1	Title: The conserved, secreted protease inhibitor MLT-11 is necessary for C.
2	elegans molting and embryogenesis
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14	inhibitor
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#### 21 ABSTRACT

22 Apical extracellular matrices (aECMs) are associated with all epithelia and form a 23 protective layer against biotic and abiotic threats in the environment. C. elegans molting 24 offers a powerful entry point to understanding developmentally programmed aECM 25 remodeling. Several protease inhibitors are implicated in molting, but their functions 26 remain poorly understood. Here we characterize *mlt-11*, an unusual protease inhibitor 27 with 10 conserved Kunitz domains. MLT-11 oscillates and is localized in the cuticle and 28 in lysosomes in larvae and in the embryonic sheath starting at the 3-fold embryo stage. 29 *mlt-11* (RNAi) produced a developmental delay, motility defects, failed apolysis, and a defective cuticle barrier. mlt-11 null and C-terminal Kunitz domain deletion mutants are 30 embryonic lethal while N-terminal deletions cause a rolling phenotype indicative of cuticle 31 32 structure abnormalities. *mlt-11* activity is primarily necessary in seam and hypodermal 33 cells and accordingly mlt-11 (RNAi) causes defects in localization of the collagens ROL-34 6 and BLI-1 over the cuticle. *mlt-11* (RNAi) molting phenotypes can be suppressed by 35 genetically inhibiting endocytosis. Our model is that MLT-11 is acting in the aECM to coordinate remodeling and timely ecdysis. 36

#### 37 INTRODUCTION

Specialized extracellular matrices cover the apical surface of all epithelial cells and form the skin in almost all animals (Li Zheng et al., 2020). These apical extracellular matrices (aECMs) also line the lumen of internal tubular epithelia to form a protective layer against biotic and abiotic threats (Li Zheng et al., 2020). Despite their importance, understanding the structure and dynamics of aECM components in development and disease remains challenging.

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45 *C. elegans* is emerging as a powerful model to study aECM structure and remodeling. 46 They have a collagen-based ECM so understanding its assembly may provide insight into 47 mammalian skin (Page and Johnstone, 2007). The components of the cuticle are 48 secreted by hypodermal and seam cells and are assembled in distinct layers (Page and 49 Johnstone, 2007). During each larval stage animals must build a new aECM underneath 50 the old one, separate the old aECM (apolysis) and then shed it (ecdysis) (Lažetić and

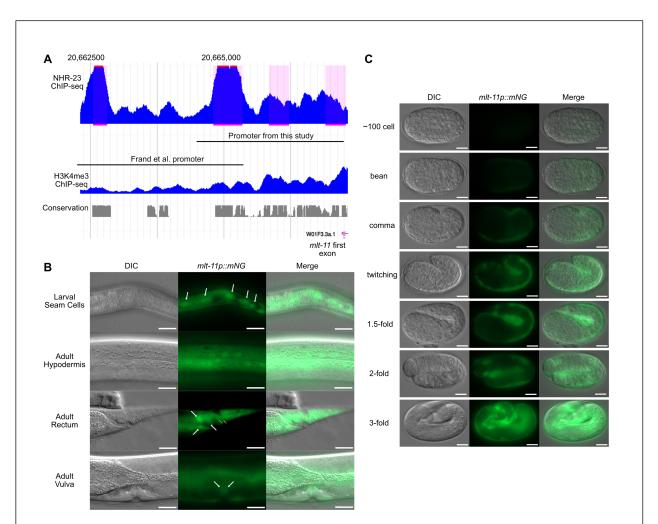
Fay, 2017b). A specialized, transient structure known as the pre-cuticle is thought to pattern the new cuticle and is then shed during ecdysis (Cohen and Sundaram, 2020). The sheath is a similar structure in embryos which ensures embryonic integrity and directs force during elongation (Vuong-Brender et al., 2017). The vulval aECM has recently been shown to be highly dynamic, and specialized aECMs also line the rectum and excretory system (Cohen et al., 2019; Cohen et al., 2020; Gill et al., 2016).

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58 A major guestion is how is the aECM remodeled during molting? Proteases are required 59 for ecdysis in both C. elegans and in parasitic nematodes, presumably by promoting 60 apolysis, though some are thought to function in collagen processing (Davis et al., 2004; 61 Hashmi et al., 2004; Kim et al., 2011; Stepek et al., 2011). Protease inhibitors have been 62 implicated in molting through RNAi screening, and have been suggested to suppress 63 ecdysis (Frand et al., 2005; Lažetić and Fay, 2017b). BLI-5 has homology to the Kunitz 64 domain family of protease inhibitors and mutations cause molting defects. However, recombinant BLI-5 enhanced the activity of two serine proteases from distinct classes 65 66 (Page et al., 2006; Stepek et al., 2010). MLT-11 is another putative protease inhibitor in 67 the Kunitz family and *mlt-11 (RNAi)* causes molting defects (Frand et al., 2005). *mlt-11* 68 mRNA oscillates, peaking mid molt and its expression is regulated by NHR-23, a nuclear 69 hormone receptor transcription factor necessary for molting (Frand et al., 2005). However, 70 *mlt-11* remains poorly characterized.

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72 Here we demonstrate that MLT-11 is localized to the cuticle, lysosomes, the rectal 73 epithelium, excretory duct lumen, and vulval lumen. It is also secreted into the 74 extracellular space in embryos before localizing to the cuticle prior to hatching. *mlt-11* null 75 alleles cause embryonic lethality, characterized by disorganization of adherens junctions. RNAi in larvae causes developmental delay, apolysis, and ecdysis defects. *mlt-11* activity 76 77 in seam cells is necessary for molting and a normal developmental rate. mlt-11 78 inactivation causes a defective cuticle barrier and aberrant localization of the collagens 79 ROL-6 and BLI-1. Genetic data suggests that MLT-11 acts in the aECM. This work 80 provides the first insight into how MLT-11 functions to promote embryogenesis and aECM 81 integrity during molting.



**Fig. 1.** *mlt-11* is expressed in larval and embryonic epidermal cells. (A) Genome browser track of *mlt-11* promoter depicting NHR-23 and H3K4me3 ChIP-seq peaks and conservation calculated across 26 nematode species. The promoter used in Fig. 1B and 1C and Frand et al. (2005) are indicated. Genomic sequence on chromosome V is indicated above. *mlt-11p::mNeonGreen (mNG)*, DIC, and overlay images of the indicated larval and adult (B) and embryonic (C) stages. In B, white arrows indicate seam cells (top), rectal epithelial cells (middle) and vulval cells (bottom) and yellow arrows indicate hypodermal cells near rectum. Images are representative of 40 animals examined over two biological replicates. Scale bars in B are 20  $\mu$ m and in C are 10  $\mu$ m.

## 82 **RESULTS**

## 83 *mlt-11* is expressed in embryonic, larval, and adult epidermal cells

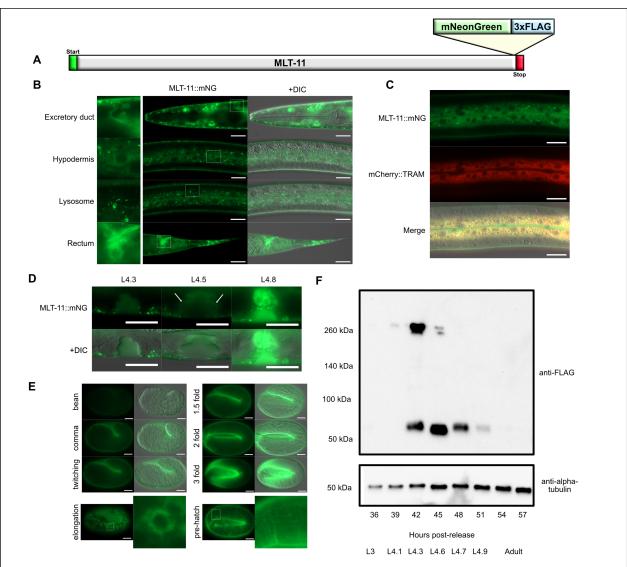
- *mlt-11* has been reported to be an NHR-23 target gene (Frand et al., 2005). There are
- four NHR-23 ChIP-seq peaks in the *mlt-11* promoter (Johnson et al., 2022), and the
- sequences under these peaks are highly conserved in other nematodes (Fig. 1A; see
- 87 Conservation track). There are additional areas of the promoter which display elevated

conserved sequence, which may indicate other regulatory elements (Fig. 1A). We used
2.8 kilobases of upstream sequence to create a single copy *mlt-11p::NLS::mNeonGreen*promoter reporter. We note that this sequence differs in part from the promoter used by
Frand et al., 2005 (Fig 1A). Expression in embryos was first detected at the bean stage
in posterior epithelial cells and persisted through the 3-fold stage spreading more
anteriorly (Fig. 1C). Expression was detected in hypodermal, rectal and vulval cells in
both larvae and adults as well as seam cells in larvae (Fig. 1B).

