Table 2.3. Proteins identified and quantified 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
O61848|O61848_CAEEL Protein K03E5.2, isoform a OS=Caenorhabditis elegans GN=CELE_K03E5.2 PE=2 SV=2; H2KZW0|H2KZW0_CAEEL Protein K03E5.2, isoform b OS=Caenorhabditis elegans GN=CELE_K03E5.2 PE=4 SV=1; H2KZW1|H2KZW1_CAEEL Protein K03E5.2, isoform d	2.61
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
Q18529|Q18529_CAEEL Protein C39D10.7 OS=Caenorhabditis elegans GN=C39D10.7 PE=1 SV=3	2.14
Q09936|YSE2_CAEEL Uncharacterized protein C53C9.2 OS=Caenorhabditis elegans GN=C53C9.2 PE=3 SV=2	1.98
O45577|O45577_CAEEL Protein CPF-2 OS=Caenorhabditis elegans GN=cpf-2 PE=4 SV=1	1.93
P90879|P90879_CAEEL Protein F49C12.9 OS=Caenorhabditis elegans GN=CELE_F49C12.9 PE=1 SV=1	1.88
Q09665|TNNC2_CAEEL Troponin C, isoform 2 OS=Caenorhabditis elegans GN=tnc-2 PE=2 SV=1	1.85
O44727|O44727_CAEEL Protein CPN-4 OS=Caenorhabditis elegans GN=cpn-4 PE=4 SV=3	1.72
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
Q9BL56|Q9BL56_CAEEL Protein Y65B4A.8 OS=Caenorhabditis elegans GN=CELE_Y65B4A.8 PE=3 SV=3	1.68

Q18547|Q18547_CAEEL Protein RFC-3 OS=Caenorhabditis elegans GN=rfc-3 PE=1 SV=1	1.52
Q21754|Q21754_CAEEL Protein PLC-4 OS=Caenorhabditis elegans GN=plc-4 PE=4 SV=1	1.52
P55956|ASP3_CAEEL Aspartic protease 3 OS=Caenorhabditis elegans GN=asp-3 PE=1 SV=2	1.51
Q94207|Q94207_CAEEL Protein F38A5.7 OS=Caenorhabditis elegans GN=CELE_F38A5.7 PE=1 SV=1	1.50
Q9U3N4|INX6_CAEEL Innexin-6 OS=Caenorhabditis elegans GN=inx-6 PE=2 SV=1	1.47
Q7Z072|Q7Z072_CAEEL Protein TNT-2, isoform a OS=Caenorhabditis elegans GN=tnt-2 PE=2 SV=1; Q7Z071|Q7Z071_CAEEL Protein TNT-2, isoform b OS=Caenorhabditis elegans GN=tnt-2 PE=2 SV=1	1.46
Q8IG33|Q8IG33_CAEEL Protein BMY-1 OS=Caenorhabditis elegans GN=bmy-1 PE=1 SV=1	1.34
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
G5ED75|G5ED75_CAEEL Kinesin like protein (Klp-7) OS=Caenorhabditis elegans GN=klp-7 PE=2 SV=1; Q9XU12|Q9XU12_CAEEL Protein KLP-7, isoform a OS=Caenorhabditis elegans GN=klp-7 PE=2 SV=1; Q8MYB5|Q8MYB5_CAEEL Kinesin OS=Caenorhabditis elegans GN=KLP	1.29
P02567|MYO1_CAEEL Myosin-1 OS=Caenorhabditis elegans GN=let-75 PE=2 SV=3	1.28
Q17778|NUC1_CAEEL Deoxyribonuclease-2 OS=Caenorhabditis elegans GN=nuc-1 PE=3 SV=1	1.27
O17620|O17620_CAEEL Protein C29F7.1 OS=Caenorhabditis elegans GN=C29F7.1 PE=4 SV=1	1.27
O44144|O44144_CAEEL Protein PERM-4 OS=Caenorhabditis elegans GN=perm-4 PE=4 SV=1	1.26
Q6QUR0|Q6QUR0_CAEEL Serine or cysteine protease inhibitor OS=Caenorhabditis elegans GN=SRP-2 PE=2 SV=1; O17365|O17365_CAEEL Protein SRP-2 OS=Caenorhabditis elegans GN=srp-2 PE=2 SV=1	1.26

O45379|ARL3_CAEEL ADP-ribosylation factor-like protein 3 OS=Caenorhabditis elegans GN=arl-3 PE=1 SV=1	1.25
Q7JP52|Q7JP52_CAEEL Protein HSP-17, isoform b OS=Caenorhabditis elegans GN=hsp-17 PE=2 SV=1; Q20660|Q20660_CAEEL Protein HSP-17, isoform a OS=Caenorhabditis elegans GN=hsp-17 PE=2 SV=1	1.22
P12845|MYO2_CAEEL Myosin-2 OS=Caenorhabditis elegans GN=myo-2 PE=2 SV=2	1.21
P34696|HSP11_CAEEL Heat shock protein Hsp-16.1/Hsp-16.11 OS=Caenorhabditis elegans GN=hsp-16.1 PE=2 SV=1; Q21062|Q21062_CAEEL Heat shock protein 16-1 OS=Caenorhabditis elegans PE=2 SV=1	1.21
P34328|HSP10_CAEEL Heat shock protein Hsp-12.2 OS=Caenorhabditis elegans GN=hsp-12.2 PE=3 SV=1	1.20
Q18625|Q18625_CAEEL Protein LEC-4 OS=Caenorhabditis elegans GN=lec-4 PE=2 SV=1; Q9GNP5|Q9GNP5_CAEEL Galectin LEC-4 OS=Caenorhabditis elegans GN=lec-4 PE=2 SV=1	1.17
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
Q9XXI6|Q9XXI6_CAEEL Protein Y17G7B.10, isoform a OS=Caenorhabditis elegans GN=CELE_Y17G7B.10 PE=2 SV=2; Q9XXI5|Q9XXI5_CAEEL Protein Y17G7B.10, isoform b OS=Caenorhabditis elegans GN=CELE_Y17G7B.10 PE=2 SV=1	1.12
P34444-3|YL86_CAEEL Isoform c of Uncharacterized protein F54C8.6 OS=Caenorhabditis elegans GN=F54C8.6	1.09
A4UVK2|A4UVK2_CAEEL Protein C44C10.9, isoform b OS=Caenorhabditis elegans GN=C44C10.9 PE=2 SV=1; J7SF86|J7SF86_CAEEL Protein C44C10.9, isoform d OS=Caenorhabditis elegans GN=C44C10.9 PE=4 SV=1	1.09
Q9BL07|PLBL3_CAEEL Putative phospholipase B-like 3 OS=Caenorhabditis elegans GN=Y54F10AM.8 PE=1 SV=1	1.09
Q965G5|Q965G5_CAEEL Protein MAK-2, isoform b OS=Caenorhabditis elegans GN=mak-2 PE=4 SV=2; H2KZB0|H2KZB0_CAEEL Protein MAK-2, isoform a OS=Caenorhabditis elegans GN=mak-2 PE=4 SV=1	1.07

Q22670|RBGPR_CAEEL Rab3 GTPase-activating protein regulatory subunit OS=Caenorhabditis elegans GN=rbg-2 PE=3 SV=1; Q22670-2|RBGPR_CAEEL Isoform b of Rab3 GTPase-activating protein regulatory subunit OS=Caenorhabditis elegans GN=rbg-2	1.07
P34885|KPC1B_CAEEL Protein kinase C-like 1B OS=Caenorhabditis elegans GN=pkc-1 PE=2 SV=2; P34885-2|KPC1B_CAEEL Isoform b of Protein kinase C-like 1B OS=Caenorhabditis elegans GN=pkc-1; H9G2Y7|H9G2Y7_CAEEL Protein PKC-1, isoform c OS=Caenorhabditi	1.06
Q9TZF3|Q9TZF3_CAEEL Protein INS-31 OS=Caenorhabditis elegans GN=ins-31 PE=4 SV=1	1.05
H2L0J4|H2L0J4_CAEEL Protein T07D3.9, isoform b OS=Caenorhabditis elegans GN=CELE_T07D3.9 PE=4 SV=1; O16725|O16725_CAEEL Protein T07D3.9, isoform a OS=Caenorhabditis elegans GN=CELE_T07D3.9 PE=4 SV=3	1.02
G5EFP4|G5EFP4_CAEEL Protein SYM-1 OS=Caenorhabditis elegans GN=sym-1 PE=2 SV=1	1.01
Q18012|Q18012_CAEEL Protein C15C7.5 OS=Caenorhabditis elegans GN=C15C7.5 PE=4 SV=1	1.00
D6R8W9|D6R8W9_CAEEL Protein RBC-1, isoform a OS=Caenorhabditis elegans GN=rbc-1 PE=4 SV=4; J7S122|J7S122_CAEEL Protein RBC-1, isoform b OS=Caenorhabditis elegans GN=rbc-1 PE=4 SV=2	1.00
Q22308|Q22308_CAEEL Protein DDX-19, isoform a OS=Caenorhabditis elegans GN=ddx-19 PE=2 SV=2; B7WN80|B7WN80_CAEEL Protein DDX-19, isoform d OS=Caenorhabditis elegans GN=ddx-19 PE=2 SV=1; O18056|O18056_CAEEL Protein DDX-19, isoform b OS=Caenorhabdi	1.00
O16319|O16319_CAEEL Protein C10B5.3 OS=Caenorhabditis elegans GN=C10B5.3 PE=4 SV=2	0.99
Q9NEZ5|Q9NEZ5_CAEEL Protein UNC-95 OS=Caenorhabditis elegans GN=unc-95 PE=1 SV=2	0.99
Q21831|Q21831_CAEEL Protein SNFC-5 OS=Caenorhabditis elegans GN=snfc-5 PE=1 SV=1	0.96
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

D9PTN8|D9PTN8_CAEEL Protein Y43F8B.1, isoform e OS=Caenorhabditis elegans GN=CELE_Y43F8B.1 PE=2 SV=1; B7FAR9|B7FAR9_CAEEL Protein Y43F8B.1, isoform d OS=Caenorhabditis elegans GN=CELE_Y43F8B.1 PE=2 SV=1	0.95
Q19661|Q19661_CAEEL Protein F21C10.9 OS=Caenorhabditis elegans GN=CELE_F21C10.9 PE=4 SV=3	0.93
Q09531|YQP4_CAEEL Uncharacterized protein F07F6.4 OS=Caenorhabditis elegans GN=F07F6.4 PE=4 SV=2	0.93
F5GU60|F5GU60_CAEEL Protein T21F4.1, isoform b OS=Caenorhabditis elegans GN=CELE_T21F4.1 PE=4 SV=1; H2KZS0|H2KZS0_CAEEL Protein T21F4.1, isoform a OS=Caenorhabditis elegans GN=CELE_T21F4.1 PE=4 SV=1	0.93
Q21243|Q21243_CAEEL Protein ACDH-8 OS=Caenorhabditis elegans GN=acdh-8 PE=3 SV=1	0.90
Q09596|GST5_CAEEL Probable glutathione S-transferase 5 OS=Caenorhabditis elegans GN=gst-5 PE=1 SV=1; G3MTX8|G3MTX8_CAEEL Protein GST-5, isoform c OS=Caenorhabditis elegans GN=gst-5 PE=2 SV=1	0.90
Q21000|Q21000_CAEEL Protein MYO-5 OS=Caenorhabditis elegans GN=myo-5 PE=4 SV=1	0.89
P91253|GST7_CAEEL Probable glutathione S-transferase 7 OS=Caenorhabditis elegans GN=gst-7 PE=3 SV=1	0.87
O01884|COQ6_CAEEL Probable ubiquinone biosynthesis monooxygenase coq-6 OS=Caenorhabditis elegans GN=coq-6 PE=3 SV=2	0.87
G5EF01|G5EF01_CAEEL Protein TBB-6 OS=Caenorhabditis elegans GN=tbb-6 PE=3 SV=1	0.86
G5ED31|G5ED31_CAEEL Protein UCR-2.1, isoform a OS=Caenorhabditis elegans GN=ucr-2.1 PE=2 SV=1; G5EDD1|G5EDD1_CAEEL Protein UCR-2.1, isoform b OS=Caenorhabditis elegans GN=ucr-2.1 PE=2 SV=1	0.86
O17612|O17612_CAEEL Protein ECH-1 OS=Caenorhabditis elegans GN=ech-1 PE=4 SV=1	0.85
Q9BKU2|Q9BKU2_CAEEL Protein Y37E3.11, isoform a OS=Caenorhabditis elegans GN=CELE_Y37E3.11 PE=2 SV=1; A9D2X7|A9D2X7_CAEEL Protein Y37E3.11, isoform b OS=Caenorhabditis elegans GN=CELE_Y37E3.11 PE=2 SV=1	0.85

G5EFS2|G5EFS2_CAEEL Neural RNA-binding protein MSI-1 OS=Caenorhabditis elegans GN=msi-1 PE=2 SV=1	0.85
Q9BL33|Q9BL33_CAEEL Protein Y71H2AM.4 OS=Caenorhabditis elegans GN=CELE_Y71H2AM.4 PE=4 SV=1	0.84
Q20992|Q20992_CAEEL Acyl-coenzyme A oxidase OS=Caenorhabditis elegans GN=CELE_F58F9.7 PE=3 SV=1	0.84
G5EFE3|G5EFE3_CAEEL Protein H03A11.2 OS=Caenorhabditis elegans GN=CELE_H03A11.2 PE=4 SV=2	0.83
P34442|PTP5_CAEEL Probable tyrosine-protein phosphatase F54C8.4 OS=Caenorhabditis elegans GN=F54C8.4 PE=2 SV=1	0.83
Q27371|TNNT_CAEEL Troponin T OS=Caenorhabditis elegans GN=mup-2 PE=2 SV=1	0.83
Q9NAF4|Q9NAF4_CAEEL Protein OIG-3 OS=Caenorhabditis elegans GN=oig-3 PE=4 SV=1	0.83
O45228|PROD_CAEEL Proline dehydrogenase 1, mitochondrial OS=Caenorhabditis elegans GN=B0513.5 PE=3 SV=2	0.83
P98080|UCR1_CAEEL Cytochrome b-c1 complex subunit 1, mitochondrial OS=Caenorhabditis elegans GN=ucr-1 PE=3 SV=2	0.80
P91001|CSN5_CAEEL COP9 signalosome complex subunit 5 OS=Caenorhabditis elegans GN=csn-5 PE=1 SV=1	0.78
Q9U3K2|Q9U3K2_CAEEL Protein F10B5.8 OS=Caenorhabditis elegans GN=CELE_F10B5.8 PE=4 SV=2	0.78
Q9XWL1|Q9XWL1_CAEEL Protein TTR-17 OS=Caenorhabditis elegans GN=ttr-17 PE=4 SV=1	0.77
Q95XP5|Q95XP5_CAEEL Protein MCA-3, isoform b OS=Caenorhabditis elegans GN=mca-3 PE=2 SV=1; O76832|O76832_CAEEL Calcium ATPase OS=Caenorhabditis elegans GN=mca-3 PE=2 SV=1	0.77
Q9TXT9|Q9TXT9_CAEEL Protein BCMO-2 OS=Caenorhabditis elegans GN=bcmo-2 PE=4 SV=2	0.77
Q21465|Q21465_CAEEL Protein M02D8.1 OS=Caenorhabditis elegans GN=CELE_M02D8.1 PE=4 SV=1	0.76
G5EC87|G5EC87_CAEEL Protein ZK1307.8 OS=Caenorhabditis elegans GN=CELE_ZK1307.8 PE=4 SV=1	0.76

P91127|YBYK_CAEEL TPPP family protein C32E8.3 OS=Caenorhabditis elegans GN=C32E8.3 PE=1 SV=1	0.76
Q86B36|Q86B36_CAEEL Protein FARS-1, isoform b OS=Caenorhabditis elegans GN=fars-1 PE=2 SV=1; Q9GYS8|Q9GYS8_CAEEL Protein FARS-1, isoform a OS=Caenorhabditis elegans GN=fars-1 PE=2 SV=1	0.75
Q10937-2|YWS1_CAEEL Isoform b of Uncharacterized protein B0310.1 OS=Caenorhabditis elegans GN=B0310.1; Q10937|YWS1_CAEEL Uncharacterized protein B0310.1 OS=Caenorhabditis elegans GN=B0310.1 PE=4 SV=2	0.75
Q93930|Q93930_CAEEL Protein PRX-14 OS=Caenorhabditis elegans GN=prx-14 PE=4 SV=1	0.74
P34329|PDIA4_CAEEL Probable protein disulfide-isomerase A4 OS=Caenorhabditis elegans GN=C14B9.2 PE=3 SV=2	0.74
Q95ZR6|Q95ZR6_CAEEL Protein K09G1.1, isoform b OS=Caenorhabditis elegans GN=CELE_K09G1.1 PE=2 SV=1	0.74
Q23098|Q23098_CAEEL Protein NUO-6 OS=Caenorhabditis elegans GN=nuo-6 PE=4 SV=2	0.73
Q21624-2|CORO_CAEEL Isoform a of Coronin-like protein cor-1 OS=Caenorhabditis elegans GN=cor-1; Q21624|CORO_CAEEL Coronin-like protein cor-1 OS=Caenorhabditis elegans GN=cor-1 PE=3 SV=2; Q21624-4|CORO_CAEEL Isoform d of Coronin-like protein cor-1	0.73
O17799|O17799_CAEEL Major sperm protein OS=Caenorhabditis elegans GN=CELE_F13A7.1 PE=3 SV=1	0.73
Q19564|OXDD1_CAEEL D-aspartate oxidase 1 OS=Caenorhabditis elegans GN=F18E3.7 PE=1 SV=1	0.72
H2L0I3|H2L0I3_CAEEL Protein LFI-1, isoform d OS=Caenorhabditis elegans GN=lfi-1 PE=4 SV=1; Q45EJ8|Q45EJ8_CAEEL Protein LFI-1, isoform b OS=Caenorhabditis elegans GN=lfi-1 PE=4 SV=1	0.72
Q17334|ADH1_CAEEL Alcohol dehydrogenase 1 OS=Caenorhabditis elegans GN=sodh-1 PE=1 SV=2	0.72
Q17512|Q17512_CAEEL Protein B0491.5 OS=Caenorhabditis elegans GN=B0491.5 PE=4 SV=1	0.72
Q86NJ7|Q86NJ7_CAEEL Protein DHS-2, isoform c OS=Caenorhabditis elegans GN=dhs-2 PE=2 SV=1; O01758|O01758_CAEEL Protein DHS-2, isoform a OS=Caenorhabditis elegans GN=dhs-2 PE=2 SV=2	0.72

Q19126|Q19126_CAEEL Protein ASB-2 OS=Caenorhabditis elegans GN=asb-2 PE=4 SV=1	0.71
Q9U263|Q9U263_CAEEL Protein SET-26 OS=Caenorhabditis elegans GN=set-26 PE=4 SV=3; O44498|O44498_CAEEL Protein SET-9 OS=Caenorhabditis elegans GN=set-9 PE=4 SV=1	0.71
Q20203|Q20203_CAEEL Calsequestrin OS=Caenorhabditis elegans GN=csq-1 PE=3 SV=1	0.71
Q18596|Q18596_CAEEL Protein C44B7.7 OS=Caenorhabditis elegans GN=C44B7.7 PE=4 SV=1	0.71
Q18968|Q18968_CAEEL Protein SCP-1, isoform a OS=Caenorhabditis elegans GN=scp-1 PE=2 SV=3	0.71
P90758|P90758_CAEEL Protein C27A7.5, isoform a OS=Caenorhabditis elegans GN=C27A7.5 PE=2 SV=2; Q9U3P0|Q9U3P0_CAEEL Protein C27A7.5, isoform c OS=Caenorhabditis elegans GN=C27A7.5 PE=2 SV=1; A5Z2U5|A5Z2U5_CAEEL Protein C27A7.5, isoform d OS=Caenor	0.70
Q7YZT6-2|TPS1_CAEEL Isoform b of Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1 OS=Caenorhabditis elegans GN=tps-1; Q7YZT6|TPS1_CAEEL Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1 OS=Caenorhabditis elegans GN=tps-1 PE=2 SV=1	0.70
P90789|NDUB7_CAEEL NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7 OS=Caenorhabditis elegans GN=D2030.4 PE=3 SV=1	0.69
Q3HKC4|Q3HKC4_CAEEL Protein PCYT-1, isoform b OS=Caenorhabditis elegans GN=pcyt-1 PE=2 SV=1; P49583|PCY1_CAEEL Putative choline-phosphate cytidylyltransferase OS=Caenorhabditis elegans GN=F08C6.2 PE=2 SV=2	0.69
P34384|YLPD_CAEEL Uncharacterized protein F02A9.4b OS=Caenorhabditis elegans GN=F02A9.4 PE=2 SV=3	0.69
Q8I4I4|Q8I4I4_CAEEL Protein F49E2.2, isoform b OS=Caenorhabditis elegans GN=CELE_F49E2.2 PE=2 SV=1; Q20621|Q20621_CAEEL Protein F49E2.2, isoform a OS=Caenorhabditis elegans GN=CELE_F49E2.2 PE=2 SV=3; A6ZJ46|A6ZJ46_CAEEL Protein F49E2.2, isoform c	0.69
Q9TXI3|Q9TXI3_CAEEL Protein F23C8.6 OS=Caenorhabditis elegans GN=CELE_F23C8.6 PE=4 SV=1	0.69
H2KZA3|H2KZA3_CAEEL Protein PQN-22, isoform a OS=Caenorhabditis elegans GN=pqn-22 PE=4 SV=2; Q9TY23|Q9TY23_CAEEL Protein PQN-22, isoform b OS=Caenorhabditis elegans GN=pqn-22 PE=4 SV=2	0.69

Q20684|Q20684_CAEEL Protein LEC-2, isoform a OS=Caenorhabditis elegans GN=lec-2 PE=2 SV=2	0.69
P52874|CLP1_CAEEL Protein clpf-1 OS=Caenorhabditis elegans GN=clpf-1 PE=2 SV=2	0.69
H2KZS2|H2KZS2_CAEEL Protein T23E7.2, isoform a OS=Caenorhabditis elegans GN=CELE_T23E7.2 PE=4 SV=2; H2KZS3|H2KZS3_CAEEL Protein T23E7.2, isoform b OS=Caenorhabditis elegans GN=CELE_T23E7.2 PE=4 SV=2; H2KZS4|H2KZS4_CAEEL Protein T23E7.2, isoform c	0.68
Q9N5K1|Q9N5K1_CAEEL Protein SACY-1 OS=Caenorhabditis elegans GN=sacy-1 PE=3 SV=1	0.68
Q65XX4|Q65XX4_CAEEL Protein Y47G6A.15 OS=Caenorhabditis elegans GN=CELE_Y47G6A.15 PE=4 SV=1	0.68
Q9XUN9|TNNI3_CAEEL Troponin I 3 OS=Caenorhabditis elegans GN=tni-3 PE=2 SV=1	0.68
Q6A2D2|Q6A2D2_CAEEL Protein HPO-34, isoform c OS=Caenorhabditis elegans GN=hpo-34 PE=2 SV=1; E3W743|E3W743_CAEEL Protein HPO-34, isoform d OS=Caenorhabditis elegans GN=hpo-34 PE=2 SV=1; Q93636|Q93636_CAEEL Protein HPO-34, isoform b OS=Caenorhabdi	0.67
P90904|P90904_CAEEL Protein K02B12.7 OS=Caenorhabditis elegans GN=CELE_K02B12.7 PE=4 SV=1	0.67
Q23084|Q23084_CAEEL Protein SET-30 OS=Caenorhabditis elegans GN=set-30 PE=4 SV=3	0.67
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
Q09975|Q09975_CAEEL Protein LYS-8 OS=Caenorhabditis elegans GN=lys-8 PE=1 SV=2	0.67
Q19589|Q19589_CAEEL Protein F19C7.2 OS=Caenorhabditis elegans GN=CELE_F19C7.2 PE=4 SV=2; Q19590|Q19590_CAEEL Protein F19C7.4 OS=Caenorhabditis elegans GN=CELE_F19C7.4 PE=4 SV=2	0.66
Q09512|TTL12_CAEEL Tubulin--tyrosine ligase-like protein 12 OS=Caenorhabditis elegans GN=ttll-12 PE=4 SV=1	0.66

Q23050|Q23050_CAEEL Protein T25F10.6, isoform a OS=Caenorhabditis elegans GN=CELE_T25F10.6 PE=4 SV=1; H2L0M6|H2L0M6_CAEEL Protein T25F10.6, isoform b OS=Caenorhabditis elegans GN=CELE_T25F10.6 PE=4 SV=1	0.66
Q93637|Q93637_CAEEL Protein HPO-34, isoform a OS=Caenorhabditis elegans GN=hpo-34 PE=1 SV=3	0.66
Q9N350|Q9N350_CAEEL Protein Y55F3BR.6 OS=Caenorhabditis elegans GN=CELE_Y55F3BR.6 PE=1 SV=3	0.66
P34676|PCP5_CAEEL Prolyl carboxy peptidase like protein 5 OS=Caenorhabditis elegans GN=pcp-5 PE=1 SV=1; P34676-2|PCP5_CAEEL Isoform b of Prolyl carboxy peptidase like protein 5 OS=Caenorhabditis elegans GN=pcp-5	0.65
D9N122|D9N122_CAEEL Protein EHS-1, isoform b OS=Caenorhabditis elegans GN=ehs-1 PE=2 SV=1; Q9BIF4|Q9BIF4_CAEEL EHS-1 OS=Caenorhabditis elegans GN=ehs-1 PE=2 SV=1	0.65
O02267|O02267_CAEEL Protein F45H10.3 OS=Caenorhabditis elegans GN=CELE_F45H10.3 PE=4 SV=1	0.64
Q9U2U0|Q9U2U0_CAEEL Protein UAF-2 OS=Caenorhabditis elegans GN=uaf-2 PE=4 SV=1	0.64
Q27473|Q27473_CAEEL Annexin OS=Caenorhabditis elegans GN=nex-3 PE=3 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
H2L048|H2L048_CAEEL Protein F46H5.7, isoform a OS=Caenorhabditis elegans GN=CELE_F46H5.7 PE=4 SV=1; Q8MQ42|Q8MQ42_CAEEL Protein F46H5.7, isoform b OS=Caenorhabditis elegans GN=CELE_F46H5.7 PE=4 SV=1	0.64
P90850|YCF2E_CAEEL Uncharacterized peptidase C1-like protein F26E4.3 OS=Caenorhabditis elegans GN=F26E4.3 PE=1 SV=3	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
Q19663|Q19663_CAEEL Protein F21C10.7 OS=Caenorhabditis elegans GN=CELE_F21C10.7 PE=4 SV=2	0.63

Q9N3D3|Q9N3D3_CAEEL Protein Y54E10BR.4 OS=Caenorhabditis elegans GN=CELE_Y54E10BR.4 PE=4 SV=2	0.63
O02658|O02658_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=gsp-3 PE=2 SV=1	0.63
Q22285|TTR46_CAEEL Transthyretin-like protein 46 OS=Caenorhabditis elegans GN=ttr-46 PE=3 SV=1	0.63
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
O62265|O62265_CAEEL Protein F57C2.5 OS=Caenorhabditis elegans GN=CELE_F57C2.5 PE=4 SV=1	0.63
Q20173|Q20173_CAEEL Protein F38E9.5 OS=Caenorhabditis elegans GN=CELE_F38E9.5 PE=4 SV=2	0.62
Q09629|KADY_CAEEL Probable adenylate kinase isoenzyme ZK673.2 OS=Caenorhabditis elegans GN=ZK673.2 PE=3 SV=1	0.62
Q9U3K1|Q9U3K1_CAEEL Protein F11A10.6, isoform a OS=Caenorhabditis elegans GN=CELE_F11A10.6 PE=2 SV=1	0.62
Q17764|Q17764_CAEEL Protein C06H2.2 OS=Caenorhabditis elegans GN=C06H2.2 PE=4 SV=3	0.62
Q27492|Q27492_CAEEL DNA-directed RNA polymerase OS=Caenorhabditis elegans GN=rpc-2 PE=3 SV=2	0.62
P55326|YZG1_CAEEL Uncharacterized protein F13E6.1 OS=Caenorhabditis elegans GN=F13E6.1 PE=3 SV=2	0.62
B1Q250|B1Q250_CAEEL Protein UGT-26, isoform b OS=Caenorhabditis elegans GN=ugt-26 PE=3 SV=1; H2KYQ0|H2KYQ0_CAEEL Protein UGT-26, isoform a OS=Caenorhabditis elegans GN=ugt-26 PE=3 SV=1	0.61
Q95Y67|Q95Y67_CAEEL Protein PES-4 OS=Caenorhabditis elegans GN=pes-4 PE=4 SV=3	0.61
Q18421|GRPE_CAEEL GrpE protein homolog, mitochondrial OS=Caenorhabditis elegans GN=C34C12.8 PE=1 SV=1	0.61
O17352|O17352_CAEEL Protein AAGR-4 OS=Caenorhabditis elegans GN=aagr-4 PE=4 SV=3	0.60
O18054|PFD3_CAEEL Probable prefoldin subunit 3 OS=Caenorhabditis elegans GN=pfd-3 PE=3 SV=1	0.60

Q9U2Q8|Q9U2Q8_CAEEL Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=fkb-2 PE=2 SV=1; Q27462|Q27462_CAEEL Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=FKBP-2 PE=2 SV=1	0.60
H2FLK8|H2FLK8_CAEEL Protein LEA-1, isoform l OS=Caenorhabditis elegans GN=lea-1 PE=4 SV=1; H2FLL1|H2FLL1_CAEEL Protein LEA-1, isoform k OS=Caenorhabditis elegans GN=lea-1 PE=4 SV=1; H2FLK9|H2FLK9_CAEEL Protein LEA-1, isoform j OS=Caenorhabditis e	0.60
Q8IG23|Q8IG23_CAEEL Protein AQP-1, isoform b OS=Caenorhabditis elegans GN=aqp-1 PE=2 SV=1	0.60
Q9XWT3|Q9XWT3_CAEEL Protein Y62H9A.6 OS=Caenorhabditis elegans GN=CELE_Y62H9A.6 PE=4 SV=1	0.59
O02207|O02207_CAEEL Protein C01A2.3 OS=Caenorhabditis elegans GN=C01A2.3 PE=3 SV=2	0.59
Q20877|Q20877_CAEEL Protein F56D3.1 OS=Caenorhabditis elegans GN=CELE_F56D3.1 PE=4 SV=2	0.59
O62055|O62055_CAEEL Protein C09F9.2 OS=Caenorhabditis elegans GN=C09F9.2 PE=4 SV=1	0.59
Q2L6V1|Q2L6V1_CAEEL Protein MRPL-47, isoform b OS=Caenorhabditis elegans GN=mrpl-47 PE=2 SV=1; Q2L6V2|Q2L6V2_CAEEL Protein MRPL-47, isoform a OS=Caenorhabditis elegans GN=mrpl-47 PE=2 SV=1	0.59
Q9N5E4|Q9N5E4_CAEEL Protein T02H6.11 OS=Caenorhabditis elegans GN=CELE_T02H6.11 PE=4 SV=1	0.59
O45630|O45630_CAEEL Sodium-calcium exchanger OS=Caenorhabditis elegans PE=2 SV=1; H2KYP3|H2KYP3_CAEEL Protein NCX-2, isoform b OS=Caenorhabditis elegans GN=ncx-2 PE=4 SV=1	0.59
O45625|O45625_CAEEL Protein H19N07.3, isoform a OS=Caenorhabditis elegans GN=CELE_H19N07.3 PE=2 SV=1; E9P8A3|E9P8A3_CAEEL Protein H19N07.3, isoform b OS=Caenorhabditis elegans GN=CELE_H19N07.3 PE=2 SV=1	0.59
O45380|TPS2_CAEEL Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 2 OS=Caenorhabditis elegans GN=tps-2 PE=2 SV=3	0.58
Q9TZ69|Q9TZ69_CAEEL Protein UBC-20 OS=Caenorhabditis elegans GN=ubc-20 PE=3 SV=1	0.58

Q18598|Q18598_CAEEL Protein PMP-2 OS=Caenorhabditis elegans GN=pmp-2 PE=3 SV=1	0.58
Q23655|NLT1_CAEEL Non-specific lipid-transfer protein-like OS=Caenorhabditis elegans GN=nlt-1 PE=4 SV=1	0.58
P91321|P91321_CAEEL Protein F53E10.1 OS=Caenorhabditis elegans GN=CELE_F53E10.1 PE=4 SV=1	0.57
H2KZL1|H2KZL1_CAEEL Protein W04B5.3, isoform c OS=Caenorhabditis elegans GN=CELE_W04B5.3 PE=4 SV=1; Q9UA61|Q9UA61_CAEEL Protein W04B5.3, isoform a OS=Caenorhabditis elegans GN=CELE_W04B5.3 PE=4 SV=2; H2KZL0|H2KZL0_CAEEL Protein W04B5.3, isoform b	0.57
Q9N5M3|Q9N5M3_CAEEL Protein H20J04.6 OS=Caenorhabditis elegans GN=CELE_H20J04.6 PE=4 SV=2	0.57
Q20140|KAD1_CAEEL Adenylate kinase isoenzyme 1 OS=Caenorhabditis elegans GN=F38B2.4 PE=2 SV=1	0.57
B3GWA1|B3GWA1_CAEEL Protein PSF-1, isoform a OS=Caenorhabditis elegans GN=psf-1 PE=2 SV=1; B3GWA0|B3GWA0_CAEEL Protein PSF-1, isoform c OS=Caenorhabditis elegans GN=psf-1 PE=2 SV=1; Q8I7K5|Q8I7K5_CAEEL Protein PSF-1, isoform d OS=Caenorhabditis e	0.57
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
Q9XXA2|Q9XXA2_CAEEL Protein EBP-2 OS=Caenorhabditis elegans GN=ebp-2 PE=4 SV=1	0.56
Q8I8G9|Q8I8G9_CAEEL ADR-1E OS=Caenorhabditis elegans GN=adr-1 PE=2 SV=1; Q86GC2|Q86GC2_CAEEL Protein ADR-1, isoform e OS=Caenorhabditis elegans GN=adr-1 PE=2 SV=1; Q86GC3|Q86GC3_CAEEL Protein ADR-1, isoform d OS=Caenorhabditis elegans GN=adr-1 PE	0.56
Q22161|Q22161_CAEEL Protein SFXN-1.5 OS=Caenorhabditis elegans GN=sfxn-1.5 PE=4 SV=1	0.56
Q9XUT0|Q9XUT0_CAEEL Protein K08E3.4 OS=Caenorhabditis elegans GN=CELE_K08E3.4 PE=4 SV=1	0.55
Q21012|ENOPH_CAEEL Enolase-phosphatase E1 OS=Caenorhabditis elegans GN=F58H1.3 PE=3 SV=3	0.55

Q21793|Q21793_CAEEL Protein PQN-53, isoform a OS=Caenorhabditis elegans GN=pqn-53 PE=4 SV=2	0.55
O17754|O17754_CAEEL Protein EGL-21 OS=Caenorhabditis elegans GN=egl-21 PE=4 SV=1	0.55
B3WFW9|B3WFW9_CAEEL Protein C41G7.9, isoform a OS=Caenorhabditis elegans GN=C41G7.9 PE=2 SV=1; C7FZU5|C7FZU5_CAEEL Protein C41G7.9, isoform b OS=Caenorhabditis elegans GN=C41G7.9 PE=2 SV=1	0.55
Q21432|NAS11_CAEEL Zinc metalloproteinase nas-11 OS=Caenorhabditis elegans GN=nas-11 PE=1 SV=2; Q21432-2|NAS11_CAEEL Isoform b of Zinc metalloproteinase nas-11 OS=Caenorhabditis elegans GN=nas-11	0.55
Q19948-2|YPP4_CAEEL Isoform b of Uncharacterized protein F32A5.4 OS=Caenorhabditis elegans GN=F32A5.4; Q19948|YPP4_CAEEL Uncharacterized protein F32A5.4 OS=Caenorhabditis elegans GN=F32A5.4 PE=1 SV=1	0.55
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
P32744|CLAS2_CAEEL Protein CLASP-2 OS=Caenorhabditis elegans GN=cls-2 PE=1 SV=3; K8ESK4|K8ESK4_CAEEL Protein CLS-2, isoform b OS=Caenorhabditis elegans GN=cls-2 PE=4 SV=1	0.54
P12456|TBB1_CAEEL Tubulin beta-1 chain OS=Caenorhabditis elegans GN=mec-7 PE=2 SV=1	0.54
Q18075|Q18075_CAEEL Protein C18B2.4 OS=Caenorhabditis elegans GN=C18B2.4 PE=4 SV=1	0.54
G5EDP0|G5EDP0_CAEEL Protein Y32F6A.5, isoform a OS=Caenorhabditis elegans GN=CELE_Y32F6A.5 PE=4 SV=1	0.54
Q9U1Y9|Q9U1Y9_CAEEL Protein SKR-4 OS=Caenorhabditis elegans GN=skr-4 PE=4 SV=1	0.54
Q21525|Q21525_CAEEL Protein M05D6.6 OS=Caenorhabditis elegans GN=CELE_M05D6.6 PE=4 SV=1	0.53

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
Q20157|MPU1_CAEEL Mannose-P-dolichol utilization defect 1 protein homolog OS=Caenorhabditis elegans GN=F38E1.9 PE=3 SV=1	0.53
Q9XWK3|Q9XWK3_CAEEL Protein NPP-4 OS=Caenorhabditis elegans GN=npp-4 PE=4 SV=1	0.53
Q19652|Q19652_CAEEL Protein F20D6.2 OS=Caenorhabditis elegans GN=CELE_F20D6.2 PE=4 SV=1	0.53
H1ZUV6|H1ZUV6_CAEEL Protein F57C9.1, isoform c OS=Caenorhabditis elegans GN=CELE_F57C9.1 PE=4 SV=1; O01824|PDXK_CAEEL Putative pyridoxal kinase OS=Caenorhabditis elegans GN=F57C9.1 PE=2 SV=2; G8JXZ7|G8JXZ7_CAEEL Protein F57C9.1, isoform b OS=Caen	0.53
Q20058|Q20058_CAEEL Protein F35G12.12 OS=Caenorhabditis elegans GN=CELE_F35G12.12 PE=1 SV=3	0.53
Q20330|Q20330_CAEEL Protein TTM-4 OS=Caenorhabditis elegans GN=ttm-4 PE=4 SV=2	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
G5EBP5|G5EBP5_CAEEL Protein ZC247.1 OS=Caenorhabditis elegans GN=CELE_ZC247.1 PE=4 SV=1	0.52
G5EC31|G5EC31_CAEEL Protein ALH-6, isoform a OS=Caenorhabditis elegans GN=alh-6 PE=2 SV=1; G4RZC3|G4RZC3_CAEEL Protein ALH-6, isoform d OS=Caenorhabditis elegans GN=alh-6 PE=2 SV=1; Q86N72|Q86N72_CAEEL Protein ALH-6, isoform b OS=Caenorhabditis e	0.52
G4SQY7|G4SQY7_CAEEL Protein T27A1.5, isoform a OS=Caenorhabditis elegans GN=CELE_T27A1.5 PE=2 SV=2	0.52
Q86DC6|IFD1_CAEEL Intermediate filament protein ifd-1 OS=Caenorhabditis elegans GN=ifd-1 PE=3 SV=2; Q86DC6-2|IFD1_CAEEL Isoform b of Intermediate filament protein ifd-1 OS=Caenorhabditis elegans GN=ifd-1	0.52
Q19079|Q19079_CAEEL Protein DPY-3 OS=Caenorhabditis elegans GN=dpy-3 PE=4 SV=1	0.52

Q21752|VDAC_CAEEL Probable voltage-dependent anion-selective channel OS=Caenorhabditis elegans GN=R05G6.7 PE=3 SV=2	0.52
P90790|P90790_CAEEL Protein D2030.3 OS=Caenorhabditis elegans GN=CELE_D2030.3 PE=4 SV=1	0.52
O16999|ZPR1_CAEEL Zinc finger protein ZPR1 homolog OS=Caenorhabditis elegans GN=W03F9.1 PE=3 SV=2	0.51
Q1RPT9|Q1RPT9_CAEEL Protein NCX-1, isoform b OS=Caenorhabditis elegans GN=ncx-1 PE=2 SV=1; G5EF08|G5EF08_CAEEL Protein NCX-1, isoform a OS=Caenorhabditis elegans GN=ncx-1 PE=2 SV=1	0.51
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
H2KYH5|H2KYH5_CAEEL Protein C07A12.7, isoform b OS=Caenorhabditis elegans GN=C07A12.7 PE=4 SV=1; Q95QX5|Q95QX5_CAEEL Protein C07A12.7, isoform a OS=Caenorhabditis elegans GN=C07A12.7 PE=2 SV=1	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
Q18846|KS6A2_CAEEL Putative ribosomal protein S6 kinase alpha-2 OS=Caenorhabditis elegans GN=rskn-2 PE=3 SV=2	0.51
Q20745-2|UNC84_CAEEL Isoform b of Nuclear migration and anchoring protein unc-84 OS=Caenorhabditis elegans GN=unc-84; Q20745|UNC84_CAEEL Nuclear migration and anchoring protein unc-84 OS=Caenorhabditis elegans GN=unc-84 PE=1 SV=2	0.51
Q9BLA0|Q9BLA0_CAEEL Protein C36E6.1, isoform b OS=Caenorhabditis elegans GN=C36E6.1 PE=4 SV=1	0.51
O76649|O76649_CAEEL Protein F25E5.7 OS=Caenorhabditis elegans GN=CELE_F25E5.7 PE=4 SV=2	0.51
Q21854|Q21854_CAEEL Protein TAG-147 OS=Caenorhabditis elegans GN=tag-147 PE=4 SV=1	0.51
Q17963|WDR51_CAEEL WD repeat-containing protein wdr-5.1 OS=Caenorhabditis elegans GN=wdr-5.1 PE=1 SV=1	0.51
Q9TYW7|Q9TYW7_CAEEL Protein GRD-3 OS=Caenorhabditis elegans GN=grd-3 PE=4 SV=2	0.50

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
Q94050|Q94050_CAEEL Protein SNA-2 OS=Caenorhabditis elegans GN=sna-2 PE=4 SV=1	0.50
Q86S61|Q86S61_CAEEL Protein UGT-31 OS=Caenorhabditis elegans GN=ugt-31 PE=4 SV=1	0.50
Q17526|Q17526_CAEEL Protein TSP-11 OS=Caenorhabditis elegans GN=tsp-11 PE=4 SV=5	0.50
Q9XVM0|Q9XVM0_CAEEL Protein LETM-1, isoform a OS=Caenorhabditis elegans GN=letm-1 PE=2 SV=1; Q9XVL7|Q9XVL7_CAEEL Protein LETM-1, isoform b OS=Caenorhabditis elegans GN=letm-1 PE=2 SV=1	0.50
Q9N3Y1|Q9N3Y1_CAEEL Protein Y42H9AR.1 OS=Caenorhabditis elegans GN=CELE_Y42H9AR.1 PE=4 SV=1	0.50
Q9GYF1|TNNI2_CAEEL Troponin I 2 OS=Caenorhabditis elegans GN=unc-27 PE=2 SV=2	0.50
G5EBV4|G5EBV4_CAEEL Galectin LEC-10 OS=Caenorhabditis elegans GN=lec-10 PE=2 SV=1	0.49
Q10462|CAH5_CAEEL Putative carbonic anhydrase 5 OS=Caenorhabditis elegans GN=cah-5 PE=3 SV=3	0.49
Q7JLB0|Q7JLB0_CAEEL Protein RET-1, isoform e OS=Caenorhabditis elegans GN=ret-1 PE=2 SV=1	0.49
Q21225|Q21225_CAEEL Protein VACL-14 OS=Caenorhabditis elegans GN=vacl-14 PE=4 SV=1	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

Q7YXB9|Q7YXB9_CAEEL Protein F32A7.5, isoform b OS=Caenorhabditis elegans GN=CELE_F32A7.5 PE=2 SV=1; H2FLK1|H2FLK1_CAEEL Protein F32A7.5, isoform d OS=Caenorhabditis elegans GN=CELE_F32A7.5 PE=4 SV=1; Q7YXB8|Q7YXB8_CAEEL Protein F32A7.5, isoform c	0.49
Q20521|Q20521_CAEEL Protein F47B8.8 OS=Caenorhabditis elegans GN=CELE_F47B8.8 PE=4 SV=1	0.49
Q7YTG7|Q7YTG7_CAEEL Protein D2030.2, isoform b OS=Caenorhabditis elegans GN=CELE_D2030.2 PE=2 SV=1; P90788|P90788_CAEEL Protein D2030.2, isoform a OS=Caenorhabditis elegans GN=CELE_D2030.2 PE=2 SV=1	0.49
Q18550|Q18550_CAEEL Protein C39H7.4 OS=Caenorhabditis elegans GN=C39H7.4 PE=4 SV=1	0.48
Q8ITY9|Q8ITY9_CAEEL Protein R148.5, isoform b OS=Caenorhabditis elegans GN=CELE_R148.5 PE=4 SV=1; H2KZA6|H2KZA6_CAEEL Protein R148.5, isoform a OS=Caenorhabditis elegans GN=CELE_R148.5 PE=4 SV=1	0.48
Q18028|Q18028_CAEEL Protein PRX-3, isoform a OS=Caenorhabditis elegans GN=prx-3 PE=2 SV=2	0.48
Q23091|Q23091_CAEEL Protein ZK742.4 OS=Caenorhabditis elegans GN=CELE_ZK742.4 PE=4 SV=1	0.48
Q18167|Q18167_CAEEL Protein C25G4.6 OS=Caenorhabditis elegans GN=C25G4.6 PE=4 SV=1	0.48
P24887|NU1M_CAEEL NADH-ubiquinone oxidoreductase chain 1 OS=Caenorhabditis elegans GN=nd1 PE=2 SV=2; G5EDL6|G5EDL6_CAEEL NADH-ubiquinone oxidoreductase chain 1 OS=Caenorhabditis elegans GN=ND1 PE=2 SV=1; G4XR16|G4XR16_CAEEL NADH-ubiquinone oxidor	0.47
O61880|O61880_CAEEL Protein F59B1.2 OS=Caenorhabditis elegans GN=CELE_F59B1.2 PE=4 SV=1	0.47
Q95X39|Q95X39_CAEEL Protein MRPL-9 OS=Caenorhabditis elegans GN=mrpl-9 PE=4 SV=2	0.47
Q9XVS9|Q9XVS9_CAEEL Protein DHS-22 OS=Caenorhabditis elegans GN=dhs-22 PE=3 SV=1	0.47
P35603-2|AP2M_CAEEL Isoform b of AP-2 complex subunit mu OS=Caenorhabditis elegans GN=dpy-23; P35603|AP2M_CAEEL AP-2 complex subunit mu OS=Caenorhabditis elegans GN=dpy-23 PE=2 SV=2	0.47

Q23320|Q23320_CAEEL Protein ZC443.1 OS=Caenorhabditis elegans GN=CELE_ZC443.1 PE=4 SV=2	0.47
H2KYY4|H2KYY4_CAEEL Protein PAT-12, isoform c OS=Caenorhabditis elegans GN=pat-12 PE=4 SV=1; H2KYY3|H2KYY3_CAEEL Protein PAT-12, isoform b OS=Caenorhabditis elegans GN=pat-12 PE=4 SV=1; Q95QA6|Q95QA6_CAEEL Protein PAT-12, isoform a OS=Caenorhabdi	0.47
P34552-3|ALX1_CAEEL Isoform c of Apoptosis-linked gene 2-interacting protein X 1 OS=Caenorhabditis elegans GN=alx-1; P34552|ALX1_CAEEL Apoptosis-linked gene 2-interacting protein X 1 OS=Caenorhabditis elegans GN=alx-1 PE=1 SV=3; P34552-2|ALX1_CAE	0.47
Q95ZJ1-2|GALT5_CAEEL Isoform b of Polypeptide N-acetylgalactosaminyltransferase 5 OS=Caenorhabditis elegans GN=gly-5; Q95ZJ1-3|GALT5_CAEEL Isoform c of Polypeptide N-acetylgalactosaminyltransferase 5 OS=Caenorhabditis elegans GN=gly-5; Q95ZJ1|GAL	0.47
Q93615|ETFA_CAEEL Probable electron transfer flavoprotein subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=F27D4.1 PE=3 SV=2	0.47
H2KZ73|H2KZ73_CAEEL Protein NOAH-1, isoform a OS=Caenorhabditis elegans GN=noah-1 PE=4 SV=2; Q8T3B7|Q8T3B7_CAEEL Protein NOAH-1, isoform b OS=Caenorhabditis elegans GN=noah-1 PE=4 SV=3; H8W3Y1|H8W3Y1_CAEEL Protein NOAH-1, isoform c OS=Caenorhabdi	0.46
Q9U2A1|Q9U2A1_CAEEL Protein Y48B6A.13, isoform a OS=Caenorhabditis elegans GN=CELE_Y48B6A.13 PE=2 SV=1; Q9U294|Q9U294_CAEEL Protein Y48B6A.13, isoform b OS=Caenorhabditis elegans GN=CELE_Y48B6A.13 PE=2 SV=1	0.46
P34462|VATD_CAEEL V-type proton ATPase subunit D OS=Caenorhabditis elegans GN=vha-14 PE=3 SV=1	0.46
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
Q95XN1|Q95XN1_CAEEL Protein Y71G12B.10 OS=Caenorhabditis elegans GN=CELE_Y71G12B.10 PE=4 SV=1	0.46
Q19876|Q19876_CAEEL Protein THN-2 OS=Caenorhabditis elegans GN=thn-2 PE=4 SV=1; Q19874|Q19874_CAEEL Protein THN-1 OS=Caenorhabditis elegans GN=thn-1 PE=4 SV=1	0.46

