Table 2.4. Proteins previously known to be expressed in the pharynx from LC-MS/MS analysis of *myo-2*::Thr412Gly-*Ce*PheRS animals fed with triply labeled *E. coli* ("heavy" arginine, "heavy" lysine and Azf) for 24 hours.

Protein	$\log_2 (H/L)_E/(H/L)_U$
Q95XD1|Q95XD1_CAEEL Protein SHL-1 OS=Caenorhabditis elegans GN=shl-1 PE=4 SV=2	2.81
Q93839|Q93839_CAEEL Acyl-coenzyme A oxidase OS=Caenorhabditis elegans GN=CELE_F59F4.1 PE=3 SV=2	2.29
O44572|TNNI4_CAEEL Troponin I 4 OS=Caenorhabditis elegans GN=tni-4 PE=2 SV=2	2.19
Q09665|TNNC2_CAEEL Troponin C, isoform 2 OS=Caenorhabditis elegans GN=tnc-2 PE=2 SV=1	1.85
H2KYP4|H2KYP4_CAEEL Protein NCX-2, isoform d OS=Caenorhabditis elegans GN=ncx-2 PE=4 SV=1; H2KYP2|H2KYP2_CAEEL Protein NCX-2, isoform a OS=Caenorhabditis elegans GN=ncx-2 PE=4 SV=1	1.69
Q9U3N4|INX6_CAEEL Innexin-6 OS=Caenorhabditis elegans GN=inx-6 PE=2 SV=1	1.47
P19626|MLR2_CAEEL Myosin regulatory light chain 2 OS=Caenorhabditis elegans GN=mlc-2 PE=1 SV=1; P19625|MLR1_CAEEL Myosin regulatory light chain 1 OS=Caenorhabditis elegans GN=mlc-1 PE=4 SV=1	1.30
P02567|MYO1_CAEEL Myosin-1 OS=Caenorhabditis elegans GN=let-75 PE=2 SV=3	1.28
P12845|MYO2_CAEEL Myosin-2 OS=Caenorhabditis elegans GN=myo-2 PE=2 SV=2	1.21
Q86GU1|Q86GU1_CAEEL Protein HSP-25, isoform b OS=Caenorhabditis elegans GN=hsp-25 PE=2 SV=1; Q17849|Q17849_CAEEL Protein HSP-25, isoform a OS=Caenorhabditis elegans GN=hsp-25 PE=2 SV=1; Q5H9M9|Q5H9M9_CAEEL Protein HSP-25, isoform c OS=Caenorhabdi	1.14
G5EFX2|G5EFX2_CAEEL Protein PKN-1, isoform a OS=Caenorhabditis elegans GN=pkn-1 PE=2 SV=1; G5EGE3|G5EGE3_CAEEL Protein PKN-1, isoform b OS=Caenorhabditis elegans GN=pkn-1 PE=2 SV=1	0.96

Q09519|Q09519_CAEEL Protein UTX-1 OS=Caenorhabditis elegans GN=utx-1 PE=4 SV=1	0.95
Q21000|Q21000_CAEEL Protein MYO-5 OS=Caenorhabditis elegans GN=myo-5 PE=4 SV=1	0.89
P34442|PTP5_CAEEL Probable tyrosine-protein phosphatase F54C8.4 OS=Caenorhabditis elegans GN=F54C8.4 PE=2 SV=1	0.83
Q9NAF4|Q9NAF4_CAEEL Protein OIG-3 OS=Caenorhabditis elegans GN=oig-3 PE=4 SV=1	0.83
P91001|CSN5_CAEEL COP9 signalosome complex subunit 5 OS=Caenorhabditis elegans GN=csn-5 PE=1 SV=1	0.78
Q19564|OXDD1_CAEEL D-aspartate oxidase 1 OS=Caenorhabditis elegans GN=F18E3.7 PE=1 SV=1	0.72
Q9TXI3|Q9TXI3_CAEEL Protein F23C8.6 OS=Caenorhabditis elegans GN=CELE_F23C8.6 PE=4 SV=1	0.69
Q01630-3|UNC33_CAEEL Isoform III of Protein unc-33 OS=Caenorhabditis elegans GN=unc-33; Q01630-2|UNC33_CAEEL Isoform II of Protein unc-33 OS=Caenorhabditis elegans GN=unc-33; Q01630|UNC33_CAEEL Protein unc-33 OS=Caenorhabditis elegans GN=unc-33 P	0.67
Q9U2U0|Q9U2U0_CAEEL Protein UAF-2 OS=Caenorhabditis elegans GN=uaf-2 PE=4 SV=1	0.64
G5EEP9|G5EEP9_CAEEL Protein FRM-1, isoform a OS=Caenorhabditis elegans GN=frm-1 PE=2 SV=1; G5EBP4|G5EBP4_CAEEL Protein FRM-1, isoform e OS=Caenorhabditis elegans GN=frm-1 PE=2 SV=1; G5EEG8|G5EEG8_CAEEL Protein FRM-1, isoform d OS=Caenorhabditis e	0.64
P53014|MLE_CAEEL Myosin, essential light chain OS=Caenorhabditis elegans GN=mlc-3 PE=1 SV=1; B6EU49|B6EU49_CAEEL Alkali myosin light chain long isoform OS=Caenorhabditis elegans GN=mlc-3 PE=2 SV=1	0.64
P91283|P91283_CAEEL Protein ATP-3, isoform a OS=Caenorhabditis elegans GN=atp-3 PE=2 SV=1; Q7JNG1|Q7JNG1_CAEEL Protein ATP-3, isoform b OS=Caenorhabditis elegans GN=atp-3 PE=2 SV=1	0.63
Q20173|Q20173_CAEEL Protein F38E9.5 OS=Caenorhabditis elegans GN=CELE_F38E9.5 PE=4 SV=2	0.62
P55326|YZG1_CAEEL Uncharacterized protein F13E6.1 OS=Caenorhabditis elegans GN=F13E6.1 PE=3 SV=2	0.62

Q95Y67|Q95Y67_CAEEL Protein PES-4 OS=Caenorhabditis elegans GN=pes-4 PE=4 SV=3	0.61
O18054|PFD3_CAEEL Probable prefoldin subunit 3 OS=Caenorhabditis elegans GN=pfd-3 PE=3 SV=1	0.60
Q8IG23|Q8IG23_CAEEL Protein AQP-1, isoform b OS=Caenorhabditis elegans GN=aqp-1 PE=2 SV=1	0.60
Q9TZ69|Q9TZ69_CAEEL Protein UBC-20 OS=Caenorhabditis elegans GN=ubc-20 PE=3 SV=1	0.58
P37806-3|UNC87_CAEEL Isoform c of Protein unc-87 OS=Caenorhabditis elegans GN=unc-87; P37806|UNC87_CAEEL Protein unc-87 OS=Caenorhabditis elegans GN=unc-87 PE=1 SV=3	0.57
Q22370|Q22370_CAEEL Protein UCR-2.2 OS=Caenorhabditis elegans GN=ucr-2.2 PE=3 SV=2	0.55
C7FZU4|C7FZU4_CAEEL Protein NID-1, isoform c OS=Caenorhabditis elegans GN=nid-1 PE=2 SV=1; C7FZU3|C7FZU3_CAEEL Protein NID-1, isoform b OS=Caenorhabditis elegans GN=nid-1 PE=2 SV=1; Q93791|Q93791_CAEEL Protein NID-1, isoform a OS=Caenorhabditis e	0.54
P91821|P91821_CAEEL Protein SET-18, isoform a OS=Caenorhabditis elegans GN=set-18 PE=2 SV=1; Q8I4F7|Q8I4F7_CAEEL Protein SET-18, isoform b OS=Caenorhabditis elegans GN=set-18 PE=2 SV=1	0.53
Q22866|TPM1_CAEEL Tropomyosin isoforms a/b/d/f OS=Caenorhabditis elegans GN=lev-11 PE=1 SV=1; Q22866-2|TPM1_CAEEL Isoform d of Tropomyosin isoforms a/b/d/f OS=Caenorhabditis elegans GN=lev-11; K8FDX2|K8FDX2_CAEEL Protein LEV-11, isoform g OS=Caen	0.52
Q21752|VDAC_CAEEL Probable voltage-dependent anion-selective channel OS=Caenorhabditis elegans GN=R05G6.7 PE=3 SV=2	0.52
Q1HB04|Q1HB04_CAEEL Protein T07F10.1, isoform b OS=Caenorhabditis elegans GN=CELE_T07F10.1 PE=2 SV=1; Q22317|Q22317_CAEEL Protein T07F10.1, isoform a OS=Caenorhabditis elegans GN=CELE_T07F10.1 PE=2 SV=2	0.51
O17218|O17218_CAEEL Protein RPS-22, isoform a OS=Caenorhabditis elegans GN=rps-22 PE=2 SV=1; A8WIR1|A8WIR1_CAEEL Protein RPS-22, isoform b OS=Caenorhabditis elegans GN=rps-22 PE=2 SV=1	0.51

O61304|O61304_CAEEL HCO3 transporter OS=Caenorhabditis elegans PE=2 SV=1; G5EC65|G5EC65_CAEEL Anion transporter ABTS-1 OS=Caenorhabditis elegans GN=abts-1 PE=2 SV=1; G5EDF4|G5EDF4_CAEEL Protein ABTS-1, isoform b OS=Caenorhabditis elegans GN=abts-	0.50
Q9GYF1|TNNI2_CAEEL Troponin I 2 OS=Caenorhabditis elegans GN=unc-27 PE=2 SV=2	0.50
Q10462|CAH5_CAEEL Putative carbonic anhydrase 5 OS=Caenorhabditis elegans GN=cah-5 PE=3 SV=3	0.49
G5EE55|G5EE55_CAEEL Protein NRFL-1, isoform c OS=Caenorhabditis elegans GN=nrfl-1 PE=2 SV=1; G5EFP7|G5EFP7_CAEEL Protein NRFL-1, isoform d OS=Caenorhabditis elegans GN=nrfl-1 PE=2 SV=1; G5EDM4|G5EDM4_CAEEL Protein NRFL-1, isoform a OS=Caenorhabdi	0.49
G5EEJ9|G5EEJ9_CAEEL Protein UNC-26, isoform a OS=Caenorhabditis elegans GN=unc-26 PE=2 SV=1; G5ECL2|G5ECL2_CAEEL Protein UNC-26, isoform b OS=Caenorhabditis elegans GN=unc-26 PE=2 SV=1	0.49
Q4PIU9|Q4PIU9_CAEEL Protein SAX-7, isoform b OS=Caenorhabditis elegans GN=sax-7 PE=2 SV=1; Q53U87|Q53U87_CAEEL Protein SAX-7, isoform c OS=Caenorhabditis elegans GN=sax-7 PE=2 SV=1; Q18100|Q18100_CAEEL Protein SAX-7, isoform a OS=Caenorhabditis e	0.46
H2KYZ6|H2KYZ6_CAEEL Protein FRM-4, isoform a OS=Caenorhabditis elegans GN=frm-4 PE=4 SV=1; Q95Q79|Q95Q79_CAEEL Protein FRM-4, isoform b OS=Caenorhabditis elegans GN=frm-4 PE=4 SV=1; H2KYZ7|H2KYZ7_CAEEL Protein FRM-4, isoform c OS=Caenorhabditis e	0.46
H2KYJ5|H2KYJ5_CAEEL Protein MTCH-1, isoform a OS=Caenorhabditis elegans GN=mtch-1 PE=3 SV=1	0.45
P10567|MYSP_CAEEL Paramyosin OS=Caenorhabditis elegans GN=unc-15 PE=1 SV=1	0.45
G5EFH4|G5EFH4_CAEEL Protein SRP-6 OS=Caenorhabditis elegans GN=srp-6 PE=1 SV=1; O01461|O01461_CAEEL Protein SRP-5 OS=Caenorhabditis elegans GN=srp-5 PE=3 SV=2	0.45
Q9N4I3|Q9N4I3_CAEEL Protein Y71F9AL.9 OS=Caenorhabditis elegans GN=CELE_Y71F9AL.9 PE=4 SV=1	0.45
Q8MXD8|Q8MXD8_CAEEL Protein KETN-1, isoform c OS=Caenorhabditis elegans GN=ketn-1 PE=2 SV=1; H2L076|H2L076_CAEEL Protein KETN-1, isoform a OS=Caenorhabditis elegans GN=ketn-1 PE=4 SV=1; Q5PY59|Q5PY59_CAEEL Kettin OS=Caenorhabditis elegans GN=F54E	0.44

G5ECP9|G5ECP9_CAEEL Protein VAB-10, isoform h OS=Caenorhabditis elegans GN=vab-10 PE=2 SV=1; G5EFW2|G5EFW2_CAEEL Protein VAB-10, isoform d OS=Caenorhabditis elegans GN=vab-10 PE=2 SV=1; Q86NF9|Q86NF9_CAEEL VAB-10A protein OS=Caenorhabditis elegan	0.43
G5EE12|G5EE12_CAEEL Protein CASH-1 OS=Caenorhabditis elegans GN=cash-1 PE=4 SV=1	0.42
Q21746|Q21746_CAEEL Protein SGT-1 OS=Caenorhabditis elegans GN=sgt-1 PE=1 SV=1	0.42
Q9XWM1|Q9XWM1_CAEEL Protein OIG-2 OS=Caenorhabditis elegans GN=oig-2 PE=4 SV=1	0.42
O18250|O18250_CAEEL Protein EPS-8, isoform a OS=Caenorhabditis elegans GN=eps-8 PE=2 SV=3; G5ED33|G5ED33_CAEEL Epidermal growth factor receptor pathway substrate 8 splice variant A OS=Caenorhabditis elegans GN=eps-8 PE=1 SV=1; Q7YTG1|Q7YTG1_CAEEL	0.42
Q10901-2|EAA1_CAEEL Isoform b of Excitatory amino acid transporter OS=Caenorhabditis elegans GN=glt-1; Q10901|EAA1_CAEEL Excitatory amino acid transporter OS=Caenorhabditis elegans GN=glt-1 PE=1 SV=2	0.41
Q09601|NUP53_CAEEL Nucleoporin NUP53 OS=Caenorhabditis elegans GN=npp-19 PE=3 SV=2; Q09601-2|NUP53_CAEEL Isoform a of Nucleoporin NUP53 OS=Caenorhabditis elegans GN=npp-19	0.41
Q9BKU4|PHB1_CAEEL Mitochondrial prohibitin complex protein 1 OS=Caenorhabditis elegans GN=phb-1 PE=1 SV=1	0.41
G5EEE5|G5EEE5_CAEEL Long chain polyunsaturated fatty acid elongation enzyme OS=Caenorhabditis elegans GN=elo-1 PE=2 SV=1	0.41
O16000-2|STX1A_CAEEL Isoform a of Syntaxin-1A homolog OS=Caenorhabditis elegans GN=unc-64; O16000|STX1A_CAEEL Syntaxin-1A homolog OS=Caenorhabditis elegans GN=unc-64 PE=1 SV=1; O16000-3|STX1A_CAEEL Isoform c of Syntaxin-1A homolog OS=Caenorhabdit	0.41
G5EE67|G5EE67_CAEEL Protein SKR-3 OS=Caenorhabditis elegans GN=skr-3 PE=2 SV=1	0.41
Q09232|ORAI_CAEEL Protein orai OS=Caenorhabditis elegans GN=orai-1 PE=2 SV=1; B6VQ32|B6VQ32_CAEEL Protein ORAI-1, isoform a OS=Caenorhabditis elegans GN=orai-1 PE=2 SV=2	0.40
G5EFV4|G5EFV4_CAEEL High mobility group protein 1.1 OS=Caenorhabditis elegans GN=hmg-1.1 PE=4 SV=1	0.40