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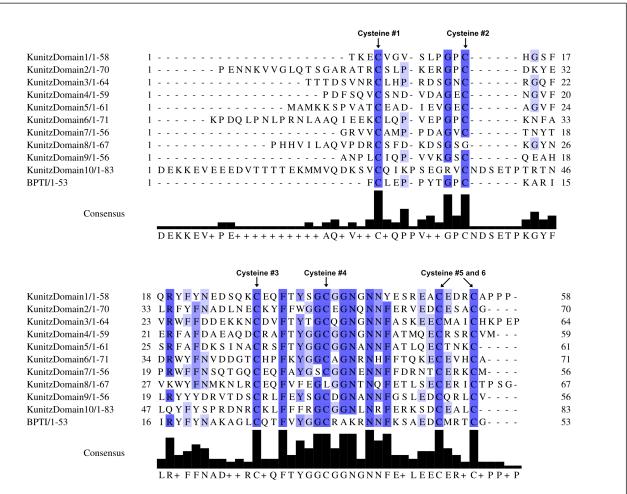
#### 96 MLT-11 is an oscillating secreted protein that localizes to the aECM and lysosomes

97 To determine where MLT-11 localized, we knocked an *mNeonGreen::3xFLAG* cassette 98 into the 3' end of the gene producing a C-terminal translational fusion that labels all 99 described *mlt-11* isoforms (Fig. 2A). MLT-11::mNeonGreen::3xFLAG (MLT-11::mNG) 100 was detected in the excretory duct, hypodermal cells, seam cells and the rectum (Fig. 101 2B). In the hypodermis MLT-11::mNG was non-nuclear and either diffuse through the 102 cytoplasm or in bright punctae, lysosomal based on morphology (Miao et al., 2020). The 103 cytoplasmic expression was reminiscent of secreted proteins. We confirmed that this 104 pattern reflected localization to the endoplasmic reticulum through co-localization with an 105 mCherry::TRAM marker (Fig. 2C)(Chen et al., 2012). MLT-11::mNG localization in the 106 vulva was dynamic. In early L4 (stage 4.3 by vulva morphology) MLT-11::mNG was 107 lumenal and by mid-L4 (stage 4.5) we saw expression within the vulD cell (Fig. 2D). In late L4 (stage 4.8) MLT-11::mNG was robustly expressed in vulD and in the vulval lumen 108 109 (Fig. 2D). In embryos, MLT-11::mNG was first observed at the bean stage (Fig. 2E). From 110 this stage to the 3-fold stage MLT-11::mNG appeared to be secreted, localizing in the 111 space between the embryo and the eggshell with enrichment at the embryo epidermis 112 (Fig. 2E). During elongation, MLT-11::mNG perinuclear expression was observed, 113 reminiscent of the collagen DPY-7 localization to embryonic endoplasmic reticulum 114 (McMahon et al., 2003). Before hatching there was a striking shift in MLT-11::mNG 115 localization where it labeled annuli in the aECM (Fig. 2E). Immunoblotting revealed that 116 MLT-11 oscillates, and three isoforms were detected (Fig. 2F). Two isoforms are large 117 (260 kDa) and align with the predicted size of full-length MLT-11 isoforms with an mNG 118 tag (268.5-371.4 kDa); these isoforms peak in early L4 and rapidly disappear (Fig. 2H).



**Fig. 2. MLT-11 localization.** (A) Schematic of *mlt-11::mNG::3xFLAG* knock-in. (B) MLT-11::mNG localization in the indicated tissues along with DIC overlay. Boxes on the left are magnified cellular or subcellular structures within the larger images to the right. (C) MLT-11::mNG overlay with mCherry::TRAM. (D) MLT-11::mNG vulval localization in the indicated L4 stages. (E) MLT-11::mNG localization in the indicated embryonic stages. Images are representative of 40 animals examined over two biological replicates. Scale bars in B and C are 20  $\mu$ m and in E are 10  $\mu$ m. (H) Immunoblotting with the indicated antibodies of *mlt-11::mNG::3xFLAG* lysates harvested at the indicated time points post-release. A developmental stage for each time point as determined by vulva morphology is provided (Mok et al., 2015).

- 119 A ~50-70 kDa band smaller than any predicted isoform appears in early L4 and persists
- 120 until late L4 (Fig. 2H). Together, these data indicate that MLT-11 is an oscillating secreted
- 121 protein with dynamic localization to aECM in embryos and larvae.
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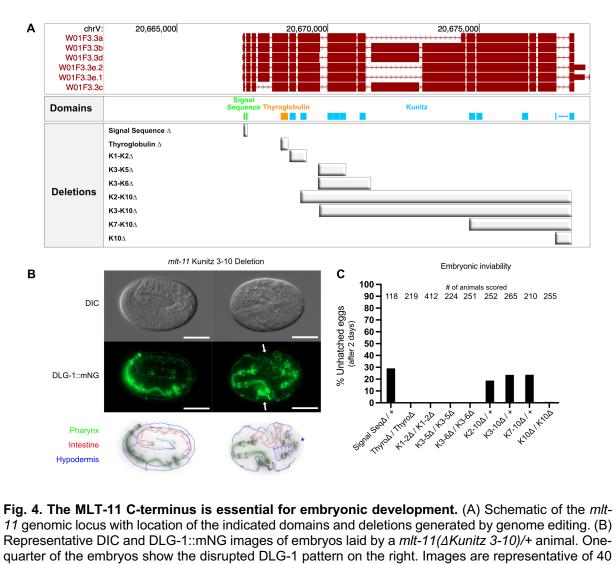
**Fig. 3. MLT-11 Kunitz domain alignment.** Alignment of the ten MLT-11 Kunitz domains to Bovine Pancreatic Trypsin Inhibitor (BPTI). Positions of the six cysteine residues critical for the structure of each Kunitz domain are indicated above.

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## 125 *mlt-11* is an essential gene required for embryogenesis and molting

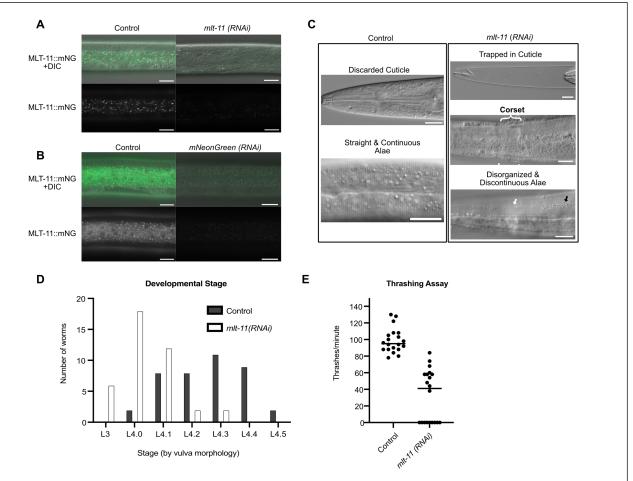
126 MLT-11 is predicted to be a large protein (234-341 kDA) with a signal sequence, a 127 thyroglobulin domain, and 10 Kunitz protease inhibitor domains (Fig. 3, 4A). A key feature 128 of Kunitz domains is the presence of 6 conserved cysteine residues which form three 129 disulfide bonds critical for stabilizing the domain (Ranasinghe and McManus, 2013; Fig. 130 3). While Kunitz domain 8 may not be active as it is missing cysteines in the second and fourth position, the remaining Kunitz domains appear functional as they contain key 131 132 conserved residues (Fig. 3). To gain insight into MLT-11 structure and function, we 133 generated a deletion series to determine which domains were necessary for *mlt-11* 134 function. Homozygous deletion of the signal sequence, Kunitz domains 2-10, 3-10, or 7-

10 caused embryonic lethality. We balanced the mutations genetically by crossing to a strain with a *myo-2p::GFP::unc-54 3'UTR* cassette inserted into F46B3.7, a gene roughly 40kb away. We never observed progeny from balanced mutant worms lacking GFP. There was no evidence of haploinsufficiency as we could maintain balanced deletion strains. Additionally, these balanced worms produced roughly 25% dead embryos, a rate expected for a homozygous lethal mutation (Fig. 4C). In contrast, Kunitz domain 10 appeared dispensable for development as deletion animals were viable (Fig. 4C).



Representative DIC and DLG-1::mNG images of embryos laid by a *mit-11*( $\Delta Kunitz$  3-10)/+ animal. Onequarter of the embryos show the disrupted DLG-1 pattern on the right. Images are representative of 40 animals examined over two biological replicates. White arrows show invaginations of the outer membrane in homozygous mutant embryos. Blue star indicates the suspected aggregation of epithelial cells in homozygous mutant embryos. Scale bars are 20 µm. (C) Embryonic viability of the indicated *mlt-11* deletion mutants.

Deletion of Kunitz domains 1-2, 3-5 and 3-6 were completely viable, producing no dead 142 143 eggs as homozygotes, but instead had coordination defects rolling to the right during 144 forward movement. Given MLT-11::mNG expression in embryos (Fig. 2), we next 145 examined the nature of the embryonic lethality in *mlt-11* deletion mutants using a DLG-146 1::mNG allele to mark adherens junctions (Heppert et al., 2018). In control embryos, DLG-147 1::mNG labeled adherens junctions in the pharynx, intestine, and hypodermis (Fig 4B). In 148 contrast, Kunitz 3-10<sup>1</sup> embryos matched to the same stage displayed severe 149 disorganization (Fig. 4B). The pharynx and foregut adherens junctions appeared wild



**Fig. 5.** *mlt-11* knockdown causes developmental delay, molting defects, and reduction of motility. (A and B) Images of MLT-11:::mNG in control, *mlt-11 (RNAi)*, or *mNeonGreen*(RNAi) animals with and without a DIC merge. (C) Representative images of molting defects in *mlt-11 (RNAi)* animals. The bracket highlights a corset phenotype, the white arrow a discontinuous alae and the black arrow, residual cuticle material stuck onto the alae following ecdysis. In A-C Scale bars are 20 µm and images are representative of 40 animals examined over two biological replicates. (D) Animals were synchronized by a timed egg lay on control or *mlt-11 (RNAi)* plates and scored for developmental stage 48 hours later using vulval development (Mok et al., 2015). Data are pooled from two independent replicates (E) 20 L4 animals grown on control or *mlt-11 (RNAi)* plates were picked into a drop of M9+gelatin and thrashes were counted for one minute.

