CAEEL]
O02215	7.32	2	49.76	131.6	cbl-1	Protein CBL-1, isoform a OS=Caenorhabditis elegans GN=cbl-1 PE=2 SV=3 - [O02215_CAEEL]
Q9N4J8	11.05	5	60.42	311.5	cct-3	Protein CCT-3 OS=Caenorhabditis elegans GN=cct-3 PE=2 SV=3 - [Q9N4J8_CAEEL]
G8JY43	17.95	4	47.64	378.9	cct-6	Protein CCT-6, isoform b OS=Caenorhabditis elegans GN=cct-6 PE=3 SV=1 - [G8JY43_CAEEL]
Q19973	4.28	1	42.25	120.0	cec-5	Protein CEC-5 OS=Caenorhabditis elegans GN=cec-5 PE=2 SV=1 - [Q19973_CAEEL]
Q19824	11.88	3	40.77	221.5	cee-1	Protein CEE-1 OS=Caenorhabditis elegans GN=cee-1 PE=1 SV=1 - [Q19824_CAEEL]
P91306	55.43	8	29.39	754.1	cey-2	Protein CEY-2 OS=Caenorhabditis elegans GN=cey-2 PE=2 SV=1 - [P91306_CAEEL]
P91398	27.92	5	29.23	422.4	cey-3	Protein CEY-3 OS=Caenorhabditis elegans GN=cey-3 PE=2 SV=1 - [P91398_CAEEL]
G5EDV3	37.07	9	32.40	902.9	cey-4	Protein CEY-4 OS=Caenorhabditis elegans GN=cey-4 PE=4 SV=1 - [G5EDV3_CAEEL]
P32744	1.27	1	112.21	108.3	cls-2	Protein CLASP-2 OS=Caenorhabditis elegans GN=cls-2 PE=1 SV=3 - [CLAS2_CAEEL]
Q22966	12.72	2	19.89	101.2	clec-1	Protein CLEC-1 OS=Caenorhabditis elegans GN=clec-1 PE=2 SV=1 - [Q22966_CAEEL]
B7WNB3	11.38	1	19.08	104.6	clec-146	Protein CLEC-146, isoform b OS=Caenorhabditis elegans GN=clec-146 PE=4 SV=1 - [B7WNB3_CAEEL]
Q7Z121	26.9	3	16.97	301.5	clec-266	Protein CLEC-266, isoform c OS=Caenorhabditis elegans GN=clec-266 PE=2 SV=1 - [Q7Z121_CAEEL]
Q9N4B1	1.8	1	86.23	134.9	clp-7	Protein CLP-7 OS=Caenorhabditis elegans GN=clp-7 PE=2 SV=1 - [Q9N4B1_CAEEL]
Q86MP1	4.53	2	30.14	111.0	col-95	Protein COL-95 OS=Caenorhabditis elegans GN=col-95 PE=2 SV=1 - [Q86MP1_CAEEL]
O45734	21.66	6	38.09	711.6	cpl-1	Protein CPL-1, isoform a OS=Caenorhabditis elegans GN=cpl-1 PE=2 SV=1 - [O45734_CAEEL]
O01542	45.07	5	15.50	538.9	cpn-3	Protein CPN-3 OS=Caenorhabditis elegans GN=cpn-3 PE=2 SV=1 - [O01542_CAEEL]
Q8MQC6	20.63	4	42.25	298.7	cpr-6	Protein CPR-6, isoform b OS=Caenorhabditis elegans GN=cpr-6 PE=2 SV=1 - [Q8MQC6_CAEEL]
Q9U2F2	2.95	3	89.31	137.3	cpt-1	Protein CPT-1 OS=Caenorhabditis elegans GN=cpt-1 PE=2 SV=3 - [Q9U2F2_CAEEL]
Q27GU1	6.34	4	98.64	236.9	csr-1	Protein CSR-1, isoform b OS=Caenorhabditis elegans GN=csr-1 PE=2 SV=1 - [Q27GU1_CAEEL]
Q18853	47.02	8	30.95	1151.9	cyc-1	Protein CYC-1 OS=Caenorhabditis elegans GN=cyc-1 PE=2 SV=1 - [Q18853_CAEEL]
Q9XUS9	7.93	3	76.27	297.2	cyk-4	Protein CYK-4 OS=Caenorhabditis elegans GN=cyk-4 PE=2 SV=1 - [Q9XUS9_CAEEL]
Q27531	21.75	6	56.54	612.3	cyp-14a5	Protein CYP-14A5 OS=Caenorhabditis elegans GN=cyp-14a5 PE=2 SV=1 - [Q27531_CAEEL]
G5EGT6	2.42	1	56.78	174.6	cyp-31a2	Protein CYP-31A2 OS=Caenorhabditis elegans GN=cyp-31a2 PE=3 SV=1 - [G5EGT6_CAEEL]
Q86NC6	9.58	2	25.96	109.9	cysl-3	Protein CYSL-3, isoform b OS=Caenorhabditis elegans GN=cysl-3 PE=2 SV=1 - [Q86NC6_CAEEL]
Q18943	30.32	6	20.57	680.2	D1054.10	Protein D1054.10 OS=Caenorhabditis elegans GN=D1054.10 PE=2 SV=1 - [Q18943_CAEEL]
Q18947	28.08	6	33.74	429.2	D1054.11	Protein D1054.11 OS=Caenorhabditis elegans GN=D1054.11 PE=2 SV=1 - [Q18947_CAEEL]
P91194	8.26	2	41.08	154.3	D2092.4	Protein D2092.4 OS=Caenorhabditis elegans GN=D2092.4 PE=2 SV=2 - [P91194_CAEEL]
Q9N363	18.98	4	36.53	280.1	dcap-1	Protein DCAP-1 OS=Caenorhabditis elegans GN=dcap-1 PE=2 SV=1 - [Q9N363_CAEEL]
Q22308	6.16	4	108.20	214.3	ddx-19	Protein DDX-19, isoform a OS=Caenorhabditis elegans GN=ddx-19 PE=2 SV=2 - [Q22308_CAEEL]

O01815	18.98	5	45.66	303.8	dhod-1	Protein DHOD-1 OS=Caenorhabditis elegans GN=dhod-1 PE=2 SV=1 - [O01815_CAEEL]
Q9XX28	10.14	2	31.22	135.7	dhs-11	Protein DHS-11 OS=Caenorhabditis elegans GN=dhs-11 PE=2 SV=1 - [Q9XX28_CAEEL]
Q9N5G3	8.6	2	29.97	213.1	dhs-14	Protein DHS-14 OS=Caenorhabditis elegans GN=dhs-14 PE=2 SV=1 - [Q9N5G3_CAEEL]
Q9U1Y6	11.72	3	43.14	237.2	dhs-24	Protein DHS-24 OS=Caenorhabditis elegans GN=dhs-24 PE=2 SV=3 - [Q9U1Y6_CAEEL]
Q19246	43.55	7	25.46	556.2	dhs-25	Protein DHS-25 OS=Caenorhabditis elegans GN=dhs-25 PE=2 SV=2 - [Q19246_CAEEL]
Q21481	27.98	8	46.23	431.2	dhs-28	Protein DHS-28 OS=Caenorhabditis elegans GN=dhs-28 PE=2 SV=1 - [Q21481_CAEEL]
Q09979	19.86	6	45.45	394.9	dhs-6	Protein DHS-6 OS=Caenorhabditis elegans GN=dhs-6 PE=2 SV=3 - [Q09979_CAEEL]
Q9N538	33.86	9	35.05	896.7	dhs-9	Protein DHS-9 OS=Caenorhabditis elegans GN=dhs-9 PE=2 SV=1 - [Q9N538_CAEEL]
Q17967	14.64	5	53.40	397.1	pdi-1	Protein disulfide-isomerase 1 OS=Caenorhabditis elegans GN=pdi-1 PE=3 SV=1 - [PDI1_CAEEL]
P90994	19.25	4	19.66	163.9	djr-1.1	Protein DJR-1.1 OS=Caenorhabditis elegans GN=djr-1.1 PE=2 SV=1 - [P90994_CAEEL]
Q20774	31.42	7	36.24	606.9	dnj-13	Protein DNJ-13 OS=Caenorhabditis elegans GN=dnj-13 PE=2 SV=1 - [Q20774_CAEEL]
Q9U1W0	10.36	4	66.83	280.1	dnj-29	Protein DNJ-29, isoform a OS=Caenorhabditis elegans GN=dnj-29 PE=2 SV=1 - [Q9U1W0_CAEEL]
Q95Y44	11.76	2	27.70	157.7	dnj-30	Protein DNJ-30 OS=Caenorhabditis elegans GN=dnj-30 PE=2 SV=1 - [Q95Y44_CAEEL]
Q9TYJ7	10.88	2	26.93	138.7	dpm-1	Protein DPM-1 OS=Caenorhabditis elegans GN=dpm-1 PE=2 SV=2 - [Q9TYJ7_CAEEL]
G5EC91	22.76	5	27.36	386.9	dpy-11	Protein DPY-11 OS=Caenorhabditis elegans GN=dpy-11 PE=2 SV=1 - [G5EC91_CAEEL]
Q8MXD9	22.54	5	33.14	352.4	E02D9.1	Protein E02D9.1, isoform b OS=Caenorhabditis elegans GN=E02D9.1 PE=2 SV=1 - [Q8MXD9_CAEEL]
Q23315	13.4	8	125.12	579.5	ears-1	Protein EARS-1 OS=Caenorhabditis elegans GN=ears-1 PE=2 SV=1 - [Q23315_CAEEL]
P90735	9.04	7	110.93	458.2	eat-6	Protein EAT-6 OS=Caenorhabditis elegans GN=eat-6 PE=2 SV=1 - [P90735_CAEEL]
Q09603	14.81	4	42.08	186.0	ech-4	Protein ECH-4 OS=Caenorhabditis elegans GN=ech-4 PE=2 SV=1 - [Q09603_CAEEL]
O45106	11.85	3	31.44	191.2	ech-5	Protein ECH-5 OS=Caenorhabditis elegans GN=ech-5 PE=2 SV=3 - [O45106_CAEEL]
Q9NEZ8	18.75	4	27.85	482.2	ech-7	Protein ECH-7 OS=Caenorhabditis elegans GN=ech-7 PE=2 SV=1 - [Q9NEZ8_CAEEL]
Q21740	21.2	7	62.60	490.2	edc-3	Protein EDC-3 OS=Caenorhabditis elegans GN=edc-3 PE=1 SV=1 - [Q21740_CAEEL]
H9G359	30.35	6	21.66	403.8	eef-1B.2	Protein EEF-1B.2, isoform c OS=Caenorhabditis elegans GN=eef-1B.2 PE=4 SV=1 - [H9G359_CAEEL]
Q814K9	16.89	5	41.98	366.9	eef-1g	Protein EEF-1G, isoform b OS=Caenorhabditis elegans GN=eef-1g PE=2 SV=1 - [Q814K9_CAEEL]
G3MU53	5.6	4	93.35	130.5	eef-2	Protein EEF-2, isoform b OS=Caenorhabditis elegans GN=eef-2 PE=4 SV=1 - [G3MU53_CAEEL]
Q967F1	34.86	2	12.37	150.1	eif-1	Protein EIF-1 OS=Caenorhabditis elegans GN=eif-1 PE=2 SV=1 - [Q967F1_CAEEL]
Q9TXU7	11.57	2	24.38	106.3	eif-1.a	Protein EIF-1.A OS=Caenorhabditis elegans GN=eif-1.a PE=2 SV=1 - [Q9TXU7_CAEEL]
Q9BKS1	29.84	3	13.80	214.4	elc-1	Protein ELC-1 OS=Caenorhabditis elegans GN=elc-1 PE=1 SV=1 - [Q9BKS1_CAEEL]
Q20303	8.03	1	31.65	145.3	elo-6	Protein ELO-6 OS=Caenorhabditis elegans GN=elo-6 PE=2 SV=1 - [Q20303_CAEEL]
Q7YTG1	10.06	5	96.61	301.9	eps-8	Protein EPS-8, isoform d OS=Caenorhabditis elegans GN=eps-8 PE=2 SV=2 - [Q7YTG1_CAEEL]
Q95QM8	10.25	7	79.49	511.4	F07A11.2	Protein F07A11.2, isoform b OS=Caenorhabditis elegans GN=F07A11.2 PE=2 SV=1 - [Q95QM8_CAEEL]
G5ECF6	8.23	2	35.27	118.8	F07B7.2	Protein F07B7.2 OS=Caenorhabditis elegans GN=F07B7.2 PE=4 SV=1 - [G5ECF6_CAEEL]
Q19257	9.32	2	34.08	126.1	F09E5.7	Protein F09E5.7 OS=Caenorhabditis elegans GN=F09E5.7 PE=2 SV=1 - [Q19257_CAEEL]
Q8MNT7	6.06	2	40.12	133.7	F09F7.4	Protein F09F7.4, isoform b OS=Caenorhabditis elegans GN=F09F7.4 PE=2 SV=1 - [Q8MNT7_CAEEL]
Q19303	15.69	2	17.49	174.9	F10E7.6	Protein F10E7.6 OS=Caenorhabditis elegans GN=F10E7.6 PE=2 SV=1 - [Q19303_CAEEL]
Q7JMA4	0.97	1	151.58	108.1	F11C1.5	Protein F11C1.5, isoform b OS=Caenorhabditis elegans GN=F11C1.5 PE=2 SV=2 - [Q7JMA4_CAEEL]
Q9GUC8	5.45	4	105.95	116.0	F14F9.4	Protein F14F9.4 OS=Caenorhabditis elegans GN=F14F9.4 PE=2 SV=1 - [Q9GUC8_CAEEL]
O61522	10.64	1	16.11	122.9	F17E9.4	Protein F17E9.4 OS=Caenorhabditis elegans GN=F17E9.4 PE=2 SV=2 - [O61522_CAEEL]
Q93535	10.37	3	50.77	389.1	F20D1.3	Protein F20D1.3 OS=Caenorhabditis elegans GN=F20D1.3 PE=2 SV=2 - [Q93535_CAEEL]
Q93545	19.68	3	26.75	150.0	F20G2.2	Protein F20G2.2 OS=Caenorhabditis elegans GN=F20G2.2 PE=2 SV=1 - [Q93545_CAEEL]
Q19680	3.27	2	61.04	118.3	F21D5.1	Protein F21D5.1 OS=Caenorhabditis elegans GN=F21D5.1 PE=3 SV=1 - [Q19680_CAEEL]
G5EE80	5.44	2	54.93	175.4	F21D5.7	Protein F21D5.7 OS=Caenorhabditis elegans GN=F21D5.7 PE=4 SV=1 - [G5EE80_CAEEL]
Q19699	10.14	8	79.25	434.0	F22B3.4	Protein F22B3.4 OS=Caenorhabditis elegans GN=F22B3.4 PE=2 SV=1 - [Q19699_CAEEL]
Q19714	12.37	2	21.29	135.0	F22B5.10	Protein F22B5.10 OS=Caenorhabditis elegans GN=F22B5.10 PE=2 SV=1 - [Q19714_CAEEL]
Q9GZE9	16.2	5	47.26	354.3	F22F7.1	Protein F22F7.1, isoform a OS=Caenorhabditis elegans GN=F22F7.1 PE=2 SV=1 - [Q9GZE9_CAEEL]
Q9TXI4	35.69	7	27.62	411.1	F23C8.5	Protein F23C8.5 OS=Caenorhabditis elegans GN=F23C8.5 PE=2 SV=2 - [Q9TXI4_CAEEL]
Q9TXI3	28.29	3	22.47	246.3	F23C8.6	Protein F23C8.6 OS=Caenorhabditis elegans GN=F23C8.6 PE=2 SV=1 - [Q9TXI3_CAEEL]
Q93568	14.8	4	21.72	167.5	F25H2.4	Protein F25H2.4 OS=Caenorhabditis elegans GN=F25H2.4 PE=1 SV=1 - [Q93568_CAEEL]
Q8I7G8	14.74	5	40.50	443.9	F26B1.2	Protein F26B1.2, isoform c OS=Caenorhabditis elegans GN=F26B1.2 PE=2 SV=1 - [Q8I7G8_CAEEL]
Q22972	7.46	2	42.21	138.9	F28A12.4	Protein F28A12.4 OS=Caenorhabditis elegans GN=F28A12.4 PE=2 SV=1 - [Q22972_CAEEL]
Q95R11	8.39	2	17.06	168.9	F28B3.10	Protein F28B3.10 OS=Caenorhabditis elegans GN=F28B3.10 PE=2 SV=1 - [Q95R11_CAEEL]



Q93622	18.67	2	17.16	121.3	F28C6.8	Protein F28C6.8 OS=Caenorhabditis elegans GN=F28C6.8 PE=2 SV=1 - [Q93622_CAEEL]
Q814K3	13.89	3	33.07	140.0	F30F8.9	Protein F30F8.9, isoform b OS=Caenorhabditis elegans GN=F30F8.9 PE=2 SV=1 - [Q814K3_CAEEL]
O62198	26.33	6	35.50	482.8	F32A11.1	Protein F32A11.1 OS=Caenorhabditis elegans GN=F32A11.1 PE=2 SV=1 - [O62198_CAEEL]
Q7YXB9	3.93	2	80.23	217.5	F32A7.5	Protein F32A7.5, isoform b OS=Caenorhabditis elegans GN=F32A7.5 PE=2 SV=1 - [Q7YXB9_CAEEL]
O45430	14.61	6	73.71	428.7	F32B6.2	Protein F32B6.2 OS=Caenorhabditis elegans GN=F32B6.2 PE=2 SV=2 - [O45430_CAEEL]
Q9U3H0	34.36	7	25.10	396.2	F32D8.5	Protein F32D8.5, isoform b OS=Caenorhabditis elegans GN=F32D8.5 PE=2 SV=1 - [Q9U3H0_CAEEL]
O44781	6.77	2	45.45	221.0	F33D11.10	Protein F33D11.10 OS=Caenorhabditis elegans GN=F33D11.10 PE=2 SV=1 - [O44781_CAEEL]
Q20034	17.82	2	19.60	161.1	F35D11.4	Protein F35D11.4 OS=Caenorhabditis elegans GN=F35D11.4 PE=2 SV=2 - [Q20034_CAEEL]
Q9N5U5	12.71	4	60.27	182.3	F35F11.1	Protein F35F11.1 OS=Caenorhabditis elegans GN=F35F11.1 PE=2 SV=3 - [Q9N5U5_CAEEL]
Q20062	22.61	5	21.84	215.7	F35G2.2	Protein F35G2.2 OS=Caenorhabditis elegans GN=F35G2.2 PE=1 SV=1 - [Q20062_CAEEL]
P90860	25.15	3	19.53	2008.7	F36A2.7	Protein F36A2.7 OS=Caenorhabditis elegans GN=F36A2.7 PE=2 SV=1 - [P90860_CAEEL]
O44400	16.01	7	61.41	574.3	F37C4.5	Protein F37C4.5 OS=Caenorhabditis elegans GN=F37C4.5 PE=1 SV=3 - [F37C4_CAEEL]
Q94207	26.63	3	19.16	121.8	F38A5.7	Protein F38A5.7 OS=Caenorhabditis elegans GN=F38A5.7 PE=1 SV=1 - [Q94207_CAEEL]
O45496	7.32	2	35.40	127.2	F39B2.3	Protein F39B2.3 OS=Caenorhabditis elegans GN=F39B2.3 PE=2 SV=1 - [O45496_CAEEL]
H2L297	3.37	1	35.54	150.5	F40F8.11	Protein F40F8.11, isoform b OS=Caenorhabditis elegans GN=F40F8.11 PE=4 SV=1 - [H2L297_CAEEL]
O44509	35.91	5	21.24	512.2	F42G8.10	Protein F42G8.10, isoform a OS=Caenorhabditis elegans GN=F42G8.10 PE=2 SV=1 - [O44509_CAEEL]
O45518	16.13	4	42.12	368.7	F44G3.2	Protein F44G3.2 OS=Caenorhabditis elegans GN=F44G3.2 PE=2 SV=1 - [O45518_CAEEL]
O02267	25.6	3	18.43	243.2	F45H10.3	Protein F45H10.3 OS=Caenorhabditis elegans GN=F45H10.3 PE=2 SV=1 - [O02267_CAEEL]
Q20476	41.01	7	20.36	435.8	F46G10.1	Protein F46G10.1, isoform a OS=Caenorhabditis elegans GN=F46G10.1 PE=1 SV=3 - [Q20476_CAEEL]
O01572	12.24	2	27.01	244.7	F48C1.6	Protein F48C1.6 OS=Caenorhabditis elegans GN=F48C1.6 PE=2 SV=1 - [O01572_CAEEL]
Q9GPA1	17.56	3	31.22	212.3	F48E3.4	Protein F48E3.4 OS=Caenorhabditis elegans GN=F48E3.4 PE=2 SV=3 - [Q9GPA1_CAEEL]
Q27GQ5	4.11	1	46.42	112.4	F49C12.7	Protein F49C12.7, isoform c OS=Caenorhabditis elegans GN=F49C12.7 PE=2 SV=1 - [Q27GQ5_CAEEL]
P90879	10.82	3	34.71	170.1	F49C12.9	Protein F49C12.9 OS=Caenorhabditis elegans GN=F49C12.9 PE=1 SV=1 - [P90879_CAEEL]
Q20616	23.21	10	73.45	1220.0	F49E12.1	Protein F49E12.1 OS=Caenorhabditis elegans GN=F49E12.1 PE=4 SV=1 - [Q20616_CAEEL]
Q9N5S7	20.62	4	30.19	321.7	F49H12.5	Protein F49H12.5 OS=Caenorhabditis elegans GN=F49H12.5 PE=2 SV=1 - [Q9N5S7_CAEEL]
O45552	52.54	12	41.26	1537.8	F53A2.7	Protein F53A2.7 OS=Caenorhabditis elegans GN=F53A2.7 PE=2 SV=2 - [O45552_CAEEL]
P91997	23.23	5	33.45	273.5	F53F1.2	Protein F53F1.2 OS=Caenorhabditis elegans GN=F53F1.2 PE=2 SV=1 - [P91997_CAEEL]
O17891	6.82	1	24.99	112.9	F55B11.2	Protein F55B11.2 OS=Caenorhabditis elegans GN=F55B11.2 PE=4 SV=2 - [O17891_CAEEL]
G5EC22	7.92	2	37.38	256.2	F55G11.4	Protein F55G11.4 OS=Caenorhabditis elegans GN=F55G11.4 PE=4 SV=1 - [G5EC22_CAEEL]
P90889	6.25	1	22.03	127.0	F55H12.4	Protein F55H12.4 OS=Caenorhabditis elegans GN=F55H12.4 PE=2 SV=1 - [P90889_CAEEL]
O44517	6.47	2	38.75	124.4	F56A11.5	Protein F56A11.5 OS=Caenorhabditis elegans GN=F56A11.5 PE=2 SV=1 - [O44517_CAEEL]
H2L085	5.85	1	20.90	112.6	F56B3.11	Protein F56B3.11, isoform b OS=Caenorhabditis elegans GN=F56B3.11 PE=4 SV=1 - [H2L085_CAEEL]
Q9TZ65	18.49	5	45.66	213.8	F56F11.4	Protein F56F11.4, isoform a OS=Caenorhabditis elegans GN=F56F11.4 PE=2 SV=2 - [Q9TZ65_CAEEL]
Q8IA68	12.48	4	57.07	283.8	F57B10.3	Protein F57B10.3, isoform b OS=Caenorhabditis elegans GN=F57B10.3 PE=2 SV=1 - [Q8IA68_CAEEL]
O44734	5.22	1	31.56	102.9	F57B10.8	Protein F57B10.8 OS=Caenorhabditis elegans GN=F57B10.8 PE=2 SV=1 - [O44734_CAEEL]
Q9XUW5	27.09	10	60.39	514.9	F58E10.3	Protein F58E10.3, isoform a OS=Caenorhabditis elegans GN=F58E10.3 PE=2 SV=1 - [Q9XUW5_CAEEL]
G3MU56	6.17	3	101.67	149.0	F58G11.2	Protein F58G11.2, isoform c OS=Caenorhabditis elegans GN=F58G11.2 PE=3 SV=1 - [G3MU56_CAEEL]
Q93831	23.08	7	31.22	480.9	F59C6.5	Protein F59C6.5 OS=Caenorhabditis elegans GN=F59C6.5 PE=2 SV=1 - [Q93831_CAEEL]
Q9XUB7	12.5	2	20.59	136.0	far-6	Protein FAR-6 OS=Caenorhabditis elegans GN=far-6 PE=2 SV=1 - [Q9XUB7_CAEEL]
P91871	4.59	8	289.04	556.1	fasn-1	Protein FASN-1 OS=Caenorhabditis elegans GN=fasn-1 PE=2 SV=2 - [P91871_CAEEL]
DOIIMZ7	7.67	10	240.42	579.4	fln-1	Protein FLN-1, isoform f OS=Caenorhabditis elegans GN=fln-1 PE=4 SV=1 - [DOIIMZ7_CAEEL]
Q95ZT1	12.63	2	22.56	108.7	ftt-2	Protein FTT-2, isoform b OS=Caenorhabditis elegans GN=ftt-2 PE=2 SV=2 - [Q95ZT1_CAEEL]
Q8I711	5.46	3	76.44	109.8	gars-1	Protein GARS-1, isoform b OS=Caenorhabditis elegans GN=gars-1 PE=2 SV=1 - [Q8I711_CAEEL]
B3CJ34	7.2	13	294.78	624.8	gcn-1	Protein GCN-1 OS=Caenorhabditis elegans GN=gcn-1 PE=4 SV=1 - [B3CJ34_CAEEL]
G5EBR1	8.78	2	49.99	179.1	gdi-1	Protein GDI-1, isoform a OS=Caenorhabditis elegans GN=gdi-1 PE=2 SV=1 - [G5EBR1_CAEEL]
H8ESF5	24.33	6	29.22	401.9	gln-3	Protein GLN-3, isoform c OS=Caenorhabditis elegans GN=gln-3 PE=4 SV=1 - [H8ESF5_CAEEL]
O02225	13.32	2	41.37	113.3	gln-6	Protein GLN-6 OS=Caenorhabditis elegans GN=gln-6 PE=2 SV=1 - [O02225_CAEEL]
Q3Y400	24.43	2	14.61	180.9	glrx-22	Protein GLRX-22 OS=Caenorhabditis elegans GN=glrx-22 PE=4 SV=1 - [Q3Y400_CAEEL]
Q6EZG4	12.57	3	37.92	207.7	glrx-3	Protein GLRX-3, isoform b OS=Caenorhabditis elegans GN=glrx-3 PE=2 SV=1 - [Q6EZG4_CAEEL]
A7LPE5	17.11	4	33.29	267.9	gpdh-2	Protein GPDH-2, isoform c OS=Caenorhabditis elegans GN=gpdh-2 PE=3 SV=1 - [A7LPE5_CAEEL]
O16462	16.67	1	10.87	181.0	grd-5	Protein GRD-5 OS=Caenorhabditis elegans GN=grd-5 PE=2 SV=1 - [O16462_CAEEL]

