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# Supporting Online Material for

## Redox-Active Antibiotics Control Gene Expression and Community Behavior in Divergent Bacteria

Lars E. P. Dietrich, Tracy K. Teal, Alexa Price-Whelan, Dianne K. Newman*

*To whom correspondence should be addressed. E-mail: dkn@mit.edu

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# Supporting online material

Materials and Methods
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## Materials and Methods

*Quantitative real time PCR*

*Streptomyces coelicolor* A3(2) strains were grown on R5$^{-}$ plates that were overlain with cellophane membranes (Spectrum Laboratory Products, Inc.) (*1*). Plates were incubated at 30°C for three days to allow pigment production. Then cells were treated with RNAProtect Bacteria Reagent (Qiagen) for 5 min at room temperature, scraped off the cellophane membrane and centrifuged for 10 min at 5000 *g*. Total RNA was extracted from the cell pellets using the RNeasy Plant Mini Kit (Qiagen) according to the manufacturer's instructions, including the optional DNase treatment. cDNA was generated with iScript (BioRad) and served as template for quantitative RT-PCR (Real Time 7300 PCR Machine, Applied Biosystems) using the Sybr Green detection system (Applied Biosystems). Samples were assayed in triplicate. The signal was standardized to SCO4548 (*2*) using the following equation: Relative expression = $2^{(\mathrm{CTstandard} - \mathrm{CTsample})}$, where CT (cycle time) was determined automatically by the Real Time 7300 PCR software (Applied Biosystems). Primers (Integrated DNA Technologies) for Q-RT-PCR were designed using Primer3 software (*3*). Criteria for primer design were a melting temperature of 60°C, primer length of ~20 nucleotides, and an amplified PCR fragment of 100 base pairs. The following primers were used:
SCO1697: 5'-tgcctcagattccagagaaga-3' and 5'- tcagacccttggactcgtaga-3'
SCO2478: 5'- acaccgtctccttccacaac-3' and 5'- ctggtcgagcatcgtcttg-3'
SCO2479: 5'- agatcgtcgcgacctgtg-3' and 5'- ccctggggtacacctgct-3'
SCO4266: 5'- gatgggcatcctccagttc-3' and 5'- cgttcttcgcgtactgcac-3'
SCO4548: 5'- agatcttcgagctcaacaagg-3' and 5'- gggcatctccatgatcca-3'

*Colony morphology assay*

a) *Pseudomonas aeruginosa* PA14:

Strains were grown in LB medium to late exponential phase, then 10 µl were spotted onto 1% agar plates containing 10 g/L Tryptone Broth, supplemented with 40 µg/l Congo Red and 20 µg/l Coomassie Blue as described previously (*4*). Plates were incubated at room temperature. Colonies were imaged using an Epson Perfection 2400 Photo Scanner at 600 dpi resolution, Nikon stereomicroscope or a digital microscope (Proscope).

b) *Streptomyces coelicolor* A3(2):
10 μl of a spore suspension in water was spotted onto plates with R5$^{-}$ medium. Plates were incubated at room temperature for six days. Colonies were imaged using a Nikon stereomicroscope.

*Phenazine extraction from agar plates*
Biological triplicate cultures of the wild type and each mutant were grown up overnight in LB. OD500 was normalized using spent supernatant so that all colonies would be spotted using the same cell density. Cultures were spotted three times onto an agar miniplate (10ml of 1% tryptone, 1% agar in a 60 x15 mm plate) and incubated at room temperature for 6 days. Cells were scraped off the agar surface with a spatula. Agar was submerged in 10 ml chloroform in a glass jar and nutated for 30 minutes. The chloroform was transferred to a brown glass vial and the sample was dried down under a stream of nitrogen gas. The solid was resuspended in 1 ml acetonitrile and filtered. 100 ul were loaded onto the HPLC and analyzed as described previously (*5*).

## SOM references

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## SOM Captions

Fig. S1. (**A**) The *P. aeruginosa* SoxR regulon differs from the *E. coli* paradigm. In *E. coli*, the SoxR homodimer binds to the soxRbox in the *soxS* promoter region (see also Fig. 1B). *soxR* and *soxS* are divergently transcribed. The binding of reduced SoxR to the soxRbox represses expression of *soxR* and *soxS*. Oxidation of the SoxR [2Fe-2S] cluster induces a conformational change that allows transcription of *soxS* (*6*). SoxS regulates genes involved in superoxide tolerance and detoxification. In contrast, in *P. aeruginosa*, the gene adjacent to *soxR* encodes a putative monooxygenase. Two additional soxRboxes, found elsewhere in the *P. aeruginosa* genome, regulate expression of putative drug transporters.

(**B**) SoxRbox consensus sequence. SoxR binding sites (soxRboxes) are palindromic sequences positioned between the -35 and -10 promoter elements. The promoter region upstream of *E. coli*'s *soxS* is shown. +1 marks the transcriptional start site, <u>ATG</u> the start codon in *soxS*. A position weight matrix was generated based on 12 soxRbox sites from diverse bacteria. A modified version of the program pyscangenes.py (*7*) was used to find the site energy of all motifs in 616 genomes (Table S1). Dots indicate nucleotides that are identical to those in the *E. coli* soxRbox.

Fig. S2. Phylogenetic tree based on SoxR orthologs. We constructed a phylogenetic tree based on 123 SoxR orthologs using the desktop software CLC protein workbench 3. The sequences were aligned with the ClustalW algorithm (gap open penalty = 35; gap extension penalty = 0.75; Scoring matrix = GONNET). Using this alignment we created a UPGMA (algorithm which assumes a constant rate of evolution) tree and performed a bootstrap analysis with 1000 replicates.

Fig. S3. **(A)** Structures of undecylprodigiosin and actinorhodin. Both compounds are produced by the *S. coelicolor* A3(2) parent strain M145, but not by *S. coelicolor* A3(2) M512 (Δ*redD* Δ*actII*-ORF4 (*8*)).

**(B)** Spore suspensions of the *S. coelicolor* A3(2) parent strain M145 and M512 were distributed over cellophane sheets that were placed on R5$^-$ plates and incubated at 30°C. After three days the M145 spread turned red due to the production of undecylprodigiosin, after four days it turned blue due to actinorhodin production. At day 5 we lifted the cellophane sheets of the agar plates, scraped off and prepared RNA for quantitative RT-PCR (Fig. 2).

Fig. S4. The phenazine null mutant forms smooth colonies in the presence of exogenous phenazines. **(A)** PA14 wt and the phenazine null mutant were spotted onto 1% tryptone, 1% agar plates that were supplemented with 50µM HPLC-purified pyocyanin or an equal volume of water. **(B)** 50µl cell suspensions of PA14 phenazine null mutant and the phenazine overproducer were streaked onto 1% tryptone, 1% agar plates (supplemented with Congo Red and Coomassie Blue). Image was taken after 5 days.

Fig. S5. **(A)** Genomic localization of *mexGHI-opmD*, *phzM*, *phzA1-G1*, and *phzS* in *P. aeruginosa* PA14. **(B)** Deletion of the RND efflux pump *mexGHI-opmD* results in an extended lag phase. This phenotype is dependent on phenazine production as a *mexGHI-opmD* deletion in the phenazine null-mutant does not show this phenotype. All strains were inoculated from late stationary phase cultures into 5ml LB to an OD (600nm) of 0.05, then incubated shaking (225 rpm) at 37°C.

