

```

      506                               528                               555
C.elegans CVPPIETEHEHCQSPSMKRSRCTNYSFRTLTLSTAETKVVVEFLAREAKVPRYTWVPTQV
C.briggsae ---FYRKFKENEDSLSNKRPRSQYGLQRQVKLSEKEYSKFVAFFAKEGENEISKYASAHC
      .. :** :* * **.* . * :.** **:*.* *:*:*.. : .....:

      574
C.elegans VS-----HILPTEGLERFLTAIKAGHDSVLFNANGIYTMGDMIREFEKHNDIFERIGIDS
C.briggsae LTPAQASRLDPSDKIEKFLAFVGDESAADNFRKHGLFTMLDLDKYFQVYDSAFETIGVDS
      ::      :: *:: :*:**: : : * . :*:* ** * : : * : :. ** **:*

      641
C.elegans SKLSKYYEAFLSFYRIQEAMKLPK
C.briggsae SKMEKYDDLFLHYHRVQENIR---
      **:.***: ** :*:** :

```

Figure S1 Sequence alignment of CEP-1 in *C.elegans* and *C.briggsae*.

Sequence comparison between two different species of Nematode reveals two conserved regions after residue 510. The oligomerization domain of CEP-1 is colored green, and the SAM domain of CEP-1 is colored orange.