Q93694	29.19	4	23.74	355.3	gst-24	Protein GST-24 OS=Caenorhabditis elegans GN=gst-24 PE=2 SV=2 - [Q93694_CAEEL]
Q9NAB2	6.7	1	23.59	129.6	gst-28	Protein GST-28 OS=Caenorhabditis elegans GN=gst-28 PE=2 SV=1 - [Q9NAB2_CAEEL]
Q9TYR0	18.32	4	36.85	222.1	H04M03.3	Protein H04M03.3 OS=Caenorhabditis elegans GN=H04M03.3 PE=2 SV=1 - [Q9TYR0_CAEEL]
O44897	9.45	4	90.74	292.2	haf-9	Protein HAF-9, isoform a OS=Caenorhabditis elegans GN=haf-9 PE=2 SV=2 - [O44897_CAEEL]
O16521	9.71	2	34.73	265.5	hpo-19	Protein HPO-19 OS=Caenorhabditis elegans GN=hpo-19 PE=2 SV=1 - [O16521_CAEEL]
Q93726	4.34	1	83.44	102.2	hpo-35	Protein HPO-35 OS=Caenorhabditis elegans GN=hpo-35 PE=2 SV=4 - [Q93726_CAEEL]
Q9NLD1	7.36	3	65.88	263.3	hrp-2	Protein HRP-2, isoform a OS=Caenorhabditis elegans GN=hrp-2 PE=2 SV=2 - [Q9NLD1_CAEEL]
Q9BIB7	11.84	4	61.74	227.3	hrpf-1	Protein HRP-1, isoform a OS=Caenorhabditis elegans GN=hrpf-1 PE=2 SV=1 - [Q9BIB7_CAEEL]
H2KYS1	22.83	6	43.21	390.6	hsp-43	Protein HSP-43, isoform a OS=Caenorhabditis elegans GN=hsp-43 PE=3 SV=1 - [H2KYS1_CAEEL]
Q8IA71	5.91	3	96.68	175.3	icl-1	Protein ICL-1, isoform b OS=Caenorhabditis elegans GN=icl-1 PE=2 SV=1 - [Q8IA71_CAEEL]
Q20049	23.48	7	43.55	634.7	idhg-1	Protein IDHG-1 OS=Caenorhabditis elegans GN=idhg-1 PE=2 SV=2 - [Q20049_CAEEL]
B5BM23	7.01	5	115.98	360.5	ifg-1	Protein IFG-1, isoform c OS=Caenorhabditis elegans GN=ifg-1 PE=4 SV=1 - [B5BM23_CAEEL]
Q22170	3.17	1	38.19	129.9	ile-2	Protein ILE-2 OS=Caenorhabditis elegans GN=ile-2 PE=2 SV=2 - [Q22170_CAEEL]
Q9N5V3	10.62	7	121.95	399.5	imb-3	Protein IMB-3 OS=Caenorhabditis elegans GN=imb-3 PE=2 SV=2 - [Q9N5V3_CAEEL]
Q9XVD2	27.27	3	14.69	165.4	imm-1	Protein IMM-1 OS=Caenorhabditis elegans GN=imm-1 PE=3 SV=2 - [Q9XVD2_CAEEL]
Q22505	22.97	11	75.95	917.6	immt-1	Protein IMMT-1 OS=Caenorhabditis elegans GN=immt-1 PE=2 SV=2 - [Q22505_CAEEL]
Q9XXN2	7.03	3	72.58	313.0	immt-2	Protein IMMT-2 OS=Caenorhabditis elegans GN=immt-2 PE=2 SV=2 - [Q9XXN2_CAEEL]
Q21274	3.99	1	34.69	123.1	K07C5.2	Protein K07C5.2 OS=Caenorhabditis elegans GN=K07C5.2 PE=2 SV=1 - [Q21274_CAEEL]
Q21284	10.31	4	68.97	165.6	K07E3.4	Protein K07E3.4, isoform a OS=Caenorhabditis elegans GN=K07E3.4 PE=2 SV=2 - [Q21284_CAEEL]
G5EBW5	13.1	4	42.65	200.5	K07G5.6	Protein K07G5.6 OS=Caenorhabditis elegans GN=K07G5.6 PE=4 SV=1 - [G5EBW5_CAEEL]
O45181	13.78	11	86.77	2768.2	K07H8.10	Protein K07H8.10 OS=Caenorhabditis elegans GN=K07H8.10 PE=2 SV=1 - [O45181_CAEEL]
Q69Z12	16.34	2	17.30	140.7	K08E3.10	Protein K08E3.10 OS=Caenorhabditis elegans GN=K08E3.10 PE=4 SV=1 - [Q69Z12_CAEEL]
Q69Z13	9.53	3	54.93	292.6	K08E3.5	Protein K08E3.5, isoform f OS=Caenorhabditis elegans GN=K08E3.5 PE=2 SV=1 - [Q69Z13_CAEEL]
Q21351	5.29	2	52.42	118.0	K08F4.2	Protein K08F4.2 OS=Caenorhabditis elegans GN=K08F4.2 PE=2 SV=2 - [Q21351_CAEEL]
O44995	4.42	2	55.65	144.8	K12C11.1	Protein K12C11.1 OS=Caenorhabditis elegans GN=K12C11.1 PE=2 SV=2 - [O44995_CAEEL]
Q22100	53.32	12	42.42	716.9	kat-1	Protein KAT-1 OS=Caenorhabditis elegans GN=kat-1 PE=2 SV=2 - [Q22100_CAEEL]
Q21977	2.49	2	110.65	141.2	kcc-1	Protein KCC-1 OS=Caenorhabditis elegans GN=kcc-1 PE=2 SV=1 - [Q21977_CAEEL]
H2L074	0.98	3	466.49	135.6	ketn-1	Protein KETN-1, isoform b OS=Caenorhabditis elegans GN=ketn-1 PE=4 SV=1 - [H2L074_CAEEL]
P34466	2.81	2	139.83	109.0	clu-1	Protein KIAA0664 homolog OS=Caenorhabditis elegans GN=clu-1 PE=2 SV=1 - [K0664_CAEEL]
Q4W5R4	19.28	9	69.85	793.3	laf-1	Protein LAF-1, isoform a OS=Caenorhabditis elegans GN=laf-1 PE=2 SV=1 - [Q4W5R4_CAEEL]
O44565	2.18	2	197.83	122.2	lam-1	Protein LAM-1 OS=Caenorhabditis elegans GN=lam-1 PE=4 SV=3 - [O44565_CAEEL]
H2KZ23	6.48	5	92.26	325.8	larp-1	Protein LARP-1, isoform a OS=Caenorhabditis elegans GN=larp-1 PE=4 SV=1 - [H2KZ23_CAEEL]
Q27GU2	52	6	17.31	463.5	lbp-3	Protein LBP-3, isoform b OS=Caenorhabditis elegans GN=lbp-3 PE=2 SV=1 - [Q27GU2_CAEEL]
Q3LFN1	48.18	4	15.25	280.2	lbp-9	Protein LBP-9, isoform b OS=Caenorhabditis elegans GN=lbp-9 PE=2 SV=1 - [Q3LFN1_CAEEL]
Q5ZR27	20.29	4	37.89	214.3	lec-12	Protein LEC-12, isoform b OS=Caenorhabditis elegans GN=lec-12 PE=2 SV=2 - [Q5ZR27_CAEEL]
Q8I4A5	24.89	5	24.99	260.8	lec-3	Protein LEC-3, isoform c OS=Caenorhabditis elegans GN=lec-3 PE=2 SV=1 - [Q8I4A5_CAEEL]
Q18625	39.22	9	32.39	830.2	lec-4	Protein LEC-4 OS=Caenorhabditis elegans GN=lec-4 PE=2 SV=1 - [Q18625_CAEEL]
Q9N384	45.21	4	15.97	754.2	lec-6	Protein LEC-6 OS=Caenorhabditis elegans GN=lec-6 PE=2 SV=1 - [Q9N384_CAEEL]
Q20937	0.79	2	282.04	128.4	let-711	Protein LET-711 OS=Caenorhabditis elegans GN=let-711 PE=2 SV=2 - [Q20937_CAEEL]
Q9XVL7	7.14	4	87.25	260.6	letm-1	Protein LETM-1, isoform b OS=Caenorhabditis elegans GN=letm-1 PE=2 SV=1 - [Q9XVL7_CAEEL]
Q8I7L5	9.19	2	31.89	162.3	lntl-1	Protein LNTL-1, isoform b OS=Caenorhabditis elegans GN=lntl-1 PE=2 SV=1 - [Q8I7L5_CAEEL]
Q9N4L8	19.32	2	19.98	235.5	lpd-5	Protein LPD-5 OS=Caenorhabditis elegans GN=lpd-5 PE=2 SV=2 - [Q9N4L8_CAEEL]
O62415	11.41	2	32.36	372.8	lys-1	Protein LYS-1 OS=Caenorhabditis elegans GN=lys-1 PE=2 SV=1 - [O62415_CAEEL]
Q20964	12.15	2	23.59	179.0	lys-4	Protein LYS-4 OS=Caenorhabditis elegans GN=lys-4 PE=4 SV=1 - [Q20964_CAEEL]
O16202	16.96	3	30.86	305.9	lys-7	Protein LYS-7 OS=Caenorhabditis elegans GN=lys-7 PE=2 SV=1 - [O16202_CAEEL]
O16376	10.48	6	87.93	357.1	M03F8.3	Protein M03F8.3, isoform a OS=Caenorhabditis elegans GN=M03F8.3 PE=2 SV=2 - [O16376_CAEEL]
Q21525	22.98	3	18.28	185.3	M05D6.6	Protein M05D6.6 OS=Caenorhabditis elegans GN=M05D6.6 PE=2 SV=1 - [Q21525_CAEEL]
Q21544	27.6	6	29.15	505.9	M153.1	Protein M153.1 OS=Caenorhabditis elegans GN=M153.1 PE=2 SV=1 - [Q21544_CAEEL]
P49029	18.42	3	17.63	263.3	mag-1	Protein mago nashi homolog OS=Caenorhabditis elegans GN=mag-1 PE=1 SV=2 - [MGN_CAEEL]
Q19058	16.44	3	32.70	204.7	maoc-1	Protein MAOC-1 OS=Caenorhabditis elegans GN=maoc-1 PE=1 SV=1 - [Q19058_CAEEL]
D3YT56	23.47	5	31.82	355.2	mars-1	Protein MARS-1, isoform c OS=Caenorhabditis elegans GN=mars-1 PE=4 SV=1 - [D3YT56_CAEEL]

Q9XXI9	7.6	5	99.26	251.1	mcm-2	Protein MCM-2, isoform a OS=Caenorhabditis elegans GN=mcm-2 PE=2 SV=1 - [Q9XXI9_CAEEL]
Q95XQ8	8.87	6	91.51	306.0	mcm-4	Protein MCM-4 OS=Caenorhabditis elegans GN=mcm-4 PE=2 SV=1 - [Q95XQ8_CAEEL]
O16297	12.33	7	81.57	471.1	mcm-7	Protein MCM-7 OS=Caenorhabditis elegans GN=mcm-7 PE=2 SV=1 - [O16297_CAEEL]
Q65ZB1	25.45	8	42.51	763.0	mdt-28	Protein MDT-28, isoform b OS=Caenorhabditis elegans GN=mdt-28 PE=2 SV=1 - [Q65ZB1_CAEEL]
P90992	24.84	6	33.29	378.7	misc-1	Protein MISC-1 OS=Caenorhabditis elegans GN=misc-1 PE=2 SV=2 - [P90992_CAEEL]
Q21154	23.38	3	22.07	148.5	moma-1	Protein MOMA-1 OS=Caenorhabditis elegans GN=moma-1 PE=2 SV=1 - [Q21154_CAEEL]
Q95QL2	8.29	2	24.22	111.6	mrpl-13	Protein MRPL-13 OS=Caenorhabditis elegans GN=mrpl-13 PE=4 SV=1 - [Q95QL2_CAEEL]
Q9BPN6	14.43	3	33.82	202.5	mrpl-15	Protein MRPL-15 OS=Caenorhabditis elegans GN=mrpl-15 PE=2 SV=1 - [Q9BPN6_CAEEL]
Q22140	12.5	3	27.69	121.7	mrpl-16	Protein MRPL-16 OS=Caenorhabditis elegans GN=mrpl-16 PE=2 SV=2 - [Q22140_CAEEL]
Q9N3F3	25.77	3	22.72	120.8	mrpl-17	Protein MRPL-17 OS=Caenorhabditis elegans GN=mrpl-17 PE=2 SV=2 - [Q9N3F3_CAEEL]
Q9UA63	9.64	2	23.30	103.3	mrpl-30	Protein MRPL-30 OS=Caenorhabditis elegans GN=mrpl-30 PE=2 SV=1 - [Q9UA63_CAEEL]
O02220	34.39	5	21.42	314.6	mrpl-34	Protein MRPL-34 OS=Caenorhabditis elegans GN=mrpl-34 PE=2 SV=1 - [O02220_CAEEL]
O18199	12.96	4	48.84	137.6	mrpl-37	Protein MRPL-37 OS=Caenorhabditis elegans GN=mrpl-37 PE=2 SV=3 - [O18199_CAEEL]
Q9BL86	5.08	2	48.04	128.4	mrpl-38	Protein MRPL-38 OS=Caenorhabditis elegans GN=mrpl-38 PE=4 SV=1 - [Q9BL86_CAEEL]
Q4W5T0	5.76	1	32.29	133.8	mrpl-39	Protein MRPL-39 OS=Caenorhabditis elegans GN=mrpl-39 PE=4 SV=1 - [Q4W5T0_CAEEL]
Q9TZ90	21.69	3	21.75	164.1	mrpl-40	Protein MRPL-40 OS=Caenorhabditis elegans GN=mrpl-40 PE=2 SV=1 - [Q9TZ90_CAEEL]
Q7YX52	18.6	3	14.84	155.9	mrpl-53	Protein MRPL-53 OS=Caenorhabditis elegans GN=mrpl-53 PE=4 SV=1 - [Q7YX52_CAEEL]
Q95X39	21.74	5	32.01	180.3	mrpl-9	Protein MRPL-9 OS=Caenorhabditis elegans GN=mrpl-9 PE=2 SV=2 - [Q95X39_CAEEL]
Q22470	23.53	3	27.97	150.3	mrps-18b	Protein MRPS-18B OS=Caenorhabditis elegans GN=mrps-18b PE=2 SV=1 - [Q22470_CAEEL]
Q95QS3	13.73	2	29.10	131.6	mrps-26	Protein MRPS-26 OS=Caenorhabditis elegans GN=mrps-26 PE=2 SV=1 - [Q95QS3_CAEEL]
O61791	20.99	3	18.63	186.2	mrps-6	Protein MRPS-6 OS=Caenorhabditis elegans GN=mrps-6 PE=2 SV=2 - [O61791_CAEEL]
H2KYJ5	33.33	7	37.40	509.0	mtch-1	Protein MTCH-1, isoform a OS=Caenorhabditis elegans GN=mtch-1 PE=3 SV=1 - [H2KYJ5_CAEEL]
Q19007	43.04	11	35.64	895.9	nap-1	Protein NAP-1 OS=Caenorhabditis elegans GN=nap-1 PE=2 SV=1 - [Q19007_CAEEL]
Q965X9	5.07	1	40.24	120.6	nape-2	Protein NAPE-2, isoform a OS=Caenorhabditis elegans GN=nape-2 PE=4 SV=1 - [Q965X9_CAEEL]
Q22800	7.38	3	53.80	172.5	nduf-2.2	Protein NDUF-2.2 OS=Caenorhabditis elegans GN=nduf-2.2 PE=2 SV=1 - [Q22800_CAEEL]
Q9N3D9	41.32	4	14.00	405.4	nduf-5	Protein NDUF-5 OS=Caenorhabditis elegans GN=nduf-5 PE=2 SV=1 - [Q9N3D9_CAEEL]
B6VQ96	2.88	4	164.17	146.5	nep-17	Protein NEP-17, isoform b OS=Caenorhabditis elegans GN=nep-17 PE=4 SV=1 - [B6VQ96_CAEEL]
Q5FC69	6.84	2	47.59	141.9	nkat-3	Protein NKAT-3, isoform b OS=Caenorhabditis elegans GN=nkat-3 PE=2 SV=1 - [Q5FC69_CAEEL]
Q20641	2.65	4	229.23	327.6	nmy-1	Protein NMY-1 OS=Caenorhabditis elegans GN=nmy-1 PE=2 SV=2 - [Q20641_CAEEL]
G5EBY3	3.89	5	231.10	292.1	nmy-2	Protein NMY-2 OS=Caenorhabditis elegans GN=nmy-2 PE=4 SV=1 - [G5EBY3_CAEEL]
O45012	45.59	15	54.60	1458.3	nol-5	Protein NOL-5 OS=Caenorhabditis elegans GN=nol-5 PE=2 SV=1 - [O45012_CAEEL]
P91495	9.15	11	199.52	534.9	npp-12	Protein NPP-12 OS=Caenorhabditis elegans GN=npp-12 PE=2 SV=1 - [P91495_CAEEL]
Q21021	3.72	2	92.80	214.7	npp-9	Protein NPP-9, isoform a OS=Caenorhabditis elegans GN=npp-9 PE=2 SV=2 - [Q21021_CAEEL]
O18033	9.69	3	61.13	263.5	nra-2	Protein NRA-2, isoform a OS=Caenorhabditis elegans GN=nra-2 PE=2 SV=1 - [O18033_CAEEL]
Q9UAN9	11.24	8	121.58	645.9	nra-4	Protein NRA-4, isoform a OS=Caenorhabditis elegans GN=nra-4 PE=2 SV=2 - [Q9UAN9_CAEEL]
Q09EE7	5.28	3	83.77	152.0	nsf-1	Protein NSF-1, isoform b OS=Caenorhabditis elegans GN=nsf-1 PE=2 SV=1 - [Q09EE7_CAEEL]
Q86NC2	35.45	9	30.78	646.1	nuo-2	Protein NUO-2, isoform b OS=Caenorhabditis elegans GN=nuo-2 PE=2 SV=1 - [Q86NC2_CAEEL]
O18236	26.72	3	15.04	196.1	nuo-3	Protein NUO-3, isoform b OS=Caenorhabditis elegans GN=nuo-3 PE=2 SV=1 - [O18236_CAEEL]
Q21233	21.33	6	50.83	671.9	nuo-4	Protein NUO-4, isoform a OS=Caenorhabditis elegans GN=nuo-4 PE=2 SV=1 - [Q21233_CAEEL]
Q9N4Y8	22.77	11	79.31	967.2	nuo-5	Protein NUO-5, isoform a OS=Caenorhabditis elegans GN=nuo-5 PE=2 SV=1 - [Q9N4Y8_CAEEL]
Q86S77	2.68	1	68.77	146.5	nuo-5	Protein NUO-5, isoform c OS=Caenorhabditis elegans GN=nuo-5 PE=2 SV=1 - [Q86S77_CAEEL]
Q23098	18.6	3	20.36	343.6	nuo-6	Protein NUO-6 OS=Caenorhabditis elegans GN=nuo-6 PE=2 SV=2 - [Q23098_CAEEL]
Q9BPN5	22.04	4	34.09	200.7	oig-6	Protein OIG-6 OS=Caenorhabditis elegans GN=oig-6 PE=4 SV=2 - [Q9BPN5_CAEEL]
O45346	7.94	1	20.72	118.1	osm-11	Protein OSM-11 OS=Caenorhabditis elegans GN=osm-11 PE=2 SV=1 - [O45346_CAEEL]
P91390	6.07	1	31.13	154.7	ostd-1	Protein OSTD-1 OS=Caenorhabditis elegans GN=ostd-1 PE=2 SV=1 - [P91390_CAEEL]
A7DT45	17.9	2	17.85	139.1	oxy-5	Protein OXY-5 OS=Caenorhabditis elegans GN=oxy-5 PE=4 SV=1 - [A7DT45_CAEEL]
Q7K797	31.74	10	65.05	714.4	pab-1	Protein PAB-1, isoform c OS=Caenorhabditis elegans GN=pab-1 PE=2 SV=1 - [Q7K797_CAEEL]
Q20627	4.75	3	99.95	199.2	pam-1	Protein PAM-1, isoform a OS=Caenorhabditis elegans GN=pam-1 PE=2 SV=1 - [Q20627_CAEEL]
Q22620	8.78	4	65.78	199.2	pars-1	Protein PARS-1, isoform a OS=Caenorhabditis elegans GN=pars-1 PE=2 SV=1 - [Q22620_CAEEL]
P90868	21.61	5	26.67	218.5	pbs-7	Protein PBS-7 OS=Caenorhabditis elegans GN=pbs-7 PE=2 SV=2 - [P90868_CAEEL]
Q8WQF1	28.93	8	56.91	372.4	pccb-1	Protein PCCB-1, isoform b OS=Caenorhabditis elegans GN=pccb-1 PE=2 SV=1 - [Q8WQF1_CAEEL]