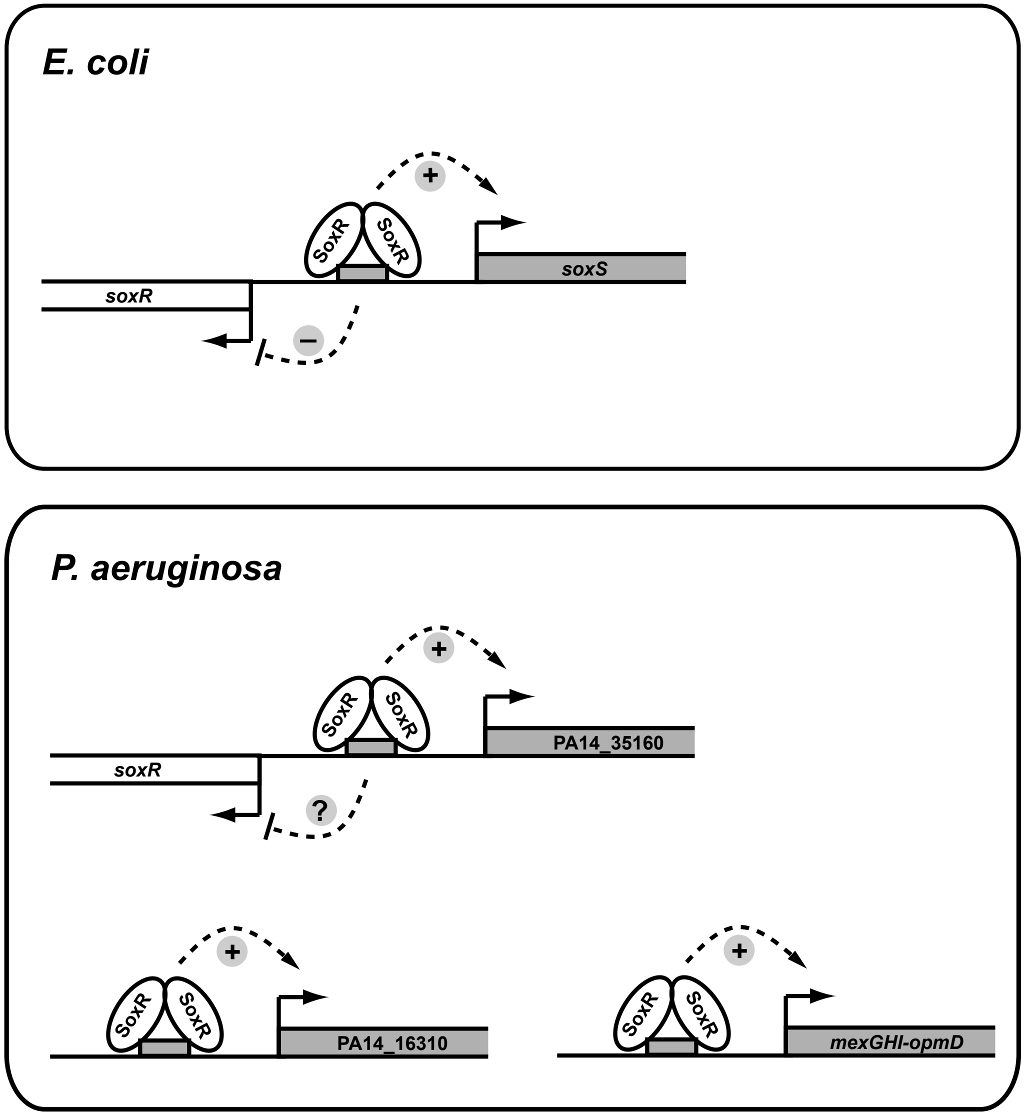
Table S1. SoxRbox analysis. 616 bacterial genomes were analyzed for the presence of soxRbox elements. Strains containing soxRbox elements are listed. Site energy was calculated such that the site energy equals 0 for the consensus site and is greater than 0 for all other sites (*7*) .

*Sequence* is the soxRbox sequence for a given site. The *operon position* indicates whether the adjacent gene/operon is located 3' (left) or 5' (right) of the soxRbox, with respect to the top strand. *Distance to start* is the distance from the soxRbox to the start of the predicted operon. *Orientation* is the orientation of the soxRbox element, using the -35 region as the start of the soxRbox motif.

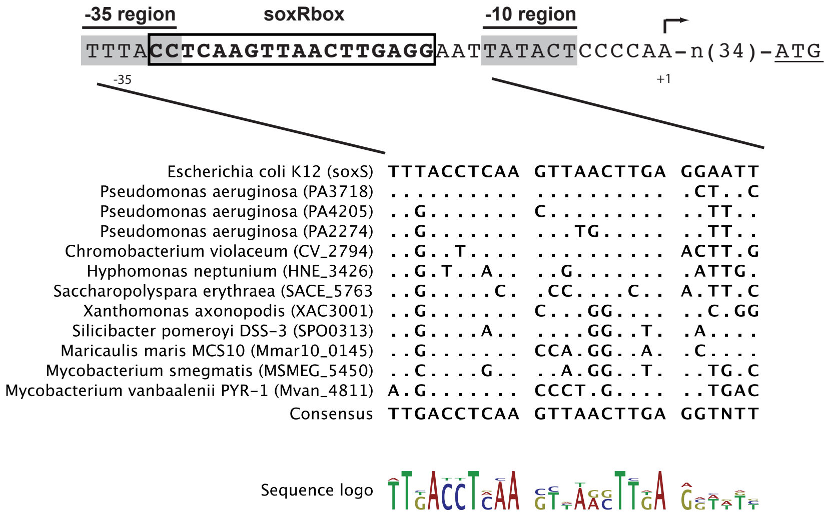
Annotations for soxRbox genes can be found at http://soxRbox.mit.edu.

**Fig. S1**
**Dietrich *et al.***

**A** **Organization of SoxR regulons in *E. coli* and *P. aeruginosa***



**B** **SoxRbox consensus sequence**



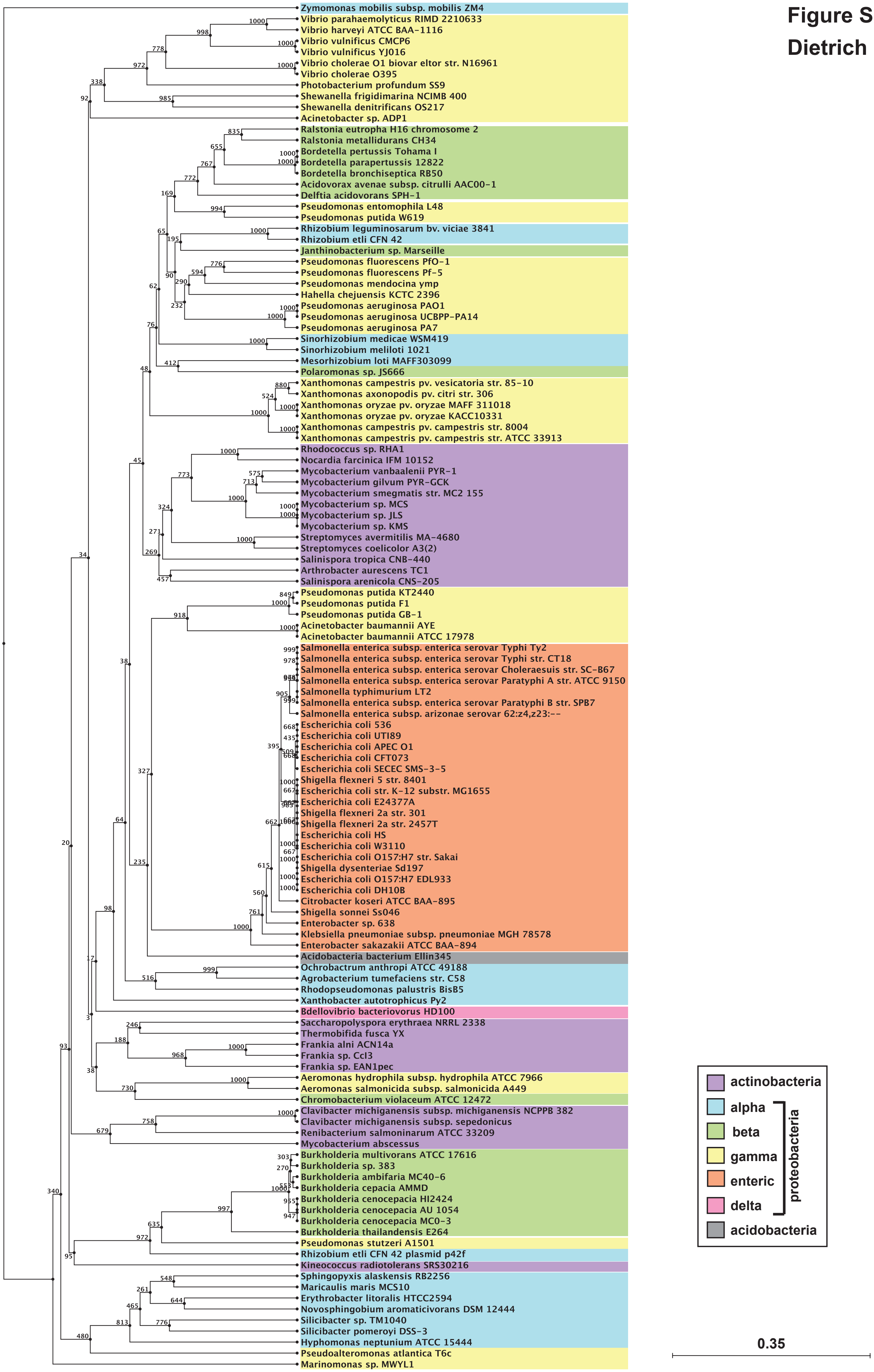
TTTA**CCTCAAGTTAACTTGAGG**AATTATACTCCCCAA-n(34)-ATG