- 150 type, but the remainder of the junctions were disorganized and there was evidence of
- 151 invaginations in the hypodermis (Fig. 4B). These data implicate the signal sequence and
- 152 Kunitz 7-10 region as being essential for embryonic development.
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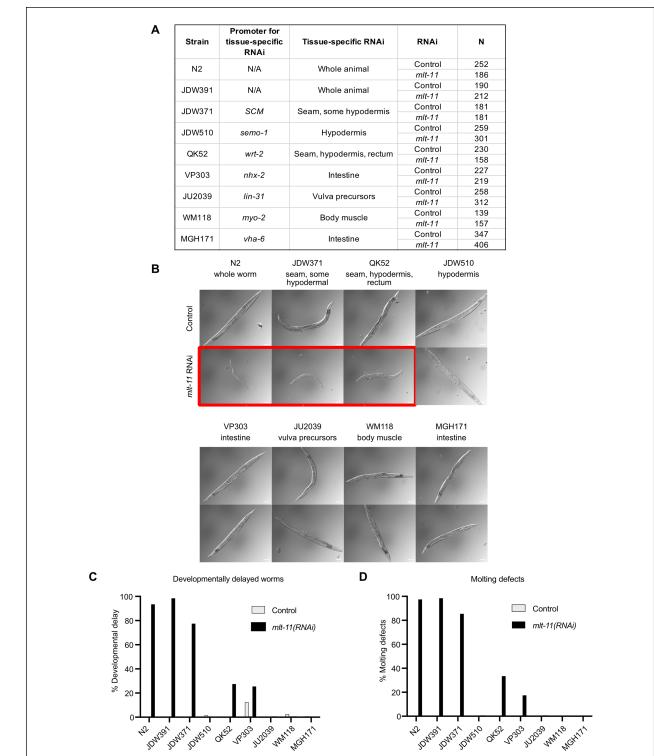
#### 154 *mlt-11* knockdown causes defective cuticle structure and function

155 As we were interested in the role of *mlt-11* in promoting molting, we turned to RNAi. Both 156 mlt-11 (RNAi) and mNeonGreen (RNAi) reduced levels of MLT-11::mNG (Fig. 5A.C), and 157 resulting phenotypes included ecdysis defects where animals were trapped in the old 158 cuticle or failed to shed the old cuticle producing a corset (Fig. 5B). We also observed 159 disorganized and discontinuous alae (Fig. 5B). mlt-11 (RNAi) animals developed more 160 slowly than control animals (Fig. 5D) and appeared to move more slowly. To test whether 161 *mlt-11* (RNAi) caused a locomotion defect, we performed a thrashing assay, scoring body 162 bends/minute. *mlt-11* RNAi caused nearly a 2.5-fold decrease in thrashing compared to 163 control animals (Fig. 5E). To determine in which tissue(s) *mlt-11* was necessary to 164 promote molting we used a set of tissue-specific RNAi strains (Fig. 6A). mlt-11 knockdown 165 in JDW371, a tissue-specific RNAi strain that restricts knockdown to seam, hypodermal, 166 and intestinal cells (Johnson et al., 2022), phenocopied *mlt-11* (RNAi) in wildtype or *mlt-*167 11::mNG (JDW391) animals with respect to developmental delay and molting defects 168 (Fig. 6A-C). *mlt-11* (RNAi) in QK52, a hypodermal and seam cell-specific RNAi strain, 169 produced less penetrant developmental delay and molting defects (Fig. 6A-C). Notably, 170 *mlt-11* (RNAi) in a hypodermal-specific RNAi strain, JDW510, produced no 171 developmental delay or molting defects, suggesting that *mlt-11* activity is necessary in 172 seam cells.

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## 174 *mlt-11* inactivation causes defects in aECM structure and function

The developmental delay and molting defects caused by seam cell specific *mlt-11 (RNAi)* were reminiscent of our recent work on *nhr-23* (Johnson et al., 2022). As NHR-23 depletion causes a defect in the cuticle barrier, we tested whether *mlt-11* inactivation also compromises this barrier. We incubated control and *mlt-11* (RNAi) animals with the cuticle impermeable, cell membrane permeable Hoechst 33258 dye and scored animals with stained nuclei. In control animals we observed no Hoechst staining while in *mlt-11* (RNAi)

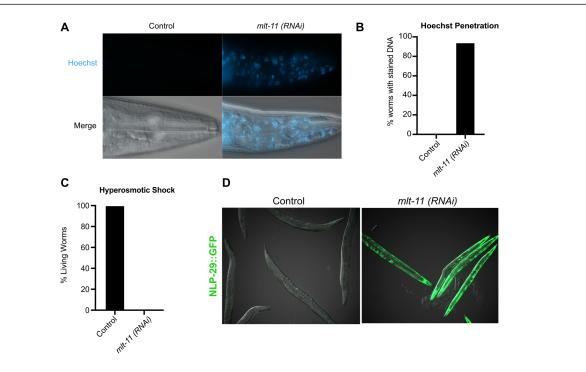


**Fig. 6.** *mlt-11* is necessary in seam cells for molting and larval development. (A) Tissue-specific RNAi strains used. A timed egg lay of animals of the indicated genotype were performed on control or *mlt-11 (RNAi)* plates and phenotypes were scored three days later. (B) Representative images of control and *mlt-11 (RNAi)* on the indicated strains. The red box highlights conditions that produced smaller larvae with molting defects. (C) Developmental delay was scored in the indicated strains grown on control or *mlt-11 (RNAi)* plates and classified as a failure to reach adulthood after 72 hours of growth. (D) Molting defects were scored in the indicated strains on control or *mlt-11 (RNAi)* plates. Scored defects included animals dragging cuticles, ecdysis failure and cuticle corsets. Tissue-specific RNAi data is from two independent replicates.

- depleted animals (Johnson et al., 2022), *mlt-11* (RNAi) also caused sensitivity to hypo-
- 183 osmotic shock (Fig. 7C) and activation of an *nlp-29::GFP* promoter reporter activated by
- 184 infection, acute stress, and physical damage to the cuticle (Fig 7D; Pujol et al., 2008;
- 185 Zugasti and Ewbank, 2009).
- 186

## 187 Weak *nekl* alleles suppress *mlt-11 (RNAi)* phenotypes

- We observed MLT-11::mNG localization to lysosomes and the aECM in the cuticle, rectal epithelium, vulva, and excretory duct (Fig. 2) and *mlt-11* inactivation caused defects in the aECM barrier function and localization of select aECM components (Fig. 7). MLT-11
- 191 could be acting directly in the aECM or could function in lysosomes, as this organelle has
- 192 been shown to play an important role in aECM remodeling during molting (Miao et al.,



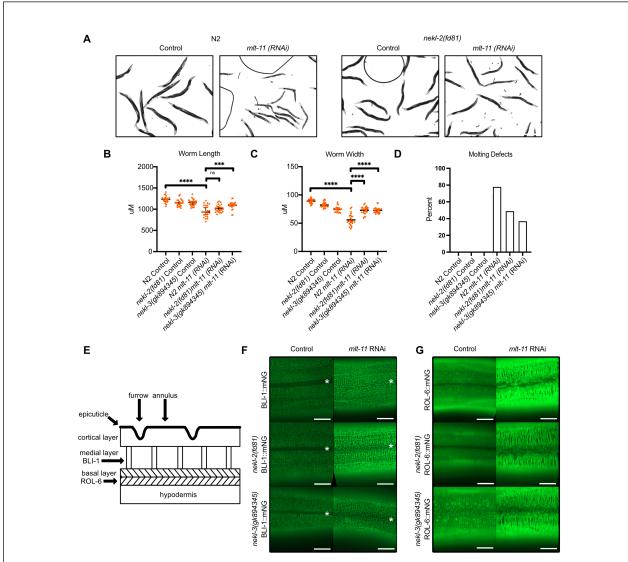
#### Fig. 7. mlt-11 knockdown causes defective aECM structure and function. (A,B)

Synchronized animals were grown on control or *mlt-11 (RNAi)* plates for 48 hours before being washed off and incubated with the cuticle impermeable/membrane permeable Hoechst 33258 dye. Representative images are shown in A. Quantitation of Hoechst 33258 nuclear staining in control and *mlt-11 (RNAi)* animals. Data from 40 worms are pooled from two independent replicates. (C) Hypoosmotic shock assay. 40 synchronized control and *mlt-11 (RNAi)* young adult animals were picked into 200  $\mu$ l of dH<sub>2</sub>0 and viability was scored 20 minutes later. Two biological replicates were performed and data pooled. (D) Representative images of animals carrying an *nlp-29p::GFP* reporter grown on control or *mlt-11 (RNAi)* plates. The reporter is activated by infection, acute stress, and physical damage to the cuticle (Pujol et al., 2008; Zugasti and Ewbank, 2009). Several biological replicates were performed and over 100 animals scored.

