Fig. S9A

```
# 1: A_Sequence: Hgr1 (2.A.76.1.5 homologue)
# 2: B_Sequence: Ssp3 (2.A.116.1.7 homologue)
# Matrix: EBLOSUM62
# Gap_penalty: 8.0
# Extend_penalty: 2.0

# Length: 188
# Identity:      60/188 (31.9%)
# Similarity:    91/188 (48.4%)
# Gaps:          27/188 (14.4%)
# Score: 138.0
#=======================================
                          1                                 2
A_Sequence         1 IGIVLLPGPNSLFVLSVATA-RGVRVGYHAACGVF----LGDSILL-LFT     44
                     : | :: ||  :  : :||| | |||      ||     || :|:| : |
B_Sequence         1 LAITMMAGPQIMSAVILATAQRAVRVSLGFVTGVLIATSLGVAIMLGIAT     50
                          1                                 2

                                           3
A_Sequence        45 ALGAA---SLLRGYPALFMVVKYVGAAYLFWVGMNLAWSAWRKWRAAGIA     91
                     ||| |          ::  |::||  | |      ||  | | ||
B_Sequence        51 ALGGAVDFGSSGDKSSVGRVIQYVLVALLI-----LA--ALRNWR----K     89
                                           3

                                                            4
A_Sequence        92 TQLVEPTA-LAAAQSAHLLAPFQRALVISLLNPKAILFLLSFFVQFIDPA    140
                      : |||   | |  ||     |:  |:: || |  :: :|:  |  :|
B_Sequence        90 RETVEPPKWLHALMSADTRKAFETGLLVVLLMPSDLMVMLTVGVH-LDQG    138
                                                            4

                                           5
A_Sequence       141 YDT--PAIPFLILSVIVMAFSAVYLSVLIVAGARLADA    176
                     : :   |:||: |: :| | : : | ||:  | | | |
B_Sequence       139 HSSFVDALPFIALTTLVAA-TPLLLRVLL--GRRAASA    173
                                           5

#---------------------------------------
============ FINISHED =============
Average Quality (AQ)     26.84 +/- 7.65
Standard score (Z):      15.0
Precise score (Z):  14.5
```