| | | | |
|---|---|---|---|
| Escherichia coli K12 (soxS) | TTTACCTCAA | GTTAACTTGA | GGAATT |
| Pseudomonas aeruginosa (PA3718) | .......... | .......... | .CT..C |
| Pseudomonas aeruginosa (PA4205) | ..G....... | C......... | ..TT.. |
| Pseudomonas aeruginosa (PA2274) | ..G....... | ...TG..... | ..TT.. |
| Chromobacterium violaceum (CV_2794) | ..G..T.... | .......... | ACTT.G |
| Hyphomonas neptunium (HNE_3426) | ..G.T..A.. | ..G....... | .ATTG. |
| Saccharopolyspara erythraea (SACE_5763 | ..G.....C. | .CC....C.. | A.TT.C |
| Xanthomonas axonopodis (XAC3001) | ..G....... | C...GG.... | ..C.GG |
| Silicibacter pomeroyi DSS-3 (SPO0313) | ..G....A.. | ....GG..T. | .A.... |
| Maricaulis maris MCS10 (Mmar10_0145) | ..G....... | CCA.GG..A. | .C.... |
| Mycobacterium smegmatis (MSMEG_5450) | ..C....G.. | ..A.GG..T. | ..TG.C |
| Mycobacterium vanbaalenii PYR-1 (Mvan_4811) | A.G....... | CCCT.G.... | ..TGAC |
| Consensus | TTGACCTCAA | GTTAACTTGA | GGTNTT |

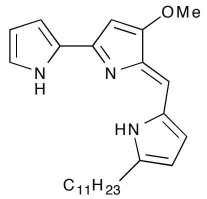
Sequence logo

**Figure S2**

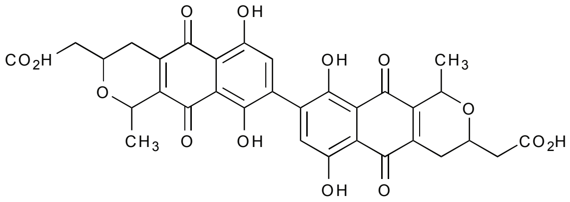
**Dietrich *et al.***



## A Pigments produced by *Streptomyces coelicolor* A3(2)

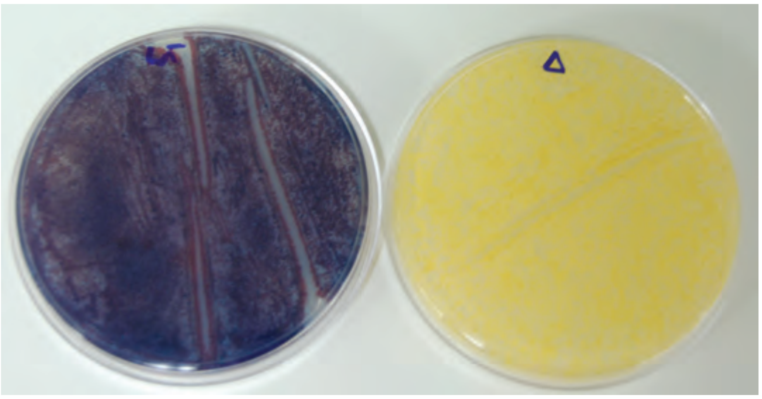


**undecylprodigiosin**



**actinorhodin**

## B Pigment production by S. coelicolor A3(2) strains



**M145** **M512**

**Figure S4**
**Dietrich *et al.***

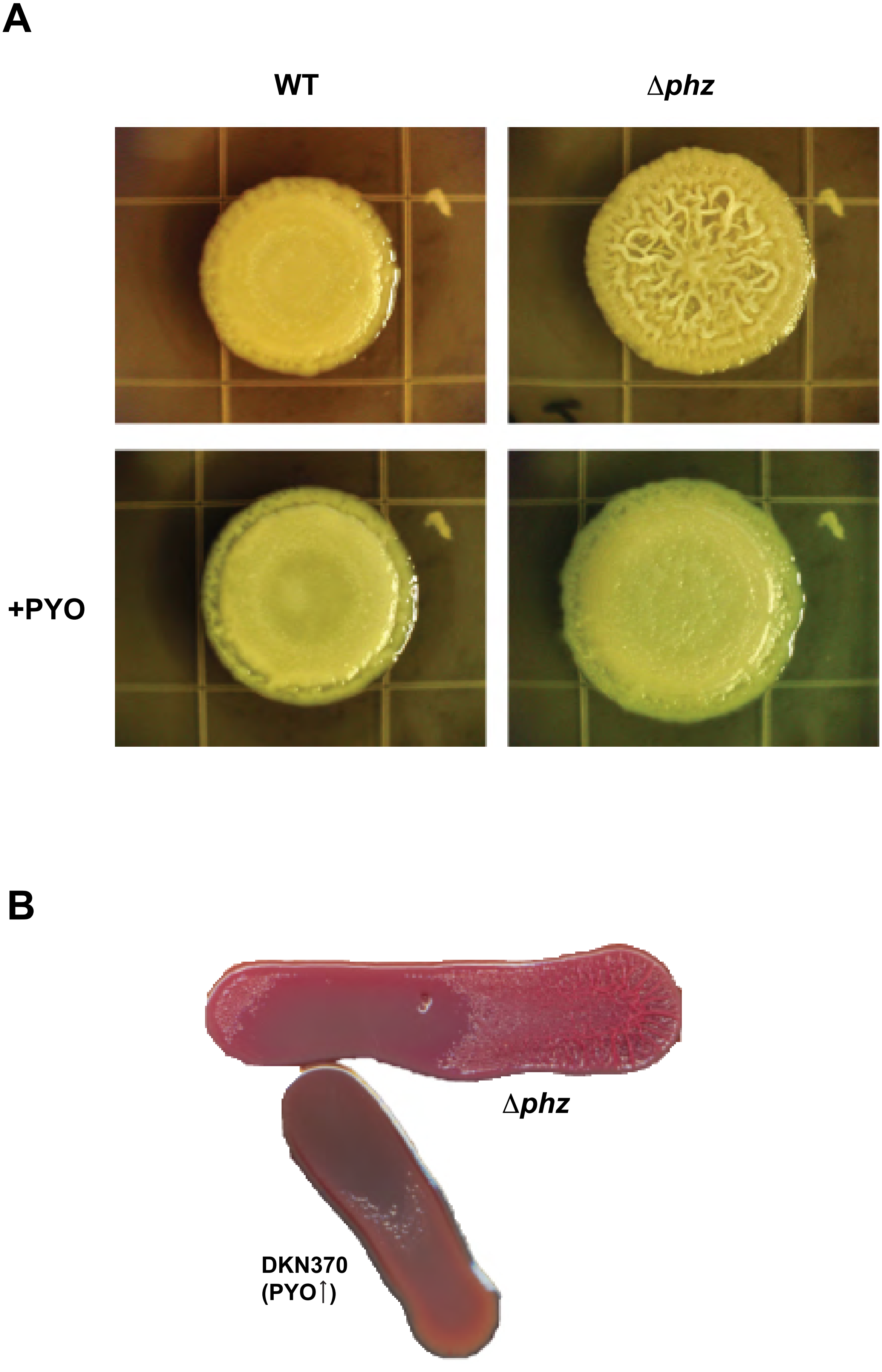
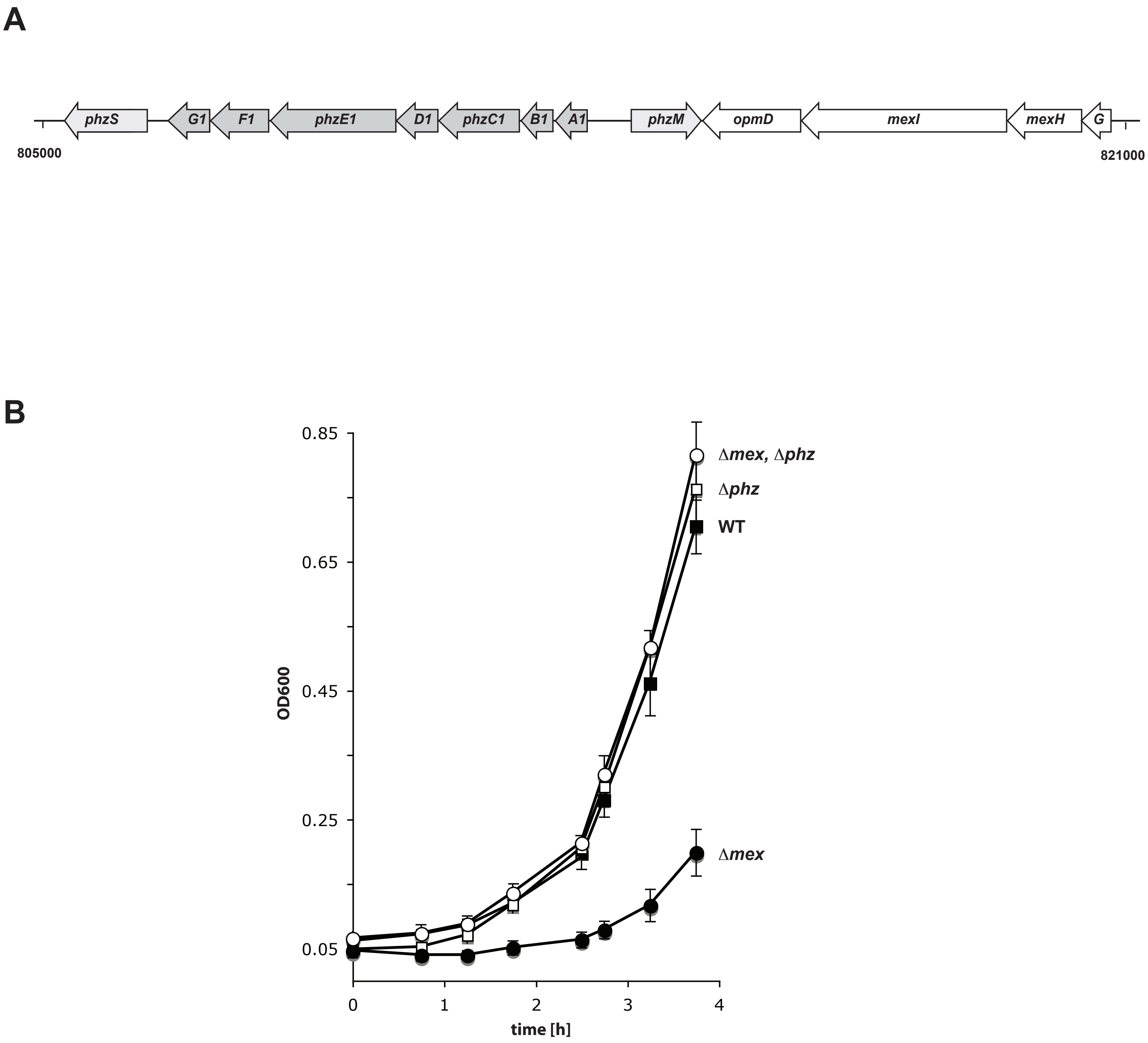


