

C.ele	A-----TTTC	AATCGGCCAAA	TTGT-----	----GCACAT	-----CCTAT	GAATTTTCCT	ACATCTATTT	TGAAAAGTAA	GC-----AAA	TTCTATGAAA	
C.bri	AGACAACCTC	AAAAAGTATA	TTGTTGAACG	ACGGCTTGGT	GACAGTCGAA	AGGCCTGAC	TAGTCGATTA	CCGGTGGTTG	GTGGACCAAA	TTTCTGGAGA	
C.rem	A-----CTC	AGAAA---AA	TTTT-----G	TTTTTTAATT	-----TCTAA	AAAATTTAAT	TGG---ATCT	TGAGTTCTCA	GT----CGAA	CTTA-AAGAA	
C.bre	G-----TGC	AAATG---TA	TTCCTATCAG	ATCTCCAGAT	-----CAGAG	AAGTTTCGAA	TGC---ATCA	AGACTTTTCA	CT----TACA	GTTC-GGATA	
	
		510	520	530	540	550	560	570	580	590	600
C.ele	ATATCTAAAG	AAAAATGGAA	AAAATTT---	--TCA-----	---AAAAGGC	ACA----GTT	TTAAGTGTTT	CC----GTCT	A---ATAAAA	AAATCCCCCT	
C.bri	ATGGAACATT	TTGTCAAAAA	TTACTTTTGG	AATTATCACA	CTATAAAAGT	CAAAGAGGAC	TCTGGGAATC	TTCAAAATTT	ATTATTAGAA	GTATGCGGAC	
C.rem	CTGGTACATT	TGAGG--AAG	CGAGACC---	-ATTG-----	---GAAAGGA	GTA---TGAG	CCACGTCATT	---AAATTGT	G---GTAAGA	-TACTTACTC	
C.bre	TCATTACAGG	ACAAGTTGAA	CGAATCC---	-TCAGTCTCA	CACGGAAGGT	GTAGTCCAAT	TGATATCATC	CA-AAACCGT	ATTTGTAGTG	-AAACTAAGT	
	
		610	620	630	640	650	660	670	680	690	700
C.ele	AAACTTCC	GGC--AAATT	GATGTTCGGC	AAATGGCAAA	TC-----	GGAAACTTGC	CGAAAAT---	-----	TACAGTTTCC	GGTAA-----	
C.bri	AAAAATGACC	CATTTATATT	CAGAAGAAAT	CTCGAAAACG	TTTTTTTTTT	GAAAACCAAG	AGAAGAATGC	GCCTGAACAG	TGATGCTTAT	CGAGGTAATA	
C.rem	AATGAAGATT	C----ACATC	CAAAAACCTGA	TCACAAGGCG	TA-----	GAAAGAACTG	TGAACTG---	-----	TAATTCTTTC	GGACG-----	
C.bre	AGAGAAGTTT	CG---AGATC	TCGTTGCCAT	CCATAAAAAA	AC-----	GAAAACGCTG	TCATGTAAAT	CCGGGA---	TGCTGCTTGC	AGACATAAAT	
	
		710	720	730	740	750	760	770	780	790	800
C.ele	-ATCGGCAAA	CCGGCAAACCT	-----GC	CTGAATTGAA	AAGTTCCGTC	AAATCGGCAA	ACCGACAACA	CCCCTGGCAC	AAATGATGGA	CATACTGAGG	
C.bri	TAAAGACTTC	AGGACTTAAC	AATAAAACAA	ATGCGTCCAG	GAATTTTTGA	AGCGGGTCTA	GCCAATGTTT	TTTTTCTTTT	TCAAAATCCC	TTTCTGTGAA	
C.rem	-ATTGGATAC	TAG-CGGAAT	-----	ACTC-T--AC	AAAT-----A	ATGAG---AA	ACCAAGACCT	GATTTTACCT	GAAAAGCTCT	TCTCCGTGAA	
C.bre	AATCTATTTT	TAA-CAGATT	TGAGAGTGGA	ATTCGT--AA	GAAT-----C	AGGAGCGAAA	ATTAATGACA	AATGACAGGT	AGTGAGATGG	AAAACCTAGGA	
	