Q9XZI6-5|PICAL_CAEEL Isoform E of Phosphatidylinositol-binding clathrin assembly protein unc-11 OS=Caenorhabditis elegans GN=unc-11; Q9XZI6-9|PICAL_CAEEL Isoform e of Phosphatidylinositol-binding clathrin assembly protein unc-11 OS=Caenorhabditis el	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
Q18076|Q18076_CAEEL Protein C18B2.5, isoform a OS=Caenorhabditis elegans GN=C18B2.5 PE=4 SV=1; H2KYV3|H2KYV3_CAEEL Protein C18B2.5, isoform b OS=Caenorhabditis elegans GN=C18B2.5 PE=4 SV=1	0.45
H2KYJ5|H2KYJ5_CAEEL Protein MTCH-1, isoform a OS=Caenorhabditis elegans GN=mtch-1 PE=3 SV=1	0.45
Q19366|DPOD2_CAEEL Probable DNA polymerase delta small subunit OS=Caenorhabditis elegans GN=F12F6.7 PE=3 SV=1	0.45
Q09442|SF3B4_CAEEL Splicing factor 3B subunit 4 OS=Caenorhabditis elegans GN=sap-49 PE=1 SV=2; Q17352|Q17352_CAEEL RRM-type RNA binding protein OS=Caenorhabditis elegans PE=2 SV=1	0.45
P10567|MYSP_CAEEL Paramyosin OS=Caenorhabditis elegans GN=unc-15 PE=1 SV=1	0.45
O62198|O62198_CAEEL Protein F32A11.1 OS=Caenorhabditis elegans GN=CELE_F32A11.1 PE=4 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
Q9NAB0|Q9NAB0_CAEEL Protein GST-39 OS=Caenorhabditis elegans GN=gst-39 PE=1 SV=1	0.45
O45525|O45525_CAEEL Protein F45H10.2 OS=Caenorhabditis elegans GN=CELE_F45H10.2 PE=4 SV=1	0.45
P43508|CPR4_CAEEL Cathepsin B-like cysteine proteinase 4 OS=Caenorhabditis elegans GN=cpr-4 PE=2 SV=1	0.45
Q9N4I3|Q9N4I3_CAEEL Protein Y71F9AL.9 OS=Caenorhabditis elegans GN=CELE_Y71F9AL.9 PE=4 SV=1	0.45
Q20143|Q20143_CAEEL Protein F38B6.4 OS=Caenorhabditis elegans GN=CELE_F38B6.4 PE=3 SV=3	0.44

O17901|COPZ_CAEEL Probable coatomer subunit zeta OS=Caenorhabditis elegans GN=F59E10.3 PE=3 SV=1	0.44
Q22170|Q22170_CAEEL Protein ILE-2 OS=Caenorhabditis elegans GN=ile-2 PE=4 SV=2	0.44
Q9N4M4|ANC1_CAEEL Nuclear anchorage protein 1 OS=Caenorhabditis elegans GN=anc-1 PE=1 SV=3; Q6IMP3|Q6IMP3_CAEEL ANC-1 OS=Caenorhabditis elegans GN=anc-1 PE=2 SV=1	0.44
P46822|KLC_CAEEL Kinesin light chain OS=Caenorhabditis elegans GN=klc-2 PE=2 SV=2; P46822-3|KLC_CAEEL Isoform 3 of Kinesin light chain OS=Caenorhabditis elegans GN=klc-2; P46822-4|KLC_CAEEL Isoform 4 of Kinesin light chain OS=Caenorhabditis elega	0.44
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
Q17688|TXNDL_CAEEL Thioredoxin domain-containing protein C06A6.5 OS=Caenorhabditis elegans GN=C06A6.5 PE=1 SV=2	0.44
P91205|P91205_CAEEL Protein IRLD-3 OS=Caenorhabditis elegans GN=irld-3 PE=4 SV=1	0.44
Q22021|ATPK_CAEEL Putative ATP synthase subunit f, mitochondrial OS=Caenorhabditis elegans GN=R53.4 PE=3 SV=1	0.44
Q17345|CNOT7_CAEEL CCR4-NOT transcription complex subunit 7 OS=Caenorhabditis elegans GN=ccf-1 PE=2 SV=1	0.44
O62421|O62421_CAEEL Protein Y32F6B.1 OS=Caenorhabditis elegans GN=CELE_Y32F6B.1 PE=4 SV=1	0.43
O16386|O16386_CAEEL Protein SAGO-1 OS=Caenorhabditis elegans GN=sago-1 PE=4 SV=1	0.43
Q9N585|Q9N585_CAEEL Protein PPW-2 OS=Caenorhabditis elegans GN=ppw-2 PE=4 SV=1	0.43
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

Q8MXS1|RAB18_CAEEL Ras-related protein Rab-18 OS=Caenorhabditis elegans GN=rab-18 PE=3 SV=1; Q8MXS1-2|RAB18_CAEEL Isoform a of Ras-related protein Rab-18 OS=Caenorhabditis elegans GN=rab-18	0.43
O44400|F37C4_CAEEL Protein F37C4.5 OS=Caenorhabditis elegans GN=F37C4.5 PE=1 SV=3	0.43
O44159|O44159_CAEEL Protein CD4.3 OS=Caenorhabditis elegans GN=CD4.3 PE=4 SV=1	0.43
O62289|O62289_CAEEL Protein TTR-51 OS=Caenorhabditis elegans GN=ttr-51 PE=4 SV=2	0.43
P90860|P90860_CAEEL Protein F36A2.7 OS=Caenorhabditis elegans GN=CELE_F36A2.7 PE=4 SV=1	0.43
E2JL04|E2JL04_CAEEL Protein IARS-2, isoform a OS=Caenorhabditis elegans GN=iars-2 PE=2 SV=1; Q7Z261|Q7Z261_CAEEL Isoleucyl-tRNA synthetase (Mitochondrial) OS=Caenorhabditis elegans GN=irs-2 PE=2 SV=1	0.42
O45904|O45904_CAEEL Protein LEC-1, isoform b OS=Caenorhabditis elegans GN=lec-1 PE=1 SV=1	0.42
P91427|PGK_CAEEL Probable phosphoglycerate kinase OS=Caenorhabditis elegans GN=pgk-1 PE=1 SV=1	0.42
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
Q95Q68|Q95Q68_CAEEL Protein C37H5.13, isoform a OS=Caenorhabditis elegans GN=C37H5.13 PE=2 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
Q22623|Q22623_CAEEL Protein MRPL-50 OS=Caenorhabditis elegans GN=mrpl-50 PE=4 SV=1	0.42

A5Z2S4|A5Z2S4_CAEEL Protein SAPS-1, isoform b OS=Caenorhabditis elegans GN=saps-1 PE=2 SV=1; Q18696|Q18696_CAEEL Protein SAPS-1, isoform a OS=Caenorhabditis elegans GN=saps-1 PE=2 SV=2; B2D6K9|B2D6K9_CAEEL Protein SAPS-1, isoform c OS=Caenorhabdi	0.42
Q86S40|ADPGK_CAEEL Probable ADP-dependent glucokinase OS=Caenorhabditis elegans GN=C50D2.7 PE=1 SV=1	0.42
Q09510|MLRH_CAEEL Probable myosin regulatory light chain OS=Caenorhabditis elegans GN=mlc-4 PE=3 SV=1	0.42
Q19983|Q19983_CAEEL Protein TSP-8 OS=Caenorhabditis elegans GN=tsp-8 PE=4 SV=1	0.42
Q19338|MON2_CAEEL Monensin-resistant homolog 2 OS=Caenorhabditis elegans GN=mon-2 PE=2 SV=2; Q19338-2|MON2_CAEEL Isoform b of Monensin-resistant homolog 2 OS=Caenorhabditis elegans GN=mon-2	0.42
O46015|O46015_CAEEL Protein TEP-1, isoform b OS=Caenorhabditis elegans GN=tep-1 PE=2 SV=2; Q7JKM0|Q7JKM0_CAEEL Protein TEP-1, isoform a OS=Caenorhabditis elegans GN=tep-1 PE=2 SV=1; Q7YTU0|Q7YTU0_CAEEL Protein TEP-1, isoform c OS=Caenorhabditis e	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
P54002|YTH3_CAEEL Putative glycosyltransferase C14A4.3 OS=Caenorhabditis elegans GN=C14A4.3 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
Q8IG45|Q8IG45_CAEEL Protein C25H3.14 OS=Caenorhabditis elegans GN=C25H3.14 PE=4 SV=1	0.41
Q9BKU4|PHB1_CAEEL Mitochondrial prohibitin complex protein 1 OS=Caenorhabditis elegans GN=phb-1 PE=1 SV=1	0.41
Q8MXS2|Q8MXS2_CAEEL Protein UAF-1, isoform d OS=Caenorhabditis elegans GN=uaf-1 PE=2 SV=1; P90978-3|U2AF2_CAEEL Isoform C of Splicing factor U2AF 65 kDa subunit OS=Caenorhabditis elegans GN=uaf-1; P90978|U2AF2_CAEEL Splicing factor U2AF 65 kDa su	0.41
P46576|SAM50_CAEEL SAM50-like protein gop-3 OS=Caenorhabditis elegans GN=gop-3 PE=2 SV=2	0.41

Q23215|Q23215_CAEEL Protein W07G4.3 OS=Caenorhabditis elegans GN=CELE_W07G4.3 PE=4 SV=2	0.41
G5EEE5|G5EEE5_CAEEL Long chain polyunsaturated fatty acid elongation enzyme OS=Caenorhabditis elegans GN=elo-1 PE=2 SV=1	0.41
O45100|ATAT1_CAEEL Alpha-tubulin N-acetyltransferase 1 OS=Caenorhabditis elegans GN=mec-17 PE=2 SV=1	0.41
G5EBF0|G5EBF0_CAEEL Protein GLO-1 OS=Caenorhabditis elegans GN=glo-1 PE=2 SV=1	0.41
Q19714|Q19714_CAEEL Protein F22B5.10 OS=Caenorhabditis elegans GN=CELE_F22B5.10 PE=4 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
C0KDV0|C0KDV0_CAEEL Potassium chloride cotransporter isoform a OS=Caenorhabditis elegans GN=kcc-2 PE=2 SV=1; G5EEC9|G5EEC9_CAEEL Potassium chloride cotransporter isoform b OS=Caenorhabditis elegans GN=kcc-2 PE=2 SV=1; H2KZC2|H2KZC2_CAEEL Protein	0.40
A8WFI3|A8WFI3_CAEEL Protein T28D9.4, isoform b OS=Caenorhabditis elegans GN=CELE_T28D9.4 PE=2 SV=1; Q10023|YSX4_CAEEL Uncharacterized protein T28D9.4 OS=Caenorhabditis elegans GN=T28D9.4 PE=2 SV=2	0.40
Q95QG8|Q95QG8_CAEEL Protein FCP-1 OS=Caenorhabditis elegans GN=fcp-1 PE=4 SV=2	0.40
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
Q21253|GELS1_CAEEL Gelsolin-like protein 1 OS=Caenorhabditis elegans GN=gsnl-1 PE=1 SV=1	0.40

Q09486|Q09486_CAEEL Protein C30G12.2 OS=Caenorhabditis elegans GN=C30G12.2 PE=3 SV=2	0.40
Q9NAB7|Q9NAB7_CAEEL Protein Y53F4B.18 OS=Caenorhabditis elegans GN=CELE_Y53F4B.18 PE=4 SV=1	0.40
G5EEH9|NUP98_CAEEL Nuclear pore complex protein Nup98-Nup96 OS=Caenorhabditis elegans GN=npp-10 PE=2 SV=1; G5EEH9-2|NUP98_CAEEL Isoform a of Nuclear pore complex protein Nup98-Nup96 OS=Caenorhabditis elegans GN=npp-10; G5EEH9-3|NUP98_CAEEL Isofor	0.40
Q17543|Q17543_CAEEL Protein C01B10.3 OS=Caenorhabditis elegans GN=C01B10.3 PE=4 SV=2	0.40
Q7JPE2|Q7JPE2_CAEEL Protein CPNA-1, isoform a OS=Caenorhabditis elegans GN=cpna-1 PE=4 SV=1; H2KYS8|H2KYS8_CAEEL Protein CPNA-1, isoform b OS=Caenorhabditis elegans GN=cpna-1 PE=4 SV=1	0.40
Q4TTA9|Q4TTA9_CAEEL Protein PRAF-3, isoform b OS=Caenorhabditis elegans GN=praf-3 PE=4 SV=1; H2KZJ7|H2KZJ7_CAEEL Protein PRAF-3, isoform a OS=Caenorhabditis elegans GN=praf-3 PE=1 SV=1	0.39
Q18246|Q18246_CAEEL Protein RAP-1 OS=Caenorhabditis elegans GN=rap-1 PE=4 SV=1	0.39
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
Q21633|Q21633_CAEEL Protein UBC-18 OS=Caenorhabditis elegans GN=ubc-18 PE=4 SV=2	0.39
O44897|O44897_CAEEL Protein HAF-9, isoform a OS=Caenorhabditis elegans GN=haf-9 PE=2 SV=2; Q8IA64|Q8IA64_CAEEL Protein HAF-9, isoform b OS=Caenorhabditis elegans GN=haf-9 PE=2 SV=1	0.39
O76830|O76830_CAEEL Aspartic protease OS=Caenorhabditis elegans PE=2 SV=1; G5EEI4|G5EEI4_CAEEL Aspartic protease 1 OS=Caenorhabditis elegans GN=asp-1 PE=2 SV=1	0.39
P90747|YE56_CAEEL Probable cation-transporting ATPase C10C6.6 OS=Caenorhabditis elegans GN=C10C6.6 PE=3 SV=3	0.39
Q9XTB5|LEM2_CAEEL LEM protein 2 OS=Caenorhabditis elegans GN=lem-2 PE=1 SV=1	0.39

O44444|O44444_CAEEL Protein C02B10.4 OS=Caenorhabditis elegans GN=C02B10.4 PE=4 SV=1	0.39
Q20636|GBB2_CAEEL Guanine nucleotide-binding protein subunit beta-2 OS=Caenorhabditis elegans GN=gpb-2 PE=1 SV=2	0.39
Q95XT5|Q95XT5_CAEEL Protein TRAP-1 OS=Caenorhabditis elegans GN=trap-1 PE=4 SV=1	0.39
O44618|O44618_CAEEL Protein SRR-4, isoform a OS=Caenorhabditis elegans GN=srr-4 PE=4 SV=2; H2KYR4|H2KYR4_CAEEL Protein SRR-4, isoform b OS=Caenorhabditis elegans GN=srr-4 PE=4 SV=1	0.39
Q17624|Q17624_CAEEL Protein ARRD-25 OS=Caenorhabditis elegans GN=arrd-25 PE=4 SV=1	0.38
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
Q966B1|Q966B1_CAEEL Protein Y50D4B.4 OS=Caenorhabditis elegans GN=CELE_Y50D4B.4 PE=4 SV=2	0.38
Q9N489|Q9N489_CAEEL Protein Y110A2AR.3, isoform a OS=Caenorhabditis elegans GN=CELE_Y110A2AR.3 PE=4 SV=1; H2L0S9|H2L0S9_CAEEL Protein Y110A2AR.3, isoform b OS=Caenorhabditis elegans GN=CELE_Y110A2AR.3 PE=4 SV=1	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
Q5FC69|Q5FC69_CAEEL Protein NKAT-3, isoform b OS=Caenorhabditis elegans GN=nkat-3 PE=2 SV=1; Q8MP09|Q8MP09_CAEEL Protein NKAT-3, isoform a OS=Caenorhabditis elegans GN=nkat-3 PE=2 SV=1	0.37

Q22392|Q22392_CAEEL Protein DHS-19 OS=Caenorhabditis elegans GN=dhs-19 PE=3 SV=1	0.37
Q20476|Q20476_CAEEL Protein F46G10.1, isoform a OS=Caenorhabditis elegans GN=CELE_F46G10.1 PE=1 SV=3	0.37
Q9TZD9|Q9TZD9_CAEEL Protein HAF-4 OS=Caenorhabditis elegans GN=haf-4 PE=3 SV=2	0.37
Q8MXR6|Q8MXR6_CAEEL Protein SQD-1, isoform a OS=Caenorhabditis elegans GN=sqd-1 PE=2 SV=1; Q4W5P0|Q4W5P0_CAEEL Protein SQD-1, isoform b OS=Caenorhabditis elegans GN=sqd-1 PE=2 SV=1	0.37
Q7JLE3|Q7JLE3_CAEEL Protein ZC434.9, isoform b OS=Caenorhabditis elegans GN=CELE_ZC434.9 PE=2 SV=2; Q23318|Q23318_CAEEL Protein ZC434.9, isoform a OS=Caenorhabditis elegans GN=CELE_ZC434.9 PE=2 SV=5; G3MU30|G3MU30_CAEEL Protein ZC434.9, isoform c	0.37
Q20965|Q20965_CAEEL Protein F58B3.6 OS=Caenorhabditis elegans GN=CELE_F58B3.6 PE=4 SV=2	0.37
Q45EK1|Q45EK1_CAEEL Protein TTR-36 OS=Caenorhabditis elegans GN=ttr-36 PE=4 SV=2	0.37
A9UJN7|A9UJN7_CAEEL Protein F25D7.4 OS=Caenorhabditis elegans GN=CELE_F25D7.4 PE=2 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
D6VPA0|D6VPA0_CAEEL Protein MATH-38 OS=Caenorhabditis elegans GN=math-38 PE=4 SV=1	0.37
O17214|FUMH_CAEEL Probable fumarate hydratase, mitochondrial OS=Caenorhabditis elegans GN=fum-1 PE=1 SV=1; Q8ITZ0|Q8ITZ0_CAEEL Protein FUM-1, isoform b OS=Caenorhabditis elegans GN=fum-1 PE=2 SV=1	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
Q93168|Q93168_CAEEL Protein C01G10.8 OS=Caenorhabditis elegans GN=C01G10.8 PE=4 SV=1	0.37

G5EGA2|G5EGA2_CAEEL Protein Y45F10B.13, isoform b OS=Caenorhabditis elegans GN=CELE_Y45F10B.13 PE=2 SV=1; G5EDA8|G5EDA8_CAEEL Protein Y45F10B.13, isoform a OS=Caenorhabditis elegans GN=CELE_Y45F10B.13 PE=2 SV=1; G5EF70|G5EF70_CAEEL Protein Y45F10	0.37
Q03600|INA1_CAEEL Integrin alpha ina-1 OS=Caenorhabditis elegans GN=ina-1 PE=1 SV=1	0.36
O62305-6|KCC2D_CAEEL Isoform f of Calcium/calmodulin-dependent protein kinase type II OS=Caenorhabditis elegans GN=unc-43; O62305-7|KCC2D_CAEEL Isoform g of Calcium/calmodulin-dependent protein kinase type II OS=Caenorhabditis elegans GN=unc-43;	0.36
Q20675|Q20675_CAEEL Protein F52E4.5 OS=Caenorhabditis elegans GN=CELE_F52E4.5 PE=4 SV=2	0.36
O16497|O16497_CAEEL Protein B0238.1 OS=Caenorhabditis elegans GN=B0238.1 PE=4 SV=1; O16496|O16496_CAEEL Protein B0238.13 OS=Caenorhabditis elegans GN=B0238.13 PE=4 SV=3	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
O45924|ODBA_CAEEL 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=Y39E4A.3 PE=1 SV=2; Q4A1S8|Q4A1S8_CAEEL Protein Y39E4A.3, isoform b OS=Caenorhabditis elegans GN=CELE_Y39E4A.3 PE=2 SV=1	0.36
P34605|TPPC3_CAEEL Probable trafficking protein particle complex subunit 3 OS=Caenorhabditis elegans GN=ZK1098.5 PE=1 SV=1	0.36
Q93339|Q93339_CAEEL Protein PRP-4 OS=Caenorhabditis elegans GN=prp-4 PE=4 SV=1	0.36
Q9N2W7|NDUAC_CAEEL Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Caenorhabditis elegans GN=Y94H6A.8 PE=3 SV=2	0.36
O44158|O44158_CAEEL Protein VPS-37 OS=Caenorhabditis elegans GN=vps-37 PE=1 SV=1	0.36
Q2EEM8|Q2EEM8_CAEEL Protein TTR-45 OS=Caenorhabditis elegans GN=ttr-45 PE=4 SV=1	0.36
Q19782|IFD2_CAEEL Intermediate filament protein ifd-2 OS=Caenorhabditis elegans GN=ifd-2 PE=3 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
Q95NM6|NUCG_CAEEL Endonuclease G, mitochondrial OS=Caenorhabditis elegans GN=cps-6 PE=1 SV=1	0.35
Q94230|Q94230_CAEEL Protein PLP-1 OS=Caenorhabditis elegans GN=plp-1 PE=4 SV=1	0.35
H2KZV5|H2KZV5_CAEEL Protein T21H3.1, isoform a OS=Caenorhabditis elegans GN=CELE_T21H3.1 PE=4 SV=1	0.35
Q9XW37|Q9XW37_CAEEL Protein Y69E1A.5 OS=Caenorhabditis elegans GN=CELE_Y69E1A.5 PE=4 SV=1	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
Q9N4L8|Q9N4L8_CAEEL Protein LPD-5 OS=Caenorhabditis elegans GN=lpd-5 PE=4 SV=2	0.35
Q19655|Q19655_CAEEL Protein F20D6.11 OS=Caenorhabditis elegans GN=CELE_F20D6.11 PE=4 SV=2	0.35
Q7JPE4|Q7JPE4_CAEEL Protein TAT-4, isoform c OS=Caenorhabditis elegans GN=tat-4 PE=2 SV=1; H2KZ37|H2KZ37_CAEEL Protein TAT-4, isoform b OS=Caenorhabditis elegans GN=tat-4 PE=4 SV=1	0.35
Q20037|Q20037_CAEEL Protein CLEC-137 OS=Caenorhabditis elegans GN=clec-137 PE=4 SV=1	0.35
G5EC98|G5EC98_CAEEL Protein CTPS-1 OS=Caenorhabditis elegans GN=ctps-1 PE=4 SV=1	0.35
O44501|O44501_CAEEL Protein FNTA-1 OS=Caenorhabditis elegans GN=fnta-1 PE=1 SV=1	0.35
Q18494|Q18494_CAEEL Protein C36A4.5 OS=Caenorhabditis elegans GN=C36A4.5 PE=4 SV=2	0.35
Q21122|F26_CAEEL Probable 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase OS=Caenorhabditis elegans GN=K02B2.1 PE=3 SV=2	0.35

Q23551-2|UNC22_CAEEL Isoform a of Twitchin OS=Caenorhabditis elegans GN=unc-22; H2FLH3|H2FLH3_CAEEL Protein UNC-22, isoform g OS=Caenorhabditis elegans GN=unc-22 PE=4 SV=1; Q23551-4|UNC22_CAEEL Isoform d of Twitchin OS=Caenorhabditis elegans GN=u	0.35
G5ECY0|G5ECY0_CAEEL MAGUK protein DLG-1 OS=Caenorhabditis elegans GN=dlg-1 PE=1 SV=1	0.35
L8E938|L8E938_CAEEL Protein DNC-1, isoform e OS=Caenorhabditis elegans GN=dnc-1 PE=4 SV=1; L8EC32|L8EC32_CAEEL Protein DNC-1, isoform d OS=Caenorhabditis elegans GN=dnc-1 PE=4 SV=1; Q23542|Q23542_CAEEL Protein DNC-1, isoform a OS=Caenorhabditis e	0.35
Q9TXI4|Q9TXI4_CAEEL Protein F23C8.5 OS=Caenorhabditis elegans GN=CELE_F23C8.5 PE=4 SV=2	0.35
Q22192|Q22192_CAEEL Protein TTR-14 OS=Caenorhabditis elegans GN=ttr-14 PE=4 SV=1	0.34
Q20647|R23A2_CAEEL 60S ribosomal protein L23a 2 OS=Caenorhabditis elegans GN=rpl-25.2 PE=3 SV=1	0.34
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
I7EVJ8|I7EVJ8_CAEEL Rab-6.1 (Fragment) OS=Caenorhabditis elegans GN=rab-6.1 PE=2 SV=1; P34213|RAB6A_CAEEL Ras-related protein Rab-6.1 OS=Caenorhabditis elegans GN=rab-6.1 PE=2 SV=1	0.34
Q9XVU3|Q9XVU3_CAEEL Protein ATGP-1, isoform a OS=Caenorhabditis elegans GN=atgp-1 PE=2 SV=2	0.34
P91918|RSMB_CAEEL Probable small nuclear ribonucleoprotein-associated protein B OS=Caenorhabditis elegans GN=snr-2 PE=3 SV=1	0.34
Q09441|YP83_CAEEL ARID domain-containing protein C08B11.3 OS=Caenorhabditis elegans GN=C08B11.3 PE=4 SV=1	0.34

B1Q254|B1Q254_CAEEL Protein C14H10.3, isoform a OS=Caenorhabditis elegans GN=C14H10.3 PE=2 SV=1; B1Q255|B1Q255_CAEEL Protein C14H10.3, isoform b OS=Caenorhabditis elegans GN=C14H10.3 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
G4SLD6|G4SLD6_CAEEL 2MDa_2 protein OS=Caenorhabditis elegans GN=ttn-1 PE=4 SV=2; G5EFF0|G5EFF0_CAEEL 2MDa_1 protein OS=Caenorhabditis elegans GN=ttn-1 PE=4 SV=1; G4SLH0|G4SLH0_CAEEL Protein TTN-1, isoform g OS=Caenorhabditis elegans GN=ttn-1 PE=2	0.34
Q20300|ELO5_CAEEL Elongation of very long chain fatty acids protein 5 OS=Caenorhabditis elegans GN=elo-5 PE=1 SV=1	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
Q21569|Q21569_CAEEL Protein LACT-3 OS=Caenorhabditis elegans GN=lact-3 PE=4 SV=1	0.34
Q20062|Q20062_CAEEL Protein F35G2.2 OS=Caenorhabditis elegans GN=CELE_F35G2.2 PE=1 SV=1	0.34
G5EEV5|G5EEV5_CAEEL 5C820 OS=Caenorhabditis elegans GN=pud-3 PE=2 SV=1; H2KZS1|H2KZS1_CAEEL Protein PUD-3, isoform a OS=Caenorhabditis elegans GN=pud-3 PE=4 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
O02325|O02325_CAEEL Protein PRMT-3, isoform a OS=Caenorhabditis elegans GN=prmt-3 PE=2 SV=2	0.33

G5EFP2|G5EFP2_CAEEL Protein ZK1321.4, isoform a OS=Caenorhabditis elegans GN=CELE_ZK1321.4 PE=2 SV=1; G5EDL9|G5EDL9_CAEEL Protein ZK1321.4, isoform b OS=Caenorhabditis elegans GN=CELE_ZK1321.4 PE=2 SV=1	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
Q17872|Q17872_CAEEL Protein NPP-23, isoform a OS=Caenorhabditis elegans GN=npp-23 PE=2 SV=2; B3GWB1|B3GWB1_CAEEL Protein NPP-23, isoform b OS=Caenorhabditis elegans GN=npp-23 PE=2 SV=1	0.33
Q8I4E2-6|LST4_CAEEL Isoform f of Sorting nexin lst-4 OS=Caenorhabditis elegans GN=lst-4; Q8I4E2-4|LST4_CAEEL Isoform d of Sorting nexin lst-4 OS=Caenorhabditis elegans GN=lst-4; Q8I4E2|LST4_CAEEL Sorting nexin lst-4 OS=Caenorhabditis elegans GN=l	0.33
Q21549|Q21549_CAEEL Protein GSS-1 OS=Caenorhabditis elegans GN=gss-1 PE=4 SV=2	0.33
G5EDB1|G5EDB1_CAEEL Protein SRAP-1, isoform c OS=Caenorhabditis elegans GN=srap-1 PE=2 SV=1; G5ECB4|G5ECB4_CAEEL Protein SRAP-1, isoform a OS=Caenorhabditis elegans GN=srap-1 PE=2 SV=1; G5ECB3|G5ECB3_CAEEL Protein SRAP-1, isoform b OS=Caenorhabdi	0.33
P90992|P90992_CAEEL Protein MISC-1 OS=Caenorhabditis elegans GN=misc-1 PE=3 SV=2	0.33
G5EFS4|DCPS_CAEEL m7GpppX diphosphatase OS=Caenorhabditis elegans GN=dcs-1 PE=1 SV=1	0.33
K8ERU3|K8ERU3_CAEEL Protein HPO-27 OS=Caenorhabditis elegans GN=hpo-27 PE=4 SV=1	0.33
Q9XWE2|Q9XWE2_CAEEL Protein Y47H9C.1 OS=Caenorhabditis elegans GN=CELE_Y47H9C.1 PE=4 SV=1	0.33
Q93831|Q93831_CAEEL Protein F59C6.5 OS=Caenorhabditis elegans GN=CELE_F59C6.5 PE=4 SV=1	0.33
Q18685|UN112_CAEEL Protein unc-112 OS=Caenorhabditis elegans GN=unc-112 PE=1 SV=1	0.33

Q9TXZ9|Q9TXZ9_CAEEL Protein YKT-6 OS=Caenorhabditis elegans GN=ykt-6 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
Q95Y96|Q95Y96_CAEEL Protein M04F3.4, isoform a OS=Caenorhabditis elegans GN=CELE_M04F3.4 PE=4 SV=4	0.33
Q7JLY3|Q7JLY3_CAEEL Protein DUR-1, isoform d OS=Caenorhabditis elegans GN=dur-1 PE=2 SV=1; D3YT34|D3YT34_CAEEL Protein DUR-1, isoform f OS=Caenorhabditis elegans GN=dur-1 PE=2 SV=1; D3YT33|D3YT33_CAEEL Protein DUR-1, isoform e OS=Caenorhabditis e	0.33
G5EGS5|G5EGS5_CAEEL Protein GBF-1, isoform a OS=Caenorhabditis elegans GN=gbf-1 PE=4 SV=1	0.33
Q9XX15|NEP1_CAEEL Ribosomal RNA small subunit methyltransferase nep-1 OS=Caenorhabditis elegans GN=Y39A1A.14 PE=3 SV=1	0.33
Q9XWP7|Q9XWP7_CAEEL Protein EIF-3.J OS=Caenorhabditis elegans GN=eif-3.j PE=4 SV=1	0.33
O02268|O02268_CAEEL Protein DRR-1 OS=Caenorhabditis elegans GN=drr-1 PE=4 SV=1	0.33
Q18910|Q18910_CAEEL Protein D1005.2 OS=Caenorhabditis elegans GN=CELE_D1005.2 PE=4 SV=2	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
Q9U1P9|Q9U1P9_CAEEL Protein Y87G2A.13 OS=Caenorhabditis elegans GN=CELE_Y87G2A.13 PE=4 SV=2	0.33
I7EVK5|I7EVK5_CAEEL Rab-11.1 (Fragment) OS=Caenorhabditis elegans GN=rab-11.1 PE=2 SV=1; O01803|O01803_CAEEL Protein RAB-11.1 OS=Caenorhabditis elegans GN=rab-11.1 PE=2 SV=1; Q94149|Q94149_CAEEL Rab11-like (Fragment) OS=Caenorhabditis elegans PE=	0.33
O45168|IFC1_CAEEL Intermediate filament protein ifc-1 OS=Caenorhabditis elegans GN=ifc-1 PE=3 SV=2	0.33
Q18803|ATPL2_CAEEL Probable ATP synthase subunit g 2, mitochondrial OS=Caenorhabditis elegans GN=asg-2 PE=3 SV=1	0.33

C9IY22|C9IY22_CAEEL Protein ZK1058.9, isoform b OS=Caenorhabditis elegans GN=CELE_ZK1058.9 PE=2 SV=1; C9IY21|C9IY21_CAEEL Protein ZK1058.9, isoform a OS=Caenorhabditis elegans GN=CELE_ZK1058.9 PE=2 SV=1	0.33
Q18599|Q18599_CAEEL Protein C44B7.10 OS=Caenorhabditis elegans GN=C44B7.10 PE=4 SV=3	0.32
Q9N4P9|Q9N4P9_CAEEL Protein EXOS-4.2 OS=Caenorhabditis elegans GN=exos-4.2 PE=4 SV=3	0.32
Q27874|PAT3_CAEEL Integrin beta pat-3 OS=Caenorhabditis elegans GN=pat-3 PE=1 SV=1	0.32
Q95R11|Q95R11_CAEEL Protein F28B3.10 OS=Caenorhabditis elegans GN=CELE_F28B3.10 PE=4 SV=1	0.32
Q9UAW8|Q9UAW8_CAEEL Protein T12B3.3 OS=Caenorhabditis elegans GN=CELE_T12B3.3 PE=4 SV=1	0.32
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
O44782|O44782_CAEEL Major sperm protein OS=Caenorhabditis elegans GN=vpr-1 PE=1 SV=1	0.32
H2L046|H2L046_CAEEL Protein TAG-163, isoform c OS=Caenorhabditis elegans GN=tag-163 PE=4 SV=1; H2L045|H2L045_CAEEL Protein TAG-163, isoform a OS=Caenorhabditis elegans GN=tag-163 PE=4 SV=1; P92160|P92160_CAEEL Protein TAG-163, isoform b OS=Caenor	0.32
Q22540|Q22540_CAEEL Protein T18D3.1 OS=Caenorhabditis elegans GN=CELE_T18D3.1 PE=4 SV=1	0.32
Q09227|YP89_CAEEL Uncharacterized protein C08B11.9 OS=Caenorhabditis elegans GN=C08B11.9 PE=2 SV=1	0.32
Q965J2|Q965J2_CAEEL Protein PGL-3, isoform b OS=Caenorhabditis elegans GN=pgl-3 PE=2 SV=1; G5EBV6|G5EBV6_CAEEL PGL-3 OS=Caenorhabditis elegans GN=pgl-3 PE=1 SV=1	0.32
O01302|O01302_CAEEL Protein T02B5.1 OS=Caenorhabditis elegans GN=CELE_T02B5.1 PE=4 SV=2	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
G5EDP6|G5EDP6_CAEEL Dimethylaniline monooxygenase [N-oxide-forming] OS=Caenorhabditis elegans GN=fmo-1 PE=2 SV=1	0.32
Q22067|AATC_CAEEL Probable aspartate aminotransferase, cytoplasmic OS=Caenorhabditis elegans GN=T01C8.5 PE=3 SV=1	0.32
Q03575|TTR5_CAEEL Transthyretin-like protein 5 OS=Caenorhabditis elegans GN=ttr-5 PE=3 SV=1	0.32
Q9NES8|Q9NES8_CAEEL Protein PPH-5, isoform a OS=Caenorhabditis elegans GN=pph-5 PE=2 SV=2	0.32
Q9U1W1|Q9U1W1_CAEEL Protein TFG-1 OS=Caenorhabditis elegans GN=tfg-1 PE=4 SV=1	0.32
O61749|SRP19_CAEEL Probable signal recognition particle 19 kDa protein OS=Caenorhabditis elegans GN=F37F2.2 PE=3 SV=4	0.31
O62349|O62349_CAEEL Protein R11H6.5 OS=Caenorhabditis elegans GN=CELE_R11H6.5 PE=4 SV=2	0.31
Q9N4Z7|Q9N4Z7_CAEEL Protein MVK-1, isoform a OS=Caenorhabditis elegans GN=mvk-1 PE=2 SV=2; Q65XY0|Q65XY0_CAEEL Protein MVK-1, isoform d OS=Caenorhabditis elegans GN=mvk-1 PE=2 SV=1; Q65XX9|Q65XX9_CAEEL Protein MVK-1, isoform b OS=Caenorhabditis e	0.31
O45106|O45106_CAEEL Protein ECH-5 OS=Caenorhabditis elegans GN=ech-5 PE=3 SV=3	0.31
Q95XS2|Q95XS2_CAEEL Protein Y38F2AR.9 OS=Caenorhabditis elegans GN=CELE_Y38F2AR.9 PE=4 SV=1	0.31
Q21233|Q21233_CAEEL Protein NUO-4, isoform a OS=Caenorhabditis elegans GN=nuo-4 PE=2 SV=1	0.31
Q17994|Q17994_CAEEL Aspartate aminotransferase OS=Caenorhabditis elegans GN=got-2.2 PE=2 SV=1	0.31

O02365|IFA2_CAEEL Intermediate filament protein ifa-2 OS=Caenorhabditis elegans GN=ifa-2 PE=1 SV=1	0.31
G5EDS2|G5EDS2_CAEEL POD-1 OS=Caenorhabditis elegans GN=pod-1 PE=2 SV=1; K8FE00|K8FE00_CAEEL Protein POD-1, isoform d OS=Caenorhabditis elegans GN=pod-1 PE=4 SV=1; K8F7Z0|K8F7Z0_CAEEL Protein POD-1, isoform b OS=Caenorhabditis elegans GN=pod-1 PE=	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
Q21828|MPC2_CAEEL Probable mitochondrial pyruvate carrier 2 OS=Caenorhabditis elegans GN=R07E5.13 PE=3 SV=2	0.30
Q8I4E0|Q8I4E0_CAEEL Protein UNC-25, isoform b OS=Caenorhabditis elegans GN=unc-25 PE=2 SV=1; G5EDB7|G5EDB7_CAEEL Glutamic acid decarboxylase OS=Caenorhabditis elegans GN=unc-25 PE=2 SV=1; Q8I4D9|Q8I4D9_CAEEL Protein UNC-25, isoform c OS=Caenorhab	0.30
Q22505|Q22505_CAEEL Protein IMMT-1 OS=Caenorhabditis elegans GN=immt-1 PE=4 SV=2	0.30
Q94055|Q94055_CAEEL Protein T14D7.1 OS=Caenorhabditis elegans GN=CELE_T14D7.1 PE=3 SV=2	0.30
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
Q20950|Q20950_CAEEL Protein F57F5.1 OS=Caenorhabditis elegans GN=CELE_F57F5.1 PE=3 SV=2	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
P52715|YUA6_CAEEL Uncharacterized serine carboxypeptidase F13S12.6 OS=Caenorhabditis elegans GN=F13D12.6 PE=3 SV=1	0.30
Q19842|PCCA_CAEEL Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Caenorhabditis elegans GN=pcca-1 PE=1 SV=1	0.30

Q18066-2|DIM_CAEEL Isoform b of Disorganized muscle protein 1 OS=Caenorhabditis elegans GN=dim-1; Q18066|DIM_CAEEL Disorganized muscle protein 1 OS=Caenorhabditis elegans GN=dim-1 PE=1 SV=3	0.30
G5EE96|G5EE96_CAEEL Oxoglutarate/malate carrier protein OS=Caenorhabditis elegans GN=CELE_K11G12.5 PE=2 SV=1	0.30
Q9XXK6|Q9XXK6_CAEEL Protein QNS-1, isoform a OS=Caenorhabditis elegans GN=qns-1 PE=2 SV=1; F3Y5P6|F3Y5P6_CAEEL Protein QNS-1, isoform b OS=Caenorhabditis elegans GN=qns-1 PE=2 SV=1	0.30
G5EFI4|G5EFI4_CAEEL Galectin LEC-5 OS=Caenorhabditis elegans GN=lec-5 PE=2 SV=1	0.30
Q966L2|Q966L2_CAEEL Protein E01A2.1, isoform a OS=Caenorhabditis elegans GN=CELE_E01A2.1 PE=1 SV=1; A9CZN9|A9CZN9_CAEEL Protein E01A2.1, isoform b OS=Caenorhabditis elegans GN=CELE_E01A2.1 PE=2 SV=1	0.30
O02485|YDJ1_CAEEL Uncharacterized protein ZK1073.1 OS=Caenorhabditis elegans GN=ZK1073.1 PE=3 SV=1	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
Q9XXQ7|Q9XXQ7_CAEEL Protein Y51A2D.8 OS=Caenorhabditis elegans GN=CELE_Y51A2D.8 PE=3 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
Q20049|Q20049_CAEEL Protein IDHG-1 OS=Caenorhabditis elegans GN=idhg-1 PE=3 SV=2	0.30
Q23281|Q23281_CAEEL Protein TOC-1, isoform a OS=Caenorhabditis elegans GN=toc-1 PE=2 SV=2	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

G5EBT3|G5EBT3_CAEEL Protein SRP-7, isoform a OS=Caenorhabditis elegans GN=srp-7 PE=2 SV=1; A9Z1L1|A9Z1L1_CAEEL Protein SRP-7, isoform d OS=Caenorhabditis elegans GN=srp-7 PE=2 SV=1; Q6QUQ5|Q6QUQ5_CAEEL Protein SRP-7, isoform c OS=Caenorhabditis e	0.30
O01869|O01869_CAEEL Protein RPS-10 OS=Caenorhabditis elegans GN=rps-10 PE=1 SV=1	0.30
Q965K3|Q965K3_CAEEL Protein DPF-3, isoform b OS=Caenorhabditis elegans GN=dpf-3 PE=4 SV=1; H2KZK7|H2KZK7_CAEEL Protein DPF-3, isoform a OS=Caenorhabditis elegans GN=dpf-3 PE=4 SV=1	0.30
P52717|YUW5_CAEEL Uncharacterized serine carboxypeptidase F41C3.5 OS=Caenorhabditis elegans GN=F41C3.5 PE=1 SV=1	0.30
Q9N425|CSN3_CAEEL COP9 signalosome complex subunit 3 OS=Caenorhabditis elegans GN=csn-3 PE=1 SV=4	0.30
Q9UAV3|Q9UAV3_CAEEL Protein UBH-1 OS=Caenorhabditis elegans GN=ubh-1 PE=4 SV=1	0.29
Q17542|Q17542_CAEEL Protein C01B10.10 OS=Caenorhabditis elegans GN=C01B10.10 PE=4 SV=3	0.29
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
Q22341|Q22341_CAEEL Protein TTR-30 OS=Caenorhabditis elegans GN=ttr-30 PE=4 SV=3	0.29
Q9N359|CSN4_CAEEL COP9 signalosome complex subunit 4 OS=Caenorhabditis elegans GN=csn-4 PE=1 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
Q9TXQ1-2|PME5_CAEEL Isoform b of Poly(ADP-ribose) polymerase pme-5 OS=Caenorhabditis elegans GN=pme-5; Q9TXQ1|PME5_CAEEL Poly(ADP-ribose) polymerase pme-5 OS=Caenorhabditis elegans GN=pme-5 PE=2 SV=1	0.29
O62277|O62277_CAEEL Protein DCT-18 OS=Caenorhabditis elegans GN=dct-18 PE=4 SV=1	0.29

Q9BL83|Q9BL83_CAEEL Protein VPS-4 OS=Caenorhabditis elegans GN=vps-4 PE=4 SV=4	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
P48162|R23A1_CAEEL 60S ribosomal protein L23a 1 OS=Caenorhabditis elegans GN=rpl-25.1 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
Q18966|Q18966_CAEEL Protein D2013.6 OS=Caenorhabditis elegans GN=CELE_D2013.6 PE=1 SV=1	0.29
Q95XX0|Q95XX0_CAEEL Protein UBC-13 OS=Caenorhabditis elegans GN=ubc-13 PE=3 SV=2	0.29
Q9N4E2|Q9N4E2_CAEEL Protein Y73C8B.3 OS=Caenorhabditis elegans GN=CELE_Y73C8B.3 PE=4 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
Q18607|Q18607_CAEEL Protein CHIL-10 OS=Caenorhabditis elegans GN=chil-10 PE=3 SV=2	0.29
Q9XXU9|VATC_CAEEL V-type proton ATPase subunit C OS=Caenorhabditis elegans GN=vha-11 PE=2 SV=1	0.29
Q20224|FABP2_CAEEL Fatty acid-binding protein homolog 2 OS=Caenorhabditis elegans GN=lbp-2 PE=1 SV=1	0.29
Q86NE0|Q86NE0_CAEEL Protein ASP-2, isoform b OS=Caenorhabditis elegans GN=asp-2 PE=2 SV=1; Q86NE1|Q86NE1_CAEEL Protein ASP-2, isoform a OS=Caenorhabditis elegans GN=asp-2 PE=2 SV=1	0.29
Q9NEQ8|Q9NEQ8_CAEEL Protein Y59A8B.8 OS=Caenorhabditis elegans GN=CELE_Y59A8B.8 PE=2 SV=2	0.29
P17329|G3P2_CAEEL Glyceraldehyde-3-phosphate dehydrogenase 2 OS=Caenorhabditis elegans GN=gpd-2 PE=3 SV=2	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
Q10013|SMD1_CAEEL Probable small nuclear ribonucleoprotein Sm D1 OS=Caenorhabditis elegans GN=snr-3 PE=3 SV=1	0.28
Q9U367|Q9U367_CAEEL Protein T16G1.9 OS=Caenorhabditis elegans GN=CELE_T16G1.9 PE=4 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
Q9GZF3|Q9GZF3_CAEEL Protein CKB-4 OS=Caenorhabditis elegans GN=ckb-4 PE=4 SV=1	0.28
Q03598|UFC1_CAEEL Ubiquitin-fold modifier-conjugating enzyme 1 OS=Caenorhabditis elegans GN=C40H1.6 PE=3 SV=1	0.28
L8E976|L8E976_CAEEL Protein K02F3.2, isoform b OS=Caenorhabditis elegans GN=CELE_K02F3.2 PE=3 SV=1; Q21153|CMC1_CAEEL Probable calcium-binding mitochondrial carrier K02F3.2 OS=Caenorhabditis elegans GN=K02F3.2 PE=3 SV=2	0.28
Q9XVS1|MCES_CAEEL mRNA cap guanine-N7 methyltransferase OS=Caenorhabditis elegans GN=tag-72 PE=3 SV=2	0.28

Q9TZQ3|PGL1_CAEEL P granule abnormality protein 1 OS=Caenorhabditis elegans GN=pgl-1 PE=1 SV=1; Q304E5|Q304E5_CAEEL Protein PGL-1, isoform b OS=Caenorhabditis elegans GN=pgl-1 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
G5EGI7|G5EGI7_CAEEL Protein ZIG-1 OS=Caenorhabditis elegans GN=zig-1 PE=2 SV=1	0.28
Q20412|NDUB2_CAEEL Probable NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial OS=Caenorhabditis elegans GN=F44G4.2 PE=2 SV=1	0.28
Q9U3C8-2|DCN1_CAEEL Isoform b of Defective in cullin neddylation protein 1 OS=Caenorhabditis elegans GN=dcn-1; Q9U3C8|DCN1_CAEEL Defective in cullin neddylation protein 1 OS=Caenorhabditis elegans GN=dcn-1 PE=1 SV=2	0.28
O62327|GPX2_CAEEL Glutathione peroxidase 2 OS=Caenorhabditis elegans GN=gpx-2 PE=3 SV=1	0.28
P91910|TBA3_CAEEL Tubulin alpha-3 chain OS=Caenorhabditis elegans GN=mec-12 PE=1 SV=1	0.28
Q9GRZ1|Q9GRZ1_CAEEL Protein EBP-1 OS=Caenorhabditis elegans GN=ebp-1 PE=4 SV=1; Q9GRZ0|Q9GRZ0_CAEEL Protein EBP-3 OS=Caenorhabditis elegans GN=ebp-3 PE=4 SV=1	0.28
Q9XTV4|Q9XTV4_CAEEL Protein MBF-1 OS=Caenorhabditis elegans GN=mbf-1 PE=4 SV=1	0.28
Q19824|Q19824_CAEEL Protein CEE-1 OS=Caenorhabditis elegans GN=cee-1 PE=1 SV=1	0.27
P34540|KINH_CAEEL Kinesin heavy chain OS=Caenorhabditis elegans GN=unc-116 PE=2 SV=2	0.27
Q9XVX5|Q9XVX5_CAEEL Protein VPS-29, isoform a OS=Caenorhabditis elegans GN=vps-29 PE=2 SV=2; Q86D99|Q86D99_CAEEL Protein VPS-29, isoform b OS=Caenorhabditis elegans GN=vps-29 PE=2 SV=1	0.27
Q95XM9|Q95XM9_CAEEL Protein Y71G12B.8 OS=Caenorhabditis elegans GN=CELE_Y71G12B.8 PE=3 SV=2	0.27

