IntaRNA 2.0 - enhanced and customizable prediction of RNA-RNA interactions
- Supplementary material -

Martin Mann¹, Patrick R. Wright¹, Rolf Backofen¹,²,*

¹Bioinformatics, Computer Science, University of Freiburg, Georges-Koehler-Allee 106, 79110 Freiburg, Germany and
²Centre for Biological Signalling Studies (BIOSS), University of Freiburg, Schaenzlestr. 18, 79104 Freiburg, Germany

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1 Energy computation details

An RNA molecule consisting of \( n \) nucleotides is described by its sequence of bases encoded by \( S \in \{A,C,G,U\}^n \) indexed from 5’ to 3’ end.

For a given pair of two RNAs \( S^1, S^2 \), we will denote with \( E^{\text{hybrid}}_{i..k} \) the minimal energy of any interaction of the subsequences \( S^1_{i..k} \) and \( S^2_{l..j} \) under the additional condition that the subsequence ends form each a base pair, i.e. \((S^1_i, S^2_j)\) and \((S^1_k, S^2_l)\) are Watson-Crick or G-U base pairs. This energy term also includes the RNA-RNA interaction initiation energy penalty as well as closing base pair penalties (if the final base pairs are not G-C).

The energy penalty \( ED^1[i,k] \) to make the subsequence \( S^1_{i..k} \) accessible is given by

\[
ED^1[i,k] = -RT \cdot \log(Pr^u[i..k]),
\]

where \( Pr^u[i..k] \) denotes the unpaired probability for subsequence \( S^1_{i..k} \) (e.g. computed via McCaskill’s algorithm [1]), \( R \) the gas constant and \( T \) the temperature of the system. \( ED^2 \) is defined analogously.

For an interaction with left/right-most base pairs \((S^1_i, S^2_j)/(S^1_k, S^2_l)\), resp., and an hybridization energy given by \( E^{\text{hybrid}} \), the overall interaction energy in \textsc{IntaRNA}v1 is defined by

\[
E_{i..k}^{v1} = E^{\text{hybrid}}_{i..k} + \begin{cases} 
ED^1[i-1,k] + E^{\text{dangle}}_{S^1_{i-1}} + E^{\text{dangle}}_{S^1_{k+1}} & \text{both ends free} \\
ED^1[i-1,k] + E^{\text{dangle}}_{S^1_{i-1}} & \text{5’-end free} \\
ED^1[i,k] + E^{\text{dangle}}_{S^1_{k+1}} & \text{3’-end free} \\
ED^1[i,k] & \text{no end free}
\end{cases}
\]

\[
+ \min \{ \text{dangling end cases for } S^2 \text{ and interval } j..l \}. \tag{2}
\]

Here, all possibilities of free ends and according dangling end contributions \( E^{\text{dangle}}[..] \) are considered while the ED penalty is extended to cover the free end positions as well.

The new \textsc{IntaRNA}v2 dangling end treatment always takes free dangling end contributions into account by weighting them with according conditional probabilities \( Pr^u \) that the position is unpaired given that the interaction site is accessible, i.e. not involved in intramolecular base pairs. For instance, the 5’-dangling-end probability for the first sequence (position \( S^1_{i-1} \)), is given by

\[
Pr^u[i-1 | i..k] = \frac{Pr^u[(i-1)..k]}{Pr^u[i..k]} = \frac{\exp(-ED^1[i-1,k]/RT)}{\exp(-ED^1[i,k]/RT)} = \frac{\exp((ED^1[i,k] - ED^1[i-1,k])/RT)}{\exp(-ED^1[i,k]/RT)} \tag{3}
\]

using the \( ED^1 \) values for \( S^1 \) given Eq. 1.

Given these probabilities, \textsc{IntaRNA}v2 computes the overall interaction energy using

\[
E_{i..k}^{v2} = E^{\text{hybrid}}_{i..k} + ED^1[i,k] + \begin{cases} 
Pr^u[i-1 | i..k] \cdot E^{\text{dangle}}_{S^1_{i-1}} + Pr^u[k+1 | i..k] \cdot E^{\text{dangle}}_{S^1_{k+1}} & \text{both ends free} \\
Pr^u[i-1 | i..k] \cdot E^{\text{dangle}}_{S^1_{i-1}} & \text{5’-end free} \\
Pr^u[k+1 | i..k] \cdot E^{\text{dangle}}_{S^1_{k+1}} & \text{3’-end free} \\
Pr^u[i,k] & \text{no end free}
\end{cases}
\]

\[
+ \begin{cases} 
ED^2[j,l] & \text{no end free} \\
Pr^u[j-1 | j..l] \cdot E^{\text{dangle}}_{S^2_{j-1}} + Pr^u[l+1 | j..l] \cdot E^{\text{dangle}}_{S^2_{l+1}} & \text{both ends free} \\
Pr^u[j-1 | j..l] \cdot E^{\text{dangle}}_{S^2_{j-1}} & \text{5’-end free} \\
Pr^u[l+1 | j..l] \cdot E^{\text{dangle}}_{S^2_{l+1}} & \text{3’-end free}
\end{cases} \tag{4}
\]
2 Minimal energy profiles of Spot42-sthA interactions

Spot42 is known to interact with its targets via three conserved accessible regions I (positions 1-10), II (20-37), and III (47-60) [2, 3] that are depicted in Figure 1. It has been shown that mainly sites I and III are important for the interaction with the target mRNA encoded by the sthA gene. The mutated sequences in Figure 1 (mutation in capital red letters) were employed in the original study [3].