Q8ITY2	12.75	5	60.61	489.1	pck-1	Protein PCK-1, isoform b OS=Caenorhabditis elegans GN=pck-1 PE=2 SV=1 - [Q8ITY2_CAEEEL]
O02286	47.09	22	73.38	1789.5	pck-2	Protein PCK-2, isoform a OS=Caenorhabditis elegans GN=pck-2 PE=2 SV=1 - [O02286_CAEEEL]
Q7JKI3	23.51	9	65.94	493.5	pck-2	Protein PCK-2, isoform c OS=Caenorhabditis elegans GN=pck-2 PE=2 SV=1 - [Q7JKI3_CAEEEL]
A3RMS2	12.13	3	41.59	498.8	pdi-2	Protein PDI-2, isoform c OS=Caenorhabditis elegans GN=pdi-2 PE=3 SV=1 - [A3RMS2_CAEEEL]
O44145	14.78	2	22.44	250.2	perm-2	Protein PERM-2 OS=Caenorhabditis elegans GN=perm-2 PE=2 SV=2 - [O44145_CAEEEL]
O44144	14.11	5	42.60	389.0	perm-4	Protein PERM-4 OS=Caenorhabditis elegans GN=perm-4 PE=2 SV=1 - [O44144_CAEEEL]
O18000	14.59	5	52.55	248.0	pes-9	Protein PES-9 OS=Caenorhabditis elegans GN=pes-9 PE=2 SV=1 - [O18000_CAEEEL]
Q1ZXU6	5.73	4	134.12	383.6	pgp-6	Protein PGP-6, isoform b OS=Caenorhabditis elegans GN=pgp-6 PE=2 SV=2 - [Q1ZXU6_CAEEEL]
Q94230	25.22	6	25.50	631.1	plp-1	Protein PLP-1 OS=Caenorhabditis elegans GN=plp-1 PE=2 SV=1 - [Q94230_CAEEEL]
H2L034	6.52	3	69.13	227.3	pmp-5	Protein PMP-5, isoform a OS=Caenorhabditis elegans GN=pmp-5 PE=3 SV=1 - [H2L034_CAEEEL]
Q22993	13.04	5	49.74	399.8	pmt-2	Protein PMT-2 OS=Caenorhabditis elegans GN=pmt-2 PE=2 SV=1 - [Q22993_CAEEEL]
B3KLZ7	10.9	5	78.01	307.9	ppw-1	Protein PPW-1, isoform d OS=Caenorhabditis elegans GN=ppw-1 PE=4 SV=1 - [B3KLZ7_CAEEEL]
Q9TY23	5.25	2	65.66	127.2	pqn-22	Protein PQN-22, isoform b OS=Caenorhabditis elegans GN=pqn-22 PE=2 SV=1 - [Q9TY23_CAEEEL]
Q9U207	1.17	1	160.87	123.8	pqn-87	Protein PQN-87, isoform a OS=Caenorhabditis elegans GN=pqn-87 PE=2 SV=3 - [Q9U207_CAEEEL]
Q8IG31	51.28	7	21.77	389.0	prdx-2	Protein PRDX-2, isoform a OS=Caenorhabditis elegans GN=prdx-2 PE=2 SV=1 - [Q8IG31_CAEEEL]
Q9U2X0	9.48	2	39.75	107.3	prmt-1	Protein PRMT-1 OS=Caenorhabditis elegans GN=prmt-1 PE=2 SV=1 - [Q9U2X0_CAEEEL]
Q20757	2.17	1	62.53	174.5	puf-5	Protein PUF-5 OS=Caenorhabditis elegans GN=puf-5 PE=2 SV=1 - [Q20757_CAEEEL]
Q18990	1.91	3	242.43	293.8	pyr-1	Protein PYR-1 OS=Caenorhabditis elegans GN=pyr-1 PE=2 SV=2 - [Q18990_CAEEEL]
Q9XVJ3	21.19	4	24.70	326.4	qdpr-1	Protein QDPR-1 OS=Caenorhabditis elegans GN=qdpr-1 PE=1 SV=1 - [Q9XVJ3_CAEEEL]
O44503	11.35	7	103.69	723.3	R02D3.1	Protein R02D3.1 OS=Caenorhabditis elegans GN=R02D3.1 PE=2 SV=1 - [O44503_CAEEEL]
Q95QC2	7.88	1	18.92	199.8	R02F2.9	Protein R02F2.9 OS=Caenorhabditis elegans GN=R02F2.9 PE=4 SV=1 - [Q95QC2_CAEEEL]
Q9XTY9	5.25	1	34.20	114.3	R03E1.2	Protein R03E1.2 OS=Caenorhabditis elegans GN=R03E1.2 PE=2 SV=1 - [Q9XTY9_CAEEEL]
Q21732	46.73	6	12.30	377.0	R04F11.2	Protein R04F11.2 OS=Caenorhabditis elegans GN=R04F11.2 PE=2 SV=1 - [Q21732_CAEEEL]
Q8WQD7	13.51	2	21.50	118.1	R04F11.5	Protein R04F11.5 OS=Caenorhabditis elegans GN=R04F11.5 PE=2 SV=1 - [Q8WQD7_CAEEEL]
Q21742	25.35	8	61.72	811.8	R05F9.6	Protein R05F9.6 OS=Caenorhabditis elegans GN=R05F9.6 PE=2 SV=1 - [Q21742_CAEEEL]
Q21763	18.12	2	17.31	242.9	R05H5.3	Protein R05H5.3 OS=Caenorhabditis elegans GN=R05H5.3 PE=2 SV=1 - [Q21763_CAEEEL]
Q93934	29.53	7	37.40	363.0	R07H5.8	Protein R07H5.8 OS=Caenorhabditis elegans GN=R07H5.8 PE=1 SV=1 - [Q93934_CAEEEL]
H9G321	9.95	2	27.72	118.6	R13H4.2	Protein R13H4.2, isoform c OS=Caenorhabditis elegans GN=R13H4.2 PE=4 SV=1 - [H9G321_CAEEEL]
Q22020	11.42	3	24.12	185.7	R53.5	Protein R53.5 OS=Caenorhabditis elegans GN=R53.5 PE=2 SV=1 - [Q22020_CAEEEL]
Q9UAQ6	30.73	4	22.53	341.0	rab-1	Protein RAB-1 OS=Caenorhabditis elegans GN=rab-1 PE=2 SV=1 - [Q9UAQ6_CAEEEL]
Q93874	12.38	2	23.37	116.7	rab-14	Protein RAB-14 OS=Caenorhabditis elegans GN=rab-14 PE=2 SV=1 - [Q93874_CAEEEL]
P91857	18.75	2	22.82	154.1	rab-5	Protein RAB-5 OS=Caenorhabditis elegans GN=rab-5 PE=1 SV=1 - [P91857_CAEEEL]
Q23146	28.71	5	23.41	187.3	rab-7	Protein RAB-7 OS=Caenorhabditis elegans GN=rab-7 PE=2 SV=1 - [Q23146_CAEEEL]
G5EFC1	17.06	3	24.01	286.7	rab-8	Protein RAB-8 OS=Caenorhabditis elegans GN=rab-8 PE=2 SV=1 - [G5EFC1_CAEEEL]
Q23451	5.26	1	34.55	117.4	rad-23	Protein RAD-23 OS=Caenorhabditis elegans GN=rad-23 PE=2 SV=2 - [Q23451_CAEEEL]
Q4W4Z2	13.39	3	40.09	158.8	rad-8	Protein RAD-8 OS=Caenorhabditis elegans GN=rad-8 PE=4 SV=2 - [Q4W4Z2_CAEEEL]
Q9N3F8	15.96	3	23.95	527.5	ral-1	Protein RAL-1, isoform a OS=Caenorhabditis elegans GN=ral-1 PE=2 SV=1 - [Q9N3F8_CAEEEL]
Q18246	14.36	2	21.23	110.7	rap-1	Protein RAP-1 OS=Caenorhabditis elegans GN=rap-1 PE=2 SV=1 - [Q18246_CAEEEL]
Q65ZK0	9.68	6	78.26	302.9	rars-1	Protein RARS-1, isoform b OS=Caenorhabditis elegans GN=rars-1 PE=2 SV=1 - [Q65ZK0_CAEEEL]
Q23188	19.37	3	24.71	119.5	ret-1	Protein RET-1, isoform b OS=Caenorhabditis elegans GN=ret-1 PE=2 SV=1 - [Q23188_CAEEEL]
Q7JLB0	17.65	3	22.61	207.6	ret-1	Protein RET-1, isoform e OS=Caenorhabditis elegans GN=ret-1 PE=2 SV=1 - [Q7JLB0_CAEEEL]
O44175	11.08	3	37.54	215.8	rfc-2	Protein RFC-2 OS=Caenorhabditis elegans GN=rfc-2 PE=2 SV=1 - [O44175_CAEEEL]
Q9GZH4	22.35	11	65.70	593.9	ribo-1	Protein RIBO-1 OS=Caenorhabditis elegans GN=ribo-1 PE=2 SV=2 - [Q9GZH4_CAEEEL]
O17694	24.46	2	16.48	237.0	ril-1	Protein RIL-1 OS=Caenorhabditis elegans GN=ril-1 PE=4 SV=1 - [O17694_CAEEEL]
Q95Q34	3.4	1	60.45	157.7	riok-2	Protein RIOK-2 OS=Caenorhabditis elegans GN=riok-2 PE=2 SV=2 - [Q95Q34_CAEEEL]
H2FLF6	31.79	4	22.20	163.0	rmd-1	Protein RMD-1, isoform b OS=Caenorhabditis elegans GN=rmd-1 PE=4 SV=1 - [H2FLF6_CAEEEL]
P90762	18.38	4	30.66	276.7	rmd-2	Protein RMD-2, isoform a OS=Caenorhabditis elegans GN=rmd-2 PE=2 SV=1 - [P90762_CAEEEL]
B2D6P1	21.33	4	25.46	253.3	rmd-2	Protein RMD-2, isoform c OS=Caenorhabditis elegans GN=rmd-2 PE=4 SV=1 - [B2D6P1_CAEEEL]
Q86S80	10.63	4	62.62	321.4	rme-1	Protein RME-1, isoform f OS=Caenorhabditis elegans GN=rme-1 PE=2 SV=1 - [Q86S80_CAEEEL]
Q21323	7.83	1	24.83	141.9	rnp-3	Protein RNP-3 OS=Caenorhabditis elegans GN=rnp-3 PE=1 SV=1 - [Q21323_CAEEEL]
Q21832	13.38	1	16.10	109.1	rnp-4	Protein RNP-4 OS=Caenorhabditis elegans GN=rnp-4 PE=2 SV=1 - [Q21832_CAEEEL]

O61711	2.57	1	64.58	120.9	rnp-8	Protein RNP-8 OS=Caenorhabditis elegans GN=rnp-8 PE=2 SV=1 - [O61711_CAEEL]
Q95Y97	17.36	3	32.02	294.5	rpa-2	Protein RPA-2 OS=Caenorhabditis elegans GN=rpa-2 PE=1 SV=1 - [Q95Y97_CAEEL]
Q19162	12.76	2	22.76	279.1	rpl-11.2	Protein RPL-11.2 OS=Caenorhabditis elegans GN=rpl-11.2 PE=2 SV=1 - [Q19162_CAEEL]
Q9XVE9	8.89	1	15.34	178.6	rpl-14	Protein RPL-14 OS=Caenorhabditis elegans GN=rpl-14 PE=2 SV=1 - [Q9XVE9_CAEEL]
G5ECE5	11.33	3	39.95	265.5	rpl-3	Protein RPL-3, isoform c OS=Caenorhabditis elegans GN=rpl-3 PE=4 SV=1 - [G5ECE5_CAEEL]
Q9XWS4	35.65	6	12.43	441.7	rpl-30	Protein RPL-30 OS=Caenorhabditis elegans GN=rpl-30 PE=2 SV=2 - [Q9XWS4_CAEEL]
B7WN95	22.22	2	9.09	205.8	rpl-32	Protein RPL-32, isoform b OS=Caenorhabditis elegans GN=rpl-32 PE=4 SV=1 - [B7WN95_CAEEL]
Q9GZH5	11.42	5	107.31	383.0	rpn-1	Protein RPN-1 OS=Caenorhabditis elegans GN=rpn-1 PE=2 SV=1 - [Q9GZH5_CAEEL]
Q22253	28.42	7	44.13	496.4	rpn-9	Protein RPN-9 OS=Caenorhabditis elegans GN=rpn-9 PE=1 SV=1 - [Q22253_CAEEL]
O01869	46.31	6	16.86	312.4	rps-10	Protein RPS-10 OS=Caenorhabditis elegans GN=rps-10 PE=1 SV=1 - [O01869_CAEEL]
Q20206	37.42	5	17.73	280.2	rps-11	Protein RPS-11 OS=Caenorhabditis elegans GN=rps-11 PE=2 SV=1 - [Q20206_CAEEL]
O18240	46.1	8	17.76	553.9	rps-18	Protein RPS-18 OS=Caenorhabditis elegans GN=rps-18 PE=3 SV=1 - [O18240_CAEEL]
Q8WQA8	36.75	5	13.23	430.5	rps-20	Protein RPS-20 OS=Caenorhabditis elegans GN=rps-20 PE=2 SV=1 - [Q8WQA8_CAEEL]
O17218	36.92	6	14.72	1173.2	rps-22	Protein RPS-22, isoform a OS=Caenorhabditis elegans GN=rps-22 PE=2 SV=1 - [O17218_CAEEL]
Q1XFY9	35.11	4	14.86	327.4	rps-24	Protein RPS-24 OS=Caenorhabditis elegans GN=rps-24 PE=2 SV=1 - [Q1XFY9_CAEEL]
O76371	16.28	4	48.10	216.6	rpt-5	Protein RPT-5 OS=Caenorhabditis elegans GN=rpt-5 PE=1 SV=1 - [O76371_CAEEL]
Q9XTT9	24.28	7	46.22	447.2	rpt-6	Protein RPT-6 OS=Caenorhabditis elegans GN=rpt-6 PE=3 SV=1 - [Q9XTT9_CAEEL]
Q19491	3.05	2	77.69	121.3	rsd-6	Protein RSD-6 OS=Caenorhabditis elegans GN=rsd-6 PE=2 SV=3 - [Q19491_CAEEL]
Q9NAH6	6.91	3	60.39	122.8	rsks-1	Protein RSKS-1 OS=Caenorhabditis elegans GN=rsks-1 PE=4 SV=2 - [Q9NAH6_CAEEL]
Q9N5K1	9.21	4	70.43	347.0	sacy-1	Protein SACY-1 OS=Caenorhabditis elegans GN=sacy-1 PE=2 SV=1 - [Q9N5K1_CAEEL]
O16386	4.2	2	98.10	116.9	sago-1	Protein SAGO-1 OS=Caenorhabditis elegans GN=sago-1 PE=2 SV=1 - [O16386_CAEEL]
Q9XU13	7.17	5	109.65	393.8	sca-1	Protein SCA-1, isoform b OS=Caenorhabditis elegans GN=sca-1 PE=2 SV=1 - [Q9XU13_CAEEL]
Q17557	13.46	6	35.63	336.3	sco-1	Protein SCO-1 OS=Caenorhabditis elegans GN=sco-1 PE=2 SV=1 - [Q17557_CAEEL]
Q94241	32.24	4	24.26	385.1	sec-22	Protein SEC-22 OS=Caenorhabditis elegans GN=sec-22 PE=4 SV=2 - [Q94241_CAEEL]
Q9U2Z1	8.04	4	89.62	167.2	sec-23	Protein SEC-23 OS=Caenorhabditis elegans GN=sec-23 PE=2 SV=2 - [Q9U2Z1_CAEEL]
Q22161	9.26	2	35.47	252.5	sfxn-1.5	Protein SFXN-1.5 OS=Caenorhabditis elegans GN=sfxn-1.5 PE=2 SV=1 - [Q22161_CAEEL]
Q9U1Y9	17.61	2	17.98	147.0	skr-4	Protein SKR-4 OS=Caenorhabditis elegans GN=skr-4 PE=2 SV=1 - [Q9U1Y9_CAEEL]
Q9XW41	15.43	3	18.77	114.1	snx-3	Protein SNX-3 OS=Caenorhabditis elegans GN=snx-3 PE=2 SV=1 - [Q9XW41_CAEEL]
G4S034	2.84	4	281.58	151.5	spc-1	Protein SPC-1, isoform a OS=Caenorhabditis elegans GN=spc-1 PE=4 SV=2 - [G4S034_CAEEL]
Q9N3T5	16.75	9	87.41	401.6	spg-7	Protein SPG-7 OS=Caenorhabditis elegans GN=spg-7 PE=2 SV=2 - [Q9N3T5_CAEEL]
Q8MXR6	23.93	5	33.45	292.9	sqd-1	Protein SQD-1, isoform a OS=Caenorhabditis elegans GN=sqd-1 PE=2 SV=1 - [Q8MXR6_CAEEL]
C6KRP6	13.3	4	40.61	201.7	sqrd-1	Protein SQRD-1, isoform c OS=Caenorhabditis elegans GN=sqrd-1 PE=4 SV=1 - [C6KRP6_CAEEL]
Q6QUQ5	6.85	2	40.49	149.6	srp-7	Protein SRP-7, isoform c OS=Caenorhabditis elegans GN=srp-7 PE=2 SV=1 - [Q6QUQ5_CAEEL]
O16259	18.44	4	36.94	307.1	sti-1	Protein STI-1 OS=Caenorhabditis elegans GN=sti-1 PE=2 SV=1 - [O16259_CAEEL]
H2FLJ1	29.63	7	35.62	948.2	stl-1	Protein STL-1, isoform a OS=Caenorhabditis elegans GN=stl-1 PE=4 SV=1 - [H2FLJ1_CAEEL]
G8JY63	11.08	2	35.88	124.4	sto-1	Protein STO-1, isoform b OS=Caenorhabditis elegans GN=sto-1 PE=4 SV=1 - [G8JY63_CAEEL]
O02642	14.64	3	33.35	209.7	sucl-2	Protein SUCL-2 OS=Caenorhabditis elegans GN=sucl-2 PE=2 SV=1 - [O02642_CAEEL]
D5MCQ9	9.9	2	32.34	143.6	sup-26	Protein SUP-26, isoform p OS=Caenorhabditis elegans GN=sup-26 PE=4 SV=1 - [D5MCQ9_CAEEL]
O62236	10.08	2	27.98	136.6	syx-7	Protein SYX-7 OS=Caenorhabditis elegans GN=syx-7 PE=2 SV=2 - [O62236_CAEEL]
Q22046	3.44	1	46.79	126.5	T01B7.5	Protein T01B7.5, isoform a OS=Caenorhabditis elegans GN=T01B7.5 PE=2 SV=2 - [Q22046_CAEEL]
Q22101	11.79	3	40.70	145.3	T02G5.7	Protein T02G5.7 OS=Caenorhabditis elegans GN=T02G5.7 PE=2 SV=1 - [Q22101_CAEEL]
A9D0C6	4.83	2	56.74	151.4	T02H6.1	Protein T02H6.1, isoform b OS=Caenorhabditis elegans GN=T02H6.1 PE=4 SV=1 - [A9D0C6_CAEEL]
Q9N5E4	46.15	6	15.11	334.9	T02H6.11	Protein T02H6.11 OS=Caenorhabditis elegans GN=T02H6.11 PE=2 SV=1 - [Q9N5E4_CAEEL]
Q22135	14.33	5	33.90	180.6	T04A8.6	Protein T04A8.6 OS=Caenorhabditis elegans GN=T04A8.6 PE=2 SV=1 - [Q22135_CAEEL]
Q22144	13.72	3	37.17	190.5	T04A8.8	Protein T04A8.8 OS=Caenorhabditis elegans GN=T04A8.8 PE=2 SV=1 - [Q22144_CAEEL]
Q22235	7.63	5	87.06	239.6	T05E11.3	Protein T05E11.3, isoform a OS=Caenorhabditis elegans GN=T05E11.3 PE=2 SV=1 - [Q22235_CAEEL]
Q8T8N8	19.94	10	75.57	1222.5	T08B2.7	Protein T08B2.7, isoform c OS=Caenorhabditis elegans GN=T08B2.7 PE=2 SV=1 - [Q8T8N8_CAEEL]
Q8T3D2	3.05	7	356.34	448.2	T08G11.1	Protein T08G11.1, isoform b OS=Caenorhabditis elegans GN=T08G11.1 PE=2 SV=1 - [Q8T3D2_CAEEL]
Q22352	21.02	6	37.29	383.3	T08H10.1	Protein T08H10.1 OS=Caenorhabditis elegans GN=T08H10.1 PE=2 SV=2 - [Q22352_CAEEL]
O76407	14.58	4	32.42	266.5	T10B5.3	Protein T10B5.3 OS=Caenorhabditis elegans GN=T10B5.3 PE=2 SV=3 - [O76407_CAEEL]
Q22437	19.46	5	49.60	320.5	T12G3.4	Protein T12G3.4 OS=Caenorhabditis elegans GN=T12G3.4 PE=2 SV=1 - [Q22437_CAEEL]