Q9XWV3|ARPC3_CAEEL Probable actin-related protein 2/3 complex subunit 3 OS=Caenorhabditis elegans GN=arx-5 PE=3 SV=1	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
Q21019|Q21019_CAEEL Protein F59A2.5 OS=Caenorhabditis elegans GN=CELE_F59A2.5 PE=4 SV=1	0.27
Q20748|ATAD3_CAEEL ATPase family AAA domain-containing protein 3 OS=Caenorhabditis elegans GN=atad-3 PE=3 SV=2	0.27
Q86NB3|Q86NB3_CAEEL Protein PMT-1, isoform d OS=Caenorhabditis elegans GN=pmt-1 PE=2 SV=1; Q23552|Q23552_CAEEL Protein PMT-1, isoform a OS=Caenorhabditis elegans GN=pmt-1 PE=2 SV=2; H2KZF5|H2KZF5_CAEEL Protein PMT-1, isoform b OS=Caenorhabditis e	0.27
Q10664|MEK2_CAEEL Dual specificity mitogen-activated protein kinase kinase mek-2 OS=Caenorhabditis elegans GN=mek-2 PE=1 SV=1	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
Q75MI6|Q75MI6_CAEEL Protein Y94H6A.10 OS=Caenorhabditis elegans GN=CELE_Y94H6A.10 PE=4 SV=1	0.27
O01590|O01590_CAEEL Protein K09H11.1 OS=Caenorhabditis elegans GN=CELE_K09H11.1 PE=3 SV=2	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
O44411-2|NOG1_CAEEL Isoform b of Probable nucleolar GTP-binding protein 1 OS=Caenorhabditis elegans GN=T07A9.9; O44411|NOG1_CAEEL Probable nucleolar GTP-binding protein 1 OS=Caenorhabditis elegans GN=T07A9.9 PE=2 SV=1	0.27
O16486|O16486_CAEEL Protein B0238.10 OS=Caenorhabditis elegans GN=B0238.10 PE=4 SV=1	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
P34479|YMJ2_CAEEL Putative amino acid permease F59B2.2 OS=Caenorhabditis elegans GN=F59B2.2 PE=3 SV=2	0.26
G5EFZ2|G5EFZ2_CAEEL Protein AC8.11 OS=Caenorhabditis elegans GN=AC8.11 PE=4 SV=1	0.26
G5EGK1|G5EGK1_CAEEL Protein TLN-1, isoform a OS=Caenorhabditis elegans GN=tln-1 PE=4 SV=1; G4S9F5|G4S9F5_CAEEL Protein TLN-1, isoform c OS=Caenorhabditis elegans GN=tln-1 PE=2 SV=1	0.26
Q93535|Q93535_CAEEL Protein F20D1.3 OS=Caenorhabditis elegans GN=CELE_F20D1.3 PE=4 SV=2	0.26
O62512|O62512_CAEEL Protein ZK550.3 OS=Caenorhabditis elegans GN=CELE_ZK550.3 PE=3 SV=3	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
O62334|O62334_CAEEL Protein AGL-1 OS=Caenorhabditis elegans GN=agl-1 PE=4 SV=1	0.26
Q18124|Q18124_CAEEL Protein C24A3.2, isoform a OS=Caenorhabditis elegans GN=C24A3.2 PE=1 SV=1	0.26
Q23629|DHTK1_CAEEL Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1 homolog, mitochondrial OS=Caenorhabditis elegans GN=ZK836.2 PE=2 SV=4; F5GUD7|F5GUD7_CAEEL Protein ZK836.2, isoform b OS=Caenorhabditis elegans GN=CELE_ZK836.2 PE=2 SV=1	0.26
H2KZJ5|H2KZJ5_CAEEL Protein GLRX-3, isoform a OS=Caenorhabditis elegans GN=glrx-3 PE=4 SV=1; Q6EZG4|Q6EZG4_CAEEL Protein GLRX-3, isoform b OS=Caenorhabditis elegans GN=glrx-3 PE=4 SV=1	0.26
O02141|O02141_CAEEL Protein C46G7.2 OS=Caenorhabditis elegans GN=C46G7.2 PE=4 SV=1	0.26

Q23069|Q23069_CAEEL Protein MOC-2 OS=Caenorhabditis elegans GN=moc-2 PE=4 SV=2	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
Q9N5A0|Q9N5A0_CAEEL Protein SPE-5 OS=Caenorhabditis elegans GN=spe-5 PE=3 SV=1	0.26
P34652|CALX_CAEEL Calnexin OS=Caenorhabditis elegans GN=cnx-1 PE=1 SV=1	0.26
Q9N2Y1|Q9N2Y1_CAEEL Protein PBO-1 OS=Caenorhabditis elegans GN=pbo-1 PE=4 SV=2	0.26
Q65ZB1|Q65ZB1_CAEEL Protein MDT-28, isoform b OS=Caenorhabditis elegans GN=mdt-28 PE=2 SV=1; Q23095|Q23095_CAEEL Protein MDT-28, isoform a OS=Caenorhabditis elegans GN=mdt-28 PE=2 SV=2; A8WHP8|A8WHP8_CAEEL Protein MDT-28, isoform c OS=Caenorhabdi	0.26
G5EGA5|G5EGA5_CAEEL Delta 12 fatty acid desaturase FAT-2 OS=Caenorhabditis elegans GN=fat-2 PE=2 SV=1	0.26
Q20264|Q20264_CAEEL Protein ACS-11 OS=Caenorhabditis elegans GN=acs-11 PE=4 SV=3	0.26
G5EFH7|G5EFH7_CAEEL Protein AGEF-1, isoform a OS=Caenorhabditis elegans GN=agef-1 PE=2 SV=1	0.26
Q8WQB3|Q8WQB3_CAEEL Protein APG-1 OS=Caenorhabditis elegans GN=apg-1 PE=4 SV=1	0.26
Q18639|Q18639_CAEEL Protein DHS-18 OS=Caenorhabditis elegans GN=dhs-18 PE=4 SV=1	0.26
Q18851|Q18851_CAEEL Protein DOD-18 OS=Caenorhabditis elegans GN=dod-18 PE=3 SV=2	0.26
P91430|UBA5_CAEEL Ubiquitin-like modifier-activating enzyme 5 OS=Caenorhabditis elegans GN=T03F1.1 PE=3 SV=1	0.26
Q86NJ8|Q86NJ8_CAEEL Protein PPW-1, isoform c OS=Caenorhabditis elegans GN=ppw-1 PE=4 SV=1; H2KYV9|H2KYV9_CAEEL Protein PPW-1, isoform a OS=Caenorhabditis elegans GN=ppw-1 PE=4 SV=1; B3KLZ7|B3KLZ7_CAEEL Protein PPW-1, isoform d OS=Caenorhabditis e	0.25

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
O02215|O02215_CAEEL Protein CBL-1, isoform a OS=Caenorhabditis elegans GN=cbl-1 PE=2 SV=3	0.25
G5EF43|G5EF43_CAEEL Transporter OS=Caenorhabditis elegans GN=snf-11 PE=2 SV=1	0.25
Q9GYI1|Q9GYI1_CAEEL Protein F29B9.11 OS=Caenorhabditis elegans GN=CELE_F29B9.11 PE=4 SV=1	0.25
P34455|ACON_CAEEL Probable aconitate hydratase, mitochondrial OS=Caenorhabditis elegans GN=aco-2 PE=1 SV=2; P34455-3|ACON_CAEEL Isoform c of Probable aconitate hydratase, mitochondrial OS=Caenorhabditis elegans GN=aco-2; P34455-2|ACON_CAEEL Isofo	0.25
G5EF37|G5EF37_CAEEL Protein PAT-10 OS=Caenorhabditis elegans GN=pat-10 PE=4 SV=1	0.25
C1P662|C1P662_CAEEL Protein Y6G8.15 OS=Caenorhabditis elegans GN=CELE_Y6G8.15 PE=4 SV=1	0.25
Q27GQ5|Q27GQ5_CAEEL Protein F49C12.7, isoform c OS=Caenorhabditis elegans GN=CELE_F49C12.7 PE=2 SV=1; Q20584|Q20584_CAEEL Protein F49C12.7, isoform a OS=Caenorhabditis elegans GN=CELE_F49C12.7 PE=2 SV=1; Q27GQ6|Q27GQ6_CAEEL Protein F49C12.7, isof	0.25
Q09983|Q09983_CAEEL Protein F30H5.3 OS=Caenorhabditis elegans GN=CELE_F30H5.3 PE=4 SV=1	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

A7LPJ5|A7LPJ5_CAEEL Protein F10A3.17 OS=Caenorhabditis elegans GN=CELE_F10A3.17 PE=4 SV=1	0.25
Q21443|LMN1_CAEEL Lamin-1 OS=Caenorhabditis elegans GN=lmn-1 PE=1 SV=2	0.25
O01816|O01816_CAEEL Protein CYTB-5.2 OS=Caenorhabditis elegans GN=cytb-5.2 PE=3 SV=1	0.25
Q8MPS2|Q8MPS2_CAEEL Protein DEB-1, isoform c OS=Caenorhabditis elegans GN=deb-1 PE=2 SV=1; P19826|VINC_CAEEL Vinculin OS=Caenorhabditis elegans GN=deb-1 PE=2 SV=1	0.25
M1ZMJ3|M1ZMJ3_CAEEL Protein PUD-4, isoform b OS=Caenorhabditis elegans GN=pud-4 PE=4 SV=1; M1ZJ62|M1ZJ62_CAEEL Protein PUD-4, isoform a OS=Caenorhabditis elegans GN=pud-4 PE=4 SV=1	0.25
Q9TYY0|Q9TYY0_CAEEL Protein M57.2 OS=Caenorhabditis elegans GN=CELE_M57.2 PE=4 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
Q23384|Q23384_CAEEL Protein NIT-1 OS=Caenorhabditis elegans GN=nit-1 PE=4 SV=1	0.25
Q22618|ADR2_CAEEL Probable double-stranded RNA-specific adenosine deaminase OS=Caenorhabditis elegans GN=adr-2 PE=2 SV=2	0.25
O62246|COPE_CAEEL Coatomer subunit epsilon OS=Caenorhabditis elegans GN=F45G2.4 PE=3 SV=1	0.24
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
Q9TXH9|Q9TXH9_CAEEL Protein UBXN-1 OS=Caenorhabditis elegans GN=ubxn-1 PE=1 SV=1	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
P46563|ALF2_CAEEL Fructose-bisphosphate aldolase 2 OS=Caenorhabditis elegans GN=aldo-2 PE=2 SV=1; G8JY45|G8JY45_CAEEL Fructose-bisphosphate aldolase OS=Caenorhabditis elegans GN=aldo-2 PE=2 SV=1	0.24
Q9NA98|Q9NA98_CAEEL Protein ARP-1 OS=Caenorhabditis elegans GN=arp-1 PE=3 SV=2	0.24
P90795|GPDM_CAEEL Probable glycerol-3-phosphate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=T25G3.4 PE=3 SV=2	0.24
Q1XFY9|Q1XFY9_CAEEL Protein RPS-24 OS=Caenorhabditis elegans GN=rps-24 PE=4 SV=1	0.24
Q93235|AT1B1_CAEEL Sodium/potassium-transporting ATPase subunit beta-1 OS=Caenorhabditis elegans GN=nkb-1 PE=1 SV=1	0.24
P29355|SEM5_CAEEL Sex muscle abnormal protein 5 OS=Caenorhabditis elegans GN=sem-5 PE=1 SV=1	0.24
Q19752|Q19752_CAEEL Protein FNTB-1 OS=Caenorhabditis elegans GN=fntb-1 PE=1 SV=1	0.24
O01257|O01257_CAEEL Protein T20D3.6 OS=Caenorhabditis elegans GN=CELE_T20D3.6 PE=4 SV=1	0.24
Q95Y85|Q95Y85_CAEEL Protein Y110A7A.6, isoform b OS=Caenorhabditis elegans GN=CELE_Y110A7A.6 PE=2 SV=1; Q9N590|Q9N590_CAEEL Protein Y110A7A.6, isoform a OS=Caenorhabditis elegans GN=CELE_Y110A7A.6 PE=1 SV=2	0.24
Q93841|PLC1_CAEEL Putative 1-acyl-sn-glycerol-3-phosphate acyltransferase acl-1 OS=Caenorhabditis elegans GN=acl-1 PE=3 SV=2	0.24
Q9XVK5|UBC12_CAEEL NEDD8-conjugating enzyme ubc-12 OS=Caenorhabditis elegans GN=ubc-12 PE=2 SV=1	0.24
O02640|MDHM_CAEEL Probable malate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=mdh-2 PE=3 SV=1	0.24
P34388|RT09_CAEEL Probable 40S ribosomal protein S9, mitochondrial OS=Caenorhabditis elegans GN=mrps-9 PE=3 SV=2	0.24
O16314|O16314_CAEEL Protein C05C8.1, isoform a OS=Caenorhabditis elegans GN=C05C8.1 PE=2 SV=3; A6PVA5|A6PVA5_CAEEL Protein C05C8.1, isoform b OS=Caenorhabditis elegans GN=C05C8.1 PE=2 SV=1	0.24

Q11189|RT17_CAEEL 28S ribosomal protein S17, mitochondrial OS=Caenorhabditis elegans GN=mrps-17 PE=3 SV=2	0.24
Q9NLD1|Q9NLD1_CAEEL Protein HRP-2, isoform a OS=Caenorhabditis elegans GN=hrp-2 PE=2 SV=2	0.24
Q9N3H3|Q9N3H3_CAEEL Protein Y53G8AL.2 OS=Caenorhabditis elegans GN=CELE_Y53G8AL.2 PE=4 SV=2	0.23
O45569|O45569_CAEEL Protein NEP-17, isoform a OS=Caenorhabditis elegans GN=nep-17 PE=2 SV=1; B6VQ96|B6VQ96_CAEEL Protein NEP-17, isoform b OS=Caenorhabditis elegans GN=nep-17 PE=2 SV=1	0.23
Q95ZJ9|Q95ZJ9_CAEEL Protein Y10G11A.1, isoform a OS=Caenorhabditis elegans GN=CELE_Y10G11A.1 PE=2 SV=2; E4MYG2|E4MYG2_CAEEL Protein Y10G11A.1, isoform b OS=Caenorhabditis elegans GN=CELE_Y10G11A.1 PE=2 SV=1	0.23
Q20448|Q20448_CAEEL Protein ZTF-7 OS=Caenorhabditis elegans GN=ztf-7 PE=4 SV=1	0.23
O17274|O17274_CAEEL Protein LGC-34 OS=Caenorhabditis elegans GN=lgc-34 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
Q65ZB8|Q65ZB8_CAEEL Protein ACS-19, isoform b OS=Caenorhabditis elegans GN=acs-19 PE=2 SV=1; Q18496|Q18496_CAEEL Protein ACS-19, isoform a OS=Caenorhabditis elegans GN=acs-19 PE=2 SV=1	0.23
Q21649|Q21649_CAEEL Protein R02F2.7 OS=Caenorhabditis elegans GN=CELE_R02F2.7 PE=4 SV=3	0.23
Q9U3I6|Q9U3I6_CAEEL Protein UFD-1, isoform b OS=Caenorhabditis elegans GN=ufd-1 PE=2 SV=1; Q19584|UFD1_CAEEL Ubiquitin fusion degradation protein 1 homolog OS=Caenorhabditis elegans GN=ufd-1 PE=2 SV=1	0.23
P34255|YKA3_CAEEL Uncharacterized protein B0303.3 OS=Caenorhabditis elegans GN=B0303.3 PE=3 SV=1	0.23
P34346|KAD2_CAEEL Adenylate kinase OS=Caenorhabditis elegans GN=let-754 PE=3 SV=2	0.23
P02566|MYO4_CAEEL Myosin-4 OS=Caenorhabditis elegans GN=unc-54 PE=4 SV=1	0.23

Q9N3B0|ARMET_CAEEL MANF/CDNF-like protein OS=Caenorhabditis elegans GN=Y54G2A.23 PE=3 SV=2	0.23
Q20011|Q20011_CAEEL Protein NLP-24 OS=Caenorhabditis elegans GN=nlp-24 PE=4 SV=2	0.23
Q93968|Q93968_CAEEL Protein T01H8.2 OS=Caenorhabditis elegans GN=CELE_T01H8.2 PE=4 SV=1	0.23
O61708|O61708_CAEEL Protein PQN-59 OS=Caenorhabditis elegans GN=pqn-59 PE=2 SV=2	0.23
P91373|P91373_CAEEL Protein K11H12.8, isoform a OS=Caenorhabditis elegans GN=CELE_K11H12.8 PE=4 SV=1	0.23
Q9N4A5|Q9N4A5_CAEEL Protein Y77E11A.1 OS=Caenorhabditis elegans GN=CELE_Y77E11A.1 PE=3 SV=1	0.23
Q17832|Q17832_CAEEL Protein C08H9.2, isoform a OS=Caenorhabditis elegans GN=C08H9.2 PE=2 SV=2; B3GWB2|B3GWB2_CAEEL Protein C08H9.2, isoform b OS=Caenorhabditis elegans GN=C08H9.2 PE=2 SV=1	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
Q20798|HRD1_CAEEL E3 ubiquitin-protein ligase hrd-1 OS=Caenorhabditis elegans GN=sel-11 PE=3 SV=1	0.23
P45971|OST48_CAEEL Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Caenorhabditis elegans GN=T09A5.11 PE=3 SV=1	0.23
O61955-2|IF4E3_CAEEL Isoform b of Eukaryotic translation initiation factor 4E-3 OS=Caenorhabditis elegans GN=ife-3; O61955-3|IF4E3_CAEEL Isoform c of Eukaryotic translation initiation factor 4E-3 OS=Caenorhabditis elegans GN=ife-3; O61955|IF4E3_C	0.23
Q17763|Q17763_CAEEL Protein ATP-5 OS=Caenorhabditis elegans GN=atp-5 PE=4 SV=2	0.23
O17730|THT2_CAEEL Putative thiosulfate sulfurtransferase D2023.5 OS=Caenorhabditis elegans GN=D2023.5 PE=3 SV=1	0.23
Q22529|Q22529_CAEEL Protein T16G12.6 OS=Caenorhabditis elegans GN=CELE_T16G12.6 PE=4 SV=1	0.23

P91917|OLA1_CAEEL Obg-like ATPase 1 OS=Caenorhabditis elegans GN=tag-210 PE=2 SV=1; E2JL06|E2JL06_CAEEL Protein OLA-1, isoform b OS=Caenorhabditis elegans GN=ola-1 PE=2 SV=1	0.23
O62332|O62332_CAEEL Protein IMB-2, isoform a OS=Caenorhabditis elegans GN=imb-2 PE=2 SV=1	0.23
Q9U3K7|Q9U3K7_CAEEL Protein DPT-1, isoform a OS=Caenorhabditis elegans GN=dpt-1 PE=2 SV=3; G5ECW7|G5ECW7_CAEEL Protein DPT-1, isoform b OS=Caenorhabditis elegans GN=dpt-1 PE=2 SV=1	0.23
Q9XWK2|Q9XWK2_CAEEL Protein Y54E5A.5 OS=Caenorhabditis elegans GN=CELE_Y54E5A.5 PE=4 SV=1	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
Q95XN2|Q95XN2_CAEEL Protein MPPA-1 OS=Caenorhabditis elegans GN=mppa-1 PE=3 SV=2	0.23
Q9N5A2|Q9N5A2_CAEEL Protein Y104H12D.2 OS=Caenorhabditis elegans GN=CELE_Y104H12D.2 PE=4 SV=2	0.22
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
Q93619|Q93619_CAEEL Protein TAG-173 OS=Caenorhabditis elegans GN=tag-173 PE=4 SV=1	0.22
Q9XUY5|AT1B3_CAEEL Probable sodium/potassium-transporting ATPase subunit beta-3 OS=Caenorhabditis elegans GN=nkb-3 PE=3 SV=1	0.22
Q18091|Q18091_CAEEL Protein C18E9.5 OS=Caenorhabditis elegans GN=C18E9.5 PE=4 SV=3	0.22
Q9U3Q0|Q9U3Q0_CAEEL Protein MRPS-22 OS=Caenorhabditis elegans GN=mrps-22 PE=4 SV=1	0.22
Q21274|Q21274_CAEEL Protein K07C5.2 OS=Caenorhabditis elegans GN=CELE_K07C5.2 PE=4 SV=1	0.22
Q94010|Q94010_CAEEL Protein T08G11.1, isoform a OS=Caenorhabditis elegans GN=CELE_T08G11.1 PE=2 SV=1; Q8T3D2|Q8T3D2_CAEEL Protein T08G11.1, isoform b OS=Caenorhabditis elegans GN=CELE_T08G11.1 PE=2 SV=1	0.22

Q9N3T5|Q9N3T5_CAEEL Protein SPG-7 OS=Caenorhabditis elegans GN=spg-7 PE=3 SV=2	0.22
Q965Y1|Q965Y1_CAEEL Methionine aminopeptidase OS=Caenorhabditis elegans GN=map-1 PE=3 SV=2	0.22
Q95XP6|Q95XP6_CAEEL Protein MCA-3, isoform a OS=Caenorhabditis elegans GN=mca-3 PE=2 SV=1; Q8MXS0|Q8MXS0_CAEEL Protein MCA-3, isoform c OS=Caenorhabditis elegans GN=mca-3 PE=2 SV=1; B7CED8|B7CED8_CAEEL Protein MCA-3, isoform d OS=Caenorhabditis e	0.22
Q93353|IDH3B_CAEEL Probable isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=idhb-1 PE=3 SV=1	0.22
Q19642|Q19642_CAEEL Protein CZW-1 OS=Caenorhabditis elegans GN=czw-1 PE=4 SV=1	0.22
G5EDR3|G5EDR3_CAEEL PP2A-B regulatory subunit PR55/B OS=Caenorhabditis elegans GN=sur-6 PE=2 SV=1	0.22
H2KZQ9|H2KZQ9_CAEEL Protein F13B9.1, isoform c OS=Caenorhabditis elegans GN=CELE_F13B9.1 PE=4 SV=1; Q95ZV3|Q95ZV3_CAEEL Protein F13B9.1, isoform b OS=Caenorhabditis elegans GN=CELE_F13B9.1 PE=4 SV=2; H2KZQ8|H2KZQ8_CAEEL Protein F13B9.1, isoform a	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
Q95QV3|Q95QV3_CAEEL Protein RAB-3, isoform a OS=Caenorhabditis elegans GN=rab-3 PE=2 SV=1; I7F488|I7F488_CAEEL Rab-3 (Fragment) OS=Caenorhabditis elegans GN=rab-3 PE=2 SV=1; Q94986|RAB3_CAEEL Ras-related protein Rab-3 OS=Caenorhabditis elegans GN	0.22
H2KZX4|H2KZX4_CAEEL Protein T13C2.6, isoform a OS=Caenorhabditis elegans GN=CELE_T13C2.6 PE=4 SV=1; Q7JP80|Q7JP80_CAEEL Protein T13C2.6, isoform b OS=Caenorhabditis elegans GN=CELE_T13C2.6 PE=4 SV=1	0.22

Q95ZI4|Q95ZI4_CAEEL Protein LEC-3, isoform b OS=Caenorhabditis elegans GN=lec-3 PE=2 SV=1; Q09581|LEC3_CAEEL 32 kDa beta-galactoside-binding lectin lec-3 OS=Caenorhabditis elegans GN=lec-3 PE=2 SV=3; I2HAG1|I2HAG1_CAEEL Protein LEC-3, isoform f O	0.22
P91390|P91390_CAEEL Protein OSTD-1 OS=Caenorhabditis elegans GN=ostd-1 PE=4 SV=1	0.22
Q21086|GNL3_CAEEL Guanine nucleotide-binding protein-like 3 homolog OS=Caenorhabditis elegans GN=nst-1 PE=3 SV=1	0.22
O45552|O45552_CAEEL Protein F53A2.7 OS=Caenorhabditis elegans GN=CELE_F53A2.7 PE=3 SV=2	0.22
P34525|SPCS3_CAEEL Probable signal peptidase complex subunit 3 OS=Caenorhabditis elegans GN=K12H4.4 PE=1 SV=1	0.22
Q9N4V3|Q9N4V3_CAEEL Protein Y47D9A.1, isoform a OS=Caenorhabditis elegans GN=CELE_Y47D9A.1 PE=2 SV=1; Q9N4V2|Q9N4V2_CAEEL Protein Y47D9A.1, isoform b OS=Caenorhabditis elegans GN=CELE_Y47D9A.1 PE=2 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
Q20287|Q20287_CAEEL Protein F41G3.6 OS=Caenorhabditis elegans GN=CELE_F41G3.6 PE=4 SV=2	0.22
P91240|SRP72_CAEEL Signal recognition particle subunit SRP72 OS=Caenorhabditis elegans GN=F08D12.1 PE=3 SV=2	0.22
O62140|O62140_CAEEL Acyl-coenzyme A oxidase OS=Caenorhabditis elegans GN=acox-1 PE=2 SV=1; Q2L6T9|Q2L6T9_CAEEL Acyl-coenzyme A oxidase OS=Caenorhabditis elegans GN=acox-1 PE=2 SV=1; Q7JK62|Q7JK62_CAEEL Acyl-coenzyme A oxidase OS=Caenorhabditis el	0.22
P46561|ATPB_CAEEL ATP synthase subunit beta, mitochondrial OS=Caenorhabditis elegans GN=atp-2 PE=1 SV=2	0.21
Q9U1Q7|Q9U1Q7_CAEEL Protein EMB-4, isoform a OS=Caenorhabditis elegans GN=emb-4 PE=2 SV=4	0.21
Q17750|UFL1_CAEEL E3 UFM1-protein ligase 1 homolog OS=Caenorhabditis elegans GN=C06G3.9 PE=3 SV=1	0.21

O02236|O02236_CAEEL Protein TBC-14 OS=Caenorhabditis elegans GN=tbc-14 PE=4 SV=2	0.21
Q9GUF2|Q9GUF2_CAEEL Protein ACP-6 OS=Caenorhabditis elegans GN=acp-6 PE=4 SV=2	0.21
Q9GZH4|Q9GZH4_CAEEL Protein RIBO-1 OS=Caenorhabditis elegans GN=ribo-1 PE=4 SV=2	0.21
Q18680-4|IPYR_CAEEL Isoform d of Probable inorganic pyrophosphatase 1 OS=Caenorhabditis elegans GN=pyp-1; Q18680-2|IPYR_CAEEL Isoform a of Probable inorganic pyrophosphatase 1 OS=Caenorhabditis elegans GN=pyp-1; Q18680-3|IPYR_CAEEL Isoform c of P	0.21
P54412|EF1G_CAEEL Probable elongation factor 1-gamma OS=Caenorhabditis elegans GN=F17C11.9 PE=2 SV=1; Q8I4K9|Q8I4K9_CAEEL Protein EEF-1G, isoform b OS=Caenorhabditis elegans GN=eef-1g PE=2 SV=1; Q2PJ76|Q2PJ76_CAEEL Protein EEF-1G, isoform c OS=Ca	0.21
Q9XXR4|Q9XXR4_CAEEL Protein TTR-24, isoform a OS=Caenorhabditis elegans GN=ttr-24 PE=4 SV=1; H2KMI9|H2KMI9_CAEEL Protein TTR-24, isoform b OS=Caenorhabditis elegans GN=ttr-24 PE=4 SV=1	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
Q19086|Q19086_CAEEL Protein DPF-4 OS=Caenorhabditis elegans GN=dpf-4 PE=4 SV=2	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
Q9U2C3|Q9U2C3_CAEEL Protein RAB-35 OS=Caenorhabditis elegans GN=rab-35 PE=2 SV=1	0.21
Q22347|ACADM_CAEEL Probable medium-chain specific acyl-CoA dehydrogenase 10, mitochondrial OS=Caenorhabditis elegans GN=acdh-10 PE=2 SV=1	0.21
Q18678|SYSC_CAEEL Probable serine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=srs-2 PE=3 SV=1	0.21

Q9U2H9|EF1B2_CAEEL Probable elongation factor 1-beta/1-delta 2 OS=Caenorhabditis elegans GN=eef-1B.2 PE=1 SV=4; Q9U2H9-3|EF1B2_CAEEL Isoform c of Probable elongation factor 1-beta/1-delta 2 OS=Caenorhabditis elegans GN=eef-1B.2; Q9U2H9-4|EF1B2_CA	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
O62102|O62102_CAEEL Proteasome subunit beta type OS=Caenorhabditis elegans GN=pbs-2 PE=1 SV=1	0.21
O17732|PYC1_CAEEL Pyruvate carboxylase 1 OS=Caenorhabditis elegans GN=pyc-1 PE=1 SV=1	0.21
G5ECE7|G5ECE7_CAEEL Protein C34E7.4 OS=Caenorhabditis elegans GN=C34E7.4 PE=4 SV=1	0.21
P53596|SUCA_CAEEL Probable succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=C05G5.4 PE=3 SV=1	0.21
Q9XVP0|RS15_CAEEL 40S ribosomal protein S15 OS=Caenorhabditis elegans GN=rps-15 PE=1 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
Q3Y3Z9|Q3Y3Z9_CAEEL Protein C01B10.11 OS=Caenorhabditis elegans GN=C01B10.11 PE=4 SV=3	0.20
O61843|O61843_CAEEL Protein UNC-57, isoform a OS=Caenorhabditis elegans GN=unc-57 PE=2 SV=3; A5A8Q9|A5A8Q9_CAEEL Protein UNC-57, isoform c OS=Caenorhabditis elegans GN=unc-57 PE=2 SV=1; B1V8A0|B1V8A0_CAEEL Protein UNC-57, isoform d OS=Caenorhabdi	0.20
P34657|YOTB_CAEEL Uncharacterized protein ZK632.12 OS=Caenorhabditis elegans GN=ZK632.12 PE=1 SV=2	0.20
G5EG78|G5EG78_CAEEL Protein PXN-2 OS=Caenorhabditis elegans GN=pxn-2 PE=4 SV=1	0.20
Q8MXT1|Q8MXT1_CAEEL Protein PRDX-6 OS=Caenorhabditis elegans GN=prdx-6 PE=4 SV=1	0.20

Q10129|RT16_CAEEL Probable 28S ribosomal protein S16, mitochondrial OS=Caenorhabditis elegans GN=mrps-16 PE=3 SV=2	0.20
Q8WQ99|Q8WQ99_CAEEL Protein CSNK-1 OS=Caenorhabditis elegans GN=csnk-1 PE=3 SV=1	0.20
Q21154|Q21154_CAEEL Protein MOMA-1 OS=Caenorhabditis elegans GN=moma-1 PE=4 SV=1	0.20
Q21824|TDX1_CAEEL Probable peroxiredoxin prdx-3 OS=Caenorhabditis elegans GN=prdx-3 PE=1 SV=1	0.20
G8JY40|G8JY40_CAEEL Protein CPR-6, isoform c OS=Caenorhabditis elegans GN=cpr-6 PE=2 SV=1; Q8MQC6|Q8MQC6_CAEEL Protein CPR-6, isoform b OS=Caenorhabditis elegans GN=cpr-6 PE=2 SV=1; P43510|CPR6_CAEEL Cathepsin B-like cysteine proteinase 6 OS=Caen	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
Q22352|Q22352_CAEEL Protein T08H10.1 OS=Caenorhabditis elegans GN=CELE_T08H10.1 PE=4 SV=2	0.20
Q18036|Q18036_CAEEL Protein C16A3.5 OS=Caenorhabditis elegans GN=C16A3.5 PE=4 SV=1	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
Q9N5C4|Q9N5C4_CAEEL Protein W02H5.8 OS=Caenorhabditis elegans GN=CELE_W02H5.8 PE=4 SV=1	0.20
P12844|MYO3_CAEEL Myosin-3 OS=Caenorhabditis elegans GN=myo-3 PE=2 SV=1	0.20
Q21574|Q21574_CAEEL Protein M28.8 OS=Caenorhabditis elegans GN=CELE_M28.8 PE=4 SV=1	0.20
Q9BL64|Q9BL64_CAEEL Protein Y54H5A.2 OS=Caenorhabditis elegans GN=CELE_Y54H5A.2 PE=4 SV=2	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
Q22137|Q22137_CAEEL Protein T04A8.7, isoform a OS=Caenorhabditis elegans GN=CELE_T04A8.7 PE=2 SV=1; Q86G92|Q86G92_CAEEL Protein T04A8.7, isoform b OS=Caenorhabditis elegans GN=CELE_T04A8.7 PE=2 SV=1	0.20
P42168|KC1A_CAEEL Casein kinase I isoform alpha OS=Caenorhabditis elegans GN=kin-19 PE=3 SV=1	0.20
H2KYM1|H2KYM1_CAEEL Protein C39D10.8, isoform c OS=Caenorhabditis elegans GN=C39D10.8 PE=4 SV=1; H2KYM0|H2KYM0_CAEEL Protein C39D10.8, isoform a OS=Caenorhabditis elegans GN=C39D10.8 PE=4 SV=1; Q95QR7|Q95QR7_CAEEL Protein C39D10.8, isoform b OS=C	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
Q966I8|Q966I8_CAEEL Proteasome subunit beta type OS=Caenorhabditis elegans GN=pbs-1 PE=3 SV=1	0.20
Q21193|PROF3_CAEEL Profilin-3 OS=Caenorhabditis elegans GN=pfn-3 PE=2 SV=1	0.20
G5EFB5|G5EFB5_CAEEL CPN-1 OS=Caenorhabditis elegans GN=cpn-1 PE=4 SV=1	0.20
O76630|O76630_CAEEL Protein EMC-2 OS=Caenorhabditis elegans GN=emc-2 PE=1 SV=1	0.20
Q23621|Q23621_CAEEL Glutamate dehydrogenase OS=Caenorhabditis elegans GN=gdh-1 PE=3 SV=1	0.20
Q21826|Q21826_CAEEL Protein PDCD-2, isoform a OS=Caenorhabditis elegans GN=pdcd-2 PE=2 SV=2	0.20

P53588|SUCB1_CAEEL Probable succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=F47B10.1 PE=3 SV=1	0.19
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
P28548|CSK2B_CAEEL Casein kinase II subunit beta OS=Caenorhabditis elegans GN=kin-10 PE=1 SV=2; P28548-2|CSK2B_CAEEL Isoform b of Casein kinase II subunit beta OS=Caenorhabditis elegans GN=kin-10	0.19
P45965|YNZ5_CAEEL Uncharacterized protein T09A5.5 OS=Caenorhabditis elegans GN=T09A5.5 PE=4 SV=1	0.19
Q18447|Q18447_CAEEL Protein HECD-1 OS=Caenorhabditis elegans GN=hecd-1 PE=4 SV=1	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
Q8MPW1|Q8MPW1_CAEEL Protein DEL-6, isoform a OS=Caenorhabditis elegans GN=del-6 PE=2 SV=2; Q8MPW0|Q8MPW0_CAEEL Protein DEL-6, isoform b OS=Caenorhabditis elegans GN=del-6 PE=2 SV=2	0.19
P34576-2|MUA3_CAEEL Isoform b of Transmembrane cell adhesion receptor mua-3 OS=Caenorhabditis elegans GN=mua-3; P34576|MUA3_CAEEL Transmembrane cell adhesion receptor mua-3 OS=Caenorhabditis elegans GN=mua-3 PE=1 SV=2	0.19
P54812|TERA2_CAEEL Transitional endoplasmic reticulum ATPase homolog 2 OS=Caenorhabditis elegans GN=cdc-48.2 PE=1 SV=2	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
P48727|GLC7B_CAEEL Serine/threonine-protein phosphatase PP1-beta OS=Caenorhabditis elegans GN=gsp-2 PE=2 SV=1	0.19
C0P278|C0P278_CAEEL Protein F17C8.9 OS=Caenorhabditis elegans GN=CELE_F17C8.9 PE=4 SV=1	0.19

Q95YD1|Q95YD1_CAEEL Protein GLN-1 OS=Caenorhabditis elegans GN=gln-1 PE=3 SV=2	0.19
H2KYG4|H2KYG4_CAEEL Protein BAS-1, isoform a OS=Caenorhabditis elegans GN=bas-1 PE=3 SV=1; O45137|O45137_CAEEL Protein BAS-1, isoform b OS=Caenorhabditis elegans GN=bas-1 PE=2 SV=2; Q66NI4|Q66NI4_CAEEL Aromatic L-amino acid decarboxylase (Fragmen	0.19
P34528-2|YM67_CAEEL Isoform b of Putative serine protease K12H4.7 OS=Caenorhabditis elegans GN=K12H4.7; P34528|YM67_CAEEL Putative serine protease K12H4.7 OS=Caenorhabditis elegans GN=K12H4.7 PE=3 SV=2	0.19
Q22460|BCA1_CAEEL Beta carbonic anhydrase 1 OS=Caenorhabditis elegans GN=bca-1 PE=3 SV=1	0.19
Q9N369|Q9N369_CAEEL Autophagy-related protein 3 OS=Caenorhabditis elegans GN=atg-3 PE=3 SV=1	0.19
P90849|P90849_CAEEL Protein CCO-1 OS=Caenorhabditis elegans GN=cco-1 PE=4 SV=1	0.19
Q9NAB3|Q9NAB3_CAEEL Protein GST-27 OS=Caenorhabditis elegans GN=gst-27 PE=3 SV=1	0.19
Q21884|Q21884_CAEEL Protein R09H10.5 OS=Caenorhabditis elegans GN=CELE_R09H10.5 PE=4 SV=2	0.19
H2L0E5|H2L0E5_CAEEL Protein MCT-4, isoform a OS=Caenorhabditis elegans GN=mct-4 PE=4 SV=1; Q2L6X7|Q2L6X7_CAEEL Protein MCT-4, isoform c OS=Caenorhabditis elegans GN=mct-4 PE=4 SV=1; H2L0E6|H2L0E6_CAEEL Protein MCT-4, isoform b OS=Caenorhabditis e	0.19
P91155|P91155_CAEEL Protein CDC-6 OS=Caenorhabditis elegans GN=cdc-6 PE=4 SV=1	0.19
Q23027|INX5_CAEEL Innexin-5 OS=Caenorhabditis elegans GN=inx-5 PE=3 SV=2	0.19
O76687|O76687_CAEEL Protein M01G5.3 OS=Caenorhabditis elegans GN=CELE_M01G5.3 PE=4 SV=2	0.19
G5EDY2|G5EDY2_CAEEL Protein WARS-1 OS=Caenorhabditis elegans GN=wars-1 PE=2 SV=1	0.19
Q9GSX9|RIC8_CAEEL Synembryn OS=Caenorhabditis elegans GN=ric-8 PE=1 SV=1	0.19

Q18032|Q18032_CAEEL Protein C15H9.9 OS=Caenorhabditis elegans GN=C15H9.9 PE=4 SV=1	0.19
Q19706|EIF3G_CAEEL Eukaryotic translation initiation factor 3 subunit G OS=Caenorhabditis elegans GN=eif-3.G PE=3 SV=1; K8ESE1|K8ESE1_CAEEL Eukaryotic translation initiation factor 3 subunit G OS=Caenorhabditis elegans GN=eif-3.g PE=3 SV=1	0.19
Q19286|IFB2_CAEEL Intermediate filament protein ifb-2 OS=Caenorhabditis elegans GN=ifb-2 PE=1 SV=1; M1Z854|M1Z854_CAEEL Protein IFB-2, isoform e OS=Caenorhabditis elegans GN=ifb-2 PE=4 SV=1	0.19
Q95XK4|Q95XK4_CAEEL Protein Y54F10BM.1 OS=Caenorhabditis elegans GN=CELE_Y54F10BM.1 PE=3 SV=2	0.19
Q18597|Q18597_CAEEL Protein PMP-1 OS=Caenorhabditis elegans GN=pmp-1 PE=3 SV=1	0.18
P34385|MCCB_CAEEL Probable methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Caenorhabditis elegans GN=F02A9.4 PE=2 SV=1	0.18
O76577|PSDE_CAEEL 26S proteasome non-ATPase regulatory subunit 14 OS=Caenorhabditis elegans GN=rpn-11 PE=1 SV=1	0.18
Q9U2T9|Q9U2T9_CAEEL Protein ITSN-1, isoform a OS=Caenorhabditis elegans GN=itsn-1 PE=1 SV=2; E6N0W0|E6N0W0_CAEEL Protein ITSN-1, isoform b OS=Caenorhabditis elegans GN=itsn-1 PE=2 SV=1; E6N0W1|E6N0W1_CAEEL Protein ITSN-1, isoform c OS=Caenorhabdi	0.18
Q18136|Q18136_CAEEL Protein CAL-5 OS=Caenorhabditis elegans GN=cal-5 PE=4 SV=2	0.18
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
P91455|APT_CAEEL Adenine phosphoribosyltransferase OS=Caenorhabditis elegans GN=T19B4.3 PE=2 SV=1	0.18
Q27257|DIF1_CAEEL Protein dif-1 OS=Caenorhabditis elegans GN=dif-1 PE=2 SV=1	0.18
Q17770|PDI2_CAEEL Protein disulfide-isomerase 2 OS=Caenorhabditis elegans GN=pdi-2 PE=1 SV=1; G8JY07|G8JY07_CAEEL Protein PDI-2, isoform b OS=Caenorhabditis elegans GN=pdi-2 PE=2 SV=1; A3RMS2|A3RMS2_CAEEL Protein PDI-2, isoform c OS=Caenorhabditi	0.18

P30625|KAPR_CAEEL cAMP-dependent protein kinase regulatory subunit OS=Caenorhabditis elegans GN=kin-2 PE=2 SV=3; Q0MQ68|Q0MQ68_CAEEL Protein KIN-2, isoform c OS=Caenorhabditis elegans GN=kin-2 PE=2 SV=1	0.18
Q17796|Q17796_CAEEL Protein HGRS-1 OS=Caenorhabditis elegans GN=hgrs-1 PE=4 SV=2	0.18
G5EE74|G5EE74_CAEEL NUD-1 OS=Caenorhabditis elegans GN=nud-1 PE=2 SV=1	0.18
Q09583|PSA3_CAEEL Proteasome subunit alpha type-3 OS=Caenorhabditis elegans GN=pas-7 PE=1 SV=3	0.18
Q93761|YXEK_CAEEL Uncharacterized oxidoreductase F53C11.3 OS=Caenorhabditis elegans GN=F53C11.3 PE=3 SV=1	0.18
Q17602|Q17602_CAEEL Protein NPP-14 OS=Caenorhabditis elegans GN=npp-14 PE=4 SV=1	0.18
G4SPY1|G4SPY1_CAEEL Protein Y71G10AL.1, isoform a OS=Caenorhabditis elegans GN=CELE_Y71G10AL.1 PE=2 SV=2; G4SPY0|G4SPY0_CAEEL Protein Y71G10AL.1, isoform b OS=Caenorhabditis elegans GN=CELE_Y71G10AL.1 PE=2 SV=2	0.18
G5ED27|G5ED27_CAEEL Protein HIM-4, isoform a OS=Caenorhabditis elegans GN=him-4 PE=2 SV=1; G5EG33|G5EG33_CAEEL Hemicentin OS=Caenorhabditis elegans GN=him-4 PE=2 SV=1; G5EDG4|G5EDG4_CAEEL Protein HIM-4, isoform d OS=Caenorhabditis elegans GN=him-	0.18
P35129|UBC2_CAEEL Ubiquitin-conjugating enzyme E2 2 OS=Caenorhabditis elegans GN=let-70 PE=1 SV=1	0.18
Q20053|Q20053_CAEEL Protein ASB-1 OS=Caenorhabditis elegans GN=asb-1 PE=4 SV=1	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
P30628|VPP1_CAEEL Probable V-type proton ATPase 116 kDa subunit a OS=Caenorhabditis elegans GN=unc-32 PE=2 SV=3; P30628-4|VPP1_CAEEL Isoform d of Probable V-type proton ATPase 116 kDa subunit a OS=Caenorhabditis elegans GN=unc-32; P30628-6|VPP1_C	0.18

Q22633|HPPD_CAEEL 4-hydroxyphenylpyruvate dioxygenase OS=Caenorhabditis elegans GN=hpd-1 PE=1 SV=1	0.18
G5EE04|G5EE04_CAEEL Protein HIP-1 OS=Caenorhabditis elegans GN=hip-1 PE=4 SV=1	0.18
P31161|SODM1_CAEEL Superoxide dismutase [Mn] 1, mitochondrial OS=Caenorhabditis elegans GN=sod-2 PE=1 SV=1	0.18
Q9GRZ9|Q9GRZ9_CAEEL Protein TCC-1 OS=Caenorhabditis elegans GN=tcc-1 PE=4 SV=1	0.18
Q17348|SMD3_CAEEL Small nuclear ribonucleoprotein Sm D3 OS=Caenorhabditis elegans GN=snr-1 PE=2 SV=2	0.18
Q21750|Q21750_CAEEL Protein AAGR-2 OS=Caenorhabditis elegans GN=aagr-2 PE=4 SV=3	0.18
G5EED5|G5EED5_CAEEL Protein SCM-1 OS=Caenorhabditis elegans GN=scm-1 PE=2 SV=1	0.18
Q21463|Q21463_CAEEL Asparagine synthetase OS=Caenorhabditis elegans GN=asns-2 PE=2 SV=1; Q65ZI9|Q65ZI9_CAEEL Asparagine synthetase OS=Caenorhabditis elegans GN=asns-2 PE=2 SV=1; Q8IG01|Q8IG01_CAEEL Protein ASNS-2, isoform b OS=Caenorhabditis eleg	0.18
Q5CZ47|Q5CZ47_CAEEL Protein M01F1.4, isoform b OS=Caenorhabditis elegans GN=CELE_M01F1.4 PE=2 SV=1; Q21453|Q21453_CAEEL Protein M01F1.4, isoform a OS=Caenorhabditis elegans GN=CELE_M01F1.4 PE=1 SV=2	0.18
Q17473|Q17473_CAEEL Protein TTR-18 OS=Caenorhabditis elegans GN=ttr-18 PE=4 SV=1	0.18
Q9U334|Q9U334_CAEEL Protein UNC-59 OS=Caenorhabditis elegans GN=unc-59 PE=3 SV=1	0.18
P53585|ACLY_CAEEL Probable ATP-citrate synthase OS=Caenorhabditis elegans GN=D1005.1 PE=2 SV=1	0.18
Q09236|COPD_CAEEL Probable coatomer subunit delta OS=Caenorhabditis elegans GN=C13B9.3 PE=3 SV=1	0.18
Q9NAN1|SAE2_CAEEL SUMO-activating enzyme subunit uba-2 OS=Caenorhabditis elegans GN=uba-2 PE=3 SV=3	0.18

Q9U1Q2|Q9U1Q2_CAEEL Glucose-6-phosphate isomerase OS=Caenorhabditis elegans GN=gpi-1 PE=2 SV=1; Q7K707|Q7K707_CAEEL Glucose-6-phosphate isomerase OS=Caenorhabditis elegans GN=gpi-1 PE=2 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
Q95XM5|Q95XM5_CAEEL Protein Y71G12B.6 OS=Caenorhabditis elegans GN=CELE_Y71G12B.6 PE=4 SV=1	0.17
Q05036|YLA4_CAEEL Uncharacterized protein C30C11.4 OS=Caenorhabditis elegans GN=C30C11.4 PE=1 SV=1	0.17
Q2AAB7|Q2AAB7_CAEEL Protein Y92H12A.5 OS=Caenorhabditis elegans GN=CELE_Y92H12A.5 PE=4 SV=1	0.17
G5EDE8|G5EDE8_CAEEL ERGIC-53-like protein OS=Caenorhabditis elegans GN=ile-1 PE=2 SV=1	0.17
O17622|KCY1_CAEEL UMP-CMP kinase 1 OS=Caenorhabditis elegans GN=C29F7.3 PE=1 SV=1	0.17
Q2L6U7|Q2L6U7_CAEEL Protein F55A11.6, isoform b OS=Caenorhabditis elegans GN=CELE_F55A11.6 PE=3 SV=2; P90887|P90887_CAEEL Protein F55A11.6, isoform a OS=Caenorhabditis elegans GN=CELE_F55A11.6 PE=3 SV=3; H9G2W4|H9G2W4_CAEEL Protein F55A11.6, isof	0.17
Q23191|Q23191_CAEEL Protein PUF-9 OS=Caenorhabditis elegans GN=puf-9 PE=4 SV=2	0.17
G5ECC9|G5ECC9_CAEEL Protein K11B4.1 OS=Caenorhabditis elegans GN=CELE_K11B4.1 PE=4 SV=1	0.17
Q21915|Q21915_CAEEL Protein LPD-8 OS=Caenorhabditis elegans GN=lpd-8 PE=4 SV=1	0.17
D0VWN8|D0VWN8_CAEEL Protein C10C5.1, isoform c OS=Caenorhabditis elegans GN=C10C5.1 PE=2 SV=1; H9G2S2|H9G2S2_CAEEL Protein C10C5.1, isoform d OS=Caenorhabditis elegans GN=C10C5.1 PE=4 SV=1; Q17897|Q17897_CAEEL Protein C10C5.1, isoform a OS=Caenor	0.17
Q17761|6PGD_CAEEL 6-phosphogluconate dehydrogenase, decarboxylating OS=Caenorhabditis elegans GN=T25B9.9 PE=3 SV=2	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
G5EFK5|G5EFK5_CAEEL Protein UFD-3, isoform a OS=Caenorhabditis elegans GN=ufd-3 PE=2 SV=1; G5EES6|G5EES6_CAEEL Protein UFD-3, isoform b OS=Caenorhabditis elegans GN=ufd-3 PE=2 SV=1	0.17
Q22053|FBRL_CAEEL rRNA 2-O-methyltransferase fibrillarin OS=Caenorhabditis elegans GN=fib-1 PE=3 SV=1	0.17
Q9BKT9|Q9BKT9_CAEEL Protein NPP-13, isoform a OS=Caenorhabditis elegans GN=npp-13 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
G5EFJ2|G5EFJ2_CAEEL Protein LST-3, isoform a OS=Caenorhabditis elegans GN=lst-3 PE=1 SV=2	0.17
Q95YD8|Q95YD8_CAEEL Protein IDHG-2 OS=Caenorhabditis elegans GN=idhg-2 PE=3 SV=1	0.17
Q9BHL6|Q9BHL6_CAEEL Protein AAKG-1 OS=Caenorhabditis elegans GN=aakg-1 PE=4 SV=2	0.17
O17528|TMED2_CAEEL Suppressor/enhancer of lin-12 protein 9 OS=Caenorhabditis elegans GN=sel-9 PE=1 SV=1	0.17
O61741|O61741_CAEEL Protein B0205.6 OS=Caenorhabditis elegans GN=B0205.6 PE=3 SV=2	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
Q93594-3|NCBP2_CAEEL Isoform c of Nuclear cap-binding protein subunit 2 OS=Caenorhabditis elegans GN=ncbp-2; Q93594-2|NCBP2_CAEEL Isoform b of Nuclear cap-binding protein subunit 2 OS=Caenorhabditis elegans GN=ncbp-2; Q93594|NCBP2_CAEEL Nuclear c	0.17
Q965I6|Q965I6_CAEEL Protein CARS-1, isoform b OS=Caenorhabditis elegans GN=cars-1 PE=2 SV=1; O76618|O76618_CAEEL Protein CARS-1, isoform a OS=Caenorhabditis elegans GN=cars-1 PE=2 SV=1	0.17