Mutating sites I and III has been reported to show the highest effect while the mutation of region II exhibited only minor effects. Figure 2 shows the according minimal energy profiles for the Spot42 wildtype and all three mutants. The individual mutations on their own do not completely break the regulation of sthA by Spot42 [3], which suggests additive effects of regions I and III.

![Minimal energy profile for all intermolecular index pairs covered by any predicted interaction of Spot42 and the sthA mRNA (with E<0) for different sequence variants of Spot42. Conserved accessible regions I, II and III of Spot42 known to interact with target RNAs are tagged on the right.](image)

While the mutation of region II shows (as experimentally shown) no significant effect (only a minor minimal energy increase for sites I and III of 0.5 kcal/mol), mutating region I or III breaks the respective predicted interaction site completely. On the other hand the non-mutated site stays intact and may be responsible for the remaining partial regulation of sthA by the mutant [3].
3 Supplementary Table 1

The following table contains the results for the benchmark. The first, second and third columns specify the sRNA name, locus tag and name of the target, respectively. The fourth column indicates the rank produced by an IntaRNA v1 whole genome target prediction (arguments \texttt{-p 7 -w 150 -L 100}). The fifth column shows the rank produced by an IntaRNA v2 whole genome target prediction with standard parameters (arguments \texttt{--seedBP 7 --tAccW 150 --tAccL 100 --qAccW 0 --qAccL 0}) and the sixth column shows the rank for IntaRNA v2 whole genome target predictions which enforce a seed energy $\leq -4.8$ kcal/mol (additional argument \texttt{--seedMaxE=-4.8}). Rank '-' indicates that no prediction could be made for a specific sRNA-target pair. The last column contains the references to the articles reporting the RNA pairs.