193 2020). To distinguish between these possibilities, we examined the genetic interaction 194 between *mlt-11* (RNAi) and weak *nekl* alleles, *nekl-2* and *nekl-3* encode NIMA-related 195 kinases that regulate endocytosis and are required for completion of molting (Joseph et 196 al., 2020; Lažetić and Fay, 2017a; Yochem et al., 2015). Weak nekl-2 and nekl-3 197 hypomorphs are viable but display reduced clathrin-mediated endocytosis (Joseph et al., 198 2020). We reasoned that if MLT-11 acted in the aECM then weak nekl alleles might 199 suppress the *mlt-11* (RNAi) defects by trapping more MLT-11 in the aECM. Conversely, 200 if MLT-11 activity was necessary in lysosomes then weak nekl alleles might enhance the 201 *mlt-11* (RNAi) defects by reducing the amount of MLT-11 that is trafficked to lysosomes. 202 Weak nekl-2(fd81) and nekl-3(gk894345) alleles suppressed the small body size of mlt-203 11 (RNAi) animals (Fig. 8A-C) and suppressed *mlt-11* (RNAi) molting defects (Fig 8D).

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205 NHR-23 depletion causes reduced levels and mis-localization of the medial cuticle layer 206 strut collagen BLI-1 and defective localization of the basal layer collagen ROL-6 (Johnson 207 et al., 2022), so we examined the effect of *mlt-11* (RNAi) on these markers. In control 208 animals, BLI-1::mNG localized to regularly spaced punctae in rows and was excluded 209 from the area of the aECM over seam cells (Fig. 8F). *mlt-11* (RNAi) caused BLI-1 to 210 localize to larger, irregularly spaced punctae which were also found over the seam cells 211 This exclusion zone and BLI-1::mNG organization pattern were partially (Fia. 8F). 212 restored in weak nekl allele worms grown on *mlt-11* (RNAi). ROL-6::mNG, in control 213 animals, localized to striped annuli, with an irregular but tight zipper-like pattern over 214 seam cells (Fig. 8G). mlt-11 (RNAi) animals displayed thick and aggregated ROL-6::mNG 215 with a large gap over seam cells where left and right side extensions typically meet (Fig. 216 8G). Weak nekl allele worms treated with *mlt-11* (RNAi) had a similar aggregation of 217 ROL-6::mNG over hypodermal cells, but more frequent connections across seam cells to 218 ROL-6::mNG in annuli on the opposite side. These data indicated that *mlt-11* is 219 necessary for aECM structure and MLT-11 acts in the aECM to promote development 220 and molting.



**Fig. 8. Weak** *nekl* **alleles suppress** *mlt-11* (*RNAi*) **defects.** (A) Representative images of animals of the indicated genotypes grown on control or *mlt-11* (*RNAi*) plates. Average length (B) and width (C) of animals of the indicated genotypes grown on control or *mlt-11* (*RNAi*) plates. Horizontal black lines indicate average from 2 independent experiments. Synchronized animals of the indicated genotypes were grown on control or *mlt-11* (*RNAi*) plates and scored for the number that displayed molting defects (D). Schematic displaying the primary layers and structures making up the *C. elegans* cuticle including the localization of ROL-6 and BLI-1 collagens used in (F) and (G). Representative images of *rol-6::mNG* (F) and *bli-1::mNG* (G) animals grown on control or *mlt-11* (*RNAi*) plates. Scale bars are 20 µm. Two independent experiments were performed and a minimum of 30 worms observed. In F, white stars indicate where the seam cells and alae are located.

#### 222 DISCUSSION

How aECMs are dynamically remodeled during development and disease remains poorly

understood. Using the *C. elegans* cuticle as a model aECM we demonstrate a role for the

protease inhibitor MLT-11 in promoting embryogenesis, molting, wild type developmental rate, and the aECM barrier. MLT-11::mNG oscillates and localizes to the aECM in the larval cuticle, vulva, rectum, and excretory pore, and is also in lysosomes. In embryos, MLT-11::mNG is secreted into the space between the eggshell and the embryo and then localizes to the cuticle prior to hatching. Tissue-specific RNAi data indicates that *mlt-11* primarily acts in seam cells. Depletion of *mlt-11* results in mislocalization of the collagens ROL-6 and BLI-1, and genetic data suggests that MLT-11 functions primarily in the aECM.

233 We observed three distinct phenotypes depending upon the severity of *mlt-11* mutation 234 or depletion: i) embryonic lethality; ii) larval molting defects and developmental delay; and 235 iii) rolling. Any C-terminal deletions removing Kunitz domains 7-10, including Kunitz 2-10 236 and Kunitz 3-10 deletions, produced embryonic lethality (Fig. 4). DLG-1::mNG revealed 237 severe disorganization of adherens junctions in these mutants with defects being most 238 pronounced in the hindgut and hypodermis (Fig. 4). One possibility is that MLT-11 is 239 required for embryonic sheath function. The embryonic sheath is an aECM that preserves 240 embryonic integrity and distributes force during embryo elongation (Kelley et al., 2015; 241 Vuong-Brender et al., 2017). MLT-11 is secreted during the window of morphogenesis, 242 when the embryo elongates. One model is that MLT-11 restrains protease activity to 243 ensure sheath integrity during elongation and in its absence the sheath is compromised. 244 Inactivation of sheath components has been shown to cause embryo arrest and rupturing 245 (Vuong-Brender et al., 2017). It is unclear whether the molting defects and developmental 246 delay incurred by *mlt-11* (RNAi) reflect a distinct molecular defect or arise from a similar 247 role for MLT-11 during larval aECM remodeling. The collagens ROL-6 and BLI-1 exhibited 248 aberrant localization in *mlt-11* (RNAi) treated larvae. A conditional deletion approach 249 would be ideal to create a *mlt-11* null in larvae, bypassing the embryo phenotypes.

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Our Kunitz 1-2, 3-5 and 3-6 deletions all produced a weak right roller phenotype. The mapping locus *rol-9* was recently discovered to be encoded by a gain-of-function *mlt-11* allele (Rich et al., 2022). How does a protease inhibitor mutation cause a roller phenotype? Aside from *mlt-11*, the only non-collagen roller gene is *rol-3*, which encodes a predicted receptor tyrosine kinase (Jones et al., 2013). ROL-3 is hypodermally

256 expressed and necessary for ecdysis and cuticle formation (Jones et al., 2013). rol-3 257 mutations cause defects in seam cell formation and *mlt-11* is necessary in seam cells for 258 developmental progression and molting (Fig. 6). One possibility is that weak *mlt-11* alleles 259 provide sufficient activity to promote ecdysis but elevated protease activity disrupts 260 collagen processing, leading to a roller phenotype. Interestingly, *mlt-11* (RNAi) disrupts 261 ROL-6::mNG localization and specific alleles of both *mlt-11* and *rol-6* cause a right roller 262 phenotype. In the future it will be interesting to test whether *mlt-11* and *rol-3* genetically 263 interact and whether *mlt-11* inactivation affects the localization of collagens that when 264 mutated produce left roller phenotypes.

265

266 Transcription factors regulate complex networks of genes to control cellular and 267 developmental processes. Assigning the regulation of a single regulated gene to a 268 phenotype incurred by inactivation of a given transcription is challenging. NHR-23 depletion causes developmental delay, molting defects, and defective aECM structure 269 270 and barrier function (Johnson et al., 2022). Strikingly, mlt-11 (RNAi) phenocopies NHR-271 23 depletion in many regards. Both cause developmental delays, apolysis defects, and a 272 loss of the aECM barrier function (Fig. 5-7; Johnson et al., 2022). The ROL-6::mNG 273 localization defects are highly similar, with annular disorganization and a gap over the 274 seam cells (Fig. 8; Johnson et al., 2022). Tissue-specific RNAi indicates that the seam cells 275 are a key site of action for both *nhr*-23 and *mlt*-11, though *nhr*-23 activity also appears 276 necessary in hypodermal cells (Fig. 6; Johnson et al., 2022). NHR-23-regulated genes 277 are enriched in protease inhibitors (Johnson et al., 2022), and *mlt-11* is a critical gene for 278 promoting aECM remodeling during molting (Fig. 8). An open guestion is whether MLT-279 11 is unique in mediating the NHR-23-dependent molting program or whether these 280 terminal phenotypes are a common feature of disrupting components in the NHR-23 gene 281 regulatory network. Given that *mlt-11* is a protease inhibitor gene, the common 282 phenotypes suggest that some aspects of the NHR-23 depletion phenotype may be due 283 to unrestrained protease activity. Identifying which protease(s) that MLT-11 inhibits and 284 the protease substrates is a critical future direction.