O45730|O45730_CAEEL Protein PMP-4 OS=Caenorhabditis elegans GN=pmp-4 PE=3 SV=1	0.17
Q9NA69|Q9NA69_CAEEL Protein Y57A10A.13 OS=Caenorhabditis elegans GN=CELE_Y57A10A.13 PE=4 SV=1	0.17
Q09214|YP65_CAEEL Uncharacterized protein B0495.5 OS=Caenorhabditis elegans GN=B0495.5 PE=4 SV=2	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
Q23381|MUTA_CAEEL Probable methylmalonyl-CoA mutase, mitochondrial OS=Caenorhabditis elegans GN=mmcm-1 PE=3 SV=2	0.17
Q17399|Q17399_CAEEL Protein UGT-49 OS=Caenorhabditis elegans GN=ugt-49 PE=3 SV=2	0.17
Q9N538|Q9N538_CAEEL Protein DHS-9 OS=Caenorhabditis elegans GN=dhs-9 PE=4 SV=1	0.17
O62415|O62415_CAEEL Protein LYS-1 OS=Caenorhabditis elegans GN=lys-1 PE=4 SV=1	0.17
Q22758|Q22758_CAEEL Protein T24H7.2 OS=Caenorhabditis elegans GN=CELE_T24H7.2 PE=3 SV=1	0.16
Q9XVS2|Q9XVS2_CAEEL Protein C25A1.4 OS=Caenorhabditis elegans GN=C25A1.4 PE=1 SV=1	0.16
P17343|GBB1_CAEEL Guanine nucleotide-binding protein subunit beta-1 OS=Caenorhabditis elegans GN=gpb-1 PE=2 SV=2	0.16
P34477|UBC7_CAEEL Probable ubiquitin-conjugating enzyme E2 7 OS=Caenorhabditis elegans GN=ubc-7 PE=1 SV=1	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
Q65ZH5|Q65ZH5_CAEEL Protein EGAL-1, isoform b OS=Caenorhabditis elegans GN=egal-1 PE=2 SV=1; Q17902|Q17902_CAEEL Protein EGAL-1, isoform a OS=Caenorhabditis elegans GN=egal-1 PE=1 SV=2	0.16
P91175|P91175_CAEEL Protein C50F2.3 OS=Caenorhabditis elegans GN=C50F2.3 PE=1 SV=1	0.16
H2L0I0|H2L0I0_CAEEL Protein NHR-212, isoform a OS=Caenorhabditis elegans GN=nhr-212 PE=3 SV=1; B1GRK7|B1GRK7_CAEEL Protein NHR-212, isoform b OS=Caenorhabditis elegans GN=nhr-212 PE=3 SV=1	0.16
G5EGK8|G5EGK8_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=let-92 PE=2 SV=1	0.16
O01530|ASP6_CAEEL Aspartic protease 6 OS=Caenorhabditis elegans GN=asp-6 PE=3 SV=1	0.16
Q9U1X0|Q9U1X0_CAEEL NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Caenorhabditis elegans GN=CELE_Y62E10A.6 PE=3 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
O44738|O44738_CAEEL Protein F57B10.5 OS=Caenorhabditis elegans GN=CELE_F57B10.5 PE=3 SV=1	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
Q09544|ATPD_CAEEL ATP synthase subunit delta, mitochondrial OS=Caenorhabditis elegans GN=F58F12.1 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
O76449|O76449_CAEEL Protein ZK1055.7 OS=Caenorhabditis elegans GN=CELE_ZK1055.7 PE=1 SV=1	0.16
O17406|O17406_CAEEL Protein ATTF-2 OS=Caenorhabditis elegans GN=attf-2 PE=4 SV=1	0.16
Q18787|PRS7_CAEEL 26S protease regulatory subunit 7 OS=Caenorhabditis elegans GN=rpt-1 PE=1 SV=1	0.16
Q9XWD1|Q9XWD1_CAEEL Protein ACS-5 OS=Caenorhabditis elegans GN=acs-5 PE=4 SV=1	0.16
Q9XVZ2|Q9XVZ2_CAEEL Protein Y7A5A.1 OS=Caenorhabditis elegans GN=CELE_Y7A5A.1 PE=4 SV=1	0.16
Q18310|Q18310_CAEEL Protein C29F5.1 OS=Caenorhabditis elegans GN=C29F5.1 PE=4 SV=1	0.16
Q1W0R5|Q1W0R5_CAEEL Protein F10G7.10, isoform c OS=Caenorhabditis elegans GN=CELE_F10G7.10 PE=2 SV=1; Q1W0R6|Q1W0R6_CAEEL Protein F10G7.10, isoform b OS=Caenorhabditis elegans GN=CELE_F10G7.10 PE=2 SV=1; Q1W0R7|Q1W0R7_CAEEL Protein F10G7.10, isof	0.16
Q9N5U1|Q9N5U1_CAEEL Phosphorylase OS=Caenorhabditis elegans GN=CELE_T22F3.3 PE=2 SV=1	0.16
O44156|PSA1_CAEEL Proteasome subunit alpha type-1 OS=Caenorhabditis elegans GN=pas-6 PE=1 SV=1	0.16
Q07749|ADF2_CAEEL Actin-depolymerizing factor 2, isoform c OS=Caenorhabditis elegans GN=unc-60 PE=1 SV=1	0.16
Q9XVR3|Q9XVR3_CAEEL Protein C30H6.8 OS=Caenorhabditis elegans GN=C30H6.8 PE=4 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

Q9XTW9|Q9XTW9_CAEEL Sulfurtransferase OS=Caenorhabditis elegans GN=mpst-3 PE=4 SV=2; H9G341|H9G341_CAEEL Protein MPST-3, isoform c OS=Caenorhabditis elegans GN=mpst-3 PE=4 SV=1; H9G340|H9G340_CAEEL Protein MPST-3, isoform b OS=Caenorhabditis eleg	0.15
O44412|O44412_CAEEL Protein T07A9.10 OS=Caenorhabditis elegans GN=CELE_T07A9.10 PE=4 SV=1	0.15
P49596|PP2C2_CAEEL Probable protein phosphatase 2C T23F11.1 OS=Caenorhabditis elegans GN=T23F11.1 PE=3 SV=2	0.15
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
Q9N4Y8|Q9N4Y8_CAEEL Protein NUO-5, isoform a OS=Caenorhabditis elegans GN=nuo-5 PE=2 SV=1; Q86S77|Q86S77_CAEEL Protein NUO-5, isoform c OS=Caenorhabditis elegans GN=nuo-5 PE=2 SV=1	0.15
Q09496|PPH6_CAEEL Putative serine/threonine-protein phosphatase pph-6 OS=Caenorhabditis elegans GN=pph-6 PE=3 SV=2	0.15
Q17967|PDI1_CAEEL Protein disulfide-isomerase 1 OS=Caenorhabditis elegans GN=pdi-1 PE=3 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
Q565D2|Q565D2_CAEEL Protein F49E2.5, isoform i OS=Caenorhabditis elegans GN=CELE_F49E2.5 PE=2 SV=1; Q565D1|Q565D1_CAEEL Protein F49E2.5, isoform j OS=Caenorhabditis elegans GN=CELE_F49E2.5 PE=2 SV=1; Q20626|Q20626_CAEEL Protein F49E2.5, isoform a	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

O76836|O76836_CAEEL Protein T19D12.4, isoform a OS=Caenorhabditis elegans GN=CELE_T19D12.4 PE=2 SV=1; Q2V4T0|Q2V4T0_CAEEL Protein T19D12.4, isoform b OS=Caenorhabditis elegans GN=CELE_T19D12.4 PE=2 SV=1	0.15
P91502|P91502_CAEEL Ubiquitin carboxyl-terminal hydrolase OS=Caenorhabditis elegans GN=usp-5 PE=3 SV=2	0.15
Q19202|Q19202_CAEEL Protein APY-1 OS=Caenorhabditis elegans GN=apy-1 PE=1 SV=2	0.15
H2FLJ1|H2FLJ1_CAEEL Protein STL-1, isoform a OS=Caenorhabditis elegans GN=stl-1 PE=4 SV=1	0.15
Q21481|Q21481_CAEEL Protein DHS-28 OS=Caenorhabditis elegans GN=dhs-28 PE=3 SV=1	0.15
Q17489|Q17489_CAEEL Protein UNC-44, isoform a OS=Caenorhabditis elegans GN=unc-44 PE=2 SV=1	0.15
Q10454-2|KARG1_CAEEL Isoform b of Probable arginine kinase F46H5.3 OS=Caenorhabditis elegans GN=F46H5.3; Q10454|KARG1_CAEEL Probable arginine kinase F46H5.3 OS=Caenorhabditis elegans GN=F46H5.3 PE=1 SV=2	0.15
Q95ZR2|Q95ZR2_CAEEL Protein R05D11.9 OS=Caenorhabditis elegans GN=CELE_R05D11.9 PE=4 SV=2	0.15
Q9U2Q9|GSK3_CAEEL Glycogen synthase kinase-3 OS=Caenorhabditis elegans GN=gsk-3 PE=1 SV=1	0.15
G5EFJ3|G5EFJ3_CAEEL Protein C08E8.4 OS=Caenorhabditis elegans GN=C08E8.4 PE=4 SV=1	0.15
Q9U1R7|Q9U1R7_CAEEL Protein ARX-3 OS=Caenorhabditis elegans GN=arx-3 PE=4 SV=1	0.15
A5Z2V3|A5Z2V3_CAEEL Protein C13B4.1, isoform b OS=Caenorhabditis elegans GN=C13B4.1 PE=2 SV=1; O45247|O45247_CAEEL Protein C13B4.1, isoform a OS=Caenorhabditis elegans GN=C13B4.1 PE=2 SV=3	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
A3QMC8|GMPPB_CAEEL Mannose-1-phosphate guanyltransferase beta OS=Caenorhabditis elegans GN=tag-335 PE=3 SV=1	0.15

Q19246|Q19246_CAEEL Protein DHS-25 OS=Caenorhabditis elegans GN=dhs-25 PE=3 SV=2	0.15
Q9U3H4|Q9U3H4_CAEEL Protein F31D4.9 OS=Caenorhabditis elegans GN=CELE_F31D4.9 PE=4 SV=2; I3VM39|I3VM39_CAEEL Uncharacterized protein (Fragment) OS=Caenorhabditis elegans 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
O62515|PAHX_CAEEL Probable phytanoyl-CoA dioxygenase OS=Caenorhabditis elegans GN=ZK550.6 PE=3 SV=2	0.15
Q10121|YSD2_CAEEL RutC family protein C23G10.2 OS=Caenorhabditis elegans GN=C23G10.2 PE=3 SV=3; Q10121-3|YSD2_CAEEL Isoform c of RutC family protein C23G10.2 OS=Caenorhabditis elegans GN=C23G10.2; Q10121-2|YSD2_CAEEL Isoform b of RutC family prot	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
Q21541|Q21541_CAEEL Protein M142.5 OS=Caenorhabditis elegans GN=CELE_M142.5 PE=4 SV=2	0.15
Q23495|HEAT1_CAEEL HEAT repeat-containing protein 1 homolog OS=Caenorhabditis elegans GN=toe-1 PE=2 SV=1	0.15
Q27274|RO60_CAEEL 60 kDa SS-A/Ro ribonucleoprotein homolog OS=Caenorhabditis elegans GN=rop-1 PE=2 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
Q94123|Q94123_CAEEL Aspartic protease OS=Caenorhabditis elegans GN=Ceasp1 PE=2 SV=1	0.15

P21137-9|KAPC_CAEEL Isoform i of cAMP-dependent protein kinase catalytic subunit OS=Caenorhabditis elegans GN=kin-1; P21137-5|KAPC_CAEEL Isoform d of cAMP-dependent protein kinase catalytic subunit OS=Caenorhabditis elegans GN=kin-1; P21137-3|KAP	0.15
Q09603|Q09603_CAEEL Protein ECH-4 OS=Caenorhabditis elegans GN=ech-4 PE=4 SV=1	0.15
O02086|O02086_CAEEL Protein HAF-2 OS=Caenorhabditis elegans GN=haf-2 PE=3 SV=1	0.15
Q21774|PUR8_CAEEL Adenylosuccinate lyase OS=Caenorhabditis elegans GN=R06C7.5 PE=1 SV=1; Q21774-2|PUR8_CAEEL Isoform b of Adenylosuccinate lyase OS=Caenorhabditis elegans GN=R06C7.5	0.14
Q17686|Q17686_CAEEL Protein C06A6.4, isoform a OS=Caenorhabditis elegans GN=C06A6.4 PE=2 SV=3; Q5WRS4|Q5WRS4_CAEEL Protein C06A6.4, isoform b OS=Caenorhabditis elegans GN=C06A6.4 PE=2 SV=1	0.14
Q20168|COPB2_CAEEL Probable coatomer subunit beta OS=Caenorhabditis elegans GN=F38E11.5 PE=3 SV=3	0.14
Q20034|Q20034_CAEEL Protein F35D11.4 OS=Caenorhabditis elegans GN=CELE_F35D11.4 PE=4 SV=2	0.14
G5EE80|G5EE80_CAEEL Protein F21D5.7 OS=Caenorhabditis elegans GN=CELE_F21D5.7 PE=3 SV=1	0.14
P34697-2|SODC_CAEEL Isoform b of Superoxide dismutase [Cu-Zn] OS=Caenorhabditis elegans GN=sod-1; P34697|SODC_CAEEL Superoxide dismutase [Cu-Zn] OS=Caenorhabditis elegans GN=sod-1 PE=1 SV=2	0.14
Q20848|P5CR_CAEEL Putative pyrroline-5-carboxylate reductase OS=Caenorhabditis elegans GN=F55G1.9 PE=3 SV=1	0.14
Q20762|YAO6_CAEEL Uncharacterized protein F54D1.6 OS=Caenorhabditis elegans GN=F54D1.6 PE=1 SV=4	0.14
P34519|TXTP_CAEEL Putative tricarboxylate transport protein, mitochondrial OS=Caenorhabditis elegans GN=K11H3.3 PE=3 SV=1	0.14
H2KZR1|H2KZR1_CAEEL Protein M60.4, isoform a OS=Caenorhabditis elegans GN=CELE_M60.4 PE=4 SV=1; Q7Z2A6|Q7Z2A6_CAEEL Protein M60.4, isoform b OS=Caenorhabditis elegans GN=CELE_M60.4 PE=4 SV=1	0.14
G5EG26|G5EG26_CAEEL Protein R151.10 OS=Caenorhabditis elegans GN=R151.8A PE=2 SV=1	0.14

O02158|O02158_CAEEL Protein T09B4.8 OS=Caenorhabditis elegans GN=CELE_T09B4.8 PE=3 SV=3	0.14
Q9BIC3|Q9BIC3_CAEEL Protein T08B2.7, isoform b OS=Caenorhabditis elegans GN=CELE_T08B2.7 PE=2 SV=1; Q9GYT0|Q9GYT0_CAEEL Protein T08B2.7, isoform a OS=Caenorhabditis elegans GN=CELE_T08B2.7 PE=2 SV=1; Q8T8N8|Q8T8N8_CAEEL Protein T08B2.7, isoform c	0.14
Q17557|Q17557_CAEEL Protein SCO-1 OS=Caenorhabditis elegans GN=sco-1 PE=4 SV=1	0.14
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
Q9XUN8|Q9XUN8_CAEEL Protein T20B3.1 OS=Caenorhabditis elegans GN=CELE_T20B3.1 PE=3 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
Q18965|Q18965_CAEEL Protein EAT-3 OS=Caenorhabditis elegans GN=eat-3 PE=3 SV=3	0.14
Q94272|Q94272_CAEEL Protein FAH-1 OS=Caenorhabditis elegans GN=fah-1 PE=4 SV=1	0.14
Q9U238|Q9U238_CAEEL Protein TRAP-4 OS=Caenorhabditis elegans GN=trap-4 PE=1 SV=1	0.14
D0PV95|D0PV95_CAEEL Protein LAF-1, isoform b OS=Caenorhabditis elegans GN=laf-1 PE=2 SV=1; Q4W5R4|Q4W5R4_CAEEL Protein LAF-1, isoform a OS=Caenorhabditis elegans GN=laf-1 PE=2 SV=1	0.14
O45060|O45060_CAEEL Protein C35B1.5 OS=Caenorhabditis elegans GN=C35B1.5 PE=4 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

Q9XXJ1|Q9XXJ1_CAEEL Protein Y17G7B.3 OS=Caenorhabditis elegans GN=CELE_Y17G7B.3 PE=3 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
P58798|ARPC4_CAEEL Probable actin-related protein 2/3 complex subunit 4 OS=Caenorhabditis elegans GN=arx-6 PE=3 SV=1	0.14
Q9N5F6|Q9N5F6_CAEEL Protein R193.2 OS=Caenorhabditis elegans GN=CELE_R193.2 PE=4 SV=5	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
O01460|O01460_CAEEL Protein C03G6.17 OS=Caenorhabditis elegans GN=C03G6.17 PE=4 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
Q9U2M7|AP4A_CAEEL Bis(5-nucleosyl)-tetraphosphatase [asymmetrical] OS=Caenorhabditis elegans GN=ndx-4 PE=1 SV=1	0.14
C1P641|C1P641_CAEEL Protein EPI-1, isoform d OS=Caenorhabditis elegans GN=epi-1 PE=2 SV=1; Q21313|EPI1_CAEEL Laminin-like protein epi-1 OS=Caenorhabditis elegans GN=epi-1 PE=1 SV=1; C1P640|C1P640_CAEEL Protein EPI-1, isoform c OS=Caenorhabditis e	0.14

Q9XU97|Q9XU97_CAEEL Protein F44E5.1 OS=Caenorhabditis elegans GN=CELE_F44E5.1 PE=4 SV=1	0.14
O17939|O17939_CAEEL Protein AIPL-1 OS=Caenorhabditis elegans GN=aipl-1 PE=4 SV=1	0.14
P91401|P91401_CAEEL Protein M01E11.2 OS=Caenorhabditis elegans GN=CELE_M01E11.2 PE=4 SV=1	0.14
Q19731|Q19731_CAEEL Protein EKL-1 OS=Caenorhabditis elegans GN=ekl-1 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
G5EF87|G5EF87_CAEEL Protein SWSN-1, isoform a OS=Caenorhabditis elegans GN=swsn-1 PE=1 SV=1; H8ESF3|H8ESF3_CAEEL Protein SWSN-1, isoform c OS=Caenorhabditis elegans GN=swsn-1 PE=4 SV=1; H8ESF4|H8ESF4_CAEEL Protein SWSN-1, isoform b OS=Caenorhabdi	0.13
Q9U229|Q9U229_CAEEL Protein WAH-1, isoform a OS=Caenorhabditis elegans GN=wah-1 PE=2 SV=2; K8ESD4|K8ESD4_CAEEL Protein WAH-1, isoform c OS=Caenorhabditis elegans GN=wah-1 PE=4 SV=1; Q8HJ11|Q8HJ11_CAEEL Oxidoreductase WAH-1 OS=Caenorhabditis elega	0.13
G5ED07|G5ED07_CAEEL CeERp57 OS=Caenorhabditis elegans GN=pdi-3 PE=2 SV=1	0.13
Q86B39|Q86B39_CAEEL Protein ALG-2, isoform b OS=Caenorhabditis elegans GN=alg-2 PE=2 SV=1; O16720|O16720_CAEEL Protein ALG-2, isoform a OS=Caenorhabditis elegans GN=alg-2 PE=2 SV=2	0.13
Q95YB2|Q95YB2_CAEEL Protein ACDH-9 OS=Caenorhabditis elegans GN=acdh-9 PE=3 SV=1	0.13
G5EF86|G5EF86_CAEEL Protein Y48G10A.1 OS=Caenorhabditis elegans GN=CELE_Y48G10A.1 PE=4 SV=1	0.13
Q23312|RS7_CAEEL 40S ribosomal protein S7 OS=Caenorhabditis elegans GN=rps-7 PE=3 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
G5ED95|G5ED95_CAEEL Protein Y105E8A.19 OS=Caenorhabditis elegans GN=yrs-2 PE=2 SV=1	0.13

G5EDW8|G5EDW8_CAEEL Protein VF13D12L.3 OS=Caenorhabditis elegans GN=CELE_VF13D12L.3 PE=4 SV=1	0.13
P25807|CPR1_CAEEL Gut-specific cysteine proteinase OS=Caenorhabditis elegans GN=cpr-1 PE=1 SV=2	0.13
Q21930|RL28_CAEEL 60S ribosomal protein L28 OS=Caenorhabditis elegans GN=rpl-28 PE=1 SV=3	0.13
O61793|O61793_CAEEL Protein R12E2.13 OS=Caenorhabditis elegans GN=CELE_R12E2.13 PE=1 SV=1	0.13
Q9U329|Q9U329_CAEEL Protein W09C5.8 OS=Caenorhabditis elegans GN=CELE_W09C5.8 PE=4 SV=1	0.13
Q19554|Q19554_CAEEL Protein ABCF-1 OS=Caenorhabditis elegans GN=abcf-1 PE=3 SV=1	0.13
Q965S8|EIF3I_CAEEL Eukaryotic translation initiation factor 3 subunit I OS=Caenorhabditis elegans GN=eif-3.I PE=3 SV=2	0.13
O01763|NCBP1_CAEEL Nuclear cap-binding protein subunit 1 OS=Caenorhabditis elegans GN=ncbp-1 PE=3 SV=3	0.13
P05690|VIT2_CAEEL Vitellogenin-2 OS=Caenorhabditis elegans GN=vit-2 PE=1 SV=5; G8JY38|G8JY38_CAEEL Protein VIT-2, isoform b OS=Caenorhabditis elegans GN=vit-2 PE=2 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
O18240|O18240_CAEEL Protein RPS-18 OS=Caenorhabditis elegans GN=rps-18 PE=3 SV=1	0.13
P17330|G3P3_CAEEL Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Caenorhabditis elegans GN=gpd-3 PE=3 SV=1	0.13
Q9N4J7|Q9N4J7_CAEEL Protein F54A3.2 OS=Caenorhabditis elegans GN=CELE_F54A3.2 PE=4 SV=5; A4F325|A4F325_CAEEL Protein T08D2.8 OS=Caenorhabditis elegans GN=CELE_T08D2.8 PE=4 SV=1	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
Q93871|Q93871_CAEEL Protein ENT-2 OS=Caenorhabditis elegans GN=ent-2 PE=4 SV=1	0.13
Q9N4I0|ARP3_CAEEL Actin-related protein 3 OS=Caenorhabditis elegans GN=arx-1 PE=3 SV=1	0.13
Q9TYL9|Q9TYL9_CAEEL Coatomer subunit beta OS=Caenorhabditis elegans GN=copb-1 PE=3 SV=1	0.13
G5EFT4|G5EFT4_CAEEL Aminopeptidase-1 OS=Caenorhabditis elegans GN=AP-1 PE=2 SV=1; A3QMC2|A3QMC2_CAEEL Protein C42C1.11, isoform c OS=Caenorhabditis elegans GN=C42C1.11 PE=2 SV=1	0.13
O16294|GMPR_CAEEL Probable GMP reductase OS=Caenorhabditis elegans GN=F32D1.5 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
Q09393|Q09393_CAEEL Protein F42G10.1 OS=Caenorhabditis elegans GN=CELE_F42G10.1 PE=4 SV=2	0.13
Q9BKQ9|Q9BKQ9_CAEEL Protein Y67D2.3 OS=Caenorhabditis elegans GN=CELE_Y67D2.3 PE=4 SV=1	0.13
Q95X44|Q95X44_CAEEL Protein VHA-8 OS=Caenorhabditis elegans GN=vha-8 PE=3 SV=1	0.13
Q19579|Q19579_CAEEL Protein PAB-2, isoform a OS=Caenorhabditis elegans GN=pab-2 PE=2 SV=1; Q19581|Q19581_CAEEL Protein PAB-2, isoform b OS=Caenorhabditis elegans GN=pab-2 PE=2 SV=2	0.13
O01542|O01542_CAEEL Protein CPN-3 OS=Caenorhabditis elegans GN=cpn-3 PE=4 SV=1	0.13
Q20822|SRP68_CAEEL Probable signal recognition particle subunit SRP68 OS=Caenorhabditis elegans GN=F55C5.8 PE=3 SV=2	0.13
Q18026|KYNU_CAEEL Kynureninase OS=Caenorhabditis elegans GN=flu-2 PE=2 SV=1	0.13

Q93934|Q93934_CAEEL Protein R07H5.8 OS=Caenorhabditis elegans GN=CELE_R07H5.8 PE=1 SV=1	0.13
Q7JQD2|Q7JQD2_CAEEL Elongation factor Tu homologue (Fragment) OS=Caenorhabditis elegans PE=2 SV=1; G5ECM6|G5ECM6_CAEEL Elongation factor Tu homologue OS=Caenorhabditis elegans GN=tufm-1 PE=2 SV=1	0.12
Q22253|Q22253_CAEEL Protein RPN-9 OS=Caenorhabditis elegans GN=rpn-9 PE=1 SV=1	0.12
Q9XWP0|Q9XWP0_CAEEL Protein MRPS-28 OS=Caenorhabditis elegans GN=mrps-28 PE=4 SV=1	0.12
Q9BL48|Q9BL48_CAEEL Protein SET-27 OS=Caenorhabditis elegans GN=set-27 PE=4 SV=2	0.12
Q17819|ORN_CAEEL Probable oligoribonuclease OS=Caenorhabditis elegans GN=C08B6.8 PE=2 SV=1	0.12
O45551|IF4E1_CAEEL Eukaryotic translation initiation factor 4E-1 OS=Caenorhabditis elegans GN=ife-1 PE=1 SV=2; D1MN85|D1MN85_CAEEL Protein IFE-1, isoform a OS=Caenorhabditis elegans GN=ife-1 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
G5EG85|G5EG85_CAEEL Beta-G spectrin OS=Caenorhabditis elegans GN=unc-70 PE=2 SV=1; E0AHA7|E0AHA7_CAEEL Protein UNC-70, isoform c OS=Caenorhabditis elegans GN=unc-70 PE=2 SV=1; Q9U9J8|Q9U9J8_CAEEL Beta-G spectrin OS=Caenorhabditis elegans GN=unc-7	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
P90868|P90868_CAEEL Protein PBS-7 OS=Caenorhabditis elegans GN=pbs-7 PE=4 SV=2	0.12

Q93459|NUBP1_CAEEL Cytosolic Fe-S cluster assembly factor NUBP1 homolog OS=Caenorhabditis elegans GN=F10G8.6 PE=3 SV=2	0.12
Q95Y37|Q95Y37_CAEEL Protein PLST-1 OS=Caenorhabditis elegans GN=plst-1 PE=4 SV=5	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
P52009|CYP1_CAEEL Peptidyl-prolyl cis-trans isomerase 1 OS=Caenorhabditis elegans GN=cyn-1 PE=2 SV=1	0.12
Q8WQB6|Q8WQB6_CAEEL Protein Y105E8A.3 OS=Caenorhabditis elegans GN=CELE_Y105E8A.3 PE=4 SV=2	0.12
G5EFJ8|G5EFJ8_CAEEL Protein PCP-2 OS=Caenorhabditis elegans GN=pcp-2 PE=4 SV=1	0.12
Q18822|Q18822_CAEEL Protein ALH-10 OS=Caenorhabditis elegans GN=alh-10 PE=3 SV=1	0.12
P52716|YPP3_CAEEL Uncharacterized serine carboxypeptidase F32A5.3 OS=Caenorhabditis elegans GN=F32A5.3 PE=1 SV=1	0.12
Q23487|Q23487_CAEEL Protein ZK418.9, isoform a OS=Caenorhabditis elegans GN=CELE_ZK418.9 PE=2 SV=2; Q7Z145|Q7Z145_CAEEL Protein ZK418.9, isoform b OS=Caenorhabditis elegans GN=CELE_ZK418.9 PE=2 SV=1	0.12
Q8IA89|Q8IA89_CAEEL Protein F44E7.4, isoform c OS=Caenorhabditis elegans GN=CELE_F44E7.4 PE=2 SV=1; Q8MXK1|Q8MXK1_CAEEL Protein F44E7.4, isoform b OS=Caenorhabditis elegans GN=CELE_F44E7.4 PE=2 SV=1; O16249|O16249_CAEEL Protein F44E7.4, isoform a	0.12
Q94261|EIF3M_CAEEL COP9/Signalosome and eIF3 complex-shared subunit 1 OS=Caenorhabditis elegans GN=cif-1 PE=1 SV=1	0.12

O62106|IF6_CAEEL Eukaryotic translation initiation factor 6 OS=Caenorhabditis elegans GN=eif-6 PE=3 SV=1	0.12
Q95QC2|Q95QC2_CAEEL Protein R02F2.9 OS=Caenorhabditis elegans GN=CELE_R02F2.9 PE=4 SV=1	0.12
Q18217|ULA1_CAEEL NEDD8-activating enzyme E1 regulatory subunit OS=Caenorhabditis elegans GN=ula-1 PE=3 SV=2	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
P53589|SUCB2_CAEEL Probable succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Caenorhabditis elegans GN=C50F7.4 PE=3 SV=1	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
A5Z2S3|A5Z2S3_CAEEL Protein F54B3.1, isoform b OS=Caenorhabditis elegans GN=CELE_F54B3.1 PE=2 SV=2; O62263|O62263_CAEEL Protein F54B3.1, isoform a OS=Caenorhabditis elegans GN=CELE_F54B3.1 PE=2 SV=2	0.12
H1ZUX6|H1ZUX6_CAEEL Protein ITX-1, isoform b OS=Caenorhabditis elegans GN=itx-1 PE=4 SV=1; O45000|O45000_CAEEL Protein ITX-1, isoform a OS=Caenorhabditis elegans GN=itx-1 PE=4 SV=3	0.12
Q19162|Q19162_CAEEL Protein RPL-11.2 OS=Caenorhabditis elegans GN=rpl-11.2 PE=3 SV=1	0.12
Q966L5|SRRT_CAEEL Serrate RNA effector molecule homolog OS=Caenorhabditis elegans GN=E01A2.2 PE=3 SV=1; Q966L5-2|SRRT_CAEEL Isoform b of Serrate RNA effector molecule homolog OS=Caenorhabditis elegans GN=E01A2.2	0.12
P52057|PROSC_CAEEL Proline synthase co-transcribed bacterial homolog protein OS=Caenorhabditis elegans GN=F09E5.8 PE=3 SV=1	0.11
Q9TXR7|Q9TXR7_CAEEL Protein F56B3.11, isoform a OS=Caenorhabditis elegans GN=CELE_F56B3.11 PE=4 SV=1	0.11
Q19680|Q19680_CAEEL Protein F21D5.1 OS=Caenorhabditis elegans GN=CELE_F21D5.1 PE=3 SV=1	0.11

Q19057|Q19057_CAEEL Protein ACDH-12, isoform a OS=Caenorhabditis elegans GN=acdh-12 PE=2 SV=1; Q6AHQ5|Q6AHQ5_CAEEL Protein ACDH-12, isoform b OS=Caenorhabditis elegans GN=acdh-12 PE=2 SV=1	0.11
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
Q19265|Q19265_CAEEL Protein F09E5.2 OS=Caenorhabditis elegans GN=CELE_F09E5.2 PE=4 SV=2	0.11
Q18486|COQ8_CAEEL Ubiquinone biosynthesis protein coq-8 OS=Caenorhabditis elegans GN=coq-8 PE=3 SV=2	0.11
Q86NC2|Q86NC2_CAEEL Protein NUO-2, isoform b OS=Caenorhabditis elegans GN=nuo-2 PE=2 SV=1; O01602|O01602_CAEEL Protein NUO-2, isoform a OS=Caenorhabditis elegans GN=nuo-2 PE=2 SV=2	0.11
Q22763|Q22763_CAEEL Protein NEP-22 OS=Caenorhabditis elegans GN=nep-22 PE=4 SV=2	0.11
A5HU98|A5HU98_CAEEL Protein GUK-1, isoform b OS=Caenorhabditis elegans GN=guk-1 PE=2 SV=1; P91425|P91425_CAEEL Protein GUK-1, isoform a OS=Caenorhabditis elegans GN=guk-1 PE=2 SV=2	0.11
Q19853|Q19853_CAEEL Protein F28B4.3 OS=Caenorhabditis elegans GN=CELE_F28B4.3 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
O16487|O16487_CAEEL Protein B0238.11 OS=Caenorhabditis elegans GN=B0238.11 PE=4 SV=1	0.11
D0IMZ5|D0IMZ5_CAEEL Protein FLN-1, isoform a OS=Caenorhabditis elegans GN=fln-1 PE=2 SV=1; D0IMZ7|D0IMZ7_CAEEL Protein FLN-1, isoform f OS=Caenorhabditis elegans GN=fln-1 PE=2 SV=1; D0IMZ8|D0IMZ8_CAEEL Protein FLN-1, isoform g OS=Caenorhabditis e	0.11

G4SRU7|G4SRU7_CAEEL Protein Y39A3CL.4, isoform c OS=Caenorhabditis elegans GN=CELE_Y39A3CL.4 PE=2 SV=2; Q965X3|Q965X3_CAEEL Protein Y39A3CL.4, isoform a OS=Caenorhabditis elegans GN=CELE_Y39A3CL.4 PE=2 SV=2; H2L0P9|H2L0P9_CAEEL Protein Y39A3CL.4,	0.11
O01812|FABP6_CAEEL Fatty acid-binding protein homolog 6 OS=Caenorhabditis elegans GN=lbp-6 PE=1 SV=1	0.11
Q93540|Q93540_CAEEL Protein F20D1.9 OS=Caenorhabditis elegans GN=CELE_F20D1.9 PE=3 SV=2	0.11
Q20628|Q20628_CAEEL Protein CDD-2 OS=Caenorhabditis elegans GN=cdd-2 PE=1 SV=1	0.11
Q21265|TIMPL_CAEEL Putative metalloproteinase inhibitor tag-225 OS=Caenorhabditis elegans GN=tag-225 PE=1 SV=1	0.11
Q9TYP9|Q9TYP9_CAEEL Protein MCA-2 OS=Caenorhabditis elegans GN=mca-2 PE=2 SV=2; O76833|O76833_CAEEL Calcium ATPase OS=Caenorhabditis elegans GN=mca-2 PE=2 SV=1	0.11
G5EDP2|G5EDP2_CAEEL 3-keto-acyl-CoA thiolase OS=Caenorhabditis elegans GN=daf-22 PE=2 SV=1	0.11
Q9BMU4|Q9BMU4_CAEEL Protein Y54G2A.2, isoform a OS=Caenorhabditis elegans GN=4D561 PE=2 SV=1; Q688Z6|Q688Z6_CAEEL Protein Y54G2A.2, isoform b OS=Caenorhabditis elegans GN=CELE_Y54G2A.2 PE=2 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
Q9XVF7|RL8_CAEEL 60S ribosomal protein L8 OS=Caenorhabditis elegans GN=rpl-8 PE=3 SV=1	0.11
Q27487|CATA1_CAEEL Peroxisomal catalase 1 OS=Caenorhabditis elegans GN=ctl-2 PE=2 SV=3	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
Q9U307|Q9U307_CAEEL Glutamine synthetase OS=Caenorhabditis elegans GN=gln-3 PE=2 SV=1; Q2HQL4|Q2HQL4_CAEEL Glutamine synthetase OS=Caenorhabditis elegans GN=gln-3 PE=2 SV=1; H8ESF5|H8ESF5_CAEEL Protein GLN-3, isoform c OS=Caenorhabditis elegans G	0.11
Q22601|Q22601_CAEEL Protein APA-2 OS=Caenorhabditis elegans GN=apa-2 PE=1 SV=2	0.11
Q18921|Q18921_CAEEL Protein SNAP-1 OS=Caenorhabditis elegans GN=snap-1 PE=4 SV=3	0.11
H9G2W1|H9G2W1_CAEEL Protein AC3.5, isoform b OS=Caenorhabditis elegans GN=AC3.5 PE=4 SV=1; Q17405|YQ02_CAEEL Aminopeptidase-like protein AC3.5 OS=Caenorhabditis elegans GN=AC3.5 PE=1 SV=2	0.11
P11141|HSP7F_CAEEL Heat shock 70 kDa protein F, mitochondrial OS=Caenorhabditis elegans GN=hsp-6 PE=1 SV=2	0.11
P55955|TTR16_CAEEL Transthyretin-like protein 16 OS=Caenorhabditis elegans GN=ttr-16 PE=1 SV=2	0.11
Q9XVE9|Q9XVE9_CAEEL Protein RPL-14 OS=Caenorhabditis elegans GN=rpl-14 PE=4 SV=1	0.11
Q9N4J8|Q9N4J8_CAEEL Protein CCT-3 OS=Caenorhabditis elegans GN=cct-3 PE=3 SV=3	0.11
Q19007|Q19007_CAEEL Protein NAP-1 OS=Caenorhabditis elegans GN=nap-1 PE=3 SV=1	0.11
Q93795|Q93795_CAEEL Protein HPO-31 OS=Caenorhabditis elegans GN=hpo-31 PE=3 SV=2	0.11
Q9XUI1|Q9XUI1_CAEEL Protein CLEC-94 OS=Caenorhabditis elegans GN=clec-94 PE=4 SV=1	0.11
Q21284|Q21284_CAEEL Protein K07E3.4, isoform a OS=Caenorhabditis elegans GN=CELE_K07E3.4 PE=3 SV=2	0.11
G5EC25|G5EC25_CAEEL Protein Y49A3A.1 OS=Caenorhabditis elegans GN=CELE_Y49A3A.1 PE=3 SV=1	0.11

O02082|O02082_CAEEL Protein C48E7.1 OS=Caenorhabditis elegans GN=C48E7.1 PE=4 SV=1	0.11
Q9U1Z4|Q9U1Z4_CAEEL Protein Y60A3A.9 OS=Caenorhabditis elegans GN=CELE_Y60A3A.9 PE=3 SV=1	0.11
P29691|EF2_CAEEL Elongation factor 2 OS=Caenorhabditis elegans GN=eef-2 PE=1 SV=4; P29691-2|EF2_CAEEL Isoform b of Elongation factor 2 OS=Caenorhabditis elegans GN=eef-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
P41956|C560_CAEEL Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=Caenorhabditis elegans GN=mev-1 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
A7DT40|A7DT40_CAEEL Protein F49D11.10 OS=Caenorhabditis elegans GN=CELE_F49D11.10 PE=4 SV=2	0.11
O76367|O76367_CAEEL Protein F29C4.2 OS=Caenorhabditis elegans GN=CELE_F29C4.2 PE=4 SV=1	0.11
L8E833|L8E833_CAEEL Protein W05H9.1, isoform b OS=Caenorhabditis elegans GN=CELE_W05H9.1 PE=4 SV=1; Q23179|Q23179_CAEEL Protein W05H9.1, isoform a OS=Caenorhabditis elegans GN=CELE_W05H9.1 PE=4 SV=1	0.11
H2KZG6|H2KZG6_CAEEL Protein ACDH-1, isoform a OS=Caenorhabditis elegans GN=acdh-1 PE=3 SV=1; Q8IAB6|Q8IAB6_CAEEL Protein ACDH-1, isoform b OS=Caenorhabditis elegans GN=acdh-1 PE=3 SV=1	0.11
Q20964|Q20964_CAEEL Protein LYS-4 OS=Caenorhabditis elegans GN=lys-4 PE=4 SV=1	0.10
B5QSI7|B5QSI7_CAEEL Protein GCK-3, isoform b OS=Caenorhabditis elegans GN=gck-3 PE=2 SV=1; F9UKV1|F9UKV1_CAEEL Protein GCK-3, isoform c OS=Caenorhabditis elegans GN=gck-3 PE=2 SV=1; G5EEN4|G5EEN4_CAEEL Protein GCK-3, isoform a OS=Caenorhabditis e	0.10
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

O45246|O45246_CAEEL Protein HSP-70 OS=Caenorhabditis elegans GN=hsp-70 PE=3 SV=1; G5ECU5|G5ECU5_CAEEL Protein F44E5.4 OS=Caenorhabditis elegans GN=CELE_F44E5.4 PE=3 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
Q9XW17|Q9XW17_CAEEL Protein CAR-1 OS=Caenorhabditis elegans GN=car-1 PE=4 SV=1	0.10
Q9N599|PSA4_CAEEL Proteasome subunit alpha type-4 OS=Caenorhabditis elegans GN=pas-3 PE=3 SV=2	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
P42170|RIR2_CAEEL Ribonucleoside-diphosphate reductase small chain OS=Caenorhabditis elegans GN=rnr-2 PE=3 SV=1	0.10
Q9U2M4|HOT_CAEEL Probable hydroxyacid-oxoacid transhydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y38F1A.6 PE=3 SV=1	0.10
Q09482|Q09482_CAEEL Protein C18H9.3 OS=Caenorhabditis elegans GN=C18H9.3 PE=4 SV=2	0.10
Q18198|Q18198_CAEEL Protein C26B9.5 OS=Caenorhabditis elegans GN=C26B9.5 PE=4 SV=1	0.10
P91303|VATG_CAEEL Probable V-type proton ATPase subunit G OS=Caenorhabditis elegans GN=vha-10 PE=3 SV=1	0.10
G5ECM9|G5ECM9_CAEEL Cystatin C OS=Caenorhabditis elegans GN=cpi-2 PE=2 SV=1	0.10
O17836|O17836_CAEEL Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-1 PE=2 SV=1; Q3S1I8|Q3S1I8_CAEEL Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-1 PE=2 SV=1; Q7JL40|Q7JL40_CAEEL Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-1 PE=2 SV=1; >	0.10

Q9XUS4|Q9XUS4_CAEEL Protein K08E3.5, isoform c OS=Caenorhabditis elegans GN=CELE_K08E3.5 PE=2 SV=1; Q69Z13|Q69Z13_CAEEL Protein K08E3.5, isoform f OS=Caenorhabditis elegans GN=CELE_K08E3.5 PE=2 SV=1; Q86D12|Q86D12_CAEEL Protein K08E3.5, isoform e	0.10
O01541|SYAC_CAEEL Alanine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=aars-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
Q8WSZ9|Q8WSZ9_CAEEL SKR-1 (Fragment) OS=Caenorhabditis elegans GN=skr-1 PE=2 SV=1; G5ECU1|G5ECU1_CAEEL Protein SKR-1 OS=Caenorhabditis elegans GN=skr-1 PE=1 SV=1	0.10
Q86MJ6|Q86MJ6_CAEEL Protein CKC-1, isoform b OS=Caenorhabditis elegans GN=ckc-1 PE=2 SV=1; Q22820|Q22820_CAEEL Protein CKC-1, isoform a OS=Caenorhabditis elegans GN=ckc-1 PE=2 SV=1	0.10
Q18187|Q18187_CAEEL Protein C25H3.3 OS=Caenorhabditis elegans GN=C25H3.3 PE=4 SV=2	0.10
Q9U302|Q9U302_CAEEL Protein PAB-1, isoform a OS=Caenorhabditis elegans GN=pab-1 PE=2 SV=1; Q7K798|Q7K798_CAEEL Protein PAB-1, isoform b OS=Caenorhabditis elegans GN=pab-1 PE=2 SV=1; Q17350|Q17350_CAEEL Polyadenylate-binding protein OS=Caenorhabdi	0.10
Q9U1Z6|Q9U1Z6_CAEEL Protein Y60A3A.7 OS=Caenorhabditis elegans GN=CELE_Y60A3A.7 PE=4 SV=1	0.10
P34342|RGP2_CAEEL Ran GTPase-activating protein 2 OS=Caenorhabditis elegans GN=ran-2 PE=4 SV=3; P34342-2|RGP2_CAEEL Isoform b of Ran GTPase-activating protein 2 OS=Caenorhabditis elegans GN=ran-2	0.10
Q23186|Q23186_CAEEL Protein W06A7.2, isoform a OS=Caenorhabditis elegans GN=CELE_W06A7.2 PE=4 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
O17773|O17773_CAEEL Protein F09C3.2 OS=Caenorhabditis elegans GN=CELE_F09C3.2 PE=4 SV=2	0.10
O02089|O02089_CAEEL Protein MSRA-1 OS=Caenorhabditis elegans GN=msra-1 PE=4 SV=1	0.10

Q9Y194|SGPL_CAEEL Sphingosine-1-phosphate lyase OS=Caenorhabditis elegans GN=spl-1 PE=1 SV=1	0.10
Q04833|LRP_CAEEL Low-density lipoprotein receptor-related protein OS=Caenorhabditis elegans GN=lrp-1 PE=1 SV=1	0.10
Q18885|BTF3_CAEEL Transcription factor BTF3 homolog OS=Caenorhabditis elegans GN=icd-1 PE=1 SV=1	0.10
P34574|CLH_CAEEL Probable clathrin heavy chain 1 OS=Caenorhabditis elegans GN=chc-1 PE=3 SV=1	0.10
Q9BLB6|RU2A_CAEEL Probable U2 small nuclear ribonucleoprotein A OS=Caenorhabditis elegans GN=mog-2 PE=1 SV=1	0.10
Q10657|TPIS_CAEEL Triosephosphate isomerase OS=Caenorhabditis elegans GN=tpi-1 PE=1 SV=2	0.10
P91020|P91020_CAEEL Protein C07D8.6 OS=Caenorhabditis elegans GN=C07D8.6 PE=1 SV=1	0.10
Q965N4|Q965N4_CAEEL Protein CHIN-1 OS=Caenorhabditis elegans GN=chin-1 PE=4 SV=3	0.10
Q19371|Q19371_CAEEL Protein SEC-24.1 OS=Caenorhabditis elegans GN=sec-24.1 PE=4 SV=1	0.10
Q9XWV5|RT10_CAEEL Probable 28S ribosomal protein S10, mitochondrial OS=Caenorhabditis elegans GN=mrps-10 PE=3 SV=1	0.10
Q27504|CAH3_CAEEL Putative carbonic anhydrase 3 OS=Caenorhabditis elegans GN=cah-3 PE=3 SV=1	0.10
O17907|O17907_CAEEL Protein CTG-1, isoform a OS=Caenorhabditis elegans GN=ctg-1 PE=4 SV=2; K8ES75|K8ES75_CAEEL Protein CTG-1, isoform b OS=Caenorhabditis elegans GN=ctg-1 PE=4 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
Q9XUU9|JAGN_CAEEL Protein jagunal homolog OS=Caenorhabditis elegans GN=K05C4.2 PE=3 SV=1	0.10
O18178|O18178_CAEEL Protein PPTR-1 OS=Caenorhabditis elegans GN=pptr-1 PE=1 SV=4	0.10

Q93701|Q93701_CAEEL Protein GST-19 OS=Caenorhabditis elegans GN=gst-19 PE=1 SV=1	0.09
Q93714|IDH3A_CAEEL Probable isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=idha-1 PE=1 SV=3	0.09
Q10051|PRP19_CAEEL Pre-mRNA-processing factor 19 homolog OS=Caenorhabditis elegans GN=prp-19 PE=3 SV=2	0.09
G5EDJ3|G5EDJ3_CAEEL Equilibrative nucleoside transporter 1 OS=Caenorhabditis elegans GN=ent-1 PE=2 SV=1	0.09
O45444|O45444_CAEEL Protein CLEC-63 OS=Caenorhabditis elegans GN=clec-63 PE=4 SV=1	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
P55216|CGL2_CAEEL Putative cystathionine gamma-lyase 2 OS=Caenorhabditis elegans GN=cth-2 PE=1 SV=1	0.09
Q22968|Q22968_CAEEL Aminomethyltransferase OS=Caenorhabditis elegans GN=gcst-1 PE=3 SV=1	0.09
Q22579|Q22579_CAEEL Protein T19D12.1 OS=Caenorhabditis elegans GN=CELE_T19D12.1 PE=4 SV=2	0.09
G5EGB3|G5EGB3_CAEEL Protein RAGC-1 OS=Caenorhabditis elegans GN=ragc-1 PE=4 SV=1	0.09
Q9N4K0|MOS1_CAEEL Mitochondrial inner membrane organizing system protein F54A3.5 OS=Caenorhabditis elegans GN=F54A3.5 PE=3 SV=2	0.09
P90900|IFA4_CAEEL Intermediate filament protein ifa-4 OS=Caenorhabditis elegans GN=ifa-4 PE=1 SV=2	0.09
Q1HB05|Q1HB05_CAEEL Protein CYP-25A3 OS=Caenorhabditis elegans GN=cyp-25a3 PE=3 SV=1; Q21262|Q21262_CAEEL Protein CYP-25A6 OS=Caenorhabditis elegans GN=cyp-25a6 PE=4 SV=1	0.09
Q23030|Q23030_CAEEL Protein R09F10.1 OS=Caenorhabditis elegans GN=CELE_R09F10.1 PE=3 SV=2	0.09
P48150|RS14_CAEEL 40S ribosomal protein S14 OS=Caenorhabditis elegans GN=rps-14 PE=3 SV=1	0.09