| sRNA | tar locus tag | tar name | v1  | v2  | v2 seed $\leq -4.8$ | reference |
|------|--------------|----------|-----|-----|---------------------|----------|
| ArcZ | STM1682      | tpx      | 1678| 1995| 1191                | [5]      |
| ArcZ | STM2970      | slaC     | 4433| 4420| -                   | [5]      |
| ArcZ | STM3216      | -        | 3616| 3662| -                   | [5]      |
| ArcZ | b1892        | fhlB     | 2322| 2525| 1726                | [6]      |
| ArcZ | b2741        | rpoS     | 192 | 423 | 256                 | [7]      |
| ArcZ | b3546        | eptB     | 2322| 2525| 1726                | [6]      |
| ChiX | STM0687      | yblM/chiP| 8   | 8   | 6                   | [9]      |
| ChiX | STM1313      | cedB     | 4   | 4   | 3                   | [9]      |
| ChiX | b16010       | dlpB/citA| 4   | 4   | 4                   | [10]     |
| ChiX | b0081        | chiP     | 3   | 3   | 3                   | [11]     |
| ChiX | b1737        | chiC     | 2   | 2   | 2                   | [12]     |
| CyaR | STM0833      | ompX     | 129 | 83  | 59                  | [13]     |
| CyaR | b0723        | sdiA     | 243 | 376 | 260                 | [14]     |
| CyaR | b0814        | ompX     | 118 | 70  | 58                  | [15]     |
| CyaR | b1740        | nadE     | 2332| 1813| -                   | [15]     |
| CyaR | b1824        | yobF     | 60  | 54  | 46                  | [14]     |
| CyaR | b2416        | ptsI     | 77  | 53  | 45                  | [14]     |
| CyaR | b3666        | yqaE     | 405 | 661 | 448                 | [15]     |
| CyaR | b2687        | luxS     | 690 | 556 | 379                 | [15]     |
| DsrA | b1237        | hns      | 14  | 8   | 2                   | [16]     |
| DsrA | b2741        | rpoS     | 1   | 1   | -                   | [16]     |
| DsrA | b3521        | mreB     | 1786| 1683| -                   | [17]     |
| FrmS | b0723        | sdiA     | 31  | 30  | 543                 | [18]     |
| FrmS | STM0777      | gmuA     | 1875| 1852| 1059                | [18]     |
| FrmS | b0887        | cydD     | 318 | 315 | 174                 | [19]     |
| FrmS | b1107        | nagZ     | 427 | 395 | -                   | [14]     |
| FrmS | b1479        | maeA     | 330 | 329 | 2341                | [18]     |
| FrmS | b1531        | marA     | 54  | 96  | -                   | [14]     |
| FrmS | b1656        | sodB     | 667 | 118 | 64                  | [19]     |
| FrmS | b1811        | yobA     | 5   | 5   | 5                   | [19]     |
| FrmS | b3215        | folE     | 312 | 539 | 284                 | [18]     |
| FrmS | b3240        | folX     | 367 | 515 | 271                 | [18]     |
| FrmS | b3631        | iscR     | 1   | 1   | 1                   | [14]     |
| FrmS | b3629        | metE     | 211 | 61  | 37                  | [19]     |
| FrmS | b3608        | sodA     | 770 | 1095| 591                 | [19]     |
| GevB | STM0002      | thrA     | 168 | 83  | 47                  | [20]     |
| GevB | STM0245      | metQ     | 620 | 367 | 562                 | [20]     |
| GevB | STM0399      | brntQ    | 17  | 55  | 171                 | [20]     |
| GevB | STM0862      | yblH     | 373 | 227 | 125                 | [20]     |
| GevB | STM0665      | gflI     | 109 | 131 | 100                 | [21]     |
| GevB | STM0699      | lrp      | 165 | 368 | 194                 | [20]     |
| GevB | STM1299      | gdhA     | 116 | 110 | 1824                | [21]     |
| GevB | STM1452      | tppB     | 819 | 924 | 457                 | [20]     |
| GevB | STM1746.8    | oppA     | 147 | 130 | 1187                | [21]     |
| GevB | STM2355      | argT     | 35  | 18  | 330                 | [21]     |
| GevB | STM2356      | ndk      | 35  | 78  | 2360                | [20]     |
| GevB | STM3062      | serA     | 119 | 177 | 131                 | [20]     |
| GevB | STM3064      | ictA     | 209 | 61  | 35                  | [20]     |
| GevB | STM3225      | yglU/stT | 459 | 447 | 232                 | [20]     |
| GevB | STM3564      | livK     | 47  | 133 | 80                  | [21]     |
| Gene   | STM        | Description |
|--------|------------|-------------|
| GevB   | STM3567    | livJ        |
| GevB   | STM3630    | dppA        |
| GevB   | STM3903    | ilvE        |
| GevB   | STM3999    | yilC        |
| GevB   | STM4351    | yifK        |
| GevB   | STM4398    | cycA        |
| GevB   | b1404      | csgD        |
| GevB   | b1130      | phoP        |
| GevB   | b3089      | sstT        |
| GevB   | b4208      | cycA        |
| GimZ   | b3729      | glmS        |
| MicA   | STM4231    | lasB        |
| MicA   | b0411      | tex         |
| MicA   | b0814      | ompX        |
| MicA   | b0957      | ompA        |
| MicA   | b1130      | phoP        |
| MicC   | STM1572    | ompD        |
| MicC   | b2215      | ompC        |
| MicF   | STM3066    | yahO        |
| MicF   | STM3095    | lrp         |
| MicF   | STM3248    | lprR        |
| MicF   | b0921      | phoE        |
| MicF   | b0889      | lrp         |
| MicF   | b0929      | ompF        |
| MicF   | b3912      | cpxR        |
| OmrA   | b0565      | ompF        |
| OmrA   | b1040      | csgD        |
| OmrA   | b1130      | flhD        |
| OmrA   | b2155      | cirA        |
| OmrA   | b3405      | ompR        |
| OmrB   | b0565      | ompF        |
| OmrB   | b1040      | csgD        |
| OmrB   | b1892      | flhD        |
| OmrB   | b2155      | cirA        |
| OmrB   | b3405      | ompR        |
| OxyS   | b0892      | flhD        |
| OxyS   | b2731      | flhA        |
| RprA   | b1040      | csgD        |
| RprA   | b1441      | ydaM        |
| RprA   | b2741      | rpoS        |
| RpyB   | STM0413    | tex         |
| RpyB   | STM0687    | yhiM/chiP   |
| RpyB   | STM0999    | ompF        |
| RpyB   | STM1070    | ompA        |
| RpyB   | STM1473    | ompN        |
| RpyB   | STM1530    | -           |
| RpyB   | STM1572    | ompD        |
| RpyB   | STM1732    | ompW        |
| RpyB   | STM1995    | ompS        |
| RpyB   | STM2207    | ompC        |
| RpyB   | STM2391    | faeL        |
| RpyB   | b0081      | mraZ        |
| RpyB   | b0721      | sdhC        |
| RpyB   | b0805      | fur         |
| RpyB   | b1256      | ompW        |
| RpyB   | b2215      | ompC        |
| RpyB   | b2394      | riuD        |
| RpyB   | b2518      | achB        |
| RpyB   | b2519      | csgD        |
| RpyB   | b3088      | ykgJ        |
| RpyB   | b0592      | fepB        |
| RpyB   | b0883      | fur         |
| RpyB   | b0721      | sdhC        |
| RpyB   | b0723      | sdhA        |
| Gene   | Start | End   | Length |
|--------|-------|-------|--------|
| RyhB   | 60894 | 60894 | 7      |
| RyhB   | 61107 | 61107 | 9      |
| RyhB   | 61200 | 61200 | 49     |
| RyhB   | 61352 | 61352 | 14     |
| RyhB   | 61531 | 61531 | 101    |
| RyhB   | 61658 | 61658 | 280    |
| RyhB   | 61659 | 61659 | 439    |
| RyhB   | 61778 | 61778 | 152    |
| RyhB   | 61981 | 61981 | 54     |
| RyhB   | 62069 | 62069 | 49     |
| RyhB   | 62155 | 62155 | 87     |
| RyhB   | 62200 | 62200 | 108    |
| RyhB   | 62530 | 62530 | 130    |
| RyhB   | 63365 | 63365 | 34     |
| RyhB   | 63607 | 63607 | 45     |
| RyhB   | 63942 | 63942 | 49     |
| RyhB   | 64070 | 64070 | 360    |
| RyhB   | 64122 | 64122 | 129    |
| SgrS   | STM2945|STM2945|1287    |
| SgrS   | STM2962|STM2962|95      |
| SgrS   | b1101  | b1101  | 7      |
| SgrS   | b1517  | b1517  | 1531   |
| SgrS   | b2416  | b2416  | 73     |
| Spec42 | STM2190 |STM2190|97      |
| Spec42 | b0039  | b0039  | 16      |
| Spec42 | b0720  | b0720  | 179    |
| Spec42 | b0721  | b0721  | 44     |
| Spec42 | b0728  | b0728  | 203    |
| Spec42 | b0757  | b0757  | 4      |
| Spec42 | b1136  | b1136  | 50     |
| Spec42 | b1302  | b1302  | 4      |
| Spec42 | b1398  | b1398  | 10     |
| Spec42 | b1761  | b1761  | 49     |
| Spec42 | b1901  | b1901  | 134    |
| Spec42 | b2221  | b2221  | 166    |
| Spec42 | b2702  | b2702  | 45     |
| Spec42 | b2715  | b2715  | 135    |
| Spec42 | b2801  | b2801  | 29     |
| Spec42 | b2802  | b2802  | 1634   |
| Spec42 | b3224  | b3224  | 6      |
| Spec42 | b3365  | b3365  | 46     |
| Spec42 | b3607  | b3607  | 83     |
| Spec42 | b3942  | b3942  | 882    |
| Spec42 | b4070  | b4070  | 214    |
| Spec42 | b4122  | b4122  | 241    |
| Spec42 | b4311  | b4311  | 51     |
| Spot42| STM2190 |STM2190|97      |
| Spot42| b0720  | b0720  | 179    |
| Spot42| b0721  | b0721  | 44     |
| Spot42| b0728  | b0728  | 203    |
| Spot42| b0757  | b0757  | 4      |
| Spot42| b1136  | b1136  | 50     |
| Spot42| b1302  | b1302  | 4      |
| Spot42| b1398  | b1398  | 10     |
| Spot42| b1761  | b1761  | 49     |
| Spot42| b1901  | b1901  | 134    |
| Spot42| b2221  | b2221  | 166    |
| Spot42| b2702  | b2702  | 45     |
| Spot42| b2715  | b2715  | 135    |
| Spot42| b2801  | b2801  | 29     |
| Spot42| b2802  | b2802  | 1634   |
| Spot42| b3224  | b3224  | 6      |
| Spot42| b3365  | b3365  | 46     |
| Spot42| b3607  | b3607  | 83     |
| Spot42| b3942  | b3942  | 882    |
| Spot42| b4070  | b4070  | 214    |
| Spot42| b4122  | b4122  | 241    |
| Spot42| b4311  | b4311  | 51     |
| Spot42| STM2190 |STM2190|97      |
| Spot42| b0720  | b0720  | 179    |
| Spot42| b0721  | b0721  | 44     |
| Spot42| b0728  | b0728  | 203    |
| Spot42| b0757  | b0757  | 4      |
| Spot42| b1136  | b1136  | 50     |
| Spot42| b1302  | b1302  | 4      |
| Spot42| b1398  | b1398  | 10     |
| Spot42| b1761  | b1761  | 49     |
| Spot42| b1901  | b1901  | 134    |
| Spot42| b2221  | b2221  | 166    |
| Spot42| b2702  | b2702  | 45     |
| Spot42| b2715  | b2715  | 135    |
| Spot42| b2801  | b2801  | 29     |
| Spot42| b2802  | b2802  | 1634   |
| Spot42| b3224  | b3224  | 6      |
| Spot42| b3365  | b3365  | 46     |
| Spot42| b3607  | b3607  | 83     |
| Spot42| b3942  | b3942  | 882    |
| Spot42| b4070  | b4070  | 214    |
| Spot42| b4122  | b4122  | 241    |
| Spot42| b4311  | b4311  | 51     |
4 Supplementary FASTA

