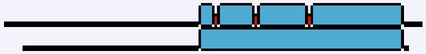
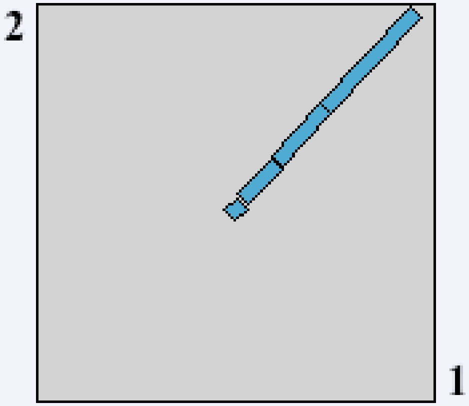
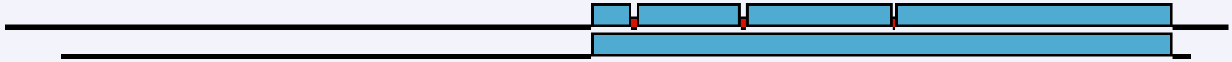
Sequence 1: lcl|1_seq_1
Length = 259 (1 .. 259)

Sequence 2: lcl|2_seq_2
Length = 244 (1 .. 244)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
 Score =  126 bits (317),  Expect = 1e-27
 Identities = 69/125 (55%), Positives = 84/125 (67%), Gaps = 5/125 (4%)

Query  128  GSEVAYKP--RRGSADGEWIQCEVLKVVADGT--RFEVRDPEPDELGNSGKVYKCNRKEL  183
            G  VA+K    R +  G+WIQC ++KV  +G   RFEV+DPEPD+ GN+G++YK     L
Sbjct  116  GMSVAFKLPYTRHNEGGDWIQCIIIKVTGEGAKQRFEVQDPEPDDDGNAGQIYKTTANHL  175

Query  184  LLIPP-GFPTKNYPPGTKVLARYPETTTFYPAIVIGTKRDGTCRLRFDGEEEVDKETEVT  242
            + IP  G P     P T VLARYPETTTFY A VI T  DG+C+LRF+GEEEV KET V
Sbjct  176  IQIPAKGTPLPPISPKTNVLARYPETTTFYRAEVIRTLPDGSCKLRFEGEEEVGKETVVE  235

Query  243  RRLVL  247
            R LVL
Sbjct  236  RHLVL  240
```