**Figure S5**
**Dietrich *et al.***



Acidobacteria bacterium Ellin345, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.30 | TTGACCTCAAGTTTACTTGAGGTTTT | left<br>right | -14<br>-97 | Acid345_3972<br>Acid345_3973-Acid345_3974 | right |

Acidovorax avenae subsp. citrulli AAC00-1, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTTTAGTTGAGGTTCC | left<br>right | -62<br>-90 | Aave_2275<br>Aave_2276 | left |
| 6.60 | TTGACCTCAACAATGGTTGAGGTTTG | left | -214 | Aave_1362 | right |

Acinetobacter baumannii ATCC 17978, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.93 | TTGACCTCAACTTAAGTTGAGGTTGG | left | -35 | A1S_0564 | left |

Acinetobacter baumannii AYE, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.93 | TTGACCTCAACTTAAGTTGAGGTTGG | left | -42 | ABAYE3195-ABAYE3196 | right |
| 7.91 | TTGACTTCAAGTGAACTTTAACTTGC | left<br>right | -9<br>-98 | ABAYE3692<br>ABAYE3693-ABAYE3694 | right |

Acinetobacter baumannii, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.93 | TTGACCTCAACTTAAGTTGAGGTTGG | left | -42 | ABSDF2956-ABSDF2957 | right |

Acinetobacter sp. ADP1, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.54 | TTGACCTCAAGTTAACTTGAGCTTTG | left<br>right | -4<br>-42 | soxR (ACIAD3082)<br>ACIAD3083-ACIAD3084 | right |

Aeromonas hydrophila subsp. hydrophila ATCC 7966, complete genome

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.03 | TTGACCTCAAGTTAGCTTTAACTTGC | left<br>right | -8<br>-90 | soxR (AHA_2710)<br>AHA_2711 | right |

**Aeromonas salmonicida subsp. salmonicida A449, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.03 | TTGACCTCAAGTTAGCTTTAACTTGC | left | -32 | ASA_1662 | left |
| | | right | -54 | soxR (ASA_1663)-ASA_1664-ASA_1665 | |

**Agrobacterium tumefaciens str. C58 chromosome circular, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.25 | TTGACCTCAACTATGGTTGAGGAATT | left | -33 | Atu2361 | left |

**Agrobacterium tumefaciens str. C58 chromosome linear, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.97 | TTGACCTCAACTATAGTTGAGGAATT | left | -68 | soxR (Atu3915) | left |
| 5.63 | TCGACCTCAACTCAAGTTGAGGTTGT | left | -108 | Atu4895 | right |

**Agrobacterium tumefaciens str. C58 plasmid At, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.36 | TTGACCTCAACTCTAGTTGAGGTTGT | left | -56 | Atu5152 | left |
| | | right | -762 | atsB (Atu5155) | |

**Arthrobacter aurescens TC1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.97 | TTGACCTCAACTTAAGTTGAGGTCCT | left | -64 | AAur_0213 | left |
| | | right | -160 | ureA (AAur_0214)-ureB (AAur_0215)-ureC (AAur_0216)-ureE (AAur_0217) | |

**Azoarcus sp. BH72, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.91 | TTGACCTCAAGTCGACTTGAACTTGC | left | -5 | soxR (azo2618)-azo2617-azo2616 | right |
| | | right | -92 | azo2619 | |

**Bacillus anthracis str. 'Ames Ancestor', complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -171 | fumC (GBAA1767) | left |

**Bacillus anthracis str. Ames, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -171 | fumC (BA1767) | left |

**Bacillus anthracis str. Sterne, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -171 | fumC (BAS1637) | left |

**Bacillus cereus ATCC 14579, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -46 | BC1711-BC1710 | left |
| | | right | -171 | fumC (BC1712) | |

**Bacillus cereus E33L, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -171 | fumC (BCZK1587) | left |

**Bacillus subtilis subsp. subtilis str. 168, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.19 | TTGACTTAAAGTTAACTTTAAGTGTT | left | -35 | yraB (BSU27000) | left |
| | | right | -498 | adhA (BSU27010) | |

**Bacillus thuringiensis str. Al Hakam, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -169 | fumC (BALH_1553) | left |

**Bacillus thuringiensis serovar konkukian str. 97-27, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.99 | TTGACCTAAACTTAAGTTTAGGCTGT | left | -46 | BT9727_1616-BT9727_1615 | left |
| | | right | -171 | fumC (BT9727_1617) | |