Q2V4T0	2.46	2	111.23	150.6	T19D12.4	Protein T19D12.4, isoform b OS=Caenorhabditis elegans GN=T19D12.4 PE=4 SV=1 - [Q2V4T0_CAEEL]
P91468	13.55	1	17.62	124.8	T20D4.7	Protein T20D4.7 OS=Caenorhabditis elegans GN=T20D4.7 PE=2 SV=1 - [P91468_CAEEL]
Q22624	1.2	1	135.45	103.7	T21B10.3	Protein T21B10.3 OS=Caenorhabditis elegans GN=T21B10.3 PE=2 SV=2 - [Q22624_CAEEL]
Q23044	25.95	8	44.40	587.9	T22B7.7	Protein T22B7.7 OS=Caenorhabditis elegans GN=T22B7.7 PE=2 SV=1 - [Q23044_CAEEL]
Q86DL2	7.36	2	50.04	144.9	T22D1.3	Protein T22D1.3, isoform b OS=Caenorhabditis elegans GN=T22D1.3 PE=2 SV=1 - [Q86DL2_CAEEL]
Q22768	4.52	1	45.47	105.5	T25B9.1	Protein T25B9.1 OS=Caenorhabditis elegans GN=T25B9.1 PE=4 SV=2 - [Q22768_CAEEL]
Q9GYK4	18.75	2	23.57	178.4	T27F7.1	Protein T27F7.1 OS=Caenorhabditis elegans GN=T27F7.1 PE=2 SV=2 - [Q9GYK4_CAEEL]
G5EGL2	15.57	4	40.78	396.4	T28D6.6	Protein T28D6.6, isoform a OS=Caenorhabditis elegans GN=T28D6.6 PE=4 SV=1 - [G5EGL2_CAEEL]
G5EBF4	5.63	2	53.20	173.8	T28H10.3	Protein T28H10.3 OS=Caenorhabditis elegans GN=T28H10.3 PE=4 SV=1 - [G5EBF4_CAEEL]
Q93619	21.58	4	40.03	276.3	tag-173	Protein TAG-173 OS=Caenorhabditis elegans GN=tag-173 PE=2 SV=1 - [Q93619_CAEEL]
Q86D21	10.96	7	79.41	283.5	tars-1	Protein TARS-1, isoform b OS=Caenorhabditis elegans GN=tars-1 PE=2 SV=1 - [Q86D21_CAEEL]
Q7JPE4	20.92	4	26.81	306.7	tat-4	Protein TAT-4, isoform c OS=Caenorhabditis elegans GN=tat-4 PE=2 SV=1 - [Q7JPE4_CAEEL]
O18688	34.52	11	49.98	5097.8	tba-1	Protein TBA-1, isoform a OS=Caenorhabditis elegans GN=tba-1 PE=2 SV=1 - [O18688_CAEEL]
G5EDD4	31.92	9	49.93	4784.6	tba-4	Protein TBA-4 OS=Caenorhabditis elegans GN=tba-4 PE=3 SV=1 - [G5EDD4_CAEEL]
O17921	54.79	19	50.21	2906.6	tbb-1	Protein TBB-1 OS=Caenorhabditis elegans GN=tbb-1 PE=2 SV=1 - [O17921_CAEEL]
Q86MP0	5.96	3	69.15	132.9	tcer-1	Protein TCER-1, isoform e OS=Caenorhabditis elegans GN=tcer-1 PE=2 SV=1 - [Q86MP0_CAEEL]
Q8IG49	5.42	1	32.58	105.9	tiar-1	Protein TIAR-1, isoform f OS=Caenorhabditis elegans GN=tiar-1 PE=2 SV=1 - [Q8IG49_CAEEL]
O17759	22.49	8	65.97	492.8	tkt-1	Protein TKT-1 OS=Caenorhabditis elegans GN=tkt-1 PE=4 SV=1 - [O17759_CAEEL]
O17287	33.03	3	12.17	144.2	tomm-22	Protein TOMM-22 OS=Caenorhabditis elegans GN=tomm-22 PE=2 SV=1 - [O17287_CAEEL]
Q95XT5	21.79	3	28.60	141.2	trap-1	Protein TRAP-1 OS=Caenorhabditis elegans GN=trap-1 PE=2 SV=1 - [Q95XT5_CAEEL]
Q9U238	43.4	4	17.40	455.2	trap-4	Protein TRAP-4 OS=Caenorhabditis elegans GN=trap-4 PE=1 SV=1 - [Q9U238_CAEEL]
Q19328	26.04	14	100.71	1379.5	tsn-1	Protein TSN-1 OS=Caenorhabditis elegans GN=tsn-1 PE=2 SV=1 - [Q19328_CAEEL]
Q17473	20.86	3	15.21	202.1	ttr-18	Protein TTR-18 OS=Caenorhabditis elegans GN=ttr-18 PE=4 SV=1 - [Q17473_CAEEL]
Q20089	8.33	1	16.29	118.7	ttr-20	Protein TTR-20 OS=Caenorhabditis elegans GN=ttr-20 PE=2 SV=1 - [Q20089_CAEEL]
Q9XXR4	18.44	2	15.29	213.1	ttr-24	Protein TTR-24, isoform a OS=Caenorhabditis elegans GN=ttr-24 PE=2 SV=1 - [Q9XXR4_CAEEL]
Q9XXQ6	29.08	3	15.23	281.0	ttr-25	Protein TTR-25, isoform a OS=Caenorhabditis elegans GN=ttr-25 PE=2 SV=1 - [Q9XXQ6_CAEEL]
Q7JMS9	28.8	3	13.60	150.5	ttr-4	Protein TTR-4 OS=Caenorhabditis elegans GN=ttr-4 PE=4 SV=1 - [Q7JMS9_CAEEL]
Q86NH9	17.86	3	15.45	275.5	ttr-41	Protein TTR-41 OS=Caenorhabditis elegans GN=ttr-41 PE=2 SV=1 - [Q86NH9_CAEEL]
O61977	18.71	2	17.32	114.8	ttr-47	Protein TTR-47 OS=Caenorhabditis elegans GN=ttr-47 PE=2 SV=1 - [O61977_CAEEL]
Q23378	17.07	2	18.55	463.6	ttr-48	Protein TTR-48 OS=Caenorhabditis elegans GN=ttr-48 PE=2 SV=1 - [Q23378_CAEEL]
G5EE48	16.43	2	22.48	107.7	ttr-50	Protein TTR-50 OS=Caenorhabditis elegans GN=ttr-50 PE=4 SV=1 - [G5EE48_CAEEL]
O62289	40.58	5	15.41	392.4	ttr-51	Protein TTR-51 OS=Caenorhabditis elegans GN=ttr-51 PE=2 SV=2 - [O62289_CAEEL]
Q95Y93	9.42	2	15.12	168.9	ttr-8	Protein TTR-8 OS=Caenorhabditis elegans GN=ttr-8 PE=2 SV=1 - [Q95Y93_CAEEL]
O01497	2.53	1	82.12	127.3	tyr-4	Protein TYR-4 OS=Caenorhabditis elegans GN=tyr-4 PE=2 SV=1 - [O01497_CAEEL]
Q9U2U0	15.79	3	30.84	148.2	uaf-2	Protein UAF-2 OS=Caenorhabditis elegans GN=uaf-2 PE=4 SV=1 - [Q9U2U0_CAEEL]
Q3S1J5	14.98	9	114.88	566.1	uba-1	Protein UBA-1, isoform b OS=Caenorhabditis elegans GN=uba-1 PE=2 SV=1 - [Q3S1J5_CAEEL]
Q95XX0	29.8	3	16.89	110.1	ubc-13	Protein UBC-13 OS=Caenorhabditis elegans GN=ubc-13 PE=2 SV=2 - [Q95XX0_CAEEL]
Q9N2W5	11.63	2	32.53	135.5	ubxn-2	Protein UBXN-2, isoform a OS=Caenorhabditis elegans GN=ubxn-2 PE=2 SV=2 - [Q9N2W5_CAEEL]
Q6A589	6.09	2	68.98	128.9	ubxn-3	Protein UBXN-3, isoform b OS=Caenorhabditis elegans GN=ubxn-3 PE=2 SV=2 - [Q6A589_CAEEL]
G5ED31	26.59	6	42.74	670.0	ucr-2.1	Protein UCR-2.1, isoform a OS=Caenorhabditis elegans GN=ucr-2.1 PE=3 SV=1 - [G5ED31_CAEEL]
Q22370	24.64	7	44.19	896.9	ucr-2.2	Protein UCR-2.2 OS=Caenorhabditis elegans GN=ucr-2.2 PE=2 SV=2 - [Q22370_CAEEL]
Q9TZ33	21.08	6	45.53	694.9	ucr-2.3	Protein UCR-2.3 OS=Caenorhabditis elegans GN=ucr-2.3 PE=2 SV=1 - [Q9TZ33_CAEEL]
O45495	14.39	2	15.91	135.2	uev-1	Protein UEV-1 OS=Caenorhabditis elegans GN=uev-1 PE=2 SV=1 - [O45495_CAEEL]
Q9GPA0	2.14	2	168.39	158.7	uggt-1	Protein UGGT-1 OS=Caenorhabditis elegans GN=uggt-1 PE=2 SV=1 - [Q9GPA0_CAEEL]
B1Q250	10.8	4	59.76	404.7	ugt-26	Protein UGT-26, isoform b OS=Caenorhabditis elegans GN=ugt-26 PE=3 SV=1 - [B1Q250_CAEEL]
Q86S69	14.56	5	54.13	400.6	ugt-29	Protein UGT-29, isoform b OS=Caenorhabditis elegans GN=ugt-29 PE=2 SV=1 - [Q86S69_CAEEL]
Q86S61	19	7	59.27	650.6	ugt-31	Protein UGT-31 OS=Caenorhabditis elegans GN=ugt-31 PE=2 SV=1 - [Q86S61_CAEEL]
O01577	35.05	7	23.58	618.0	unc-108	Protein UNC-108 OS=Caenorhabditis elegans GN=unc-108 PE=2 SV=1 - [O01577_CAEEL]
Q18685	1.81	1	82.30	105.8	unc-112	Protein unc-112 OS=Caenorhabditis elegans GN=unc-112 PE=1 SV=1 - [UN112_CAEEL]
Q17489	2.01	3	222.71	137.3	unc-44	Protein UNC-44, isoform a OS=Caenorhabditis elegans GN=unc-44 PE=2 SV=1 - [Q17489_CAEEL]
Q19437	6.72	2	43.17	146.9	upb-1	Protein UPB-1 OS=Caenorhabditis elegans GN=upb-1 PE=2 SV=1 - [Q19437_CAEEL]

G5EFK7	5.48	12	374.68	528.3	vab-10	Protein VAB-10, isoform f OS=Caenorhabditis elegans GN=vab-10 PE=4 SV=1 - [G5EFK7_CAEEL]
Q9N3F4	16.69	7	69.18	400.3	vbh-1	Protein VBH-1, isoform a OS=Caenorhabditis elegans GN=vbh-1 PE=2 SV=1 - [Q9N3F4_CAEEL]
Q95YD5	11.49	3	39.91	255.0	vha-16	Protein VHA-16 OS=Caenorhabditis elegans GN=vha-16 PE=2 SV=1 - [Q95YD5_CAEEL]
Q9TYW1	3.33	1	49.58	125.4	vha-19	Protein VHA-19 OS=Caenorhabditis elegans GN=vha-19 PE=2 SV=1 - [Q9TYW1_CAEEL]
G5EDB8	7.48	2	22.09	107.2	vha-4	Protein VHA-4 OS=Caenorhabditis elegans GN=vha-4 PE=2 SV=1 - [G5EDB8_CAEEL]
G5EEK9	9.05	6	99.25	375.9	vha-5	Protein VHA-5 OS=Caenorhabditis elegans GN=vha-5 PE=2 SV=1 - [G5EEK9_CAEEL]
Q95X44	47.79	11	25.57	1547.7	vha-8	Protein VHA-8 OS=Caenorhabditis elegans GN=vha-8 PE=2 SV=1 - [Q95X44_CAEEL]
H2KYR1	21.96	4	40.38	231.2	vig-1	Protein VIG-1, isoform a OS=Caenorhabditis elegans GN=vig-1 PE=4 SV=1 - [H2KYR1_CAEEL]
G8JY38	12.2	13	180.81	516.7	vit-2	Protein VIT-2, isoform b OS=Caenorhabditis elegans GN=vit-2 PE=4 SV=1 - [G8JY38_CAEEL]
Q9U2F6	16.88	2	25.96	117.4	vps-2	Protein VPS-2 OS=Caenorhabditis elegans GN=vps-2 PE=2 SV=1 - [Q9U2F6_CAEEL]
Q21053	2.07	1	93.79	146.9	vps-35	Protein VPS-35 OS=Caenorhabditis elegans GN=vps-35 PE=2 SV=3 - [Q21053_CAEEL]
Q19519	4.18	1	42.68	120.0	vps-36	Protein VPS-36 OS=Caenorhabditis elegans GN=vps-36 PE=2 SV=2 - [Q19519_CAEEL]
Q9BL83	5.81	2	48.07	121.4	vps-4	Protein VPS-4 OS=Caenorhabditis elegans GN=vps-4 PE=2 SV=4 - [Q9BL83_CAEEL]
Q23068	10.4	3	51.43	274.7	W01A11.1	Protein W01A11.1 OS=Caenorhabditis elegans GN=W01A11.1 PE=2 SV=1 - [Q23068_CAEEL]
O62390	25.73	6	34.40	391.8	W01F3.2	Protein W01F3.2 OS=Caenorhabditis elegans GN=W01F3.2 PE=2 SV=1 - [O62390_CAEEL]
Q5FC71	25.24	3	11.27	271.1	W02B12.15	Protein W02B12.15, isoform a OS=Caenorhabditis elegans GN=W02B12.15 PE=2 SV=1 - [Q5FC71_CAEEL]
O01780	20	3	27.07	271.8	W03F11.1	Protein W03F11.1 OS=Caenorhabditis elegans GN=W03F11.1 PE=2 SV=1 - [O01780_CAEEL]
Q9TYT8	21.62	5	24.66	241.1	W05F2.3	Protein W05F2.3 OS=Caenorhabditis elegans GN=W05F2.3 PE=2 SV=1 - [Q9TYT8_CAEEL]
Q23179	6.04	2	47.45	120.1	W05H9.1	Protein W05H9.1 OS=Caenorhabditis elegans GN=W05H9.1 PE=2 SV=1 - [Q23179_CAEEL]
G5EC98	4.02	2	75.20	130.3	W06H3.3	Protein W06H3.3 OS=Caenorhabditis elegans GN=W06H3.3 PE=4 SV=1 - [G5EC98_CAEEL]
G5EF05	6.21	9	240.72	518.8	W07E11.1	Protein W07E11.1 OS=Caenorhabditis elegans GN=W07E11.1 PE=4 SV=1 - [G5EF05_CAEEL]
Q9N5B3	32.23	7	43.01	341.0	W08E12.7	Protein W08E12.7 OS=Caenorhabditis elegans GN=W08E12.7 PE=2 SV=1 - [Q9N5B3_CAEEL]
O02109	23.68	3	25.60	361.3	W08F4.3	Protein W08F4.3 OS=Caenorhabditis elegans GN=W08F4.3 PE=2 SV=1 - [O02109_CAEEL]
H2L0M1	10.63	2	28.49	121.4	W09B6.4	Protein W09B6.4, isoform a OS=Caenorhabditis elegans GN=W09B6.4 PE=4 SV=1 - [H2L0M1_CAEEL]
Q9U329	31.43	6	20.24	527.8	W09C5.8	Protein W09C5.8 OS=Caenorhabditis elegans GN=W09C5.8 PE=2 SV=1 - [Q9U329_CAEEL]
O45011	17.79	5	44.71	474.6	W10C8.5	Protein W10C8.5 OS=Caenorhabditis elegans GN=W10C8.5 PE=2 SV=1 - [O45011_CAEEL]
G5EDY2	8.15	2	47.21	175.1	wars-1	Protein WARS-1 OS=Caenorhabditis elegans GN=wars-1 PE=2 SV=1 - [G5EDY2_CAEEL]
Q965V4	5.33	3	104.78	104.8	xpo-2	Protein XPO-2 OS=Caenorhabditis elegans GN=xpo-2 PE=2 SV=1 - [Q965V4_CAEEL]
Q9NF11	10.28	2	23.81	138.2	Y105E8B.5	Protein Y105E8B.5 OS=Caenorhabditis elegans GN=Y105E8B.5 PE=1 SV=1 - [Q9NF11_CAEEL]
Q9N584	2.12	1	74.79	133.0	Y110A7A.19	Protein Y110A7A.19 OS=Caenorhabditis elegans GN=Y110A7A.19 PE=2 SV=1 - [Q9N584_CAEEL]
Q9U2U3	6.69	1	30.43	152.6	Y116A8C.27	Protein Y116A8C.27, isoform a OS=Caenorhabditis elegans GN=Y116A8C.27 PE=4 SV=2 - [Q9U2U3_CAEEL]
Q9XXJ4	11.48	2	23.14	143.9	Y12A6A.1	Protein Y12A6A.1 OS=Caenorhabditis elegans GN=Y12A6A.1 PE=2 SV=1 - [Q9XXJ4_CAEEL]
Q9N580	7.14	2	40.61	120.3	Y17G9B.5	Protein Y17G9B.5 OS=Caenorhabditis elegans GN=Y17G9B.5 PE=2 SV=1 - [Q9N580_CAEEL]
O76616	25.73	5	34.78	377.6	Y23H5A.3	Protein Y23H5A.3 OS=Caenorhabditis elegans GN=Y23H5A.3 PE=2 SV=1 - [O76616_CAEEL]
Q9XX35	1.85	1	94.55	110.8	Y32B12B.2	Protein Y32B12B.2, isoform a OS=Caenorhabditis elegans GN=Y32B12B.2 PE=2 SV=3 - [Q9XX35_CAEEL]
Q9BKU3	18.71	4	38.87	269.9	Y37E3.10	Protein Y37E3.10 OS=Caenorhabditis elegans GN=Y37E3.10 PE=4 SV=2 - [Q9BKU3_CAEEL]
H2L0N9	18.07	10	91.76	819.9	Y37E3.17	Protein Y37E3.17, isoform a OS=Caenorhabditis elegans GN=Y37E3.17 PE=3 SV=1 - [H2L0N9_CAEEL]
D6RYE0	24.64	2	15.30	161.2	Y38C1AA.14	Protein Y38C1AA.14 OS=Caenorhabditis elegans GN=Y38C1AA.14 PE=4 SV=1 - [D6RYE0_CAEEL]
O45924	24.59	6	48.99	408.7	Y39E4A.3	Protein Y39E4A.3, isoform a OS=Caenorhabditis elegans GN=Y39E4A.3 PE=2 SV=2 - [O45924_CAEEL]
Q95XR0	11.09	4	51.20	242.3	Y39G10AR.8	Protein Y39G10AR.8 OS=Caenorhabditis elegans GN=Y39G10AR.8 PE=2 SV=1 - [Q95XR0_CAEEL]
Q9NAI5	27.53	6	35.19	515.7	Y39G8B.1	Protein Y39G8B.1, isoform a OS=Caenorhabditis elegans GN=Y39G8B.1 PE=2 SV=1 - [Q9NAI5_CAEEL]
Q9U2J0	3.8	1	55.11	156.3	Y40B1B.8	Protein Y40B1B.8 OS=Caenorhabditis elegans GN=Y40B1B.8 PE=2 SV=1 - [Q9U2J0_CAEEL]
O45934	8.74	4	66.54	133.0	Y43F4B.5	Protein Y43F4B.5, isoform a OS=Caenorhabditis elegans GN=Y43F4B.5 PE=2 SV=1 - [O45934_CAEEL]
Q9BL81	14.12	2	26.75	251.2	Y47G6A.21	Protein Y47G6A.21 OS=Caenorhabditis elegans GN=Y47G6A.21 PE=2 SV=4 - [Q9BL81_CAEEL]
Q8MXS8	34.25	6	26.84	546.2	Y47G6A.22	Protein Y47G6A.22 OS=Caenorhabditis elegans GN=Y47G6A.22 PE=2 SV=1 - [Q8MXS8_CAEEL]
G5EF86	16.79	3	31.23	198.6	Y48G10A.1	Protein Y48G10A.1 OS=Caenorhabditis elegans GN=Y48G10A.1 PE=4 SV=1 - [G5EF86_CAEEL]
Q9XWJ6	37.19	5	23.53	237.6	Y51H1A.3	Protein Y51H1A.3, isoform a OS=Caenorhabditis elegans GN=Y51H1A.3 PE=2 SV=1 - [Q9XWJ6_CAEEL]
Q9N3H3	33.64	10	48.22	599.8	Y53G8AL.2	Protein Y53G8AL.2 OS=Caenorhabditis elegans GN=Y53G8AL.2 PE=2 SV=2 - [Q9N3H3_CAEEL]
Q9N3D0	28.96	5	20.61	297.9	Y54E10BR.5	Protein Y54E10BR.5 OS=Caenorhabditis elegans GN=Y54E10BR.5 PE=2 SV=1 - [Q9N3D0_CAEEL]
Q9XWK2	17.65	2	17.43	146.8	Y54E5A.5	Protein Y54E5A.5 OS=Caenorhabditis elegans GN=Y54E5A.5 PE=2 SV=1 - [Q9XWK2_CAEEL]
C0Z3L6	18.55	2	14.71	134.6	Y54G11A.17	Protein Y54G11A.17 OS=Caenorhabditis elegans GN=Y54G11A.17 PE=4 SV=1 - [C0Z3L6_CAEEL]