> ArcZ
  gugcggccccaaacagugcuagcggccccuuauacucauauauuuacggcagcggcaccacauuauuuc
cuccgggugcagcggcagcggcaccacggcagcggcagcggcaccacggcagcggcagcggcaccacggcagu
awggccauauuauu
> CyaX
  gugacuauacacacuauauacucucucucuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuu}
5 Target sequence generation

Input: The target sequences that were used for the benchmark can be generated by performing a whole genome target prediction using the IntaRNA webserver interface. For this, "Get target RNA sequences from NCBI Genome" should be selected on the input page. Then, any FASTA file can be pasted into the query area. Next, either NC_000913 or NC_003197 need to be specified in the "Target NCBI RefSeq ID" field. NC_000913 retrieves the sequences for *Escherichia coli* and NC_003197 does the same for *Salmonella*. In the last input step, "nt up" needs to be set to 200, "nt down" needs to be set to 100 and the job can be started.

Output: On the result page "Show Input Parameters" can be selected. Here, "Target RNA (long) in FASTA" shows a link to a FASTA file with the target sequences of interest.
References

[1] J. S. McCaskill. The equilibrium partition function and base pair binding probabilities for RNA secondary structure. *Biopolymers*, 29(6-7):1105–19, 1990. [PubMed:1695107] [doi:10.1002/bip.360290621].

[2] Thorleif Møller, Thomas Franch, Christina Udesen, Kenn Gerdes, and Poul Valentin-Hansen. Spot 42 RNA mediates discoordinate expression of the *E. coli* galactose operon. *Genes Dev*, 16(13):1696–706, 2002. [PubMed:12101127] [doi:10.1101/gad.231702].

[3] Chase L. Beisel and Gisela Storz. The base-pairing RNA Spot 42 participates in a multioutput feedforward loop to help enact catabolite repression in *Escherichia coli*. *Mol Cell*, 41(3):286–97, 2011. [PubMed:21292161] [doi:10.1016/j.molcel.2010.12.027].

[4] Patrick R. Wright. *Predicting small RNA targets in prokaryotes - a challenge beyond the barriers of thermodynamic models*. PhD thesis, Albert-Ludwigs-University Freiburg, December 2016.