**Bdellovibrio bacteriovorus HD100, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.20 | TTGACCTCAAGTTAACTTGAGGTTGT | left | -7 | soxR (Bd1002) | right |
| | | right | -113 | Bd1003 | |

**Bordetella bronchiseptica RB50, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.04 | TTGACCTCAAGCTAGCTTGAGGGTCC | left | -90 | BB4154 | right |

**Bordetella pertussis Tohama I, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.04 | TTGACCTCAAGCTAGCTTGAGGGTCC | left | -141 | BP2837 | left |

**Burkholderia sp. 383 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTGAACTTGAAGTTGC | left | -2 | Bcep18194_B1905 | right |
|  |  | right | -164 | Bcep18194_B1906 |  |
| 7.70 | TTGACTTGAAGTTAACTTCAACTTTT | left | -19 | Bcep18194_B1003 | right |
|  |  | right | -87 | Bcep18194_B1004-Bcep18194_B1005-Bcep18194_B1006 |  |

**Burkholderia ambifaria MC40-6 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTGAACTTGAAGTTGC | left | -54 | BamMC406_4022 | left |
| 7.70 | TTGACTTGAAGTTAACTTCAACTTTT | left | -68 | BamMC406_4594 | left |

**Burkholderia cenocepacia AU 1054 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTGAACTTGAAGTTGC | left | -2 | Bcen_4236 | right |
|  |  | right | -164 | Bcen_4237 |  |
| 7.70 | TTGACTTGAAGTTAACTTCAACTTTT | left | -18 | Bcen_3620 | right |
|  |  | right | -87 | Bcen_3621 |  |

**Burkholderia cenocepacia HI2424 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTGAACTTGAAGTTGC | left | -112 | Bcen2424_4129 | left |
|  |  | right | -54 | Bcen2424_4130 |  |
| 7.70 | TTGACTTGAAGTTAACTTCAACTTTT | left | -35 | Bcen2424_4746-Bcen2424_4745-Bcen2424_4744 | left |
|  |  | right | -70 | Bcen2424_4747 |  |

**Burkholderia cenocepacia MC0-3 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTGAACTTGAAGTTGC | left | -2 | Bcenmc03_3389 | right |
| | | right | -158 | Bcenmc03_3390 | |
| 7.70 | TTGACTTGAAGTTAACTTCAACTTTT | left | -18 | Bcenmc03_5536 | right |
| | | right | -87 | Bcenmc03_5537-<br>Bcenmc03_5538-<br>Bcenmc03_5539 | |

**Burkholderia cepacia AMMD chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.23 | TTGACCTCAAGTGAACTTGAAGTTGC | left | -54 | Bamb_3541 | left |
| 7.70 | TTGACTTGAAGTTAACTTCAACTTTT | left | -35 | Bamb_4129 | left |
| | | right | -69 | Bamb_4130 | |

**Burkholderia multivorans ATCC 17616 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.51 | TTGACCTCAAGTGAGCTTGAAGTTGC | left | -2 | Bmul_4462 | right |
| | | right | -194 | Bmul_4463 | |
| 5.39 | TTGACTTGAAGTTAACTTGAACTTTT | left | -18 | Bmul_3929 | right |
| | | right | -87 | Bmul_3930-<br>Bmul_3931-<br>Bmul_3932 | |

**Chromobacterium violaceum ATCC 12472, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.63 | TTGACTTCAAGTTAACTTGAACTTTG | left | -7 | soxR (CV_2793) | right |
| | | right | -87 | CV_2794-<br>CV_2795 | |
| 5.33 | TTGACTTCAAGTTAACTTTAACTTTC | left | -87 | ebrB (CV_3243) | right |

**Citrobacter koseri ATCC BAA-895, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -7 | CKO_03827 | right |
| | | right | -105 | CKO_03828 | |

**Clavibacter michiganensis subsp. sepedonicus, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.68 | TTGACCTCAAGTTCGCTTGAGGTGCT | left | -11 | CMS1293 | left |

**Clostridium beijerinckii NCIMB 8052, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.81 | TTGACCTAAAGTTAACTTTAGGGTGT | left | -127 | Cbei_3182 | left |
| | | right | -79 | Cbei_3183 | |
| 6.19 | TTGACTTAAAGTTAACTTTAAGTGTT | left | -34 | Cbei_3974 | left |

**Delftia acidovorans SPH-1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.80 | TTGACCTCAACTTTGGTTGAGGTTTC | left | -54 | Daci_1188 | left |
| | | right | -101 | Daci_1189 | |

**Desulfitobacterium hafniense Y51, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.69 | TTGACCTAAAGTTAAGTTTAGGTGCT | left | -88 | DSY1467 | right |

**Enterobacter sp. 638, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.90 | TTGACCTCAAGTTAACTTTAGCTTTT | left | -41 | Ent638_2697 | left |
| | | right | -359 | Ent638_2698 | |
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -64 | Ent638_0266 | left |
| | | right | -60 | Ent638_0267 | |

**Enterobacter sakazakii ATCC BAA-894, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -53 | ESA_00114 | left |
| | | right | -59 | ESA_00115 | |

**Erythrobacter litoralis HTCC2594, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.81 | TTGACCTCAAGTCAGCTTGAGGTTGC | left | -27 | ELI_02950 | right |
| | | right | -142 | ELI_02955 | |

**Escherichia coli 536, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | ECP_4290 | left |
| | | right | -59 | ECP_4291 | |

**Escherichia coli APEC O1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -59 | soxR (APECO1_2394) | left |

**Escherichia coli CFT073, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (c5053) | left |
| | | right | -59 | soxR (c5054) | |

**Escherichia coli DH10B, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (ECDH10B_4251) | left |
| | | right | -59 | soxR (ECDH10B_4252) | |

**Escherichia coli E24377A, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (EcE24377A_4615) | left |
| | | right | -59 | soxR (EcE24377A_4616) | |

**Escherichia coli HS, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (EcHS_A4304) | left |
| | | right | -59 | soxR (EcHS_A4305) | |

**Escherichia coli str. K-12 substr. MG1655, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (b4062) | left |
| | | right | -59 | soxR (b4063) | |

**Escherichia coli O157:H7 EDL933, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (Z5661) | left |
| | | right | -59 | soxR (Z5662) | |

**Escherichia coli O157:H7 str. Sakai, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | ECs5044 | left |
| | | right | -59 | ECs5045 | |

**Escherichia coli SECEC SMS-3-5, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (EcSMS35_4524) | left |
| | | right | -59 | soxR (EcSMS35_4525) | |

**Escherichia coli UTI89, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (UTI89_C4648) | left |
| | | right | -59 | soxR (UTI89_C4649)-UTI89_C4650 | |

**Frankia sp. CcI3, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.76 | TTGACTTCAATCATGGTTGAGGTTTT | left | -113 | Francci3_1887 | right |

**Frankia sp. EAN1pec, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.87 | TTGACCTGAAGTCAACTTCAGATATT | left | -213 | Franean1_1305 | right |
| 6.36 | TTGACCTGAAGTCAGGTTTAACTTTT | left | -64 | Franean1_4948 | right |

**Hahella chejuensis KCTC 2396, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.49 | TTGACCTAAAGTTAAGTTGAGGTTTT | left | -10 | soxR (HCH_01441) | right |
| | | right | -96 | HCH_01442 | |
| 5.28 | TTGACCTCAAGTCGACTTGAGCTTGT | left | -6 | HCH_01327 | right |
| | | right | -140 | HCH_01328 | |

**Herpetosiphon aurantiacus ATCC 23779, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.78 | TTGACTTCCAGTTAACTTGAACTTGT | left | -56 | Haur_3151 | left |
| | | right | -75 | Haur_3152 | |

**Hyphomonas neptunium ATCC 15444, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.57 | TTGATCTAAAGTGAACTTGAGATTGT | left | -43 | HNE_3425 | left |
| | | right | -64 | soxR (HNE_3426) | |

**Idiomarina loihiensis L2TR, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.91 | TTGACCTAAAGTTAACTTTAAGTTGT | left | -9 | soxR_2 (IL0801) | right |
| | | right | -96 | IL0802 | |