Q9N362	7.91	2	38.43	128.3	Y55F3AM.13	Protein Y55F3AM.13 OS=Caenorhabditis elegans GN=Y55F3AM.13 PE=2 SV=1 - [Q9N362_CAEEEL]
Q8MXS6	4.14	1	47.50	165.2	Y55F3AM.3	Protein Y55F3AM.3, isoform c OS=Caenorhabditis elegans GN=Y55F3AM.3 PE=2 SV=1 - [Q8MXS6_CAEEEL]
Q9NA78	27.42	4	21.45	211.7	Y57A10A.23	Protein Y57A10A.23 OS=Caenorhabditis elegans GN=Y57A10A.23 PE=2 SV=1 - [Q9NA78_CAEEEL]
Q9NA74	41.26	9	30.71	665.7	Y57A10A.26	Protein Y57A10A.26 OS=Caenorhabditis elegans GN=Y57A10A.26 PE=2 SV=1 - [Q9NA74_CAEEEL]
Q9U210	6.44	2	42.91	128.2	Y57A10A.27	Protein Y57A10A.27 OS=Caenorhabditis elegans GN=Y57A10A.27 PE=2 SV=1 - [Q9U210_CAEEEL]
O18239	9.51	2	52.21	119.1	Y57G11C.15	Protein Y57G11C.15, isoform a OS=Caenorhabditis elegans GN=Y57G11C.15 PE=3 SV=1 - [O18239_CAEEEL]
O76630	14.29	3	33.32	238.9	Y57G7A.10	Protein Y57G7A.10 OS=Caenorhabditis elegans GN=Y57G7A.10 PE=1 SV=1 - [O76630_CAEEEL]
Q966A5	6.64	5	104.55	172.6	Y58A7A.4	Protein Y58A7A.4 OS=Caenorhabditis elegans GN=Y58A7A.4 PE=2 SV=1 - [Q966A5_CAEEEL]
Q9GRZ9	17.46	8	75.85	407.7	Y59A8A.3	Protein Y59A8A.3 OS=Caenorhabditis elegans GN=Y59A8A.3 PE=2 SV=1 - [Q9GRZ9_CAEEEL]
Q9U1Z4	5.21	1	24.51	100.4	Y60A3A.9	Protein Y60A3A.9 OS=Caenorhabditis elegans GN=Y60A3A.9 PE=2 SV=1 - [Q9U1Z4_CAEEEL]
Q9XWT5	21.5	4	24.05	338.0	Y62H9A.3	Protein Y62H9A.3 OS=Caenorhabditis elegans GN=Y62H9A.3 PE=2 SV=1 - [Q9XWT5_CAEEEL]
Q9XWS6	14.55	3	18.48	131.5	Y62H9A.5	Protein Y62H9A.5 OS=Caenorhabditis elegans GN=Y62H9A.5 PE=2 SV=2 - [Q9XWS6_CAEEEL]
G5EDQ7	16.24	1	12.91	102.7	Y66A7A.7	Protein Y66A7A.7 OS=Caenorhabditis elegans GN=Y66A7A.7 PE=4 SV=1 - [G5EDQ7_CAEEEL]
Q95PZ7	3.63	1	28.67	170.6	Y66D12A.9	Protein Y66D12A.9 OS=Caenorhabditis elegans GN=Y66D12A.9 PE=2 SV=1 - [Q95PZ7_CAEEEL]
Q9BKQ9	34.62	4	16.81	418.0	Y67D2.3	Protein Y67D2.3 OS=Caenorhabditis elegans GN=Y67D2.3 PE=2 SV=1 - [Q9BKQ9_CAEEEL]
Q95PZ1	41.38	11	15.50	1237.9	Y67H2A.5	Protein Y67H2A.5 OS=Caenorhabditis elegans GN=Y67H2A.5 PE=2 SV=1 - [Q95PZ1_CAEEEL]
Q9XW37	19.19	3	19.21	331.5	Y69E1A.5	Protein Y69E1A.5 OS=Caenorhabditis elegans GN=Y69E1A.5 PE=2 SV=1 - [Q9XW37_CAEEEL]
Q9N4H7	9.82	8	137.62	388.9	Y71F9AL.17	Protein Y71F9AL.17 OS=Caenorhabditis elegans GN=Y71F9AL.17 PE=2 SV=2 - [Q9N4H7_CAEEEL]
Q9N4I3	16.56	3	32.17	244.3	Y71F9AL.9	Protein Y71F9AL.9 OS=Caenorhabditis elegans GN=Y71F9AL.9 PE=2 SV=1 - [Q9N4I3_CAEEEL]
Q95XN3	1.71	1	112.02	142.8	Y71G12B.11	Protein Y71G12B.11, isoform b OS=Caenorhabditis elegans GN=Y71G12B.11 PE=2 SV=1 - [Q95XN3_CAEEEL]
Q9BL43	10.36	3	61.61	190.1	Y71H2AM.13	Protein Y71H2AM.13 OS=Caenorhabditis elegans GN=Y71H2AM.13 PE=2 SV=1 - [Q9BL43_CAEEEL]
Q9BL33	33.81	4	16.26	275.7	Y71H2AM.4	Protein Y71H2AM.4 OS=Caenorhabditis elegans GN=Y71H2AM.4 PE=4 SV=1 - [Q9BL33_CAEEEL]
Q9BL34	34.71	5	14.81	433.2	Y71H2AM.5	Protein Y71H2AM.5 OS=Caenorhabditis elegans GN=Y71H2AM.5 PE=2 SV=1 - [Q9BL34_CAEEEL]
Q9N4E8	3.23	1	38.37	103.5	Y71H2B.2	Protein Y71H2B.2 OS=Caenorhabditis elegans GN=Y71H2B.2 PE=2 SV=1 - [Q9N4E8_CAEEEL]
Q9GUE9	19.08	2	15.07	154.6	Y73B6BL.27	Protein Y73B6BL.27 OS=Caenorhabditis elegans GN=Y73B6BL.27 PE=4 SV=3 - [Q9GUE9_CAEEEL]
Q965S3	6.94	1	20.48	109.8	Y97E10AL.3	Protein Y97E10AL.3 OS=Caenorhabditis elegans GN=Y97E10AL.3 PE=2 SV=1 - [Q965S3_CAEEEL]
Q23258	53.85	5	11.05	1210.8	ZC373.2	Protein ZC373.2 OS=Caenorhabditis elegans GN=ZC373.2 PE=4 SV=2 - [Q23258_CAEEEL]
Q5WRS7	13.18	2	29.75	154.4	ZC477.3	Protein ZC477.3, isoform b OS=Caenorhabditis elegans GN=ZC477.3 PE=2 SV=1 - [Q5WRS7_CAEEEL]
O76449	7.02	3	63.05	177.6	ZK1055.7	Protein ZK1055.7 OS=Caenorhabditis elegans GN=ZK1055.7 PE=1 SV=1 - [O76449_CAEEEL]
Q09657	6.99	2	51.34	170.4	ZK1320.9	Protein ZK1320.9 OS=Caenorhabditis elegans GN=ZK1320.9 PE=2 SV=1 - [Q09657_CAEEEL]
Q7Z145	4.12	1	54.43	142.9	ZK418.9	Protein ZK418.9, isoform b OS=Caenorhabditis elegans GN=ZK418.9 PE=2 SV=1 - [Q7Z145_CAEEEL]
Q6EZG8	10.13	2	42.41	121.8	ZK6.11	Protein ZK6.11, isoform b OS=Caenorhabditis elegans GN=ZK6.11 PE=2 SV=1 - [Q6EZG8_CAEEEL]
Q23571	6.25	2	49.66	101.4	ZK669.4	Protein ZK669.4 OS=Caenorhabditis elegans GN=ZK669.4 PE=2 SV=1 - [Q23571_CAEEEL]
Q23597	32.38	5	24.34	480.3	ZK809.3	Protein ZK809.3 OS=Caenorhabditis elegans GN=ZK809.3 PE=2 SV=1 - [Q23597_CAEEEL]
Q23624	4.57	1	40.20	127.7	ZK829.7	Protein ZK829.7 OS=Caenorhabditis elegans GN=ZK829.7 PE=1 SV=2 - [Q23624_CAEEEL]
Q23660	3.32	1	52.95	106.2	ZK899.2	Protein ZK899.2 OS=Caenorhabditis elegans GN=ZK899.2 PE=2 SV=2 - [Q23660_CAEEEL]
Q20448	4.07	2	71.07	136.4	ztf-7	Protein ZTF-7 OS=Caenorhabditis elegans GN=ztf-7 PE=2 SV=1 - [Q20448_CAEEEL]
P49404	9.93	3	44.61	170.2	C26E6.6	Putative 39S ribosomal protein L3, mitochondrial OS=Caenorhabditis elegans GN=C26E6.6 PE=2 SV=3 - [RM03_CAEEEL]
O01513	14.21	2	21.06	116.7	C48B6.2	Putative 40S ribosomal protein S4-like OS=Caenorhabditis elegans GN=C48B6.2 PE=2 SV=1 - [YS4L_CAEEEL]
O18229	10.78	2	30.39	260.4	Y57G11C.3	Putative 6-phosphogluconolactonase OS=Caenorhabditis elegans GN=Y57G11C.3 PE=2 SV=2 - [6PGL_CAEEEL]
P46562	8.85	4	56.98	236.5	alh-9	Putative aldehyde dehydrogenase family 7 member A1 homolog OS=Caenorhabditis elegans GN=alh-9
Q27245	12.07	6	56.05	415.8	W07G4.4	Putative aminopeptidase W07G4.4 OS=Caenorhabditis elegans GN=W07G4.4 PE=1 SV=1 - [YH24_CAEEEL]
Q22021	39.22	6	18.74	415.0	R53.4	Putative ATP synthase subunit f, mitochondrial OS=Caenorhabditis elegans GN=R53.4 PE=2 SV=1 - [ATPK_CAEEEL]
P55216	17.86	5	43.07	338.1	cth-2	Putative cystathionine gamma-lyase 2 OS=Caenorhabditis elegans GN=cth-2 PE=1 SV=1 - [CGL2_CAEEEL]
O01739	16.19	4	42.48	292.1	F20H11.5	Putative D-amino-acid oxidase 1 OS=Caenorhabditis elegans GN=F20H11.5 PE=1 SV=1 - [OXDA1_CAEEEL]
Q19264	38.94	10	33.07	551.5	F09E5.3	Putative deoxyribose-phosphate aldolase OS=Caenorhabditis elegans GN=F09E5.3 PE=2 SV=1 - [DEOC_CAEEEL]
P91917	33.92	10	44.32	854.0	tag-210	Putative GTP-binding protein tag-210 OS=Caenorhabditis elegans GN=tag-210 PE=2 SV=1 - [TG210_CAEEEL]
Q9XWV2	12.96	6	65.40	536.4	Y37D8A.2	Putative phospholipase B-like 1 OS=Caenorhabditis elegans GN=Y37D8A.2 PE=1 SV=1 - [PLBL1_CAEEEL]
O62146	11.86	5	66.60	362.6	F09B12.3	Putative phospholipase B-like 2 OS=Caenorhabditis elegans GN=F09B12.3 PE=1 SV=2 - [PLBL2_CAEEEL]
Q9BL07	7.92	3	67.20	226.7	Y54F10AM.8	Putative phospholipase B-like 3 OS=Caenorhabditis elegans GN=Y54F10AM.8 PE=1 SV=1 - [PLBL3_CAEEEL]
P34528	6.27	2	56.53	109.6	K12H4.7	Putative serine protease K12H4.7 OS=Caenorhabditis elegans GN=K12H4.7 PE=2 SV=2 - [YM67_CAEEEL]



Q17703	14.33	3	34.58	233.2	stdh-1	Putative steroid dehydrogenase 1 OS=Caenorhabditis elegans GN=stdh-1 PE=2 SV=1 - [STDH1_CAEEL]
Q09517	28.16	6	34.29	354.9	let-767	Putative steroid dehydrogenase let-767 OS=Caenorhabditis elegans GN=let-767 PE=1 SV=2 - [LE767_CAEEL]
Q09541	1.67	2	150.99	159.3	F21H12.6	Putative subtilase-type proteinase F21H12.6 OS=Caenorhabditis elegans GN=F21H12.6 PE=2 SV=1 - [YQS6_CAEEL]
P52652	3.25	1	34.85	134.3	T24H10.1	Putative transcription elongation factor S-II OS=Caenorhabditis elegans GN=T24H10.1 PE=3 SV=1 - [TFS2_CAEEL]
P34519	18.91	5	34.20	225.6	K11H3.3	Putative tricarboxylate transport protein, mitochondrial OS=Caenorhabditis elegans GN=K11H3.3 PE=2 SV=1 - [TXTP_CAEEL]
Q9U2G0	2.05	3	243.68	123.6	Y46G5A.4	Putative U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Caenorhabditis elegans GN=Y46G5A.4
P50581	6.59	1	20.68	123.3	T27A8.3	Putative uncharacterized protein T27A8.3 OS=Caenorhabditis elegans GN=T27A8.3 PE=5 SV=1 - [YD43_CAEEL]
O17732	22.38	19	129.20	959.8	pyc-1	Pyruvate carboxylase 1 OS=Caenorhabditis elegans GN=pyc-1 PE=1 SV=1 - [PYC1_CAEEL]
O44451	16.48	4	38.12	189.8	C04C3.3	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C04C3.3
Q7JL40	12.99	5	57.36	407.5	pyk-1	Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-1 PE=2 SV=1 - [Q7JL40_CAEEL]
P22981	13.59	2	20.97	106.2	let-60	Ras protein let-60 OS=Caenorhabditis elegans GN=let-60 PE=1 SV=1 - [LET60_CAEEL]
Q22038	16.67	2	21.62	193.3	rho-1	Ras-like GTP-binding protein rhoA OS=Caenorhabditis elegans GN=rho-1 PE=2 SV=1 - [RHO1_CAEEL]
P34213	16.59	3	23.24	209.1	rab-6.1	Ras-related protein Rab-6.1 OS=Caenorhabditis elegans GN=rab-6.1 PE=2 SV=1 - [RAB6A_CAEEL]
Q18211	5.8	2	61.45	190.7	ran-3	Regulator of chromosome condensation OS=Caenorhabditis elegans GN=ran-3 PE=2 SV=1 - [RCC1_CAEEL]
P53016	8.98	2	37.68	189.3	rfc-4	Replication factor C subunit 4 OS=Caenorhabditis elegans GN=rfc-4 PE=1 SV=1 - [RFC4_CAEEL]
Q03604	8.25	3	88.91	155.9	rrr-1	Ribonucleoside-diphosphate reductase large subunit OS=Caenorhabditis elegans GN=rrr-1 PE=2 SV=1 - [RIR1_CAEEL]
P42170	8.4	3	44.26	200.6	rrr-2	Ribonucleoside-diphosphate reductase small chain OS=Caenorhabditis elegans GN=rrr-2 PE=2 SV=1 - [RIR2_CAEEL]
Q95QB6	10.06	2	34.51	106.6	R151.2	Ribose-phosphate pyrophosphokinase OS=Caenorhabditis elegans GN=R151.2 PE=2 SV=1 - [Q95QB6_CAEEL]
Q9N3F0	7.74	2	33.44	105.4	Y54E10A.10	Ribosome production factor 2 homolog OS=Caenorhabditis elegans GN=Y54E10A.10 PE=2 SV=1 - [RPF2_CAEEL]
P90783	9.41	3	49.87	169.1	C55A6.9	RNA polymerase II-associated factor 1 homolog OS=Caenorhabditis elegans GN=C55A6.9 PE=2 SV=2 - [PAF1_CAEEL]
Q22053	39.2	12	36.36	1687.9	fib-1	rRNA 2'-O-methyltransferase fibrillar OS=Caenorhabditis elegans GN=fib-1 PE=2 SV=1 - [FBRL_CAEEL]
P46576	12.9	5	47.10	434.1	gop-3	SAM50-like protein gop-3 OS=Caenorhabditis elegans GN=gop-3 PE=2 SV=2 - [SAM50_CAEEL]
P50432	26.82	10	55.73	658.9	mel-32	Serine hydroxymethyltransferase OS=Caenorhabditis elegans GN=mel-32 PE=1 SV=2 - [GLYC_CAEEL]
Q09422	16.2	3	32.47	212.6	pgam-5	Serine/threonine-protein phosphatase Pgam5, mitochondrial OS=Caenorhabditis elegans GN=pgam-5
Q27497	13.68	3	37.18	160.6	gsp-1	Serine/threonine-protein phosphatase PP1-alpha OS=Caenorhabditis elegans GN=gsp-1 PE=2 SV=2 - [GLC7A_CAEEL]
P48727	26.13	7	37.77	306.7	gsp-2	Serine/threonine-protein phosphatase PP1-beta OS=Caenorhabditis elegans GN=gsp-2 PE=2 SV=1 - [GLC7B_CAEEL]
P29355	9.21	1	26.19	108.4	sem-5	Sex muscle abnormal protein 5 OS=Caenorhabditis elegans GN=sem-5 PE=1 SV=1 - [SEM5_CAEEL]
P91240	10.71	4	71.37	288.8	F08D12.1	Signal recognition particle 72 kDa protein homolog OS=Caenorhabditis elegans GN=F08D12.1 PE=3 SV=2 - [SRP72_CAEEL]
Q8WSZ9	7.65	1	19.32	192.7	skr-1	SKR-1 (Fragment) OS=Caenorhabditis elegans GN=skr-1 PE=2 SV=1 - [Q8WSZ9_CAEEL]
P55853	16.48	1	10.22	104.1	smo-1	Small ubiquitin-related modifier OS=Caenorhabditis elegans GN=smo-1 PE=1 SV=1 - [SUMO_CAEEL]
Q93235	18.44	4	36.65	169.1	nkb-1	Sodium/potassium-transporting ATPase subunit beta-1 OS=Caenorhabditis elegans GN=nkb-1 PE=1 SV=1 - [AT1B1_CAEEL]
Q9Y194	4.71	2	61.06	103.8	spl-1	Sphingosine-1-phosphate lyase OS=Caenorhabditis elegans GN=spl-1 PE=2 SV=1 - [SGPL_CAEEL]
Q18212	7.53	3	48.46	218.0	hel-1	Spliceosome RNA helicase DDX39B homolog OS=Caenorhabditis elegans GN=hel-1 PE=2 SV=1 - [DX39B_CAEEL]
Q17322	13.79	5	59.31	220.9	sta	STE12 transcriptional activator OS=Caenorhabditis elegans GN=sta PE=2 SV=1 - [Q17322_CAEEL]
Q20363	85.53	11	17.83	1297.7	sip-1	Stress-induced protein 1 OS=Caenorhabditis elegans GN=sip-1 PE=1 SV=1 - [SIP1_CAEEL]
Q09508	24.92	10	70.35	910.8	sdha-1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Caenorhabditis elegans GN=sdha-1
Q09545	25.17	6	32.87	206.1	sdhb-1	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Caenorhabditis elegans GN=sdhb-1
P34697	22.22	2	18.69	140.4	sod-1	Superoxide dismutase [Cu-Zn] OS=Caenorhabditis elegans GN=sod-1 PE=1 SV=2 - [SODC_CAEEL]
P31161	36.2	6	24.52	577.3	sod-2	Superoxide dismutase [Mn] 1, mitochondrial OS=Caenorhabditis elegans GN=sod-2 PE=1 SV=1 - [SODM1_CAEEL]
P34703	1.91	2	175.71	106.0	emb-5	Suppressor of Ty 6 homolog OS=Caenorhabditis elegans GN=emb-5 PE=1 SV=1 - [SPT6H_CAEEL]
O02495	33.03	3	12.02	338.7	snb-1	Synaptobrevin-1 OS=Caenorhabditis elegans GN=snb-1 PE=1 SV=1 - [SYB1_CAEEL]
P41988	12.2	5	58.77	235.6	cct-1	T-complex protein 1 subunit alpha OS=Caenorhabditis elegans GN=cct-1 PE=2 SV=2 - [TCPA_CAEEL]
P47207	11.15	3	56.94	199.4	cct-2	T-complex protein 1 subunit beta OS=Caenorhabditis elegans GN=cct-2 PE=1 SV=2 - [TCPB_CAEEL]
P47208	24.26	9	58.35	609.1	cct-4	T-complex protein 1 subunit delta OS=Caenorhabditis elegans GN=cct-4 PE=2 SV=1 - [TCPD_CAEEL]
P47209	12.73	5	59.37	261.8	cct-5	T-complex protein 1 subunit epsilon OS=Caenorhabditis elegans GN=cct-5 PE=1 SV=1 - [TCPE_CAEEL]
Q9N358	9.49	4	59.70	122.6	cct-8	T-complex protein 1 subunit theta OS=Caenorhabditis elegans GN=cct-8 PE=1 SV=3 - [TCPQ_CAEEL]
Q20683	8.38	1	19.64	136.9	F52H3.5	Tetratricopeptide repeat protein 36 homolog OS=Caenorhabditis elegans GN=F52H3.5 PE=2 SV=1 - [TTC36_CAEEL]
Q02335	6.15	3	64.83	170.3	ZK370.8	TPR repeat-containing protein ZK370.8 OS=Caenorhabditis elegans GN=ZK370.8 PE=2 SV=3 - [YOL8_CAEEL]
Q966C7	32.29	7	35.25	378.1	Y24D9A.8	Transaldolase OS=Caenorhabditis elegans GN=Y24D9A.8 PE=2 SV=1 - [Q966C7_CAEEL]
Q21338	7.7	6	133.27	336.1	spt-5	Transcription elongation factor SPT5 OS=Caenorhabditis elegans GN=spt-5 PE=2 SV=3 - [SPT5H_CAEEL]
Q9U7E0	1.03	1	156.10	103.7	xnp-1	Transcriptional regulator ATRX homolog OS=Caenorhabditis elegans GN=xnp-1 PE=1 SV=1 - [ATRX_CAEEL]