[5] Kai Papenfort, Nelly Said, Tim Welsink, Sacha Lucchini, Jay C. D. Hinton, and Jorg Vogel. Specific and pleiotropic patterns of mRNA regulation by ArcZ, a conserved, Hfq-dependent small RNA. *Mol Microbiol*, 74(1):139–58, 2009. [PubMed:19732340] [doi:10.1111/j.1365-2958.2009.06857.x].

[6] Nicholas De Lay and Susan Gottesman. A complex network of small non-coding RNAs regulate motility in *Escherichia coli*. *Mol Microbiol*, 86(3):524–38, 2012. [PubMed:22925049] [doi:10.1111/j.1365-2958.2012.08209.x].

[7] Pierre Mandin and Susan Gottesman. Integrating anaerobic/aerobic sensing and the general stress response through the ArcZ small RNA. *EMBO J*, 29(18):3094–107, 2010. [PubMed:20683441] [PubMed Central:PMC2944060] [doi:10.1038/emboj.2010.179].

[8] Kyung Moon, David A. Six, Hyun-Jung Lee, Christian R. H. Raetz, and Susan Gottesman. Complex transcriptional and post-transcriptional regulation of an enzyme for lipopolysaccharide modification. *Mol Microbiol*, 89(1):52–64, 2013. [PubMed:23659637] [PubMed Central:PMC3765083] [doi:10.1111/mmi.12257].

[9] Nara Figueroa-Bossi, Martina Valentini, Laurette Malleret, Francesca Fiorini, and Lionello Bossi. Caught at its own game: regulatory small RNA inactivated by an inducible transcript mimicking its target. *Genes Dev*, 23(17):2004–15, 2009. [PubMed:19638370] [PubMed Central:PMC2751969] [doi:10.1101/gad.541609].

[10] Pierre Mandin and Susan Gottesman. A genetic approach for finding small RNAs regulators of genes of interest identifies RybC as regulating the DpiA/DpiB two-component system. *Mol Microbiol*, 72(3):551–65, 2009. [PubMed:19426207] [PubMed Central:PMC2714224] [doi:10.1111/j.1365-2958.2009.06665.x].

[11] Anders Aamann Rasmussen, Jesper Johansen, Jesper S. Nielsen, Martin Overgaard, Birgitte Kallipolitis, and Poul Valentin-Hansen. A conserved small RNA promotes silencing of the outer membrane protein YfbM. *Mol Microbiol*, 72(3):566–77, 2009. [PubMed:19400782] [doi:10.1111/j.1365-2958.2009.06688.x].

[12] Martin Overgaard, Jesper Johansen, Jakob Møller-Jensen, and Poul Valentin-Hansen. Switching off small RNA regulation with trap-mRNA. *Mol Microbiol*, 73(5):790–800, 2009. [PubMed:19682266] [doi:10.1111/j.1365-2958.2009.06807.x].

[13] Kai Papenfort, Verena Pfeiffer, Sacha Lucchini, Avinash Sonawane, Jay C. D. Hinton, and Jorg Vogel. Systematic deletion of *Salmonella* small RNA genes identifies CyaR, a conserved CRP-dependent riboregulator of OmpX synthesis. *Mol Microbiol*, 68(4):890–906, 2008. [PubMed:18399940] [doi:10.1111/j.1365-2958.2008.06189.x].
[14] Patrick R. Wright, Andreas S. Richter, Kai Papenfort, Martin Mann, Jorg Vogel, Wolfgang R. Hess, Rolf Backofen, and Jens Georg. Comparative genomics boosts target prediction for bacterial small RNAs. *Proc Natl Acad Sci USA*, 110(37):E3487–96, 2013. [PubMed:23980183] [PubMed Central:PMC3773804] [doi:10.1073/pnas.1305248110].

[15] Nicholas De Lay and Susan Gottesman. The Crp-activated small noncoding regulatory RNA CyaR (RyeE) links nutritional status to group behavior. *J Bacteriol*, 191(2):461–76, 2009. [PubMed:18978044] [PubMed Central:PMC2620814] [doi:10.1128/JB.01157-08].

[16] R. A. Lease, M. E. Cusick, and M. Belfort. Riboregulation in *Escherichia coli*: DsrA RNA acts by RNA:RNA interactions at multiple loci. *Proc Natl Acad Sci USA*, 95(21):12456–61, 1998. [PubMed:9770507].

[17] Bastien Cayrol, Emilie Fortas, Claire Martret, Grzegorz Cech, Anna Kloska, Stephane Caulet, Marion Barbet, Sylvain Trepont, Sergio Marco, Aziz Taghbalout, Florent Busi, Grzegorz Wegrzyń, and Veronique Arluison. Riboregulation of the bacterial actin-homolog MreB by DsrA small noncoding RNA. *Integr Biol (Camb)*, 7(1):128–41, 2015. [PubMed:25407044] [doi:10.1039/c4ib00102h].

[18] Sylvain Durand and Gisela Storz. Reprogramming of anaerobic metabolism by the FnrS small RNA. *Mol Microbiol*, 75(5):1215–31, 2010. [PubMed:20075074] [PubMed Central:PMC2941437] [doi:10.1111/j.1365-2958.2010.07044.x].

[19] Anders Boysen, Jakob Moller-Jensen, Birgitte Kallipolitis, Poul Valentin-Hansen, and Martin Overgaard. Translational regulation of gene expression by an anaerobically induced small non-coding RNA in *Escherichia coli*. *Journal of Biological Chemistry*, 285(14):10690–702, 2010. [PubMed:20075074] [PubMed Central:PMC2856277] [doi:10.1074/jbc.M109.089755].