O18155|O18155_CAEEL Protein T28D6.7 OS=Caenorhabditis elegans GN=CELE_T28D6.7 PE=4 SV=2	0.09
Q27389|RL13A_CAEEL 60S ribosomal protein L13a OS=Caenorhabditis elegans GN=rpl-16 PE=2 SV=1	0.09
Q9U2D2|Q9U2D2_CAEEL Protein CKU-70 OS=Caenorhabditis elegans GN=cku-70 PE=4 SV=3	0.09
Q21962|Q21962_CAEEL Protein R12C12.1, isoform a OS=Caenorhabditis elegans GN=CELE_R12C12.1 PE=2 SV=1	0.09
P34313|BUD31_CAEEL Protein BUD31 homolog OS=Caenorhabditis elegans GN=C07A9.2 PE=2 SV=1	0.09
Q20932|BYN1_CAEEL Cell adhesion protein byn-1 OS=Caenorhabditis elegans GN=byn-1 PE=3 SV=2	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
Q23089|Q23089_CAEEL Protein XPO-1, isoform a OS=Caenorhabditis elegans GN=xpo-1 PE=2 SV=2	0.09
G5EC91|G5EC91_CAEEL Protein DPY-11 OS=Caenorhabditis elegans GN=dpy-11 PE=2 SV=1	0.09
O17003|O17003_CAEEL Protein T23B12.4 OS=Caenorhabditis elegans GN=CELE_T23B12.4 PE=4 SV=2	0.09
Q9NES7|Q9NES7_CAEEL Protein Y39B6A.1 OS=Caenorhabditis elegans GN=CELE_Y39B6A.1 PE=4 SV=1	0.09
Q9TYK1|GAR1_CAEEL Probable H/ACA ribonucleoprotein complex subunit 1-like protein OS=Caenorhabditis elegans GN=Y66H1A.4 PE=3 SV=2	0.09
O62388|O62388_CAEEL Ribosomal protein L37 OS=Caenorhabditis elegans GN=CELE_W01D2.1 PE=3 SV=1; P49622|RL37_CAEEL 60S ribosomal protein L37 OS=Caenorhabditis elegans GN=rpl-37 PE=3 SV=2	0.09
Q7YX30|Q7YX30_CAEEL Protein F26D2.16 OS=Caenorhabditis elegans GN=CELE_F26D2.16 PE=4 SV=1	0.09

Q23382|Q23382_CAEEL Protein CCDC-47 OS=Caenorhabditis elegans GN=ccdc-47 PE=1 SV=1	0.09
O45934|O45934_CAEEL Protein Y43F4B.5, isoform a OS=Caenorhabditis elegans GN=CELE_Y43F4B.5 PE=2 SV=1; Q86DA0|Q86DA0_CAEEL Protein Y43F4B.5, isoform b OS=Caenorhabditis elegans GN=CELE_Y43F4B.5 PE=2 SV=1	0.09
Q95PZ1|Q95PZ1_CAEEL Protein Y67H2A.5 OS=Caenorhabditis elegans GN=CELE_Y67H2A.5 PE=4 SV=1	0.09
O62250|TIM16_CAEEL Mitochondrial import inner membrane translocase subunit tim-16 OS=Caenorhabditis elegans GN=tim-16 PE=3 SV=1	0.09
O76654|O76654_CAEEL Protein TRY-8 OS=Caenorhabditis elegans GN=try-8 PE=4 SV=1	0.09
Q9N5K2|RPAB1_CAEEL DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Caenorhabditis elegans GN=rpb-5 PE=3 SV=1	0.09
Q95Q95-2|TOR_CAEEL Isoform b of Target of rapamycin homolog OS=Caenorhabditis elegans GN=let-363; Q95Q95|TOR_CAEEL Target of rapamycin homolog OS=Caenorhabditis elegans GN=let-363 PE=2 SV=3	0.09
K8ESM2|K8ESM2_CAEEL Protein Y16B4A.2 OS=Caenorhabditis elegans GN=CELE_Y16B4A.2 PE=4 SV=1	0.09
B2D6P1|B2D6P1_CAEEL Protein RMD-2, isoform c OS=Caenorhabditis elegans GN=rmd-2 PE=2 SV=1; P90762|P90762_CAEEL Protein RMD-2, isoform a OS=Caenorhabditis elegans GN=rmd-2 PE=2 SV=1; Q8MQB5|Q8MQB5_CAEEL Protein RMD-2, isoform b OS=Caenorhabditis e	0.09
Q17361|UBP14_CAEEL Ubiquitin carboxyl-terminal hydrolase 14 OS=Caenorhabditis elegans GN=usp-14 PE=2 SV=2	0.09
Q95008|PSA5_CAEEL Proteasome subunit alpha type-5 OS=Caenorhabditis elegans GN=pas-5 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
Q20875|DHX15_CAEEL Putative pre-mRNA-splicing factor ATP-dependent RNA helicase F56D2.6 OS=Caenorhabditis elegans GN=F56D2.6 PE=2 SV=1; G8JY03|G8JY03_CAEEL Protein F56D2.6, isoform b OS=Caenorhabditis elegans GN=CELE_F56D2.6 PE=2 SV=1	0.09
O76384|O76384_CAEEL Protein MMS-19 OS=Caenorhabditis elegans GN=mms-19 PE=4 SV=2	0.09

O76371|O76371_CAEEL Protein RPT-5 OS=Caenorhabditis elegans GN=rpt-5 PE=1 SV=1	0.09
Q18990|Q18990_CAEEL Protein PYR-1 OS=Caenorhabditis elegans GN=pyr-1 PE=3 SV=2	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
Q21763|Q21763_CAEEL Protein R05H5.3 OS=Caenorhabditis elegans GN=CELE_R05H5.3 PE=4 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
O17643|O17643_CAEEL Isocitrate dehydrogenase [NADP] OS=Caenorhabditis elegans GN=idh-2 PE=3 SV=1	0.09
I7FN66|I7FN66_CAEEL Rab-7 (Fragment) OS=Caenorhabditis elegans GN=rab-7 PE=2 SV=1; Q23146|Q23146_CAEEL Protein RAB-7 OS=Caenorhabditis elegans GN=rab-7 PE=3 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
Q18164|DPYD_CAEEL Dihydropyrimidine dehydrogenase [NADP(+)] OS=Caenorhabditis elegans GN=dpyd-1 PE=3 SV=2	0.08
O02155|O02155_CAEEL Protein T09B4.5, isoform a OS=Caenorhabditis elegans GN=CELE_T09B4.5 PE=2 SV=1	0.08
Q20719|NDUV2_CAEEL Probable NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Caenorhabditis elegans GN=F53F4.10 PE=1 SV=1	0.08
Q20819|EFTS_CAEEL Elongation factor Ts, mitochondrial OS=Caenorhabditis elegans GN=tsfm-1 PE=2 SV=1	0.08
Q17499|Q17499_CAEEL Protein B0395.3 OS=Caenorhabditis elegans GN=B0395.3 PE=3 SV=1	0.08
P54216|ALF1_CAEEL Fructose-bisphosphate aldolase 1 OS=Caenorhabditis elegans GN=aldo-1 PE=1 SV=1	0.08

Q22875-2|SHOC2_CAEEL Isoform b of Leucine-rich repeat protein soc-2 OS=Caenorhabditis elegans GN=soc-2; Q22875|SHOC2_CAEEL Leucine-rich repeat protein soc-2 OS=Caenorhabditis elegans GN=soc-2 PE=1 SV=3	0.08
O17921|O17921_CAEEL Protein TBB-1 OS=Caenorhabditis elegans GN=tbb-1 PE=3 SV=1	0.08
G4SL51|G4SL51_CAEEL Protein PQN-52, isoform c OS=Caenorhabditis elegans GN=pqn-52 PE=2 SV=1	0.08
Q21929|DCXR_CAEEL Probable L-xylulose reductase OS=Caenorhabditis elegans GN=dhs-21 PE=3 SV=2	0.08
Q9U2X0|Q9U2X0_CAEEL Protein PRMT-1 OS=Caenorhabditis elegans GN=prmt-1 PE=4 SV=1	0.08
G5EDD4|G5EDD4_CAEEL Protein TBA-4 OS=Caenorhabditis elegans GN=tba-4 PE=3 SV=1	0.08
P46550|TCPZ_CAEEL T-complex protein 1 subunit zeta OS=Caenorhabditis elegans GN=cct-6 PE=1 SV=1; G8JY43|G8JY43_CAEEL Protein CCT-6, isoform b OS=Caenorhabditis elegans GN=cct-6 PE=2 SV=1	0.08
G5EES9|G5EES9_CAEEL Protein Y54E10A.3 OS=Caenorhabditis elegans GN=txl PE=2 SV=1	0.08
Q9XVJ3|Q9XVJ3_CAEEL Protein QDPR-1 OS=Caenorhabditis elegans GN=qdpr-1 PE=1 SV=1	0.08
Q966E7|Q966E7_CAEEL Protein Y104H12D.3 OS=Caenorhabditis elegans GN=CELE_Y104H12D.3 PE=3 SV=2	0.08
Q9U3P5|Q9U3P5_CAEEL Protein TRAM-1, isoform a OS=Caenorhabditis elegans GN=tram-1 PE=2 SV=1; Q9XXK7|Q9XXK7_CAEEL Protein TRAM-1, isoform b OS=Caenorhabditis elegans GN=tram-1 PE=2 SV=1	0.08
Q20829|Q20829_CAEEL Protein AMAN-1 OS=Caenorhabditis elegans GN=aman-1 PE=4 SV=2	0.08
Q18785|MIF2_CAEEL MIF-like protein mif-2 OS=Caenorhabditis elegans GN=mif-2 PE=2 SV=1; G3MU38|G3MU38_CAEEL Protein MIF-2, isoform c OS=Caenorhabditis elegans GN=mif-2 PE=2 SV=1; D6R8W7|D6R8W7_CAEEL Protein MIF-2, isoform b OS=Caenorhabditis elega	0.08
P34689|GLH1_CAEEL ATP-dependent RNA helicase glh-1 OS=Caenorhabditis elegans GN=glh-1 PE=1 SV=3	0.08

P34460|EF1B1_CAEEL Probable elongation factor 1-beta/1-delta 1 OS=Caenorhabditis elegans GN=eef-1B.1 PE=1 SV=1	0.08
Q9N3D9|Q9N3D9_CAEEL Protein NDUF-5 OS=Caenorhabditis elegans GN=nduf-5 PE=4 SV=1	0.08
P52713|MMSA_CAEEL Probable methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Caenorhabditis elegans GN=alh-8 PE=1 SV=1	0.08
O16520|ERF1_CAEEL Eukaryotic peptide chain release factor subunit 1 OS=Caenorhabditis elegans GN=erf-1 PE=3 SV=2	0.08
Q20430|Q20430_CAEEL Protein MRPL-14, isoform b OS=Caenorhabditis elegans GN=mrpl-14 PE=3 SV=2	0.08
P34690|TBA2_CAEEL Tubulin alpha-2 chain OS=Caenorhabditis elegans GN=tba-2 PE=2 SV=1	0.08
G5EBR1|G5EBR1_CAEEL Protein GDI-1, isoform a OS=Caenorhabditis elegans GN=gdi-1 PE=2 SV=1; Q2V4S2|Q2V4S2_CAEEL Protein GDI-1, isoform b OS=Caenorhabditis elegans GN=gdi-1 PE=2 SV=1	0.08
P34500|TTR2_CAEEL Transthyretin-like protein 2 OS=Caenorhabditis elegans GN=ttr-2 PE=1 SV=1	0.08
G5ECS9|G5ECS9_CAEEL Protein CPT-2, isoform a OS=Caenorhabditis elegans GN=cpt-2 PE=2 SV=2; G5EFE6|G5EFE6_CAEEL Protein CPT-2, isoform b OS=Caenorhabditis elegans GN=cpt-2 PE=2 SV=2	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
Q8ITV7|Q8ITV7_CAEEL Protein Y44E3A.6, isoform a OS=Caenorhabditis elegans GN=CELE_Y44E3A.6 PE=2 SV=1; Q8ITV6|Q8ITV6_CAEEL Protein Y44E3A.6, isoform b OS=Caenorhabditis elegans GN=CELE_Y44E3A.6 PE=2 SV=1	0.08

Q9N5V3|Q9N5V3_CAEEL Protein IMB-3 OS=Caenorhabditis elegans GN=imb-3 PE=4 SV=2	0.08
Q20655|14332_CAEEL 14-3-3-like protein 2 OS=Caenorhabditis elegans GN=ftt-2 PE=1 SV=1; Q95ZT1|Q95ZT1_CAEEL Protein FTT-2, isoform b OS=Caenorhabditis elegans GN=ftt-2 PE=2 SV=2	0.08
P10771|H11_CAEEL Histone H1.1 OS=Caenorhabditis elegans GN=his-24 PE=1 SV=4	0.08
Q86S66-2|NACA_CAEEL Isoform b of Nascent polypeptide-associated complex subunit alpha OS=Caenorhabditis elegans GN=Y65B4BR.5	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
O17606|YK4P_CAEEL UPF0160 protein C27H6.8 OS=Caenorhabditis elegans GN=C27H6.8 PE=3 SV=2	0.08
P47991|RL6_CAEEL 60S ribosomal protein L6 OS=Caenorhabditis elegans GN=rpl-6 PE=1 SV=1	0.08
P91871|P91871_CAEEL Protein FASN-1 OS=Caenorhabditis elegans GN=fasn-1 PE=4 SV=2	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
D6R8W5|D6R8W5_CAEEL Protein NSTP-10, isoform b OS=Caenorhabditis elegans GN=nstp-10 PE=2 SV=1; Q968A5|FUCT1_CAEEL GDP-fucose transporter OS=Caenorhabditis elegans GN=C50F4.14 PE=1 SV=1	0.08
Q93545|Q93545_CAEEL Protein F20G2.2 OS=Caenorhabditis elegans GN=CELE_F20G2.2 PE=3 SV=1	0.08
Q95YC6|Q95YC6_CAEEL Protein C45B2.1 OS=Caenorhabditis elegans GN=C45B2.1 PE=4 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
Q9U2Z1|Q9U2Z1_CAEEL Protein SEC-23 OS=Caenorhabditis elegans GN=sec-23 PE=4 SV=2	0.08

Q93244|Q93244_CAEEL Cysteine synthase OS=Caenorhabditis elegans GN=cysl-1 PE=1 SV=2	0.07
Q93573|TCTP_CAEEL Translationally-controlled tumor protein homolog OS=Caenorhabditis elegans GN=tct-1 PE=1 SV=1	0.07
Q27245|YH24_CAEEL Putative aminopeptidase W07G4.4 OS=Caenorhabditis elegans GN=W07G4.4 PE=1 SV=1	0.07
Q95ZW2|Q95ZW2_CAEEL Ribulose-phosphate 3-epimerase OS=Caenorhabditis elegans GN=CELE_F08F8.7 PE=3 SV=1	0.07
Q09501|IFP1_CAEEL Intermediate filament protein ifp-1 OS=Caenorhabditis elegans GN=ifp-1 PE=3 SV=1	0.07
P34286|PSB1_CAEEL Proteasome subunit beta type-1 OS=Caenorhabditis elegans GN=pbs-6 PE=1 SV=2	0.07
P52899|ODPA_CAEEL Probable pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Caenorhabditis elegans GN=T05H10.6 PE=2 SV=1; Q8I111|Q8I111_CAEEL Protein PDHA-1, isoform b OS=Caenorhabditis elegans GN=pdha-1 PE=2 SV=1	0.07
Q22496|Q22496_CAEEL Protein HPO-5 OS=Caenorhabditis elegans GN=hpo-5 PE=4 SV=2	0.07
P49049|IMP2_CAEEL Intramembrane protease 2 OS=Caenorhabditis elegans GN=imp-2 PE=1 SV=1	0.07
Q17475|Q17475_CAEEL Protein B0334.3, isoform b OS=Caenorhabditis elegans GN=B0334.3 PE=2 SV=2; Q17474|Q17474_CAEEL Protein B0334.3, isoform a OS=Caenorhabditis elegans GN=B0334.3 PE=2 SV=2	0.07
Q9N358|TCPQ_CAEEL T-complex protein 1 subunit theta OS=Caenorhabditis elegans GN=cct-8 PE=1 SV=3	0.07
O62107|O62107_CAEEL Protein GALE-1, isoform a OS=Caenorhabditis elegans GN=gale-1 PE=2 SV=1; Q564Q1|Q564Q1_CAEEL Protein GALE-1, isoform b OS=Caenorhabditis elegans GN=gale-1 PE=2 SV=1	0.07
B1PEX0|B1PEX0_CAEEL NADH dehydrogenase subunit 5 (Fragment) OS=Caenorhabditis elegans GN=ND5 PE=4 SV=1; P24896|NU5M_CAEEL NADH-ubiquinone oxidoreductase chain 5 OS=Caenorhabditis elegans GN=nd5 PE=3 SV=2; G4XR36|G4XR36_CAEEL NADH dehydrogenase su	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
Q9XW92|VATA_CAEEL V-type proton ATPase catalytic subunit A OS=Caenorhabditis elegans GN=vha-13 PE=1 SV=3	0.07
Q9U2D9|GYS_CAEEL Probable glycogen [starch] synthase OS=Caenorhabditis elegans GN=gsy-1 PE=3 SV=1	0.07
Q9XX11|Q9XX11_CAEEL Protein Y39A1A.21, isoform a OS=Caenorhabditis elegans GN=CELE_Y39A1A.21 PE=4 SV=1	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
Q17574|MTRR_CAEEL Putative methionine synthase reductase OS=Caenorhabditis elegans GN=tag-165 PE=3 SV=1	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
O02056|RL4_CAEEL 60S ribosomal protein L4 OS=Caenorhabditis elegans GN=rpl-4 PE=1 SV=3	0.07
Q9N4G8|Q9N4G8_CAEEL Protein YOP-1 OS=Caenorhabditis elegans GN=yop-1 PE=4 SV=1	0.07
Q09979|Q09979_CAEEL Protein DHS-6 OS=Caenorhabditis elegans GN=dhs-6 PE=4 SV=3	0.07
Q20230|KCY2_CAEEL UMP-CMP kinase 2 OS=Caenorhabditis elegans GN=F40F8.1 PE=1 SV=1	0.07
Q8I4I9|Q8I4I9_CAEEL Protein HDA-5 OS=Caenorhabditis elegans GN=hda-5 PE=2 SV=1	0.07
P91495|P91495_CAEEL Protein NPP-12 OS=Caenorhabditis elegans GN=npp-12 PE=4 SV=1	0.07
Q18786|SMD2_CAEEL Probable small nuclear ribonucleoprotein Sm D2 OS=Caenorhabditis elegans GN=snr-4 PE=1 SV=1	0.07

Q27888|LDH_CAEEL L-lactate dehydrogenase OS=Caenorhabditis elegans GN=ldh-1 PE=2 SV=1	0.07
G5EG13|G5EG13_CAEEL Protein DHS-12 OS=Caenorhabditis elegans GN=dhs-12 PE=3 SV=1	0.07
Q17880|Q17880_CAEEL Protein NUO-1 OS=Caenorhabditis elegans GN=nuo-1 PE=4 SV=1	0.07
Q8MNS3|Q8MNS3_CAEEL Protein F42G9.1, isoform b OS=Caenorhabditis elegans GN=CELE_F42G9.1 PE=2 SV=1; P49595|PP2C1_CAEEL Probable protein phosphatase 2C F42G9.1 OS=Caenorhabditis elegans GN=F42G9.1 PE=2 SV=2	0.07
Q21926|SYIC_CAEEL Isoleucine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=irs-1 PE=3 SV=1	0.07
Q02335|YOL8_CAEEL TPR repeat-containing protein ZK370.8 OS=Caenorhabditis elegans GN=ZK370.8 PE=4 SV=3	0.07
G5EFY6|G5EFY6_CAEEL Protein SEC-31 OS=Caenorhabditis elegans GN=sec-31 PE=4 SV=1	0.07
Q09251|RN121_CAEEL RING finger protein 121 OS=Caenorhabditis elegans GN=rnf-121 PE=3 SV=1	0.07
Q8WTL6|Q8WTL6_CAEEL Protein HPO-29 OS=Caenorhabditis elegans GN=hpo-29 PE=4 SV=2	0.06
O18239|O18239_CAEEL Protein Y57G11C.15, isoform a OS=Caenorhabditis elegans GN=CELE_Y57G11C.15 PE=2 SV=1; G3MU88|G3MU88_CAEEL Protein Y57G11C.15, isoform b OS=Caenorhabditis elegans GN=CELE_Y57G11C.15 PE=2 SV=1	0.06
Q95YD5|Q95YD5_CAEEL Protein VHA-16 OS=Caenorhabditis elegans GN=vha-16 PE=4 SV=1	0.06
O45499|RS26_CAEEL 40S ribosomal protein S26 OS=Caenorhabditis elegans GN=rps-26 PE=3 SV=1	0.06
Q20758|ARL1_CAEEL ADP-ribosylation factor-like protein 1 OS=Caenorhabditis elegans GN=arl-1 PE=3 SV=2	0.06
Q17598|TM104_CAEEL Transmembrane protein 104 homolog OS=Caenorhabditis elegans GN=C03A3.2 PE=1 SV=2	0.06
G5EDV3|G5EDV3_CAEEL Protein CEY-4 OS=Caenorhabditis elegans GN=cey-4 PE=4 SV=1	0.06

O02286|O02286_CAEEL Protein PCK-2, isoform a OS=Caenorhabditis elegans GN=pck-2 PE=2 SV=1; Q7JKI2|Q7JKI2_CAEEL Protein PCK-2, isoform d OS=Caenorhabditis elegans GN=pck-2 PE=2 SV=1; Q7JKI3|Q7JKI3_CAEEL Protein PCK-2, isoform c OS=Caenorhabditis e	0.06
G5EBI0|G5EBI0_CAEEL 4D656 OS=Caenorhabditis elegans GN=4D656 PE=2 SV=1	0.06
Q11117|LMP1_CAEEL LAMP family protein lmp-1 OS=Caenorhabditis elegans GN=lmp-1 PE=2 SV=1	0.06
Q09657|Q09657_CAEEL Protein ZK1320.9 OS=Caenorhabditis elegans GN=CELE_ZK1320.9 PE=4 SV=1	0.06
Q9N4H7|Q9N4H7_CAEEL Protein Y71F9AL.17 OS=Caenorhabditis elegans GN=CELE_Y71F9AL.17 PE=4 SV=2	0.06
P18948-2|VIT6_CAEEL Isoform a of Vitellogenin-6 OS=Caenorhabditis elegans GN=vit-6; P18948|VIT6_CAEEL Vitellogenin-6 OS=Caenorhabditis elegans GN=vit-6 PE=1 SV=5	0.06
O17915|RAN_CAEEL GTP-binding nuclear protein ran-1 OS=Caenorhabditis elegans GN=ran-1 PE=1 SV=1	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
G3MU56|G3MU56_CAEEL Protein F58G11.2, isoform c OS=Caenorhabditis elegans GN=CELE_F58G11.2 PE=2 SV=1; G3MU57|G3MU57_CAEEL Protein F58G11.2, isoform b OS=Caenorhabditis elegans GN=CELE_F58G11.2 PE=2 SV=1; P90897|P90897_CAEEL Protein F58G11.2, isof	0.06
O01578|MPC1_CAEEL Probable mitochondrial pyruvate carrier 1 OS=Caenorhabditis elegans GN=F53F10.3 PE=3 SV=2	0.06
I2HA98|I2HA98_CAEEL Protein PAH-1, isoform b OS=Caenorhabditis elegans GN=pah-1 PE=4 SV=1; P90925|PH4H_CAEEL Probable phenylalanine-4-hydroxylase 1 OS=Caenorhabditis elegans GN=pah-1 PE=1 SV=2; Q9XYQ5|Q9XYQ5_CAEEL Phenylalanine hydroxylase OS=Cae	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
P34604|EI2BA_CAEEL Probable translation initiation factor eIF-2B subunit alpha OS=Caenorhabditis elegans GN=ZK1098.4 PE=1 SV=1	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
D5MCQ2|D5MCQ2_CAEEL Protein SUP-26, isoform g OS=Caenorhabditis elegans GN=sup-26 PE=2 SV=1; D5MCQ6|D5MCQ6_CAEEL Protein SUP-26, isoform m OS=Caenorhabditis elegans GN=sup-26 PE=2 SV=1; D5MCQ9|D5MCQ9_CAEEL Protein SUP-26, isoform p OS=Caenorhabdi	0.06
Q9U2K8|Q9U2K8_CAEEL Protein ABCE-1 OS=Caenorhabditis elegans GN=abce-1 PE=3 SV=1	0.06
P34517|GPDH2_CAEEL Probable glycerol-3-phosphate dehydrogenase 2 OS=Caenorhabditis elegans GN=gpdh-2 PE=2 SV=2; A7LPE6|A7LPE6_CAEEL Protein GPDH-2, isoform d OS=Caenorhabditis elegans GN=gpdh-2 PE=2 SV=1; Q7JMU1|Q7JMU1_CAEEL Protein GPDH-2, isofo	0.06
P41847|DRE2_CAEEL Anamorsin homolog OS=Caenorhabditis elegans GN=T20B12.7 PE=3 SV=1	0.06
P34815-2|UNC18_CAEEL Isoform a of Putative acetylcholine regulator unc-18 OS=Caenorhabditis elegans GN=unc-18; P34815|UNC18_CAEEL Putative acetylcholine regulator unc-18 OS=Caenorhabditis elegans GN=unc-18 PE=2 SV=3	0.06
P52011|CYP3_CAEEL Peptidyl-prolyl cis-trans isomerase 3 OS=Caenorhabditis elegans GN=cyn-3 PE=1 SV=1	0.06
P90916|LIN53_CAEEL Probable histone-binding protein lin-53 OS=Caenorhabditis elegans GN=lin-53 PE=1 SV=2	0.06
O17680|METK1_CAEEL Probable S-adenosylmethionine synthase 1 OS=Caenorhabditis elegans GN=sams-1 PE=1 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
Q5DX36|Q5DX36_CAEEL Protein C33F10.14 OS=Caenorhabditis elegans GN=C33F10.14 PE=4 SV=1	0.06
Q8WQF1|Q8WQF1_CAEEL Protein PCCB-1, isoform b OS=Caenorhabditis elegans GN=pccb-1 PE=2 SV=1; Q20676|Q20676_CAEEL Protein PCCB-1, isoform a OS=Caenorhabditis elegans GN=pccb-1 PE=2 SV=1	0.06

G5EGP4|G5EGP4_CAEEL Protein VHA-6 OS=Caenorhabditis elegans GN=vha-6 PE=2 SV=1	0.06
H2L0N9|H2L0N9_CAEEL Protein Y37E3.17, isoform a OS=Caenorhabditis elegans GN=CELE_Y37E3.17 PE=3 SV=1; Q6AW03|Q6AW03_CAEEL Protein Y37E3.17, isoform b OS=Caenorhabditis elegans GN=CELE_Y37E3.17 PE=3 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
O02621|GPX1_CAEEL Glutathione peroxidase 1 OS=Caenorhabditis elegans GN=gpx-1 PE=3 SV=1	0.06
O45430|O45430_CAEEL Protein MCCC-1 OS=Caenorhabditis elegans GN=mccc-1 PE=4 SV=2	0.06
Q19825|SYRC_CAEEL Probable arginine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=rrt-1 PE=2 SV=2; Q65ZK0|Q65ZK0_CAEEL Protein RARS-1, isoform b OS=Caenorhabditis elegans GN=rars-1 PE=2 SV=1	0.06
Q9NAI5|Q9NAI5_CAEEL Protein Y39G8B.1, isoform a OS=Caenorhabditis elegans GN=CELE_Y39G8B.1 PE=2 SV=1; Q9U2J6|Q9U2J6_CAEEL Protein Y39G8B.1, isoform b OS=Caenorhabditis elegans GN=CELE_Y39G8B.1 PE=2 SV=1	0.06
Q9N584|Q9N584_CAEEL Protein Y110A7A.19 OS=Caenorhabditis elegans GN=CELE_Y110A7A.19 PE=4 SV=1	0.06
Q20589|Q20589_CAEEL Protein F49C12.12 OS=Caenorhabditis elegans GN=CELE_F49C12.12 PE=4 SV=1	0.06

H2KYP1|H2KYP1_CAEEL Protein LNTL-1, isoform a OS=Caenorhabditis elegans GN=lntl-1 PE=1 SV=1; Q8I7L5|Q8I7L5_CAEEL Protein LNTL-1, isoform b OS=Caenorhabditis elegans GN=lntl-1 PE=4 SV=1	0.06
Q9XUW5|Q9XUW5_CAEEL Protein F58E10.3, isoform a OS=Caenorhabditis elegans GN=CELE_F58E10.3 PE=3 SV=1	0.06
Q9TYW0|Q9TYW0_CAEEL Clustered mitochondria protein homolog OS=Caenorhabditis elegans GN=clu-1 PE=2 SV=1; P34466|CLU_CAEEL Clustered mitochondria protein homolog OS=Caenorhabditis elegans GN=clu-1 PE=2 SV=1	0.06
Q17413|UCK_CAEEL Probable uridine-cytidine kinase OS=Caenorhabditis elegans GN=B0001.4 PE=3 SV=2	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
Q19131|Q19131_CAEEL Protein NPP-5 OS=Caenorhabditis elegans GN=npp-5 PE=4 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
Q9GS00|CSN1_CAEEL COP9 signalosome complex subunit 1 OS=Caenorhabditis elegans GN=csn-1 PE=1 SV=1	0.05
G5EFM9|G5EFM9_CAEEL Molting protein MLT-1 OS=Caenorhabditis elegans GN=nekl-3 PE=2 SV=1	0.05
O18154|O18154_CAEEL Protein TBA-7 OS=Caenorhabditis elegans GN=tba-7 PE=3 SV=1	0.05
Q9N357|Q9N357_CAEEL Protein Y55F3AR.2 OS=Caenorhabditis elegans GN=CELE_Y55F3AR.2 PE=4 SV=2	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

Q9XWD5|Q9XWD5_CAEEL Protein Y47H9C.7 OS=Caenorhabditis elegans GN=CELE_Y47H9C.7 PE=3 SV=1	0.05
Q9U2F2|Q9U2F2_CAEEL Protein CPT-1 OS=Caenorhabditis elegans GN=cpt-1 PE=3 SV=3	0.05
Q18406|EXOC5_CAEEL Exocyst complex component 5 OS=Caenorhabditis elegans GN=sec-10 PE=3 SV=1	0.05
E9RKC7|E9RKC7_CAEEL Protein Y95B8A.8 OS=Caenorhabditis elegans GN=CELE_Y95B8A.8 PE=4 SV=1	0.05
B3CJ34|B3CJ34_CAEEL Protein GCN-1 OS=Caenorhabditis elegans GN=gcn-1 PE=4 SV=2	0.05
Q19420|IMPA1_CAEEL Inositol monophosphatase ttx-7 OS=Caenorhabditis elegans GN=ttx-7 PE=1 SV=3; Q19420-2|IMPA1_CAEEL Isoform b of Inositol monophosphatase ttx-7 OS=Caenorhabditis elegans GN=ttx-7	0.05
Q9XUV0|Q9XUV0_CAEEL Proteasome subunit beta type OS=Caenorhabditis elegans GN=pbs-5 PE=3 SV=1	0.05
P54811|TERA1_CAEEL Transitional endoplasmic reticulum ATPase homolog 1 OS=Caenorhabditis elegans GN=cdc-48.1 PE=1 SV=1	0.05
Q20329|Q20329_CAEEL Protein F42C5.9 OS=Caenorhabditis elegans GN=CELE_F42C5.9 PE=3 SV=1	0.05
Q19070|Q19070_CAEEL Eft-1 protein OS=Caenorhabditis elegans GN=eft-1 PE=2 SV=1; Q23463|Q23463_CAEEL Protein EFTU-2 OS=Caenorhabditis elegans GN=eftu-2 PE=2 SV=1	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
D3YT36|D3YT36_CAEEL Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-2 PE=2 SV=1; Q23539|Q23539_CAEEL Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-2 PE=2 SV=2; D3YT37|D3YT37_CAEEL Pyruvate kinase OS=Caenorhabditis elegans GN=pyk-2 PE=2 SV=1	0.05

P46562|AL7A1_CAEEL Putative aldehyde dehydrogenase family 7 member A1 homolog OS=Caenorhabditis elegans GN=alh-9 PE=3 SV=2	0.05
Q20206|Q20206_CAEEL Protein RPS-11 OS=Caenorhabditis elegans GN=rps-11 PE=3 SV=1	0.05
Q19339|Q19339_CAEEL Protein ACS-14 OS=Caenorhabditis elegans GN=acs-14 PE=4 SV=1	0.05
P36609|NCS2_CAEEL Neuronal calcium sensor 2 OS=Caenorhabditis elegans GN=ncs-2 PE=2 SV=2	0.05
P90829|DPOD1_CAEEL DNA polymerase delta catalytic subunit OS=Caenorhabditis elegans GN=F10C2.4 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
Q94246|Q94246_CAEEL Protein GFI-1 OS=Caenorhabditis elegans GN=gfi-1 PE=4 SV=1; Q94247|Q94247_CAEEL Protein F57F4.4 OS=Caenorhabditis elegans GN=CELE_F57F4.4 PE=4 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
Q20967|Q20967_CAEEL Protein LYS-5 OS=Caenorhabditis elegans GN=lys-5 PE=4 SV=1	0.05
Q95Y24|Q95Y24_CAEEL Protein Y41D4A.4 OS=Caenorhabditis elegans GN=CELE_Y41D4A.4 PE=4 SV=1	0.05
Q22562|Q22562_CAEEL Protein T19B10.2 OS=Caenorhabditis elegans GN=CELE_T19B10.2 PE=4 SV=2	0.05
Q93796|NRF5_CAEEL Nose resistant to fluoxetine protein 5 OS=Caenorhabditis elegans GN=nrf-5 PE=1 SV=2	0.05
Q03577|SYDC_CAEEL Aspartate--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=drs-1 PE=3 SV=1	0.05
Q09580-3|GUAA_CAEEL Isoform c of Probable GMP synthase [glutamine-hydrolyzing] OS=Caenorhabditis elegans GN=M106.4; Q09580-2|GUAA_CAEEL Isoform a of Probable GMP synthase [glutamine-hydrolyzing] OS=Caenorhabditis elegans GN=M106.4; Q09580|GUAA_CA	0.05
Q21300|Q21300_CAEEL Protein K07G5.4 OS=Caenorhabditis elegans GN=CELE_K07G5.4 PE=4 SV=1	0.05

Q09289|ADRM1_CAEEL Proteasomal ubiquitin receptor ADRM1 homolog OS=Caenorhabditis elegans GN=C56G2.7 PE=3 SV=2	0.05
Q21219|PEPT1_CAEEL Peptide transporter family 1 OS=Caenorhabditis elegans GN=pept-1 PE=2 SV=2	0.05
Q20310|Q20310_CAEEL Protein F42A10.5 OS=Caenorhabditis elegans GN=CELE_F42A10.5 PE=4 SV=1	0.05
B1Q251|B1Q251_CAEEL Protein M106.8 OS=Caenorhabditis elegans GN=CELE_M106.8 PE=4 SV=1	0.05
G5EFC4|G5EFC4_CAEEL Protein D1081.8 OS=Caenorhabditis elegans GN=CELE_D1081.8 PE=4 SV=1	0.05
O44512|O44512_CAEEL Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Caenorhabditis elegans GN=isp-1 PE=3 SV=1	0.05
G5EEQ8|G5EEQ8_CAEEL Protein T08A11.2 OS=Caenorhabditis elegans GN=CELE_T08A11.2 PE=4 SV=1	0.05
Q23670|TOP2_CAEEL Probable DNA topoisomerase 2 OS=Caenorhabditis elegans GN=K12D12.1 PE=3 SV=2	0.05
G5EEI9|G5EEI9_CAEEL Protein K11D9.3 OS=Caenorhabditis elegans GN=CELE_K11D9.3 PE=4 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
Q9XUT9|Q9XUT9_CAEEL Protein K06G5.1, isoform a OS=Caenorhabditis elegans GN=CELE_K06G5.1 PE=2 SV=1; Q5WRM0|Q5WRM0_CAEEL Protein K06G5.1, isoform b OS=Caenorhabditis elegans GN=CELE_K06G5.1 PE=2 SV=1	0.04
Q9N5T2|Q9N5T2_CAEEL Protein F45D11.14 OS=Caenorhabditis elegans GN=CELE_F45D11.14 PE=2 SV=1; G5EFS5|G5EFS5_CAEEL Protein F45D11.15 OS=Caenorhabditis elegans GN=CELE_F45D11.15 PE=4 SV=1	0.04
Q10663|GCP_CAEEL Bifunctional glyoxylate cycle protein OS=Caenorhabditis elegans GN=gei-7 PE=1 SV=2; Q8IA71|Q8IA71_CAEEL Protein ICL-1, isoform b OS=Caenorhabditis elegans GN=icl-1 PE=2 SV=1	0.04
Q19264|DEOC_CAEEL Putative deoxyribose-phosphate aldolase OS=Caenorhabditis elegans GN=F09E5.3 PE=3 SV=1	0.04

Q19818|Q19818_CAEEL Protein NHL-2 OS=Caenorhabditis elegans GN=nhl-2 PE=4 SV=2	0.04
Q09541|YQS6_CAEEL Putative subtilase-type proteinase F21H12.6 OS=Caenorhabditis elegans GN=F21H12.6 PE=3 SV=1	0.04
O44511|O44511_CAEEL Protein SPH-1 OS=Caenorhabditis elegans GN=sph-1 PE=4 SV=2	0.04
Q07750-1|ADF1_CAEEL Isoform a of Actin-depolymerizing factor 1, isoforms a/b OS=Caenorhabditis elegans GN=unc-60	0.04
Q21217|GABT_CAEEL Probable 4-aminobutyrate aminotransferase, mitochondrial OS=Caenorhabditis elegans GN=gta-1 PE=1 SV=1; N1NVC4|N1NVC4_CAEEL Protein GTA-1, isoform b OS=Caenorhabditis elegans GN=gta-1 PE=4 SV=1	0.04
Q9BL09|Q9BL09_CAEEL Protein Y48G8AL.13 OS=Caenorhabditis elegans GN=CELE_Y48G8AL.13 PE=4 SV=1	0.04
Q9U354|Q9U354_CAEEL Protein VPS-25 OS=Caenorhabditis elegans GN=vps-25 PE=4 SV=1	0.04
Q9XWP1|Q9XWP1_CAEEL Protein Y43F8C.7 OS=Caenorhabditis elegans GN=CELE_Y43F8C.7 PE=4 SV=1	0.04
Q19324|Q19324_CAEEL Protein RPN-5 OS=Caenorhabditis elegans GN=rpn-5 PE=4 SV=1	0.04
H2L0J5|H2L0J5_CAEEL Cysteine synthase OS=Caenorhabditis elegans GN=cysl-3 PE=3 SV=1; O01592|O01592_CAEEL Cysteine synthase OS=Caenorhabditis elegans GN=cysl-3 PE=2 SV=1; Q86NC6|Q86NC6_CAEEL Protein CYSL-3, isoform b OS=Caenorhabditis elegans GN=c	0.04
G5EC10|G5EC10_CAEEL Galectin LEC-9 OS=Caenorhabditis elegans GN=lec-9 PE=2 SV=1	0.04
Q19766|TOM20_CAEEL Mitochondrial import receptor subunit TOM20 homolog OS=Caenorhabditis elegans GN=tomm-20 PE=1 SV=1	0.04
Q20219|Q20219_CAEEL Protein F40F4.6 OS=Caenorhabditis elegans GN=CELE_F40F4.6 PE=4 SV=2	0.04
P50140|CH60_CAEEL Chaperonin homolog Hsp-60, mitochondrial OS=Caenorhabditis elegans GN=hsp-60 PE=1 SV=2; G8JYF5|G8JYF5_CAEEL Protein HSP-60, isoform b OS=Caenorhabditis elegans GN=hsp-60 PE=2 SV=1	0.04

Q9TYY8|Q9TYY8_CAEEL Ubiquitin carboxyl-terminal hydrolase OS=Caenorhabditis elegans GN=CELE_H34C03.2 PE=3 SV=1	0.04
G5EEH6|G5EEH6_CAEEL Isovaleryl-CoA dehydrogenase OS=Caenorhabditis elegans GN=ivd-1 PE=2 SV=1	0.04
Q9BL46|Q9BL46_CAEEL Protein Y71H2AM.11 OS=Caenorhabditis elegans GN=CELE_Y71H2AM.11 PE=4 SV=4	0.04
P91477|PSB2_CAEEL Proteasome subunit beta type-2 OS=Caenorhabditis elegans GN=pbs-4 PE=3 SV=2	0.04
Q7KPV7|Q7KPV7_CAEEL Protein ZK697.14 OS=Caenorhabditis elegans GN=CELE_ZK697.14 PE=3 SV=1	0.04
P34382|FAR1_CAEEL Fatty-acid and retinol-binding protein 1 OS=Caenorhabditis elegans GN=far-1 PE=2 SV=1	0.04
Q9U3L5|Q9U3L5_CAEEL Protein C47B2.2 OS=Caenorhabditis elegans GN=C47B2.2 PE=4 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
P46554|LCMT1_CAEEL Probable leucine carboxyl methyltransferase 1 OS=Caenorhabditis elegans GN=B0285.4 PE=3 SV=1	0.04
G5EDF9|G5EDF9_CAEEL ABC transporter PGP-2 OS=Caenorhabditis elegans GN=pgp-2 PE=2 SV=1	0.04
G5EBJ8|G5EBJ8_CAEEL Major sperm protein OS=Caenorhabditis elegans GN=CELE_Y59E9AR.1 PE=3 SV=1	0.04
Q20012|Q20012_CAEEL Protein DHS-20 OS=Caenorhabditis elegans GN=dhs-20 PE=4 SV=3	0.04
Q9XVJ2|GNPI_CAEEL Probable glucosamine-6-phosphate isomerase OS=Caenorhabditis elegans GN=T03F6.3 PE=1 SV=1	0.04
G5EBL8|G5EBL8_CAEEL Protein T07C4.10 OS=Caenorhabditis elegans GN=CELE_T07C4.10 PE=4 SV=1	0.04
P55954|COX5A_CAEEL Cytochrome c oxidase subunit 5A, mitochondrial OS=Caenorhabditis elegans GN=cco-2 PE=1 SV=2	0.04

G5EGL2|G5EGL2_CAEEL Protein T28D6.6, isoform a OS=Caenorhabditis elegans GN=CELE_T28D6.6 PE=2 SV=1; G2HK05|G2HK05_CAEEL Protein T28D6.6, isoform b OS=Caenorhabditis elegans GN=CELE_T28D6.6 PE=2 SV=1	0.04
Q21603|Q21603_CAEEL Protein UGT-62 OS=Caenorhabditis elegans GN=ugt-62 PE=3 SV=1	0.04
H2L099|H2L099_CAEEL Protein GCK-1, isoform a OS=Caenorhabditis elegans GN=gck-1 PE=4 SV=1; Q6ABW4|Q6ABW4_CAEEL Protein GCK-1, isoform d OS=Caenorhabditis elegans GN=gck-1 PE=4 SV=1; H2L0A1|H2L0A1_CAEEL Protein GCK-1, isoform c OS=Caenorhabditis e	0.04
P34183-2|SYH_CAEEL Isoform a of Histidine--tRNA ligase OS=Caenorhabditis elegans GN=hrs-1; P34183|SYH_CAEEL Histidine--tRNA ligase OS=Caenorhabditis elegans GN=hrs-1 PE=2 SV=3	0.04
Q18758|Q18758_CAEEL Protein KLO-1 OS=Caenorhabditis elegans GN=klo-1 PE=3 SV=1	0.04
O02639|RL19_CAEEL 60S ribosomal protein L19 OS=Caenorhabditis elegans GN=rpl-19 PE=3 SV=1	0.04
G5EG54|G5EG54_CAEEL Protein CPT-5 OS=Caenorhabditis elegans GN=cpt-5 PE=4 SV=1	0.04
P91128|RL13_CAEEL 60S ribosomal protein L13 OS=Caenorhabditis elegans GN=rpl-13 PE=3 SV=1	0.04
O44750|O44750_CAEEL Protein APP-1 OS=Caenorhabditis elegans GN=app-1 PE=1 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
O17345|O17345_CAEEL Protein TTR-6 OS=Caenorhabditis elegans GN=ttr-6 PE=4 SV=1	0.04
Q18476|Q18476_CAEEL Protein C35A5.8 OS=Caenorhabditis elegans GN=C35A5.8 PE=4 SV=3	0.04
Q8WQD7|Q8WQD7_CAEEL Protein R04F11.5 OS=Caenorhabditis elegans GN=CELE_R04F11.5 PE=4 SV=1	0.04

Q9N393|Q9N393_CAEEL Protein Y54H5A.1 OS=Caenorhabditis elegans GN=CELE_Y54H5A.1 PE=4 SV=2	0.04
Q19102|Q19102_CAEEL Protein ARD-1 OS=Caenorhabditis elegans GN=ard-1 PE=3 SV=1	0.04
Q9U300|Q9U300_CAEEL Protein Y106G6H.5 OS=Caenorhabditis elegans GN=CELE_Y106G6H.5 PE=3 SV=2	0.04
Q23378|Q23378_CAEEL Protein TTR-48 OS=Caenorhabditis elegans GN=ttr-48 PE=4 SV=1	0.04
Q9XU15|Q9XU15_CAEEL Protein H25P06.1 OS=Caenorhabditis elegans GN=CELE_H25P06.1 PE=3 SV=1	0.04
Q7Z1Q3|Q7Z1Q3_CAEEL Protein ALH-12, isoform a OS=Caenorhabditis elegans GN=alh-12 PE=2 SV=1; Q7Z1Q2|Q7Z1Q2_CAEEL Protein ALH-12, isoform b OS=Caenorhabditis elegans GN=alh-12 PE=2 SV=1	0.04
Q8WQA8|Q8WQA8_CAEEL Protein RPS-20 OS=Caenorhabditis elegans GN=rps-20 PE=3 SV=1	0.03
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
O61787|INX16_CAEEL Innexin-16 OS=Caenorhabditis elegans GN=inx-16 PE=3 SV=2	0.03
G4RYA5|G4RYA5_CAEEL Protein F38A1.8 OS=Caenorhabditis elegans GN=CELE_F38A1.8 PE=4 SV=1	0.03
O45503|MTX1_CAEEL Metaxin-1 homolog OS=Caenorhabditis elegans GN=mtx-1 PE=1 SV=1	0.03
Q966C7|Q966C7_CAEEL Transaldolase OS=Caenorhabditis elegans GN=CELE_Y24D9A.8 PE=3 SV=1	0.03
Q18823|LAM2_CAEEL Laminin-like protein lam-2 OS=Caenorhabditis elegans GN=lam-2 PE=1 SV=3	0.03

Q3T978|Q3T978_CAEEL Protein ACDH-11, isoform b OS=Caenorhabditis elegans GN=acdh-11 PE=2 SV=1; Q9XWZ2|Q9XWZ2_CAEEL Protein ACDH-11, isoform a OS=Caenorhabditis elegans GN=acdh-11 PE=2 SV=1	0.03
O02115|PCNA_CAEEL Proliferating cell nuclear antigen OS=Caenorhabditis elegans GN=pcn-1 PE=1 SV=3	0.03
Q9GZI3|Q9GZI3_CAEEL Protein POD-2, isoform a OS=Caenorhabditis elegans GN=pod-2 PE=2 SV=1; H2L0M0|H2L0M0_CAEEL Protein POD-2, isoform c OS=Caenorhabditis elegans GN=pod-2 PE=4 SV=1	0.03
P91914|RL27_CAEEL 60S ribosomal protein L27 OS=Caenorhabditis elegans GN=rpl-27 PE=2 SV=1	0.03
Q17335|ADHX_CAEEL Alcohol dehydrogenase class-3 OS=Caenorhabditis elegans GN=H24K24.3 PE=2 SV=1; Q17335-2|ADHX_CAEEL Isoform b of Alcohol dehydrogenase class-3 OS=Caenorhabditis elegans GN=H24K24.3	0.03
O18650|RS19_CAEEL 40S ribosomal protein S19 OS=Caenorhabditis elegans GN=rps-19 PE=2 SV=1	0.03
Q22620|Q22620_CAEEL Protein PARS-1, isoform a OS=Caenorhabditis elegans GN=pars-1 PE=2 SV=1; Q65ZK5|Q65ZK5_CAEEL Protein PARS-1, isoform b OS=Caenorhabditis elegans GN=pars-1 PE=2 SV=1	0.03
Q9BL15|Q9BL15_CAEEL Protein Y48G8AL.5 OS=Caenorhabditis elegans GN=CELE_Y48G8AL.5 PE=4 SV=4	0.03
Q23571|ODB2_CAEEL Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Caenorhabditis elegans GN=ZK669.4 PE=3 SV=1	0.03
P34339|EIF3A_CAEEL Eukaryotic translation initiation factor 3 subunit A OS=Caenorhabditis elegans GN=egl-45 PE=3 SV=1	0.03
O62431|SYQ_CAEEL Probable glutamine--tRNA ligase OS=Caenorhabditis elegans GN=ers-1 PE=2 SV=1; D3YT95|D3YT95_CAEEL Protein QARS-1, isoform b OS=Caenorhabditis elegans GN=qars-1 PE=2 SV=1	0.03
Q21021|Q21021_CAEEL Protein NPP-9, isoform a OS=Caenorhabditis elegans GN=npp-9 PE=2 SV=2; Q86G90|Q86G90_CAEEL Protein NPP-9, isoform b OS=Caenorhabditis elegans GN=npp-9 PE=1 SV=1	0.03
O17107|O17107_CAEEL Protein K06H6.6 OS=Caenorhabditis elegans GN=CELE_K06H6.6 PE=4 SV=1	0.03
O61217|O61217_CAEEL Purine nucleoside phosphorylase OS=Caenorhabditis elegans GN=CELE_K02D7.1 PE=3 SV=1	0.03