P54811	22.5	11	89.73	842.2	cdc-48.1	Transitional endoplasmic reticulum ATPase homolog 1 OS=Caenorhabditis elegans GN=cdc-48.1 PE=1 SV=1 - [TERA1_CAEEL]
P54812	20.49	10	89.58	726.4	cdc-48.2	Transitional endoplasmic reticulum ATPase homolog 2 OS=Caenorhabditis elegans GN=cdc-48.2 PE=1 SV=2 - [TERA2_CAEEL]
Q93573	66.85	10	20.53	772.7	tct-1	Translationally-controlled tumor protein homolog OS=Caenorhabditis elegans GN=tct-1 PE=1 SV=1 - [TCTP_CAEEL]
Q23424	5.68	3	87.41	396.9	fzo-1	Transmembrane GTPase fzo-1 OS=Caenorhabditis elegans GN=fzo-1 PE=2 SV=1 - [FZO1_CAEEL]
Q22288	36.15	2	14.49	206.8	ttr-15	Transthyretin-like protein 15 OS=Caenorhabditis elegans GN=ttr-15 PE=2 SV=1 - [TTR15_CAEEL]
P34500	39.19	6	15.69	653.5	ttr-2	Transthyretin-like protein 2 OS=Caenorhabditis elegans GN=ttr-2 PE=1 SV=1 - [TTR2_CAEEL]
Q10657	54.25	10	26.56	700.1	tpi-1	Triosephosphate isomerase OS=Caenorhabditis elegans GN=tpi-1 PE=1 SV=2 - [TPIS_CAEEL]
Q9GYF1	10.74	2	27.54	164.7	unc-27	Troponin I 2 OS=Caenorhabditis elegans GN=unc-27 PE=2 SV=2 - [TNNI2_CAEEL]
P46579	7.22	2	40.45	149.2	wars-2	Tryptophan-tRNA ligase, mitochondrial OS=Caenorhabditis elegans GN=wars-2 PE=2 SV=3 - [SYWM_CAEEL]
P34690	34.6	11	49.88	5098.6	tba-2	Tubulin alpha-2 chain OS=Caenorhabditis elegans GN=tba-2 PE=2 SV=1 - [TBA2_CAEEL]
P91910	14	4	50.08	195.6	mec-12	Tubulin alpha-3 chain OS=Caenorhabditis elegans GN=mec-12 PE=1 SV=1 - [TBA3_CAEEL]
P52274	11.5	3	50.46	382.1	tba-8	Tubulin alpha-8 chain OS=Caenorhabditis elegans GN=tba-8 PE=2 SV=2 - [TBA8_CAEEL]
P52275	55.56	20	50.31	2902.4	tbb-2	Tubulin beta-2 chain OS=Caenorhabditis elegans GN=tbb-2 PE=2 SV=1 - [TBB2_CAEEL]
Q9XTQ6	2.22	1	66.71	100.9	tbh-1	Tyramine beta-hydroxylase OS=Caenorhabditis elegans GN=tbh-1 PE=1 SV=2 - [TBH1_CAEEL]
O44512	22.46	5	29.69	608.1	isp-1	Ubiquinol-cytochrome c reductase iron-sulfur subunit OS=Caenorhabditis elegans GN=isp-1 PE=2 SV=1 - [O44512_CAEEL]
P91428	6.93	1	26.21	166.3	coq-4	Ubiquinone biosynthesis protein coq-4, mitochondrial OS=Caenorhabditis elegans GN=coq-4 PE=2 SV=2 - [COQ4_CAEEL]
Q17361	10.43	3	55.84	307.5	usp-14	Ubiquitin carboxyl-terminal hydrolase 14 OS=Caenorhabditis elegans GN=usp-14 PE=2 SV=2 - [UBP14_CAEEL]
Q19905	8.73	3	52.72	169.2	sqv-4	UDP-glucose 6-dehydrogenase OS=Caenorhabditis elegans GN=sqv-4 PE=1 SV=1 - [UGDH_CAEEL]
Q6LD30	40.62	10	39.71	604.2	unc-87	Unc-87 protein OS=Caenorhabditis elegans GN=unc-87 PE=2 SV=1 - [Q6LD30_CAEEL]
P34280	6.56	2	40.80	142.0	C02F5.3	Uncharacterized GTP-binding protein C02F5.3 OS=Caenorhabditis elegans GN=C02F5.3 PE=2 SV=2 - [YKK3_CAEEL]
Q09475	4.43	6	193.97	391.3	C28H8.3	Uncharacterized helicase C28H8.3 OS=Caenorhabditis elegans GN=C28H8.3 PE=2 SV=2 - [YP93_CAEEL]
Q21276	41.36	14	54.48	2629.2	K07C5.4	Uncharacterized NOP5 family protein K07C5.4 OS=Caenorhabditis elegans GN=K07C5.4 PE=2 SV=1 - [YZVL_CAEEL]
Q93761	21.41	4	33.37	224.9	F53C11.3	Uncharacterized oxidoreductase F53C11.3 OS=Caenorhabditis elegans GN=F53C11.3 PE=2 SV=1 - [YXEK_CAEEL]
P34255	19.42	7	47.84	441.8	B0303.3	Uncharacterized protein B0303.3 OS=Caenorhabditis elegans GN=B0303.3 PE=2 SV=1 - [YKA3_CAEEL]
P34304	2.64	1	72.31	179.7	C06E1.9	Uncharacterized protein C06E1.9 OS=Caenorhabditis elegans GN=C06E1.9 PE=2 SV=2 - [YKQ9_CAEEL]
Q18232	6.99	1	21.18	101.3	C26F1.3	Uncharacterized protein C26F1.3 OS=Caenorhabditis elegans GN=C26F1.3 PE=2 SV=1 - [YBRI_CAEEL]
Q05036	31.06	13	86.84	869.8	C30C11.4	Uncharacterized protein C30C11.4 OS=Caenorhabditis elegans GN=C30C11.4 PE=1 SV=1 - [YLA4_CAEEL]
P34384	8.63	3	44.35	224.3	F02A9.4	Uncharacterized protein F02A9.4b OS=Caenorhabditis elegans GN=F02A9.4 PE=2 SV=3 - [YLPD_CAEEL]
Q19753	5.88	4	108.36	160.2	F23B12.7	Uncharacterized protein F23B12.7 OS=Caenorhabditis elegans GN=F23B12.7 PE=2 SV=1 - [YU00_CAEEL]
P34526	41.24	3	11.52	249.0	K12H4.5	Uncharacterized protein K12H4.5 OS=Caenorhabditis elegans GN=K12H4.5 PE=2 SV=1 - [YM65_CAEEL]
Q629J5	12.61	3	37.98	282.9	R144.12	Uncharacterized protein R144.12 OS=Caenorhabditis elegans GN=R144.12 PE=4 SV=1 - [YRRC_CAEEL]
Q9BPN8	5.49	2	71.04	121.5	Y92H12BR.3	Uncharacterized protein Y92H12BR.3 OS=Caenorhabditis elegans GN=Y92H12BR.3 PE=1 SV=2 - [Y92H3_CAEEL]
Q23280	32.57	6	19.42	286.0	ZC395.10	Uncharacterized protein ZC395.10 OS=Caenorhabditis elegans GN=ZC395.10 PE=2 SV=1 - [YOCA_CAEEL]
P34748	21.8	2	15.38	168.3	ZK1098.7	Uncharacterized protein ZK1098.7 OS=Caenorhabditis elegans GN=ZK1098.7 PE=2 SV=1 - [YO67_CAEEL]
Q09359	9.32	2	31.15	115.4	ZK1307.1	Uncharacterized protein ZK1307.1 OS=Caenorhabditis elegans GN=ZK1307.1 PE=2 SV=1 - [YS11_CAEEL]
P34669	6.34	2	37.66	112.6	ZK686.3	Uncharacterized protein ZK686.3 OS=Caenorhabditis elegans GN=ZK686.3 PE=2 SV=1 - [YO13_CAEEL]
P52717	8.53	3	53.61	311.9	F41C3.5	Uncharacterized serine carboxypeptidase F41C3.5 OS=Caenorhabditis elegans GN=F41C3.5 PE=1 SV=1 - [YUW5_CAEEL]
Q8WQG1	17.57	2	24.95	156.1	C35D10.1	UPF0480 protein C35D10.1 OS=Caenorhabditis elegans GN=C35D10.1 PE=3 SV=1 - [YLC1_CAEEL]
Q21898	10.65	1	16.94	124.0	vha-1	V-type proton ATPase 16 kDa proteolipid subunit 1 OS=Caenorhabditis elegans GN=vha-1 PE=2 SV=1 - [VATL1_CAEEL]
P34546	7.45	1	16.40	119.8	vha-2	V-type proton ATPase 16 kDa proteolipid subunit 2/3 OS=Caenorhabditis elegans GN=vha-2 PE=2 SV=2 - [VATL2_CAEEL]
Q9XW92	23.1	10	66.42	882.8	vha-13	V-type proton ATPase catalytic subunit A OS=Caenorhabditis elegans GN=vha-13 PE=1 SV=3 - [VATA_CAEEL]
Q9XXU9	21.35	7	43.43	761.3	vha-11	V-type proton ATPase subunit C OS=Caenorhabditis elegans GN=vha-11 PE=2 SV=1 - [VATC_CAEEL]
P34462	21.01	4	28.77	392.7	vha-14	V-type proton ATPase subunit D OS=Caenorhabditis elegans GN=vha-14 PE=2 SV=1 - [VATD_CAEEL]
Q9U1Q4	14.76	11	118.85	636.8	vrs-2	Valine-tRNA ligase OS=Caenorhabditis elegans GN=vrs-2 PE=1 SV=1 - [SYV_CAEEL]
P55155	42.95	67	187.95	9017.4	vit-1	Vitellogenin-1 OS=Caenorhabditis elegans GN=vit-1 PE=1 SV=2 - [VIT1_CAEEL]
P05690	61.13	91	187.60	#####	vit-2	Vitellogenin-2 OS=Caenorhabditis elegans GN=vit-2 PE=1 SV=5 - [VIT2_CAEEL]
Q9N4J2	44.67	67	186.41	8882.6	vit-3	Vitellogenin-3 OS=Caenorhabditis elegans GN=vit-3 PE=1 SV=1 - [VIT3_CAEEL]
P18947	42.79	66	186.19	9173.4	vit-4	Vitellogenin-4 OS=Caenorhabditis elegans GN=vit-4 PE=1 SV=3 - [VIT4_CAEEL]
P06125	52.28	78	186.32	#####	vit-5	Vitellogenin-5 OS=Caenorhabditis elegans GN=vit-5 PE=2 SV=2 - [VIT5_CAEEL]
P18948	53.85	79	193.20	#####	vit-6	Vitellogenin-6 OS=Caenorhabditis elegans GN=vit-6 PE=1 SV=5 - [VIT6_CAEEL]
XA1000	33.82	6	30.97	687.1	Q35-YFP Fusion protein	YFP Fusion protein

Q21432	10.19	4	64.99	271.0	nas-11
G5EEM5	3.32	3	156.09	135.9	zyg-9

Zinc metalloproteinase nas-11 OS=Caenorhabditis elegans GN=nas-11 PE=1 SV=2 - [NAS11\_CAEEL]  
Zygote defective protein 9 OS=Caenorhabditis elegans GN=zyg-9 PE=1 SV=1 - [ZYG9\_CAEEL]

**Table S4**

Uniprot ID	Coverage [%]	# Peptides	MW [kDa]	Score	Gene name	Description
P41932	11.69	3	28.17	184.29	par-5	14-3-3-like protein 1 OS=Caenorhabditis elegans GN=par-5 PE=1 SV=2 - [14331_CAEEL]
Q20655	17.34	4	28.05	221.95	ftt-2	14-3-3-like protein 2 OS=Caenorhabditis elegans GN=ftt-2 PE=1 SV=1 - [14332_CAEEL]
P36573	45.88	9	31.79	414.20	lec-1	32 kDa beta-galactoside-binding lectin OS=Caenorhabditis elegans GN=lec-1 PE=1 SV=1 - [LEC1_CAEEL]
P49196	25	3	15.06	277.74	rps-12	40S ribosomal protein S12 OS=Caenorhabditis elegans GN=rps-12 PE=1 SV=2 - [RS12_CAEEL]
P51404	27.81	4	17.31	125.80	rps-13	40S ribosomal protein S13 OS=Caenorhabditis elegans GN=rps-13 PE=2 SV=2 - [RS13_CAEEL]
P48150	50	8	16.24	292.58	rps-14	40S ribosomal protein S14 OS=Caenorhabditis elegans GN=rps-14 PE=2 SV=1 - [RS14_CAEEL]
Q9XVP0	24.5	3	17.23	62.62	rps-15	40S ribosomal protein S15 OS=Caenorhabditis elegans GN=rps-15 PE=1 SV=3 - [RS15_CAEEL]
Q22054	43.75	7	16.31	329.14	rps-16	40S ribosomal protein S16 OS=Caenorhabditis elegans GN=rps-16 PE=1 SV=3 - [RS16_CAEEL]
O01692	23.08	2	14.93	153.89	rps-17	40S ribosomal protein S17 OS=Caenorhabditis elegans GN=rps-17 PE=2 SV=2 - [RS17_CAEEL]
O18650	40.41	5	16.31	128.08	rps-19	40S ribosomal protein S19 OS=Caenorhabditis elegans GN=rps-19 PE=2 SV=1 - [RS19_CAEEL]
P51403	26.47	4	28.94	114.35	rps-2	40S ribosomal protein S2 OS=Caenorhabditis elegans GN=rps-2 PE=2 SV=1 - [RS2_CAEEL]
Q19877	16.08	2	15.86	78.98	rps-23	40S ribosomal protein S23 OS=Caenorhabditis elegans GN=rps-23 PE=2 SV=1 - [RS23_CAEEL]
P52821	24.79	4	12.90	220.40	rps-25	40S ribosomal protein S25 OS=Caenorhabditis elegans GN=rps-25 PE=2 SV=1 - [RS25_CAEEL]
O45499	30.77	3	13.24	250.86	rps-26	40S ribosomal protein S26 OS=Caenorhabditis elegans GN=rps-26 PE=2 SV=1 - [RS26_CAEEL]
P48152	32.39	6	27.30	404.89	rps-3	40S ribosomal protein S3 OS=Caenorhabditis elegans GN=rps-3 PE=2 SV=1 - [RS3_CAEEL]
P48154	22.57	5	28.94	188.60	rps-1	40S ribosomal protein S3a OS=Caenorhabditis elegans GN=rps-1 PE=2 SV=2 - [RS3A_CAEEL]
Q9N3X2	32.82	8	29.03	365.68	rps-4	40S ribosomal protein S4 OS=Caenorhabditis elegans GN=rps-4 PE=1 SV=1 - [RS4_CAEEL]
P49041	38.57	6	23.14	315.22	rps-5	40S ribosomal protein S5 OS=Caenorhabditis elegans GN=rps-5 PE=2 SV=1 - [RS5_CAEEL]
Q9NEN6	18.29	5	28.12	224.76	rps-6	40S ribosomal protein S6 OS=Caenorhabditis elegans GN=rps-6 PE=1 SV=1 - [RS6_CAEEL]
Q23312	11.34	2	22.04	117.49	rps-7	40S ribosomal protein S7 OS=Caenorhabditis elegans GN=rps-7 PE=2 SV=1 - [RS7_CAEEL]
P48156	38.46	7	23.74	455.78	rps-8	40S ribosomal protein S8 OS=Caenorhabditis elegans GN=rps-8 PE=2 SV=1 - [RS8_CAEEL]
Q20228	31.22	7	21.94	198.65	rps-9	40S ribosomal protein S9 OS=Caenorhabditis elegans GN=rps-9 PE=2 SV=1 - [RS9_CAEEL]
P46769	39.86	8	30.68	300.45	rps-0	40S ribosomal protein SA OS=Caenorhabditis elegans GN=rps-0 PE=1 SV=3 - [RSSA_CAEEL]
G5EEV5	17.44	2	19.42	57.78	5C820	5C820 OS=Caenorhabditis elegans GN=5C820 PE=2 SV=1 - [G5EEV5_CAEEL]
Q93572	45.19	8	33.75	648.39	rpa-0	60S acidic ribosomal protein P0 OS=Caenorhabditis elegans GN=rpa-0 PE=1 SV=3 - [RLA0_CAEEL]
O01504	61.68	4	10.81	244.73	rpa-2	60S acidic ribosomal protein P2 OS=Caenorhabditis elegans GN=rpa-2 PE=2 SV=2 - [RLA2_CAEEL]
Q09533	11.21	3	24.73	142.56	rpl-10	60S ribosomal protein L10 OS=Caenorhabditis elegans GN=rpl-10 PE=2 SV=1 - [RL10_CAEEL]
Q9N414	17.59	5	24.12	296.73	rpl-10a	60S ribosomal protein L10a OS=Caenorhabditis elegans GN=rpl-10a PE=2 SV=1 - [RL10A_CAEEL]
P61866	16.97	2	17.82	89.55	rpl-12	60S ribosomal protein L12 OS=Caenorhabditis elegans GN=rpl-12 PE=2 SV=1 - [RL12_CAEEL]
P91128	23.67	4	23.74	94.74	rpl-13	60S ribosomal protein L13 OS=Caenorhabditis elegans GN=rpl-13 PE=2 SV=1 - [RL13_CAEEL]
Q27389	13.37	2	22.98	106.14	rpl-16	60S ribosomal protein L13a OS=Caenorhabditis elegans GN=rpl-16 PE=2 SV=1 - [RL13A_CAEEL]
P91374	12.75	2	24.11	126.56	rpl-15	60S ribosomal protein L15 OS=Caenorhabditis elegans GN=rpl-15 PE=2 SV=1 - [RL15_CAEEL]
Q9BL19	13.9	2	21.50	231.53	rpl-17	60S ribosomal protein L17 OS=Caenorhabditis elegans GN=rpl-17 PE=2 SV=1 - [RL17_CAEEL]
O45946	36.17	6	20.98	357.21	rpl-18	60S ribosomal protein L18 OS=Caenorhabditis elegans GN=rpl-18 PE=3 SV=1 - [RL18_CAEEL]
O44480	24.44	5	20.95	427.80	rpl-20	60S ribosomal protein L18a OS=Caenorhabditis elegans GN=rpl-20 PE=2 SV=2 - [RL18A_CAEEL]
O02639	13.13	2	23.64	107.61	rpl-19	60S ribosomal protein L19 OS=Caenorhabditis elegans GN=rpl-19 PE=2 SV=1 - [RL19_CAEEL]
P34334	18.01	2	18.30	242.74	rpl-21	60S ribosomal protein L21 OS=Caenorhabditis elegans GN=rpl-21 PE=1 SV=3 - [RL21_CAEEL]
P52819	30.77	5	14.94	260.29	rpl-22	60S ribosomal protein L22 OS=Caenorhabditis elegans GN=rpl-22 PE=1 SV=3 - [RL22_CAEEL]

P48158	32.86	3	14.94	171.86	rpl-23	60S ribosomal protein L23 OS=Caenorhabditis elegans GN=rpl-23 PE=2 SV=1 - [RL23_CAEEL]
O01868	15.72	2	17.77	68.70	rpl-24.1	60S ribosomal protein L24 OS=Caenorhabditis elegans GN=rpl-24.1 PE=2 SV=1 - [RL24_CAEEL]
P91914	30.15	5	15.72	248.07	rpl-27	60S ribosomal protein L27 OS=Caenorhabditis elegans GN=rpl-27 PE=2 SV=1 - [RL27_CAEEL]
Q21930	15.87	2	13.72	188.15	rpl-28	60S ribosomal protein L28 OS=Caenorhabditis elegans GN=rpl-28 PE=1 SV=3 - [RL28_CAEEL]
Q9U332	14.75	2	14.25	89.64	rpl-31	60S ribosomal protein L31 OS=Caenorhabditis elegans GN=rpl-31 PE=2 SV=1 - [RL31_CAEEL]
P34662	21.95	2	14.19	145.57	rpl-35	60S ribosomal protein L35 OS=Caenorhabditis elegans GN=rpl-35 PE=2 SV=1 - [RL35_CAEEL]
P49180	13.71	2	13.76	135.82	rpl-33	60S ribosomal protein L35a OS=Caenorhabditis elegans GN=rpl-33 PE=1 SV=3 - [RL35A_CAEEL]
P49181	27.88	4	11.88	181.63	rpl-36	60S ribosomal protein L36 OS=Caenorhabditis elegans GN=rpl-36 PE=1 SV=3 - [RL36_CAEEL]
O02056	23.48	7	38.64	417.81	rpl-4	60S ribosomal protein L4 OS=Caenorhabditis elegans GN=rpl-4 PE=1 SV=3 - [RL4_CAEEL]
P49405	35.49	7	33.37	375.69	rpl-5	60S ribosomal protein L5 OS=Caenorhabditis elegans GN=rpl-5 PE=2 SV=1 - [RL5_CAEEL]
P47991	28.57	6	24.30	241.93	rpl-6	60S ribosomal protein L6 OS=Caenorhabditis elegans GN=rpl-6 PE=1 SV=1 - [RL6_CAEEL]
O01802	27.46	7	28.11	452.91	rpl-7	60S ribosomal protein L7 OS=Caenorhabditis elegans GN=rpl-7 PE=1 SV=1 - [RL7_CAEEL]
Q966C6	26.79	6	30.16	299.21	rpl-7A	60S ribosomal protein L7a OS=Caenorhabditis elegans GN=rpl-7A PE=1 SV=3 - [RL7A_CAEEL]
Q9XVF7	15.77	4	28.19	137.88	rpl-8	60S ribosomal protein L8 OS=Caenorhabditis elegans GN=rpl-8 PE=1 SV=1 - [RL8_CAEEL]
Q95Y90	34.92	5	21.49	261.28	rpl-9	60S ribosomal protein L9 OS=Caenorhabditis elegans GN=rpl-9 PE=1 SV=1 - [RL9_CAEEL]
P10984	34.04	9	41.75	426.16	act-2	Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=2 SV=3 - [ACT2_CAEEL]
Q07750	8.49	2	23.56	50.24	unc-60	Actin-depolymerizing factor 1, isoforms a/b OS=Caenorhabditis elegans GN=unc-60 PE=2 SV=2 - [ADF1_CAEEL]
P27604	8.47	3	47.51	195.58	ahcy-1	Adenosylhomocysteinase OS=Caenorhabditis elegans GN=ahcy-1 PE=1 SV=1 - [SAHH_CAEEL]
Q10943	13.26	2	20.51	103.89	arf-1.2	ADP-ribosylation factor 1-like 2 OS=Caenorhabditis elegans GN=arf-1.2 PE=2 SV=2 - [ARF12_CAEEL]
Q17334	32.95	9	37.67	507.44	sodh-1	Alcohol dehydrogenase 1 OS=Caenorhabditis elegans GN=sodh-1 PE=1 SV=2 - [ADH1_CAEEL]
G5EEA8	33.85	9	35.67	588.40	nex-1	Annexin OS=Caenorhabditis elegans GN=nex-1 PE=2 SV=1 - [G5EEA8_CAEEL]
Q27473	27.13	6	36.07	225.57	nex-3	Annexin OS=Caenorhabditis elegans GN=nex-3 PE=2 SV=1 - [Q27473_CAEEL]
Q8MYM9	16.2	2	17.45	32.47	Y39B6A.34	APOPT family protein Y39B6A.34, mitochondrial OS=Caenorhabditis elegans GN=Y39B6A.34 PE=2 SV=1 - [APOP1_CAEEL]
Q17994	7.73	2	45.59	89.14	got-2.2	Aspartate aminotransferase OS=Caenorhabditis elegans GN=got-2.2 PE=2 SV=1 - [Q17994_CAEEL]
Q95XJ0	27.76	6	32.36	341.56	Y69A2AR.18	ATP synthase gamma chain OS=Caenorhabditis elegans GN=Y69A2AR.18 PE=2 SV=1 - [Q95XJ0_CAEEL]
Q9XXK1	16.17	9	57.75	685.25	H28O16.1	ATP synthase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=H28O16.1 PE=1 SV=1 - [ATPA_CAEEL]
P46561	24.54	9	57.49	659.03	atp-2	ATP synthase subunit beta, mitochondrial OS=Caenorhabditis elegans GN=atp-2 PE=1 SV=2 - [ATPB_CAEEL]
G5ED07	11.07	4	54.89	195.56	pdi-3	CeERp57 OS=Caenorhabditis elegans GN=pdi-3 PE=2 SV=1 - [G5ED07_CAEEL]
P98080	20.59	7	51.70	440.74	ucr-1	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Caenorhabditis elegans GN=ucr-1 PE=2 SV=2 - [UCR1_CAEEL]
P19974	23.42	2	12.23	141.62	cyc-2.1	Cytochrome c 2.1 OS=Caenorhabditis elegans GN=cyc-2.1 PE=1 SV=2 - [CYC21_CAEEL]
P55954	17.82	2	20.10	48.27	cco-2	Cytochrome c oxidase subunit 5A, mitochondrial OS=Caenorhabditis elegans GN=cco-2 PE=1 SV=2 - [COX5A_CAEEL]
Q18066	8.13	3	71.80	230.97	dim-1	Disorganized muscle protein 1 OS=Caenorhabditis elegans GN=dim-1 PE=1 SV=3 - [DIM_CAEEL]
Q22799	25.84	2	10.34	91.65	dlc-1	Dynein light chain 1, cytoplasmic OS=Caenorhabditis elegans GN=dlc-1 PE=1 SV=1 - [DYL1_CAEEL]
P53013	21.38	7	50.64	1452.93	eft-3	Elongation factor 1-alpha OS=Caenorhabditis elegans GN=eft-3 PE=2 SV=1 - [EF1A_CAEEL]
Q27527	8.06	2	46.59	92.38	enol-1	Enolase OS=Caenorhabditis elegans GN=enol-1 PE=1 SV=3 - [ENO_CAEEL]
P27639	7.46	2	45.38	163.73	inf-1	Eukaryotic initiation factor 4A OS=Caenorhabditis elegans GN=inf-1 PE=2 SV=1 - [IF4A_CAEEL]
Q21693	15.35	2	25.71	69.09	ife-2	Eukaryotic translation initiation factor 4E-2 OS=Caenorhabditis elegans GN=ife-2 PE=1 SV=1 - [IF4E2_CAEEL]
P34563	25.47	2	17.86	210.98	iff-1	Eukaryotic translation initiation factor 5A-1 OS=Caenorhabditis elegans GN=iff-1 PE=1 SV=1 - [IF5A1_CAEEL]
Q20751	32.3	3	17.94	121.05	iff-2	Eukaryotic translation initiation factor 5A-2 OS=Caenorhabditis elegans GN=iff-2 PE=2 SV=1 - [IF5A2_CAEEL]
P34686	8.52	2	30.77	71.23	cap-2	F-actin-capping protein subunit beta OS=Caenorhabditis elegans GN=cap-2 PE=2 SV=1 - [CAPZB_CAEEL]