285

Why does MLT-11 have so many Kunitz domains? The extensively studied bovine 286 287 pancreatic trypsin inhibitor has a single Kunitz domain (Ascenzi et al., 2003), as do other 288 proteins such as Alzheimer Precursor Protein (Beckmann et al., 2016). Others such as 289 Tissue Factor Pathway Inhibitor and *C. elegans* MEC-9 have multiple Kunitz domains 290 (Broze and Girard, 2012; Du et al., 1996). One possibility was that the large number of 291 Kunitz domains in *C. elegans* MLT-11 arose through recent duplication. Arguing against 292 this possibility many *Caenorhabdid* species, as well as more distantly related nematodes 293 (P. pacificus, O. vovlulus, B. malayi) have large MLT-11 homologs with predicted signal 294 sequences and 10 Kunitz domains (Fig. S1). In C. elegans, Kunitz domains 1-6 and 10 295 appear dispensable whereas deletion of Kunitz domains 7-9 causes embryonic lethality 296 (Fig. 4). Notably, there is additional sequence flanking Kunitz domain 9 that is conserved 297 (Fig. S1). Interestingly, our immunoblotting experiments detect a smaller isoform of 50-298 70 kDa that could be produced by cleavage at or near the start of Kunitz domain 9. An 299 interesting approach would be to exogenously express a C-terminal fragment of *mlt-11* 300 containing Kunitz domains 7-10 in worms with an endogenous null allele of *mlt-11* to see 301 if this region is sufficient to rescue embryonic inviability. We would reasonably expect 302 these rescued worms to be right rollers as our deletion strains lacking Kunitz 1-2, 3-5 and 303 3-6 are right rollers.

304

305 Our data could suggest that the different Kunitz domains may play distinct roles, or that 306 their location within the protein is important. Kunitz domains work as competitive protease 307 inhibitors, which would suggest that MLT-11 could serve as a scaffold to bind to and 308 inactivate proteases. Kunitz domains tend to inactivate serine proteases, yet there are no 309 serine proteases implicated in molting (Frand et al., 2005). nas-37, an astacin 310 metalloprotease, peaks in expression 30 minutes after *mlt-11* mRNA peaks in expression 311 and genes expressed at similar points in development often function in common 312 processes (Davis et al., 2004; Farrell et al., 2018; Hendriks et al., 2014; Meeuse et al., 313 2020). MLT-11 may regulate uncharacterized protease inhibitors or could inactivate 314 different classes of protease inhibitors. An unusual family of Kunitz domain protease 315 inhibitors from the parasitic nematode *Fasciola hepatica* was shown to inhibit cathepsin 316 proteases, not serine proteases (Smith et al., 2020). Alternatively, MLT-11 may not

function as a protease inhibitor. The Kunitz domain containing molting factor BLI-5 was shown to enhance the activity of two serine proteases, rather than inhibit them (Stepek et al., 2010). Similarly, the ADM-2 protease regulates molting by modulating levels of the low-density lipoprotein receptor–related protein, LRP-1, through a mechanism independent of its protease activity (Joseph et al., 2022).

322

## 323 Future perspective

Our characterization of MLT-11 provides an entry point into understanding how proteases and protease inhibitors interact to promote aECM remodeling. Going forward, exploring whether MLT-11 plays roles in specialized aECM such as the vulval lumen, excretory duct, and glial socket cuticle will be important. As proteases are important targets to combat parasitic nematode infections, understanding how they are regulated during development by endogenous protease inhibitors will be critical to develop novel approaches to combat this group of devastating pathogens.

## 331 MATERIALS AND METHODS

## 332 Strains and culture

333 *C. elegans* were cultured as originally described (Brenner, 1974), except worms were 334 grown on MYOB media instead of NGM. MYOB agar was made as previously described 335 (Church et al., 1995).

336 Strains created by injection in the Ward Lab and used in this study:

Name	Genotype
JDW330	rde-1 (ne300) V.; jsTi1493 [mosL loxP mex-5p FLP sl2 mNeonGreen rpl-28p FRT GFP-HIS 58 FRT3 mosR] IV (Johnson et al., 2022)
JDW371	jsTi1493 {mosL loxP [wrdSi72( <b>SCMp::pes-10delta::rde-1 CDS+3'UTR</b> )] FRT3::mosR} IV ; rde-1(ne300) V (Johnson et al., 2022)
JDW380	jsTi1493 {mosL loxP [wrdSi72( <b>mlt-11(-2.8kb)p::mNeonGreen(dpi)::tbb-2 3'UTR</b> )] FRT3::mosR} IV

JDW383	<i>mlt-11(wrd78[<b>mlt-11 Kunitz 2-10 deletion</b>]),</i> oxTi633 [eft-3p::tdTomato::H2B::unc-54 3'UTR / F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V.
JDW385	him-8(e1489) IV; mlt-11(wrd80[ <b>mlt-11 Kunitz 7-10 deletion</b> ]), oxTi633 [eft- 3p::tdTomato::H2B::unc-54 3'UTR] / F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V
JDW386	him-8(e1489) IV ; mlt-11(wrd81[ <b>mlt-11 Kunitz 10 deletion</b> ]), oxTi633 [eft- 3p::tdTomato::H2B::unc-54 3'UTR] V
JDW387	mlt-11(wrd82[ <b>mlt-11 Kunitz 3-10 deletion</b> ]) , oxTi633 [eft-3p::tdTomato::H2B::unc-54 3'UTR] / F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V
JDW389	bli-1(wrd84[linker::mNeonGreen::3xFLAG::linker])
JDW391	mlt-11(wrd86[C-terminal mNeonGreen::3xFLAG]) V
JDW458	rol-6(wrd117[rol-6::C-term mNeonGreen (dpi)::3xFLAG::linker]) (Johnson et al., 2022)
JDW497	mlt-11(wrd122[ <b>mlt-11 Kunitz 3-6 deletion</b> ]), oxTi633 [eft-3p::tdTomato::H2B::unc-54 3' UTR] V
JDW503	mlt-11(wrd124[ <b>mlt-11 thyroglobulin domain deletion</b> ]) , oxTi633 [eft- 3p::tdTomato::H2B::unc-54 3'UTR + Cbr-unc-119(+)] V
JDW504	mlt-11(wrd125[ <b>mlt-11 Kunitz 3-5 deletion</b> ]) , oxTi633 [eft-3p::tdTomato::H2B::unc-54 3'UTR] + Cbr-unc-119(+)] V
JDW510	jsTi1493 {mosL loxP [wrdSi97( <b>suro-1p::rde-1 CDS+3'UTR</b> )] FRT3::mosR} IV ; rde-1 (ne300) V (Johnson <i>et al.</i> , 2022)
JDW512	wrdEx40[dpy-7p::mCherry::TRAM::unc-54 3' UTR]; mlt-11(wrd86[C-terminal mNeonGreen::3xFLAG]) V

# 337 Strains created by crossing in the Ward Lab and used in this study:

Strain	Genotype	Crossing	Crossing
		strain 1	strain 2

JDW359	ezls2 III [fkh-6::GFP + unc-119(+)] ; him-8(e1489) IV ;	DZ325	VC4276
	F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V.		
JDW401	mlt-11(wrd82[mlt-11 Kunitz 3-10 deletion]) , oxTi633 [eft- 3p::tdTomato::H2B::unc-54 3'UTR] / F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V. dlg- 1(cp301[dlg-1::mNG-C1^3xFlag]) X	JDW387	LP598
JDW511	ezIs2 [fkh-6::GFP + unc-119(+)] / + III ; him-8(e1489) / + IV ; mlt-11(wrd126[mlt-11 signal sequence deletionmNG::3xFLAG]) / F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V	EG7968	JDW359
JDW516	bli-1(wrd84[linker::mNeonGreen::3xFLAG::linker]) II ; nekl-3(gk894345) X	WY1141	JDW389
JDW517	rol-6(wrd117[rol-6::C-term-mNeonGreen (dpi)::3xFLAG::linker]) II ; nekl-3(gk894345) X	WY1141	JDW458
JDW522	nekl-2(fd81); rol-6(wrd117[rol-6::C-term-mNeonGreen (dpi)::3xFLAG::linker]) II	WY1122	JDW458
JDW526	nekl-2(fd81);bli- 1(wrd84[linker::mNeonGreen::3xFLAG::linker]) II	WY1122	JDW389

## 338 Strains provided by the *Caenorhabditis* Genetics Center:

N2	Wild-type
QK52	rde-1(ne219) V ; xkls99(wrt-2p::rde-1::unc-54 3'UTR) (Melo and Ruvkun, 2012)
VP303	rde-1(ne219) V ; kbls7[nhx-2p::rde-1 + rol-6(su1006)]) (Espelt et al., 2005)
JU2039	<i>mfls70 [lin-31p::rde-1 + myo2p::GFP] IV ; rde-1(ne219) V</i> (Barkoulas et al., 2013)
WM118	rde-1(ne300) V ; nels9(nels9 [myo-3::HA::RDE-1 + rol-6(su1006)]) X (Watts et al., 2020)

MGH171	alxIs9 [vha-6p::sid-1::SL2::GFP] sid-1(qt9) V ; alxIs9 (Melo and Ruvkun, 2012)
WY1122	nekl-2(fd81[Y84L,G88A]) I (Lažetić and Fay, 2017a)
WY1141 nekl-3(gk894345) X (Lažetić and Fay, 2017a)	
DZ325	ezls2 III [fkh-6::GFP + unc-119(+)] ; him-8(e1489) IV (Chang et al., 2004)
VC4276	F46B3.7(gk5359[loxP + myo-2p::GFP::unc-54 3' UTR + rps-27p::neoR::unc-54 3' UTR + loxP]) V (Au et al., 2019)
LP598	<i>dlg-1(cp301[dlg-1::mNG-C1^3xFlag]) X</i> (Heppert et al., 2018)
EG7968	unc-119(ed3) III; oxTi633 [eft-3p::tdTomato::H2B::unc-54 3'UTR + Cbr-unc-119(+)] V (Frøkjær-Jensen et al., 2014)

339

## 340 Other strains

NM5548 *jsSi1579 jsSi1706 jsSi1726[loxP myo-2p FRT nlsCyOFP myo-2 3' mex-5p FLP D5 glh-2 3' FRT3] II* was a gift from Dr. Michael Nonet and will be described elsewhere.
The sequence of this landing pad can be found on the Nonet lab website
(https://sites.wustl.edu/nonetlab/rmce-insertion-strains/ -last edited 6-4-2022) and is
inserted at an sgRNA within 50 base pairs away from the ttTi5605 insertion site.