Q8IAA5|Q8IAA5_CAEEL Protein Y50D7A.10 OS=Caenorhabditis elegans GN=CELE_Y50D7A.10 PE=4 SV=2	0.03
Q20627|Q20627_CAEEL Protein PAM-1, isoform a OS=Caenorhabditis elegans GN=pam-1 PE=2 SV=1; Q4TT88|Q4TT88_CAEEL Protein PAM-1, isoform b OS=Caenorhabditis elegans GN=pam-1 PE=2 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
Q18655|Q18655_CAEEL Protein C46C2.2 OS=Caenorhabditis elegans GN=C46C2.2 PE=4 SV=2	0.03
D3YT31|D3YT31_CAEEL Protein T12G3.2, isoform e OS=Caenorhabditis elegans GN=CELE_T12G3.2 PE=2 SV=1	0.03
Q22498|COPG_CAEEL Probable coatomer subunit gamma OS=Caenorhabditis elegans GN=T14G10.5 PE=2 SV=1; Q2XN02|Q2XN02_CAEEL Coatomer subunit gamma OS=Caenorhabditis elegans GN=CELE_T14G10.5 PE=2 SV=1; F5GUA3|F5GUA3_CAEEL Coatomer subunit gamma OS=Caen	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
Q21285|Q21285_CAEEL Protein DAO-3 OS=Caenorhabditis elegans GN=dao-3 PE=3 SV=2	0.03
G5EF48|G5EF48_CAEEL Protein Y63D3A.8 OS=Caenorhabditis elegans GN=CELE_Y63D3A.8 PE=4 SV=1	0.03
O45946|RL18_CAEEL 60S ribosomal protein L18 OS=Caenorhabditis elegans GN=rpl-18 PE=3 SV=1	0.03
Q8MXR2|Q8MXR2_CAEEL Protein HRPF-2 OS=Caenorhabditis elegans GN=hrpf-2 PE=4 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

P48152|RS3_CAEEL 40S ribosomal protein S3 OS=Caenorhabditis elegans GN=rps-3 PE=3 SV=1	0.03
O44326|HMP2_CAEEL Protein humpback-2 OS=Caenorhabditis elegans GN=hmp-2 PE=1 SV=1; H2L2I2|H2L2I2_CAEEL Protein HMP-2, isoform b OS=Caenorhabditis elegans GN=hmp-2 PE=4 SV=1	0.03
P46975|STT3_CAEEL Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3 OS=Caenorhabditis elegans GN=T12A2.2 PE=1 SV=1	0.03
O17895|O17895_CAEEL Protein HAF-3 OS=Caenorhabditis elegans GN=haf-3 PE=3 SV=2	0.03
G5EE46|G5EE46_CAEEL Protein F54D5.12 OS=Caenorhabditis elegans GN=CELE_F54D5.12 PE=4 SV=1	0.03
O02328|EIF3C_CAEEL Eukaryotic translation initiation factor 3 subunit C OS=Caenorhabditis elegans GN=eif-3.C 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
Q93694|Q93694_CAEEL Protein GST-24 OS=Caenorhabditis elegans GN=gst-24 PE=3 SV=2	0.03
H2KYJ2|H2KYJ2_CAEEL Protein TTR-59, isoform b OS=Caenorhabditis elegans GN=ttr-59 PE=4 SV=1	0.03
Q9XTT9|Q9XTT9_CAEEL Protein RPT-6 OS=Caenorhabditis elegans GN=rpt-6 PE=4 SV=1	0.03
Q23500|ACOC_CAEEL Probable cytoplasmic aconitate hydratase OS=Caenorhabditis elegans GN=aco-1 PE=1 SV=1	0.03
Q9XWI1|Q9XWI1_CAEEL Protein Y54E2A.4 OS=Caenorhabditis elegans GN=CELE_Y54E2A.4 PE=4 SV=2	0.03
Q21559|Q21559_CAEEL Protein ALY-3, isoform a OS=Caenorhabditis elegans GN=aly-3 PE=4 SV=1	0.03
Q9GYK2|ITBL_CAEEL Uncharacterized integrin beta-like protein C05D9.3 OS=Caenorhabditis elegans GN=C05D9.3 PE=1 SV=3	0.03
P91997|P91997_CAEEL Protein F53F1.2 OS=Caenorhabditis elegans GN=CELE_F53F1.2 PE=4 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
Q23526|Q23526_CAEEL Protein ZK546.2, isoform a OS=Caenorhabditis elegans GN=CELE_ZK546.2 PE=2 SV=4; Q7JPD6|Q7JPD6_CAEEL Protein ZK546.2, isoform c OS=Caenorhabditis elegans GN=CELE_ZK546.2 PE=2 SV=1; Q95PW8|Q95PW8_CAEEL Protein ZK546.2, isoform b	0.02
O02266|O02266_CAEEL Protein ALH-7, isoform a OS=Caenorhabditis elegans GN=alh-7 PE=2 SV=2; G3MU66|G3MU66_CAEEL Protein ALH-7, isoform b OS=Caenorhabditis elegans GN=alh-7 PE=2 SV=1	0.02
Q23315|Q23315_CAEEL Protein EARS-1 OS=Caenorhabditis elegans GN=ears-1 PE=3 SV=1	0.02
O16298|O16298_CAEEL Protein HPO-18 OS=Caenorhabditis elegans GN=hpo-18 PE=4 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
O17135|O17135_CAEEL Protein FBXA-72 OS=Caenorhabditis elegans GN=fbxa-72 PE=4 SV=1	0.02
Q9BI73|Q9BI73_CAEEL Ribose-phosphate pyrophosphokinase OS=Caenorhabditis elegans GN=CELE_R151.2 PE=2 SV=3; Q21994|Q21994_CAEEL Ribose-phosphate pyrophosphokinase OS=Caenorhabditis elegans GN=CELE_R151.2 PE=2 SV=2; Q6AHR3|Q6AHR3_CAEEL Ribose-phosp	0.02
Q19722|SYNC_CAEEL Asparagine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=nrs-1 PE=3 SV=1	0.02
P34599|MTX2_CAEEL Metaxin-2 homolog OS=Caenorhabditis elegans GN=mtx-2 PE=2 SV=3	0.02
Q22054|RS16_CAEEL 40S ribosomal protein S16 OS=Caenorhabditis elegans GN=rps-16 PE=1 SV=3	0.02
A7LPF3|A7LPF3_CAEEL Protein F43D9.3, isoform b OS=Caenorhabditis elegans GN=CELE_F43D9.3 PE=2 SV=4; Q20364|Q20364_CAEEL Protein F43D9.3, isoform a OS=Caenorhabditis elegans GN=CELE_F43D9.3 PE=2 SV=4	0.02

O45502|O45502_CAEEL Protein DNJ-12 OS=Caenorhabditis elegans GN=dnj-12 PE=1 SV=1	0.02
Q94218-2|UFSP_CAEEL Isoform b of Probable Ufm1-specific protease OS=Caenorhabditis elegans GN=F38A5.1; Q94218|UFSP_CAEEL Probable Ufm1-specific protease OS=Caenorhabditis elegans GN=F38A5.1 PE=3 SV=1	0.02
P32740|NNRD_CAEEL ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Caenorhabditis elegans GN=R107.2 PE=3 SV=3	0.02
G5EFZ1|G5EFZ1_CAEEL Cofactor-independent phosphoglycerate mutase OS=Caenorhabditis elegans GN=CELE_F57B10.3 PE=2 SV=1	0.02
O01692|RS17_CAEEL 40S ribosomal protein S17 OS=Caenorhabditis elegans GN=rps-17 PE=3 SV=2	0.02
G5ECG7|G5ECG7_CAEEL Microsomal triglyceride transfer protein OS=Caenorhabditis elegans GN=dsc-4 PE=2 SV=1	0.02
C6KRP5|C6KRP5_CAEEL Protein SQRD-1, isoform b OS=Caenorhabditis elegans GN=sqrd-1 PE=2 SV=1; C6KRP6|C6KRP6_CAEEL Protein SQRD-1, isoform c OS=Caenorhabditis elegans GN=sqrd-1 PE=2 SV=1; O62133|O62133_CAEEL Protein SQRD-1, isoform a OS=Caenorhabdi	0.02
Q22288|TTR15_CAEEL Transthyretin-like protein 15 OS=Caenorhabditis elegans GN=ttr-15 PE=3 SV=1	0.02
P49041|RS5_CAEEL 40S ribosomal protein S5 OS=Caenorhabditis elegans GN=rps-5 PE=3 SV=1	0.02
Q93568|Q93568_CAEEL Protein F25H2.4 OS=Caenorhabditis elegans GN=CELE_F25H2.4 PE=1 SV=1	0.02
K8F7V7|K8F7V7_CAEEL Protein W07E11.1, isoform b OS=Caenorhabditis elegans GN=CELE_W07E11.1 PE=4 SV=1	0.02
O45011|O45011_CAEEL Protein W10C8.5 OS=Caenorhabditis elegans GN=CELE_W10C8.5 PE=3 SV=1	0.02
Q95XS1|Q95XS1_CAEEL Protein TRAP-3 OS=Caenorhabditis elegans GN=trap-3 PE=4 SV=1	0.02
O16369|O16369_CAEEL Protein APS-1 OS=Caenorhabditis elegans GN=aps-1 PE=4 SV=1	0.02

Q9NEN6|RS6_CAEEL 40S ribosomal protein S6 OS=Caenorhabditis elegans GN=rps-6 PE=1 SV=1; I2HAF8|I2HAF8_CAEEL 40S ribosomal protein S6 OS=Caenorhabditis elegans GN=rps-6 PE=3 SV=1; I2HAF9|I2HAF9_CAEEL Protein RPS-6, isoform c OS=Caenorhabditis eleg	0.02
O45012|O45012_CAEEL Protein NOL-5 OS=Caenorhabditis elegans GN=nol-5 PE=4 SV=1	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
Q9NF11|Q9NF11_CAEEL Protein Y105E8B.5 OS=Caenorhabditis elegans GN=CELE_Y105E8B.5 PE=1 SV=1	0.02
O76360|EGL4_CAEEL cGMP-dependent protein kinase egl-4 OS=Caenorhabditis elegans GN=egl-4 PE=1 SV=2; O76360-2|EGL4_CAEEL Isoform b of cGMP-dependent protein kinase egl-4 OS=Caenorhabditis elegans GN=egl-4; O76360-5|EGL4_CAEEL Isoform e of cGMP-dep	0.02
P20163|HSP7D_CAEEL Heat shock 70 kDa protein D OS=Caenorhabditis elegans GN=hsp-4 PE=1 SV=2	0.02
Q21832|Q21832_CAEEL Protein RNP-4 OS=Caenorhabditis elegans GN=rnp-4 PE=4 SV=1	0.02
Q8I4C5|Q8I4C5_CAEEL Protein FAAH-4, isoform b OS=Caenorhabditis elegans GN=faah-4 PE=2 SV=1; Q9U217|Q9U217_CAEEL Protein FAAH-4, isoform a OS=Caenorhabditis elegans GN=faah-4 PE=2 SV=1	0.02
I7FXD3|I7FXD3_CAEEL Rab-5 (Fragment) OS=Caenorhabditis elegans GN=rab-5 PE=2 SV=1; P91857|P91857_CAEEL Protein RAB-5 OS=Caenorhabditis elegans GN=rab-5 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
P24894|COX2_CAEEL Cytochrome c oxidase subunit 2 OS=Caenorhabditis elegans GN=cox-2 PE=2 SV=2; G5EGS6|G5EGS6_CAEEL Cytochrome c oxidase subunit 2 OS=Caenorhabditis elegans GN=COX2 PE=2 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
O02642|O02642_CAEEL Protein SUCL-2 OS=Caenorhabditis elegans GN=sucl-2 PE=3 SV=1	0.02

O44985|O44985_CAEEL Protein TEG-4 OS=Caenorhabditis elegans GN=teg-4 PE=4 SV=1	0.02
O17953|DLDH_CAEEL Dihydrolipoyl dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=dld-1 PE=2 SV=2	0.02
P91350|P91350_CAEEL Protein NPP-6, isoform a OS=Caenorhabditis elegans GN=npp-6 PE=2 SV=1; Q8T8M4|Q8T8M4_CAEEL Protein NPP-6, isoform b OS=Caenorhabditis elegans GN=npp-6 PE=2 SV=1	0.02
G5EGB1|G5EGB1_CAEEL Galectin LEC-2 OS=Caenorhabditis elegans GN=lec-2 PE=2 SV=1	0.02
G5ED41|CAND1_CAEEL Cullin-associated NEDD8-dissociated protein 1 OS=Caenorhabditis elegans GN=cand-1 PE=1 SV=1	0.02
Q9BKS2|Q9BKS2_CAEEL Protein Y82E9BR.14, isoform a OS=Caenorhabditis elegans GN=CELE_Y82E9BR.14 PE=4 SV=1; H2L0G7|H2L0G7_CAEEL Protein Y82E9BR.14, isoform b OS=Caenorhabditis elegans GN=CELE_Y82E9BR.14 PE=4 SV=1	0.02
Q09567|Q09567_CAEEL Protein F48E8.3 OS=Caenorhabditis elegans GN=CELE_F48E8.3 PE=4 SV=3	0.02
Q95Y15|Q95Y15_CAEEL Protein NPP-8, isoform b OS=Caenorhabditis elegans GN=npp-8 PE=2 SV=4	0.02
Q9U296|Q9U296_CAEEL Malic enzyme OS=Caenorhabditis elegans GN=men-1 PE=3 SV=1	0.01
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
Q8IA68|Q8IA68_CAEEL Protein F57B10.3, isoform b OS=Caenorhabditis elegans GN=CELE_F57B10.3 PE=2 SV=1	0.01
Q09285|YQK1_CAEEL KH domain-containing protein C56G2.1 OS=Caenorhabditis elegans GN=C56G2.1/C56G2.2 PE=4 SV=2; Q09285-2|YQK1_CAEEL Isoform b of KH domain-containing protein C56G2.1 OS=Caenorhabditis elegans GN=C56G2.1/C56G2.2	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

O44503|O44503_CAEEL Protein R02D3.1 OS=Caenorhabditis elegans GN=CELE_R02D3.1 PE=4 SV=1	0.01
B5BM23|B5BM23_CAEEL Protein IFG-1, isoform c OS=Caenorhabditis elegans GN=ifg-1 PE=2 SV=1; Q7JMF0|Q7JMF0_CAEEL Protein IFG-1, isoform b OS=Caenorhabditis elegans GN=ifg-1 PE=2 SV=1; Q21531|Q21531_CAEEL Protein IFG-1, isoform a OS=Caenorhabditis e	0.01
M1ZJV8|M1ZJV8_CAEEL Protein Y69A2AR.16, isoform b OS=Caenorhabditis elegans GN=CELE_Y69A2AR.16 PE=4 SV=1; Q95XI7|Q95XI7_CAEEL Protein Y69A2AR.16, isoform a OS=Caenorhabditis elegans GN=CELE_Y69A2AR.16 PE=4 SV=2	0.01
O16521|O16521_CAEEL Protein HPO-19 OS=Caenorhabditis elegans GN=hpo-19 PE=4 SV=1	0.01
Q9XTI0|3HIDH_CAEEL Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=B0250.5 PE=3 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
Q71JP7|Q71JP7_CAEEL ABC6 protein OS=Caenorhabditis elegans GN=W09D6.6 PE=2 SV=1; G5EFD4|G5EFD4_CAEEL Heavy metal tolerance factor 1 OS=Caenorhabditis elegans GN=hmt-1 PE=2 SV=1	0.01
Q07750|ADF1_CAEEL Actin-depolymerizing factor 1, isoforms a/b OS=Caenorhabditis elegans GN=unc-60 PE=1 SV=2	0.01
O01802|RL7_CAEEL 60S ribosomal protein L7 OS=Caenorhabditis elegans GN=rpl-7 PE=1 SV=1	0.01
Q19468|MBOA7_CAEEL Lysophospholipid acyltransferase 7 OS=Caenorhabditis elegans GN=mboa-7 PE=1 SV=2	0.01
Q22240|Q22240_CAEEL Ubiquitin carboxyl-terminal hydrolase OS=Caenorhabditis elegans GN=CELE_T05H10.1 PE=3 SV=2	0.01
Q21338|SPT5H_CAEEL Transcription elongation factor SPT5 OS=Caenorhabditis elegans GN=spt-5 PE=3 SV=3	0.01
Q65ZI3|Q65ZI3_CAEEL Protein DHS-30 OS=Caenorhabditis elegans GN=dhs-30 PE=3 SV=1; H2L0K8|H2L0K8_CAEEL Protein T25G12.13 OS=Caenorhabditis elegans GN=CELE_T25G12.13 PE=3 SV=1	0.01
P49196|RS12_CAEEL 40S ribosomal protein S12 OS=Caenorhabditis elegans GN=rps-12 PE=1 SV=2	0.01

O61521|O61521_CAEEL Protein F17E9.5 OS=Caenorhabditis elegans GN=CELE_F17E9.5 PE=1 SV=1	0.01
P34546|VATL2_CAEEL V-type proton ATPase 16 kDa proteolipid subunit 2/3 OS=Caenorhabditis elegans GN=vha-2 PE=2 SV=2	0.01
Q8I4I0|Q8I4I0_CAEEL Protein F55H12.5 OS=Caenorhabditis elegans GN=CELE_F55H12.5 PE=4 SV=1	0.01
Q9XW63|Q9XW63_CAEEL Protein Y75B8A.24 OS=Caenorhabditis elegans GN=CELE_Y75B8A.24 PE=4 SV=2	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
O45218|ADAS_CAEEL Alkyldihydroxyacetonephosphate synthase OS=Caenorhabditis elegans GN=ads-1 PE=2 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
Q20970|SYMC_CAEEL Methionine--tRNA ligase, cytoplasmic OS=Caenorhabditis elegans GN=mrs-1 PE=2 SV=1; D3YT55|D3YT55_CAEEL Protein MARS-1, isoform b OS=Caenorhabditis elegans GN=mars-1 PE=2 SV=1	0.01
Q9GZH5|Q9GZH5_CAEEL Protein RPN-1 OS=Caenorhabditis elegans GN=rpn-1 PE=4 SV=1	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
Q19058|Q19058_CAEEL Protein MAOC-1 OS=Caenorhabditis elegans GN=maoc-1 PE=1 SV=1	0.01

Q95XX1-2|PNCB_CAEEL Isoform a of Nicotinate phosphoribosyltransferase OS=Caenorhabditis elegans GN=Y54G2A.17; Q95XX1|PNCB_CAEEL Nicotinate phosphoribosyltransferase OS=Caenorhabditis elegans GN=Y54G2A.17 PE=3 SV=3; Q95XX1-3|PNCB_CAEEL Isoform c o	0.01
Q09590|Q09590_CAEEL NADPH--cytochrome P450 reductase OS=Caenorhabditis elegans GN=emb-8 PE=3 SV=1	0.01
P10299|GSTP1_CAEEL Glutathione S-transferase P OS=Caenorhabditis elegans GN=gst-1 PE=1 SV=1	0.01
P47209|TCPE_CAEEL T-complex protein 1 subunit epsilon OS=Caenorhabditis elegans GN=cct-5 PE=1 SV=1; Q8WQG4|Q8WQG4_CAEEL Protein CCT-5, isoform b OS=Caenorhabditis elegans GN=cct-5 PE=2 SV=1	0.01
P53489|ARP2_CAEEL Actin-related protein 2 OS=Caenorhabditis elegans GN=arx-2 PE=3 SV=1	0.01
Q22531|Q22531_CAEEL Protein T16G12.1 OS=Caenorhabditis elegans GN=CELE_T16G12.1 PE=4 SV=4	0.01
Q9XV52|EFGM_CAEEL Elongation factor G, mitochondrial OS=Caenorhabditis elegans GN=F29C12.4 PE=3 SV=1	0.01
Q95PZ0|CSN6_CAEEL COP9 signalosome complex subunit 6 OS=Caenorhabditis elegans GN=csn-6 PE=1 SV=1; C5VUK2|C5VUK2_CAEEL Protein CSN-6, isoform b OS=Caenorhabditis elegans GN=csn-6 PE=2 SV=1	0.01
Q965V4|Q965V4_CAEEL Protein XPO-2 OS=Caenorhabditis elegans GN=xpo-2 PE=4 SV=1	0.01
M1ZK05|M1ZK05_CAEEL Protein SEC-16, isoform b OS=Caenorhabditis elegans GN=sec-16 PE=4 SV=1; P34643|YOQ5_CAEEL Uncharacterized protein ZK512.5 OS=Caenorhabditis elegans GN=ZK512.5 PE=3 SV=1	0.01
Q9XUP3|EIF3K_CAEEL Eukaryotic translation initiation factor 3 subunit K OS=Caenorhabditis elegans GN=eif-3.K PE=2 SV=1	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
P04255|H2B1_CAEEL Histone H2B 1 OS=Caenorhabditis elegans GN=his-11 PE=1 SV=4; Q27894|H2B2_CAEEL Histone H2B 2 OS=Caenorhabditis elegans GN=his-4 PE=1 SV=3; Q27876|H2B4_CAEEL Probable histone H2B 4 OS=Caenorhabditis elegans GN=his-48 PE=3 SV=3; >s	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
Q09422|PGAM5_CAEEL Serine/threonine-protein phosphatase Pgam5, mitochondrial OS=Caenorhabditis elegans GN=pgam-5 PE=3 SV=2	0.00
P91154|P91154_CAEEL 60S ribosome subunit biogenesis protein NIP7 homolog OS=Caenorhabditis elegans GN=C43E11.9 PE=3 SV=1	0.00
Q9U1Q4|SYV_CAEEL Valine--tRNA ligase OS=Caenorhabditis elegans GN=vrs-2 PE=1 SV=1	0.00
O45495|O45495_CAEEL Protein UEV-1 OS=Caenorhabditis elegans GN=uev-1 PE=4 SV=1	0.00
Q9BL27|Q9BL27_CAEEL Protein Y71H2AR.1 OS=Caenorhabditis elegans GN=CELE_Y71H2AR.1 PE=4 SV=1	0.00
Q9N362|Q9N362_CAEEL Protein Y55F3AM.13 OS=Caenorhabditis elegans GN=CELE_Y55F3AM.13 PE=4 SV=1	0.00
Q21473|Q21473_CAEEL Protein AQP-7 OS=Caenorhabditis elegans GN=aqp-7 PE=3 SV=2	0.00
Q19687|Q19687_CAEEL Protein F21D5.3, isoform a OS=Caenorhabditis elegans GN=CELE_F21D5.3 PE=2 SV=2	0.00
G5ECR6|G5ECR6_CAEEL Aldose 1-epimerase OS=Caenorhabditis elegans GN=C01B4.6 PE=3 SV=1	0.00
Q95Y90|RL9_CAEEL 60S ribosomal protein L9 OS=Caenorhabditis elegans GN=rpl-9 PE=3 SV=1	0.00
P34650|MPI_CAEEL Probable mannose-6-phosphate isomerase OS=Caenorhabditis elegans GN=ZK632.4 PE=3 SV=3	0.00

P34524|BRX1_CAEEL Ribosome biogenesis protein BRX1 homolog OS=Caenorhabditis elegans GN=K12H4.3 PE=3 SV=1	0.00
Q9XW79|PP4C1_CAEEL Serine/threonine-protein phosphatase 4 catalytic subunit 1 OS=Caenorhabditis elegans GN=pph-4.1 PE=1 SV=1	0.00
Q9N3X2|RS4_CAEEL 40S ribosomal protein S4 OS=Caenorhabditis elegans GN=rps-4 PE=1 SV=1	0.00
O62178|O62178_CAEEL Protein RME-8, isoform b OS=Caenorhabditis elegans GN=rme-8 PE=2 SV=3; G5ED36|G5ED36_CAEEL Endocytosis protein RME-8 OS=Caenorhabditis elegans GN=rme-8 PE=2 SV=1	0.00
O62103|O62103_CAEEL Protein PRX-11 OS=Caenorhabditis elegans GN=prx-11 PE=4 SV=1	0.00
Q9N4I4|RL10A_CAEEL 60S ribosomal protein L10a OS=Caenorhabditis elegans GN=rpl-10a PE=2 SV=1; Q95Y46|Q95Y46_CAEEL Ribosomal protein OS=Caenorhabditis elegans GN=rpl-1 PE=2 SV=1; Q9U3B1|Q9U3B1_CAEEL Ribosomal protein (Fragment) OS=Caenorhabditis e	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
Q9BKU5|Q9BKU5_CAEEL Protein Y37E3.8, isoform a OS=Caenorhabditis elegans GN=CELE_Y37E3.8 PE=3 SV=1; Q9BKU6|Q9BKU6_CAEEL Protein Y37E3.8, isoform b OS=Caenorhabditis elegans GN=CELE_Y37E3.8 PE=3 SV=1	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
Q9TVW5|MSP77_CAEEL Major sperm protein 77/79 OS=Caenorhabditis elegans GN=msp-77 PE=2 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
P34334|RL21_CAEEL 60S ribosomal protein L21 OS=Caenorhabditis elegans GN=rpl-21 PE=1 SV=3	0.00
Q9U2U3|Q9U2U3_CAEEL Protein Y116A8C.27, isoform a OS=Caenorhabditis elegans GN=CELE_Y116A8C.27 PE=2 SV=2; D3NQA8|D3NQA8_CAEEL Protein Y116A8C.27, isoform b OS=Caenorhabditis elegans GN=CELE_Y116A8C.27 PE=2 SV=1	0.00
Q21544|Q21544_CAEEL Protein M153.1 OS=Caenorhabditis elegans GN=CELE_M153.1 PE=4 SV=1	0.00
P50880|RL3_CAEEL 60S ribosomal protein L3 OS=Caenorhabditis elegans GN=rpl-3 PE=2 SV=1; G5ECE5|G5ECE5_CAEEL Protein RPL-3, isoform c OS=Caenorhabditis elegans GN=rpl-3 PE=2 SV=1; G5EEC0|G5EEC0_CAEEL Protein RPL-3, isoform d OS=Caenorhabditis eleg	0.00
Q04908|PSMD3_CAEEL 26S proteasome non-ATPase regulatory subunit 3 OS=Caenorhabditis elegans GN=rpn-3 PE=1 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
Q9TYX1|Q9TYX1_CAEEL Protein DPF-5 OS=Caenorhabditis elegans GN=dpf-5 PE=4 SV=2	0.00
O45166|FOLT2_CAEEL Folate-like transporter 2 OS=Caenorhabditis elegans GN=folt-2 PE=3 SV=1	0.00
O16927|SRP14_CAEEL Signal recognition particle 14 kDa protein OS=Caenorhabditis elegans GN=F25G6.8 PE=3 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
O17919|DKC1_CAEEL Putative H/ACA ribonucleoprotein complex subunit 4 OS=Caenorhabditis elegans GN=K01G5.5 PE=3 SV=1	0.00
G5EFP3|G5EFP3_CAEEL Protein MRP-4 OS=Caenorhabditis elegans GN=mrp-4 PE=3 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

Q21436|Q21436_CAEEL Protein NPP-3 OS=Caenorhabditis elegans GN=npp-3 PE=4 SV=1	0.00
Q18211|RCC1_CAEEL Regulator of chromosome condensation OS=Caenorhabditis elegans GN=ran-3 PE=4 SV=1	0.00
G5EBT8|G5EBT8_CAEEL Protein F17C11.12, isoform b OS=Caenorhabditis elegans GN=CELE_F17C11.12 PE=2 SV=1; G5EC34|G5EC34_CAEEL Protein F17C11.12, isoform a OS=Caenorhabditis elegans GN=CELE_F17C11.12 PE=2 SV=1	0.00
P34446|PAT2_CAEEL Integrin alpha pat-2 OS=Caenorhabditis elegans GN=pat-2 PE=1 SV=1	0.00
Q21773|DHP1_CAEEL Dihydropyrimidinase 1 OS=Caenorhabditis elegans GN=dhp-1 PE=1 SV=2	0.00
H9G321|H9G321_CAEEL Protein R13H4.2, isoform c OS=Caenorhabditis elegans GN=CELE_R13H4.2 PE=4 SV=1	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
Q8MNT7|Q8MNT7_CAEEL Protein F09F7.4, isoform b OS=Caenorhabditis elegans GN=CELE_F09F7.4 PE=2 SV=1; Q19278|Q19278_CAEEL Protein F09F7.4, isoform a OS=Caenorhabditis elegans GN=CELE_F09F7.4 PE=2 SV=1	0.00
Q22037-3|ROA1_CAEEL Isoform c of Heterogeneous nuclear ribonucleoprotein A1 OS=Caenorhabditis elegans GN=hrp-1; Q22037-2|ROA1_CAEEL Isoform b of Heterogeneous nuclear ribonucleoprotein A1 OS=Caenorhabditis elegans GN=hrp-1; Q22037|ROA1_CAEEL Hete	0.00
O44906|O44906_CAEEL Protein PCK-1, isoform a OS=Caenorhabditis elegans GN=pck-1 PE=2 SV=2; Q8ITY2|Q8ITY2_CAEEL Protein PCK-1, isoform b OS=Caenorhabditis elegans GN=pck-1 PE=2 SV=1; Q8ITY0|Q8ITY0_CAEEL Protein PCK-1, isoform d OS=Caenorhabditis e	0.00
Q9N5R9|SPT16_CAEEL FACT complex subunit spt-16 OS=Caenorhabditis elegans GN=spt-16 PE=3 SV=1	-0.01
B5U8N2|B5U8N2_CAEEL Protein RET-1, isoform g OS=Caenorhabditis elegans GN=ret-1 PE=2 SV=1	-0.01

Q23237|PSB3_CAEEL Proteasome subunit beta type-3 OS=Caenorhabditis elegans GN=pbs-3 PE=1 SV=1	-0.01
P41942|YKB4_CAEEL Uncharacterized protein B0272.4 OS=Caenorhabditis elegans GN=B0272.4 PE=3 SV=1; H2B4M6|H2B4M6_CAEEL Putative uncharacterized protein B04272.1 (Fragment) OS=Caenorhabditis elegans GN=B04272.1 PE=2 SV=1	-0.01
O17759|O17759_CAEEL Protein TKT-1 OS=Caenorhabditis elegans GN=tkt-1 PE=4 SV=1	-0.01
P90994|P90994_CAEEL Protein DJR-1.1 OS=Caenorhabditis elegans GN=djr-1.1 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
B7WN92|B7WN92_CAEEL Protein CTG-2, isoform b OS=Caenorhabditis elegans GN=ctg-2 PE=2 SV=1; Q22467|Q22467_CAEEL Protein CTG-2, isoform a OS=Caenorhabditis elegans GN=ctg-2 PE=2 SV=2	-0.01
Q95QQ4|Q95QQ4_CAEEL Protein C55F2.1, isoform b OS=Caenorhabditis elegans GN=C55F2.1 PE=2 SV=3; Q7JNV5|Q7JNV5_CAEEL Protein C55F2.1, isoform c OS=Caenorhabditis elegans GN=C55F2.1 PE=2 SV=1; Q95QQ5|Q95QQ5_CAEEL Protein C55F2.1, isoform a OS=Caenor	-0.01
O44952|LONM_CAEEL Lon protease homolog, mitochondrial OS=Caenorhabditis elegans GN=C34B2.6 PE=3 SV=1	-0.01
O17892|O17892_CAEEL Protein F55B11.1 OS=Caenorhabditis elegans GN=CELE_F55B11.1 PE=4 SV=1	-0.01
Q22972|Q22972_CAEEL Protein ASP-13 OS=Caenorhabditis elegans GN=asp-13 PE=3 SV=1	-0.01
O76512|RENT1_CAEEL Regulator of nonsense transcripts 1 OS=Caenorhabditis elegans GN=smg-2 PE=1 SV=1	-0.01
Q21215|GBLP_CAEEL Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Caenorhabditis elegans GN=rack-1 PE=1 SV=3	-0.01
Q9N3C9|Q9N3C9_CAEEL Protein RPB-7 OS=Caenorhabditis elegans GN=rpb-7 PE=4 SV=1	-0.01
O17785|O17785_CAEEL Protein F11A5.9 OS=Caenorhabditis elegans GN=CELE_F11A5.9 PE=4 SV=2	-0.01

Q9BPN8|Y92H3_CAEEL Uncharacterized protein Y92H12BR.3 OS=Caenorhabditis elegans GN=Y92H12BR.3 PE=1 SV=2; Q9BPN8-2|Y92H3_CAEEL Isoform b of Uncharacterized protein Y92H12BR.3 OS=Caenorhabditis elegans GN=Y92H12BR.3	-0.01
Q20772|GCDH_CAEEL Probable glutaryl-CoA dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=F54D5.7 PE=1 SV=1	-0.01
Q95Y88|Q95Y88_CAEEL Protein R13A5.9 OS=Caenorhabditis elegans GN=CELE_R13A5.9 PE=4 SV=1	-0.01
Q9TYL2|Q9TYL2_CAEEL Protein Y25C1A.13 OS=Caenorhabditis elegans GN=CELE_Y25C1A.13 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
Q21551|Q21551_CAEEL Protein CHCH-3 OS=Caenorhabditis elegans GN=chch-3 PE=4 SV=1	-0.01
Q9NEI6|Q9NEI6_CAEEL Protein MRPS-35, isoform a OS=Caenorhabditis elegans GN=mrps-35 PE=2 SV=1; D4YWC8|D4YWC8_CAEEL Protein MRPS-35, isoform b OS=Caenorhabditis elegans GN=mrps-35 PE=2 SV=1	-0.01
Q9XW16|PROF1_CAEEL Profilin-1 OS=Caenorhabditis elegans GN=pfn-1 PE=2 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
P34673|YO23_CAEEL Uncharacterized protein ZK688.3 OS=Caenorhabditis elegans GN=ZK688.3 PE=3 SV=1	-0.01
G5EET8|G5EET8_CAEEL Protein PUD-1.1 OS=Caenorhabditis elegans GN=pud-1.2 PE=4 SV=1	-0.01
Q19416|Q19416_CAEEL Protein DYLT-1 OS=Caenorhabditis elegans GN=dylt-1 PE=4 SV=2	-0.01
O45815|O45815_CAEEL Protein ACT-5 OS=Caenorhabditis elegans GN=act-5 PE=3 SV=1	-0.01
O45679|O45679_CAEEL Cysteine synthase OS=Caenorhabditis elegans GN=cysl-2 PE=3 SV=1	-0.01

Q18801-3|GMD1_CAEEL Isoform c of GDP-mannose 4,6 dehydratase 1 OS=Caenorhabditis elegans GN=bre-1; Q18801-4|GMD1_CAEEL Isoform d of GDP-mannose 4,6 dehydratase 1 OS=Caenorhabditis elegans GN=bre-1; Q18801-2|GMD1_CAEEL Isoform a of GDP-mannose 4,6	-0.01
Q19713|SYFB_CAEEL Phenylalanine--tRNA ligase beta subunit OS=Caenorhabditis elegans GN=frs-2 PE=1 SV=2	-0.01
Q9NAH6|Q9NAH6_CAEEL Protein RSKS-1 OS=Caenorhabditis elegans GN=rsks-1 PE=4 SV=2	-0.01
Q18115|PSMD1_CAEEL 26S proteasome non-ATPase regulatory subunit 1 OS=Caenorhabditis elegans GN=rpn-2 PE=3 SV=4; Q18115-2|PSMD1_CAEEL Isoform a of 26S proteasome non-ATPase regulatory subunit 1 OS=Caenorhabditis elegans GN=rpn-2	-0.01
G3MU81|G3MU81_CAEEL Ubiquitin carboxyl-terminal hydrolase OS=Caenorhabditis elegans GN=math-33 PE=2 SV=1; O45624|O45624_CAEEL Ubiquitin carboxyl-terminal hydrolase OS=Caenorhabditis elegans GN=math-33 PE=2 SV=1; G3MU79|G3MU79_CAEEL Ubiquitin carb	-0.01
Q965N8|Q965N8_CAEEL Protein Y46E12BL.2 OS=Caenorhabditis elegans GN=CELE_Y46E12BL.2 PE=4 SV=1	-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
P91529|RPC6_CAEEL Probable DNA-directed RNA polymerase III subunit RPC6 OS=Caenorhabditis elegans GN=W09C3.4 PE=3 SV=1	-0.01
O17861|YVRI_CAEEL GILT-like protein F37H8.5 OS=Caenorhabditis elegans GN=F37H8.5 PE=1 SV=1	-0.01
Q9N4X8|GSTPA_CAEEL Glutathione S-transferase P 10 OS=Caenorhabditis elegans GN=gst-10 PE=1 SV=3; Q9N5R3|Q9N5R3_CAEEL Protein F56A4.3 OS=Caenorhabditis elegans GN=CELE_F56A4.3 PE=4 SV=2	-0.02
Q9GRY9|Q9GRY9_CAEEL Protein Y59A8B.10, isoform a OS=Caenorhabditis elegans GN=CELE_Y59A8B.10 PE=1 SV=1	-0.02
G5EDB8|G5EDB8_CAEEL Protein VHA-4 OS=Caenorhabditis elegans GN=vha-4 PE=2 SV=1	-0.02
G5ECV9|G5ECV9_CAEEL Protein ALH-3 OS=Caenorhabditis elegans GN=alh-3 PE=3 SV=1	-0.02

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
O17395|O17395_CAEEL Protein AAT-3 OS=Caenorhabditis elegans GN=aat-3 PE=4 SV=2	-0.02
P34669|OST3_CAEEL Probable dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3 OS=Caenorhabditis elegans GN=ZK686.3 PE=3 SV=2	-0.02
P54889|ALH13_CAEEL Probable delta-1-pyrroline-5-carboxylate synthase OS=Caenorhabditis elegans GN=alh-13 PE=2 SV=1; Q9BI69|Q9BI69_CAEEL Protein ALH-13, isoform b OS=Caenorhabditis elegans GN=alh-13 PE=2 SV=2	-0.02
G5ECR0|G5ECR0_CAEEL Protein T25C12.3 OS=Caenorhabditis elegans GN=CELE_T25C12.3 PE=4 SV=1	-0.02
Q21018|CRI3_CAEEL Conserved regulator of innate immunity protein 3 OS=Caenorhabditis elegans GN=cri-3 PE=1 SV=2	-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
Q19459-2|GSLG1_CAEEL Isoform b of Golgi apparatus protein 1 homolog OS=Caenorhabditis elegans GN=F14E5.2; Q19459|GSLG1_CAEEL Golgi apparatus protein 1 homolog OS=Caenorhabditis elegans GN=F14E5.2 PE=1 SV=1	-0.02
Q19052|EIF2A_CAEEL Eukaryotic translation initiation factor 2A OS=Caenorhabditis elegans GN=E04D5.1 PE=3 SV=2	-0.02
Q9TYV5|Q9TYV5_CAEEL Protein NOL-1 OS=Caenorhabditis elegans GN=nol-1 PE=4 SV=2	-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
O16785|PARV_CAEEL Paralyzed arrest at two-fold protein 6 OS=Caenorhabditis elegans GN=pat-6 PE=1 SV=1	-0.02
O01504|RLA2_CAEEL 60S acidic ribosomal protein P2 OS=Caenorhabditis elegans GN=rpa-2 PE=3 SV=2	-0.02

O01572|O01572_CAEEL Protein F48C1.6 OS=Caenorhabditis elegans GN=CELE_F48C1.6 PE=4 SV=1	-0.02
O17695|HDA1_CAEEL Histone deacetylase 1 OS=Caenorhabditis elegans GN=hda-1 PE=1 SV=1	-0.02
P34662|RL35_CAEEL 60S ribosomal protein L35 OS=Caenorhabditis elegans GN=rpl-35 PE=3 SV=1	-0.02
Q09444|UBH4_CAEEL Probable ubiquitin carboxyl-terminal hydrolase ubh-4 OS=Caenorhabditis elegans GN=ubh-4 PE=3 SV=2	-0.02
O61791|O61791_CAEEL Protein MRPS-6 OS=Caenorhabditis elegans GN=mrps-6 PE=4 SV=2	-0.02
P37165|RS27A_CAEEL Ubiquitin-like protein 1-40S ribosomal protein S27a OS=Caenorhabditis elegans GN=ubl-1 PE=1 SV=2	-0.02
O61856|ILVBL_CAEEL Acetolactate synthase-like protein OS=Caenorhabditis elegans GN=T26C12.1 PE=3 SV=2	-0.02
Q19341|3HAO_CAEEL 3-hydroxyanthranilate 3,4-dioxygenase OS=Caenorhabditis elegans GN=haao-1 PE=1 SV=2	-0.02
O01927|O01927_CAEEL Protein C13C4.5 OS=Caenorhabditis elegans GN=C13C4.5 PE=4 SV=1	-0.02
Q09432|Q09432_CAEEL Sodium/hydrogen exchanger OS=Caenorhabditis elegans GN=nhx-2 PE=2 SV=2; Q8T5S1|Q8T5S1_CAEEL Sodium/hydrogen exchanger OS=Caenorhabditis elegans GN=nhx-2 PE=2 SV=1	-0.02
Q19545|Q19545_CAEEL Protein TAG-184 OS=Caenorhabditis elegans GN=tag-184 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
P91420|P91420_CAEEL Serine/threonine-protein phosphatase OS=Caenorhabditis elegans GN=gsp-4 PE=3 SV=1	-0.02
Q17571|Q17571_CAEEL Protein AQP-2, isoform a OS=Caenorhabditis elegans GN=aqp-2 PE=2 SV=1; Q7JMQ6|Q7JMQ6_CAEEL Protein AQP-2, isoform b OS=Caenorhabditis elegans GN=aqp-2 PE=2 SV=1	-0.02
Q20306|Q20306_CAEEL Protein ABCF-3 OS=Caenorhabditis elegans GN=abcf-3 PE=3 SV=1	-0.02

Q9XWS4|Q9XWS4_CAEEL Protein RPL-30, isoform a OS=Caenorhabditis elegans GN=rpl-30 PE=3 SV=2; I2HAJ2|I2HAJ2_CAEEL Protein RPL-30, isoform c OS=Caenorhabditis elegans GN=rpl-30 PE=4 SV=1	-0.02
P48154|RS3A_CAEEL 40S ribosomal protein S3a OS=Caenorhabditis elegans GN=rps-1 PE=3 SV=2	-0.03
Q8I711|Q8I711_CAEEL Protein GARS-1, isoform b OS=Caenorhabditis elegans GN=gars-1 PE=2 SV=1; Q10039|SYG_CAEEL Glycine--tRNA ligase OS=Caenorhabditis elegans GN=grs-1 PE=2 SV=2	-0.03
Q09489|Q09489_CAEEL Protein C32D5.8, isoform a OS=Caenorhabditis elegans GN=C32D5.8 PE=2 SV=1	-0.03
Q93169|MTNA_CAEEL Methylthioribose-1-phosphate isomerase OS=Caenorhabditis elegans GN=C01G10.9 PE=3 SV=1	-0.03
Q27488|PSA2_CAEEL Proteasome subunit alpha type-2 OS=Caenorhabditis elegans GN=pas-2 PE=1 SV=1	-0.03
Q9N4A7|SEC13_CAEEL Protein SEC13 homolog OS=Caenorhabditis elegans GN=npp-20 PE=3 SV=1	-0.03
Q18224|Q18224_CAEEL Protein NTL-9 OS=Caenorhabditis elegans GN=ntl-9 PE=4 SV=2	-0.03
P06125|VIT5_CAEEL Vitellogenin-5 OS=Caenorhabditis elegans GN=vit-5 PE=2 SV=2	-0.03
Q22922|Q22922_CAEEL Protein CDD-1 OS=Caenorhabditis elegans GN=cdd-1 PE=4 SV=1	-0.03
Q9U1Q3|Q9U1Q3_CAEEL Protein CYN-15 OS=Caenorhabditis elegans GN=cyn-15 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
Q95PZ7|Q95PZ7_CAEEL Protein Y66D12A.9 OS=Caenorhabditis elegans GN=CELE_Y66D12A.9 PE=4 SV=1	-0.03
G5EBF3|G5EBF3_CAEEL Protein PUD-2.1 OS=Caenorhabditis elegans GN=pud-2.1 PE=4 SV=1	-0.03
Q19978|YV6L_CAEEL Uncharacterized protein F32G8.4 OS=Caenorhabditis elegans GN=F32G8.4 PE=3 SV=3	-0.03
P49405|RL5_CAEEL 60S ribosomal protein L5 OS=Caenorhabditis elegans GN=rpl-5 PE=3 SV=1	-0.03

Q2EEM5|Q2EEM5_CAEEL Protein USO-1, isoform b OS=Caenorhabditis elegans GN=uso-1 PE=2 SV=1; G5EGG0|G5EGG0_CAEEL Protein USO-1, isoform a OS=Caenorhabditis elegans GN=uso-1 PE=1 SV=1	-0.03
P41932|14331_CAEEL 14-3-3-like protein 1 OS=Caenorhabditis elegans GN=par-5 PE=1 SV=2	-0.03
Q09359|YS11_CAEEL Uncharacterized protein ZK1307.1 OS=Caenorhabditis elegans GN=ZK1307.1 PE=2 SV=1	-0.03
Q9N2Z6|Q9N2Z6_CAEEL Protein PTR-21 OS=Caenorhabditis elegans GN=ptr-21 PE=4 SV=1	-0.03
O01260|O01260_CAEEL Protein T20D3.11, isoform a OS=Caenorhabditis elegans GN=CELE_T20D3.11 PE=2 SV=3; B9WRT3|B9WRT3_CAEEL Protein T20D3.11, isoform b OS=Caenorhabditis elegans GN=CELE_T20D3.11 PE=2 SV=2	-0.03
Q9BKR9|Q9BKR9_CAEEL Protein Y82E9BR.16, isoform a OS=Caenorhabditis elegans GN=CELE_Y82E9BR.16 PE=2 SV=1; Q7Z1Q8|Q7Z1Q8_CAEEL Protein Y82E9BR.16, isoform b OS=Caenorhabditis elegans GN=CELE_Y82E9BR.16 PE=2 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
Q9U3Q6|Q9U3Q6_CAEEL Protein UGT-22 OS=Caenorhabditis elegans GN=ugt-22 PE=3 SV=1	-0.03
G5ED43|G5ED43_CAEEL Dimethylaniline monooxygenase [N-oxide-forming] OS=Caenorhabditis elegans GN=fmo-5 PE=2 SV=1	-0.03
Q20937|Q20937_CAEEL Protein LET-711 OS=Caenorhabditis elegans GN=let-711 PE=4 SV=3	-0.03
P50432-2|GLYC_CAEEL Isoform a of Serine hydroxymethyltransferase OS=Caenorhabditis elegans GN=mel-32; P50432|GLYC_CAEEL Serine hydroxymethyltransferase OS=Caenorhabditis elegans GN=mel-32 PE=1 SV=2	-0.03
P52819|RL22_CAEEL 60S ribosomal protein L22 OS=Caenorhabditis elegans GN=rpl-22 PE=1 SV=3	-0.03
Q95017|UBC9_CAEEL SUMO-conjugating enzyme UBC9 OS=Caenorhabditis elegans GN=ubc-9 PE=1 SV=1	-0.03
P91079|SPTC1_CAEEL Serine palmitoyltransferase 1 OS=Caenorhabditis elegans GN=sptl-1 PE=2 SV=1	-0.03