Q17543|Q17543_CAEEL Protein C01B10.3 OS=Caenorhabditis elegans GN=C01B10.3 PE=4 SV=2	0.40
G5EEA4|G5EEA4_CAEEL Protein LIM-9, isoform c OS=Caenorhabditis elegans GN=lim-9 PE=2 SV=1; G5ECN3|G5ECN3_CAEEL Protein LIM-9, isoform a OS=Caenorhabditis elegans GN=lim-9 PE=2 SV=1; G5EF39|G5EF39_CAEEL LIM-9 isoform OS=Caenorhabditis elegans GN=l	0.39
Q20636|GBB2_CAEEL Guanine nucleotide-binding protein subunit beta-2 OS=Caenorhabditis elegans GN=gpb-2 PE=1 SV=2	0.39
P90901-4|IFA1_CAEEL Isoform d of Intermediate filament protein ifa-1 OS=Caenorhabditis elegans GN=ifa-1; P90901-2|IFA1_CAEEL Isoform b of Intermediate filament protein ifa-1 OS=Caenorhabditis elegans GN=ifa-1; G5ECT5|G5ECT5_CAEEL Protein IFA-1, i	0.38
Q95ZQ4-3|AAPK2_CAEEL Isoform c of 5-AMP-activated protein kinase catalytic subunit alpha-2 OS=Caenorhabditis elegans GN=aak-2; Q95ZQ4-2|AAPK2_CAEEL Isoform a of 5-AMP-activated protein kinase catalytic subunit alpha-2 OS=Caenorhabditis elegans GN=	0.38
H2L0Q8|H2L0Q8_CAEEL Protein FEH-1, isoform c OS=Caenorhabditis elegans GN=feh-1 PE=4 SV=1; Q8WQE2|Q8WQE2_CAEEL FEH-1 protein (Fragment) OS=Caenorhabditis elegans GN=feh-1 PE=2 SV=1; H2L0Q7|H2L0Q7_CAEEL Protein FEH-1, isoform b OS=Caenorhabditis e	0.38
Q09610|LEC8_CAEEL Probable galaptin lec-8 OS=Caenorhabditis elegans GN=lec-8 PE=2 SV=2	0.37
G5EBH7|G5EBH7_CAEEL Calumenin-like protein OS=Caenorhabditis elegans GN=calu-1 PE=2 SV=1	0.37
Q22392|Q22392_CAEEL Protein DHS-19 OS=Caenorhabditis elegans GN=dhs-19 PE=3 SV=1	0.37
I7FXD6|I7FXD6_CAEEL Rab-10 (Fragment) OS=Caenorhabditis elegans GN=rab-10 PE=2 SV=1; Q94148|Q94148_CAEEL Protein RAB-10 OS=Caenorhabditis elegans GN=rab-10 PE=2 SV=2	0.37
I2HAA7|I2HAA7_CAEEL Protein UNC-68, isoform d OS=Caenorhabditis elegans GN=unc-68 PE=4 SV=1; I2HAA6|I2HAA6_CAEEL Protein UNC-68, isoform c OS=Caenorhabditis elegans GN=unc-68 PE=4 SV=1; P91905|P91905_CAEEL Ryanodine receptor OS=Caenorhabditis ele	0.37
Q03600|INA1_CAEEL Integrin alpha ina-1 OS=Caenorhabditis elegans GN=ina-1 PE=1 SV=1	0.36

Q9BI72|Q9BI72_CAEEL Protein EPN-1, isoform a OS=Caenorhabditis elegans GN=epn-1 PE=2 SV=1; Q9BI71|Q9BI71_CAEEL Protein EPN-1, isoform b OS=Caenorhabditis elegans GN=epn-1 PE=2 SV=1	0.36
O44158|O44158_CAEEL Protein VPS-37 OS=Caenorhabditis elegans GN=vps-37 PE=1 SV=1	0.36
Q7JMT5|Q7JMT5_CAEEL Annexin OS=Caenorhabditis elegans GN=nex-2 PE=2 SV=1; Q27512|Q27512_CAEEL Annexin OS=Caenorhabditis elegans GN=nex-2 PE=2 SV=2	0.35
Q03206|RAC1_CAEEL Ras-related protein ced-10 OS=Caenorhabditis elegans GN=ced-10 PE=1 SV=2; Q03206-2|RAC1_CAEEL Isoform b of Ras-related protein ced-10 OS=Caenorhabditis elegans GN=ced-10	0.35
Q19655|Q19655_CAEEL Protein F20D6.11 OS=Caenorhabditis elegans GN=CELE_F20D6.11 PE=4 SV=2	0.35
G5ECY0|G5ECY0_CAEEL MAGUK protein DLG-1 OS=Caenorhabditis elegans GN=dlg-1 PE=1 SV=1	0.35
Q93873|NDUS2_CAEEL Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Caenorhabditis elegans GN=gas-1 PE=3 SV=2	0.34
P34343|NU133_CAEEL Nuclear pore complex protein 15 OS=Caenorhabditis elegans GN=npp-15 PE=3 SV=4	0.34
Q7KPV0|Q7KPV0_CAEEL Protein GSA-1 OS=Caenorhabditis elegans GN=gsa-1 PE=4 SV=1; G5EF72|G5EF72_CAEEL G protein a(S) subunit OS=Caenorhabditis elegans PE=2 SV=1	0.34
Q86DB5|Q86DB5_CAEEL Protein GSR-1, isoform b OS=Caenorhabditis elegans GN=gsr-1 PE=2 SV=1; Q93379|Q93379_CAEEL Protein GSR-1, isoform a OS=Caenorhabditis elegans GN=gsr-1 PE=2 SV=2	0.34
G4SRS5|G4SRS5_CAEEL Protein ABTM-1 OS=Caenorhabditis elegans GN=abtm-1 PE=2 SV=1; Q71JP9|Q71JP9_CAEEL ABC7 protein OS=Caenorhabditis elegans GN=Y74C10AM.1 PE=2 SV=1	0.34
O16259|STIP1_CAEEL Stress-induced-phosphoprotein 1 OS=Caenorhabditis elegans GN=sti-1 PE=1 SV=1	0.34
Q9U2F6|Q9U2F6_CAEEL Protein VPS-2 OS=Caenorhabditis elegans GN=vps-2 PE=4 SV=1	0.33

G5EDV6|G5EDV6_CAEEL Protein K10C8.3, isoform c OS=Caenorhabditis elegans GN=CELE_K10C8.3 PE=2 SV=1; G5ECX8|G5ECX8_CAEEL Protein K10C8.3, isoform a OS=Caenorhabditis elegans GN=CELE_K10C8.3 PE=2 SV=1	0.33
G4S185|G4S185_CAEEL Protein ANAT-1, isoform b OS=Caenorhabditis elegans GN=anat-1 PE=2 SV=2; G5EDH7|G5EDH7_CAEEL Protein ANAT-1, isoform a OS=Caenorhabditis elegans GN=anat-1 PE=2 SV=2	0.33
Q09221|CPNA2_CAEEL Copine family protein 2 OS=Caenorhabditis elegans GN=cpna-2 PE=2 SV=4; Q09221-4|CPNA2_CAEEL Isoform d of Copine family protein 2 OS=Caenorhabditis elegans GN=cpna-2; Q09221-2|CPNA2_CAEEL Isoform a of Copine family protein 2 OS=	0.33
P91149|P91149_CAEEL Protein EXOC-7 OS=Caenorhabditis elegans GN=exoc-7 PE=4 SV=1	0.33
Q21549|Q21549_CAEEL Protein GSS-1 OS=Caenorhabditis elegans GN=gss-1 PE=4 SV=2	0.33
P90992|P90992_CAEEL Protein MISC-1 OS=Caenorhabditis elegans GN=misc-1 PE=3 SV=2	0.33
K8ERU3|K8ERU3_CAEEL Protein HPO-27 OS=Caenorhabditis elegans GN=hpo-27 PE=4 SV=1	0.33
Q21693|IF4E2_CAEEL Eukaryotic translation initiation factor 4E-2 OS=Caenorhabditis elegans GN=ife-2 PE=1 SV=1	0.33
H2L023|H2L023_CAEEL Adenylyl cyclase-associated protein OS=Caenorhabditis elegans GN=cas-1 PE=3 SV=1; Q95YA9|Q95YA9_CAEEL Adenylyl cyclase-associated protein OS=Caenorhabditis elegans GN=cas-1 PE=3 SV=1	0.33
O45168|IFC1_CAEEL Intermediate filament protein ifc-1 OS=Caenorhabditis elegans GN=ifc-1 PE=3 SV=2	0.33
Q9N3F8|Q9N3F8_CAEEL Protein RAL-1, isoform a OS=Caenorhabditis elegans GN=ral-1 PE=4 SV=1; H2L0Q6|H2L0Q6_CAEEL Protein RAL-1, isoform b OS=Caenorhabditis elegans GN=ral-1 PE=4 SV=1	0.32
G5EEA8|G5EEA8_CAEEL Annexin OS=Caenorhabditis elegans GN=nex-1 PE=2 SV=1	0.32

Q94263|MIRO_CAEEL Mitochondrial Rho GTPase OS=Caenorhabditis elegans GN=K08F11.5 PE=3 SV=1; Q94180|Q94180_CAEEL Protein MIRO-2 OS=Caenorhabditis elegans GN=miro-2 PE=4 SV=1; Q9BL82|Q9BL82_CAEEL Protein Y47G6A.27 OS=Caenorhabditis elegans GN=miro-	0.32
Q23624|Q23624_CAEEL Protein ZK829.7 OS=Caenorhabditis elegans GN=CELE_ZK829.7 PE=1 SV=2	0.32
Q22067|AATC_CAEEL Probable aspartate aminotransferase, cytoplasmic OS=Caenorhabditis elegans GN=T01C8.5 PE=3 SV=1	0.32
O45106|O45106_CAEEL Protein ECH-5 OS=Caenorhabditis elegans GN=ech-5 PE=3 SV=3	0.31
P39055|DYN1_CAEEL Dynamin OS=Caenorhabditis elegans GN=dyn-1 PE=1 SV=3; Q9U9I9|Q9U9I9_CAEEL Dynamin OS=Caenorhabditis elegans GN=dyn-1 PE=1 SV=1; P39055-2|DYN1_CAEEL Isoform b of Dynamin OS=Caenorhabditis elegans GN=dyn-1	0.31
Q9TZC8|Q9TZC8_CAEEL Protein Y71H10B.1, isoform a OS=Caenorhabditis elegans GN=CELE_Y71H10B.1 PE=2 SV=2; Q95X21|Q95X21_CAEEL Protein Y71H10B.1, isoform b OS=Caenorhabditis elegans GN=CELE_Y71H10B.1 PE=2 SV=1; Q86MI3|Q86MI3_CAEEL Protein Y71H10B.1,	0.30
Q21067|IFC2_CAEEL Intermediate filament protein ifc-2 OS=Caenorhabditis elegans GN=ifc-2 PE=1 SV=3; G8JY94|G8JY94_CAEEL Protein IFC-2, isoform d OS=Caenorhabditis elegans GN=ifc-2 PE=2 SV=1; Q21067-2|IFC2_CAEEL Isoform b of Intermediate filament	0.30
Q9N384|Q9N384_CAEEL Protein LEC-6 OS=Caenorhabditis elegans GN=lec-6 PE=1 SV=1; Q21057|Q21057_CAEEL Galectin OS=Caenorhabditis elegans PE=2 SV=1	0.30
Q95Q50|Q95Q50_CAEEL Protein GYG-1, isoform b OS=Caenorhabditis elegans GN=gyg-1 PE=4 SV=1; H2KYQ6|H2KYQ6_CAEEL Protein GYG-1, isoform c OS=Caenorhabditis elegans GN=gyg-1 PE=4 SV=1; H2KYQ5|H2KYQ5_CAEEL Protein GYG-1, isoform a OS=Caenorhabditis e	0.30
Q9XXK1-4|ATPA_CAEEL Isoform d of ATP synthase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=H28O16.1; Q9XXK1|ATPA_CAEEL ATP synthase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=H28O16.1 PE=1 SV=1; Q9XXK1-3|ATPA_CAEEL Iso	0.30
P52717|YUW5_CAEEL Uncharacterized serine carboxypeptidase F41C3.5 OS=Caenorhabditis elegans GN=F41C3.5 PE=1 SV=1	0.30

Q22235|Q22235_CAEEL Protein ENPL-1, isoform a OS=Caenorhabditis elegans GN=enpl-1 PE=2 SV=1; E9P859|E9P859_CAEEL Protein ENPL-1, isoform b OS=Caenorhabditis elegans GN=enpl-1 PE=2 SV=1	0.29
Q17941-2|AKT1_CAEEL Isoform b of Serine/threonine-protein kinase akt-1 OS=Caenorhabditis elegans GN=akt-1; Q17941|AKT1_CAEEL Serine/threonine-protein kinase akt-1 OS=Caenorhabditis elegans GN=akt-1 PE=1 SV=2; Q17941-3|AKT1_CAEEL Isoform c of Seri	0.29
Q21342|Q21342_CAEEL Protein EAK-7 OS=Caenorhabditis elegans GN=eak-7 PE=4 SV=1	0.29
Q18359|NDUA5_CAEEL Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Caenorhabditis elegans GN=C33A12.1 PE=3 SV=1	0.29
I7FW32|I7FW32_CAEEL Rab-1 (Fragment) OS=Caenorhabditis elegans GN=rab-1 PE=2 SV=1; Q9UAQ6|Q9UAQ6_CAEEL Protein RAB-1 OS=Caenorhabditis elegans GN=rab-1 PE=2 SV=1	0.29
Q27527|ENO_CAEEL Enolase OS=Caenorhabditis elegans GN=enol-1 PE=1 SV=3; Q27527-3|ENO_CAEEL Isoform c of Enolase OS=Caenorhabditis elegans GN=enol-1; Q27527-2|ENO_CAEEL Isoform b of Enolase OS=Caenorhabditis elegans GN=enol-1	0.29
O01761-6|UNC89_CAEEL Isoform f of Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89; O01761|UNC89_CAEEL Muscle M-line assembly protein unc-89 OS=Caenorhabditis elegans GN=unc-89 PE=1 SV=3; O01761-7|UNC89_CAEEL Isoform g of	0.29
O01685|O01685_CAEEL Protein C32F10.8, isoform a OS=Caenorhabditis elegans GN=C32F10.8 PE=2 SV=2; Q86GU3|Q86GU3_CAEEL Protein C32F10.8, isoform b OS=Caenorhabditis elegans GN=C32F10.8 PE=2 SV=1	0.28
P50305|METK3_CAEEL Probable S-adenosylmethionine synthase 3 OS=Caenorhabditis elegans GN=sams-3 PE=1 SV=1	0.28
G5EG62|G5EG62_CAEEL Protein UNC-45 OS=Caenorhabditis elegans GN=unc-45 PE=1 SV=1	0.28
P51875|GNAO_CAEEL Guanine nucleotide-binding protein G(o) subunit alpha OS=Caenorhabditis elegans GN=goa-1 PE=1 SV=3	0.28
P34308-2|CAN_CAEEL Isoform b of Calpain clp-1 OS=Caenorhabditis elegans GN=clp-1; P34308-4|CAN_CAEEL Isoform d of Calpain clp-1 OS=Caenorhabditis elegans GN=clp-1; P34308|CAN_CAEEL Calpain clp-1 OS=Caenorhabditis elegans GN=clp-1 PE=3 SV=4	0.28

