

- 1 -

piece 1, NC_000913, uvrA_ssbt, config: linear, direction: +, begin: 4271865, end: 4272167

5' c g a t c a c a a c c g g t t a a t t a t g a c a a a t t g a c t t g a a t q a a t a t a c a g t t a t t g g a a t g c a t t t a c c c g g a g t t g t g t a 3'
 - arg - ser - gln - thr - val - asn - tyr - asp - thr - asn - - - - - fMet - his - tyr - pro - glu - cys - cys - val -
 - asp - his - lys - arg - leu - ile - met - thr - glm - ile - asp - leu - asn - glu - tyr - thr - val - leu - glu - cys - ile - thr - arg - ser - val - val -
 - ile - thr - asn - gly - - - - - fMet - thr - - fMet - asn - ile - gln - tyr - trp - asn - ala - leu - pro - gly - val - leu - cys - asn -

[----] sd-(7)-ir 4271965 Gap 3.7 bits
[-----] sd-ir 4271965 uvrA ssb+ total 11.5 bits

orf 21 codons

p35 4.8 bits p10 2.7 bits p10 6.9 bits

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... | p35-p10 4272027 total 4.8 bits

Diagram illustrating the structure of a sequence with various segments labeled p35, p10, and gaps. The segments are color-coded: purple for p35, blue for p10, and green for gaps.

- p35-p10 4272067 total 5.2 bits**: A purple segment followed by a blue segment.
- p35 3.8 bits**: A purple segment.
- p10 3.0 bits**: A blue segment.
- p35-(22)-p10 4272070 Gap 2.3 bits**: A purple segment followed by a blue segment, separated by a green gap.
- p35-p10 4272070 total 4.4 bits**: A purple segment followed by a blue segment.
- p35 1.4 bits**: A purple segment.
- p35-(24)-p10 4272096 Gap 2.4 bit**: A purple segment followed by a blue segment, separated by a green gap.
- p35-p10 4272096 total 5.9 bits**: A purple segment followed by a blue segment.

Sequence alignment diagram showing the amino acid sequence of p10 (5.8 bits) aligned with a reference sequence. The alignment highlights conserved residues in green and divergent residues in red. Domains p10, sd, and [] are indicated by colored boxes. A red circle marks a stop codon at the end of the sequence.

... -----} p35-(23)-p10 4272110 Gap 1.4 bits
... -----| p35-p10 4272110 total 7.8 bits