[20] Cynthia M. Sharma, Kai Papenfort, Sandy R. Pernitzsch, Hans-Joachim Mollenkopf, Jay C. D. Hinton, and Jorg Vogel. Pervasive post-transcriptional control of genes involved in amino acid metabolism by the Hfq-dependent GcvB small RNA. *Mol Microbiol*, 81(5):1144–65, 2011. [PubMed:21696468] [doi:10.1111/j.1365-2958.2011.07751.x].

[21] Cynthia M. Sharma, Fabien Darfeuille, Titia H. Plantinga, and Jorg Vogel. A small RNA regulates multiple ABC transporter mRNAs by targeting C/A-rich elements inside and upstream of ribosome-binding sites. *Genes Dev*, 21(21):2804–17, 2007. [PubMed:17974919] [PubMed Central:PMC2045133] [doi:10.1101/gad.447207].

[22] Qi Yang, Nara Figueroa-Bossi, and Lionello Bossi. Translation enhancing ACA motifs and their silencing by a bacterial small regulatory RNA. *PLoS Genet*, 10(1):e1004026, 2014. [PubMed:24391513] [PubMed Central:PMC3879156] [doi:10.1371/journal.pgen.1004026].

[23] Mikkel Girke Jorgensen, Jesper S. Nielsen, Anders Boysen, Thomas Franch, Jakob Moller-Jensen, and Poul Valentin-Hansen. Small regulatory RNAs control the multi-cellular adhesive lifestyle of *Escherichia coli*. *Mol Microbiol*, 84(1):36–50, 2012. [PubMed:22250746] [doi:10.1111/j.1365-2958.2012.07976.x].

[24] Audrey Coornaert, Claude Chiaruttini, Mathias Springer, and Maude Guillier. Post-transcriptional control of the *Escherichia coli* PhoQ-PhoP two-component system by multiple sRNAs involves a novel pairing region of GcvB. *PLoS Genet*, 9(1):e1003156, 2013. [PubMed:23300478] [PubMed Central:PMC3556696] [doi:10.1371/journal.pgen.1003156].

[25] Sarah C. Pulvermacher, Lorraine T. Stauffer, and George V. Stauffer. The small RNA GcvB regulates *sstT* mRNA expression in *Escherichia coli*. *J Bacteriol*, 191(1):238–48, 2009. [PubMed:18952787] [doi:10.1128/ JB.00915-08].

[26] Sarah C. Pulvermacher, Lorraine T. Stauffer, and George V. Stauffer. Role of the sRNA GcvB in regulation of *cycA* in *Escherichia coli*. *Microbiology*, 155(Pt 1):106–14, 2009. [PubMed:19118351] [doi:10.1099/mic.0.023508-0].
[27] Johannes H. Urban and Jörg Vogel. Two seemingly homologous noncoding RNAs act hierarchically to activate glmS mRNA translation. *PLoS Biol*, 6(3):e64, 2008. [PubMed:18351803] [doi:10.1371/journal.pbio.0060064].

[28] Lionello Bossi and Nara Figueroa-Bossi. A small RNA downregulates LamB maltoporin in *Salmonella*. *Mol Microbiol*, 65(3):799–810, 2007. [PubMed:17608792] [doi:10.1111/j.1365-2958.2007.05829.x].

[29] Emily B. Gogol, Virgil A. Rhodius, Kai Papenfort, Jorg Vogel, and Carol A. Gross. Small RNAs endow a transcriptional activator with essential repressor functions for single-tier control of a global stress regulon. *Proc Natl Acad Sci USA*, 108(31):12875–80, 2011. [PubMed:21768388] [PubMed Central:PMC3150882] [doi:10.1073/pnas.1109379108].

[30] Klas I. Udekwu, Fabien Darfeuille, Jorg Vogel, Johan Reimegård, Erik Holmqvist, and E. Gerhart H. Wagner. Hfq-dependent regulation of OmpA synthesis is mediated by an antisense RNA. *Genes Dev*, 19(19):2355–66, 2005. [PubMed:16204185] [PubMed Central:PMC1240044] [doi:10.1101/gad.354405].

[31] Audrey Coornaert, Alisa Lu, Pierre Mandin, Mathias Springer, Susan Gottesman, and Maude Guillier. MicA sRNA links the PhoP regulon to cell envelope stress. *Mol Microbiol*, 76(2):467–79, 2010. [PubMed:20345657] [PubMed Central:PMC2925231] [doi:10.1111/j.1365-2958.2010.07115.x].

[32] Verena Pfleiffer, Kai Papenfort, Sacha Lucchini, Jay C. D. Hinton, and Jorg Vogel. Coding sequence targeting by MicC RNA reveals bacterial mRNA silencing downstream of translational initiation. *Nat Struct Mol Biol*, 16(8):840–6, 2009. [PubMed:19620966] [doi:10.1038/nsmb.1631].

[33] Shuo Chen, Aixia Zhang, Lawrence B. Blyn, and Gisela Storz. MicC, a second small-RNA regulator of Omp protein expression in *Escherichia coli*. *J Bacteriol*, 186(20):6689–97, 2004. [PubMed:15466019] [doi:10.1128/JB.186.20.6689-6697.2004].