		810	820	830	840	850	860	870	880	890	900
C.ele	CAATTTGCCG	GT-----	-----TT	TCCAATTGCA	GGAAATTTT-	---CAATTCC	GGCAGTGTGC	CGA-----	TTTGCCGGAA	ATTTTAATTC	
C.bri	AAATGATGCC	GTGAGATGAA	GTCCCAAATT	TAGAAAAGTT	TCAAACATTG	AAACAACACA	TTTGAGGAAT	AGGCTCTTCT	TATTTTAGTA	GCCAAGCAAC	
C.rem	GAAA-----	CT-----	-----	---AAAAACA	ACTGTCTT--	---CACTTGA	AATGAAG---	-----	-----TGAAA	ACAAAAAAGA	
C.bre	GAAGGTTTCT	CT-----	-----	---CAAAGTT	TTGACCTT--	---CAGTCCA	ACTGAAGAGT	-----T	TTCGATGGAA	GTTGAAACAA	


```

1400
C.ele AAAAAAGAAGA GCCTTTCGGT TTGGAGAGTA GGGTCTAATA ATCCCCCGTG CTCTTCAAAT CATTGTGCCA ACACACAGAC ACACTTTATG TGTGCTCACA
C.bri AAGAAGAAGA GTCTTC---- --GGAGAAGA GCGTCTAATA ATCCCTG--- --CTTCAAAT CATTGTGCCA ACACA~~GAC ACACTTTATG GG~~CCAGAA
C.rem ---AAGAAGA GCCTC----- -----GGA GCGTCTAATA ATCCCTG--- --CTTCAAAT CATTGTGCCA ACACA~~~~C ACACTTTATG TG--CCCA--
C.bre ---AAGAAGA GCCTC----- -----GGA GCGTCTAATA ATCCCTG--- --CTTCAAAT CATTGTGCCA ACACA~~~~C ACACTTTATG TGTGCCCA--

.....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
1410 1420 1430 1440 1450 1460 1470 1480 1490

1500
C.ele CACACACGCT ATTTGAAGAG CGAAGACGAC GAC-----G ACGCATTTCAG A-GCTCTTTT CCACGAAATT TGCTCCATCT TTCCACAATC
C.bri C---CACGCT ATTTGAAGAG CAACGACGAC GAT-GACG-- AGCGCCAAG AGGTCTCCAG A-GCT-CTTT TCACAAATTC ----TCTTCT TTCAA-AACC
C.rem ----CACGCT ATTTGAAGAG CGAAGAAGAC GACCGA---T GACGACCTCG ACGTCTTCAG ACGCT-CTTT TCAAAAAATT ----CTTTCT TTTCA-AATC
C.bre ----CACGCT ATTTGAAGAG CGAAGAAGAC GTCCGACGAT GACGACGACG ACGTCTTCAG ACCCTTCTTT TCACGAATTT ----CTTATT TTTTCG-AATT

.....|.....| .....|.....| .....|.....| .....|.....| .....|..
1510 1520 1530 1540
C.ele TGTCTTTCCT GTGAGACGAC AGCGTCACAT TTATTTTCATT ACAGATG
C.bri GGTGGTTCCT TTCAAGT--- --TTGT--GT TTCCT-TACA G-ACATG
C.rem GGTCTTCCTG CT-ACAT--- --TT----AT TTCGT-TACA GAAGATG
C.bre TGTCTTACTT CTCATAC--- --CTCTCAAT TTCGTATTTT ACAGATG

```

C.ele=*C. elegans*; *C.bri*=*C. briggsae*; *C.rem*=*C. remanei*; *C.bre*=*C. brenneri*. All genomic sequences are available on Wormbase (<http://wormbase.org/>). Alignment was carried out using BioEdit (Hall, 1999) ClustalW Multiple Alignment function and was edited manually. All sequences terminate with the start codon of the *unc-47* ortholog.

1. Hall, T.A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucl. Acids. Symp. Ser. 41:95-98.