

- 1 -

piece 1, NC\_000913, rhaT\_sodA-, config: linear, direction: -, begin: 4098862, end: 4098529

5' \*4098860 \* \*4098850 \* \*4098840 \* \*4098830 \* \*4098820 \* \*4098810 \* \*4098800 \* \*4098790 \*  
- ile - arg - gln - gly - trp - gln - gly - ile - ala - his - ile - his - leu - gln - tyr - cys - arg - ala - ala - asp - cys -  
- thr - ala - gly - met - ala - gly - tyr - ser - ser - tyr - ser - pro - val - leu - ser - gly - gly - arg - leu - leu - met - pro - arg - lys - gln - leu -  
... ] NC\_000913.sodA

p35 2.1 bits

5' \*4098780 \* \*4098770 \* \*4098760 \* \*4098750 \* \*4098740 \* \*4098730 \* \*4098720 \* \*4098710 \*  
- fMet - ile - leu - lys - met - ile - ile - ASN - ala - val - leu - phe - val - arg - val - trp - phe - cys - arg - lys -  
- val - his - tyr - ser - red box ir rhaT\_sodA- [###] orf 6 codons {----} ... sd-(13)-ir 4098691 Gap  
... p35-(24)-p10 4098772 Gap 2.4 bits ir rhaT\_sodA- ... sd

... p35-p10 4098772 total 5.5 bits p35 6.4 bits ir rhaT\_sodA- {----} ... sd-ir 4098691 rhaT\_sodA-

{----} sd {----} sd-(10)-ir 4098748 Gap 2.7 bits p35 3.5 bits {----} ... sd-(15)-ir 4098689 Gap  
{----} sd-(9)-ir 4098760 Gap 2.3 bits p10 3.8 bits {----} ... sd-ir 4098760 rhaT\_sodA- total 5.5 bits  
|----| sd-ir 4098760 rhaT\_sodA- total 5.5 bits p10 5.9 bits {----} ... p10

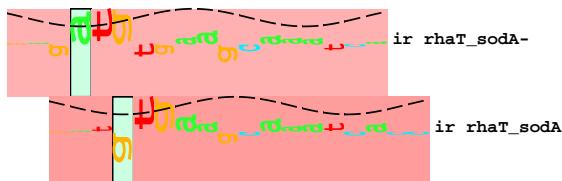
{----} sd {----} sd-(8)-ir 4098738 Gap 2.4 bits |----| sd-ir 4098748 rhaT\_sodA- total 11.0 bits {----} p35-(24)-p10 4098703 Gap 2.4 bits  
|----| sd-ir 4098738 rhaT\_sodA- total 5.4 bits p35-(22)-p10 4098731 Gap 2.3 bits {----} p35-p10 4098703 total 4.6 bits  
|----| p35-p10 4098731 total 7.8 bits

5' \*4098700 \* \*4098690 \* \*4098680 \* \*4098670 \* \*4098660 \* \*4098650 \* \*4098640 \* \*4098630 \* \*4098620 \*  
- met - pro - glu - met - red box sd {----} orf 25 codons |----| sd-ir 4098691 rhaT\_sodA- total 7.6 bits  
- ala - arg - asp - val - lys - gln - ile - thr - his - leu - met - pro - red box orf 10 codons {----} sd-ir 4098691 rhaT\_sodA- total 7.6 bits  
... sd-(13)-ir 4098691 Gap 4.6 bits {----} sd-(15)-ir 4098689 Gap 6.0 bits

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... -----| sd-ir 4098689 rhoT\_sodA- total 7.2 bits

. p10 3.6 bits



The figure shows a protein sequence alignment at the top and a secondary structure diagram below it. The sequence is aligned with a reference sequence, showing amino acid substitutions (e.g., ile, asp, ser, thr, phe, thr, leu, ile, ser, ser, glu, met) and stop codons (red dots). The secondary structure is indicated by green arrows and dashed lines, with labels for fMet, sd, and [-]. A legend at the bottom right identifies the color scheme for the sequence.

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{-----} sd-(9)-ir 4098548 Gap 2.3 bits  
|-----| sd-ir 4098548 rhaT_sodA- total 15.0 bits
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5' c g a t t a c g a t 3'

-ile - thr -

\* \*4098530

... NC\_000913.rhAT