**Janthinobacterium sp. Marseille, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 0.29 | TTGACCTCAAGTTAAGTTGAGGTTTT | left | -8 | mma_1929 | right |
| | | right | -169 | mma_1930 | |

**Kineococcus radiotolerans SRS30216, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.07 | TTGACCTCAAGTCCGCTTGAGCAGGT | left | -11 | Krad_2687 | left |
| | | right | -382 | Krad_2688 | |

**Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -51 | soxS (KPN_04462) | left |
| | | right | -86 | soxR (KPN_04463) | |
| 3.00 | TTGATCTCAAGTTAACTTGAGGTTGT | left | -202 | KPN_01860 | right |
| | | right | -88 | KPN_01861 | |

**Lactobacillus casei ATCC 334, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.21 | TTGACCTAAAGCTAACTTTAGGGGTT | left | -30 | LSEI_0442 | right |
| | | right | -167 | LSEI_0443 | |

**Lactobacillus sakei subsp. sakei 23K, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.47 | TTGACCTCAAGTCAGCTTGAGGTTGT | left | -89 | LSA0238 | right |

**Lactobacillus salivarius UCC118, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.09 | TTGACTTCAAGTTAACTTGAAGTTTT | left | -124 | LSL_0710-LSL_0711-LSL_0712 | right |

**Lactococcus lactis subsp. cremoris MG1363, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.56 | TTGCTCTCAAGTTAACTTGAGGGTTT | left | -33 | pcaC (llmg_2230) | left |
| | | right | -69 | rmeD (llmg_2231) | |

**Lactococcus lactis subsp. cremoris SK11, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.56 | TTGCTCTCAAGTTAACTTGAGGGTTT | left | -33 | LACR_2239 | left |
| | | right | -69 | LACR_2240 | |

**Lactococcus lactis subsp. lactis Il1403, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.06 | TTGCCCTCAAGTTAACTTGAAGGTTT | left | -34 | pcaC (L35675) | left |
| | | right | -69 | rmeD (L35965) | |

**Maricaulis maris MCS10, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.17 | TTGACCTCAACCAAGGTTAAGCAATT | left | -3 | Mmar10_0144 | right |
| | | right | -103 | Mmar10_0145 | |

**Marinomonas sp. MWYL1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.72 | TTGACCTCAACTTAAGTTCAGGTTGC | left | -99 | Mmwyl1_1994 | left |
| | | right | -59 | Mmwyl1_1995 | |

**Mesorhizobium loti MAFF303099, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.06 | TTGACCTCAACTTAAGTTGAGATTGT | left | -104 | mlr7819 | right |
| 4.26 | TTGACCTCAAGTTATGTTGAGCTTGT | left | -66 | mlr2720 | left |

**Mycobacterium abscessus chromosome Chromosome, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.48 | TTGACCTCAAGTCCAGTTGAGGATTT | left | -180 | MAB_4665c | left |
| 5.05 | TTGACCTCAAGTGCGCTTGAGATTTT | left | -4 | MAB_4677c | right |
| | | right | -65 | MAB_4678-MAB_4679 | |

**Mycobacterium gilvum PYR-GCK, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.33 | TTGACCTGAAGGTTGGTTGAGGTTGC | left | -12 | Mflv_1248 | left |

**Mycobacterium sp. JLS, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.86 | TTGACCTGAACTTTGGTTGAGGTCTT | left | -13 | Mjls_1491 | left |
| | | right | -108 | Mjls_1492 | |
| 7.91 | TTGACCTGAACTTTGGTTGAGGTCGG | left | -32 | Mjls_2737 | right |
| | | right | -64 | Mjls_2738 | |

**Mycobacterium sp. KMS, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.86 | TTGACCTGAACTTTGGTTGAGGTCTT | left | -13 | Mkms_1515 | left |
| | | right | -180 | Mkms_1516 | |
| 7.91 | TTGACCTGAACTTTGGTTGAGGTCGG | left | -32 | Mkms_2751 | right |
| | | right | -64 | Mkms_2752 | |

**Mycobacterium sp. MCS, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.86 | TTGACCTGAACTTTGGTTGAGGTCTT | left | -13 | Mmcs_1493 | left |
| | | right | -180 | Mmcs_1494 | |
| 7.91 | TTGACCTGAACTTTGGTTGAGGTCGG | left | -32 | Mmcs_2707 | right |
| | | right | -64 | Mmcs_2708 | |

**Mycobacterium smegmatis str. MC2 155, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.01 | TTCACCTGAAGTAAGGTTTAGGTGTC | left | -20 | arcA (MSMEG_5448) | right |
| | | right | -58 | soxR (MSMEG_5450) | |
| 7.23 | TTGACCTCAACCTCACTTGAGGTGCC | left | -171 | MSMEG_0572-MSMEG_0571-MSMEG_0570-MSMEG_0569-MSMEG_0568-MSMEG_0567-MSMEG_0566-MSMEG_0565-MSMEG_0564 | right |
| | | right | -170 | MSMEG_0574 | |
| 7.33 | TTGACCTCATCATTGGTTGAGGTTTT | left | -11 | MSMEG_5661 | left |
| | | right | -130 | prrA (MSMEG_5662)-MSMEG_5663 | |

**Mycoplasma penetrans HF-2, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.87 | TTGACTTAAACTTAGGTTTAAGTTGT | left | -32 | MYPE6210 | left |
| | | right | -275 | MYPE6220 | |

**Myxococcus xanthus DK 1622, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.60 | TTGACCTCAAGTCGACTTGAACTGGC | left | -46 | MXAN_6982 | left |
| | | right | -56 | MXAN_6983 | |

**Nocardia farcinica IFM 10152, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.46 | TTGACTTCAAGTGAACTTGAAATTTT | left | -66 | nfa33330 | left |
| | | right | -76 | nfa33340 | |
| 7.12 | TTGACCTCAACATTGGTTGAGGAAGC | left | -54 | nfa29630-nfa29620 | left |

**Novosphingobium aromaticivorans DSM 12444, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.25 | TTGATCTCAAGCTAACTTGAGGTTGC | left | -49 | Saro_0953-Saro_0952 | left |
| | | right | -128 | Saro_0954 | |

**Ochrobactrum anthropi ATCC 49188 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.17 | TTGACCTCAACCAAGGTTGAGGAACT | left | -536 | Oant_2947 | right |
| | | right | -86 | Oant_2948 | |

**Pelotomaculum thermopropionicum SI, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.64 | TTTACCTCAAGTCAACTTAAGGTGGA | left | -139 | PTH_2806 | left |

**Photobacterium profundum SS9 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.37 | TTGACCTCAAGTTAACCTGAGGCACT | left | -23 | PBPRB1505 | right |
| | | right | -91 | PBPRB1506 | |

**Polaromonas sp. JS666, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.89 | TTGACCTCAACTTTACTTGAGGTTTT | left | -10 | Bpro_1373 | right |
| | | right | -112 | Bpro_1374 | |

**Pseudoalteromonas atlantica T6c, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.47 | TTGATCTAAAGTTAGCTTTAGATATT | left | -43 | Patl_1581 | left |
| | | right | -73 | Patl_1582 | |

**Pseudomonas aeruginosa PAO1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 0.59 | TTGACCTCAACTTAACTTGAGGTTTT | left | -154 | mexG (PA4205)-mexH (PA4206)-mexI (PA4207)-opmD (PA4208) | right |
| 1.59 | TTGACCTCAAGTTTGCTTGAGGTTTT | left | -7 | PA2273 | right |
|  |  | right | -96 | PA2274 |  |
| 2.23 | TTTACCTCAAGTTAACTTGAGCTATC | left | -60 | PA3718 | left |

**Pseudomonas aeruginosa PA7, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.30 | TTGACCTCAAGTTTACTTGAGGTTTT | left | -44 | PSPA7_2966 | left |
|  |  | right | -59 | soxR (PSPA7_2967) |  |
| 2.52 | TTTACCTCAAGTTAAGTTGAGCTATC | left | -115 | PSPA7_1403 | right |
| 3.18 | TTGACCTCAACTTAAGTTGAGGTTCT | left | -103 | PSPA7_0893-PSPA7_0892-PSPA7_0891-PSPA7_0890 | left |