Q21166|SUR5_CAEEL Acetoacetyl-CoA synthetase OS=Caenorhabditis elegans GN=sur-5 PE=2 SV=1	0.28
Q27497|GLC7A_CAEEL Serine/threonine-protein phosphatase PP1-alpha OS=Caenorhabditis elegans GN=gsp-1 PE=2 SV=2; G3MU14|G3MU14_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=gsp-1 PE=2 SV=1	0.28
Q9XTV4|Q9XTV4_CAEEL Protein MBF-1 OS=Caenorhabditis elegans GN=mbf-1 PE=4 SV=1	0.28
P34540|KINH_CAEEL Kinesin heavy chain OS=Caenorhabditis elegans GN=unc-116 PE=2 SV=2	0.27
Q95002|Q95002_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=tax-6 PE=2 SV=1; Q86MD4|Q86MD4_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=tax-6 PE=2 SV=2; Q0G819|Q0G819_CAEEL Serine/threonine-pro	0.27
G5EDC6|G5EDC6_CAEEL Novel small G protein indispensable for equal chromosome segregation OS=Caenorhabditis elegans GN=arl-8 PE=2 SV=1	0.27
Q11067|PDIA6_CAEEL Probable protein disulfide-isomerase A6 OS=Caenorhabditis elegans GN=tag-320 PE=3 SV=1	0.27
H2KYS1|H2KYS1_CAEEL Protein HSP-43, isoform a OS=Caenorhabditis elegans GN=hsp-43 PE=3 SV=1; B0M0L8|B0M0L8_CAEEL Protein HSP-43, isoform b OS=Caenorhabditis elegans GN=hsp-43 PE=3 SV=2	0.27
Q7Z135|Q7Z135_CAEEL Protein HID-1, isoform b OS=Caenorhabditis elegans GN=hid-1 PE=2 SV=1; G5EG65|G5EG65_CAEEL HID-1 OS=Caenorhabditis elegans GN=hid-1 PE=2 SV=1	0.26
Q9U3F8|Q9U3F8_CAEEL Protein AAGR-3, isoform b OS=Caenorhabditis elegans GN=aagr-3 PE=2 SV=1; Q20239|Q20239_CAEEL Protein AAGR-3, isoform a OS=Caenorhabditis elegans GN=aagr-3 PE=2 SV=1; J7SA48|J7SA48_CAEEL Protein AAGR-3, isoform c OS=Caenorhabdi	0.26
O61967-2|LAP1_CAEEL Isoform a of Protein lap1 OS=Caenorhabditis elegans GN=let-413; O61967|LAP1_CAEEL Protein lap1 OS=Caenorhabditis elegans GN=let-413 PE=1 SV=3	0.26
Q06561-2|UNC52_CAEEL Isoform a of Basement membrane proteoglycan OS=Caenorhabditis elegans GN=unc-52; Q06561|UNC52_CAEEL Basement membrane proteoglycan OS=Caenorhabditis elegans GN=unc-52 PE=1 SV=2; H9G349|H9G349_CAEEL Protein UNC-52, isoform n O	0.26

G5EGA5|G5EGA5_CAEEL Delta 12 fatty acid desaturase FAT-2 OS=Caenorhabditis elegans GN=fat-2 PE=2 SV=1	0.26
G5EDQ4|G5EDQ4_CAEEL CLE-1C protein OS=Caenorhabditis elegans GN=cle-1 PE=4 SV=1; G5EDV5|G5EDV5_CAEEL CLE-1B protein OS=Caenorhabditis elegans GN=cle-1 PE=4 SV=1; Q9U9K7|Q9U9K7_CAEEL CLE-1A protein OS=Caenorhabditis elegans PE=2 SV=1; G5EF89|G5	0.25
Q95Q55|Q95Q55_CAEEL Protein F38A5.2, isoform b OS=Caenorhabditis elegans GN=CELE_F38A5.2 PE=4 SV=2; H2KZA2|H2KZA2_CAEEL Protein F38A5.2, isoform a OS=Caenorhabditis elegans GN=CELE_F38A5.2 PE=4 SV=1	0.25
Q2XMZ9|Q2XMZ9_CAEEL Protein C12D8.1, isoform c OS=Caenorhabditis elegans GN=C12D8.1 PE=2 SV=1; Q17935|Q17935_CAEEL Protein C12D8.1, isoform a OS=Caenorhabditis elegans GN=C12D8.1 PE=2 SV=1; Q17936|Q17936_CAEEL Protein C12D8.1, isoform b OS=Caenor	0.25
O01813|O01813_CAEEL Protein ANT-1.2 OS=Caenorhabditis elegans GN=ant-1.2 PE=2 SV=1; B4YEQ8|B4YEQ8_CAEEL Mitochondrial adenine nucleotide translocase 1.2 (Fragment) OS=Caenorhabditis elegans PE=2 SV=1	0.25
Q8WTM6|ARPC2_CAEEL Probable actin-related protein 2/3 complex subunit 2 OS=Caenorhabditis elegans GN=arx-4 PE=3 SV=1	0.25
Q21301|Q21301_CAEEL Protein CRML-1 OS=Caenorhabditis elegans GN=crml-1 PE=4 SV=1	0.24
Q9N589|Q9N589_CAEEL Protein MTM-1 OS=Caenorhabditis elegans GN=mtm-1 PE=4 SV=2	0.24
G5EDJ6|G5EDJ6_CAEEL Auxilin OS=Caenorhabditis elegans GN=dnj-25 PE=2 SV=1; D7SFQ6|D7SFQ6_CAEEL Protein DNJ-25, isoform c OS=Caenorhabditis elegans GN=dnj-25 PE=2 SV=1; D7SFQ5|D7SFQ5_CAEEL Protein DNJ-25, isoform b OS=Caenorhabditis elegans GN=dnj	0.24
Q9XW41|Q9XW41_CAEEL Protein SNX-3 OS=Caenorhabditis elegans GN=snx-3 PE=4 SV=1	0.24
O02640|MDHM_CAEEL Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-2 PE=3 SV=1	0.24
Q11189|RT17_CAEEL 28S ribosomal protein S17, mitochondrial OS=Caenorhabditis elegans GN=mrps-17 PE=3 SV=2	0.24

Q9N3H3|Q9N3H3_CAEEL Protein Y53G8AL.2 OS=Caenorhabditis elegans GN=CELE_Y53G8AL.2 PE=4 SV=2	0.23
Q20448|Q20448_CAEEL Protein ZTF-7 OS=Caenorhabditis elegans GN=ztf-7 PE=4 SV=1	0.23
O44451|ODPB_CAEEL Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C04C3.3 PE=1 SV=2	0.23
P34346|KAD2_CAEEL Adenylate kinase OS=Caenorhabditis elegans GN=let-754 PE=3 SV=2	0.23
Q20011|Q20011_CAEEL Protein NLP-24 OS=Caenorhabditis elegans GN=nlp-24 PE=4 SV=2	0.23
D0VWL8|D0VWL8_CAEEL Protein FLN-2, isoform d OS=Caenorhabditis elegans GN=fln-2 PE=2 SV=1; D0VWL7|D0VWL7_CAEEL Protein FLN-2, isoform c OS=Caenorhabditis elegans GN=fln-2 PE=2 SV=1; D0VWL6|D0VWL6_CAEEL Protein FLN-2, isoform a OS=Caenorhabditis e	0.23
G5EGU1|G5EGU1_CAEEL EGL-30 OS=Caenorhabditis elegans GN=egl-30 PE=2 SV=1; Q8T3G5|Q8T3G5_CAEEL Protein EGL-30, isoform b OS=Caenorhabditis elegans GN=egl-30 PE=2 SV=1	0.23
G4S034|G4S034_CAEEL Protein SPC-1, isoform a OS=Caenorhabditis elegans GN=spc-1 PE=2 SV=2; Q21408|Q21408_CAEEL Protein SPC-1, isoform b OS=Caenorhabditis elegans GN=spc-1 PE=2 SV=2	0.22
Q93353|IDH3B_CAEEL Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=idhb-1 PE=3 SV=1	0.22
Q09509-3|FOLC_CAEEL Isoform c of Putative folylpolyglutamate synthase OS=Caenorhabditis elegans GN=F25B5.6; Q09509|FOLC_CAEEL Putative folylpolyglutamate synthase OS=Caenorhabditis elegans GN=F25B5.6 PE=3 SV=1; Q09509-2|FOLC_CAEEL Isoform b of Pu	0.22
G5ECZ0|G5ECZ0_CAEEL Myosin IA OS=Caenorhabditis elegans GN=hum-5 PE=2 SV=1	0.22
Q10943|ARF12_CAEEL ADP-ribosylation factor 1-like 2 OS=Caenorhabditis elegans GN=arf-1.2 PE=2 SV=2	0.22
P91390|P91390_CAEEL Protein OSTD-1 OS=Caenorhabditis elegans GN=ostd-1 PE=4 SV=1	0.22
Q7Z1P1|Q7Z1P1_CAEEL Protein MEK-1, isoform b OS=Caenorhabditis elegans GN=mek-1 PE=2 SV=1; Q21307|Q21307_CAEEL Protein MEK-1, isoform a OS=Caenorhabditis elegans GN=mek-1 PE=2 SV=2	0.22

O44565|O44565_CAEEL Protein LAM-1 OS=Caenorhabditis elegans GN=lam-1 PE=4 SV=3	0.22
P46561|ATPB_CAEEL ATP synthase subunit beta, mitochondrial OS=Caenorhabditis elegans GN=atp-2 PE=1 SV=2	0.21
Q9TXC0|Q9TXC0_CAEEL Alpha-ACTININ=ACTIN-binding protein (Fragment) OS=Caenorhabditis elegans PE=2 SV=1; Q23158|Q23158_CAEEL Protein ATN-1, isoform a OS=Caenorhabditis elegans GN=atn-1 PE=1 SV=1; H2L2C9|H2L2C9_CAEEL Protein ATN-1, isoform c OS=Cae	0.21
Q9UB28|Q9UB28_CAEEL Myotactin form B OS=Caenorhabditis elegans GN=let-805 PE=2 SV=1; Q9UB29|Q9UB29_CAEEL Myotactin form A OS=Caenorhabditis elegans GN=let-805 PE=2 SV=1	0.21
Q02328-2|SLAP2_CAEEL Isoform b of Huntington interacting protein related 1 OS=Caenorhabditis elegans GN=hipr-1; Q02328|SLAP2_CAEEL Huntington interacting protein related 1 OS=Caenorhabditis elegans GN=hipr-1 PE=3 SV=3	0.21
P0DM42|ACT3_CAEEL Actin-3 OS=Caenorhabditis elegans GN=act-3 PE=1 SV=1; P0DM41|ACT1_CAEEL Actin-1 OS=Caenorhabditis elegans GN=act-1 PE=1 SV=1	0.20
P34657|YOTB_CAEEL Uncharacterized protein ZK632.12 OS=Caenorhabditis elegans GN=ZK632.12 PE=1 SV=2	0.20
Q10129|RT16_CAEEL Probable 28S ribosomal protein S16, mitochondrial OS=Caenorhabditis elegans GN=mrps-16 PE=3 SV=2	0.20
H2KZV8|H2KZV8_CAEEL Protein MLP-1, isoform b OS=Caenorhabditis elegans GN=mlp-1 PE=4 SV=1; Q9GP94|Q9GP94_CAEEL Protein MLP-1, isoform a OS=Caenorhabditis elegans GN=mlp-1 PE=2 SV=2; L8E6X8|L8E6X8_CAEEL Protein MLP-1, isoform d OS=Caenorhabditis e	0.20
Q20780|Q20780_CAEEL Protein ALH-1, isoform a OS=Caenorhabditis elegans GN=alh-1 PE=2 SV=3; Q8IG19|Q8IG19_CAEEL Protein ALH-1, isoform b OS=Caenorhabditis elegans GN=alh-1 PE=2 SV=1	0.20
O01868|RL24_CAEEL 60S ribosomal protein L24 OS=Caenorhabditis elegans GN=rpl-24.1 PE=3 SV=1	0.20
H2KYD7|H2KYD7_CAEEL Protein VEM-1, isoform a OS=Caenorhabditis elegans GN=vem-1 PE=4 SV=1; Q7YZW5|Q7YZW5_CAEEL Protein VEM-1, isoform b OS=Caenorhabditis elegans GN=vem-1 PE=4 SV=1	0.20

O76258|O76258_CAEEL Protein TSG-101 OS=Caenorhabditis elegans GN=tsg-101 PE=1 SV=2	0.20
P52013|CYP5_CAEEL Peptidyl-prolyl cis-trans isomerase 5 OS=Caenorhabditis elegans GN=cyn-5 PE=1 SV=2	0.20
P42168|KC1A_CAEEL Casein kinase I isoform alpha OS=Caenorhabditis elegans GN=kin-19 PE=3 SV=1	0.20
Q9N4F3|Q9N4F3_CAEEL Protein APB-1, isoform a OS=Caenorhabditis elegans GN=apb-1 PE=2 SV=2; Q7YZG8|Q7YZG8_CAEEL Protein APB-1, isoform c OS=Caenorhabditis elegans GN=apb-1 PE=2 SV=1	0.20
Q23621|Q23621_CAEEL Glutamate dehydrogenase OS=Caenorhabditis elegans GN=gdh-1 PE=3 SV=1	0.20
G5EC78|G5EC78_CAEEL Protein UBQL-1, isoform b OS=Caenorhabditis elegans GN=ubql-1 PE=2 SV=1; G5EFF7|G5EFF7_CAEEL Protein UBQL-1, isoform a OS=Caenorhabditis elegans GN=ubql-1 PE=2 SV=1; O18672|O18672_CAEEL F15C11.2 (Fragment) OS=Caenorhabditis el	0.19
Q22716|Q22716_CAEEL Protein RPL-32, isoform a OS=Caenorhabditis elegans GN=rpl-32 PE=2 SV=1; B7WN95|B7WN95_CAEEL Protein RPL-32, isoform b OS=Caenorhabditis elegans GN=rpl-32 PE=2 SV=1	0.19
Q93565|Q93565_CAEEL Protein TLI-1 OS=Caenorhabditis elegans GN=tli-1 PE=4 SV=2	0.19
G5EE56|G5EE56_CAEEL Protein SRC-1 OS=Caenorhabditis elegans GN=src-1 PE=2 SV=1	0.19
Q9N369|Q9N369_CAEEL Autophagy-related protein 3 OS=Caenorhabditis elegans GN=atg-3 PE=3 SV=1	0.19
Q8I7H7|Q8I7H7_CAEEL Protein C37C3.2, isoform c OS=Caenorhabditis elegans GN=C37C3.2 PE=2 SV=1; Q22918|IF5_CAEEL Eukaryotic translation initiation factor 5 OS=Caenorhabditis elegans GN=C37C3.2 PE=2 SV=2; Q22918-2|IF5_CAEEL Isoform b of Eukaryotic	0.18
Q17796|Q17796_CAEEL Protein HGRS-1 OS=Caenorhabditis elegans GN=hgrs-1 PE=4 SV=2	0.18
Q19130|Q19130_CAEEL Protein F07A11.2, isoform a OS=Caenorhabditis elegans GN=CELE_F07A11.2 PE=2 SV=1; Q95QM8|Q95QM8_CAEEL Protein F07A11.2, isoform b OS=Caenorhabditis elegans GN=CELE_F07A11.2 PE=2 SV=1	0.18