Q93454|NPP17_CAEEL Nucleoporin-17 OS=Caenorhabditis elegans GN=npp-17 PE=1 SV=1	-0.03
O16309|O16309_CAEEL Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=fkb-3 PE=4 SV=1	-0.03
Q86NC1|Q86NC1_CAEEL Phosphorylase OS=Caenorhabditis elegans GN=CELE_T22F3.3 PE=2 SV=1	-0.03
Q18660|Q18660_CAEEL Protein ACS-17 OS=Caenorhabditis elegans GN=acs-17 PE=4 SV=2	-0.03
A0A9S2|A0A9S2_CAEEL Protein Y38F2AR.12, isoform a OS=Caenorhabditis elegans GN=CELE_Y38F2AR.12 PE=2 SV=2	-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
Q9XX28|Q9XX28_CAEEL Protein DHS-11 OS=Caenorhabditis elegans GN=dhs-11 PE=3 SV=1	-0.03
Q09996|SYLC_CAEEL Leucine--tRNA ligase OS=Caenorhabditis elegans GN=lrs-1 PE=3 SV=2	-0.04
G4SF15|G4SF15_CAEEL Protein Y39G10AR.9, isoform a OS=Caenorhabditis elegans GN=CELE_Y39G10AR.9 PE=2 SV=2; Q95XR3|Q95XR3_CAEEL Protein Y39G10AR.9, isoform b OS=Caenorhabditis elegans GN=CELE_Y39G10AR.9 PE=2 SV=2	-0.04
Q23424|FZO1_CAEEL Transmembrane GTPase fzo-1 OS=Caenorhabditis elegans GN=fzo-1 PE=3 SV=1	-0.04
Q18020|Q18020_CAEEL Protein ASP-10, isoform a OS=Caenorhabditis elegans GN=asp-10 PE=2 SV=1; E0AHB8|E0AHB8_CAEEL Protein ASP-10, isoform b OS=Caenorhabditis elegans GN=asp-10 PE=2 SV=1	-0.04
Q09607|GST36_CAEEL Probable glutathione S-transferase gst-36 OS=Caenorhabditis elegans GN=gst-36 PE=3 SV=2	-0.04
Q19724|NDUS6_CAEEL Probable NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Caenorhabditis elegans GN=nduf-6 PE=3 SV=1	-0.04
Q17633|Q17633_CAEEL Protein C04G2.9 OS=Caenorhabditis elegans GN=C04G2.9 PE=4 SV=2	-0.04

Q17593|Q17593_CAEEL Protein C02G6.2 OS=Caenorhabditis elegans GN=C02G6.2 PE=3 SV=2	-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
G5EFC8|G5EFC8_CAEEL Protein DAP-3 OS=Caenorhabditis elegans GN=dap-3 PE=2 SV=1	-0.04
Q22038|RHO1_CAEEL Ras-like GTP-binding protein rhoA OS=Caenorhabditis elegans GN=rho-1 PE=2 SV=1	-0.04
O44480|RL18A_CAEEL 60S ribosomal protein L18a OS=Caenorhabditis elegans GN=rpl-20 PE=3 SV=2	-0.04
P52821|RS25_CAEEL 40S ribosomal protein S25 OS=Caenorhabditis elegans GN=rps-25 PE=3 SV=1	-0.04
Q9U283|Q9U283_CAEEL Protein Y48G10A.3 OS=Caenorhabditis elegans GN=CELE_Y48G10A.3 PE=4 SV=1	-0.04
D6RYD3|D6RYD3_CAEEL Protein Y58A7A.1, isoform b OS=Caenorhabditis elegans GN=CELE_Y58A7A.1 PE=2 SV=1; Q966A8|Q966A8_CAEEL Protein Y58A7A.1, isoform a OS=Caenorhabditis elegans GN=CELE_Y58A7A.1 PE=2 SV=1	-0.04
O17157|O17157_CAEEL Protein C24H12.4, isoform a OS=Caenorhabditis elegans GN=C24H12.4 PE=2 SV=2; Q95X81|Q95X81_CAEEL Protein C24H12.4, isoform b OS=Caenorhabditis elegans GN=C24H12.4 PE=2 SV=1	-0.04
P10984|ACT2_CAEEL Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=3 SV=3	-0.04
G5ED01|G5ED01_CAEEL Protein INOS-1 OS=Caenorhabditis elegans GN=inos-1 PE=4 SV=1	-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

Q21276|YZVL_CAEEL Uncharacterized NOP5 family protein K07C5.4 OS=Caenorhabditis elegans GN=K07C5.4 PE=3 SV=1	-0.04
O45148|O45148_CAEEL Protein DLST-1 OS=Caenorhabditis elegans GN=dlst-1 PE=3 SV=2	-0.04
P34559|ECHM_CAEEL Probable enoyl-CoA hydratase, mitochondrial OS=Caenorhabditis elegans GN=ech-6 PE=1 SV=1	-0.04
G5EBJ7|G5EBJ7_CAEEL Fructose-1,6-bisphosphatase OS=Caenorhabditis elegans GN=fbp-1 PE=2 SV=1	-0.04
P48156|RS8_CAEEL 40S ribosomal protein S8 OS=Caenorhabditis elegans GN=rps-8 PE=3 SV=1	-0.04
Q94269|Q94269_CAEEL Protein K10C2.1 OS=Caenorhabditis elegans GN=CELE_K10C2.1 PE=4 SV=2	-0.04
Q9N5Y2|TECR_CAEEL Probable very-long-chain enoyl-CoA reductase art-1 OS=Caenorhabditis elegans GN=art-1 PE=3 SV=1	-0.04
Q22781|Q22781_CAEEL Protein ACDH-7 OS=Caenorhabditis elegans GN=acdh-7 PE=3 SV=2	-0.04
H2KZ95|H2KZ95_CAEEL Protein Y48G9A.9, isoform a OS=Caenorhabditis elegans GN=CELE_Y48G9A.9 PE=4 SV=1; Q7YZG5|Q7YZG5_CAEEL Protein Y48G9A.9, isoform b OS=Caenorhabditis elegans GN=CELE_Y48G9A.9 PE=4 SV=1	-0.05
Q23652|Q23652_CAEEL Protein ZK863.4 OS=Caenorhabditis elegans GN=CELE_ZK863.4 PE=4 SV=2	-0.05
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
Q8MXJ7|Q8MXJ7_CAEEL Aldehyde dehydrogenase OS=Caenorhabditis elegans GN=alh-4 PE=2 SV=1; O16518|O16518_CAEEL Aldehyde dehydrogenase OS=Caenorhabditis elegans GN=alh-4 PE=2 SV=2; Q86S57|Q86S57_CAEEL Aldehyde dehydrogenase OS=Caenorhabditis elegans	-0.05
Q9XVD2|Q9XVD2_CAEEL Protein IMMP-1 OS=Caenorhabditis elegans GN=immp-1 PE=3 SV=2	-0.05

H2L034|H2L034_CAEEL Protein PMP-5, isoform a OS=Caenorhabditis elegans GN=pmp-5 PE=3 SV=1; H2L035|H2L035_CAEEL Protein PMP-5, isoform c OS=Caenorhabditis elegans GN=pmp-5 PE=4 SV=1; Q86S26|Q86S26_CAEEL Protein PMP-5, isoform b OS=Caenorhabditis e	-0.05
O01804|O01804_CAEEL Aspartate aminotransferase OS=Caenorhabditis elegans GN=got-2.1 PE=3 SV=3	-0.05
P50464|UNC97_CAEEL LIM domain-containing protein unc-97 OS=Caenorhabditis elegans GN=unc-97 PE=1 SV=1	-0.05
Q19969|IMA3_CAEEL Importin subunit alpha-3 OS=Caenorhabditis elegans GN=ima-3 PE=1 SV=2	-0.05
Q9U2Y2|CK5P3_CAEEL CDK5RAP3-like protein OS=Caenorhabditis elegans GN=Y113G7B.16 PE=3 SV=1	-0.05
Q9XXQ6|Q9XXQ6_CAEEL Protein TTR-25, isoform a OS=Caenorhabditis elegans GN=ttr-25 PE=2 SV=1	-0.05
O01686|O01686_CAEEL Oxysterol-binding protein OS=Caenorhabditis elegans GN=obr-4 PE=2 SV=2; Q8I7N6|Q8I7N6_CAEEL Oxysterol-binding protein OS=Caenorhabditis elegans GN=obr-4 PE=2 SV=1	-0.05
O44509|O44509_CAEEL Protein F42G8.10, isoform a OS=Caenorhabditis elegans GN=CELE_F42G8.10 PE=2 SV=1; Q86MF9|Q86MF9_CAEEL Protein F42G8.10, isoform b OS=Caenorhabditis elegans GN=CELE_F42G8.10 PE=2 SV=1	-0.05
Q18813|Q18813_CAEEL Protein C53D6.7 OS=Caenorhabditis elegans GN=C53D6.7 PE=4 SV=3	-0.05
Q9NAE2|HUTU_CAEEL Probable urocanate hydratase OS=Caenorhabditis elegans GN=Y51H4A.7 PE=3 SV=2	-0.05
O44557|O44557_CAEEL Protein T08B1.1 OS=Caenorhabditis elegans GN=CELE_T08B1.1 PE=4 SV=2	-0.05
Q966I7|Q966I7_CAEEL Protein K08D12.3, isoform a OS=Caenorhabditis elegans GN=CELE_K08D12.3 PE=2 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
Q9BPN5|Q9BPN5_CAEEL Protein OIG-6 OS=Caenorhabditis elegans GN=oig-6 PE=4 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
O17694|O17694_CAEEL Protein RIL-1 OS=Caenorhabditis elegans GN=ril-1 PE=4 SV=1	-0.05
Q20502|HUTH_CAEEL Probable histidine ammonia-lyase OS=Caenorhabditis elegans GN=F47B10.2 PE=1 SV=1	-0.05
B0M0L9|B0M0L9_CAEEL Protein C17C3.1, isoform e OS=Caenorhabditis elegans GN=C17C3.1 PE=2 SV=1; H2KYT6|H2KYT6_CAEEL Protein C17C3.1, isoform b OS=Caenorhabditis elegans GN=C17C3.1 PE=4 SV=1; Q9BIA9|Q9BIA9_CAEEL Protein C17C3.1, isoform a OS=Caenor	-0.05
Q22020|Q22020_CAEEL Protein R53.5 OS=Caenorhabditis elegans GN=CELE_R53.5 PE=4 SV=1	-0.05
P91522|P91522_CAEEL Protein FBXA-64 OS=Caenorhabditis elegans GN=fbxa-64 PE=4 SV=2	-0.05
P61866|RL12_CAEEL 60S ribosomal protein L12 OS=Caenorhabditis elegans GN=rpl-12 PE=3 SV=1	-0.05
Q19869-2|RL26_CAEEL Isoform b of 60S ribosomal protein L26 OS=Caenorhabditis elegans GN=rpl-26; Q19869-3|RL26_CAEEL Isoform c of 60S ribosomal protein L26 OS=Caenorhabditis elegans GN=rpl-26; Q19869|RL26_CAEEL 60S ribosomal protein L26 OS=Caenorh	-0.05
Q9BIB8|Q9BIB8_CAEEL Protein IMB-1 OS=Caenorhabditis elegans GN=imb-1 PE=4 SV=3	-0.05
Q9GZH3|IMDH_CAEEL Inosine-5-monophosphate dehydrogenase OS=Caenorhabditis elegans GN=T22D1.3 PE=2 SV=2; Q86DL2|Q86DL2_CAEEL Inosine-5-monophosphate dehydrogenase OS=Caenorhabditis elegans GN=CELE_T22D1.3 PE=2 SV=2	-0.05
Q95Y54|Q95Y54_CAEEL Protein Y71D11A.3, isoform a OS=Caenorhabditis elegans GN=CELE_Y71D11A.3 PE=2 SV=1; Q8T8B9|ACMSD_CAEEL 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase OS=Caenorhabditis elegans GN=acmsd PE=2 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

Q9XWJ6|Q9XWJ6_CAEEL Protein Y51H1A.3, isoform a OS=Caenorhabditis elegans GN=CELE_Y51H1A.3 PE=2 SV=1; Q9XWJ5|Q9XWJ5_CAEEL Protein Y51H1A.3, isoform b OS=Caenorhabditis elegans GN=CELE_Y51H1A.3 PE=2 SV=1	-0.06
P52872|DAD1_CAEEL Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit dad-1 OS=Caenorhabditis elegans GN=dad-1 PE=3 SV=1	-0.06
Q9N431|Q9N431_CAEEL Protein Y38C1AA.7 OS=Caenorhabditis elegans GN=CELE_Y38C1AA.7 PE=1 SV=1	-0.06
Q9N492|Q9N492_CAEEL Protein PINN-1 OS=Caenorhabditis elegans GN=pinn-1 PE=4 SV=2	-0.06
Q21230|IF2B_CAEEL Eukaryotic translation initiation factor 2 subunit 2 OS=Caenorhabditis elegans GN=K04G2.1 PE=3 SV=4	-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
P48053|YPD1_CAEEL Uncharacterized protein C05D11.1 OS=Caenorhabditis elegans GN=C05D11.1 PE=1 SV=2	-0.06
O45089|O45089_CAEEL Protein FAAH-3 OS=Caenorhabditis elegans GN=faah-3 PE=4 SV=2	-0.06
O62216|O62216_CAEEL Protein F33H2.6 OS=Caenorhabditis elegans GN=CELE_F33H2.6 PE=4 SV=2	-0.06
G5EC71|G5EC71_CAEEL Protein GST-20 OS=Caenorhabditis elegans GN=gst-20 PE=4 SV=1	-0.06
Q22508|Q22508_CAEEL Protein TAG-18 OS=Caenorhabditis elegans GN=tag-18 PE=4 SV=1	-0.06
Q20641|Q20641_CAEEL Protein NMY-1 OS=Caenorhabditis elegans GN=nmy-1 PE=4 SV=2	-0.06
O17607|O17607_CAEEL Protein RUVB-1 OS=Caenorhabditis elegans GN=ruvb-1 PE=1 SV=2	-0.06

Q7Z1P7|Q7Z1P7_CAEEL Protein R08E3.1, isoform b OS=Caenorhabditis elegans GN=CELE_R08E3.1 PE=2 SV=1; Q21850|Q21850_CAEEL Protein R08E3.1, isoform a OS=Caenorhabditis elegans GN=CELE_R08E3.1 PE=2 SV=5	-0.06
Q20616|Q20616_CAEEL Protein F49E12.1 OS=Caenorhabditis elegans GN=CELE_F49E12.1 PE=4 SV=1	-0.06
Q23120|RSP2_CAEEL Probable splicing factor, arginine/serine-rich 2 OS=Caenorhabditis elegans GN=rsp-2 PE=3 SV=1	-0.06
Q27GU2|Q27GU2_CAEEL Protein LBP-3, isoform b OS=Caenorhabditis elegans GN=lbp-3 PE=2 SV=1; Q20222|FABP3_CAEEL Fatty acid-binding protein homolog 3 OS=Caenorhabditis elegans GN=lbp-3 PE=2 SV=2	-0.06
Q21702|Q21702_CAEEL Protein R04B5.5 OS=Caenorhabditis elegans GN=CELE_R04B5.5 PE=3 SV=1	-0.06
P91856|SERC_CAEEL Probable phosphoserine aminotransferase OS=Caenorhabditis elegans GN=F26H9.5 PE=3 SV=1	-0.06
Q17539|Q17539_CAEEL Protein C01B10.8 OS=Caenorhabditis elegans GN=C01B10.8 PE=1 SV=1	-0.06
Q18853|Q18853_CAEEL Protein CYC-1 OS=Caenorhabditis elegans GN=cyc-1 PE=4 SV=1	-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
Q8MXS8|Q8MXS8_CAEEL Protein Y47G6A.22 OS=Caenorhabditis elegans GN=CELE_Y47G6A.22 PE=4 SV=1	-0.06
O16519|GAD1_CAEEL Gastrulation defective protein 1 OS=Caenorhabditis elegans GN=gad-1 PE=1 SV=1	-0.06
Q20634|Q20634_CAEEL Protein F52A8.5 OS=Caenorhabditis elegans GN=CELE_F52A8.5 PE=3 SV=1	-0.06
G5EEM5|ZYG9_CAEEL Zygote defective protein 9 OS=Caenorhabditis elegans GN=zyg-9 PE=1 SV=1	-0.07
P52015|CYP7_CAEEL Peptidyl-prolyl cis-trans isomerase 7 OS=Caenorhabditis elegans GN=cyn-7 PE=1 SV=2	-0.07

Q09474|T23O_CAEEL Tryptophan 2,3-dioxygenase OS=Caenorhabditis elegans GN=C28H8.11 PE=1 SV=1; Q8I7L6|Q8I7L6_CAEEL Protein TDO-2, isoform b OS=Caenorhabditis elegans GN=tdo-2 PE=2 SV=1	-0.07
Q18315|Q18315_CAEEL Protein C29H12.2 OS=Caenorhabditis elegans GN=C29H12.2 PE=4 SV=1	-0.07
Q9U1Q5|Q9U1Q5_CAEEL Protein Y87G2A.2 OS=Caenorhabditis elegans GN=CELE_Y87G2A.2 PE=4 SV=3	-0.07
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
O17586|PSA6_CAEEL Proteasome subunit alpha type-6 OS=Caenorhabditis elegans GN=pas-1 PE=1 SV=1	-0.07
Q8I4N3|NDC1_CAEEL Nucleoporin ndc-1 OS=Caenorhabditis elegans GN=npp-22 PE=3 SV=1	-0.07
Q5FC79|SFXN5_CAEEL Sideroflexin-5 OS=Caenorhabditis elegans GN=sfxn-5 PE=3 SV=1	-0.07
O18693|O18693_CAEEL Protein ACS-2 OS=Caenorhabditis elegans GN=acs-2 PE=4 SV=1	-0.07
P22981|LET60_CAEEL Ras protein let-60 OS=Caenorhabditis elegans GN=let-60 PE=1 SV=1	-0.07
Q9XWV2|PLBL1_CAEEL Putative phospholipase B-like 1 OS=Caenorhabditis elegans GN=Y37D8A.2 PE=1 SV=1	-0.07
P51404|RS13_CAEEL 40S ribosomal protein S13 OS=Caenorhabditis elegans GN=rps-13 PE=3 SV=2	-0.07
Q17663|Q17663_CAEEL Protein AMT-4 OS=Caenorhabditis elegans GN=amt-4 PE=4 SV=3	-0.07
O45781|O45781_CAEEL Protein DRR-2 OS=Caenorhabditis elegans GN=drr-2 PE=4 SV=1	-0.07
G5EBW5|G5EBW5_CAEEL Protein K07G5.6 OS=Caenorhabditis elegans GN=CELE_K07G5.6 PE=4 SV=1	-0.07
Q22101|Q22101_CAEEL Protein T02G5.7 OS=Caenorhabditis elegans GN=CELE_T02G5.7 PE=3 SV=1	-0.07

O17621|O17621_CAEEL Protein C29F7.2 OS=Caenorhabditis elegans GN=C29F7.2 PE=4 SV=2	-0.07
P62784|H4_CAEEL Histone H4 OS=Caenorhabditis elegans GN=his-1 PE=1 SV=2	-0.07
Q2L6Y6|Q2L6Y6_CAEEL Protein R151.7, isoform a OS=Caenorhabditis elegans GN=CELE_R151.7 PE=2 SV=1; H2L001|H2L001_CAEEL Protein R151.7, isoform b OS=Caenorhabditis elegans GN=CELE_R151.7 PE=4 SV=1	-0.07
Q9NAQ2|Q9NAQ2_CAEEL Protein JC8.2 OS=Caenorhabditis elegans GN=CELE_JC8.2 PE=4 SV=2	-0.07
Q9BL61|Q9BL61_CAEEL Protein Y65B4A.6 OS=Caenorhabditis elegans GN=CELE_Y65B4A.6 PE=3 SV=2; O44781|O44781_CAEEL Protein F33D11.10 OS=Caenorhabditis elegans GN=CELE_F33D11.10 PE=3 SV=1	-0.07
Q5WRT8|Q5WRT8_CAEEL Protein NPP-21, isoform a OS=Caenorhabditis elegans GN=npp-21 PE=2 SV=1; Q5WRT9|Q5WRT9_CAEEL Protein NPP-21, isoform b OS=Caenorhabditis elegans GN=npp-21 PE=2 SV=1; Q1NZ34|Q1NZ34_CAEEL Protein NPP-21, isoform c OS=Caenorhabdi	-0.07
Q9XVA6|Q9XVA6_CAEEL Protein CYP-37A1 OS=Caenorhabditis elegans GN=cyp-37a1 PE=3 SV=2	-0.07
O44408|O44408_CAEEL Protein KGB-1 OS=Caenorhabditis elegans GN=kgb-1 PE=1 SV=2	-0.08
Q9XWU3|Q9XWU3_CAEEL Protein Y41C4A.11 OS=Caenorhabditis elegans GN=CELE_Y41C4A.11 PE=4 SV=1	-0.08
Q9XXF9|Q9XXF9_CAEEL Protein Y37A1B.5, isoform a OS=Caenorhabditis elegans GN=CELE_Y37A1B.5 PE=2 SV=1; D3NQ99|D3NQ99_CAEEL Protein Y37A1B.5, isoform b OS=Caenorhabditis elegans GN=CELE_Y37A1B.5 PE=2 SV=1	-0.08
Q09216|YP67_CAEEL Uncharacterized protein B0495.7 OS=Caenorhabditis elegans GN=B0495.7 PE=1 SV=2	-0.08
Q7YWP5|Q7YWP5_CAEEL Protein Y46G5A.35 OS=Caenorhabditis elegans GN=CELE_Y46G5A.35 PE=4 SV=1	-0.08
Q7YX71|Q7YX71_CAEEL Protein C26C6.9 OS=Caenorhabditis elegans GN=C26C6.9 PE=4 SV=1	-0.08
Q21554|DDB1_CAEEL DNA damage-binding protein 1 OS=Caenorhabditis elegans GN=ddb-1 PE=1 SV=2	-0.08

Q9UAY9|Q9UAY9_CAEEL Protein RPAC-40 OS=Caenorhabditis elegans GN=rpac-40 PE=4 SV=2	-0.08
Q23588|Q23588_CAEEL Protein UPP-1 OS=Caenorhabditis elegans GN=upp-1 PE=4 SV=2	-0.08
Q19781|Q19781_CAEEL Protein F25E2.3 OS=Caenorhabditis elegans GN=CELE_F25E2.3 PE=4 SV=2	-0.08
Q27535|KARG2_CAEEL Probable arginine kinase ZC434.8 OS=Caenorhabditis elegans GN=ZC434.8 PE=3 SV=1	-0.08
Q07085|EST2_CAEEL Esterase CM06B1 OS=Caenorhabditis elegans GN=F13H6.3 PE=3 SV=3	-0.08
Q09475|YP93_CAEEL Uncharacterized helicase C28H8.3 OS=Caenorhabditis elegans GN=C28H8.3 PE=3 SV=2	-0.08
Q20223|FABP1_CAEEL Fatty acid-binding protein homolog 1 OS=Caenorhabditis elegans GN=lbp-1 PE=1 SV=1	-0.08
P34595-2|YOD3_CAEEL Isoform b of Uncharacterized protein ZC262.3 OS=Caenorhabditis elegans GN=ZC262.3; P34595|YOD3_CAEEL Uncharacterized protein ZC262.3 OS=Caenorhabditis elegans GN=ZC262.3 PE=1 SV=2	-0.08
Q21241|Q21241_CAEEL Protein K05F1.5 OS=Caenorhabditis elegans GN=CELE_K05F1.5 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
Q23660|Q23660_CAEEL Protein ZK899.2 OS=Caenorhabditis elegans GN=CELE_ZK899.2 PE=4 SV=2	-0.08
Q23195|Q23195_CAEEL Protein W06B4.2 OS=Caenorhabditis elegans GN=CELE_W06B4.2 PE=4 SV=1	-0.08
I7F493|I7F493_CAEEL Rab-8 (Fragment) OS=Caenorhabditis elegans GN=rab-8 PE=2 SV=1; G5EFC1|G5EFC1_CAEEL Protein RAB-8 OS=Caenorhabditis elegans GN=rab-8 PE=2 SV=1; Q94147|Q94147_CAEEL Rab8-like (Fragment) OS=Caenorhabditis elegans PE=2 SV=1	-0.08
O01593|O01593_CAEEL Protein R08E5.3 OS=Caenorhabditis elegans GN=CELE_R08E5.3 PE=4 SV=1	-0.08

Q17899|Q17899_CAEEL Protein C10C5.4 OS=Caenorhabditis elegans GN=C10C5.4 PE=4 SV=2; Q17900|Q17900_CAEEL Protein C10C5.5 OS=Caenorhabditis elegans GN=C10C5.5 PE=4 SV=2; Q17898|Q17898_CAEEL Protein C10C5.3 OS=Caenorhabditis elegans GN=C10C5.3 PE=4	-0.09
Q18493|UAP1_CAEEL Probable UDP-N-acetylglucosamine pyrophosphorylase OS=Caenorhabditis elegans GN=C36A4.4 PE=3 SV=2; A4UVJ9|A4UVJ9_CAEEL Protein K06B9.2 OS=Caenorhabditis elegans GN=CELE_K06B9.2 PE=4 SV=1	-0.09
Q18967|EIF3F_CAEEL Eukaryotic translation initiation factor 3 subunit F OS=Caenorhabditis elegans GN=eif-3.F PE=3 SV=1	-0.09
Q95PX8|Q95PX8_CAEEL Protein TCER-1, isoform b OS=Caenorhabditis elegans GN=tcer-1 PE=2 SV=1; Q95PX7|Q95PX7_CAEEL Protein TCER-1, isoform a OS=Caenorhabditis elegans GN=tcer-1 PE=2 SV=1; Q86MP0|Q86MP0_CAEEL Protein TCER-1, isoform e OS=Caenorhabdi	-0.09
Q18600|YTV2_CAEEL Uncharacterized zinc metalloprotease C44B7.11 OS=Caenorhabditis elegans GN=C44B7.11 PE=1 SV=4	-0.09
Q20277|Q20277_CAEEL Protein FIPR-21 OS=Caenorhabditis elegans GN=fipr-21 PE=4 SV=1	-0.09
Q18186|Q18186_CAEEL Protein C25H3.4 OS=Caenorhabditis elegans GN=C25H3.4 PE=4 SV=4	-0.09
Q9GZH2|Q9GZH2_CAEEL Protein RUVB-2 OS=Caenorhabditis elegans GN=ruvb-2 PE=1 SV=1	-0.09
B5BM33|B5BM33_CAEEL Protein C27A7.1, isoform c OS=Caenorhabditis elegans GN=C27A7.1 PE=2 SV=1; E1B6U2|E1B6U2_CAEEL Protein C27A7.1, isoform d OS=Caenorhabditis elegans GN=C27A7.1 PE=2 SV=1; P90754-2|ENPP1_CAEEL Isoform b of Ectonucleotide pyropho	-0.09
P51403|RS2_CAEEL 40S ribosomal protein S2 OS=Caenorhabditis elegans GN=rps-2 PE=3 SV=1	-0.09
Q9XUG1|Q9XUG1_CAEEL Protein CLEC-197 OS=Caenorhabditis elegans GN=clec-197 PE=4 SV=2	-0.09
Q19257|Q19257_CAEEL Protein F09E5.7 OS=Caenorhabditis elegans GN=CELE_F09E5.7 PE=4 SV=1	-0.09

H2L2J6|H2L2J6_CAEEL Protein PQN-27, isoform c OS=Caenorhabditis elegans GN=pqn-27 PE=4 SV=1; H2L2J5|H2L2J5_CAEEL Protein PQN-27, isoform b OS=Caenorhabditis elegans GN=pqn-27 PE=4 SV=1; O02238|O02238_CAEEL Protein PQN-27, isoform a OS=Caenorhabdi	-0.09
G5EGA6|G5EGA6_CAEEL Protein DHRS-4 OS=Caenorhabditis elegans GN=dhrs-4 PE=4 SV=1	-0.09
Q17556|Q17556_CAEEL Protein C01F1.3, isoform a OS=Caenorhabditis elegans GN=C01F1.3 PE=2 SV=1	-0.09
O61742|O61742_CAEEL Protein RPN-10 OS=Caenorhabditis elegans GN=rpn-10 PE=4 SV=2	-0.09
Q17949|DOHH_CAEEL Deoxyhypusine hydroxylase OS=Caenorhabditis elegans GN=tag-242 PE=3 SV=1	-0.09
Q21890-3|YF64_CAEEL Isoform c of Uncharacterized protein R102.4 OS=Caenorhabditis elegans GN=R102.4; C6KRK8|C6KRK8_CAEEL Protein R102.4, isoform d OS=Caenorhabditis elegans GN=CELE_R102.4 PE=2 SV=1; Q21890-2|YF64_CAEEL Isoform a of Uncharacterize	-0.09
P90889|P90889_CAEEL Protein F55H12.4 OS=Caenorhabditis elegans GN=CELE_F55H12.4 PE=4 SV=1	-0.09
Q9BL17|Q9BL17_CAEEL Protein HAF-6 OS=Caenorhabditis elegans GN=haf-6 PE=3 SV=3	-0.09
Q23202|SBDS_CAEEL Ribosome maturation protein SBDS OS=Caenorhabditis elegans GN=sbds-1 PE=3 SV=2	-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
Q18581|ACN1_CAEEL Inactive angiotensin-converting enzyme-related protein OS=Caenorhabditis elegans GN=acn-1 PE=1 SV=2	-0.09
O45279|O45279_CAEEL Protein C30H6.7, isoform a OS=Caenorhabditis elegans GN=C30H6.7 PE=3 SV=1	-0.10
O02108|CDC37_CAEEL Probable Hsp90 co-chaperone cdc37 OS=Caenorhabditis elegans GN=cdc-37 PE=2 SV=1; Q336L8|Q336L8_CAEEL Protein CDC-37, isoform b OS=Caenorhabditis elegans GN=cdc-37 PE=2 SV=1	-0.10
O45713|O45713_CAEEL Protein R09B3.3 OS=Caenorhabditis elegans GN=CELE_R09B3.3 PE=1 SV=1	-0.10

Q9N4N3|Q9N4N3_CAEEL Protein PERM-3 OS=Caenorhabditis elegans GN=perm-3 PE=4 SV=1	-0.10
Q9N477|Q9N477_CAEEL Protein Y23H5B.5 OS=Caenorhabditis elegans GN=CELE_Y23H5B.5 PE=4 SV=2	-0.10
O17040|HACD_CAEEL Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase hpo-8 OS=Caenorhabditis elegans GN=hpo-8 PE=3 SV=2	-0.10
Q9N302|Q9N302_CAEEL Protein ACS-13 OS=Caenorhabditis elegans GN=acs-13 PE=4 SV=1	-0.10
Q23451|Q23451_CAEEL Protein RAD-23 OS=Caenorhabditis elegans GN=rad-23 PE=4 SV=2	-0.10
Q2PJ74|Q2PJ74_CAEEL Protein AMAN-2 OS=Caenorhabditis elegans GN=aman-2 PE=4 SV=1	-0.10
P19974|CYC21_CAEEL Cytochrome c 2.1 OS=Caenorhabditis elegans GN=cyc-2.1 PE=1 SV=2	-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
Q22743|Q22743_CAEEL Protein RAGA-1 OS=Caenorhabditis elegans GN=raga-1 PE=4 SV=1	-0.10
G5EDZ2|G5EDZ2_CAEEL Protein UMPS-1 OS=Caenorhabditis elegans GN=umps-1 PE=3 SV=1	-0.11
O62390|O62390_CAEEL Protein W01F3.2 OS=Caenorhabditis elegans GN=CELE_W01F3.2 PE=4 SV=1	-0.11
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
Q20728|TBCB_CAEEL Tubulin-specific chaperone B OS=Caenorhabditis elegans GN=F53F4.3 PE=1 SV=1	-0.11

P34487|YMJB_CAEEL Uncharacterized protein F59B2.12 OS=Caenorhabditis elegans GN=F59B2.12 PE=4 SV=2	-0.11
Q9XWW1|SPCS2_CAEEL Probable signal peptidase complex subunit 2 OS=Caenorhabditis elegans GN=Y37D8A.10 PE=1 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
Q9BL81|Q9BL81_CAEEL Protein Y47G6A.21 OS=Caenorhabditis elegans GN=CELE_Y47G6A.21 PE=4 SV=4	-0.11
A3QMC5|A3QMC5_CAEEL Protein RPL-34 OS=Caenorhabditis elegans GN=rpl-34 PE=4 SV=1	-0.11
Q22368|Q22368_CAEEL Protein T10B10.3 OS=Caenorhabditis elegans GN=CELE_T10B10.3 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
Q18983|Q18983_CAEEL Protein D2045.2 OS=Caenorhabditis elegans GN=CELE_D2045.2 PE=4 SV=3	-0.11
Q95XN6|Q95XN6_CAEEL Protein LSM-6 OS=Caenorhabditis elegans GN=lsm-6 PE=4 SV=1	-0.11
Q94300|RL11_CAEEL 60S ribosomal protein L11 OS=Caenorhabditis elegans GN=rpl-11.1 PE=3 SV=1	-0.11
Q22993|Q22993_CAEEL Protein PMT-2 OS=Caenorhabditis elegans GN=pmt-2 PE=4 SV=1	-0.11
O61861|O61861_CAEEL Actin-related protein 2/3 complex subunit 5 OS=Caenorhabditis elegans GN=arx-7 PE=3 SV=1	-0.11
O16315|O16315_CAEEL Protein C05C8.7 OS=Caenorhabditis elegans GN=C05C8.7 PE=3 SV=1	-0.11
Q17428|PORED_CAEEL Polyprenol reductase OS=Caenorhabditis elegans GN=B0024.13 PE=3 SV=2	-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
Q18074|Q18074_CAEEL Protein C18B2.3 OS=Caenorhabditis elegans GN=C18B2.3 PE=4 SV=2	-0.11
Q23092|FABP4_CAEEL Fatty acid-binding protein homolog 4 OS=Caenorhabditis elegans GN=lbp-4 PE=3 SV=1	-0.12
Q21898|VATL1_CAEEL V-type proton ATPase 16 kDa proteolipid subunit 1 OS=Caenorhabditis elegans GN=vha-1 PE=2 SV=1	-0.12
O01600|O01600_CAEEL Protein T10E9.4 OS=Caenorhabditis elegans GN=CELE_T10E9.4 PE=4 SV=2	-0.12
Q9BKS1|Q9BKS1_CAEEL Protein ELC-1 OS=Caenorhabditis elegans GN=elc-1 PE=1 SV=1	-0.12
B5BM32|B5BM32_CAEEL Protein NXF-1, isoform b OS=Caenorhabditis elegans GN=nxf-1 PE=2 SV=1; Q9XVS7|NXF1_CAEEL Nuclear RNA export factor 1 OS=Caenorhabditis elegans GN=nxf-1 PE=1 SV=1	-0.12
Q8I7G8|Q8I7G8_CAEEL Protein F26B1.2, isoform c OS=Caenorhabditis elegans GN=CELE_F26B1.2 PE=2 SV=1; P91277|P91277_CAEEL Protein F26B1.2, isoform a OS=Caenorhabditis elegans GN=CELE_F26B1.2 PE=1 SV=1	-0.12
Q965S9|Q965S9_CAEEL Protein Y74C10AR.2 OS=Caenorhabditis elegans GN=CELE_Y74C10AR.2 PE=4 SV=2	-0.12
Q9U3C1|Q9U3C1_CAEEL Protein NPP-1, isoform b OS=Caenorhabditis elegans GN=npp-1 PE=2 SV=1; Q21295|Q21295_CAEEL Protein NPP-1, isoform a OS=Caenorhabditis elegans GN=npp-1 PE=2 SV=3; Q9U3B9|Q9U3B9_CAEEL Protein NPP-1, isoform c OS=Caenorhabditis e	-0.12
P91148|NDX7_CAEEL Putative nudix hydrolase 7 OS=Caenorhabditis elegans GN=ndx-7 PE=3 SV=2	-0.12
Q18964|WDFY2_CAEEL WD repeat and FYVE domain-containing protein 2 OS=Caenorhabditis elegans GN=wdfy-2 PE=1 SV=1	-0.12
Q5R3Y2|Q5R3Y2_CAEEL Protein F28H1.4, isoform b OS=Caenorhabditis elegans GN=CELE_F28H1.4 PE=2 SV=1; P83386|P83386_CAEEL Protein F28H1.4, isoform a OS=Caenorhabditis elegans GN=CELE_F28H1.4 PE=2 SV=2	-0.12

G8JYG1|G8JYG1_CAEEL Protein NXT-1, isoform b OS=Caenorhabditis elegans GN=nxt-1 PE=2 SV=1; Q9U757|NXT1_CAEEL NTF2-related export protein OS=Caenorhabditis elegans GN=nxt-1 PE=1 SV=1	-0.12
O61709|O61709_CAEEL Protein R119.3 OS=Caenorhabditis elegans GN=CELE_R119.3 PE=4 SV=2	-0.12
Q23295|Q23295_CAEEL Protein MPPB-1 OS=Caenorhabditis elegans GN=mppb-1 PE=3 SV=2	-0.12
Q20117|GSH1_CAEEL Glutamate--cysteine ligase OS=Caenorhabditis elegans GN=gcs-1 PE=1 SV=2	-0.12
Q9N4B1|Q9N4B1_CAEEL Protein CLP-7 OS=Caenorhabditis elegans GN=clp-7 PE=4 SV=2	-0.12
P55163|GEX3_CAEEL Membrane-associated protein gex-3 OS=Caenorhabditis elegans GN=gex-3 PE=1 SV=2	-0.12
Q7Z2A5|Q7Z2A5_CAEEL Protein MOP-25.1, isoform b OS=Caenorhabditis elegans GN=mop-25.1 PE=2 SV=1; Q21643|Q21643_CAEEL Protein MOP-25.1, isoform a OS=Caenorhabditis elegans GN=mop-25.1 PE=2 SV=2	-0.12
O76430|O76430_CAEEL Protein C24B9.3, isoform a OS=Caenorhabditis elegans GN=C24B9.3 PE=4 SV=2; H2KZ02|H2KZ02_CAEEL Protein C24B9.3, isoform b OS=Caenorhabditis elegans GN=C24B9.3 PE=4 SV=1	-0.12
P18334|CSK2A_CAEEL Casein kinase II subunit alpha OS=Caenorhabditis elegans GN=kin-3 PE=1 SV=1	-0.13
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
P92005|P92005_CAEEL Protein CPZ-2 OS=Caenorhabditis elegans GN=cpz-2 PE=3 SV=1	-0.13
Q22768|Q22768_CAEEL Protein T25B9.1 OS=Caenorhabditis elegans GN=CELE_T25B9.1 PE=4 SV=2	-0.13
G5EGT7|G5EGT7_CAEEL Eukaryotic translation initiation factor eIF5B OS=Caenorhabditis elegans GN=iffb-1 PE=2 SV=1	-0.13

Q17409|Q17409_CAEEL Alpha-1 tubulin OS=Caenorhabditis elegans GN=tba-1 PE=2 SV=1; O18688|O18688_CAEEL Protein TBA-1, isoform a OS=Caenorhabditis elegans GN=tba-1 PE=2 SV=1; H2L2E8|H2L2E8_CAEEL Protein TBA-1, isoform b OS=Caenorhabditis elegans GN	-0.13
Q10578|RPB2_CAEEL DNA-directed RNA polymerase II subunit RPB2 OS=Caenorhabditis elegans GN=rpb-2 PE=2 SV=2	-0.13
Q23493|Q23493_CAEEL Protein TAG-231 OS=Caenorhabditis elegans GN=tag-231 PE=4 SV=1	-0.13
P34497|GLNA_CAEEL Probable glutamine synthetase OS=Caenorhabditis elegans GN=gln-2 PE=3 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
Q21210|Q21210_CAEEL Protein K04C2.2 OS=Caenorhabditis elegans GN=CELE_K04C2.2 PE=4 SV=1	-0.13
Q09438|MTAP_CAEEL S-methyl-5-thioadenosine phosphorylase OS=Caenorhabditis elegans GN=B0228.7 PE=3 SV=2	-0.13
Q95QB1|Q95QB1_CAEEL Protein T13H5.8 OS=Caenorhabditis elegans GN=CELE_T13H5.8 PE=4 SV=1	-0.13
H2L0C0|H2L0C0_CAEEL Protein EMC-1, isoform a OS=Caenorhabditis elegans GN=emc-1 PE=4 SV=1; Q86S39|Q86S39_CAEEL Protein EMC-1, isoform b OS=Caenorhabditis elegans GN=emc-1 PE=4 SV=1	-0.14
G5ED21|G5ED21_CAEEL DNA-directed RNA polymerase OS=Caenorhabditis elegans GN=rpoa-1 PE=2 SV=1	-0.14
O44995|O44995_CAEEL Protein K12C11.1 OS=Caenorhabditis elegans GN=CELE_K12C11.1 PE=3 SV=2	-0.14
Q8IG34|Q8IG34_CAEEL Protein F09C12.8 OS=Caenorhabditis elegans GN=CELE_F09C12.8 PE=4 SV=1	-0.14
A7DT45|A7DT45_CAEEL Protein OXY-5 OS=Caenorhabditis elegans GN=oxy-5 PE=4 SV=1	-0.14

Q21351|Q21351_CAEEL Protein K08F4.2 OS=Caenorhabditis elegans GN=CELE_K08F4.2 PE=4 SV=2	-0.14
Q9NAB4|Q9NAB4_CAEEL Protein GST-26 OS=Caenorhabditis elegans GN=gst-26 PE=3 SV=1	-0.14
H2KY88|H2KY88_CAEEL Protein F56C9.10, isoform a OS=Caenorhabditis elegans GN=CELE_F56C9.10 PE=4 SV=1; Q8MQ22|Q8MQ22_CAEEL Protein F56C9.10, isoform b OS=Caenorhabditis elegans GN=CELE_F56C9.10 PE=4 SV=1	-0.14
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
G5EC23|G5EC23_CAEEL Host cell factor 1 OS=Caenorhabditis elegans GN=hcf-1 PE=1 SV=1	-0.14
G5EBK4|G5EBK4_CAEEL Protein ATG-7 OS=Caenorhabditis elegans GN=atg-7 PE=4 SV=1	-0.14
Q18577|Q18577_CAEEL Protein C42D4.1 OS=Caenorhabditis elegans GN=C42D4.1 PE=4 SV=1; Q22670-2|RBGPR_CAEEL Isoform b of Rab3 GTPase-activating protein regulatory subunit OS=Caenorhabditis elegans GN=rbg-2; Q22670|RBGPR_CAEEL Rab3 GTPase-activating	-0.14
Q9XUE5|Q9XUE5_CAEEL Protein NOAH-2 OS=Caenorhabditis elegans GN=noah-2 PE=4 SV=1	-0.14
Q19555|Q19555_CAEEL Protein SCC-3 OS=Caenorhabditis elegans GN=scc-3 PE=4 SV=1	-0.14
G5EF60-3|STIM1_CAEEL Isoform c of Stromal interaction molecule 1 OS=Caenorhabditis elegans GN=stim-1; G5EF60-2|STIM1_CAEEL Isoform b of Stromal interaction molecule 1 OS=Caenorhabditis elegans GN=stim-1; G5EF60|STIM1_CAEEL Stromal interaction mol	-0.15
P91180|P91180_CAEEL Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=fkb-5 PE=2 SV=1; Q95Q60|Q95Q60_CAEEL Peptidyl-prolyl cis-trans isomerase OS=Caenorhabditis elegans GN=fkb-5 PE=2 SV=1	-0.15
Q18905|CGP1_CAEEL GTP-binding protein cgp-1 OS=Caenorhabditis elegans GN=cgp-1 PE=2 SV=2	-0.15
O18000|O18000_CAEEL Protein PES-9 OS=Caenorhabditis elegans GN=pes-9 PE=4 SV=1	-0.15

G5EFF9|G5EFF9_CAEEL Protein F11A3.2, isoform a OS=Caenorhabditis elegans GN=CELE_F11A3.2 PE=2 SV=1; G5EG28|G5EG28_CAEEL Protein F11A3.2, isoform b OS=Caenorhabditis elegans GN=CELE_F11A3.2 PE=2 SV=1	-0.15
Q9XWN7|Q9XWN7_CAEEL Protein Y43F8C.13 OS=Caenorhabditis elegans GN=CELE_Y43F8C.13 PE=4 SV=1	-0.15
O17687|O17687_CAEEL Protein NASP-2 OS=Caenorhabditis elegans GN=nasp-2 PE=4 SV=1	-0.15
P34712|PGP1_CAEEL Multidrug resistance protein pgp-1 OS=Caenorhabditis elegans GN=pgp-1 PE=1 SV=2	-0.15
Q03567|YLD2_CAEEL Uncharacterized transporter C38C10.2 OS=Caenorhabditis elegans GN=C38C10.2 PE=1 SV=2	-0.15
Q22134|Q22134_CAEEL Amidophosphoribosyltransferase OS=Caenorhabditis elegans GN=CELE_T04A8.5 PE=3 SV=1	-0.15
G5EFW8|G5EFW8_CAEEL Mitochondrial adenine nucleotide translocase 1.3 OS=Caenorhabditis elegans GN=ant-1.3 PE=2 SV=1; G5EFU2|G5EFU2_CAEEL Mitochondrial adenine nucleotide translocase 1.4 OS=Caenorhabditis elegans GN=ant-1.4 PE=2 SV=1	-0.15
Q9NAG5|Q9NAG5_CAEEL Protein Y48C3A.3 OS=Caenorhabditis elegans GN=CELE_Y48C3A.3 PE=4 SV=1	-0.15
O44183|O44183_CAEEL Protein ZC416.6 OS=Caenorhabditis elegans GN=CELE_ZC416.6 PE=4 SV=2	-0.15
O76463|NFT1_CAEEL Nitrilase and fragile histidine triad fusion protein NitFhit OS=Caenorhabditis elegans GN=nft-1 PE=1 SV=1	-0.15
P91398|P91398_CAEEL Protein CEY-3 OS=Caenorhabditis elegans GN=cey-3 PE=4 SV=1	-0.15
P49180|RL35A_CAEEL 60S ribosomal protein L35a OS=Caenorhabditis elegans GN=rpl-33 PE=1 SV=3	-0.15
Q20363|SIP1_CAEEL Stress-induced protein 1 OS=Caenorhabditis elegans GN=sip-1 PE=1 SV=1	-0.15
O45110|O45110_CAEEL Protein MRPL-2 OS=Caenorhabditis elegans GN=mrpl-2 PE=4 SV=3	-0.15
Q9N3F7|Q9N3F7_CAEEL Protein Y53G8AR.9 OS=Caenorhabditis elegans GN=CELE_Y53G8AR.9 PE=4 SV=1	-0.15

G5EFH8|G5EFH8_CAEEL Protein CBS-1, isoform a OS=Caenorhabditis elegans GN=cbs-1 PE=4 SV=1; H9G2P9|H9G2P9_CAEEL Protein CBS-1, isoform b OS=Caenorhabditis elegans GN=cbs-1 PE=4 SV=1	-0.16
Q22135|Q22135_CAEEL Protein T04A8.6 OS=Caenorhabditis elegans GN=CELE_T04A8.6 PE=4 SV=1	-0.16
O17636|O17636_CAEEL Protein ETHE-1 OS=Caenorhabditis elegans GN=ethe-1 PE=4 SV=1	-0.16
Q9XUY4|Q9XUY4_CAEEL Protein F55F3.2, isoform a OS=Caenorhabditis elegans GN=CELE_F55F3.2 PE=2 SV=2; Q8MQ23|Q8MQ23_CAEEL Protein F55F3.2, isoform b OS=Caenorhabditis elegans GN=CELE_F55F3.2 PE=2 SV=1	-0.16
O61219|O61219_CAEEL Protein K07H8.3 OS=Caenorhabditis elegans GN=CELE_K07H8.3 PE=4 SV=1	-0.16
P53703|CCHL_CAEEL Probable cytochrome c-type heme lyase OS=Caenorhabditis elegans GN=cchl-1 PE=3 SV=1	-0.16
Q27532|H33L2_CAEEL Histone H3.3-like type 2 OS=Caenorhabditis elegans GN=his-74 PE=3 SV=3	-0.16
Q95Y71|RM45_CAEEL Probable 39S ribosomal protein L45, mitochondrial OS=Caenorhabditis elegans GN=mrpl-45 PE=3 SV=3	-0.16
Q95QH5|Q95QH5_CAEEL Protein F32A5.2, isoform b OS=Caenorhabditis elegans GN=CELE_F32A5.2 PE=4 SV=1; H2KZ53|H2KZ53_CAEEL Protein F32A5.2, isoform a OS=Caenorhabditis elegans GN=CELE_F32A5.2 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
Q22528|Q22528_CAEEL Protein EKL-6 OS=Caenorhabditis elegans GN=ekl-6 PE=4 SV=2	-0.16
Q21568|NH2L1_CAEEL NHP2-like protein 1 homolog OS=Caenorhabditis elegans GN=M28.5 PE=3 SV=1	-0.16
Q8I136-2|GALT4_CAEEL Isoform b of Polypeptide N-acetylgalactosaminyltransferase 4 OS=Caenorhabditis elegans GN=gly-4; C6S3M5|C6S3M5_CAEEL Protein GLY-4, isoform c OS=Caenorhabditis elegans GN=gly-4 PE=2 SV=1; Q8I136|GALT4_CAEEL Polypeptide N-acet	-0.16
Q9TZ33|Q9TZ33_CAEEL Protein UCR-2.3 OS=Caenorhabditis elegans GN=ucr-2.3 PE=3 SV=1	-0.16

