

Table S2. Non EF-hand with calcium/metal binding motif proteins in *Caenorhabditis*

UniProtID/gi	Predicted Name	Organism	Length	Other domain	PE	Molecular Function	Source	Biological function	Source
A8Y1Z6	CBR-DYB-1	<i>C. briggsae</i>	622	zf_zz	P	CaB, ZnB	IEA		
A8XM20	Uncharacterized	<i>C. briggsae</i>	1276	ww, zz_zf, zz_c2h2	P	ZnB	IEA		
Q9Y048	Dystrobrevin-1	<i>C. elegans</i>	590	zf_zz, zz_zf	T	cytoplasm	IEA	synaptic specificity	IMP
						glycoprotein	IDA	locomotion, muscle homeostasis, synaptic transmission, sarcomere organization	IMP, IGI
Q9TW65	Dystrophin-1	<i>C. elegans</i>	3674	calponin homology	T	transporter	IMP	locomotory behaviour, synaptic transmission	IMP
						actin binding, ZnB	IEA	homeostasis	IMP
								sarcomere organization	IGI
A8XMK5	CBR-PLL-1	<i>C. briggsae</i>	1083	X, Y, C2	P	CaB, PLC, signal transducer	IEA	ST, metabolic	IEA
A8XRA5	CBR-PLC-1	<i>C. briggsae</i>	1917	R, X, Y, C2, RA	P	CaB, PLC, signal transducer, exchange factor	IEA	metabolic, ST	IEA
A8XTZ1	CBR-PLC-3	<i>C. briggsae</i>	1308	X, SH2, SH3, PH, Y, C2	P	PLC, signal transducer	IEA	ST, phospholipid catabolic	IEA
A8X232	CBR-EGL-8	<i>C. briggsae</i>	1528	X, Y, C2	P	PLC, CaB, signal transducer	IEA	ST, lipid catabolic	IEA

Q9U6B9	PLC beta	<i>C. elegans</i>	1418	X, Y, C2	T	PLC, CaB, signal transducer	IEA	ST, lipid catabolic	IEA
Q8IA75	PLC	<i>C. elegans</i>	1075	X, Y, C2	T	PLC, CaB, signal transducer	IEA	ST, lipid catabolic	IEA
								pronuclear migration	IMP
Q95X30	Egg laying defective protein- 8	<i>C. elegans</i>	1491	X, Y, C2	T	CaB, PLC, signal transducer	IEA	ST, lipid metabolic	IEA
Q22070	T01E8.3	<i>C. elegans</i>	1350	X, Y, C2 , PH, SH3, SH2	T	PLC	IEA	ST, phospholipid catabolic	IEA
						signal transducer	IEA	endocytosis, reproduction	IMP
Q95X29	Egg laying defective protein- 8	<i>C. elegans</i>	1431	X, Y, C2	T	PLC, CaB	IEA	signaling pathway, embryo development, insemination, growth & locomotion regulation, oviposition regulation, oviposition regulation, spicule insertion	IMP
						signal transducer	IEA	ST, lipid metabolic	IEA
Q9TVI2	PLC210	<i>C. elegans</i>	1898	X, Y, C2 , RA, R	T	signal transducer	IEA	lipid metabolic, ST	IEA
						CaB, PLC, exchange factor	IEA	reproduction	IMP
Q7JM51	F31B12.1b	<i>C. elegans</i>	1868	X, Y, C2 , RA, R	T	signal transducer, CaB, PLC, exchange factor	IEA	lipid metabolic, ST	IEA

Q9XWB7	Y75B12B.6	<i>C. elegans</i>	896	X, Y	T	CaB, PLC	IEA	lipid metabolic, ST	IEA
B3GWB0	F31B12.1f	<i>C. elegans</i>	1886	X, Y, C2 , RA, R	P	signal transducer, CaB, PLC, exchange factor	IEA	lipid metabolic, ST	IEA
B2D6L1	F31B12.1d	<i>C. elegans</i>	1875	X, Y, C2 , RA, R	P	signal transducer, CaB, PLC, exchange factor	IEA	lipid metabolic, ST	IEA
Q8IA76	PLC like protein 1	<i>C. elegans</i>	1068	X, Y, C2	T	signal transducer, CaB, PLC	IEA	ST, lipid metabolic	IEA
B2G4Y4	Phosphoinositide PLC-epsilon	<i>C. elegans</i>	1878	X, Y, C2 , RA, R	T	signal transducer, CaB, PLC, exchange factor	IEA	lipid metabolic, ST	IEA
Q6EZG7	Egg laying defective protein- 8	<i>C. elegans</i>	592	X	T	CaB, PLC	IEA	ST, lipid metabolic	IEA
A8Y2J4	CBR-OST-1	<i>C. briggsae</i>	264	KAZAL, Ost	P	CaB	IEA	ST	IEA
A8XBD1	Uncharacterized	<i>C. briggsae</i>	275	Thr	P	CaB	IEA	ST	IEA
Q86GV1	Uncharacterized	<i>C. elegans</i>	234	Thr	T	CaB	IEA	ST	IEA
O44466	Uncharacterized	<i>C. elegans</i>	226	Thr	T	CaB	IEA	ST	IEA
P34714	SPARC	<i>C. elegans</i>	264	KAZAL, Ost	T	CaB	IEA	ST	IEA
								reproduction, growth regulation, embryo & larval development	IMP
Q4TTR2	Osteonectin	<i>C. remanei</i> (<i>C.</i>	106		T	CaB	IEA		

		<i>vulgaris)</i>							
002159	HP T09B4.4	<i>C. elegans</i>	142		T	CaB	IEA		

SH2- Src homology 2; IMP- Inferred from Mutant Phenotype; SH3- Src homology 3; IGI-Inferred from genetic interaction; PH- Pleckstrin homology; IEA- Inferred from Electronic Annotation; RA- Ras-associating; zf_zz- Zinc finger, ZZ type; zz_c2h2- Zinc finger, C2H2 type; X- Phosphatidylinositol- specific phospholipase X; Y- Phosphatidylinositol-specific phospholipase Y; R-Ras guanine-nucleotide exchange factors catalytic; Thr- Thyroglobulin; CaB- Calcium Binding; PLC- Phospholipase C; ZnB- zinc Binding; ST- Signal transduction; P- Predicted; T- Transcript; IDA -Inferred from Direct Assay; KAZAL- Kazal domain profile; Ost- Osteonectin domain; UniProtID/gi- UniProtID number/gi number. All the functions of a protein deduced through one common technique have been put in a one row of the respective protein. If the technique differed for the particular function of the protein then it is kept in the next row of the respective protein.