[34] Colin P. Corcoran, Dimitri Podkaminski, Kai Papenfort, Johannes H. Urban, Jay C. D. Hinton, and Jorg Vogel. Superfolder GFP reporters validate diverse new mRNA targets of the classic porin regulator, MicF RNA. *Mol Microbiol*, 84(3):428–45, 2012. [PubMed:22458297] [doi:10.1111/j.1365-2958.2012.08031.x].

[35] Erik Holmqvist, Cecilia Unoson, Johan Reimegard, and E. Gerhart H. Wagner. A mixed double negative feedback loop between the sRNA MicF and the global regulator Lrp. *Mol Microbiol*, 84(3):414–27, 2012. [PubMed:22234810] [doi:10.1111/j.1365-2958.2012.07994.x].

[36] T. Suzuki, C. Ueguchi, and T. Mizuno. H-NS regulates OmpF expression through micF antisense RNA in *Escherichia coli*. *J Bacteriol*, 178(12):3650–3, 1996. [PubMed:8655567] [PubMed Central:PMC178139].

[37] Maude Guillier and Susan Gottesman. The 5’ end of two redundant sRNAs is involved in the regulation of multiple targets, including their own regulator. *Nucleic Acids Res*, 36(21):6781–94, 2008. [PubMed:18953042] [PubMed Central:PMC2588501] [doi:10.1093/nar/gkn742].

[38] Erik Holmqvist, Johan Reimegård, Maaike Sterk, Nina Grantcharova, Ute Römling, and Eduard Gerhart Heinrich Wagner. Two antisense RNAs target the transcriptional regulator CsgD to inhibit curli synthesis. *EMBO J*, 29(11):1840–50, 2010. [PubMed:20407422] [PubMed Central:PMC2885931] [doi:10.1038/emboj.2010.73].

[39] S. Altuvia, A. Zhang, L. Argaman, A. Tiwari, and G. Storz. The *Escherichia coli* OxyS regulatory RNA represses flhA translation by blocking ribosome binding. *EMBO J*, 17(20):6069–75, 1998. [PubMed:9774350] [PubMed Central:PMC1170933] [doi:10.1093/emboj/17.20.6069].

[40] Franziska Miika, Susan Busse, Alexandra Possling, Janine Berkhof, Natalia Tschowri, Nicole Sommerfeldt, Mihaela Pruteanu, and Regine Hengge. Targeting of csgD by the small regulatory RNA RprA links stationary phase, biofilm formation and cell envelope stress in *Escherichia coli*. *Mol Microbiol*, 84(1):51–65, 2012. [PubMed:22356413] [PubMed Central:PMC3465796] [doi:10.1111/j.1365-2958.2012.08002.x].
[41] Nadim Majdalani, David Hernandez, and Susan Gottesman. Regulation and mode of action of the second small RNA activator of RpoS translation, RprA. *Mol Microbiol*, 46(3):813–26, 2002. [PubMed:12410838].

[42] Kai Papenfort, Marie Bouvier, Franziska Mika, Cynthia M. Sharma, and Jörg Vogel. Evidence for an autonomous 5’ target recognition domain in an Hfq-associated small RNA. *Proc Natl Acad Sci USA*, 107(17):20435–40, 2010. [PubMed:21059903] [PubMed Central:PMC2996696] [doi:10.1073/pnas.1009784107].

[43] Roberto Balbontín, Francesca Fiorini, Nara Figueroa-Bossi, Josep Casadesús, and Lionello Bossi. Recognition of heptameric seed sequence underlies multi-target regulation by RybB small RNA in *Salmonella enterica*. *Mol Microbiol*, 78(2):380–94, 2010. [PubMed:20979336].

[44] Marie Bouvier, Cynthia M. Sharma, Franziska Mika, Knud H. Nierhaus, and Jorg Vogel. Small RNA binding to 5’ mRNA coding region inhibits translational initiation. *Mol Cell*, 32(6):827–37, 2008. [PubMed:19111662] [doi:10.1016/j.molcel.2008.10.027].

[45] Patrick R. Wright. hlIntaRNA - Comparative prediction of sRNA targets in prokaryotes. Diplomarbeit, Albert Ludwigs University Freiburg, March 2012.

[46] Guillaume Desnoyers and Eric Masse. Noncanonical repression of translation initiation through small RNA recruitment of the RNA chaperone Hfq. *Genes Dev*, 26(7):726–39, 2012. [PubMed:22474262] [PubMed Central:PMC3323883] [doi:10.1101/gad.182493.111].

[47] Jesper Johansen, Anders Aamann Rasmussen, Martin Overgaard, and Poul Valentin-Hansen. Conserved small non-coding RNAs that belong to the sigmaE regulon: role in down-regulation of outer membrane proteins. J Mol Biol, 364(1):1–8, 2006. [PubMed:17007876] [doi:10.1016/j.jmb.2006.09.004].

[48] Julie-Anna M. Benjamin and Eric Masse. The iron-sensing aconitase B binds its own mRNA to prevent sRNA-induced mRNA cleavage. *Nucleic Acids Res*, 42(15):10023–36, 2014. [PubMed:25092924] [PubMed Central:PMC4150767] [doi:10.1093/nar/gku649].

[49] Jing Wang, William Rennie, Chaochun Liu, Charles S. Carmack, Karine Prevost, Marie-Pier Caron, Eric Masse, Ye Ding, and Joseph T. Wade. Identification of bacterial sRNA regulatory targets using ribosome profiling. *Nucleic Acids Res*, 43(21):10308–20, 2015. [PubMed:26546513] [PubMed Central:PMC4666370] [doi:10.1093/nar/gkv1158].