Q20224	14.29	2	18.83	58.25	lbp-2	Fatty acid-binding protein homolog 2 OS=Caenorhabditis elegans GN=lbp-2 PE=1 SV=1 - [FABP2_CAEEL]
O02323	29.93	3	16.16	231.43	lbp-7	Fatty acid-binding protein homolog 7 OS=Caenorhabditis elegans GN=lbp-7 PE=1 SV=1 - [FABP7_CAEEL]
G8JY45	18.15	3	28.00	178.67	aldo-2	Fructose-bisphosphate aldolase OS=Caenorhabditis elegans GN=aldo-2 PE=3 SV=1 - [G8JY45_CAEEL]
G5EGB1	46.04	8	31.28	692.64	lec-2	Galectin LEC-2 OS=Caenorhabditis elegans GN=lec-2 PE=2 SV=1 - [G5EGB1_CAEEL]
Q23621	4.29	2	58.76	106.92	gdh-1	Glutamate dehydrogenase OS=Caenorhabditis elegans GN=gdh-1 PE=2 SV=1 - [Q23621_CAEEL]
P10299	22.12	3	23.89	178.98	gst-1	Glutathione S-transferase P OS=Caenorhabditis elegans GN=gst-1 PE=1 SV=1 - [GSTP1_CAEEL]
P17329	12.9	3	36.43	165.33	gpd-2	Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Caenorhabditis elegans GN=gpd-2 PE=3 SV=2 - [G3P2_CAEEL]
Q21215	21.23	5	35.81	252.01	rack-1	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Caenorhabditis elegans GN=rack-1 PE=1 SV=3 - [GBLP_CAEEL]
P09446	10.31	5	69.68	187.95	hsp-1	Heat shock 70 kDa protein A OS=Caenorhabditis elegans GN=hsp-1 PE=1 SV=2 - [HSP7A_CAEEL]
P27420	11.8	5	72.98	225.82	hsp-3	Heat shock 70 kDa protein C OS=Caenorhabditis elegans GN=hsp-3 PE=1 SV=2 - [HSP7C_CAEEL]
P09588	23.62	2	13.40	52.14	his-3	Histone H2A OS=Caenorhabditis elegans GN=his-3 PE=1 SV=2 - [H2A_CAEEL]
P04255	27.87	3	13.49	173.22	his-11	Histone H2B 1 OS=Caenorhabditis elegans GN=his-11 PE=1 SV=4 - [H2B1_CAEEL]
P62784	41.75	4	11.36	173.60	his-1	Histone H4 OS=Caenorhabditis elegans GN=his-1 PE=1 SV=2 - [H4_CAEEL]
P05634	33.86	4	14.23	167.33	msp-10	Major sperm protein 10/36/56/76 OS=Caenorhabditis elegans GN=msp-10 PE=2 SV=4 - [MSP10_CAEEL]
Q8IA49	17.58	3	29.09	594.96	mdh-1	Malate dehydrogenase OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1 - [Q8IA49_CAEEL]
Q9BKU4	44.36	7	29.97	1098.00	phb-1	Mitochondrial prohibitin complex protein 1 OS=Caenorhabditis elegans GN=phb-1 PE=1 SV=1 - [PHB1_CAEEL]
P50093	11.9	3	32.65	238.70	phb-2	Mitochondrial prohibitin complex protein 2 OS=Caenorhabditis elegans GN=phb-2 PE=1 SV=2 - [PHB2_CAEEL]
P19625	77.06	10	18.61	361.58	mlc-1	Myosin regulatory light chain 1 OS=Caenorhabditis elegans GN=mlc-1 PE=2 SV=1 - [MLR1_CAEEL]
P02566	15.16	20	224.99	866.07	unc-54	Myosin-4 OS=Caenorhabditis elegans GN=unc-54 PE=4 SV=1 - [MYO4_CAEEL]
Q86S66	20.3	3	22.06	195.10	Y65B4BR.5 / icd-2 / $\alpha$ NAC	Nascent polypeptide-associated complex subunit alpha OS=Caenorhabditis elegans GN=Y65B4BR.5 PE=1 SV=1 - [NACA_CAEEL]
Q9XVK5	8.89	2	21.09	52.91	ubc-12	NEDD8-conjugating enzyme ubc-12 OS=Caenorhabditis elegans GN=ubc-12 PE=2 SV=1 - [UBC12_CAEEL]
P36609	13.16	2	21.97	81.19	ncs-2	Neuronal calcium sensor 2 OS=Caenorhabditis elegans GN=ncs-2 PE=2 SV=2 - [NCS2_CAEEL]
Q21568	26.56	2	13.99	104.91	M28.5	NHP2-like protein 1 homolog OS=Caenorhabditis elegans GN=M28.5 PE=2 SV=1 - [NH2L1_CAEEL]
Q93576	18.3	2	17.11	108.08	ndk-1	Nucleoside diphosphate kinase OS=Caenorhabditis elegans GN=ndk-1 PE=1 SV=1 - [Q93576_CAEEL]
P52013	8.82	2	21.91	96.47	cyn-5	Peptidyl-prolyl cis-trans isomerase 5 OS=Caenorhabditis elegans GN=cyn-5 PE=1 SV=2 - [CYP5_CAEEL]
P52015	64.91	8	18.39	343.69	cyn-7	Peptidyl-prolyl cis-trans isomerase 7 OS=Caenorhabditis elegans GN=cyn-7 PE=1 SV=2 - [CYP7_CAEEL]
Q27462	27.78	2	11.62	42.79	FKBP-2	Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=FKBP-2 PE=2 SV=1 - [Q27462_CAEEL]
P40614	16.47	5	36.65	168.76	F01G4.6	Phosphate carrier protein, mitochondrial OS=Caenorhabditis elegans GN=F01G4.6 PE=2 SV=1 - [MPCP_CAEEL]
Q21217	4.55	3	53.02	138.06	gta-1	Probable 4-aminobutyrate aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=gta-1 PE=1 SV=1 - [GABT_CAEEL]
Q8WTM6	5.65	2	34.46	43.01	arx-4	Probable actin-related protein 2/3 complex subunit 2 OS=Caenorhabditis elegans GN=arx-4 PE=2 SV=1 - [ARPC2_CAEEL]
Q20140	28.57	4	22.58	170.29	F38B2.4	Probable adenylate kinase isoenzyme F38B2.4 OS=Caenorhabditis elegans GN=F38B2.4 PE=2 SV=1 - [KAD1_CAEEL]
Q10454	25.25	7	44.14	526.05	F46H5.3	Probable arginine kinase F46H5.3 OS=Caenorhabditis elegans GN=F46H5.3 PE=1 SV=2 - [KARG1_CAEEL]
Q27535	8.06	2	40.36	122.22	ZC434.8	Probable arginine kinase ZC434.8 OS=Caenorhabditis elegans GN=ZC434.8 PE=1 SV=1 - [KARG2_CAEEL]
Q18803	17.56	2	14.82	120.56	asg-2	Probable ATP synthase subunit g 2, mitochondrial OS=Caenorhabditis elegans GN=asg-2 PE=2 SV=1 - [ATPL2_CAEEL]
P34575	7.05	3	51.51	161.70	cts-1	Probable citrate synthase, mitochondrial OS=Caenorhabditis elegans GN=cts-1 PE=1 SV=1 - [CISY_CAEEL]
Q20779	44.53	6	14.73	232.41	tag-174	Probable cytochrome c oxidase subunit 6A, mitochondrial OS=Caenorhabditis elegans GN=tag-174 PE=2 SV=1 - [COX6A_CAEEL]
Q93615	14.76	3	34.43	99.43	F27D4.1	Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F27D4.1 PE=2 SV=2 - [ETFA_CAEEL]
P34460	15.96	2	22.69	37.19	F54H12.6	Probable elongation factor 1-beta/1-delta 1 OS=Caenorhabditis elegans GN=F54H12.6 PE=1 SV=1 - [EF1B1_CAEEL]
P34559	11.46	2	31.15	118.74	ech-6	Probable enoyl-CoA hydratase, mitochondrial OS=Caenorhabditis elegans GN=ech-6 PE=1 SV=1 - [ECHM_CAEEL]
O62327	13.5	2	18.14	121.16	R05H10.5	Probable glutathione peroxidase R05H10.5 OS=Caenorhabditis elegans GN=R05H10.5 PE=2 SV=1 - [GPX2_CAEEL]

Q93714	6.42	2	38.44	96.10	F43G9.1	Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F43G9.1 PE=1 SV=3 - [IDH3A_CAEEL]
Q93353	9.5	2	41.53	52.52	C37E2.1	Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C37E2.1 PE=2 SV=1 - [IDH3B_CAEEL]
O02640	42.23	8	35.10	330.78	mdh-1	Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1 - [MDHM_CAEEL]
Q9N2W7	17.81	2	17.06	78.76	Y94H6A.8	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Caenorhabditis elegans GN=Y94H6A.8 PE=2 SV=2 - [NDUAC_CAEEL]
Q18359	17.33	2	17.32	120.18	C33A12.1	Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Caenorhabditis elegans GN=C33A12.1 PE=3 SV=1 - [NDUA5_CAEEL]
Q20412	20.63	3	18.47	125.72	F44G4.2	Probable NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial OS=Caenorhabditis elegans GN=F44G4.2
Q20719	8.79	2	26.22	52.87	F53F4.10	Probable NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Caenorhabditis elegans GN=F53F4.10 PE=1 SV=1 - [NDUV2_CAEEL]
Q94360	12.56	2	21.90	193.38	nduf-7	Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Caenorhabditis elegans GN=nduf-7 PE=2 SV=1 - [NDUS7_CAEEL]
Q18040	10.19	3	46.42	162.52	C16A3.10	Probable ornithine aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=3 - [OAT_CAEEL]
P91427	10.31	3	44.09	123.45	pgk-1	Probable phosphoglycerate kinase OS=Caenorhabditis elegans GN=pgk-1 PE=1 SV=1 - [PGK_CAEEL]
Q11067	7.27	2	47.70	127.83	tag-320	Probable protein disulfide-isomerase A6 OS=Caenorhabditis elegans GN=tag-320 PE=2 SV=1 - [PDIA6_CAEEL]
P50305	4.95	2	44.01	143.01	sams-3	Probable S-adenosylmethionine synthase 3 OS=Caenorhabditis elegans GN=sams-3 PE=1 SV=1 - [METK3_CAEEL]
P91303	25.4	3	14.48	160.02	vha-10	Probable V-type proton ATPase subunit G OS=Caenorhabditis elegans GN=vha-10 PE=2 SV=1 - [VATG_CAEEL]
Q21752	60.07	14	29.94	1703.12	R05G6.7	Probable voltage-dependent anion-selective channel OS=Caenorhabditis elegans GN=R05G6.7 PE=2 SV=2 - [VDAC_CAEEL]
O44156	10.38	2	28.29	125.86	pas-6	Proteasome subunit alpha type-1 OS=Caenorhabditis elegans GN=pas-6 PE=1 SV=1 - [PSA1_CAEEL]
Q27488	16.45	2	25.32	148.14	pas-2	Proteasome subunit alpha type-2 OS=Caenorhabditis elegans GN=pas-2 PE=1 SV=1 - [PSA2_CAEEL]
Q9XUV0	7.39	2	31.21	81.76	pbs-5	Proteasome subunit beta type OS=Caenorhabditis elegans GN=pbs-5 PE=3 SV=1 - [Q9XUV0_CAEEL]
P34286	12.79	2	28.91	61.12	pbs-6	Proteasome subunit beta type-1 OS=Caenorhabditis elegans GN=pbs-6 PE=1 SV=2 - [PSB1_CAEEL]
Q9GUF2	6.56	2	43.00	131.77	acp-6	Protein ACP-6 OS=Caenorhabditis elegans GN=acp-6 PE=2 SV=2 - [Q9GUF2_CAEEL]
Q6A8K1	50.83	12	40.40	1461.43	act-4	Protein ACT-4, isoform c OS=Caenorhabditis elegans GN=act-4 PE=2 SV=1 - [Q6A8K1_CAEEL]
O45815	29.6	7	41.85	705.52	act-5	Protein ACT-5 OS=Caenorhabditis elegans GN=act-5 PE=2 SV=1 - [O45815_CAEEL]
O45865	39	10	33.02	1549.89	ant-1.1	Protein ANT-1.1, isoform a OS=Caenorhabditis elegans GN=ant-1.1 PE=2 SV=1 - [O45865_CAEEL]
Q86CZ8	18.84	4	22.60	138.31	ant-1.1	Protein ANT-1.1, isoform c OS=Caenorhabditis elegans GN=ant-1.1 PE=2 SV=1 - [Q86CZ8_CAEEL]
Q19102	10.47	2	27.13	50.78	ard-1	Protein ARD-1 OS=Caenorhabditis elegans GN=ard-1 PE=2 SV=1 - [Q19102_CAEEL]
Q20053	7.64	2	34.35	156.96	asb-1	Protein ASB-1 OS=Caenorhabditis elegans GN=asb-1 PE=2 SV=1 - [Q20053_CAEEL]
Q19126	15.74	4	34.92	199.23	asb-2	Protein ASB-2 OS=Caenorhabditis elegans GN=asb-2 PE=2 SV=1 - [Q19126_CAEEL]
Q21966	2.93	2	49.25	166.82	asp-4	Protein ASP-4 OS=Caenorhabditis elegans GN=asp-4 PE=2 SV=1 - [Q21966_CAEEL]
P91283	51.69	10	22.38	582.04	atp-3	Protein ATP-3, isoform a OS=Caenorhabditis elegans GN=atp-3 PE=2 SV=1 - [P91283_CAEEL]
Q17763	34.03	5	21.78	275.25	atp-5	Protein ATP-5 OS=Caenorhabditis elegans GN=atp-5 PE=2 SV=2 - [Q17763_CAEEL]
P91020	10.41	2	35.17	120.98	C07D8.6	Protein C07D8.6 OS=Caenorhabditis elegans GN=C07D8.6 PE=1 SV=1 - [P91020_CAEEL]
B3GWB2	1.73	2	101.76	48.62	C08H9.2	Protein C08H9.2, isoform b OS=Caenorhabditis elegans GN=C08H9.2 PE=4 SV=1 - [B3GWB2_CAEEL]
Q17993	18.95	2	21.60	46.78	C14F11.6	Protein C14F11.6 OS=Caenorhabditis elegans GN=C14F11.6 PE=2 SV=1 - [Q17993_CAEEL]
Q18036	46.01	5	19.35	209.83	C16A3.5	Protein C16A3.5 OS=Caenorhabditis elegans GN=C16A3.5 PE=2 SV=1 - [Q18036_CAEEL]
Q18074	15.25	2	26.62	71.89	C18B2.3	Protein C18B2.3 OS=Caenorhabditis elegans GN=C18B2.3 PE=2 SV=2 - [Q18074_CAEEL]
Q18095	31.07	4	12.08	90.49	C18E9.4	Protein C18E9.4 OS=Caenorhabditis elegans GN=C18E9.4 PE=2 SV=1 - [Q18095_CAEEL]
D7SFJ4	15.3	2	21.73	101.29	C25H3.9	Protein C25H3.9, isoform b OS=Caenorhabditis elegans GN=C25H3.9 PE=4 SV=1 - [D7SFJ4_CAEEL]
O17622	16.23	2	21.19	40.26	C29F7.3	Protein C29F7.3 OS=Caenorhabditis elegans GN=C29F7.3 PE=2 SV=1 - [O17622_CAEEL]
O44955	22.81	2	20.09	40.98	C34B2.8	Protein C34B2.8 OS=Caenorhabditis elegans GN=C34B2.8 PE=2 SV=1 - [O44955_CAEEL]
O45060	45.7	5	16.95	171.21	C35B1.5	Protein C35B1.5 OS=Caenorhabditis elegans GN=C35B1.5 PE=2 SV=1 - [O45060_CAEEL]
Q18599	12.74	4	50.72	180.34	C44B7.10	Protein C44B7.10 OS=Caenorhabditis elegans GN=C44B7.10 PE=2 SV=3 - [Q18599_CAEEL]

