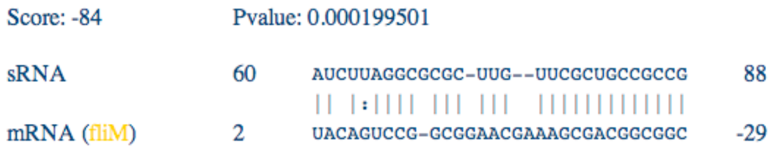
Proposed alignment from TargetRNA analysis of *sra* genes interactions (e < 10^{-3})

➡ *sra32 targets*

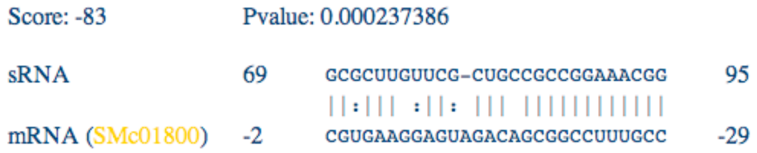
1- fliM : Flagellar motor switch transmembrane protein



```
Score: -84               Pvalue: 0.000199501

sRNA                     60      AUCUUAGGCGCGC-UUG--UUCGCUGCCGCCG      88
                                 || |:|||| ||| |||  |||||||||||||
mRNA (fliM)              2       UACAGUCCG-GCGGAACGAAAGCGACGGCGGC      -29
```

2- SMc01800 = transmembrane cytochrome C oxidase



```
Score: -83               Pvalue: 0.000237386

sRNA                     69      GCGCUUGUUCG-CUGCCGCCGGAAACGG      95
                                 ||:||| :||: ||| ||||||||||||
mRNA (SMc01800)          -2      CGUGAAGGAGUAGACAGCGGCCUUUGCC      -29
```

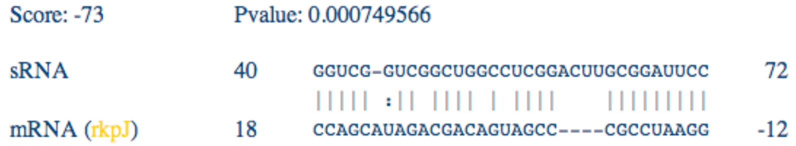
➡ *sra33 targets*

1- SMc00899 = hypothetical protein

```
Score: -78               Pvalue: 0.000301856

sRNA                     2       CCAUGAUGCUCAGGUCCGCCGCAU-CU-CCUGGGUCGUGGGGUCGGUC      47
                                 || ||||||||||  ||: |: || || ||||| || ||   |||:||
mRNA (SMc00899)          19      GGAACUACGAGUCGCGGUAGUCUACGAAGGACCAAGGAC---AGCUAG      -26
```

2- rkpJ = capsular polysaccharide biosynthesis/export protein

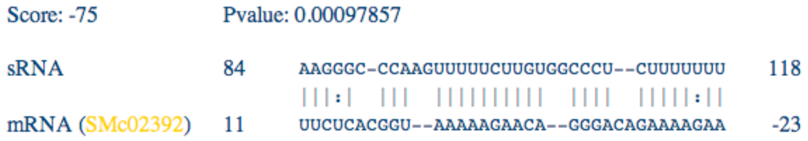


```
Score: -73               Pvalue: 0.000749566

sRNA                     40      GGUCG-GUCGGCUGGCCUCGGACUUGCGGAUUCC      72
                                 ||||| :|| |||| | ||||    |||||||||
mRNA (rkpJ)              18      CCAGCAUAGACGACAGUAGCC----CGCCUAAGG      -12
```

➡ *sra41 copie 1 target*

1- SMc02392 = hypothetical protein



```
Score: -75               Pvalue: 0.00097857

sRNA                     84      AAGGGC-CCAAGUUUUUCUUGUGGCCCU--CUUUUUUU      118
                                 |||:|  |||  ||||||||||  ||||  |||||:||
mRNA (SMc02392)          11      UUCUCACGGU--AAAAAGAACA--GGGACAGAAAAGAA      -23
```

➡ *sra41 copie 2 target*

1- SMc00317 = hypothetical protein

```
1        SMc00317 hypothetical protein

Score: -80               Pvalue: 0.000214469

sRNA                     23      CUCCCCAGCCGCUGCAGCAGCUGUUCC      49
                                 |||||  |||||||||| |||  ||||
mRNA (SMc00317)          -4      GAGGGAGCGGCGACGUCUUCGCGAAGG      -30
```

