

A.

```

      10      20      30      40      50      60      70      80      90     100
Ov496 SEDFERQLAYYATTWTSKDILEVLAMMPGNRAQKELIQGKLNEEAERWRRNPPQAGGGLTVDQIMGVGTNQAAAQANMDQARQICLQWVISALRAVR
Seq 1 .....
Seq 2 .....T.....
Seq 3 .....I.....

      110     120     130     140     150     160     170     180     190     200
Ov496 HMAHRPGNPLVKQKSNEPYEDFAARLLEAIDAEPVTQPIKEYLKLTLSTYNASSDCQKQMDRVLGQRVQQASVEEKMQACRDVGSEGFKMQLLAQALRP
Seq 1 .....
Seq 2 .....N.....
Seq 3 .....

      210     220     230     240     250     260
Ov496 ERKKGIGPAQRCYNCGKPGHRARQCRQGIICHNCGKRGHMOKDCRGKKTGMQSGNGRRGL
Seq 1 ...E.....V.....
Seq 2 ...E.....
Seq 3 ...E.....
```

B.

```

      10      20      30      40      50      60      70      80      90     100
697   SEDFERQLAYYATTWTSKDILEVLAMMPGNRAQKELIQGKLNEEAERWVRQNPVLTVDQIMGVGTNQQASQANMDQARQICLQWVINALRSVRHM
Seq 1 .....
Seq 2 .....-.....
Seq 3 .....

      110     120     130     140     150     160     170     180     190     200
697   SHRPGNPLVKQKNNESYEDFIARLLEAIDAEPVADPIKTYLKVTLSTYNASTDCQKQMDRVLGTRVQQATVEEKMQACRDVGSEGFKMQLLAQALRPER
Seq 1 .....T.....
Seq 2 .....T.....
Seq 3 .....T.....

      210     220     230     240     250
697   KARNQEIGQKCYNCGKPGHLARQCRQGIICHHCGKRGHMOKDCRQKK-QQGNTKRGF
Seq 1 .....K....NG...
Seq 2 .....K....NG...
Seq 3 .....K....NG...
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