Supporting information

Title of the manuscript: Immunization with *Brugia malayi* Calreticulin protein generates robust anti-parasitic immunity and offers protection during experimental Lymphatic filariasis

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Number of Pages: 1

Number of Figures: 1

Results

Figure S1: ClustalW multiple sequence alignment of Calreticulin protein from *Brugia malayi* (bm) and *Wuchereria bancrofti* (w) showing 97% homology.

Supplementary figure 1

10/9/2020 CLUSTALW Result

CLUSTALW Result

[clustalw.aln][clustalw.dnd][readme]

Select tree menu Exec

```
 CLUSTAL 2.1 Multiple Sequence Alignments


Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: w           404 aa
Sequence 2: bm          404 aa
Start of Pairwise alignments
Aligning...



Sequences (1:2) Aligned. Score: 97.0297
Guide tree file created:   [clustalw.dnd]

There are 1 groups
Start of Multiple Alignment

Aligning...
Group 1: Sequences:   2      Score:6764
Alignment Score 2577

CLUSTAL-Alignment file created  [clustalw.aln]
```

clustalw.aln

```
CLUSTAL 2.1 multiple sequence alignment


w               MQLYLLLGLVCFSVVSAKVYFKEEFSDDDWEKRWIKSKHKDDFGKWEISHGKFYGDAAKD
bm              MQLYLLLGLVCFSAVSAKIYFKEEFSDDDWEKRWIKSKHKDDFGKWEISHGKFYGDAVKD
                *************.****:************************************.**

w               KGLKTAQDAKFYSIGAKFEKGFSNKGKSLVVQFSVKHEQDIDCGGGYVKLMASNVNLEDF
bm              RGLKTAQDAKFYSIGAKFEKGFSNKGKSLVVQFSVKHEQDIDCGGGYIKLMASDVNLEDF
                :*********************************************:*****:******

w               HGETPYHIMFGPDICGPGTKKVHVIFHYKGRNHMIKKDIRCKDDVFTHLYTLIVNSDNTY
bm              HGETPYHIMFGPDICGPGTKKVHVIFHYKGRNHMIKKDIRCKDDVFTHLYTLIVNSDNTY
                ************************************************************

w               EVQINGEKVESGELEADWDFLPPKKIKDPDAKKPEDWDEREYIDDEDDKKPEDWDKPEHI
bm              EVQINGEKVESGELEADWDFLPPKKIKDPDAKKPEDWDEREYIDDEDDKKPEDWDKPEHI
                ************************************************************

w               PDPDAKKPEDWDDEMDGEWEPPMVDNPEYKGEWKPKQKKNPAYKGKWIHPEIDNPDYTPD
bm              PDPDAKKPEDWDDEMDGEWEPPMVDNPEYKGEWKPKQKKNPAYKGKWIHPEIDNPDYTPD
                ************************************************************

w               DDLYIYEDIGAIGFDLWQVKSGTIFDDIIVTDNVEEAKKFGEKTLKKTKEGEKKMKEKQD
bm              DDLYLYGDIGAVGFDLWQVKSGTIFDDVIVTDSVEEAKKFGEKTLKKTKEGEKKMKEKQD
                ****:* ****:***************:****.**************************

w               EEEEKKRKEEEEKKKEEEKEDEDKEEEEKEEDEKKKDDETHEEL
bm              EEEEKKRKEEEEKKKEEEKEEEDKEEEEKEEDEKKKDDETHEEL
                *******************:**********************
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https://www.genome.jp/tools-bin/clustalw