Q17348|SMD3_CAEEL Small nuclear ribonucleoprotein Sm D3 OS=Caenorhabditis elegans GN=snr-1 PE=2 SV=2	0.18
Q09236|COPD_CAEEL Probable coatomer subunit delta OS=Caenorhabditis elegans GN=C13B9.3 PE=3 SV=1	0.18
P34685|CAPZA_CAEEL F-actin-capping protein subunit alpha OS=Caenorhabditis elegans GN=cap-1 PE=2 SV=1	0.18
O17622|KCY1_CAEEL UMP-CMP kinase 1 OS=Caenorhabditis elegans GN=C29F7.3 PE=1 SV=1	0.17
Q9TYN2|Q9TYN2_CAEEL Protein Y37E11B.5 OS=Caenorhabditis elegans GN=CELE_Y37E11B.5 PE=4 SV=1	0.17
P40614|MPCP_CAEEL Phosphate carrier protein, mitochondrial OS=Caenorhabditis elegans GN=F01G4.6 PE=2 SV=1; G5ECU3|G5ECU3_CAEEL Protein F01G4.6, isoform b OS=Caenorhabditis elegans GN=CELE_F01G4.6 PE=2 SV=1	0.17
Q964N4|Q964N4_CAEEL Transmembrane matrix receptor MUP-4 OS=Caenorhabditis elegans PE=2 SV=1; Q21281|Q21281_CAEEL Protein MUP-4 OS=Caenorhabditis elegans GN=mup-4 PE=2 SV=4	0.17
O17528|TMED2_CAEEL Suppressor/enhancer of lin-12 protein 9 OS=Caenorhabditis elegans GN=sel-9 PE=1 SV=1	0.17
Q86S80|Q86S80_CAEEL Protein RME-1, isoform f OS=Caenorhabditis elegans GN=rme-1 PE=2 SV=1; G5EEU7|G5EEU7_CAEEL Protein RME-1, isoform c OS=Caenorhabditis elegans GN=rme-1 PE=2 SV=1; Q8WSP1|Q8WSP1_CAEEL Protein RME-1, isoform e OS=Caenorhabditis e	0.17
Q09517|LE767_CAEEL Very-long-chain 3-oxooacyl-coA reductase let-767 OS=Caenorhabditis elegans GN=let-767 PE=1 SV=2; C1P622|C1P622_CAEEL Protein LET-767, isoform b OS=Caenorhabditis elegans GN=let-767 PE=2 SV=1	0.17
Q23223|MTR4_CAEEL mRNA transport homolog 4 OS=Caenorhabditis elegans GN=mtr-4 PE=3 SV=1	0.17
Q93576|Q93576_CAEEL Protein NDK-1 OS=Caenorhabditis elegans GN=ndk-1 PE=1 SV=1	0.17
P17343|GBB1_CAEEL Guanine nucleotide-binding protein subunit beta-1 OS=Caenorhabditis elegans GN=gpb-1 PE=2 SV=2	0.16
Q19289|IFB1_CAEEL Intermediate filament protein ifb-1 OS=Caenorhabditis elegans GN=ifb-1 PE=1 SV=1	0.16

C4ALD5|C4ALD5_CAEEL Protein UNC-73, isoform i OS=Caenorhabditis elegans GN=unc-73 PE=2 SV=1; O61528|O61528_CAEEL Guanine nucleotide exchange factor UNC-73A OS=Caenorhabditis elegans GN=unc-73 PE=2 SV=1; Q7JNG4|Q7JNG4_CAEEL Protein UNC-73, isoform	0.16
Q11190|ETFD_CAEEL Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Caenorhabditis elegans GN=let-721 PE=1 SV=2	0.16
P91175|P91175_CAEEL Protein C50F2.3 OS=Caenorhabditis elegans GN=C50F2.3 PE=1 SV=1	0.16
G5EGK8|G5EGK8_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=let-92 PE=2 SV=1	0.16
G5EFL5|G5EFL5_CAEEL Protein ALP-1, isoform d OS=Caenorhabditis elegans GN=alp-1 PE=1 SV=1; G5EEL1|G5EEL1_CAEEL Protein ALP-1, isoform b OS=Caenorhabditis elegans GN=alp-1 PE=1 SV=1; G5EFG1|G5EFG1_CAEEL Protein ALP-1, isoform e OS=Caenorhabditis e	0.16
Q19749|ODP2_CAEEL Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Caenorhabditis elegans GN=F23B12.5 PE=1 SV=1	0.16
Q22888|IF4E4_CAEEL Eukaryotic translation initiation factor 4E-4 OS=Caenorhabditis elegans GN=ife-4 PE=2 SV=1	0.16
P52652|TFS2_CAEEL Putative transcription elongation factor S-II OS=Caenorhabditis elegans GN=T24H10.1 PE=3 SV=1	0.16
Q23166|Q23166_CAEEL Protein W04G3.5, isoform a OS=Caenorhabditis elegans GN=CELE_W04G3.5 PE=2 SV=1; D0VWN5|D0VWN5_CAEEL Protein W04G3.5, isoform b OS=Caenorhabditis elegans GN=CELE_W04G3.5 PE=2 SV=1	0.16
Q9NG00|Q9NG00_CAEEL Putative integrin-linked kinase OS=Caenorhabditis elegans GN=ilk PE=2 SV=1; Q9TZC4|Q9TZC4_CAEEL Protein PAT-4 OS=Caenorhabditis elegans GN=pat-4 PE=1 SV=1	0.15
P30642|EIF3D_CAEEL Eukaryotic translation initiation factor 3 subunit D OS=Caenorhabditis elegans GN=eif-3.D PE=1 SV=1	0.15
P49029|MGN_CAEEL Protein mago nashi homolog OS=Caenorhabditis elegans GN=mag-1 PE=1 SV=2	0.15
P50093|PHB2_CAEEL Mitochondrial prohibitin complex protein 2 OS=Caenorhabditis elegans GN=phb-2 PE=1 SV=2	0.15

Q6BEV4|Q6BEV4_CAEEL Protein UFD-2, isoform c OS=Caenorhabditis elegans GN=ufd-2 PE=2 SV=1; Q09349|UBE4_CAEEL Probable ubiquitin conjugation factor E4 OS=Caenorhabditis elegans GN=ufd-2 PE=2 SV=1; Q95QB5|Q95QB5_CAEEL Protein UFD-2, isoform b OS=Ca	0.15
Q19202|Q19202_CAEEL Protein APY-1 OS=Caenorhabditis elegans GN=apy-1 PE=1 SV=2	0.15
Q17489|Q17489_CAEEL Protein UNC-44, isoform a OS=Caenorhabditis elegans GN=unc-44 PE=2 SV=1	0.15
G5ECK7|G5ECK7_CAEEL Protein DLI-1, isoform b OS=Caenorhabditis elegans GN=dli-1 PE=2 SV=1; G5ED34|G5ED34_CAEEL Protein DLI-1, isoform a OS=Caenorhabditis elegans GN=dli-1 PE=2 SV=1	0.15
P52275|TBB2_CAEEL Tubulin beta-2 chain OS=Caenorhabditis elegans GN=tbb-2 PE=3 SV=1	0.15
Q18688|HSP90_CAEEL Heat shock protein 90 OS=Caenorhabditis elegans GN=daf-21 PE=1 SV=1	0.15
Q09450|SCOT_CAEEL Probable succinyl-CoA:3-ketoacid coenzyme A transferase, mitochondrial OS=Caenorhabditis elegans GN=C05C10.3 PE=3 SV=1	0.15
N1NVB5|N1NVB5_CAEEL Protein KCC-1, isoform b OS=Caenorhabditis elegans GN=kcc-1 PE=4 SV=1; N1NV09|N1NV09_CAEEL Protein KCC-1, isoform a OS=Caenorhabditis elegans GN=kcc-1 PE=4 SV=1	0.15
Q10576|P4HA1_CAEEL Prolyl 4-hydroxylase subunit alpha-1 OS=Caenorhabditis elegans GN=dpy-18 PE=1 SV=2	0.15
Q09543|2AAA_CAEEL Probable serine/threonine-protein phosphatase PP2A regulatory subunit OS=Caenorhabditis elegans GN=paa-1 PE=3 SV=2	0.15
Q93572|RLA0_CAEEL 60S acidic ribosomal protein P0 OS=Caenorhabditis elegans GN=rpa-0 PE=1 SV=3	0.14
O16997|O16997_CAEEL Protein W03F9.10 OS=Caenorhabditis elegans GN=CELE_W03F9.10 PE=1 SV=1	0.14
G5EDY8|G5EDY8_CAEEL Dynamin-related protein OS=Caenorhabditis elegans GN=drp-1 PE=2 SV=1; Q8WQC9|Q8WQC9_CAEEL Protein DRP-1, isoform b OS=Caenorhabditis elegans GN=drp-1 PE=2 SV=1	0.14
Q18090|TOM40_CAEEL Mitochondrial import receptor subunit TOM40 homolog OS=Caenorhabditis elegans GN=C18E9.6 PE=3 SV=1	0.14

H2KYN5|H2KYN5_CAEEL Protein ATG-18, isoform b OS=Caenorhabditis elegans GN=atg-18 PE=4 SV=1; O16466|O16466_CAEEL Protein ATG-18, isoform a OS=Caenorhabditis elegans GN=atg-18 PE=4 SV=1	0.14
Q9UAV5|Q9UAV5_CAEEL Malate dehydrogenase OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1; Q8IA49|Q8IA49_CAEEL Malate dehydrogenase OS=Caenorhabditis elegans GN=mdh-1 PE=2 SV=1; Q8IA50|Q8IA50_CAEEL Protein MDH-1, isoform c OS=Caenorhabditis elegans G	0.14
H2L0B9|H2L0B9_CAEEL Protein FGT-1, isoform a OS=Caenorhabditis elegans GN=fgt-1 PE=3 SV=1; O44827|O44827_CAEEL Protein FGT-1, isoform b OS=Caenorhabditis elegans GN=fgt-1 PE=3 SV=2	0.14
Q9GPA0|Q9GPA0_CAEEL Protein UGGT-1 OS=Caenorhabditis elegans GN=uggt-1 PE=4 SV=1	0.14
Q95XJ0|Q95XJ0_CAEEL Protein Y69A2AR.18, isoform a OS=Caenorhabditis elegans GN=CELE_Y69A2AR.18 PE=2 SV=1; Q95XI9|Q95XI9_CAEEL Protein Y69A2AR.18, isoform b OS=Caenorhabditis elegans GN=CELE_Y69A2AR.18 PE=2 SV=1; Q86DM7|Q86DM7_CAEEL Protein Y69A2A	0.14
Q9XW10|PAD1_CAEEL Protein pad-1 OS=Caenorhabditis elegans GN=pad-1 PE=2 SV=2	0.14
O01974|EIF3H_CAEEL Eukaryotic translation initiation factor 3 subunit H OS=Caenorhabditis elegans GN=eif-3.H PE=1 SV=2	0.14
Q17449|FAAH1_CAEEL Fatty acid amide hydrolase 1 OS=Caenorhabditis elegans GN=faah-1 PE=2 SV=1; Q17449-2|FAAH1_CAEEL Isoform b of Fatty acid amide hydrolase 1 OS=Caenorhabditis elegans GN=faah-1	0.14
P91401|P91401_CAEEL Protein M01E11.2 OS=Caenorhabditis elegans GN=CELE_M01E11.2 PE=4 SV=1	0.14
I7FW40|I7FW40_CAEEL Rab-14 (Fragment) OS=Caenorhabditis elegans GN=rab-14 PE=2 SV=1; Q93874|Q93874_CAEEL Protein RAB-14 OS=Caenorhabditis elegans GN=rab-14 PE=2 SV=1	0.13
G3MU69|G3MU69_CAEEL Protein ANT-1.1, isoform d OS=Caenorhabditis elegans GN=ant-1.1 PE=2 SV=1	0.13
Q21930|RL28_CAEEL 60S ribosomal protein L28 OS=Caenorhabditis elegans GN=rpl-28 PE=1 SV=3	0.13
Q19554|Q19554_CAEEL Protein ABCF-1 OS=Caenorhabditis elegans GN=abcf-1 PE=3 SV=1	0.13

P34575|CISY_CAEEL Probable citrate synthase, mitochondrial OS=Caenorhabditis elegans GN=cts-1 PE=1 SV=1	0.13
Q11176|WDR1_CAEEL Actin-interacting protein 1 OS=Caenorhabditis elegans GN=unc-78 PE=1 SV=1; Q11176-2|WDR1_CAEEL Isoform b of Actin-interacting protein 1 OS=Caenorhabditis elegans GN=unc-78	0.13
P27420|HSP7C_CAEEL Heat shock 70 kDa protein C OS=Caenorhabditis elegans GN=hsp-3 PE=1 SV=2	0.13
Q9BKQ5|Q9BKQ5_CAEEL Protein REP-1, isoform a OS=Caenorhabditis elegans GN=rep-1 PE=4 SV=1	0.13
Q21742|Q21742_CAEEL Protein R05F9.6 OS=Caenorhabditis elegans GN=CELE_R05F9.6 PE=3 SV=1	0.13
Q9TYL9|Q9TYL9_CAEEL Coatomer subunit beta OS=Caenorhabditis elegans GN=copb-1 PE=3 SV=1	0.13
Q18864|SURF4_CAEEL Surfeit locus protein 4 homolog OS=Caenorhabditis elegans GN=sft-4 PE=2 SV=1	0.13
P47207|TCPB_CAEEL T-complex protein 1 subunit beta OS=Caenorhabditis elegans GN=cct-2 PE=1 SV=2	0.13
Q20822|SRP68_CAEEL Probable signal recognition particle subunit SRP68 OS=Caenorhabditis elegans GN=F55C5.8 PE=3 SV=2	0.13
Q93934|Q93934_CAEEL Protein R07H5.8 OS=Caenorhabditis elegans GN=CELE_R07H5.8 PE=1 SV=1	0.13
Q17819|ORN_CAEEL Probable oligoribonuclease OS=Caenorhabditis elegans GN=C08B6.8 PE=2 SV=1	0.12
G5EDZ7|G5EDZ7_CAEEL Cadmium-inducible lysosomal protein CDR-4 OS=Caenorhabditis elegans GN=cdr-4 PE=2 SV=1	0.12
Q23280|YOCA_CAEEL Uncharacterized protein ZC395.10 OS=Caenorhabditis elegans GN=ZC395.10 PE=3 SV=1	0.12
Q22100|Q22100_CAEEL Protein KAT-1 OS=Caenorhabditis elegans GN=kat-1 PE=3 SV=2	0.12
O45865|O45865_CAEEL Protein ANT-1.1, isoform a OS=Caenorhabditis elegans GN=ant-1.1 PE=2 SV=1; Q17407|Q17407_CAEEL ADP/ATP translocase OS=Caenorhabditis elegans PE=2 SV=1	0.12
P34686|CAPZB_CAEEL F-actin-capping protein subunit beta OS=Caenorhabditis elegans GN=cap-2 PE=2 SV=1	0.12