Q27476|Q27476_CAEEL Protein CYP-25A2 OS=Caenorhabditis elegans GN=cyp-25a2 PE=3 SV=2; Q27477|Q27477_CAEEL Protein CYP-25A1 OS=Caenorhabditis elegans GN=cyp-25a1 PE=3 SV=3	-0.17
E1B6R8|E1B6R8_CAEEL Protein EMC-5 OS=Caenorhabditis elegans GN=emc-5 PE=4 SV=1	-0.17
P08898|H3_CAEEL Histone H3 OS=Caenorhabditis elegans GN=his-2 PE=1 SV=4; K7ZUH9|K7ZUH9_CAEEL Histone H3 OS=Caenorhabditis elegans GN=his-40 PE=3 SV=1; Q10453|H331_CAEEL Histone H3.3 type 1 OS=Caenorhabditis elegans GN=his-71 PE=2 SV=2; Q9U281|	-0.17
O44954|O44954_CAEEL Protein SDHA-2 OS=Caenorhabditis elegans GN=sdha-2 PE=4 SV=1	-0.17
G5EER7|G5EER7_CAEEL Protein TAG-10, isoform b OS=Caenorhabditis elegans GN=tag-10 PE=2 SV=1; B8ZX16|B8ZX16_CAEEL P52CeGA (Fragment) OS=Caenorhabditis elegans GN=tag-10 PE=2 SV=1; G5EG67|G5EG67_CAEEL Protein TAG-10, isoform a OS=Caenorhabditis ele	-0.17
D3YT94|D3YT94_CAEEL Protein FAT-6, isoform c OS=Caenorhabditis elegans GN=fat-6 PE=2 SV=1; D3YT93|D3YT93_CAEEL Protein FAT-6, isoform b OS=Caenorhabditis elegans GN=fat-6 PE=2 SV=1; G5EGN2|G5EGN2_CAEEL Protein FAT-6, isoform a OS=Caenorhabditis e	-0.17
P34492-2|YMQ1_CAEEL Isoform b of Putative NipSnap protein K02D10.1 OS=Caenorhabditis elegans GN=K02D10.1; P34492|YMQ1_CAEEL Putative NipSnap protein K02D10.1 OS=Caenorhabditis elegans GN=K02D10.1 PE=2 SV=4	-0.17
P91416|MTND1_CAEEL 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase homolog 1 OS=Caenorhabditis elegans GN=T01D1.4 PE=3 SV=1	-0.17
Q8MQ99|Q8MQ99_CAEEL Protein C51E3.9, isoform a OS=Caenorhabditis elegans GN=C51E3.9 PE=4 SV=1; G3MU39|G3MU39_CAEEL Protein C51E3.9, isoform b OS=Caenorhabditis elegans GN=C51E3.9 PE=4 SV=1	-0.17
Q9TYV3|Q9TYV3_CAEEL Protein W07E6.2 OS=Caenorhabditis elegans GN=CELE_W07E6.2 PE=4 SV=1	-0.17
O01755|O01755_CAEEL Protein APM-1 OS=Caenorhabditis elegans GN=apm-1 PE=4 SV=2	-0.18
Q10457|PUR6_CAEEL Probable multifunctional protein ADE2 OS=Caenorhabditis elegans GN=B0286.3 PE=1 SV=1	-0.18

O02225|O02225_CAEEL Protein GLN-6 OS=Caenorhabditis elegans GN=gln-6 PE=3 SV=1	-0.18
Q9XVF1|Q9XVF1_CAEEL Protein C04F12.1 OS=Caenorhabditis elegans GN=C04F12.1 PE=4 SV=1	-0.18
O16619|O16619_CAEEL Protein DHS-13 OS=Caenorhabditis elegans GN=dhs-13 PE=4 SV=1	-0.18
P30627|GLBH_CAEEL Globin-like protein OS=Caenorhabditis elegans GN=glb-1 PE=1 SV=2	-0.18
O44739|BAG1_CAEEL BAG family molecular chaperone regulator 1 OS=Caenorhabditis elegans GN=bag-1 PE=1 SV=1	-0.18
Q09225|NRF6_CAEEL Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3	-0.18
O16214|O16214_CAEEL Protein F17A9.4 OS=Caenorhabditis elegans GN=CELE_F17A9.4 PE=4 SV=1	-0.18
Q19478|Q19478_CAEEL Protein FAR-3 OS=Caenorhabditis elegans GN=far-3 PE=4 SV=1	-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
Q19133|Q19133_CAEEL Protein F07A11.5 OS=Caenorhabditis elegans GN=CELE_F07A11.5 PE=4 SV=2	-0.18
Q9Y041|HGD_CAEEL Homogentisate 1,2-dioxygenase OS=Caenorhabditis elegans GN=hgo-1 PE=1 SV=2	-0.18
Q95YF3|CGH1_CAEEL ATP-dependent RNA helicase cgh-1 OS=Caenorhabditis elegans GN=cgh-1 PE=1 SV=1	-0.19
Q18994|Q18994_CAEEL Protein D2085.3 OS=Caenorhabditis elegans GN=CELE_D2085.3 PE=4 SV=1	-0.19
Q9BKU3|Q9BKU3_CAEEL Protein Y37E3.10 OS=Caenorhabditis elegans GN=CELE_Y37E3.10 PE=4 SV=2	-0.19
Q19743|H13_CAEEL Histone H1.3 OS=Caenorhabditis elegans GN=hil-3 PE=2 SV=3	-0.19
Q23188|Q23188_CAEEL Protein RET-1, isoform b OS=Caenorhabditis elegans GN=ret-1 PE=2 SV=1	-0.19

P49181|RL36_CAEEL 60S ribosomal protein L36 OS=Caenorhabditis elegans GN=rpl-36 PE=1 SV=3	-0.19
Q9GYJ9|Q9GYJ9_CAEEL Protein SNX-1 OS=Caenorhabditis elegans GN=snx-1 PE=1 SV=1	-0.19
Q7YTF9|Q7YTF9_CAEEL Protein ZK858.6, isoform b OS=Caenorhabditis elegans GN=CELE_ZK858.6 PE=2 SV=1; B3WFW5|B3WFW5_CAEEL Protein ZK858.6, isoform a OS=Caenorhabditis elegans GN=CELE_ZK858.6 PE=2 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
P34280|YKK3_CAEEL Uncharacterized GTP-binding protein C02F5.3 OS=Caenorhabditis elegans GN=C02F5.3 PE=3 SV=2	-0.19
O01422|CSN2_CAEEL COP9 signalosome complex subunit 2 OS=Caenorhabditis elegans GN=csn-2 PE=1 SV=2	-0.19
Q9NEZ8|Q9NEZ8_CAEEL Protein ECH-7 OS=Caenorhabditis elegans GN=ech-7 PE=3 SV=1	-0.19
O02252|O02252_CAEEL Protein PCP-3 OS=Caenorhabditis elegans GN=pcp-3 PE=4 SV=2	-0.19
Q22028|Q22028_CAEEL Protein DNJ-16, isoform a OS=Caenorhabditis elegans GN=dnj-16 PE=2 SV=1; C1P627|C1P627_CAEEL Protein DNJ-16, isoform b OS=Caenorhabditis elegans GN=dnj-16 PE=2 SV=1	-0.20
Q8ITV4|Q8ITV4_CAEEL Protein H14E04.2, isoform d OS=Caenorhabditis elegans GN=CELE_H14E04.2 PE=4 SV=1; H2L0A4|H2L0A4_CAEEL Protein H14E04.2, isoform a OS=Caenorhabditis elegans GN=CELE_H14E04.2 PE=4 SV=1; H2L0A5|H2L0A5_CAEEL Protein H14E04.2, isof	-0.20
Q21925|Q21925_CAEEL Protein R11A8.5 OS=Caenorhabditis elegans GN=CELE_R11A8.5 PE=4 SV=1	-0.20
P49404|RM03_CAEEL Putative 39S ribosomal protein L3, mitochondrial OS=Caenorhabditis elegans GN=mrps-18C PE=3 SV=3	-0.20
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

Q5CZ43|Q5CZ43_CAEEL Protein TRR-1, isoform c OS=Caenorhabditis elegans GN=trr-1 PE=2 SV=1; Q6A4L2|Q6A4L2_CAEEL Protein TRR-1, isoform b OS=Caenorhabditis elegans GN=trr-1 PE=2 SV=1; G5EEV2|G5EEV2_CAEEL Protein TRR-1, isoform a OS=Caenorhabditis e	-0.21
Q9U2V9|Q9U2V9_CAEEL Methionine aminopeptidase OS=Caenorhabditis elegans GN=map-2 PE=3 SV=1; H1UBK1|H1UBK1_CAEEL Methionine aminopeptidase OS=Caenorhabditis elegans GN=map-2 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
Q9TZL9|Q9TZL9_CAEEL Protein FARD-1 OS=Caenorhabditis elegans GN=fard-1 PE=4 SV=1	-0.21
O01815|O01815_CAEEL Protein DHOD-1 OS=Caenorhabditis elegans GN=dhod-1 PE=4 SV=1	-0.21
Q18038|Q18038_CAEEL Protein LET-716 OS=Caenorhabditis elegans GN=let-716 PE=4 SV=3	-0.21
G5EDZ9|G5EDZ9_CAEEL Cystatin OS=Caenorhabditis elegans GN=cpi-1 PE=2 SV=1	-0.21
Q9N3W5|Q9N3W5_CAEEL Protein CLEC-72 OS=Caenorhabditis elegans GN=clec-72 PE=4 SV=3; Q9N3X0|Q9N3X0_CAEEL Protein CLEC-70 OS=Caenorhabditis elegans GN=clec-70 PE=4 SV=2	-0.21
Q27511|H2AV_CAEEL Histone H2A.V OS=Caenorhabditis elegans GN=htz-1 PE=3 SV=3	-0.21
P34713|PGP3_CAEEL Multidrug resistance protein pgp-3 OS=Caenorhabditis elegans GN=pgp-3 PE=2 SV=2	-0.21
Q19437|Q19437_CAEEL Protein UPB-1 OS=Caenorhabditis elegans GN=upb-1 PE=4 SV=1	-0.21
Q27493|Q27493_CAEEL DNA-directed RNA polymerase OS=Caenorhabditis elegans GN=rpoa-2 PE=3 SV=1	-0.21
Q9N3F2|Q9N3F2_CAEEL Protein Y54E10A.6 OS=Caenorhabditis elegans GN=CELE_Y54E10A.6 PE=4 SV=1	-0.21
Q95XD0|Q95XD0_CAEEL Protein EXOS-2 OS=Caenorhabditis elegans GN=exos-2 PE=4 SV=1	-0.21

Q9NA75|Q9NA75_CAEEL Protein Y57A10A.10 OS=Caenorhabditis elegans GN=CELE_Y57A10A.10 PE=4 SV=2	-0.21
G5EEN1|G5EEN1_CAEEL Protein FARS-2, isoform c OS=Caenorhabditis elegans GN=fars-2 PE=2 SV=1; G5ECI8|G5ECI8_CAEEL Mitochondrial phenylalanyl-tRNA synthetase OS=Caenorhabditis elegans GN=fars-2 PE=2 SV=1	-0.21
Q9GUP2|Q9GUP2_CAEEL Protein EEL-1 OS=Caenorhabditis elegans GN=eel-1 PE=4 SV=2	-0.21
Q23591|Q23591_CAEEL Protein ZK792.5 OS=Caenorhabditis elegans GN=CELE_ZK792.5 PE=4 SV=2	-0.21
Q960A1|Q960A1_CAEEL Protein GAD-3 OS=Caenorhabditis elegans GN=gad-3 PE=4 SV=3	-0.22
P90778|P90778_CAEEL Protein C55A6.3 OS=Caenorhabditis elegans GN=C55A6.3 PE=4 SV=3	-0.22
Q9N3D0|Q9N3D0_CAEEL Protein Y54E10BR.5 OS=Caenorhabditis elegans GN=CELE_Y54E10BR.5 PE=4 SV=1	-0.22
Q20065|P4HA2_CAEEL Prolyl 4-hydroxylase subunit alpha-2 OS=Caenorhabditis elegans GN=phy-2 PE=1 SV=1	-0.22
O76689|SNF6_CAEEL Sodium-dependent acetylcholine transporter OS=Caenorhabditis elegans GN=snf-6 PE=1 SV=4	-0.22
P16356|RPB1_CAEEL DNA-directed RNA polymerase II subunit RPB1 OS=Caenorhabditis elegans GN=ama-1 PE=1 SV=3	-0.22
Q22824|Q22824_CAEEL Protein CGR-1 OS=Caenorhabditis elegans GN=cgr-1 PE=4 SV=3	-0.22
B3GWC0|B3GWC0_CAEEL Protein NDX-9, isoform b OS=Caenorhabditis elegans GN=ndx-9 PE=2 SV=1; Q19427|NPY1_CAEEL NADH pyrophosphatase OS=Caenorhabditis elegans GN=ndx-9 PE=1 SV=3	-0.22
Q17390|CUL2_CAEEL Cullin-2 OS=Caenorhabditis elegans GN=cul-2 PE=1 SV=3; Q17390-4|CUL2_CAEEL Isoform 4 of Cullin-2 OS=Caenorhabditis elegans GN=cul-2; Q17390-3|CUL2_CAEEL Isoform 3 of Cullin-2 OS=Caenorhabditis elegans GN=cul-2; Q17390-2|CUL2_	-0.22
O01615|AN322_CAEEL Acidic leucine-rich nuclear phosphoprotein 32-related protein 2 OS=Caenorhabditis elegans GN=T19H12.2 PE=3 SV=1	-0.22

B0M0N9|B0M0N9_CAEEL Protein GLNA-1, isoform a OS=Caenorhabditis elegans GN=glna-1 PE=3 SV=1; B0M0P0|B0M0P0_CAEEL Protein GLNA-1, isoform b OS=Caenorhabditis elegans GN=glna-1 PE=3 SV=1; B6VQ90|B6VQ90_CAEEL Protein GLNA-1, isoform c OS=Caenorhabdi	-0.23
O16297|O16297_CAEEL Protein MCM-7 OS=Caenorhabditis elegans GN=mcm-7 PE=3 SV=1	-0.23
Q21770|GCC7_CAEEL Germ cell-expressed protein R06C7.1 OS=Caenorhabditis elegans GN=R06C7.1 PE=2 SV=1	-0.23
G5ECA0|G5ECA0_CAEEL Protein MPST-5 OS=Caenorhabditis elegans GN=mpst-5 PE=4 SV=1; P91247|THT1_CAEEL Putative thiosulfate sulfurtransferase F11G11.9 OS=Caenorhabditis elegans GN=F11G11.9 PE=3 SV=1	-0.23
G5EF53|G5EF53_CAEEL Protein SWSN-4 OS=Caenorhabditis elegans GN=swsn-4 PE=2 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
P34563|IF5A1_CAEEL Eukaryotic translation initiation factor 5A-1 OS=Caenorhabditis elegans GN=iff-1 PE=1 SV=1; G1K0V8|G1K0V8_CAEEL Protein IFF-1, isoform b OS=Caenorhabditis elegans GN=iff-1 PE=2 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
G5ECF8|G5ECF8_CAEEL Protein Y59E9AL.2 OS=Caenorhabditis elegans GN=CELE_Y59E9AL.2 PE=4 SV=1	-0.24
Q9U1Y6|Q9U1Y6_CAEEL Protein DHS-24 OS=Caenorhabditis elegans GN=dhs-24 PE=4 SV=3	-0.24

A5JYX4|A5JYX4_CAEEL Protein DHS-3, isoform a OS=Caenorhabditis elegans GN=dhs-3 PE=2 SV=1; A5JYX5|A5JYX5_CAEEL Protein DHS-3, isoform b OS=Caenorhabditis elegans GN=dhs-3 PE=2 SV=1	-0.24
Q9N5G3|Q9N5G3_CAEEL Protein DHS-14 OS=Caenorhabditis elegans GN=dhs-14 PE=4 SV=1	-0.24
O16575|O16575_CAEEL Protein SCL-15 OS=Caenorhabditis elegans GN=scl-15 PE=4 SV=1	-0.24
H2L0I7|H2L0I7_CAEEL Protein HUM-8, isoform a OS=Caenorhabditis elegans GN=hum-8 PE=4 SV=1; Q6EZG5|Q6EZG5_CAEEL Protein HUM-8, isoform b OS=Caenorhabditis elegans GN=hum-8 PE=4 SV=2	-0.24
Q05062|CDC42_CAEEL Cell division control protein 42 homolog OS=Caenorhabditis elegans GN=cdc-42 PE=1 SV=2	-0.24
O01965|O01965_CAEEL Protein ARI-1 OS=Caenorhabditis elegans GN=ari-1 PE=4 SV=3	-0.24
Q8MXH7|Q8MXH7_CAEEL Protein C11D2.7 OS=Caenorhabditis elegans GN=C11D2.7 PE=4 SV=1	-0.25
O62146|PLBL2_CAEEL Putative phospholipase B-like 2 OS=Caenorhabditis elegans GN=F09B12.3 PE=1 SV=2	-0.25
P34260|VP33A_CAEEL Vacuolar protein sorting-associated protein 33A OS=Caenorhabditis elegans GN=vps-33.1 PE=1 SV=4	-0.25
Q19864|Q19864_CAEEL Protein CPF-1 OS=Caenorhabditis elegans GN=cpf-1 PE=4 SV=1	-0.25
Q18553|Q18553_CAEEL Protein C39H7.1 OS=Caenorhabditis elegans GN=C39H7.1 PE=3 SV=1; O62426|O62426_CAEEL Protein Y38H8A.3 OS=Caenorhabditis elegans GN=CELE_Y38H8A.3 PE=3 SV=1	-0.25
Q22129|Q22129_CAEEL Protein T03G6.3 OS=Caenorhabditis elegans GN=CELE_T03G6.3 PE=4 SV=2	-0.25
Q9BL36|Q9BL36_CAEEL Protein Y71H2AM.6, isoform a OS=Caenorhabditis elegans GN=CELE_Y71H2AM.6 PE=2 SV=1	-0.25
Q18408|Q18408_CAEEL Protein IMP-3 OS=Caenorhabditis elegans GN=imp-3 PE=4 SV=3	-0.25
Q9N4Z0|L2HDH_CAEEL L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Caenorhabditis elegans GN=Y45G12B.3 PE=3 SV=2	-0.25

P46559|KICB2_CAEEL Choline kinase B2 OS=Caenorhabditis elegans GN=ckb-2 PE=1 SV=2	-0.25
Q9N3Q8|DAF25_CAEEL Dauer abnormal formation protein 25 OS=Caenorhabditis elegans GN=daf-25 PE=1 SV=2	-0.26
P34355|ACOX_CAEEL Probable peroxisomal acyl-coenzyme A oxidase OS=Caenorhabditis elegans GN=C48B4.1 PE=3 SV=1	-0.26
Q20228|RS9_CAEEL 40S ribosomal protein S9 OS=Caenorhabditis elegans GN=rps-9 PE=3 SV=1	-0.26
O18212|O18212_CAEEL Protein Y53C12A.3 OS=Caenorhabditis elegans GN=CELE_Y53C12A.3 PE=4 SV=2	-0.26
Q9NAM7|PHYD1_CAEEL Phytanoyl-CoA dioxygenase domain-containing protein 1 homolog OS=Caenorhabditis elegans GN=Y105C5B.9 PE=3 SV=1	-0.26
Q9XUB7|Q9XUB7_CAEEL Protein FAR-6 OS=Caenorhabditis elegans GN=far-6 PE=4 SV=1	-0.26
Q9N361|RT25_CAEEL Probable 28S ribosomal protein S25, mitochondrial OS=Caenorhabditis elegans GN=mrps-25 PE=3 SV=1	-0.26
Q17974|Q17974_CAEEL Protein C14C10.4 OS=Caenorhabditis elegans GN=C14C10.4 PE=4 SV=1	-0.26
Q19698|Q19698_CAEEL Protein ILYS-5, isoform a OS=Caenorhabditis elegans GN=ilys-5 PE=4 SV=1	-0.27
O16202|O16202_CAEEL Protein LYS-7 OS=Caenorhabditis elegans GN=lys-7 PE=4 SV=1	-0.27
Q21993|PFD5_CAEEL Probable prefoldin subunit 5 OS=Caenorhabditis elegans GN=pfd-5 PE=2 SV=1	-0.27
Q23232|WDR4_CAEEL tRNA (guanine-N(7)-)-methyltransferase subunit wdr-4 OS=Caenorhabditis elegans GN=Y102E9.2 PE=2 SV=1; G8XYY6|G8XYY6_CAEEL Protein Y102E9.2, isoform b OS=Caenorhabditis elegans GN=CELE_Y102E9.2 PE=2 SV=1	-0.27
Q17378|Q17378_CAEEL Sel-1 protein OS=Caenorhabditis elegans GN=sel-1 PE=2 SV=1; G5EFG0|G5EFG0_CAEEL Protein SEL-1 OS=Caenorhabditis elegans GN=sel-1 PE=2 SV=1	-0.27

Q5FC71|Q5FC71_CAEEL Protein W02B12.15, isoform a OS=Caenorhabditis elegans GN=CELE_W02B12.15 PE=2 SV=1; A7LPG5|A7LPG5_CAEEL Protein W02B12.15, isoform b OS=Caenorhabditis elegans GN=CELE_W02B12.15 PE=2 SV=1; Q9NL51|Q9NL51_CAEEL Kinesin like prote	-0.27
Q21986|NAA25_CAEEL N-terminal acetyltransferase B complex subunit NAA25 homolog OS=Caenorhabditis elegans GN=R13F6.10 PE=3 SV=3	-0.27
C2BR91|C2BR91_CAEEL Protein C39B5.5 OS=Caenorhabditis elegans GN=C39B5.5 PE=4 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
P91913|RLA1_CAEEL 60S acidic ribosomal protein P1 OS=Caenorhabditis elegans GN=rla-1 PE=3 SV=2	-0.28
Q9N3A9|Q9N3A9_CAEEL Protein Y54G2A.4 OS=Caenorhabditis elegans GN=CELE_Y54G2A.4 PE=4 SV=3	-0.28
Q9N4N4|Q9N4N4_CAEEL Protein SWSN-6 OS=Caenorhabditis elegans GN=swsn-6 PE=3 SV=2	-0.28
G5EGP8|G5EGP8_CAEEL Cathepsin Z-like enzyme OS=Caenorhabditis elegans GN=cpz-1 PE=3 SV=1	-0.28
Q23445|SAR1_CAEEL GTP-binding protein SAR1 OS=Caenorhabditis elegans GN=ZK180.4 PE=3 SV=1	-0.28
G5ECJ8|G5ECJ8_CAEEL Dimethylaniline monooxygenase [N-oxide-forming] OS=Caenorhabditis elegans GN=fmo-3 PE=2 SV=1	-0.28
Q19311|PUR4_CAEEL Probable phosphoribosylformylglycinamidine synthase OS=Caenorhabditis elegans GN=F10F2.2 PE=3 SV=3	-0.29
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

Q27485|Q27485_CAEEL Histone H2A OS=Caenorhabditis elegans GN=his-35 PE=3 SV=1; P09588|H2A_CAEEL Histone H2A OS=Caenorhabditis elegans GN=his-3 PE=1 SV=2; J7S164|J7S164_CAEEL Histone H2A OS=Caenorhabditis elegans GN=his-57 PE=3 SV=1; J7SA65|J7S	-0.29
P91544|P91544_CAEEL Protein ZC204.12 OS=Caenorhabditis elegans GN=CELE_ZC204.12 PE=4 SV=1	-0.29
O17772|O17772_CAEEL Protein PES-7 OS=Caenorhabditis elegans GN=pes-7 PE=4 SV=2	-0.29
O44443|YC2BA_CAEEL EGF-like domain-containing protein C02B10.3 OS=Caenorhabditis elegans GN=C02B10.3 PE=1 SV=2	-0.30
Q9XUE6|PMM_CAEEL Probable phosphomannomutase OS=Caenorhabditis elegans GN=F52B11.2 PE=3 SV=2; Q9XUE6-2|PMM_CAEEL Isoform a of Probable phosphomannomutase OS=Caenorhabditis elegans GN=F52B11.2	-0.30
H2KZV7|H2KZV7_CAEEL Protein T04C9.1, isoform b OS=Caenorhabditis elegans GN=CELE_T04C9.1 PE=4 SV=1; H2KZV6|H2KZV6_CAEEL Protein T04C9.1, isoform a OS=Caenorhabditis elegans GN=CELE_T04C9.1 PE=4 SV=1	-0.31
Q9U2A8|RL37A_CAEEL 60S ribosomal protein L37a OS=Caenorhabditis elegans GN=rpl-43 PE=3 SV=3	-0.31
P91374|RL15_CAEEL 60S ribosomal protein L15 OS=Caenorhabditis elegans GN=rpl-15 PE=3 SV=1	-0.31
Q18946|Q18946_CAEEL Protein D1054.8 OS=Caenorhabditis elegans GN=CELE_D1054.8 PE=1 SV=1	-0.32
Q2L6U9|Q2L6U9_CAEEL Protein R07E3.1, isoform b OS=Caenorhabditis elegans GN=CELE_R07E3.1 PE=2 SV=1; Q21810|Q21810_CAEEL Protein R07E3.1, isoform a OS=Caenorhabditis elegans GN=CELE_R07E3.1 PE=2 SV=1	-0.32
Q21484|Q21484_CAEEL Protein HAT-1 OS=Caenorhabditis elegans GN=hat-1 PE=4 SV=2	-0.32
O45496|O45496_CAEEL Protein F39B2.3 OS=Caenorhabditis elegans GN=CELE_F39B2.3 PE=4 SV=1	-0.32
O01634|INX12_CAEEL Innexin-12 OS=Caenorhabditis elegans GN=inx-12 PE=1 SV=1	-0.33
O44175|O44175_CAEEL Protein RFC-2 OS=Caenorhabditis elegans GN=rfc-2 PE=4 SV=1	-0.33

Q0G821|Q0G821_CAEEL Protein UGT-23, isoform b OS=Caenorhabditis elegans GN=ugt-23 PE=2 SV=1; Q93242|Q93242_CAEEL Protein UGT-23, isoform a OS=Caenorhabditis elegans GN=ugt-23 PE=2 SV=1	-0.33
Q8MXH3|Q8MXH3_CAEEL Protein T09A12.5 OS=Caenorhabditis elegans GN=CELE_T09A12.5 PE=4 SV=1	-0.34
Q9GYQ7|Q9GYQ7_CAEEL Protein XPO-3 OS=Caenorhabditis elegans GN=xpo-3 PE=4 SV=3	-0.34
P18947|VIT4_CAEEL Vitellogenin-4 OS=Caenorhabditis elegans GN=vit-4 PE=1 SV=3	-0.34
Q21966|Q21966_CAEEL Protein ASP-4 OS=Caenorhabditis elegans GN=asp-4 PE=3 SV=1	-0.34
Q21353|EAA3_CAEEL Putative sodium-dependent excitatory amino acid transporter glt-3 OS=Caenorhabditis elegans GN=glt-3 PE=1 SV=1	-0.35
P41877|ISW1_CAEEL Chromatin-remodeling complex ATPase chain isw-1 OS=Caenorhabditis elegans GN=isw-1 PE=1 SV=2	-0.35
Q09582|METH_CAEEL Probable methionine synthase OS=Caenorhabditis elegans GN=nos-1 PE=1 SV=1	-0.35
P34556|CDK1_CAEEL Cyclin-dependent kinase 1 OS=Caenorhabditis elegans GN=cdk-1 PE=1 SV=1	-0.35
P34475|TBG_CAEEL Tubulin gamma chain OS=Caenorhabditis elegans GN=tbg-1 PE=2 SV=1	-0.36
H2L0D5|H2L0D5_CAEEL Protein LRON-7, isoform b OS=Caenorhabditis elegans GN=lron-7 PE=4 SV=1; Q21164|Q21164_CAEEL Protein LRON-7, isoform a OS=Caenorhabditis elegans GN=lron-7 PE=4 SV=2	-0.36
Q3LFN1|Q3LFN1_CAEEL Protein LBP-9, isoform b OS=Caenorhabditis elegans GN=lbp-9 PE=2 SV=1; Q965W1|FABP9_CAEEL Fatty acid-binding protein homolog 9 OS=Caenorhabditis elegans GN=lbp-9 PE=2 SV=1	-0.36
P91343|WDR12_CAEEL Ribosome biogenesis protein WDR12 homolog OS=Caenorhabditis elegans GN=tag-345 PE=3 SV=1	-0.36
G5EC97|G5EC97_CAEEL Protein CYP-29A2 OS=Caenorhabditis elegans GN=cyp-29a2 PE=3 SV=1	-0.36
Q9U1V9|Q9U1V9_CAEEL Protein DNJ-29, isoform b OS=Caenorhabditis elegans GN=dnj-29 PE=2 SV=1; Q9U1W0|Q9U1W0_CAEEL Protein DNJ-29, isoform a OS=Caenorhabditis elegans GN=dnj-29 PE=2 SV=1	-0.36

Q27GU1|Q27GU1_CAEEL Protein CSR-1, isoform b OS=Caenorhabditis elegans GN=csr-1 PE=4 SV=1; H2KZD5|H2KZD5_CAEEL Protein CSR-1, isoform a OS=Caenorhabditis elegans GN=csr-1 PE=4 SV=1	-0.36
Q9XW38|Q9XW38_CAEEL Protein Y69E1A.2 OS=Caenorhabditis elegans GN=CELE_Y69E1A.2 PE=4 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
O17731|O17731_CAEEL Protein D2023.4 OS=Caenorhabditis elegans GN=CELE_D2023.4 PE=4 SV=1	-0.37
Q21452|LIAS_CAEEL Lipoyl synthase, mitochondrial OS=Caenorhabditis elegans GN=M01F1.3 PE=3 SV=1	-0.37
Q95Q18|LACB2_CAEEL Beta-lactamase-like protein 2 homolog OS=Caenorhabditis elegans GN=Y53F4B.39 PE=3 SV=1; Q95Q18-2|LACB2_CAEEL Isoform b of Beta-lactamase-like protein 2 homolog OS=Caenorhabditis elegans GN=Y53F4B.39	-0.37
Q20546|Q20546_CAEEL Protein F47G9.1 OS=Caenorhabditis elegans GN=CELE_F47G9.1 PE=4 SV=1	-0.37
G5ECU4|G5ECU4_CAEEL Protein ZK829.1 OS=Caenorhabditis elegans GN=CELE_ZK829.1 PE=4 SV=1	-0.38
P91408|AGT2L_CAEEL Alanine--glyoxylate aminotransferase 2-like OS=Caenorhabditis elegans GN=T01B11.2 PE=2 SV=1; G8JY42|G8JY42_CAEEL Protein T01B11.2, isoform b OS=Caenorhabditis elegans GN=CELE_T01B11.2 PE=2 SV=1	-0.38
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
Q20375|SPTC2_CAEEL Serine palmitoyltransferase 2 OS=Caenorhabditis elegans GN=sptl-2 PE=2 SV=1; Q20375-2|SPTC2_CAEEL Isoform b of Serine palmitoyltransferase 2 OS=Caenorhabditis elegans GN=sptl-2	-0.38
Q9XXA7|NEUFC_CAEEL Neuferricin homolog OS=Caenorhabditis elegans GN=tag-131 PE=3 SV=1	-0.39
Q17848|I5P1_CAEEL Probable type I inositol 1,4,5-trisphosphate 5-phosphatase OS=Caenorhabditis elegans GN=ipp-5 PE=2 SV=2	-0.39

P53016|RFC4_CAEEL Replication factor C subunit 4 OS=Caenorhabditis elegans GN=rfc-4 PE=1 SV=1	-0.39
Q9TW67|NGLY1_CAEEL Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase OS=Caenorhabditis elegans GN=png-1 PE=1 SV=1	-0.39
O45181|O45181_CAEEL Protein K07H8.10 OS=Caenorhabditis elegans GN=CELE_K07H8.10 PE=4 SV=1	-0.39
P17331|G3P4_CAEEL Glyceraldehyde-3-phosphate dehydrogenase 4 OS=Caenorhabditis elegans GN=gpd-4 PE=3 SV=1; P04970|G3P1_CAEEL Glyceraldehyde-3-phosphate dehydrogenase 1 OS=Caenorhabditis elegans GN=gpd-1 PE=1 SV=1	-0.40
P34703|SPT6H_CAEEL Suppressor of Ty 6 homolog OS=Caenorhabditis elegans GN=emb-5 PE=1 SV=1	-0.40
Q9BIB7|Q9BIB7_CAEEL Protein HRPF-1, isoform a OS=Caenorhabditis elegans GN=hrpf-1 PE=4 SV=1; H2KZN0|H2KZN0_CAEEL Protein HRPF-1, isoform b OS=Caenorhabditis elegans GN=hrpf-1 PE=4 SV=1	-0.40
O17271|HEH1_CAEEL Putative protein heh-1 OS=Caenorhabditis elegans GN=heh-1 PE=3 SV=2	-0.41
Q17389|CUL1_CAEEL Cullin-1 OS=Caenorhabditis elegans GN=cul-1 PE=1 SV=1	-0.41
Q17432|Q17432_CAEEL Protein B0035.3 OS=Caenorhabditis elegans GN=B0035.3 PE=4 SV=1	-0.42
P24893|COX1_CAEEL Cytochrome c oxidase subunit 1 OS=Caenorhabditis elegans GN=cox-1 PE=2 SV=2; B1PEX9|B1PEX9_CAEEL Cytochrome c oxidase subunit 1 OS=Caenorhabditis elegans GN=COX1 PE=2 SV=1; B1PEW7|B1PEW7_CAEEL Cytochrome c oxidase subunit 1 OS=C	-0.42
P17140|CO4A2_CAEEL Collagen alpha-2(IV) chain OS=Caenorhabditis elegans GN=let-2 PE=1 SV=2; P17140-2|CO4A2_CAEEL Isoform II of Collagen alpha-2(IV) chain OS=Caenorhabditis elegans GN=let-2	-0.43
H9G337|H9G337_CAEEL Protein C27A7.6, isoform d OS=Caenorhabditis elegans GN=C27A7.6 PE=4 SV=1; G5ED11|G5ED11_CAEEL Protein C27A7.6, isoform a OS=Caenorhabditis elegans GN=C27A7.6 PE=4 SV=1; H9G2Z4|H9G2Z4_CAEEL Protein C27A7.6, isoform c OS=Caenor	-0.43
Q93315|Q93315_CAEEL Protein CYTB-5.1 OS=Caenorhabditis elegans GN=cytb-5.1 PE=3 SV=2	-0.43

Q2XN11|Q2XN11_CAEEL Protein CKA-2, isoform b OS=Caenorhabditis elegans GN=cka-2 PE=2 SV=1; Q22942|Q22942_CAEEL Protein CKA-2, isoform a OS=Caenorhabditis elegans GN=cka-2 PE=1 SV=2	-0.43
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
G5EGE0|G5EGE0_CAEEL Protein TAT-5, isoform b OS=Caenorhabditis elegans GN=tat-5 PE=2 SV=1; G5EE81|G5EE81_CAEEL Protein TAT-5, isoform c OS=Caenorhabditis elegans GN=tat-5 PE=2 SV=1; G5EBH1|G5EBH1_CAEEL Protein TAT-5, isoform a OS=Caenorhabditis e	-0.44
Q21916|Q21916_CAEEL Protein R10H10.3 OS=Caenorhabditis elegans GN=CELE_R10H10.3 PE=2 SV=1	-0.44
O61710|O61710_CAEEL Protein R119.2 OS=Caenorhabditis elegans GN=CELE_R119.2 PE=3 SV=3	-0.44
D7SFI3|D7SFI3_CAEEL Protein C02D5.4 OS=Caenorhabditis elegans GN=C02D5.4 PE=3 SV=1	-0.44
Q19294|Q19294_CAEEL Protein MAT-3 OS=Caenorhabditis elegans GN=mat-3 PE=4 SV=2	-0.45
Q965E3|Q965E3_CAEEL Condensin complex subunit 1 OS=Caenorhabditis elegans GN=dpy-28 PE=2 SV=1; Q9U2M1|Q9U2M1_CAEEL Condensin complex subunit 1 OS=Caenorhabditis elegans GN=dpy-28 PE=3 SV=2	-0.46
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
G5EF83|G5EF83_CAEEL Protein K01G5.9 OS=Caenorhabditis elegans GN=CELE_K01G5.9 PE=4 SV=1	-0.46
O45394|O45394_CAEEL Protein F22B8.7 OS=Caenorhabditis elegans GN=CELE_F22B8.7 PE=4 SV=2	-0.47
G5EEG7|G5EEG7_CAEEL Protein SMU-1 OS=Caenorhabditis elegans GN=smu-1 PE=2 SV=1	-0.47
Q95Y79|Q95Y79_CAEEL Protein ZIG-9 OS=Caenorhabditis elegans GN=zig-9 PE=4 SV=3	-0.48
H2KYN3|H2KYN3_CAEEL Protein ACDH-13, isoform a OS=Caenorhabditis elegans GN=acdh-13 PE=4 SV=1	-0.49

Q18258|Q18258_CAEEL Protein VPS-22 OS=Caenorhabditis elegans GN=vps-22 PE=4 SV=2	-0.49
Q19329|TSR1_CAEEL Pre-rRNA-processing protein TSR1 homolog OS=Caenorhabditis elegans GN=tag-151 PE=3 SV=1	-0.51
Q8IA86|Q8IA86_CAEEL Protein CATP-3, isoform b OS=Caenorhabditis elegans GN=catp-3 PE=2 SV=1; O16331|O16331_CAEEL Protein CATP-3, isoform a OS=Caenorhabditis elegans GN=catp-3 PE=2 SV=2	-0.51
Q18926|Q18926_CAEEL Protein D1022.4 OS=Caenorhabditis elegans GN=CELE_D1022.4 PE=4 SV=1	-0.51
Q09622|PUF12_CAEEL Pumilio domain-containing protein 12 OS=Caenorhabditis elegans GN=puf-12 PE=4 SV=1	-0.52
D3YT56|D3YT56_CAEEL Protein MARS-1, isoform c OS=Caenorhabditis elegans GN=mars-1 PE=2 SV=1	-0.52
Q9XWW2|Q9XWW2_CAEEL Protein MRG-1, isoform a OS=Caenorhabditis elegans GN=mrg-1 PE=2 SV=1; A7DTF0|A7DTF0_CAEEL Protein MRG-1, isoform b OS=Caenorhabditis elegans GN=mrg-1 PE=2 SV=1	-0.53
P41992-2|GGTB2_CAEEL Isoform b of Probable geranylgeranyl transferase type-2 subunit beta OS=Caenorhabditis elegans GN=ggtb-1; P41992|GGTB2_CAEEL Probable geranylgeranyl transferase type-2 subunit beta OS=Caenorhabditis elegans GN=ggtb-1 PE=3 SV=2	-0.54
O44665|NLP28_CAEEL Neuropeptide-like protein 28 OS=Caenorhabditis elegans GN=nlp-28 PE=3 SV=1; O44664|NLP29_CAEEL Neuropeptide-like protein 29 OS=Caenorhabditis elegans GN=nlp-29 PE=2 SV=1; O44662|NLP31_CAEEL Neuropeptide-like protein 31 OS=Caeno	-0.55
Q11174|CHIT_CAEEL Probable endochitinase OS=Caenorhabditis elegans GN=cht-1 PE=1 SV=1	-0.56
G5EFD7|G5EFD7_CAEEL Protein F46C5.9 OS=Caenorhabditis elegans GN=CELE_F46C5.9 PE=4 SV=1	-0.57
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
G5EET2|G5EET2_CAEEL Deoxyuridinetriphosphatase OS=Caenorhabditis elegans GN=dut-1 PE=2 SV=1	-0.59

Q23083|Q23083_CAEEL Protein ZC8.6 OS=Caenorhabditis elegans GN=CELE_ZC8.6 PE=4 SV=4	-0.61
Q965Q8|XYLT_CAEEL Xylosyltransferase sqv-6 OS=Caenorhabditis elegans GN=sqv-6 PE=1 SV=3	-0.62
I2HA91|I2HA91_CAEEL Protein F28C6.8, isoform b OS=Caenorhabditis elegans GN=CELE_F28C6.8 PE=4 SV=1; Q93622|Q93622_CAEEL Protein F28C6.8, isoform a OS=Caenorhabditis elegans GN=CELE_F28C6.8 PE=4 SV=1	-0.63
Q10010|YSV4_CAEEL Uncharacterized protein T19C3.4 OS=Caenorhabditis elegans GN=T19C3.4 PE=3 SV=1	-0.64
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
Q95XQ8|Q95XQ8_CAEEL Protein MCM-4 OS=Caenorhabditis elegans GN=mcm-4 PE=3 SV=1	-0.66
Q9XUF9|Q9XUF9_CAEEL Protein C49C3.4 OS=Caenorhabditis elegans GN=C49C3.4 PE=4 SV=1	-0.66
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
Q22869|Q22869_CAEEL Non-muscle myosin heavy chain II OS=Caenorhabditis elegans GN=nmy-2 PE=2 SV=1; G5EBY3|G5EBY3_CAEEL Protein NMY-2 OS=Caenorhabditis elegans GN=nmy-2 PE=2 SV=1	-0.66
O18215|O18215_CAEEL Protein Y53C12B.1 OS=Caenorhabditis elegans GN=CELE_Y53C12B.1 PE=4 SV=1	-0.67
Q9N303|Q9N303_CAEEL Protein DEPS-1 OS=Caenorhabditis elegans GN=deps-1 PE=4 SV=1	-0.72
P90786|P90786_CAEEL Protein PRG-1 OS=Caenorhabditis elegans GN=prg-1 PE=4 SV=1	-0.73
Q9U2Z5|Q9U2Z5_CAEEL Protein Y106G6H.14 OS=Caenorhabditis elegans GN=CELE_Y106G6H.14 PE=4 SV=1	-0.75

O17944|O17944_CAEEL Protein K10C3.5, isoform a OS=Caenorhabditis elegans GN=CELE_K10C3.5 PE=2 SV=2; Q564S2|Q564S2_CAEEL Protein K10C3.5, isoform b OS=Caenorhabditis elegans GN=CELE_K10C3.5 PE=2 SV=1	-0.75
G5ECL1|G5ECL1_CAEEL Protein M05D6.2 OS=Caenorhabditis elegans GN=CELE_M05D6.2 PE=4 SV=1	-0.75
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
Q9NEQ0|Q9NEQ0_CAEEL Protein FAT-1 OS=Caenorhabditis elegans GN=fat-1 PE=2 SV=1; Q21056|Q21056_CAEEL Fatty acid desaturase OS=Caenorhabditis elegans GN=fat PE=2 SV=1	-0.76
P46557|MNP1_CAEEL Matrix non-peptidase homolog 1 OS=Caenorhabditis elegans GN=mnp-1 PE=1 SV=1	-0.77
Q20713|Q20713_CAEEL Protein F53B3.5 OS=Caenorhabditis elegans GN=CELE_F53B3.5 PE=4 SV=3	-0.78
I2HA81|I2HA81_CAEEL Protein F15B9.10, isoform b OS=Caenorhabditis elegans GN=CELE_F15B9.10 PE=4 SV=1; A5Z2T9|A5Z2T9_CAEEL Protein F15B9.10, isoform a OS=Caenorhabditis elegans GN=CELE_F15B9.10 PE=4 SV=1	-0.79
Q9XW42|ANM7_CAEEL Protein arginine N-methyltransferase 7 OS=Caenorhabditis elegans GN=prmt-7 PE=3 SV=2	-0.79
O16303|O16303_CAEEL Protein DNJ-19 OS=Caenorhabditis elegans GN=dnj-19 PE=3 SV=1	-0.82
Q9XUR4|Q9XUR4_CAEEL Protein T05F1.2 OS=Caenorhabditis elegans GN=CELE_T05F1.2 PE=4 SV=1	-0.82
P41996|CPG2_CAEEL Chondroitin proteoglycan-2 OS=Caenorhabditis elegans GN=cpg-2 PE=1 SV=3	-0.82
O44729|O44729_CAEEL Protein PRP-17 OS=Caenorhabditis elegans GN=prp-17 PE=4 SV=2	-0.82
C6KRJ0|C6KRJ0_CAEEL Protein HUM-4, isoform c OS=Caenorhabditis elegans GN=hum-4 PE=2 SV=2; B6VQ62|B6VQ62_CAEEL Protein HUM-4, isoform b OS=Caenorhabditis elegans GN=hum-4 PE=2 SV=2; D3YT14|D3YT14_CAEEL Protein HUM-4, isoform e OS=Caenorhabditis e	-0.83

Q9U376|Q9U376_CAEEL Protein T07C4.3, isoform b OS=Caenorhabditis elegans GN=CELE_T07C4.3 PE=2 SV=1; Q22290|Q22290_CAEEL Protein T07C4.3, isoform a OS=Caenorhabditis elegans GN=CELE_T07C4.3 PE=1 SV=1	-0.83
Q9N2M4|Q9N2M4_CAEEL Rh-like protein-2 OS=Caenorhabditis elegans PE=2 SV=1; Q22947|Q22947_CAEEL Protein RHR-1 OS=Caenorhabditis elegans GN=rhr-1 PE=2 SV=1	-0.84
P91013|P91013_CAEEL Protein DHS-1 OS=Caenorhabditis elegans GN=dhs-1 PE=4 SV=1	-0.85
Q9U2G5|Q9U2G5_CAEEL Protein MRP-7 OS=Caenorhabditis elegans GN=mrp-7 PE=3 SV=3	-0.90
Q6EZG8|Q6EZG8_CAEEL Protein ZK6.11, isoform b OS=Caenorhabditis elegans GN=CELE_ZK6.11 PE=4 SV=1; H2L0Q1|H2L0Q1_CAEEL Protein ZK6.11, isoform a OS=Caenorhabditis elegans GN=CELE_ZK6.11 PE=4 SV=1	-0.92
O44566|O44566_CAEEL Protein W03F8.4 OS=Caenorhabditis elegans GN=CELE_W03F8.4 PE=3 SV=1	-0.92
Q9TYS3|Q9TYS3_CAEEL Ferritin OS=Caenorhabditis elegans GN=ftn-2 PE=1 SV=1	-0.92
Q09297|NDX6_CAEEL Putative nudix hydrolase 6 OS=Caenorhabditis elegans GN=ndx-6 PE=3 SV=2	-0.96
Q960A6|Q960A6_CAEEL Protein CLEC-219 OS=Caenorhabditis elegans GN=clec-219 PE=4 SV=1	-1.02
Q20390|PPT1_CAEEL Palmitoyl-protein thioesterase 1 OS=Caenorhabditis elegans GN=ppt-1 PE=2 SV=2	-1.06
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
Q18943|Q18943_CAEEL Protein D1054.10 OS=Caenorhabditis elegans GN=CELE_D1054.10 PE=4 SV=1	-1.17
Q8MXQ7|CDKAL_CAEEL Threonylcarbamoyladenosine tRNA methylthiotransferase OS=Caenorhabditis elegans GN=Y92H12BL.1 PE=3 SV=2	-1.19

Q21323|Q21323_CAEEL Protein RNP-3 OS=Caenorhabditis elegans GN=rnp-3 PE=1 SV=1	-1.31
Q22694|Q22694_CAEEL Protein T23F11.2 OS=Caenorhabditis elegans GN=CELE_T23F11.2 PE=4 SV=1; O62342|O62342_CAEEL Protein R07E5.15 OS=Caenorhabditis elegans GN=CELE_R07E5.15 PE=4 SV=1; Q7YTH0|Q7YTH0_CAEEL Protein F17C8.7 OS=Caenorhabditis elegans GN	-1.34
H2L0C4|H2L0C4_CAEEL Protein ABTS-4, isoform d OS=Caenorhabditis elegans GN=abts-4 PE=4 SV=1; Q45EK3|Q45EK3_CAEEL Protein ABTS-4, isoform b OS=Caenorhabditis elegans GN=abts-4 PE=2 SV=1; Q58G79|Q58G79_CAEEL Anion transporter ABTS-4b OS=Caenorhabdi	-1.36
Q17938|DAF36_CAEEL Cholesterol desaturase daf-36 OS=Caenorhabditis elegans GN=daf-36 PE=1 SV=2	-1.37
P54688|BCAT_CAEEL Branched-chain-amino-acid aminotransferase, cytosolic OS=Caenorhabditis elegans GN=bcat-1 PE=2 SV=2	-1.47
Q17802|CPG1_CAEEL Chondroitin proteoglycan 1 OS=Caenorhabditis elegans GN=cpg-1 PE=1 SV=1; Q17802-2|CPG1_CAEEL Isoform b of Chondroitin proteoglycan 1 OS=Caenorhabditis elegans GN=cpg-1	-1.60
Q86FP2|Q86FP2_CAEEL Protein CATP-7, isoform b OS=Caenorhabditis elegans GN=catp-7 PE=2 SV=1; Q9N323|Q9N323_CAEEL Protein CATP-7, isoform a OS=Caenorhabditis elegans GN=catp-7 PE=2 SV=3; Q3V5J8|Q3V5J8_CAEEL Protein CATP-7, isoform d OS=Caenorhabdi	-2.09
Q09591|MIX1_CAEEL Mitotic chromosome and X-chromosome-associated protein mix-1 OS=Caenorhabditis elegans GN=mix-1 PE=1 SV=2	-2.11
Q18677|DHP2_CAEEL Dihydropyrimidinase 2 OS=Caenorhabditis elegans GN=dhp-2 PE=1 SV=1	-2.29
G5EGH6|G5EGH6_CAEEL Protein FAT-7 OS=Caenorhabditis elegans GN=fat-7 PE=2 SV=1	-2.36
Q9NEU2|SDA1_CAEEL Protein SDA1 homolog OS=Caenorhabditis elegans GN=pro-3 PE=1 SV=4	-2.38
O45819|O45819_CAEEL Protein GYG-2 OS=Caenorhabditis elegans GN=gyg-2 PE=4 SV=1	-2.62