1- SMc01118 = hypothetical protein

```
2        SMc01118 hypothetical protein

Score: -76               Pvalue: 0.000443528

sRNA                     5       GCAUCU-AGCGGCUUUCUCCUCCCCAGCCGCUGC      37
                                 |||| | ||| ||  |||||||||| ||  ||||
mRNA (SMc01118)          4       CGUAAAGUCGGCGCCAGAGGAGGGGACGCGGACG      -30
```

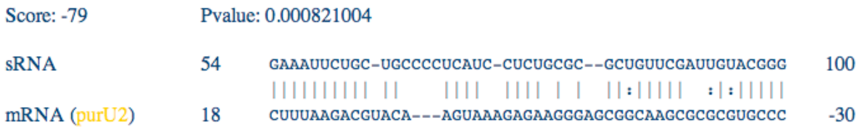
➡ *sra12b targets*

1- SMc03123 = hypothetical transcriptional regulatory protein

```
Score: -91            Pvalue: 0.000110731

sRNA             50   AUCAGAAAUUCUGCUGCCCC-U-CAUCCUC--UGCG-CGCUGUUCGAUUGU   95
                      |||||   |||||||||||| | ||:||:|  |||: |||||: || :|||
mRNA (SMc03123)  20   UAGUCA--AAGACGACGGGGUACGUGGGGGGGACGUUGCGACGCGCAGACA  -29
```

2- purU2 = formyltetrahydrofolate deformylase

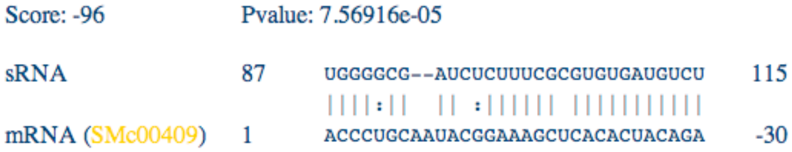


```
Score: -79          Pvalue: 0.000821004

sRNA           54   GAAAUUCUGC-UGCCCCUCAUC-CUCUGCGC--GCUGUUCGAUUGUACGGG   100
                    |||||||||| ||    ||||  |||| | |  ||:|||||  :|:|||||
mRNA (purU2)   18   CUUUAAGACGUACA---AGUAAAGAGAAGGGAGCGGCAAGCGCGCGUGCCC   -30
```

➡ *sra34 targets*

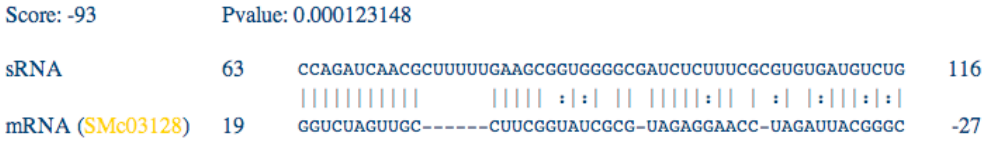
1- SMc00409 = hypothetical signal peptide protein



```
Score: -96            Pvalue: 7.56916e-05

sRNA             87   UGGGGCG--AUCUCUUUCGCGUGUGAUGUCU   115
                      ||||:||  || :|||||| |||||||||||
mRNA (SMc00409)  1    ACCCUGCAAUACGGAAAGCUCACACUACAGA   -30
```

2- SMc03128 = transport system permease ABC transporter protein



```
Score: -93            Pvalue: 0.000123148

sRNA             63   CCAGAUCAACGCUUUUUGAAGCGGUGGGGCGAUCUCUUUCGCGUGUGAUGUCUG   116
                      |||||||||||      ||||| :|:| || |||||:|| | :| |:|||:|:|
mRNA (SMc03128)  19   GGUCUAGUUGC------CUUCGGUAUCGCG-UAGAGGAACC-UAGAUUACGGGC   -27
```

➡ *sra66 targets*

1- tolR = putative transport transmembrane protein

```
Score: -84            Pvalue: 0.000756567

sRNA            172   GCUAAAUGCACAUACCCCUCCAUGCUUGG---CCGUGCUUUCUGGGCG   216
                      ||:|| ||| ||||||| || | || |||   |||||||||  || ||
mRNA (tolR)      18   CGGUUGACG-GUAUGGGUAG-U-CGCACCAGAGGCACGAAACUCCAGC   -27
```