346

## 347 Genome Editing

348 All plasmids used are listed in Table S1. Annotated plasmid sequence files are provided 349 in File S1. Specific cloning details and primers used are available upon request. JDW380 350 jsTi1493 {mosL loxP [wrdSi72(mlt-11(-2.8kb)p::mNeonGreen(dpi)::tbb-2 3'UTR)] 351 FRT3::mosR} IV was created by recombination-mediated cassette exchange 352 (RMCE)(Nonet, 2020). A 2.8 kb mlt-11 promoter fragment was initially Gibson cloned into 353 the NLS::mScarlet (dpi)::tbb-2 3'UTR vector pJW1841 (Ashley et al., 2021) to generate 354 pJW1934. The mScarlet cassette was then replaced with mNeonGreen (dpi) to generate 355 pJW2229. The mlt-11p (-2.8kb) mNeonGreen (dpi)-tbb-2 3'UTR fragment was PCR amplified from pJW2229 and Gibson cloned into SphI-HF+SpeI-HF double digested 356 357 RMCE integration vector pLF3FShC to produce pJW2337. This vector was integrated into 358 NM5179 and the SEC was excised as previously described (Nonet, 2020).

359

360 *mlt-11* deletion strains were created by injection of Cas9 ribonucleoprotein complexes 361 (RNPs)(Paix et al., 2014; Paix et al., 2015) [700 ng/µl IDT Cas9, 115 ng/µl each crRNA 362 and 250 ng/µl IDT tracrRNA], oligonucleotide repair template (110 ng/µl) and pSEM229 co-injection marker (25 ng/µl)(El Mouridi et al., 2020) for screening into strain EG7968. 363 364 Where possible, we selected "GGNGG" crRNA targets as these have been the most 365 robust in our hand and support efficient editing (Farboud and Meyer, 2015). F1s expressing the co-injection marker were isolated to lay eggs and screened by PCR for 366 367 the deletion. F2 progeny of a verified F1 deletion mutant were crossed to JDW359 males 368 expressing myo-2::GFP to genetically balance the mutation. Genotyping primers are 369 provided in Table S2. JDW389 and JDW391 and were created by injection of RNPs [700 370 ng/µl IDT Cas9, 115 ng/µl crRNA and 250 ng/µl IDT tracrRNA] and a dsDNA repair 371 template (25-50 ng/ul) created by PCR amplification of a plasmid template into N2 372 animals (Paix et al., 2014; Paix et al., 2015)(Table S1). PCR products were melted to 373 boost editing efficiency, as previously described (Ghanta and Mello, 2020). For the *mlt*-374 11 C-terminal knock-in, the mNeonGreen::3xFLAG cassette was inserted right at the 375 double-strand break and a stop codon followed the 3xFLAG sequence. We re-coded the 376 sequence between the insert and native stop codon and placed it in 5' to the mNeonGreen 377 3xFLAG insertion (File S2). Sequences of CRISPR/Cas9-mediated genome edits are 378 provided in File S2. crRNAs used are provided in Table S3. F1 progeny were screened by mNeonGreen expression. JDW512 wrdEx40[dpy-7p::mCherry::TRAM::unc-54 3' 379 380 UTR]; mlt-11(wrd86[C-terminal mNeonGreen::3xFLAG]) V was generated by injection of 381 a dpy-7p::mCherry::tram-1::unc-54 3'UTR vector (25 ng/µl)(Chen et al., 2012) into 382 JDW391. F1 progeny were screened by mCherry::TRAM expression.

383

#### 384 Imaging

Synchronized animals were collected from MYOB, control, or auxin plates by either picking or washing off plates. For washing, 1000  $\mu$ l of M9 + 2% gelatin was added to the plate or well, agitated to suspend animals in M9+gelatin, and then transferred to a 1.5 ml tube. Animals were spun at 700xg for 1 min. The media was then aspirated off and animals were resuspended in 500 $\mu$ l M9 + 2% gelatin with 5 mM levamisole. 12  $\mu$ l of

animals in M9 +gel with levamisole solution were placed on slides with a 2% agarose pad 390 391 and secured with a coverslip. For picking, animals were transferred to a 10 µl drop of 392 M9+5 mM levamisole on a 2% agarose pad on a slide and secured with a coverslip. 393 Images were acquired using a Plan-Apochromat 40x/1.3 Oil DIC lens or a Plan-Apochromat 63x/1.4 Oil DIC lens on an AxioImager M2 microscope (Carl Zeiss 394 395 Microscopy, LLC) equipped with a Colibri 7 LED light source and an Axiocam 506 mono 396 camera. Acquired images were processed through Fiji software (version: 2.0.0- rc-397 69/1.52p). For direct comparisons within a figure, we set the exposure conditions to avoid 398 pixel saturation of the brightest sample and kept equivalent exposure for imaging of the 399 other samples.

400

#### 401 Western Blot

402 For the western blot in Fig. X JDW391 animals were synchronized by alkaline bleaching 403 (dx.doi.org/10.17504/protocols.io.j8nlkkyxdl5r/v1) and released on MYOB plates. 404 Animals were harvested at the indicated time points by picking thirty animals into 30 µl of 405 M9+0.05% gelatin. Laemmli sample buffer was added to 1X and then samples were 406 immediately incubated for five minutes at 95°C. Lysates were stored at -80°C until 407 resolution by SDS-PAGE. Lysates were resolved using precast 4-20% MiniProtean TGX 408 Stain Free Gels (Bio-Rad) with a Spectra<sup>™</sup> Multicolor Broad Range Protein Ladder 409 (Thermo; # 26623) protein standard. For the anti-FLAG blots, proteins were transferred 410 to a polyvinylidene difluoride membrane by wet transfer using Towbin buffer (25 mM Tris. 411 192 mM glycine, 20% methanol, pH 8.3) supplemented with 0.1% SDS and 30V was 412 applied for 16 hours in a cold room. The buffer was chilled prior to use and a freezer back 413 was added to the transfer container. For the anti-Tubulin blots, a semi-dry transfer with a 414 TransBlot Turbo (Bio-Rad) was performed. Blots and washes were performed as 415 previously described (Johnson et al., 2022, 23). Anti-FLAG blots used horseradish 416 peroxidase (HRP) conjugated anti-FLAG M2 (Sigma-Aldrich, A8592-5x1MG, Lot 417 #SLCB9703) at a 1:2000 dilution. Mouse anti-alpha-Tubulin 12G10 (Developmental Studies Hybridoma Bank; "-c" concentrated supernatant) was used at 1:4000 and Digital 418 419 anti-mouse (Kindle Biosciences LLC, R1005) diluted 1:20,000 was used as the 2°. Blots 420 were incubated for 5 minutes with 1 ml of Supersignal West Femto Maximum Sensitivity

Substrate (Thermo Fisher Scientific, 34095) and the final blot were imaged using the
'chemi high-resolution' setting on a Bio-Rad ChemiDoc MP System.

423

#### 424 RNAi Knockdown

RNA interference experiments were performed as in Johnson *et al.* (2022). Control RNAi
used either an empty L4440 or high-efficiency T444T RNAi vector (Sturm et al., 2018).
The *mlt-11 (RNAi)* vector was streaked from the Ahringer library (Kamath et al., 2003).
The *mNeonGreen*(RNAi) vector was generated by synthesizing a cDNA fragment and
cloning it into T444T. Synthesis and cloning were performed by Twist Bioscience. Vector
sequences are provided in File S1.

- 431
- 432

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442

## 443 **Competing interests**

- 444 The authors declare no competing or financial interests.
- 445

## 446 Author Contributions

- 447 Conceptualization: J.M.R, J.D.W.
- 448 Methodology: J.M.R, J.D.W.
- 449 Validation: J.M.R, J.D.W.
- 450 Formal analysis: J.M.R, J.D.W.
- 451 Resources: J.M.R, J.D.W.

