

CLUSTAL O(1.2.4) multiple sequence alignment

```
XP_005463512.2    MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTE    60
AAN39284.1        MARTKQTARKSTGGKAPRKQLATKVARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTE    60
                    *****.*****

XP_005463512.2    LLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTI    120
AAN39284.1        LLIRKLPFQRLMREIAQDFKTDLRFQSSAVMALQEACESYLVGLFEDTNLCVIHAKRVTI    120
                    *****.******.*.******.******

XP_005463512.2    MPKDIQLARRIRGRGLKI 139
AAN39284.1        MPKDIQLARRIRGERA--- 136
                    *****.
```