Q9XW17	7.35	2	37.59	159.55	car-1	Protein CAR-1 OS=Caenorhabditis elegans GN=car-1 PE=2 SV=1 - [Q9XW17_CAEEL]
P91306	17.6	2	29.39	215.63	cey-2	Protein CEY-2 OS=Caenorhabditis elegans GN=cey-2 PE=2 SV=1 - [P91306_CAEEL]
G5EDV3	16.33	3	32.40	157.18	cey-4	Protein CEY-4 OS=Caenorhabditis elegans GN=cey-4 PE=4 SV=1 - [G5EDV3_CAEEL]
H9G333	29.29	5	21.82	308.65	cpl-1	Protein CPL-1, isoform b OS=Caenorhabditis elegans GN=cpl-1 PE=4 SV=1 - [H9G333_CAEEL]
O01542	28.17	4	15.50	378.81	cpn-3	Protein CPN-3 OS=Caenorhabditis elegans GN=cpn-3 PE=2 SV=1 - [O01542_CAEEL]
P92005	5.78	2	53.14	173.00	cpz-2	Protein CPZ-2 OS=Caenorhabditis elegans GN=cpz-2 PE=2 SV=1 - [P92005_CAEEL]
Q18853	18.6	3	30.95	267.75	cyc-1	Protein CYC-1 OS=Caenorhabditis elegans GN=cyc-1 PE=2 SV=1 - [Q18853_CAEEL]
O01816	34.04	3	15.62	145.48	cytb-5.2	Protein CYTB-5.2 OS=Caenorhabditis elegans GN=cytb-5.2 PE=3 SV=1 - [O01816_CAEEL]
Q18943	22.87	4	20.57	131.21	D1054.10	Protein D1054.10 OS=Caenorhabditis elegans GN=D1054.10 PE=2 SV=1 - [Q18943_CAEEL]
Q21481	10.55	3	46.23	163.14	dhs-28	Protein DHS-28 OS=Caenorhabditis elegans GN=dhs-28 PE=2 SV=1 - [Q21481_CAEEL]
Q9TYJ7	10.88	2	26.93	94.98	dpm-1	Protein DPM-1 OS=Caenorhabditis elegans GN=dpm-1 PE=2 SV=2 - [Q9TYJ7_CAEEL]
G5EC91	10.98	2	27.36	121.61	dpy-11	Protein DPY-11 OS=Caenorhabditis elegans GN=dpy-11 PE=2 SV=1 - [G5EC91_CAEEL]
G8JY74	6.06	2	47.12	102.82	eef-1A.2	Protein EEF-1A.2, isoform d OS=Caenorhabditis elegans GN=eef-1A.2 PE=4 SV=1 - [G8JY74_CAEEL]
H9G360	17.3	6	25.48	588.56	eef-1	Protein EEF-1B.2, isoform d OS=Caenorhabditis elegans GN=eef-1B.2 PE=4 SV=1 - [H9G360_CAEEL]
Q8I4K9	16.62	3	41.98	133.01	eef-1g	Protein EEF-1G, isoform b OS=Caenorhabditis elegans GN=eef-1g PE=2 SV=1 - [Q8I4K9_CAEEL]
G3MU53	5	2	93.35	154.02	eef-2	Protein EEF-2, isoform b OS=Caenorhabditis elegans GN=eef-2 PE=4 SV=1 - [G3MU53_CAEEL]
Q19303	15.69	2	17.49	110.78	F10E7.6	Protein F10E7.6 OS=Caenorhabditis elegans GN=F10E7.6 PE=2 SV=1 - [Q19303_CAEEL]
G5EBF3	20.78	2	17.42	130.96	F15E11.1	Protein F15E11.1 OS=Caenorhabditis elegans GN=F15E11.1 PE=4 SV=1 - [G5EBF3_CAEEL]
Q9TXI4	9.41	2	27.62	128.61	F23C8.5	Protein F23C8.5 OS=Caenorhabditis elegans GN=F23C8.5 PE=2 SV=2 - [Q9TXI4_CAEEL]
P90860	25.15	3	19.53	200.97	F36A2.7	Protein F36A2.7 OS=Caenorhabditis elegans GN=F36A2.7 PE=2 SV=1 - [P90860_CAEEL]
Q86MF9	45	3	6.95	111.27	F42G8.10	Protein F42G8.10, isoform b OS=Caenorhabditis elegans GN=F42G8.10 PE=2 SV=1 - [Q86MF9_CAEEL]
Q9XU97	44.87	4	8.86	121.26	F44E5.1	Protein F44E5.1 OS=Caenorhabditis elegans GN=F44E5.1 PE=2 SV=1 - [Q9XU97_CAEEL]
Q20476	15.17	2	20.36	104.70	F46G10.1	Protein F46G10.1, isoform a OS=Caenorhabditis elegans GN=F46G10.1 PE=1 SV=3 - [Q20476_CAEEL]
O01572	12.24	2	27.01	133.80	F48C1.6	Protein F48C1.6 OS=Caenorhabditis elegans GN=F48C1.6 PE=2 SV=1 - [O01572_CAEEL]
Q9N5S7	19.46	4	30.19	173.94	F49H12.5	Protein F49H12.5 OS=Caenorhabditis elegans GN=F49H12.5 PE=2 SV=1 - [Q9N5S7_CAEEL]
P91997	10.44	2	33.45	63.25	F53F1.2	Protein F53F1.2 OS=Caenorhabditis elegans GN=F53F1.2 PE=2 SV=1 - [P91997_CAEEL]
Q93831	8.08	2	31.22	119.87	F59C6.5	Protein F59C6.5 OS=Caenorhabditis elegans GN=F59C6.5 PE=2 SV=1 - [Q93831_CAEEL]
Q95ZT1	12.63	2	22.56	113.20	ftt-2	Protein FTT-2, isoform b OS=Caenorhabditis elegans GN=ftt-2 PE=2 SV=2 - [Q95ZT1_CAEEL]
Q3Y400	33.59	3	14.61	258.18	glrx-22	Protein GLRX-22 OS=Caenorhabditis elegans GN=glrx-22 PE=4 SV=1 - [Q3Y400_CAEEL]
Q9NAB3	18.18	2	23.20	82.56	gst-27	Protein GST-27 OS=Caenorhabditis elegans GN=gst-27 PE=2 SV=1 - [Q9NAB3_CAEEL]
Q5H9M9	14.81	2	12.41	52.50	hsp-25	Protein HSP-25, isoform c OS=Caenorhabditis elegans GN=hsp-25 PE=2 SV=1 - [Q5H9M9_CAEEL]
B5BM25	1.45	2	77.51	146.23	ifg-1	Protein IFG-1, isoform e OS=Caenorhabditis elegans GN=ifg-1 PE=4 SV=1 - [B5BM25_CAEEL]
Q9XVD2	23.48	2	14.69	64.59	immp-1	Protein IMMP-1 OS=Caenorhabditis elegans GN=immp-1 PE=3 SV=2 - [Q9XVD2_CAEEL]
Q27GU2	18	2	17.31	63.64	lbp-3	Protein LBP-3, isoform b OS=Caenorhabditis elegans GN=lbp-3 PE=2 SV=1 - [Q27GU2_CAEEL]
Q18625	17.67	3	32.39	185.43	lec-4	Protein LEC-4 OS=Caenorhabditis elegans GN=lec-4 PE=2 SV=1 - [Q18625_CAEEL]
Q20964	19.63	3	23.59	143.52	lys-4	Protein LYS-4 OS=Caenorhabditis elegans GN=lys-4 PE=4 SV=1 - [Q20964_CAEEL]
P49029	28.95	3	17.63	252.59	mag-1	Protein mago nashi homolog OS=Caenorhabditis elegans GN=mag-1 PE=1 SV=2 - [MGN_CAEEL]
Q9GP94	36.84	2	10.30	78.84	mlp-1	Protein MLP-1, isoform a OS=Caenorhabditis elegans GN=mlp-1 PE=2 SV=2 - [Q9GP94_CAEEL]
Q21154	15.92	2	22.07	55.43	moma-1	Protein MOMA-1 OS=Caenorhabditis elegans GN=moma-1 PE=2 SV=1 - [Q21154_CAEEL]
Q7YX52	24.03	3	14.84	94.68	mrpl-53	Protein MRPL-53 OS=Caenorhabditis elegans GN=mrpl-53 PE=4 SV=1 - [Q7YX52_CAEEL]



H2KYJ5	15.2	3	37.40	394.13	mtch-1	Protein MTCH-1, isoform a OS=Caenorhabditis elegans GN=mtch-1 PE=3 SV=1 - [H2KYJ5_CAEEL]
Q9N3D9	37.19	4	14.00	214.84	nduf-5	Protein NDUF-5 OS=Caenorhabditis elegans GN=nduf-5 PE=2 SV=1 - [Q9N3D9_CAEEL]
Q86NC2	19.4	5	30.78	297.60	nuo-2	Protein NUO-2, isoform b OS=Caenorhabditis elegans GN=nuo-2 PE=2 SV=1 - [Q86NC2_CAEEL]
Q23098	18.6	3	20.36	122.25	nuo-6	Protein NUO-6 OS=Caenorhabditis elegans GN=nuo-6 PE=2 SV=2 - [Q23098_CAEEL]
Q7K797	4.27	2	65.05	84.79	pab-1	Protein PAB-1, isoform c OS=Caenorhabditis elegans GN=pab-1 PE=2 SV=1 - [Q7K797_CAEEL]
Q7JKI3	9.88	4	65.94	174.51	pck-2	Protein PCK-2, isoform c OS=Caenorhabditis elegans GN=pck-2 PE=2 SV=1 - [Q7JKI3_CAEEL]
O44145	14.78	2	22.44	62.25	perm-2	Protein PERM-2 OS=Caenorhabditis elegans GN=perm-2 PE=2 SV=2 - [O44145_CAEEL]
Q8IG31	37.95	5	21.77	225.56	prdx-2	Protein PRDX-2, isoform a OS=Caenorhabditis elegans GN=prdx-2 PE=2 SV=1 - [Q8IG31_CAEEL]
Q21732	35.51	2	12.30	456.69	R04F11.2	Protein R04F11.2 OS=Caenorhabditis elegans GN=R04F11.2 PE=2 SV=1 - [Q21732_CAEEL]
Q21763	18.12	2	17.31	130.34	R05H5.3	Protein R05H5.3 OS=Caenorhabditis elegans GN=R05H5.3 PE=2 SV=1 - [Q21763_CAEEL]
H9G321	16.74	3	27.72	90.40	R13H4.2	Protein R13H4.2, isoform c OS=Caenorhabditis elegans GN=R13H4.2 PE=4 SV=1 - [H9G321_CAEEL]
Q22020	23.74	2	24.12	106.13	R53.5	Protein R53.5 OS=Caenorhabditis elegans GN=R53.5 PE=2 SV=1 - [Q22020_CAEEL]
Q23146	17.22	3	23.41	166.88	rab-7	Protein RAB-7 OS=Caenorhabditis elegans GN=rab-7 PE=2 SV=1 - [Q23146_CAEEL]
Q7JLB0	17.16	2	22.61	57.37	ret-1	Protein RET-1, isoform e OS=Caenorhabditis elegans GN=ret-1 PE=2 SV=1 - [Q7JLB0_CAEEL]
O17694	43.17	4	16.48	121.72	ril-1	Protein RIL-1 OS=Caenorhabditis elegans GN=ril-1 PE=4 SV=1 - [O17694_CAEEL]
Q9U1X9	19.09	2	10.86	82.09	rla-2	Protein RLA-2 OS=Caenorhabditis elegans GN=rla-2 PE=4 SV=1 - [Q9U1X9_CAEEL]
B2D6P1	14.67	2	25.46	108.60	rmd-2	Protein RMD-2, isoform c OS=Caenorhabditis elegans GN=rmd-2 PE=4 SV=1 - [B2D6P1_CAEEL]
Q19162	13.78	2	22.76	399.97	rpl-11.2	Protein RPL-11.2 OS=Caenorhabditis elegans GN=rpl-11.2 PE=2 SV=1 - [Q19162_CAEEL]
Q9XVE9	17.78	2	15.34	165.49	rpl-14	Protein RPL-14 OS=Caenorhabditis elegans GN=rpl-14 PE=2 SV=1 - [Q9XVE9_CAEEL]
Q9XWS4	45.22	5	12.43	337.56	rpl-30	Protein RPL-30 OS=Caenorhabditis elegans GN=rpl-30 PE=2 SV=2 - [Q9XWS4_CAEEL]
O01869	35.57	4	16.86	211.57	rps-10	Protein RPS-10 OS=Caenorhabditis elegans GN=rps-10 PE=1 SV=1 - [O01869_CAEEL]
Q20206	20	2	17.73	92.51	rps-11	Protein RPS-11 OS=Caenorhabditis elegans GN=rps-11 PE=2 SV=1 - [Q20206_CAEEL]
O18240	36.36	4	17.76	217.14	rps-18	Protein RPS-18 OS=Caenorhabditis elegans GN=rps-18 PE=3 SV=1 - [O18240_CAEEL]
Q8WQA8	38.46	6	13.23	198.11	rps-20	Protein RPS-20 OS=Caenorhabditis elegans GN=rps-20 PE=2 SV=1 - [Q8WQA8_CAEEL]
O17218	25.38	4	14.72	278.54	rps-22	Protein RPS-22, isoform a OS=Caenorhabditis elegans GN=rps-22 PE=2 SV=1 - [O17218_CAEEL]
A8WIR1	30.69	3	11.54	151.04	rps-22	Protein RPS-22, isoform b OS=Caenorhabditis elegans GN=rps-22 PE=3 SV=1 - [A8WIR1_CAEEL]
Q1XFY9	22.14	3	14.86	82.55	rps-24	Protein RPS-24 OS=Caenorhabditis elegans GN=rps-24 PE=2 SV=1 - [Q1XFY9_CAEEL]
H2FLJ1	7.1	2	35.62	148.01	stl-1	Protein STL-1, isoform a OS=Caenorhabditis elegans GN=stl-1 PE=4 SV=1 - [H2FLJ1_CAEEL]
Q9N5E4	46.92	7	15.11	282.38	T02H6.11	Protein T02H6.11 OS=Caenorhabditis elegans GN=T02H6.11 PE=2 SV=1 - [Q9N5E4_CAEEL]
Q22352	7.51	2	37.29	85.95	T08H10.1	Protein T08H10.1 OS=Caenorhabditis elegans GN=T08H10.1 PE=2 SV=2 - [Q22352_CAEEL]
Q7JPE4	6.28	2	26.81	110.93	tat-4	Protein TAT-4, isoform c OS=Caenorhabditis elegans GN=tat-4 PE=2 SV=1 - [Q7JPE4_CAEEL]
G5EDD4	14.06	4	49.93	152.37	tba-4	Protein TBA-4 OS=Caenorhabditis elegans GN=tba-4 PE=3 SV=1 - [G5EDD4_CAEEL]
O17921	5.79	2	50.21	67.04	tbb-1	Protein TBB-1 OS=Caenorhabditis elegans GN=tbb-1 PE=2 SV=1 - [O17921_CAEEL]
O17287	58.72	5	12.17	267.58	tomm-22	Protein TOMM-22 OS=Caenorhabditis elegans GN=tomm-22 PE=2 SV=1 - [O17287_CAEEL]
Q9U238	67.3	7	17.40	400.05	trap-4	Protein TRAP-4 OS=Caenorhabditis elegans GN=trap-4 PE=1 SV=1 - [Q9U238_CAEEL]
Q19328	3.5	2	100.71	137.71	tsn-1	Protein TSN-1 OS=Caenorhabditis elegans GN=tsn-1 PE=2 SV=1 - [Q19328_CAEEL]
Q23378	17.07	2	18.55	33.87	ttr-48	Protein TTR-48 OS=Caenorhabditis elegans GN=ttr-48 PE=2 SV=1 - [Q23378_CAEEL]
G5ED31	17.8	5	42.74	377.62	ucr-2.1	Protein UCR-2.1, isoform a OS=Caenorhabditis elegans GN=ucr-2.1 PE=3 SV=1 - [G5ED31_CAEEL]
Q22370	7.82	2	44.19	116.29	ucr-2.2	Protein UCR-2.2 OS=Caenorhabditis elegans GN=ucr-2.2 PE=2 SV=2 - [Q22370_CAEEL]
Q9TZ33	6.79	2	45.53	200.06	ucr-2.3	Protein UCR-2.3 OS=Caenorhabditis elegans GN=ucr-2.3 PE=2 SV=1 - [Q9TZ33_CAEEL]

Q95YD5	21.26	4	39.91	340.70	vha-16	Protein VHA-16 OS=Caenorhabditis elegans GN=vha-16 PE=2 SV=1 - [Q95YD5_CAEEL]
Q95X44	11.95	2	25.57	242.85	vha-8	Protein VHA-8 OS=Caenorhabditis elegans GN=vha-8 PE=2 SV=1 - [Q95X44_CAEEL]
G8JY38	6.35	8	180.81	315.15	vit-2	Protein VIT-2, isoform b OS=Caenorhabditis elegans GN=vit-2 PE=4 SV=1 - [G8JY38_CAEEL]
Q5FC71	13.59	2	11.27	135.67	W02B12.15	Protein W02B12.15, isoform a OS=Caenorhabditis elegans GN=W02B12.15 PE=2 SV=1 - [Q5FC71_CAEEL]
Q9TZE0	35.29	2	11.11	45.78	W04C9.2	Protein W04C9.2 OS=Caenorhabditis elegans GN=W04C9.2 PE=2 SV=1 - [Q9TZE0_CAEEL]
Q9U329	37.71	7	20.24	269.13	W09C5.8	Protein W09C5.8 OS=Caenorhabditis elegans GN=W09C5.8 PE=2 SV=1 - [Q9U329_CAEEL]
O45011	14.79	5	44.71	178.21	W10C8.5	Protein W10C8.5 OS=Caenorhabditis elegans GN=W10C8.5 PE=2 SV=1 - [O45011_CAEEL]
Q9BKU6	23.86	2	9.80	46.78	Y37E3.8	Protein Y37E3.8, isoform b OS=Caenorhabditis elegans GN=Y37E3.8 PE=2 SV=1 - [Q9BKU6_CAEEL]
Q9XWP1	14.41	2	26.31	76.54	Y43F8C.7	Protein Y43F8C.7 OS=Caenorhabditis elegans GN=Y43F8C.7 PE=2 SV=1 - [Q9XWP1_CAEEL]
Q9XWJ6	14.57	2	23.53	128.04	Y51H1A.3	Protein Y51H1A.3, isoform a OS=Caenorhabditis elegans GN=Y51H1A.3 PE=2 SV=1 - [Q9XWJ6_CAEEL]
Q9N3H3	5.57	2	48.22	128.47	Y53G8AL.2	Protein Y53G8AL.2 OS=Caenorhabditis elegans GN=Y53G8AL.2 PE=2 SV=2 - [Q9N3H3_CAEEL]
O76630	13.27	2	33.32	191.51	Y57G7A.10	Protein Y57G7A.10 OS=Caenorhabditis elegans GN=Y57G7A.10 PE=1 SV=1 - [O76630_CAEEL]
Q9GRZ9	7.54	2	75.85	62.63	Y59A8A.3	Protein Y59A8A.3 OS=Caenorhabditis elegans GN=Y59A8A.3 PE=2 SV=1 - [Q9GRZ9_CAEEL]
Q9XWG2	13.04	2	10.20	93.13	Y63D3A.7	Protein Y63D3A.7 OS=Caenorhabditis elegans GN=Y63D3A.7 PE=2 SV=2 - [Q9XWG2_CAEEL]
Q9BKK9	30.13	3	16.81	172.36	Y67D2.3	Protein Y67D2.3 OS=Caenorhabditis elegans GN=Y67D2.3 PE=2 SV=1 - [Q9BKK9_CAEEL]
Q95PZ1	40.69	7	15.50	314.39	Y67H2A.5	Protein Y67H2A.5 OS=Caenorhabditis elegans GN=Y67H2A.5 PE=2 SV=1 - [Q95PZ1_CAEEL]
Q9BL34	58.68	6	14.81	300.61	Y71H2AM.5	Protein Y71H2AM.5 OS=Caenorhabditis elegans GN=Y71H2AM.5 PE=2 SV=1 - [Q9BL34_CAEEL]
Q23258	52.88	4	11.05	147.70	ZC373.2	Protein ZC373.2 OS=Caenorhabditis elegans GN=ZC373.2 PE=4 SV=2 - [Q23258_CAEEL]
Q23597	18.57	4	24.34	300.62	ZK809.3	Protein ZK809.3 OS=Caenorhabditis elegans GN=ZK809.3 PE=2 SV=1 - [Q23597_CAEEL]
Q23624	8.33	2	40.20	102.51	ZK829.7	Protein ZK829.7 OS=Caenorhabditis elegans GN=ZK829.7 PE=1 SV=2 - [Q23624_CAEEL]
O18229	10.41	2	30.39	79.89	Y57G11C.3	Putative 6-phosphogluconolactonase OS=Caenorhabditis elegans GN=Y57G11C.3 PE=2 SV=2 - [6PGL_CAEEL]
Q22021	39.22	7	18.74	211.39	R53.4	Putative ATP synthase subunit f, mitochondrial OS=Caenorhabditis elegans GN=R53.4 PE=2 SV=1 - [ATPK_CAEEL]
P91917	7.85	2	44.32	101.93	tag-210	Putative GTP-binding protein tag-210 OS=Caenorhabditis elegans GN=tag-210 PE=2 SV=1 - [TG210_CAEEL]
O62146	4.47	2	66.60	189.06	F09B12.3	Putative phospholipase B-like 2 OS=Caenorhabditis elegans GN=F09B12.3 PE=1 SV=2 - [PLBL2_CAEEL]
Q22038	13.54	2	21.62	161.50	rho-1	Ras-like GTP-binding protein rhoA OS=Caenorhabditis elegans GN=rho-1 PE=2 SV=1 - [RHO1_CAEEL]
P34213	10.73	2	23.24	54.68	rab-6.1	Ras-related protein Rab-6.1 OS=Caenorhabditis elegans GN=rab-6.1 PE=2 SV=1 - [RAB6A_CAEEL]
Q22053	12.78	4	36.36	255.54	fib-1	rRNA 2'-O-methyltransferase fibrillarlin OS=Caenorhabditis elegans GN=fib-1 PE=2 SV=1 - [FBRL_CAEEL]
Q27497	9.73	3	37.18	167.46	gsp-1	Serine/threonine-protein phosphatase PP1-alpha OS=Caenorhabditis elegans GN=gsp-1 PE=2 SV=2 - [GLC7A_CAEEL]
Q20363	33.96	4	17.83	309.83	sip-1	Stress-induced protein 1 OS=Caenorhabditis elegans GN=sip-1 PE=1 SV=1 - [SIP1_CAEEL]
Q09545	15.1	2	32.87	71.68	sdhb-1	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Caenorhabditis elegans GN=sdhb-1 PE=2 SV=1 - [DHSB_CAEEL]
O02495	18.35	2	12.02	167.73	snb-1	Synaptobrevin-1 OS=Caenorhabditis elegans GN=snb-1 PE=1 SV=1 - [SYB1_CAEEL]
Q966C7	6.58	2	35.25	56.46	Y24D9A.8	Transaldolase OS=Caenorhabditis elegans GN=Y24D9A.8 PE=2 SV=1 - [Q966C7_CAEEL]
Q93573	41.99	6	20.53	200.45	tct-1	Translationally-controlled tumor protein homolog OS=Caenorhabditis elegans GN=tct-1 PE=1 SV=1 - [TCTP_CAEEL]
P34500	21.62	3	15.69	223.80	ttr-2	Transthyretin-like protein 2 OS=Caenorhabditis elegans GN=ttr-2 PE=1 SV=1 - [TTR2_CAEEL]
Q10657	25.91	4	26.56	211.18	tpi-1	Triosephosphate isomerase OS=Caenorhabditis elegans GN=tpi-1 PE=1 SV=2 - [TPIS_CAEEL]
Q9GYF1	10.74	2	27.54	99.74	unc-27	Troponin I 2 OS=Caenorhabditis elegans GN=unc-27 PE=2 SV=2 - [TNNI2_CAEEL]
Q27371	7.41	2	47.01	57.63	mup-2	Troponin T OS=Caenorhabditis elegans GN=mup-2 PE=2 SV=1 - [TNNT_CAEEL]
O44512	22.46	5	29.69	293.27	isp-1	Ubiquinol-cytochrome c reductase iron-sulfur subunit OS=Caenorhabditis elegans GN=isp-1 PE=2 SV=1 - [O44512_CAEEL]
Q21276	7.82	3	54.48	216.17	K07C5.4	Uncharacterized NOP5 family protein K07C5.4 OS=Caenorhabditis elegans GN=K07C5.4 PE=2 SV=1 - [YZVL_CAEEL]
P34255	9.82	3	47.84	63.01	B0303.3	Uncharacterized protein B0303.3 OS=Caenorhabditis elegans GN=B0303.3 PE=2 SV=1 - [YKA3_CAEEL]

Q18594	9.32	2	26.28	66.85	C44B7.5	Uncharacterized protein C44B7.5 OS=Caenorhabditis elegans GN=C44B7.5 PE=1 SV=1 - [YC4B5_CAEEL]
P52717	4.9	2	53.61	86.90	F41C3.5	Uncharacterized serine carboxypeptidase F41C3.5 OS=Caenorhabditis elegans GN=F41C3.5 PE=1 SV=1 - [YUW5_CAEEL]
P05690	7.32	8	187.60	360.26	vit-2	Vitellogenin-2 OS=Caenorhabditis elegans GN=vit-2 PE=1 SV=5 - [VIT2_CAEEL]
P18948	7.27	10	193.20	507.46	vit-6	Vitellogenin-6 OS=Caenorhabditis elegans GN=vit-6 PE=1 SV=5 - [VIT6_CAEEL]