452	Data curation: J.M.R, J.D.W.
453	Writing - original draft: J.M.R, J.D.W.
454	Writing - review & editing: J.M.R, J.D.W.
455	Supervision: J.M.R, J.D.W.
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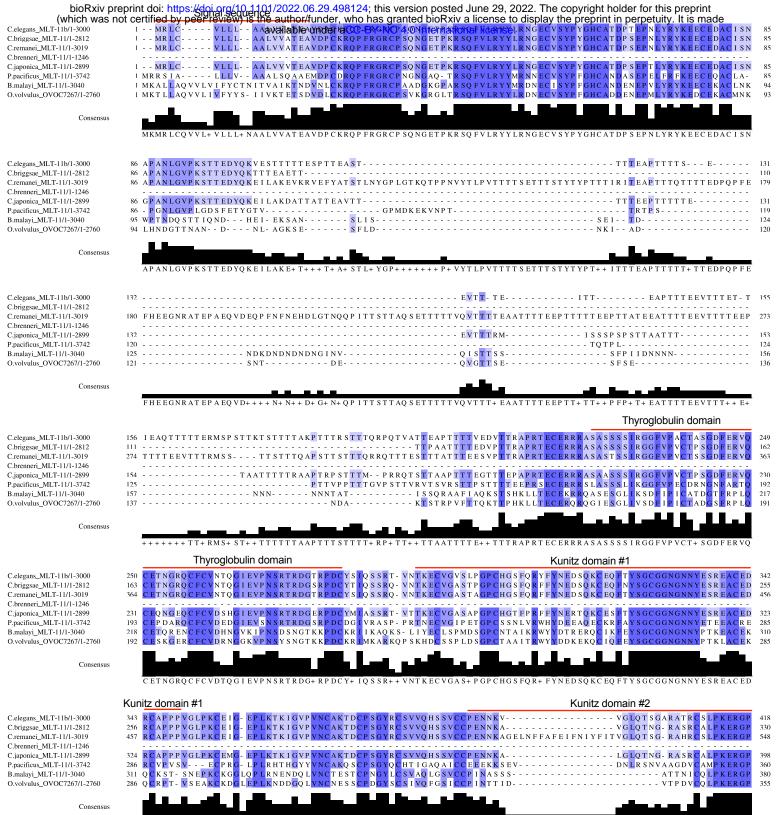
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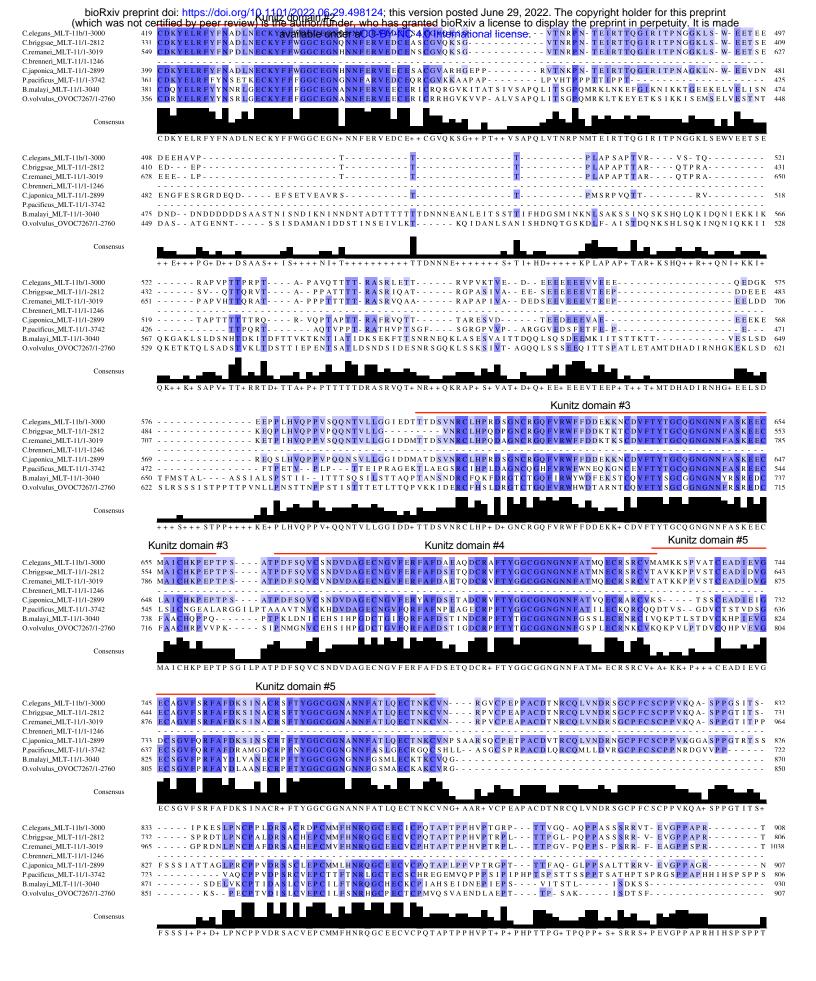
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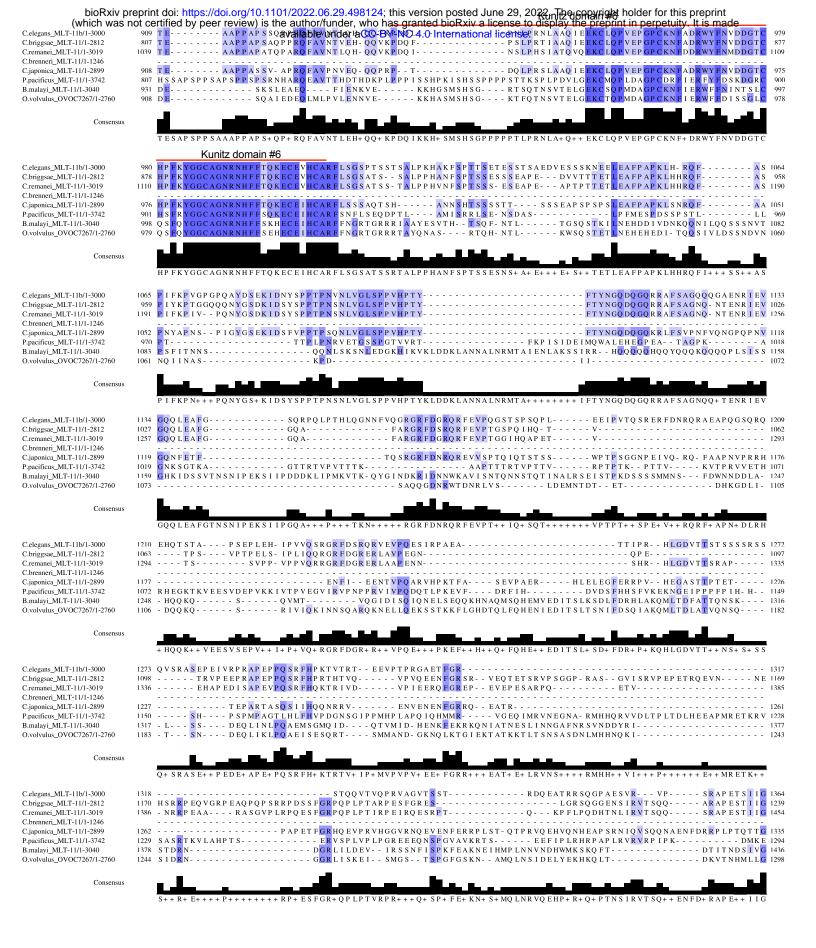
635 Figure S1. Alignment of MLT-11 homologs. MLT-11 homologs from the indicated 636 nematode species were aligned using Clustal Omega. The length in amino acids of each 637 homolog follows the species and homolog name. To the left and right of the alignment 638 are amino acid positions of the end residues for each protein. Blue shading indicates 639 conserved sequences and the histogram at the bottom depicts the degree of conservation 640 with a consensus sequence listed below. The positions of the C. elegans MLT-11 signal 641 sequence, thyroglobulin domain, and ten Kunitz domains are indicated. We note that we 642 cut off the extended P. pacificus C-terminus (amino acids 2626-3742) since no sequence aligned to it as all proteins terminated at the C. elegans MLT-11 stop codon. No predicted 643 motifs are found in the *P. pacificus* C-terminus. 644 645