**Pseudomonas aeruginosa UCBPP-PA14, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 0.59 | TTGACCTCAACTTAACTTGAGGTTTT | left | -102 | mexG (PA14_09540)-mexH (PA14_09530)-mexI (PA14_09520)-opmD (PA14_09500) | left |
| 1.59 | TTGACCTCAAGTTTGCTTGAGGTTTT | left | -44 | PA14_35160 | left |
|  |  | right | -59 | PA14_35170 |  |
| 2.23 | TTTACCTCAAGTTAACTTGAGCTATC | left | -112 | PA14_16310 | right |

**Pseudomonas entomophila L48, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.27 | TTGACCTTGAGTTAACTGGAGGTTTT | left | -48 | PSEEN3529 | left |
|  |  | right | -63 | soxR (PSEEN3530) |  |

**Pseudomonas fluorescens Pf-5, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.86 | TTGACCTTGACTTAACTAGAGGTTTT | left | -55 | PFL_4159 | left |
|  |  | right | -79 | soxR (PFL_4160) |  |

**Pseudomonas fluorescens PfO-1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.48 | TTTACCTCTAGTTAACTCGAGGTTTT | left | -50 | PflO1_3919 | left |
| | | right | -66 | PflO1_3920 | |

**Pseudomonas mendocina ymp, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.59 | TTGACCTTAAGTTAAGTTGAGGTTTT | left | -12 | Pmen_1341 | right |
| | | right | -92 | Pmen_1342 | |

**Pseudomonas putida F1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.96 | TTGACCTCAAGTAAAGTTGAGCTTTT | left | -53 | Pput_3679-Pput_3678 | left |
| | | right | -57 | Pput_3680 | |
| 6.17 | TTGACCTCGAGTTAAGTCAAGGTTTT | left | -57 | Pput_3216 | left |
| | | right | -335 | Pput_3217 | |
| 6.96 | TTGACCTTGACTTTGCTTGAGGTTTT | left | -48 | Pput_3505 | left |
| 7.02 | TTGACCTCGAGTTAGCTTAAGGTCTG | left | -443 | Pput_2251 | right |
| | | right | -89 | Pput_2252 | |

**Pseudomonas putida GB-1, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.77 | TTGACCTCAAGTTAAGTTGAGCTCTT | left | -5 | PputGB1_1579 | right |
| | | right | -105 | PputGB1_1580-PputGB1_1581 | |
| 6.96 | TTGACCTTGACTTTGCTTGAGGTTTT | left | -100 | PputGB1_1858 | right |

**Pseudomonas putida KT2440, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.75 | TCGACCTAAAGTTAAGTTGAGCTTTT | left | -6 | soxR (PP_2060) | right |
| 6.17 | TTGACCTCGAGTTAAGTCAAGGTTTT | left | -288 | PP_2505 | right |
| | | right | -55 | PP_2506 | |

**Pseudomonas putida W619, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.27 | TTGACCTTGAGTTAACTGGAGGTTTT | left | -64 | PputW619_3439 | left |

**Pseudomonas stutzeri A1501, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.98 | TTGACCTCAAGTTCGCTTGAACTTCT | left | -8 | PST_1793 | left |

**Ralstonia eutropha H16 chromosome 1, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.60 | TTGACCTCAAGTCGACTTGAACTGGC | left | -45 | h16_A0054 (H16_A0054)-h16_A0053 (H16_A0053) | left |
| | | right | -55 | h16_A0055 (H16_A0055) | |

**Ralstonia eutropha H16 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.62 | TTGACCTCAATTTAGGTTGAGGTTTG | left | -50 | h16_B2318 (H16_B2318) | left |
| | | right | -71 | h16_B2319 (H16_B2319) | |

**Ralstonia metallidurans CH34 chromosome 2, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.74 | TTGACCTCAAGCGTGCTTGAGGTTTG | left | -63 | Rmet_4538 | right |
| | | right | -85 | Rmet_4539 | |

**Renibacterium salmoninarum ATCC 33209, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.59 | TTGACCTCAAGTTAGCTTGAGGTTCT | left | -9 | soxR (RSal33209_3062)-RSal33209_3061-RSal33209_3060 | right |
| | | right | -593 | RSal33209_3063 | |
| 6.65 | TTGACCTCAACAAAGGTTGAGGGATT | left | -11 | RSal33209_3297 | left |

**Rhizobium etli CFN 42, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.88 | TTGACCTCAACCATAGTTGAGGAATT | left | -399 | RHE_CH02960 | right |
| | | right | -89 | RHE_CH02961 | |
| 6.09 | TTGACCTCAATATTAGTTGAGGTTTT | left | -6 | soxR (RHE_CH03863) | right |
| | | right | -606 | RHE_CH03864-RHE_CH03865 | |

**Rhizobium etli CFN 42 plasmid p42f, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.29 | TTAACTTCAAGTTAACTTGAACTTGT | left | -34 | RHE_PF00559-RHE_PF00558 | left |
| | | right | -77 | RHE_PF00560 | |

**Rhizobium leguminosarum bv. viciae 3841, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.38 | TTGACCTCAGGTTAACTTGAGGAATT | left | -92 | RL3412 | right |
| 3.89 | TTGACCTCAAGATTAGTTGAGGTTTT | left | -6 | RL4397 | right |
| | | right | -103 | RL4398 | |

**Rhodopseudomonas palustris BisB5, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.45 | TTGACCTCAACTAAGGTTGAGGTTCT | left | -73 | RPD_3140-RPD_3139 | left |
| | | right | -58 | RPD_3141 | |

**Saccharopolyspora erythraea NRRL 2338, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.27 | TTGACCTCGACCTTGCTTGAGCTTTT | left | -44 | SACE_4991 | right |
| | | right | -95 | SACE_4992 | |
| 7.12 | TTGACCTCCAGCCAACTCGAAGTTTC | left | -11 | SACE_5763-SACE_5762 | left |
| | | right | -98 | soxR (SACE_5764) | |

**Salinispora tropica CNB-440, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.46 | TTGACCTCAACCACGGTTGAGGTTTT | left | -42 | Strop_0660 | left |
| 6.91 | TTGATCTGAAGTTAACTTCAGGTTGT | left | -242 | Strop_4405 | right |
| | | right | -63 | Strop_4406 | |

**Salmonella enterica subsp. arizonae serovar 62:z4,z23:–, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -7<br>-105 | SARI_03411<br>SARI_03412 | right |

**Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -53<br>-59 | soxS (SC4144)<br>soxR (SC4145) | left |

**Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -53<br>-59 | soxS (SPA4081)<br>soxR (SPA4082) | left |

**Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -53<br>-59 | SPAB_05256<br>SPAB_05257 | left |

**Salmonella typhimurium LT2, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -53<br>-59 | soxS (STM4265)<br>soxR (STM4266) | left |

**Salmonella enterica subsp. enterica serovar Typhi str. CT18, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -53<br>-59 | soxS (STY4463)<br>soxR (STY4464) | left |

**Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left<br>right | -53<br>-59 | soxS (t4171)<br>soxR (t4172) | left |

**Shewanella amazonensis SB2B, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.90 | TTGACCTCAAGTTGACTTGAAGTTGT | left<br>right | -9<br>-91 | Sama_3347<br>Sama_3348 | right |

**Shewanella denitrificans OS217, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 0.98 | TTGACCTCAAGTTAGCTTGAGCTTTT | left | -38 | Sden_0647 | left |
| | | right | -271 | Sden_0648 | |
| 2.12 | TTTACCTCAAGCTAACTTGAGGTTTT | left | -33 | Sden_2124 | left |
| | | right | -145 | Sden_2125 | |

**Shewanella frigidimarina NCIMB 400, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.70 | TTTACCTCAAGTTAGCTTTAGGTATT | left | -41 | Sfri_1565 | right |
| | | right | -86 | Sfri_1566 | |

**Shewanella loihica PV-4, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.88 | TTGACCTCAAGTCGACTTGAAGTTGT | left | -42 | Shew_0422 | left |
| | | right | -61 | Shew_0423 | |

**Shigella dysenteriae Sd197, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -7 | soxR (SDY_4504) | right |
| | | right | -104 | soxS (SDY_4505) | |

**Shigella flexneri 2a str. 2457T, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (S3589) | left |
| | | right | -59 | soxR (S3590) | |