Q22494|VATH2_CAEEL Probable V-type proton ATPase subunit H 2 OS=Caenorhabditis elegans GN=vha-15 PE=3 SV=1	0.12
Q18212|DX39B_CAEEL Spliceosome RNA helicase DDX39B homolog OS=Caenorhabditis elegans GN=hel-1 PE=2 SV=1; Q86GC6|Q86GC6_CAEEL Protein HEL-1, isoform b OS=Caenorhabditis elegans GN=hel-1 PE=2 SV=1	0.12
Q9TYW1|Q9TYW1_CAEEL Protein VHA-19 OS=Caenorhabditis elegans GN=vha-19 PE=4 SV=1	0.12
O62106|IF6_CAEEL Eukaryotic translation initiation factor 6 OS=Caenorhabditis elegans GN=eif-6 PE=3 SV=1	0.12
Q9XU13|Q9XU13_CAEEL Protein SCA-1, isoform b OS=Caenorhabditis elegans GN=sca-1 PE=2 SV=1	0.12
O61199|ODO1_CAEEL 2-oxoglutarate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=T22B11.5 PE=1 SV=2	0.12
Q21053|Q21053_CAEEL Protein VPS-35 OS=Caenorhabditis elegans GN=vps-35 PE=2 SV=3; A1X3T7|A1X3T7_CAEEL Vacuolar protein sorting factor OS=Caenorhabditis elegans GN=F59G1.3 PE=2 SV=1	0.12
Q19162|Q19162_CAEEL Protein RPL-11.2 OS=Caenorhabditis elegans GN=rpl-11.2 PE=3 SV=1	0.12
H2KYR1|H2KYR1_CAEEL Protein VIG-1, isoform a OS=Caenorhabditis elegans GN=vig-1 PE=4 SV=1	0.11
P91134|PURA_CAEEL Adenylosuccinate synthetase OS=Caenorhabditis elegans GN=C37H5.6 PE=3 SV=3; P91134-2|PURA_CAEEL Isoform b of Adenylosuccinate synthetase OS=Caenorhabditis elegans GN=C37H5.6	0.11
O45903|MECR1_CAEEL Probable trans-2-enoyl-CoA reductase 1, mitochondrial OS=Caenorhabditis elegans GN=W09H1.5 PE=3 SV=1	0.11
Q19905|UGDH_CAEEL UDP-glucose 6-dehydrogenase OS=Caenorhabditis elegans GN=sqv-4 PE=1 SV=1	0.11
Q8IG31|Q8IG31_CAEEL Protein PRDX-2, isoform a OS=Caenorhabditis elegans GN=prdx-2 PE=4 SV=1; H2KZL7|H2KZL7_CAEEL Protein PRDX-2, isoform b OS=Caenorhabditis elegans GN=prdx-2 PE=4 SV=1	0.11
Q18265|Q18265_CAEEL Protein FUST-1 OS=Caenorhabditis elegans GN=fust-1 PE=4 SV=2	0.11

P49197|RS21_CAEEL 40S ribosomal protein S21 OS=Caenorhabditis elegans GN=rps-21 PE=1 SV=1	0.11
Q19087|DNPEP_CAEEL Putative aspartyl aminopeptidase OS=Caenorhabditis elegans GN=F01F1.9 PE=1 SV=1	0.11
Q95005|PSA7_CAEEL Proteasome subunit alpha type-7 OS=Caenorhabditis elegans GN=pas-4 PE=1 SV=1	0.11
G5EBH3|G5EBH3_CAEEL Protein SMA-1, isoform d OS=Caenorhabditis elegans GN=sma-1 PE=2 SV=1; G5EG97|G5EG97_CAEEL Protein SMA-1, isoform c OS=Caenorhabditis elegans GN=sma-1 PE=2 SV=1; G5EC35|G5EC35_CAEEL Beta chain spectrin homolog Sma1 OS=Caenorha	0.11
Q22601|Q22601_CAEEL Protein APA-2 OS=Caenorhabditis elegans GN=apa-2 PE=1 SV=2	0.11
Q21284|Q21284_CAEEL Protein K07E3.4, isoform a OS=Caenorhabditis elegans GN=CELE_K07E3.4 PE=3 SV=2	0.11
P53013|EF1A_CAEEL Elongation factor 1-alpha OS=Caenorhabditis elegans GN=eft-3 PE=2 SV=1; G8JY74|G8JY74_CAEEL Protein EEF-1A.2, isoform d OS=Caenorhabditis elegans GN=eef-1a.2 PE=2 SV=1	0.11
Q9XWV0|TMM33_CAEEL Transmembrane protein 33 homolog OS=Caenorhabditis elegans GN=Y37D8A.17 PE=1 SV=1	0.11
Q93896|Q93896_CAEEL Protein MCT-3 OS=Caenorhabditis elegans GN=mct-3 PE=4 SV=1	0.10
P91189|P91189_CAEEL Protein DNJ-7 OS=Caenorhabditis elegans GN=dnj-7 PE=4 SV=1	0.10
G5EET3|G5EET3_CAEEL Cadmium-inducible lysosomal protein CDR-6 OS=Caenorhabditis elegans GN=cdr-6 PE=2 SV=1	0.10
Q9UAN9|Q9UAN9_CAEEL Protein NRA-4, isoform a OS=Caenorhabditis elegans GN=nra-4 PE=4 SV=2; H2KYE0|H2KYE0_CAEEL Protein NRA-4, isoform b OS=Caenorhabditis elegans GN=nra-4 PE=4 SV=1	0.10
Q9N3F4|Q9N3F4_CAEEL Protein VBH-1, isoform a OS=Caenorhabditis elegans GN=vbh-1 PE=2 SV=1; Q95XY1|Q95XY1_CAEEL Protein VBH-1, isoform b OS=Caenorhabditis elegans GN=vbh-1 PE=2 SV=1; Q65XX1|Q65XX1_CAEEL Protein VBH-1, isoform c OS=Caenorhabditis e	0.10
Q9U2M4|HOT_CAEEL Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y38F1A.6 PE=3 SV=1	0.10

G5ECM9|G5ECM9_CAEEL Cystatin C OS=Caenorhabditis elegans GN=cpi-2 PE=2 SV=1	0.10
Q09545|DHSB_CAEEL Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Caenorhabditis elegans GN=sdhb-1 PE=2 SV=1	0.10
E9P883|E9P883_CAEEL Protein EGL-3, isoform c OS=Caenorhabditis elegans GN=egl-3 PE=2 SV=1; Q18772|Q18772_CAEEL Protein EGL-3, isoform b OS=Caenorhabditis elegans GN=egl-3 PE=2 SV=1; G5ECN9|G5ECN9_CAEEL Prohormone convertase 2 OS=Caenorhabditis el	0.10
Q18885|BTF3_CAEEL Transcription factor BTF3 homolog OS=Caenorhabditis elegans GN=icd-1 PE=1 SV=1	0.10
Q965N4|Q965N4_CAEEL Protein CHIN-1 OS=Caenorhabditis elegans GN=chin-1 PE=4 SV=3	0.10
Q27504|CAH3_CAEEL Putative carbonic anhydrase 3 OS=Caenorhabditis elegans GN=cah-3 PE=3 SV=1	0.10
Q17693|MTHR_CAEEL Probable methylenetetrahydrofolate reductase OS=Caenorhabditis elegans GN=C06A8.1 PE=2 SV=2; G8JXY2|G8JXY2_CAEEL Methylenetetrahydrofolate reductase OS=Caenorhabditis elegans GN=mthf-1 PE=2 SV=1	0.10
O18178|O18178_CAEEL Protein PPTR-1 OS=Caenorhabditis elegans GN=pptr-1 PE=1 SV=4	0.10
Q93714|IDH3A_CAEEL Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=idha-1 PE=1 SV=3	0.09
P49632|RL40_CAEEL Ubiquitin-60S ribosomal protein L40 OS=Caenorhabditis elegans GN=ubq-2 PE=3 SV=2; G8JY83|G8JY83_CAEEL Protein UBQ-1, isoform c OS=Caenorhabditis elegans GN=ubq-1 PE=2 SV=1; P0CG71|UBIQ1_CAEEL Polyubiquitin-A OS=Caenorhabditis el	0.09
Q22968|Q22968_CAEEL Aminomethyltransferase OS=Caenorhabditis elegans GN=gcst-1 PE=3 SV=1	0.09
P90900|IFA4_CAEEL Intermediate filament protein ifa-4 OS=Caenorhabditis elegans GN=ifa-4 PE=1 SV=2	0.09
P48150|RS14_CAEEL 40S ribosomal protein S14 OS=Caenorhabditis elegans GN=rps-14 PE=3 SV=1	0.09
Q09533|RL10_CAEEL 60S ribosomal protein L10 OS=Caenorhabditis elegans GN=rpl-10 PE=3 SV=1	0.09

Q19128|Q19128_CAEEL Immunoglobulin domain-containing protein F02G3.1 OS=Caenorhabditis elegans GN=ncam-1 PE=2 SV=3; Q8MQ86|Q8MQ86_CAEEL Protein NCAM-1, isoform c OS=Caenorhabditis elegans GN=ncam-1 PE=2 SV=1; Q8T3E5|Q8T3E5_CAEEL Protein NCAM-1, i	0.09
G5EC91|G5EC91_CAEEL Protein DPY-11 OS=Caenorhabditis elegans GN=dpy-11 PE=2 SV=1	0.09
Q23382|Q23382_CAEEL Protein CCDC-47 OS=Caenorhabditis elegans GN=ccdc-47 PE=1 SV=1	0.09
Q9XVR6|OTUBL_CAEEL Ubiquitin thioesterase otubain-like OS=Caenorhabditis elegans GN=otub-1 PE=1 SV=1	0.09
O76371|O76371_CAEEL Protein RPT-5 OS=Caenorhabditis elegans GN=rpt-5 PE=1 SV=1	0.09
Q86D21|Q86D21_CAEEL Protein TARS-1, isoform b OS=Caenorhabditis elegans GN=tars-1 PE=2 SV=1; P52709|SYTC_CAEEL Threonine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=trs-1 PE=2 SV=1	0.09
G8JXY9|G8JXY9_CAEEL Protein B0416.5, isoform b OS=Caenorhabditis elegans GN=B0416.5 PE=2 SV=1; Q11073|YT45_CAEEL Uncharacterized protein B0416.5 OS=Caenorhabditis elegans GN=B0416.5 PE=2 SV=1	0.09
P90735|P90735_CAEEL Protein EAT-6 OS=Caenorhabditis elegans GN=eat-6 PE=2 SV=1; Q27461|Q27461_CAEEL Na,K-ATPase alpha subunit OS=Caenorhabditis elegans GN=eat-6 PE=2 SV=1	0.08
Q9U2X0|Q9U2X0_CAEEL Protein PRMT-1 OS=Caenorhabditis elegans GN=prmt-1 PE=4 SV=1	0.08
P34690|TBA2_CAEEL Tubulin alpha-2 chain OS=Caenorhabditis elegans GN=tba-2 PE=2 SV=1	0.08
O16368|PRS4_CAEEL Probable 26S protease regulatory subunit 4 OS=Caenorhabditis elegans GN=rpt-2 PE=3 SV=1	0.08
Q9UAT3|Q9UAT3_CAEEL Protein MCT-1 OS=Caenorhabditis elegans GN=mct-2 PE=4 SV=2	0.08
Q09508|DHSA_CAEEL Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Caenorhabditis elegans GN=sdha-1 PE=1 SV=3	0.08

A8WHR6|A8WHR6_CAEEL Protein PPM-1, isoform c OS=Caenorhabditis elegans GN=ppm-1 PE=2 SV=1; Q19775|Q19775_CAEEL Protein PPM-1, isoform a OS=Caenorhabditis elegans GN=ppm-1 PE=2 SV=1; Q7JLJ3|Q7JLJ3_CAEEL Protein PPM-1, isoform b OS=Caenorhabditis e	0.08
P10771|H11_CAEEL Histone H1.1 OS=Caenorhabditis elegans GN=his-24 PE=1 SV=4	0.08
G5EFK4|G5EFK4_CAEEL ADP-ribosylation factor related (20.5 kD) (Arf-3) OS=Caenorhabditis elegans GN=arf-3 PE=2 SV=1	0.08
Q8MXD9|Q8MXD9_CAEEL Protein E02D9.1, isoform b OS=Caenorhabditis elegans GN=CELE_E02D9.1 PE=2 SV=1; Q4W4Y5|Q4W4Y5_CAEEL Protein E02D9.1, isoform c OS=Caenorhabditis elegans GN=CELE_E02D9.1 PE=2 SV=1	0.08
Q21032|Q21032_CAEEL Isocitrate dehydrogenase [NADP] OS=Caenorhabditis elegans GN=idh-1 PE=3 SV=1; H9G2T4|H9G2T4_CAEEL Isocitrate dehydrogenase [NADP] OS=Caenorhabditis elegans GN=idh-1 PE=3 SV=1	0.08
Q93244|Q93244_CAEEL Cysteine synthase OS=Caenorhabditis elegans GN=cysl-1 PE=1 SV=2	0.07
P34286|PSB1_CAEEL Proteasome subunit beta type-1 OS=Caenorhabditis elegans GN=pbs-6 PE=1 SV=2	0.07
P34496|MTSS1_CAEEL Single-stranded DNA-binding protein, mitochondrial OS=Caenorhabditis elegans GN=mtss-1 PE=2 SV=2	0.07
Q8MXS6|Q8MXS6_CAEEL Protein Y55F3AM.3, isoform c OS=Caenorhabditis elegans GN=CELE_Y55F3AM.3 PE=2 SV=1; Q9N368|Q9N368_CAEEL Protein Y55F3AM.3, isoform a OS=Caenorhabditis elegans GN=CELE_Y55F3AM.3 PE=2 SV=2	0.07
Q9TZL8|Q9TZL8_CAEEL 6-phosphofructokinase OS=Caenorhabditis elegans GN=pfk-1 PE=2 SV=2; Q95X24|Q95X24_CAEEL Protein PFK-1, isoform b OS=Caenorhabditis elegans GN=pfk-1 PE=2 SV=2	0.07
Q19901|Q19901_CAEEL Protein HUM-1 OS=Caenorhabditis elegans GN=hum-1 PE=2 SV=1; Q17382|Q17382_CAEEL Hum-1 (Fragment) OS=Caenorhabditis elegans GN=hum-1 PE=2 SV=1	0.07
Q27464|G6PD_CAEEL Glucose-6-phosphate 1-dehydrogenase OS=Caenorhabditis elegans GN=gspd-1 PE=3 SV=1	0.07
Q9N4G8|Q9N4G8_CAEEL Protein YOP-1 OS=Caenorhabditis elegans GN=yop-1 PE=4 SV=1	0.07