[50] Branislav Vecerek, Isabella Moll, and Udo Bläsi. Control of Fur synthesis by the non-coding RNA RyhB and iron-responsive decoding. *EMBO J*, 26(4):965–75, 2007. [PubMed:17268550] [PubMed Central:PMC1852835] [doi:10.1038/sj.emboj.7601553].

[51] Karine Prévost, Guillaume Desnoyers, Jean-François Jacques, François Lavoie, and Eric Massé. Small RNA-induced mRNA degradation achieved through both translation block and activated cleavage. *Genes Dev*, 25(4):385–96, 2011. [PubMed:21289064] [PubMed Central:PMC3042161] [doi:10.1101/gad.2001711].

[52] Branislav Vecerek, Isabella Moll, Taras Afonyushkin, Vladimir Kaberdin, and Udo Blasi. Interaction of the RNA chaperone Hfq with mRNAs: direct and indirect roles of Hfq in iron metabolism of *Escherichia coli*. *Mol Microbiol*, 50(3):897–909, 2003. [PubMed:14617150].

[53] Julia Bos, Yohann Duverger, Benoît Thouvenot, Claude Chiaruttini, Christiane Branlant, Mathias Springer, Bruno Charpentier, and Frederic Barras. The sRNA RyhB regulates the synthesis of the *Escherichia coli* methionine sulfoxide reductase MsrB but not MsrA. *PLoS One*, 8(5):e63647, 2013. [PubMed:23671689] [doi:10.1371/journal.pone.0063647].

[54] Karine Prévost, Hubert Salvail, Guillaume Desnoyers, Jean-François Jacques, Émilie Phaneuf, and Eric Massé. The small RNA RyhB activates the translation of *shiA* mRNA encoding a permease of shikimate, a compound involved in siderophore synthesis. *Mol Microbiol*, 64(5):1260–73, 2007. [PubMed:17542919] [doi:10.1111/j.1365-2958.2007.05733.x].
[55] Guillaume Desnoyers, Audrey Morissette, Karine Prévost, and Eric Massé. Small RNA-induced differential degradation of the polycistronic mRNA iscRSUA. *EMBO J*, 28(11):1551–61, 2009. [PubMed:19407815] [doi:10.1038/emboj.2009.116].

[56] Hubert Salvail, Pascale Lanthier-Bourbonnais, Jason Michael Sobota, Mélissa Caza, Julie-Anna M. Benjamin, Martha Eugénia Sequeira Mendia, François Lépine, Charles M. Dozois, James Imlay, and Eric Massé. A small RNA promotes siderophore production through transcriptional and metabolic remodeling. *Proc Natl Acad Sci USA*, 107(34):15223–8, 2010. [PubMed:20696910] [PubMed Central:PMC2930555] [doi:10.1073/pnas.1007805107].

[57] Kai Papenfort, Dimitri Podkaminski, Jay C. D. Hinton, and Jorg Vogel. The ancestral SgrS RNA discriminates horizontally acquired Salmonella mRNAs through a single G-U wobble pair. *Proc Natl Acad Sci USA*, 109(13):E757–64, 2012. [PubMed:2338560] [PubMed Central:PMC3323961] [doi:10.1073/pnas.1119414109].

[58] Kai Papenfort, Yan Sun, Masatoshi Miyakoshi, Carin K. Vanderpool, and Jorg Vogel. Small RNA-mediated activation of sugar phosphatase mRNA regulates glucose homeostasis. *Cell*, 153(2):426–37, 2013. [PubMed:23582330] [PubMed Central:PMC4151517] [doi:10.1016/j.cell.2013.03.003].

[59] Hiroshi Kawamoto, Yukari Koide, Teppei Morita, and Hiroji Aiba. Base-pairing requirement for RNA silencing by a bacterial small RNA and acceleration of duplex formation by Hfq. *Mol Microbiol*, 61(4):1013–22, 2006. [PubMed:16859494] [doi:10.1111/j.1365-2958.2006.05288.x].

[60] Jennifer B. Rice and Carin K. Vanderpool. The small RNA SgrS controls sugar-phosphate accumulation by regulating multiple PTS genes. *Nucleic Acids Res*, 39(9):3806–19, 2011. [PubMed:21245045] [PubMed Central:PMC3089445] [doi:10.1093/nar/gkq1219].

[61] Erik Holmqvist, Patrick R. Wright, Lei Li, Thorsten Bischler, Lars Barquist, Richard Reinhardt, Rolf Backofen, and Jorg Vogel. Global RNA recognition patterns of post-transcriptional regulators Hfq and CsrA revealed by UV crosslinking in vivo. *EMBO J*, 2016. [PubMed:27044921] [PubMed Central:PMC5207318] [doi:10.15252/embj.201593360].

[62] Chase L. Beisel, Taylor B. Updegrove, Ben J. Janson, and Gisela Storz. Multiple factors dictate target selection by Hfq-binding small RNAs. *EMBO J*, 31(8):1961–74, 2012. [PubMed:22388518] [PubMed Central:PMC3343335] [doi:10.1038/embj.2012.52].

[63] Jiandong Chen and Susan Gottesman. Spot 42 sRNA regulates arabinose-inducible araBAD promoter activity by repressing synthesis of the high-affinity low-capacity arabinose transporter. *J Bacteriol*, 2016. [PubMed:27849174] [PubMed Central:PMC5237117] [doi:10.1128/JB.00691-16].