**Shigella flexneri 2a str. 301, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (SF4122) | left |
| | | right | -59 | soxR (SF4123) | |

**Shigella flexneri 5 str. 8401, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -7 | soxR (SFV_4149) | right |
| | | right | -104 | soxS (SFV_4150) | |

**Shigella sonnei Ss046, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.02 | TTTACCTCAAGTTAACTTGAGGAATT | left | -52 | soxS (SSON_4242) | left |
| | | right | -349 | SSON_4243 | |

**Silicibacter pomeroyi DSS-3, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.78 | TTGACCTAAAGTTAGGTTTAGAAATT | left | -38 | SPO0313 | left |
| | | right | -72 | soxR (SPO0314) | |

**Silicibacter sp. TM1040 mega plasmid, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.26 | TTGAGCTAAAGTTAGGTTTAGAAATT | left | -80 | TM1040_3746 | right |
| | | right | -91 | TM1040_3747 | |

**Silicibacter sp. TM1040, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.48 | TTGATCTAAAGTGAGCTTGAGGAATT | left | -96 | TM1040_1862-TM1040_1861-TM1040_1860-TM1040_1859 | right |
| | | right | -122 | TM1040_1863 | |

**Sinorhizobium medicae WSM419, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.48 | TTGACCTCAACTTTAGTTGAGGTTCT | left | -5 | Smed_1545 | left |
| | | right | -60 | Smed_1546 | |

**Sinorhizobium meliloti 1021, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.46 | TTGACCTCAACTATAGTTGAGGTTCT | left | -44 | SMc00183 | left |
| | | right | -60 | SMc00182 | |
| 7.29 | TTGACCTCAAGTACGGTTGAGGTCGC | left | -88 | SMc03095 | right |

**Sorangium cellulosum 'So ce 56', complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.63 | TTGACCTCAAGTTGACTTGAGCTTGC | left | -45 | sce1907 | left |
| | | right | -54 | sce1908 | |

**Sphingopyxis alaskensis RB2256, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.19 | TTGACCTCCACTGCACTTGAGCTTTC | left | -37 | Sala_2373 | left |

**Streptomyces avermitilis MA-4680, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.02 | TTGACCTGAAGTTTGGTTGAGGTTGC | left | -637 | gbsA1 (SAV_1622) | right |
| | | right | -64 | SAV_1623 | |
| 6.19 | TTGACCTCAAGATTGCTTGAGGTTCT | left | -253 | SAV_7217 | right |
| | | right | -64 | SAV_7218 | |
| 6.82 | TTGACCTCAAGATTGGTTGAGGTACC | left | -328 | SAV_5664 | right |
| | | right | -82 | SAV_5665 | |

**Streptomyces coelicolor A3(2), complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.54 | TTGACCTCAAGCAAACTTGAGGTACC | left | -57 | SCO2478 | left |
| | | right | -178 | SCO2479 | |
| 7.58 | TTGACCTCAAGCAGGCTTGAGGTCGT | left | -45 | SCO4266 | left |

**Thermobifida fusca YX, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.46 | TTGACCTCAACTTTGGTTGAGGTTTT | left | -278 | Tfu_1696-Tfu_1695 | right |
| | | right | -133 | Tfu_1697 | |
| 5.90 | TTGACCTCAACCTAACCTGAGATTTG | left | -27 | Tfu_0408 | right |
| | | right | -141 | Tfu_0409 | |

**Trichodesmium erythraeum IMS101, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 5.69 | TTAACCTCAAGTTAACTTTAGATAGT | left | -1745 | Tery_1256 | right |

**Vibrio cholerae O1 biovar eltor str. N16961 chromosome II, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.41 | TTTACCTAAAGTTAACTTGAGGTATT | left | -115 | VCA0084 | right |
| | | right | -89 | VCA0085 | |

**Vibrio cholerae O395 chromosome 1, complete sequence**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 2.41 | TTTACCTAAAGTTAACTTGAGGTATT | left | -37 | VC0395_0055 | left |
| | | right | -168 | soxR (VC0395_0056) | |

### Vibrio harveyi ATCC BAA-1116 chromosome I, complete sequence

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 1.90 | TTGACCTAAAGTTAACTTGAGCTTTT | left | -35 | VIBHAR_02685 | left |
| | | right | -260 | VIBHAR_02686 | |

### Vibrio harveyi ATCC BAA-1116 chromosome II, complete sequence

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.56 | TTGACCTCAACTTCGGTTGAGGTTTT | left | -41 | VIBHAR_06924 | left |
| | | right | -274 | VIBHAR_06925 | |
| 4.10 | TTTACCTTAACTTAACTTGAGGTTTT | left | -44 | VIBHAR_04755 | left |
| | | right | -124 | VIBHAR_04756 | |
| 4.10 | TTAACCTCAACCTAGCTTGAGGTTTT | left | -129 | VIBHAR_07059 | left |
| | | right | -206 | VIBHAR_07060 | |

### Vibrio parahaemolyticus RIMD 2210633 chromosome II, complete sequence

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 3.69 | TTGACCTAAACCAAACTTGAGGTTTT | left | -99 | VPA1738 | right |
| 4.81 | TTTACCTCAAGTTTACTTGAGGTTCT | left | -89 | VPA0335 | left |
| 5.59 | TTTACCTAAACTTAGCTTGAGGTTCT | left | -163 | VPA0390 | right |
| | | right | -98 | VPA0391 | |
| 5.89 | TTTACCTCGATTTAACTTGAGGTTTT | left | -96 | VPA1685 | right |

### Vibrio vulnificus CMCP6 chromosome II, complete sequence

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 0.81 | TTGACCTCAAGTTAACTTGAGGAATT | left | -109 | VV2_1129 | right |
| 2.19 | TTTACCTCAAGTTAAGTTGAGCTTTT | left | -57 | VV2_0936 | right |
| | | right | -97 | VV2_0937 | |
| 3.40 | TTTACCTCAATTTAACTTGAGGTTTT | left | -35 | VV2_0607 | left |
| | | right | -230 | VV2_0608 | |

### Vibrio vulnificus YJ016 chromosome II, complete sequence

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 0.81 | TTGACCTCAAGTTAACTTGAGGAATT | left | -110 | VVA1655-VVA1656 | right |
| 2.19 | TTTACCTCAAGTTAAGTTGAGCTTTT | left | -57 | VVA1425 | right |
| | | right | -79 | VVA1426 | |
| 3.40 | TTTACCTCAATTTAACTTGAGGTTTT | left | -35 | VVA1158 | left |
| | | right | -230 | VVA1159 | |

**Xanthomonas campestris pv. campestris str. 8004, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.93 | TTGACCTCAACCTTGGTTGAGGCAGG | left | -166 | XC_1279 | left |
| | | right | -56 | XC_1280 | |

**Xanthomonas campestris pv. campestris str. ATCC 33913, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 6.93 | TTGACCTCAACCTTGGTTGAGGCAGG | left | -4 | soxR (XCC2831) | right |
| | | right | -729 | XCC2832 | |

**Xanthomonas campestris pv. vesicatoria str. 85-10, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.72 | TTGACCTCAACTTAGGTTGAGGCAGG | left | -4 | soxR (XCV3149) | right |
| | | right | -121 | XCV3150 | |

**Xanthomonas axonopodis pv. citri str. 306, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.72 | TTGACCTCAACTTAGGTTGAGGCAGG | left | -4 | soxR (XAC3000) | right |
| | | right | -121 | ptr (XAC3001) | |
| 7.66 | TTGACCTCAACTGCGCTTGAGGTCGT | left | -31 | XAC0314 | left |
| | | right | -278 | XAC0315 | |

**Xanthomonas oryzae pv. oryzae MAFF 311018, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 7.31 | TTGACCTCAACTCAGGTTAAGGCAGG | left | -70 | XOO1154 (XOO_1154) | left |
| | | right | -56 | XOO1155 (XOO_1155) | |

**Zymomonas mobilis subsp. mobilis ZM4, complete genome**

| Site Energy | Sequence | Operon pos | Distance to start | Genes in operon | Orientation |
|---|---|---|---|---|---|
| 4.25 | TTGACCTCAAGTTAACTTGAGGTTCA | left | -116 | ZMO0169 | left |