Q20230|KCY2_CAEEL UMP-CMP kinase 2 OS=Caenorhabditis elegans GN=F40F8.1 PE=1 SV=1	0.07
Q21926|SYIC_CAEEL Isoleucine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=irs-1 PE=3 SV=1	0.07
Q95YD5|Q95YD5_CAEEL Protein VHA-16 OS=Caenorhabditis elegans GN=vha-16 PE=4 SV=1	0.06
Q17598|TM104_CAEEL Transmembrane protein 104 homolog OS=Caenorhabditis elegans GN=C03A3.2 PE=1 SV=2	0.06
Q9N4H7|Q9N4H7_CAEEL Protein Y71F9AL.17 OS=Caenorhabditis elegans GN=CELE_Y71F9AL.17 PE=4 SV=2	0.06
O62220|AN321_CAEEL Acidic leucine-rich nuclear phosphoprotein 32-related protein 1 OS=Caenorhabditis elegans GN=F33H2.3 PE=3 SV=1	0.06
O76840-2|PPN1_CAEEL Isoform a of Papilin OS=Caenorhabditis elegans GN=mig-6; O76840|PPN1_CAEEL Papilin OS=Caenorhabditis elegans GN=mig-6 PE=1 SV=1; O76840-3|PPN1_CAEEL Isoform c of Papilin OS=Caenorhabditis elegans GN=mig-6	0.06
Q9NEW6|RSP3_CAEEL Probable splicing factor, arginine/serine-rich 3 OS=Caenorhabditis elegans GN=rsp-3 PE=1 SV=2	0.06
Q94360|NDUS7_CAEEL Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Caenorhabditis elegans GN=nduf-7 PE=3 SV=1	0.06
Q9U2K8|Q9U2K8_CAEEL Protein ABCE-1 OS=Caenorhabditis elegans GN=abce-1 PE=3 SV=1	0.06
P09446|HSP7A_CAEEL Heat shock 70 kDa protein A OS=Caenorhabditis elegans GN=hsp-1 PE=1 SV=2	0.06
G5EGP4|G5EGP4_CAEEL Protein VHA-6 OS=Caenorhabditis elegans GN=vha-6 PE=2 SV=1	0.06
Q8I4B4|Q8I4B4_CAEEL Protein CCR-4, isoform c OS=Caenorhabditis elegans GN=ccr-4 PE=2 SV=1; G5EE09|G5EE09_CAEEL CCR4 OS=Caenorhabditis elegans GN=ccr-4 PE=2 SV=1; Q9U1P4|Q9U1P4_CAEEL Protein CCR-4, isoform b OS=Caenorhabditis elegans GN=ccr-4 PE=2	0.06

Q20938-2|PS11A_CAEEL Isoform b of Probable 26S proteasome regulatory subunit rpn-6.1 OS=Caenorhabditis elegans GN=rpn-6.1; Q20938|PS11A_CAEEL Probable 26S proteasome regulatory subunit rpn-6.1 OS=Caenorhabditis elegans GN=rpn-6.1 PE=2 SV=2	0.06
Q9U332|RL31_CAEEL 60S ribosomal protein L31 OS=Caenorhabditis elegans GN=rpl-31 PE=3 SV=1; Q9U332-2|RL31_CAEEL Isoform b of 60S ribosomal protein L31 OS=Caenorhabditis elegans GN=rpl-31	0.06
Q9TZS5|Q9TZS5_CAEEL Protein CCT-7, isoform a OS=Caenorhabditis elegans GN=cct-7 PE=2 SV=2; Q86S29|Q86S29_CAEEL Protein CCT-7, isoform b OS=Caenorhabditis elegans GN=cct-7 PE=2 SV=1	0.06
O45430|O45430_CAEEL Protein MCCC-1 OS=Caenorhabditis elegans GN=mccc-1 PE=4 SV=2	0.06
Q9XUW5|Q9XUW5_CAEEL Protein F58E10.3, isoform a OS=Caenorhabditis elegans GN=CELE_F58E10.3 PE=3 SV=1	0.06
P34629|AMPL_CAEEL Leucine aminopeptidase 1 OS=Caenorhabditis elegans GN=lap-1 PE=1 SV=1	0.06
Q19626|VATB_CAEEL Probable V-type proton ATPase subunit B OS=Caenorhabditis elegans GN=vha-12 PE=1 SV=1	0.05
G5EER4|G5EER4_CAEEL GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase OS=Caenorhabditis elegans GN=ger-1 PE=2 SV=1	0.05
P30632|ASNA_CAEEL ATPase asna-1 OS=Caenorhabditis elegans GN=asna-1 PE=1 SV=1	0.05
Q20751|IF5A2_CAEEL Eukaryotic translation initiation factor 5A-2 OS=Caenorhabditis elegans GN=iff-2 PE=2 SV=1	0.05
G5EBK3|G5EBK3_CAEEL ERM-1B OS=Caenorhabditis elegans GN=erm-1 PE=2 SV=1; G5EES2|G5EES2_CAEEL ERM-1A OS=Caenorhabditis elegans GN=erm-1 PE=2 SV=1	0.05
Q9U2F2|Q9U2F2_CAEEL Protein CPT-1 OS=Caenorhabditis elegans GN=cpt-1 PE=3 SV=3	0.05
Q18040|OAT_CAEEL Probable ornithine aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=3; Q8MNV6|Q8MNV6_CAEEL Protein C16A3.10, isoform b OS=Caenorhabditis elegans GN=C16A3.10 PE=2 SV=1; Q5TYL8|Q5TYL8_CAEEL Protein C16A	0.05

Q19877|RS23_CAEEL 40S ribosomal protein S23 OS=Caenorhabditis elegans GN=rps-23 PE=3 SV=1	0.05
P48158|RL23_CAEEL 60S ribosomal protein L23 OS=Caenorhabditis elegans GN=rpl-23 PE=3 SV=1	0.05
P41938|HCDH2_CAEEL Probable 3-hydroxyacyl-CoA dehydrogenase B0272.3 OS=Caenorhabditis elegans GN=B0272.3 PE=1 SV=1	0.05
Q95Y24|Q95Y24_CAEEL Protein Y41D4A.4 OS=Caenorhabditis elegans GN=CELE_Y41D4A.4 PE=4 SV=1	0.05
Q93796|NRF5_CAEEL Nose resistant to fluoxetine protein 5 OS=Caenorhabditis elegans GN=nrf-5 PE=1 SV=2	0.05
O44512|O44512_CAEEL Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Caenorhabditis elegans GN=isp-1 PE=3 SV=1	0.05
N1NTN5|N1NTN5_CAEEL Protein C14C10.5, isoform b OS=Caenorhabditis elegans GN=C14C10.5 PE=4 SV=1; Q17971|Q17971_CAEEL Protein C14C10.5, isoform a OS=Caenorhabditis elegans GN=C14C10.5 PE=4 SV=1	0.04
Q19818|Q19818_CAEEL Protein NHL-2 OS=Caenorhabditis elegans GN=nhl-2 PE=4 SV=2	0.04
O44511|O44511_CAEEL Protein SPH-1 OS=Caenorhabditis elegans GN=sph-1 PE=4 SV=2	0.04
Q19324|Q19324_CAEEL Protein RPN-5 OS=Caenorhabditis elegans GN=rpn-5 PE=4 SV=1	0.04
G5EEH6|G5EEH6_CAEEL Isovaleryl-CoA dehydrogenase OS=Caenorhabditis elegans GN=ivd-1 PE=2 SV=1	0.04
Q10045|UNC50_CAEEL Protein unc-50 OS=Caenorhabditis elegans GN=unc-50 PE=2 SV=2	0.04
Q9N456|Q9N456_CAEEL Protein GLRX-10 OS=Caenorhabditis elegans GN=glrx-10 PE=4 SV=1	0.04
G5EDF9|G5EDF9_CAEEL ABC transporter PGP-2 OS=Caenorhabditis elegans GN=pgp-2 PE=2 SV=1	0.04
O02639|RL19_CAEEL 60S ribosomal protein L19 OS=Caenorhabditis elegans GN=rpl-19 PE=3 SV=1	0.04

Q22099|SYK_CAEEL Lysine--tRNA ligase OS=Caenorhabditis elegans GN=krs-1 PE=2 SV=1; Q95ZQ3|Q95ZQ3_CAEEL Lysine--tRNA ligase OS=Caenorhabditis elegans GN=kars-1 PE=2 SV=1; Q2XN16|Q2XN16_CAEEL Lysine--tRNA ligase OS=Caenorhabditis elegans GN=kars-1	0.04
Q8WQD7|Q8WQD7_CAEEL Protein R04F11.5 OS=Caenorhabditis elegans GN=CELE_R04F11.5 PE=4 SV=1	0.04
D7SFJ4|D7SFJ4_CAEEL Protein C25H3.9, isoform b OS=Caenorhabditis elegans GN=C25H3.9 PE=4 SV=1; H2KYV1|H2KYV1_CAEEL Protein C25H3.9, isoform a OS=Caenorhabditis elegans GN=C25H3.9 PE=4 SV=1	0.03
P41994|RPIA_CAEEL Probable-ribose 5-phosphate isomerase OS=Caenorhabditis elegans GN=rpia-1 PE=3 SV=1	0.03
Q95QU0|PCID2_CAEEL PCI domain-containing protein 2 homolog OS=Caenorhabditis elegans GN=C27F2.10 PE=3 SV=1	0.03
G4RYA5|G4RYA5_CAEEL Protein F38A1.8 OS=Caenorhabditis elegans GN=CELE_F38A1.8 PE=4 SV=1	0.03
O45622|O45622_CAEEL Protein ERFA-3, isoform a OS=Caenorhabditis elegans GN=erfa-3 PE=2 SV=2	0.03
P91243|P91243_CAEEL Protein DNJ-9 OS=Caenorhabditis elegans GN=dnj-9 PE=4 SV=2	0.03
Q19328|Q19328_CAEEL Protein TSN-1 OS=Caenorhabditis elegans GN=tsn-1 PE=4 SV=1	0.03
Q9GZE9|Q9GZE9_CAEEL Protein F22F7.1, isoform a OS=Caenorhabditis elegans GN=CELE_F22F7.1 PE=2 SV=1; Q8IA58|Q8IA58_CAEEL Protein F22F7.1, isoform b OS=Caenorhabditis elegans GN=CELE_F22F7.1 PE=2 SV=1	0.03
P41988|TCPA_CAEEL T-complex protein 1 subunit alpha OS=Caenorhabditis elegans GN=cct-1 PE=3 SV=2	0.03
G5ECX9|G5ECX9_CAEEL Cadmium-inducible lysosomal protein CDR-2 OS=Caenorhabditis elegans GN=cdr-2 PE=2 SV=1	0.03
O44549|O44549_CAEEL Protein ACDH-3 OS=Caenorhabditis elegans GN=acdh-3 PE=3 SV=1	0.03
O17626|O17626_CAEEL Protein C31C9.2 OS=Caenorhabditis elegans GN=C31C9.2 PE=3 SV=1	0.02

P27604|SAHH_CAEEL Adenosylhomocysteinase OS=Caenorhabditis elegans GN=ahcy-1 PE=1 SV=1	0.02
P27639|IF4A_CAEEL Eukaryotic initiation factor 4A OS=Caenorhabditis elegans GN=inf-1 PE=2 SV=1	0.02
O45502|O45502_CAEEL Protein DNJ-12 OS=Caenorhabditis elegans GN=dnj-12 PE=1 SV=1	0.02
O01692|RS17_CAEEL 40S ribosomal protein S17 OS=Caenorhabditis elegans GN=rps-17 PE=3 SV=2	0.02
Q20585|PSMD6_CAEEL 26S proteasome non-ATPase regulatory subunit 6 OS=Caenorhabditis elegans GN=rpn-7 PE=3 SV=1	0.02
O45418|O45418_CAEEL Protein FKB-6 OS=Caenorhabditis elegans GN=fkb-6 PE=1 SV=1	0.02
P46502|PRS6B_CAEEL Probable 26S protease regulatory subunit 6B OS=Caenorhabditis elegans GN=rpt-3 PE=3 SV=1	0.02
P34369|PRP8_CAEEL Pre-mRNA-splicing factor 8 homolog OS=Caenorhabditis elegans GN=prp-8 PE=1 SV=1	0.02
G5ECG5|G5ECG5_CAEEL Protein VAB-10, isoform g OS=Caenorhabditis elegans GN=vab-10 PE=2 SV=1; G5EFM4|G5EFM4_CAEEL Protein VAB-10, isoform b OS=Caenorhabditis elegans GN=vab-10 PE=2 SV=1; G5EDD3|G5EDD3_CAEEL Protein VAB-10, isoform c OS=Caenorhabdi	0.01
Q19317|NBEA_CAEEL Putative neurobeachin homolog OS=Caenorhabditis elegans GN=sel-2 PE=2 SV=3; K8ESP0|K8ESP0_CAEEL Protein SEL-2 OS=Caenorhabditis elegans GN=sel-2 PE=4 SV=1	0.01
Q9XWI6|EIF3B_CAEEL Eukaryotic translation initiation factor 3 subunit B OS=Caenorhabditis elegans GN=eif-3.B PE=2 SV=2	0.01
Q19468|MBOA7_CAEEL Lysophospholipid acyltransferase 7 OS=Caenorhabditis elegans GN=mboa-7 PE=1 SV=2	0.01
Q21338|SPT5H_CAEEL Transcription elongation factor SPT5 OS=Caenorhabditis elegans GN=spt-5 PE=3 SV=3	0.01
C1P636|C1P636_CAEEL Protein UBA-1, isoform c OS=Caenorhabditis elegans GN=uba-1 PE=2 SV=1; Q27481|Q27481_CAEEL Protein UBA-1, isoform a OS=Caenorhabditis elegans GN=uba-1 PE=2 SV=1; Q3S1J5|Q3S1J5_CAEEL Protein UBA-1, isoform b OS=Caenorhabditis e	0.01