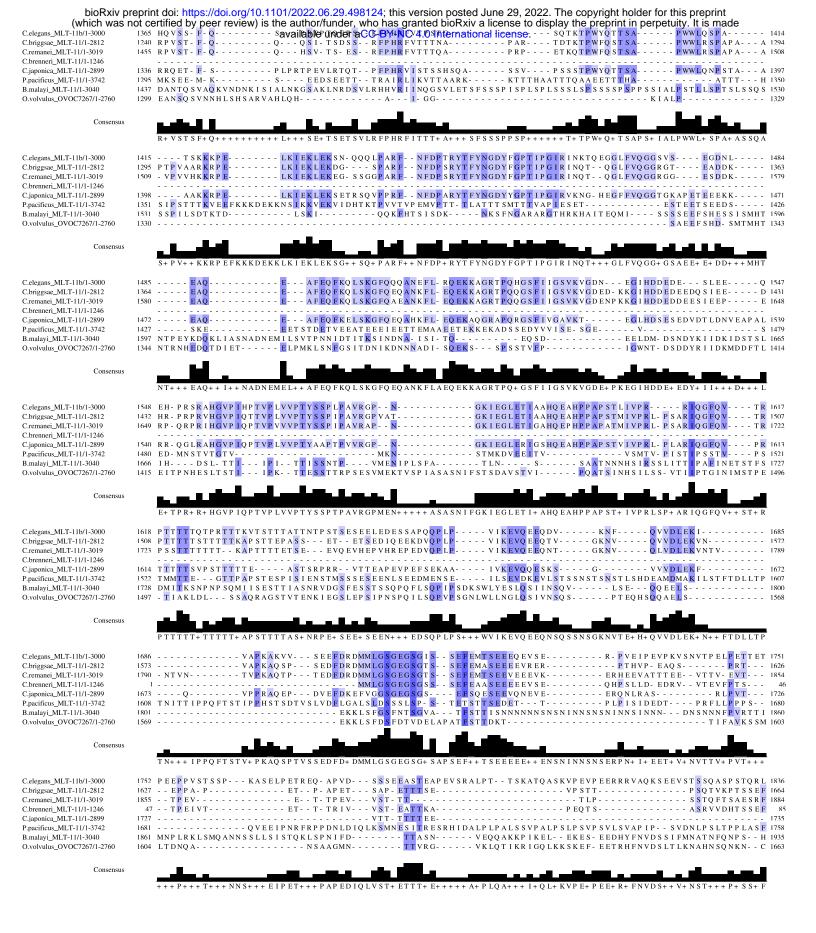
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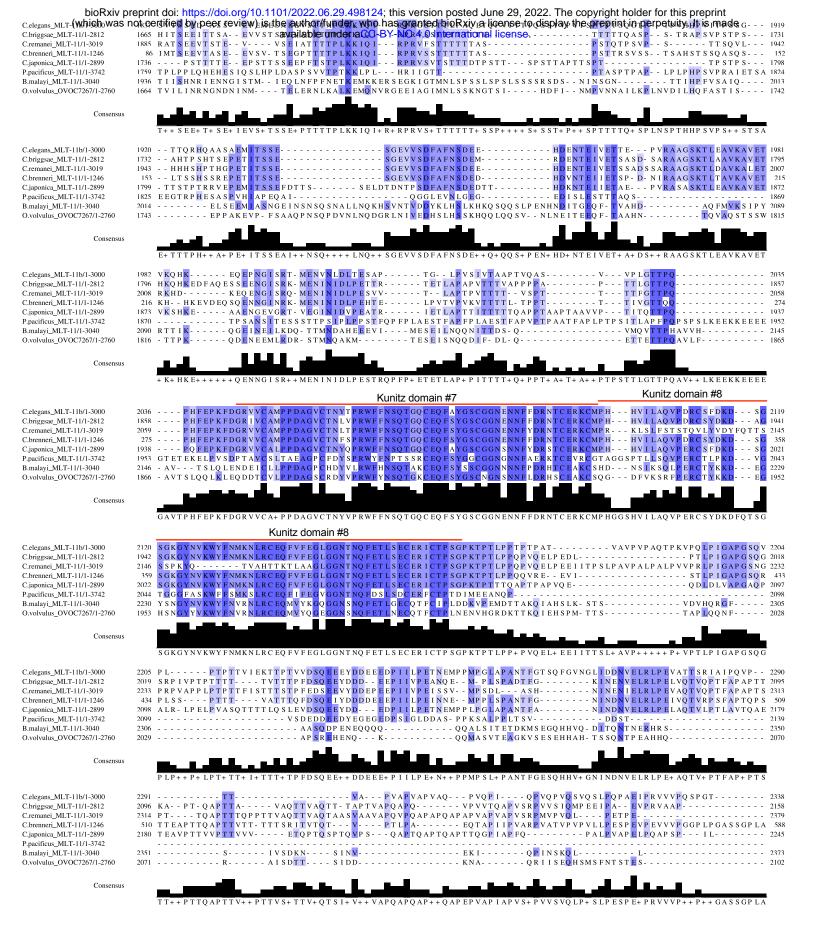


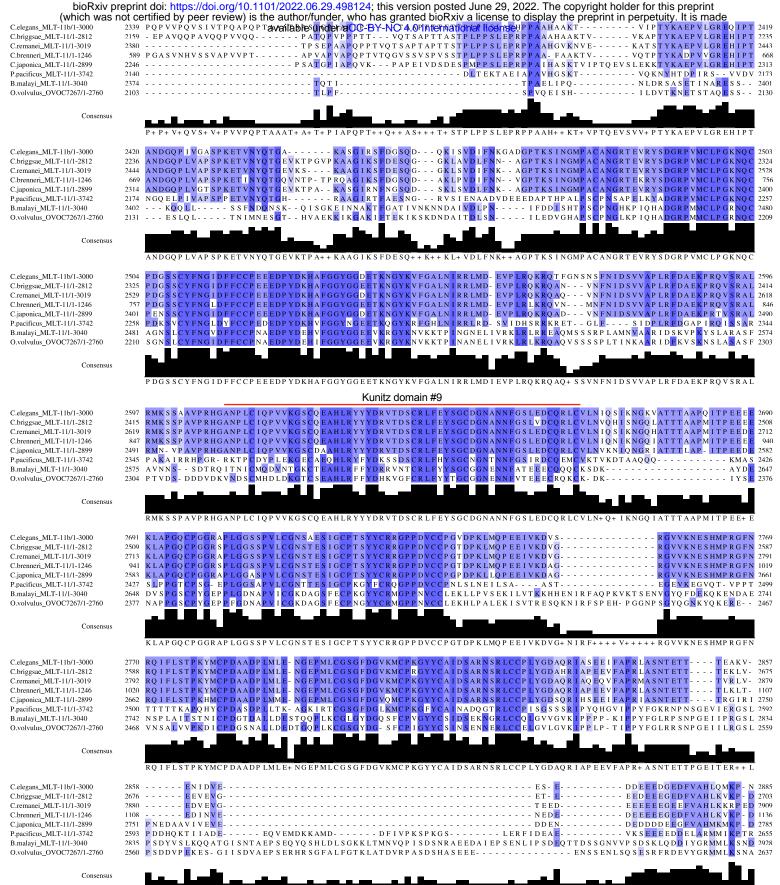
R C A P P P V G L P K C E I G L E P L K T K I G V P V N C A K T D C P S G Y R C S V V O H S S V C C P E N N K A + + L N F F A F E I F N I Y F I T V G L O T N G A R A + R C A L P K E R G P











S D D V + E + E V E + I S + + A E P S E + + + S + + D L + G + K L + + + V + P + S D S + + + E E + A I E P + E + + I + E + E Q T + + S S + N + + D E E E E G E D F V A H + K + K P N D

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C.elegans MLT-11b/1-3000	2886 KF VOV VEC LAKS - available under SACE WILD 4 OU AKS AT THE REFAT THE VALUE KEN VOV KEV COLKEVEG BOR VON DE EPT RT NLOY FYS 2968		
C.briggsae MLT-11/1-2812			
C.remanei MLT-11/1-2012	2010 KEVNVYED LAKQ		
C.brenneri MLT-11/1-1246	2210 KEYSVED-LAKE		
	115/ REGSVVED-LARE		
C.japonica_MLT-11/1-2899			
P.pacificus_MLT-11/1-3742	2656 HQ - EKQ EE - VASI ILP SIDSES - SPVFISNVPTPTLETE STVLPKETFDRSRCQLRPDEGRPCREDEVAPRTNLHYFYS 2731 2929 QAFRTQ ALYNAINNVASPEAENNEVQIDIGEMKDPFESL EYAQKSTSDRSICLLKPSEGRTCREDESPPRTNLQYFYS 3006		
B.malayi_MLT-11/1-3040			
O.volvulus_OVOC7267/1-2760	2638 QTLR SQAFILAK LAMFVALYNALGNVASPEAETNE IQIDVGEMKDPFESMEYAKKTASDRSICFLKPNEGRTCREDESPPRTNLQYFYS 2726		
Consensus	التكاولية الشابلي ويتوجد والشابي ويرب والشوي		
	+ P V S V V E+ 1 L A KQ A M F V A L Y N A+ S + + A T D L + E E G E V S I D L G + D E K P F V E E E E I T T T T E K M M V Q D + S V C Q I K P + E G R + C N E S E T P T R T N L Q Y F Y S		
	Kunitz domain #10		
C.elegans MLT-11b/1-3000	2969 PRDNRCKLFFFRGCGGNLNRFERKSDCEALCL 3000		
C.briggsae MLT-11/1-2812	2781 PRONCK LEFFRGCGGNLNR FEKSDCFALCL 2812		
C.remanei MLT-11/1-3019	2988 PRDKRCKLFFFRGCGGNLNRFEKKSDCEALCL 3019		
C.brenneri MLT-11/1-1246	1215 PKHNRCKLFFFOGCGGNLNRFEKKSDCEALCL 1246		
C.japonica_MLT-11/1-2899	2868 PRDNRCKIEFERGGONINREEKKSDCEALCI		
P.pacificus MLT-11/1-3742	2732 EVD GRCK LY FYKGCGGNENRFERK SDLEYD I SFDELLT FHY SHR FTP FLDCARTALLR I YTKYPWDEEK I EYYRGE I EKGLRDLE I YGGVT VQQ 2825		
B.malayi_MLT-11/1-3040	3007 NRDKRCKLYFYRGCGGSONRFDTKRHCELTCAGV 3040		
O.volvulus OVOC7267/1-2760	2777 TR DKR C KLY FYR G C GG SONR FDT KR HC FMT C G S V		
Consensus			

PRDNRCKLFFFRGCGGNLNRFEKKSDCEALCL+ VELLTFHYSHRFTPFLDCARTALLRIYTKYPWDEEKIEYYRGEIEKGLRDLEIYGGVTVQQ