O61792|O61792_CAEEL Protein RPN-8 OS=Caenorhabditis elegans GN=rpn-8 PE=1 SV=1	0.01
Q20121|Q20121_CAEEL Protein ACS-4 OS=Caenorhabditis elegans GN=acs-4 PE=4 SV=2	0.01
Q09EE7|Q09EE7_CAEEL Protein NSF-1, isoform b OS=Caenorhabditis elegans GN=nsf-1 PE=2 SV=1; Q94392|NSF_CAEEL Vesicle-fusing ATPase OS=Caenorhabditis elegans GN=nsf-1 PE=1 SV=2	0.01
H2KZ18|H2KZ18_CAEEL Protein C34F11.3, isoform a OS=Caenorhabditis elegans GN=C34F11.3 PE=4 SV=1; D7SFL2|D7SFL2_CAEEL Protein C34F11.3, isoform b OS=Caenorhabditis elegans GN=C34F11.3 PE=4 SV=1; H2KZ19|H2KZ19_CAEEL Protein C34F11.3, isoform c OS=C	0.01
P27798|CALR_CAEEL Calreticulin OS=Caenorhabditis elegans GN=crt-1 PE=1 SV=1	0.01
O61820|EIF3E_CAEEL Eukaryotic translation initiation factor 3 subunit E OS=Caenorhabditis elegans GN=eif-3.E PE=3 SV=1	0.00
Q8IG49|Q8IG49_CAEEL Protein TIAR-1, isoform f OS=Caenorhabditis elegans GN=tiar-1 PE=2 SV=1; Q8IG50|Q8IG50_CAEEL Protein TIAR-1, isoform e OS=Caenorhabditis elegans GN=tiar-1 PE=2 SV=1; Q95QV7|Q95QV7_CAEEL Protein TIAR-1, isoform b OS=Caenorhabdi	0.00
P46548|NMT_CAEEL Probable glycylpeptide N-tetradecanoyltransferase OS=Caenorhabditis elegans GN=nmt-1 PE=2 SV=1; Q95ZN7|Q95ZN7_CAEEL Glycylpeptide N-tetradecanoyltransferase OS=Caenorhabditis elegans GN=nmt-1 PE=2 SV=1; G8JY05|G8JY05_CAEEL Glycyl	0.00
O45495|O45495_CAEEL Protein UEV-1 OS=Caenorhabditis elegans GN=uev-1 PE=4 SV=1	0.00
Q95Y90|RL9_CAEEL 60S ribosomal protein L9 OS=Caenorhabditis elegans GN=rpl-9 PE=3 SV=1	0.00
Q9N3X2|RS4_CAEEL 40S ribosomal protein S4 OS=Caenorhabditis elegans GN=rps-4 PE=1 SV=1	0.00
Q9U2G0|U520_CAEEL Putative U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Caenorhabditis elegans GN=Y46G5A.4 PE=3 SV=1	0.00
I7KSC2|I7KSC2_CAEEL Protein CFIM-2, isoform e OS=Caenorhabditis elegans GN=cfim-2 PE=4 SV=1; Q18937|Q18937_CAEEL Protein CFIM-2, isoform a OS=Caenorhabditis elegans GN=cfim-2 PE=2 SV=3; C6KRJ2|C6KRJ2_CAEEL Protein CFIM-2, isoform c OS=Caenorhabdi	0.00

O01806|O01806_CAEEL Protein C44E4.4 OS=Caenorhabditis elegans GN=C44E4.4 PE=4 SV=1	0.00
O16658|O16658_CAEEL Protein NSTP-4 OS=Caenorhabditis elegans GN=nstp-4 PE=4 SV=3	0.00
Q9N5B3|Q9N5B3_CAEEL Protein W08E12.7 OS=Caenorhabditis elegans GN=CELE_W08E12.7 PE=4 SV=1	0.00
O61235|CATA2_CAEEL Catalase-2 OS=Caenorhabditis elegans GN=ctl-1 PE=2 SV=3; Q8MYL7|Q8MYL7_CAEEL Catalase OS=Caenorhabditis elegans GN=ctl-3 PE=3 SV=1	0.00
P47208|TCPD_CAEEL T-complex protein 1 subunit delta OS=Caenorhabditis elegans GN=cct-4 PE=2 SV=1	0.00
G5EE72|G5EE72_CAEEL Protein MRP-5, isoform b OS=Caenorhabditis elegans GN=mrp-5 PE=2 SV=1; G5EEY4|G5EEY4_CAEEL Protein MRP-5, isoform a OS=Caenorhabditis elegans GN=mrp-5 PE=2 SV=1	0.00
Q9XTQ5-2|GOB1_CAEEL Isoform b of Trehalose-phosphatase OS=Caenorhabditis elegans GN=gob-1; Q9XTQ5|GOB1_CAEEL Trehalose-phosphatase OS=Caenorhabditis elegans GN=gob-1 PE=1 SV=1	0.00
Q21773|DHP1_CAEEL Dihydropyrimidinase 1 OS=Caenorhabditis elegans GN=dhp-1 PE=1 SV=2	0.00
I7J4D2|I7J4D2_CAEEL Protein HMP-1, isoform f OS=Caenorhabditis elegans GN=hmp-1 PE=4 SV=1; I7LFF2|I7LFF2_CAEEL Protein HMP-1, isoform e OS=Caenorhabditis elegans GN=hmp-1 PE=4 SV=1; I7K4K5|I7K4K5_CAEEL Protein HMP-1, isoform d OS=Caenorhabditis e	0.00
G5EC24|G5EC24_CAEEL Tyrosine-protein phosphatase non-receptor type OS=Caenorhabditis elegans GN=ptp-2 PE=2 SV=1	0.00
O17759|O17759_CAEEL Protein TKT-1 OS=Caenorhabditis elegans GN=tkt-1 PE=4 SV=1	-0.01
Q966C6|RL7A_CAEEL 60S ribosomal protein L7a OS=Caenorhabditis elegans GN=rpl-7A PE=1 SV=3; Q966C6-2|RL7A_CAEEL Isoform c of 60S ribosomal protein L7a OS=Caenorhabditis elegans GN=rpl-7A	-0.01
O44952|LONM_CAEEL Lon protease homolog, mitochondrial OS=Caenorhabditis elegans GN=C34B2.6 PE=3 SV=1	-0.01
Q95Y88|Q95Y88_CAEEL Protein R13A5.9 OS=Caenorhabditis elegans GN=CELE_R13A5.9 PE=4 SV=1	-0.01

Q95XR0|Q95XR0_CAEEL Protein Y39G10AR.8 OS=Caenorhabditis elegans GN=CELE_Y39G10AR.8 PE=4 SV=1	-0.01
Q09476-3|PXL1_CAEEL Isoform c of Paxillin homolog 1 OS=Caenorhabditis elegans GN=pxl-1; Q09476|PXL1_CAEEL Paxillin homolog 1 OS=Caenorhabditis elegans GN=pxl-1 PE=2 SV=2; Q09476-2|PXL1_CAEEL Isoform b of Paxillin homolog 1 OS=Caenorhabditis elega	-0.01
O45815|O45815_CAEEL Protein ACT-5 OS=Caenorhabditis elegans GN=act-5 PE=3 SV=1	-0.01
Q9NAH6|Q9NAH6_CAEEL Protein RSKS-1 OS=Caenorhabditis elegans GN=rsks-1 PE=4 SV=2	-0.01
Q14V28|Q14V28_CAEEL Protein ZK822.5, isoform b OS=Caenorhabditis elegans GN=CELE_ZK822.5 PE=2 SV=1; Q23616|Q23616_CAEEL Protein ZK822.5, isoform a OS=Caenorhabditis elegans GN=CELE_ZK822.5 PE=2 SV=2	-0.01
G5EFG4|G5EFG4_CAEEL Protein ABCF-2 OS=Caenorhabditis elegans GN=abcf-2 PE=3 SV=1; Q17340|Q17340_CAEEL Putative uncharacterized protein (Fragment) OS=Caenorhabditis elegans PE=2 SV=1	-0.02
Q95QW0-2|EIF3L_CAEEL Isoform b of Eukaryotic translation initiation factor 3 subunit L OS=Caenorhabditis elegans GN=eif-3.L; Q95QW0|EIF3L_CAEEL Eukaryotic translation initiation factor 3 subunit L OS=Caenorhabditis elegans GN=eif-3.L PE=3 SV=1	-0.02
Q9U3F5|Q9U3F5_CAEEL Protein ZYX-1, isoform b OS=Caenorhabditis elegans GN=zyx-1 PE=2 SV=2; H2L2F5|H2L2F5_CAEEL Protein ZYX-1, isoform d OS=Caenorhabditis elegans GN=zyx-1 PE=4 SV=1; H2L2F6|H2L2F6_CAEEL Protein ZYX-1, isoform c OS=Caenorhabditis e	-0.02
O01927|O01927_CAEEL Protein C13C4.5 OS=Caenorhabditis elegans GN=C13C4.5 PE=4 SV=1	-0.02
Q19020|DYHC_CAEEL Dynein heavy chain, cytoplasmic OS=Caenorhabditis elegans GN=dhc-1 PE=3 SV=1	-0.02
Q22922|Q22922_CAEEL Protein CDD-1 OS=Caenorhabditis elegans GN=cdd-1 PE=4 SV=1	-0.03
Q23068|Q23068_CAEEL Protein W01A11.1 OS=Caenorhabditis elegans GN=CELE_W01A11.1 PE=4 SV=1	-0.03
P49405|RL5_CAEEL 60S ribosomal protein L5 OS=Caenorhabditis elegans GN=rpl-5 PE=3 SV=1	-0.03

O01814|FABP5_CAEEL Fatty acid-binding protein homolog 5 OS=Caenorhabditis elegans GN=lbp-5 PE=3 SV=1	-0.03
Q17948|Q17948_CAEEL Protein PPTR-2, isoform a OS=Caenorhabditis elegans GN=pptr-2 PE=2 SV=1; H9G2X3|H9G2X3_CAEEL Protein PPTR-2, isoform d OS=Caenorhabditis elegans GN=pptr-2 PE=4 SV=1; A9UJN4|A9UJN4_CAEEL Protein PPTR-2, isoform c OS=Caenorhabdi	-0.03
Q23424|FZO1_CAEEL Transmembrane GTPase fzo-1 OS=Caenorhabditis elegans GN=fzo-1 PE=3 SV=1	-0.04
Q86NI2|Q86NI2_CAEEL Protein C06G3.5, isoform b OS=Caenorhabditis elegans GN=C06G3.5 PE=4 SV=1; H2KYI5|H2KYI5_CAEEL Protein C06G3.5, isoform a OS=Caenorhabditis elegans GN=C06G3.5 PE=4 SV=1	-0.04
Q09165|DIG1_CAEEL Mesocentin OS=Caenorhabditis elegans GN=dig-1 PE=1 SV=2; Q8MQ08|Q8MQ08_CAEEL Protein DIG-1, isoform b OS=Caenorhabditis elegans GN=dig-1 PE=2 SV=2	-0.04
G5EEK9|G5EEK9_CAEEL Protein VHA-5 OS=Caenorhabditis elegans GN=vha-5 PE=2 SV=1	-0.04
Q9BL19|RL17_CAEEL 60S ribosomal protein L17 OS=Caenorhabditis elegans GN=rpl-17 PE=3 SV=1; Q9BL19-2|RL17_CAEEL Isoform b of 60S ribosomal protein L17 OS=Caenorhabditis elegans GN=rpl-17	-0.04
G5EBJ7|G5EBJ7_CAEEL Fructose-1,6-bisphosphatase OS=Caenorhabditis elegans GN=fbp-1 PE=2 SV=1	-0.04
Q22781|Q22781_CAEEL Protein ACDH-7 OS=Caenorhabditis elegans GN=acdh-7 PE=3 SV=2	-0.04
G5EFF8|G5EFF8_CAEEL Protein C30H7.2, isoform a OS=Caenorhabditis elegans GN=C30H7.2 PE=2 SV=1; Q304D5|Q304D5_CAEEL Protein C30H7.2, isoform b OS=Caenorhabditis elegans GN=C30H7.2 PE=2 SV=1	-0.05
Q9U2Y2|CK5P3_CAEEL CDK5RAP3-like protein OS=Caenorhabditis elegans GN=Y113G7B.16 PE=3 SV=1	-0.05
O17071-2|PRS10_CAEEL Isoform b of Probable 26S protease regulatory subunit 10B OS=Caenorhabditis elegans GN=rpt-4; O17071|PRS10_CAEEL Probable 26S protease regulatory subunit 10B OS=Caenorhabditis elegans GN=rpt-4 PE=1 SV=2	-0.05
P34358-2|CED7_CAEEL Isoform a of ABC transporter ced-7 OS=Caenorhabditis elegans GN=ced-7; P34358-3|CED7_CAEEL Isoform b of ABC transporter ced-7 OS=Caenorhabditis elegans GN=ced-7; P34358|CED7_CAEEL ABC transporter ced-7 OS=Caenorhabditis elegan	-0.05

O17328|O17328_CAEEL Protein MCT-6 OS=Caenorhabditis elegans GN=mct-6 PE=4 SV=2	-0.05
Q22020|Q22020_CAEEL Protein R53.5 OS=Caenorhabditis elegans GN=CELE_R53.5 PE=4 SV=1	-0.05
P61866|RL12_CAEEL 60S ribosomal protein L12 OS=Caenorhabditis elegans GN=rpl-12 PE=3 SV=1	-0.05
Q19537|RFA1_CAEEL Probable replication factor A 73 kDa subunit OS=Caenorhabditis elegans GN=rpa-1 PE=1 SV=1	-0.05
Q9N492|Q9N492_CAEEL Protein PINN-1 OS=Caenorhabditis elegans GN=pinn-1 PE=4 SV=2	-0.06
Q9TXP0|RS27_CAEEL 40S ribosomal protein S27 OS=Caenorhabditis elegans GN=rps-27 PE=1 SV=3	-0.06
P46769|RSSA_CAEEL 40S ribosomal protein SA OS=Caenorhabditis elegans GN=rps-0 PE=1 SV=3	-0.06
O17607|O17607_CAEEL Protein RUVB-1 OS=Caenorhabditis elegans GN=ruvb-1 PE=1 SV=2	-0.06
Q19200|STO1_CAEEL Stomatin-1 OS=Caenorhabditis elegans GN=sto-1 PE=2 SV=2; G8JY63|G8JY63_CAEEL Protein STO-1, isoform b OS=Caenorhabditis elegans GN=sto-1 PE=2 SV=1	-0.06
Q95QI2|Q95QI2_CAEEL Protein LIM-8, isoform b OS=Caenorhabditis elegans GN=lim-8 PE=2 SV=1; Q95QI3|Q95QI3_CAEEL Protein LIM-8, isoform a OS=Caenorhabditis elegans GN=lim-8 PE=2 SV=1; Q8MNT0|Q8MNT0_CAEEL Protein LIM-8, isoform c OS=Caenorhabditis e	-0.07
O18693|O18693_CAEEL Protein ACS-2 OS=Caenorhabditis elegans GN=acs-2 PE=4 SV=1	-0.07
O45781|O45781_CAEEL Protein DRR-2 OS=Caenorhabditis elegans GN=drr-2 PE=4 SV=1	-0.07
P62784|H4_CAEEL Histone H4 OS=Caenorhabditis elegans GN=his-1 PE=1 SV=2	-0.07
Q9XVA6|Q9XVA6_CAEEL Protein CYP-37A1 OS=Caenorhabditis elegans GN=cyp-37a1 PE=3 SV=2	-0.07
Q23588|Q23588_CAEEL Protein UPP-1 OS=Caenorhabditis elegans GN=upp-1 PE=4 SV=2	-0.08

Q86S28|Q86S28_CAEEL Protein LIN-40, isoform d OS=Caenorhabditis elegans GN=lin-40 PE=2 SV=1; Q76NP4|Q76NP4_CAEEL Protein LIN-40, isoform b OS=Caenorhabditis elegans GN=lin-40 PE=2 SV=1; O61907|O61907_CAEEL Protein LIN-40, isoform a OS=Caenorhabdi	-0.08
P90889|P90889_CAEEL Protein F55H12.4 OS=Caenorhabditis elegans GN=CELE_F55H12.4 PE=4 SV=1	-0.09
I7FN62|I7FN62_CAEEL Rab-2 (Fragment) OS=Caenorhabditis elegans GN=unc-108 PE=2 SV=1; O01577|O01577_CAEEL Protein UNC-108 OS=Caenorhabditis elegans GN=unc-108 PE=2 SV=1	-0.09
Q9N302|Q9N302_CAEEL Protein ACS-13 OS=Caenorhabditis elegans GN=acs-13 PE=4 SV=1	-0.10
Q2PJ74|Q2PJ74_CAEEL Protein AMAN-2 OS=Caenorhabditis elegans GN=aman-2 PE=4 SV=1	-0.10
Q7JMA4|Q7JMA4_CAEEL Protein F11C1.5, isoform b OS=Caenorhabditis elegans GN=CELE_F11C1.5 PE=2 SV=2; Q19346|Q19346_CAEEL Protein F11C1.5, isoform a OS=Caenorhabditis elegans GN=CELE_F11C1.5 PE=2 SV=3; B6VQ59|B6VQ59_CAEEL Protein F11C1.5, isoform d	-0.10
Q94241|Q94241_CAEEL Protein SEC-22 OS=Caenorhabditis elegans GN=sec-22 PE=4 SV=2	-0.10
P90983|P90983_CAEEL Protein RPS-29 OS=Caenorhabditis elegans GN=rps-29 PE=4 SV=2	-0.11
G5EG58|G5EG58_CAEEL Protein PGP-9 OS=Caenorhabditis elegans GN=pgp-9 PE=3 SV=1	-0.11
Q21355|GST4_CAEEL Glutathione S-transferase 4 OS=Caenorhabditis elegans GN=gst-4 PE=2 SV=1	-0.11
G5EEG4|G5EEG4_CAEEL Mitochondrial methylmalonyl-CoA epimerase OS=Caenorhabditis elegans GN=mce-1 PE=2 SV=1	-0.11
A3QMC5|A3QMC5_CAEEL Protein RPL-34 OS=Caenorhabditis elegans GN=rpl-34 PE=4 SV=1	-0.11
G5EFD1|G5EFD1_CAEEL Protein VAB-10, isoform i OS=Caenorhabditis elegans GN=vab-10 PE=2 SV=1	-0.11
P39745-2|SUR1_CAEEL Isoform a of Mitogen-activated protein kinase mpk-1 OS=Caenorhabditis elegans GN=mpk-1; P39745|SUR1_CAEEL Mitogen-activated protein kinase mpk-1 OS=Caenorhabditis elegans GN=mpk-1 PE=1 SV=2	-0.11

G5EBZ4|LE418_CAEEL Protein let-418 OS=Caenorhabditis elegans GN=let-418 PE=1 SV=1	-0.11
Q20117|GSH1_CAEEL Glutamate--cysteine ligase OS=Caenorhabditis elegans GN=gcs-1 PE=1 SV=2	-0.12
Q0G839|Q0G839_CAEEL Protein M106.3, isoform b OS=Caenorhabditis elegans GN=CELE_M106.3 PE=4 SV=1; Q0G840|Q0G840_CAEEL Protein M106.3, isoform a OS=Caenorhabditis elegans GN=CELE_M106.3 PE=4 SV=1	-0.13
O18033|O18033_CAEEL Protein NRA-2, isoform a OS=Caenorhabditis elegans GN=nra-2 PE=2 SV=1; A5JYX8|A5JYX8_CAEEL Protein NRA-2, isoform b OS=Caenorhabditis elegans GN=nra-2 PE=2 SV=1	-0.13
Q9XVQ9|Q9XVQ9_CAEEL Protein ELO-2 OS=Caenorhabditis elegans GN=elo-2 PE=4 SV=1	-0.13
O01925|O01925_CAEEL Protein MBOA-6, isoform a OS=Caenorhabditis elegans GN=mboa-6 PE=2 SV=2; Q86DC4|Q86DC4_CAEEL Protein MBOA-6, isoform b OS=Caenorhabditis elegans GN=mboa-6 PE=2 SV=1	-0.14
P34712|PGP1_CAEEL Multidrug resistance protein pgp-1 OS=Caenorhabditis elegans GN=pgp-1 PE=1 SV=2	-0.15
P91398|P91398_CAEEL Protein CEY-3 OS=Caenorhabditis elegans GN=cey-3 PE=4 SV=1	-0.15
Q22135|Q22135_CAEEL Protein T04A8.6 OS=Caenorhabditis elegans GN=CELE_T04A8.6 PE=4 SV=1	-0.16
O61219|O61219_CAEEL Protein K07H8.3 OS=Caenorhabditis elegans GN=CELE_K07H8.3 PE=4 SV=1	-0.16
Q19360|UBA3_CAEEL NEDD8-activating enzyme E1 catalytic subunit OS=Caenorhabditis elegans GN=uba-3 PE=2 SV=2	-0.16
Q9TZ33|Q9TZ33_CAEEL Protein UCR-2.3 OS=Caenorhabditis elegans GN=ucr-2.3 PE=3 SV=1	-0.16
O01755|O01755_CAEEL Protein APM-1 OS=Caenorhabditis elegans GN=apm-1 PE=4 SV=2	-0.18
Q9N2N3|Q9N2N3_CAEEL Protein MRP-1, isoform a OS=Caenorhabditis elegans GN=mrp-1 PE=2 SV=1; Q95QE2|Q95QE2_CAEEL Protein MRP-1, isoform b OS=Caenorhabditis elegans GN=mrp-1 PE=2 SV=1; Q8MQ16|Q8MQ16_CAEEL Protein MRP-1, isoform c OS=Caenorhabditis e	-0.18

Q9Y041|HGD_CAEEL Homogentisate 1,2-dioxygenase OS=Caenorhabditis elegans GN=hgo-1 PE=1 SV=2	-0.18
Q18994|Q18994_CAEEL Protein D2085.3 OS=Caenorhabditis elegans GN=CELE_D2085.3 PE=4 SV=1	-0.19
Q9GYJ9|Q9GYJ9_CAEEL Protein SNX-1 OS=Caenorhabditis elegans GN=snx-1 PE=1 SV=1	-0.19
Q1ZXU6|Q1ZXU6_CAEEL Protein PGP-6, isoform b OS=Caenorhabditis elegans GN=pgp-6 PE=2 SV=2; G1K0X0|G1K0X0_CAEEL Protein PGP-6, isoform c OS=Caenorhabditis elegans GN=pgp-6 PE=2 SV=1; Q22656|Q22656_CAEEL Protein PGP-6, isoform a OS=Caenorhabditis e	-0.19
O01422|CSN2_CAEEL COP9 signalosome complex subunit 2 OS=Caenorhabditis elegans GN=csn-2 PE=1 SV=2	-0.19
O45734|O45734_CAEEL Protein CPL-1, isoform a OS=Caenorhabditis elegans GN=cpl-1 PE=3 SV=1; H9G333|H9G333_CAEEL Protein CPL-1, isoform b OS=Caenorhabditis elegans GN=cpl-1 PE=3 SV=1	-0.21
Q23121|RSP1_CAEEL Probable splicing factor, arginine/serine-rich 1 OS=Caenorhabditis elegans GN=rsp-1 PE=3 SV=1; Q23121-2|RSP1_CAEEL Isoform b of Probable splicing factor, arginine/serine-rich 1 OS=Caenorhabditis elegans GN=rsp-1; Q23121-3|RSP1_C	-0.21
P34713|PGP3_CAEEL Multidrug resistance protein pgp-3 OS=Caenorhabditis elegans GN=pgp-3 PE=2 SV=2	-0.21
Q27493|Q27493_CAEEL DNA-directed RNA polymerase OS=Caenorhabditis elegans GN=rpoa-2 PE=3 SV=1	-0.21
Q9GUP2|Q9GUP2_CAEEL Protein EEL-1 OS=Caenorhabditis elegans GN=eel-1 PE=4 SV=2	-0.21
O16297|O16297_CAEEL Protein MCM-7 OS=Caenorhabditis elegans GN=mcm-7 PE=3 SV=1	-0.23
Q93890|SRF3_CAEEL UDP-galactose/UDP-N-acetylglucosamine transporter srf-3 OS=Caenorhabditis elegans GN=srf-3 PE=1 SV=5; G5EFD3|G5EFD3_CAEEL Protein SRF-3, isoform b OS=Caenorhabditis elegans GN=srf-3 PE=2 SV=1	-0.23
O16454|O16454_CAEEL Protein TAG-196 OS=Caenorhabditis elegans GN=tag-196 PE=3 SV=2	-0.23

O02161|TIM44_CAEEL Probable mitochondrial import inner membrane translocase subunit tim-44 OS=Caenorhabditis elegans GN=tim-44 PE=3 SV=1	-0.23
Q22267|PLC2_CAEEL Putative 1-acyl-sn-glycerol-3-phosphate acyltransferase acl-2 OS=Caenorhabditis elegans GN=acl-2 PE=3 SV=1; I2HA82|I2HA82_CAEEL Protein ACL-2, isoform b OS=Caenorhabditis elegans GN=acl-2 PE=4 SV=1	-0.23
O01965|O01965_CAEEL Protein ARI-1 OS=Caenorhabditis elegans GN=ari-1 PE=4 SV=3	-0.24
P46559|KICB2_CAEEL Choline kinase B2 OS=Caenorhabditis elegans GN=ckb-2 PE=1 SV=2	-0.25
Q21993|PFD5_CAEEL Probable prefoldin subunit 5 OS=Caenorhabditis elegans GN=pfd-5 PE=2 SV=1	-0.27
P90980-2|KPC2_CAEEL Isoform a of Protein kinase C-like 2 OS=Caenorhabditis elegans GN=pkc-2; P90980|KPC2_CAEEL Protein kinase C-like 2 OS=Caenorhabditis elegans GN=pkc-2 PE=2 SV=2; G8JY36|G8JY36_CAEEL Protein kinase C OS=Caenorhabditis elegans GN	-0.27
Q9N3A9|Q9N3A9_CAEEL Protein Y54G2A.4 OS=Caenorhabditis elegans GN=CELE_Y54G2A.4 PE=4 SV=3	-0.28
G5EGP8|G5EGP8_CAEEL Cathepsin Z-like enzyme OS=Caenorhabditis elegans GN=cpz-1 PE=3 SV=1	-0.28
Q03604|RIR1_CAEEL Ribonucleoside-diphosphate reductase large subunit OS=Caenorhabditis elegans GN=rnr-1 PE=3 SV=1	-0.29
Q9XW01|Q9XW01_CAEEL Protein Y54G11A.7 OS=Caenorhabditis elegans GN=CELE_Y54G11A.7 PE=4 SV=2	-0.29
E9P8A2|E9P8A2_CAEEL Protein ERFA-3, isoform b OS=Caenorhabditis elegans GN=erfa-3 PE=2 SV=1	-0.29
P91544|P91544_CAEEL Protein ZC204.12 OS=Caenorhabditis elegans GN=CELE_ZC204.12 PE=4 SV=1	-0.29
Q21353|EAA3_CAEEL Putative sodium-dependent excitatory amino acid transporter glt-3 OS=Caenorhabditis elegans GN=glt-3 PE=1 SV=1	-0.35
Q09582|METH_CAEEL Probable methionine synthase OS=Caenorhabditis elegans GN=nos-1 PE=1 SV=1	-0.35

G5EC97|G5EC97_CAEEL Protein CYP-29A2 OS=Caenorhabditis elegans GN=cyp-29a2 PE=3 SV=1	-0.36
O01683|SSP1B_CAEEL FACT complex subunit ssrp1-B OS=Caenorhabditis elegans GN=hmg-3 PE=3 SV=1; P41848|SSP1A_CAEEL FACT complex subunit SSRP1-A OS=Caenorhabditis elegans GN=hmg-4 PE=3 SV=1	-0.37
Q21452|LIAS_CAEEL Lipoyl synthase, mitochondrial OS=Caenorhabditis elegans GN=M01F1.3 PE=3 SV=1	-0.37
Q20546|Q20546_CAEEL Protein F47G9.1 OS=Caenorhabditis elegans GN=CELE_F47G9.1 PE=4 SV=1	-0.37
Q23651|ELP3_CAEEL Probable elongator complex protein 3 OS=Caenorhabditis elegans GN=elpc-3 PE=3 SV=2	-0.38
Q21038|Q21038_CAEEL Protein VER-3 OS=Caenorhabditis elegans GN=ver-3 PE=4 SV=1	-0.38
Q9TW67|NGLY1_CAEEL Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase OS=Caenorhabditis elegans GN=png-1 PE=1 SV=1	-0.39
P34703|SPT6H_CAEEL Suppressor of Ty 6 homolog OS=Caenorhabditis elegans GN=emb-5 PE=1 SV=1	-0.40
P17139-2|CO4A1_CAEEL Isoform b of Collagen alpha-1(IV) chain OS=Caenorhabditis elegans GN=emb-9; P17139|CO4A1_CAEEL Collagen alpha-1(IV) chain OS=Caenorhabditis elegans GN=emb-9 PE=1 SV=5	-0.44
P34537|BRE1_CAEEL E3 ubiquitin-protein ligase bre-1 OS=Caenorhabditis elegans GN=rfp-1 PE=1 SV=2; P34537-2|BRE1_CAEEL Isoform a of E3 ubiquitin-protein ligase bre-1 OS=Caenorhabditis elegans GN=rfp-1	-0.46
Q6A582|Q6A582_CAEEL Protein ZBP-1, isoform b OS=Caenorhabditis elegans GN=zbp-1 PE=2 SV=1; K8ERX1|K8ERX1_CAEEL Protein ZBP-1, isoform d OS=Caenorhabditis elegans GN=zbp-1 PE=4 SV=1; Q21605|Q21605_CAEEL Protein ZBP-1, isoform a OS=Caenorhabditis e	-0.58
Q8WSL9|Q8WSL9_CAEEL Protein H43I07.3 OS=Caenorhabditis elegans GN=CELE_H43I07.3 PE=4 SV=1	-0.64
Q19240|Q19240_CAEEL Protein UNC-115, isoform a OS=Caenorhabditis elegans GN=unc-115 PE=2 SV=2; Q95QM5|Q95QM5_CAEEL Protein UNC-115, isoform b OS=Caenorhabditis elegans GN=unc-115 PE=1 SV=1; O77133|O77133_CAEEL Putative actin-binding protein UNC-1	-0.65

D5MCN2|D5MCN2_CAEEL Protein LARP-1, isoform b OS=Caenorhabditis elegans GN=larp-1 PE=4 SV=2; H2KZ23|H2KZ23_CAEEL Protein LARP-1, isoform a OS=Caenorhabditis elegans GN=larp-1 PE=4 SV=1	-0.66
O18215|O18215_CAEEL Protein Y53C12B.1 OS=Caenorhabditis elegans GN=CELE_Y53C12B.1 PE=4 SV=1	-0.67
Q95XU3|Q95XU3_CAEEL E3 ubiquitin-protein ligase OS=Caenorhabditis elegans GN=wwp-1 PE=2 SV=2; Q9N2Z7|Q9N2Z7_CAEEL E3 ubiquitin-protein ligase OS=Caenorhabditis elegans GN=wwp-1 PE=1 SV=2	-0.75
Q9TYS3|Q9TYS3_CAEEL Ferritin OS=Caenorhabditis elegans GN=ftn-2 PE=1 SV=1	-0.92
O61815|O61815_CAEEL Protein B0511.6 OS=Caenorhabditis elegans GN=B0511.6 PE=3 SV=2	-1.06
Q19493|Q19493_CAEEL Protein F16D3.4 OS=Caenorhabditis elegans GN=CELE_F16D3.4 PE=4 SV=1	-1.11
P54688|BCAT_CAEEL Branched-chain-amino-acid aminotransferase, cytosolic OS=Caenorhabditis elegans GN=bcat-1 PE=2 SV=2	-1.47