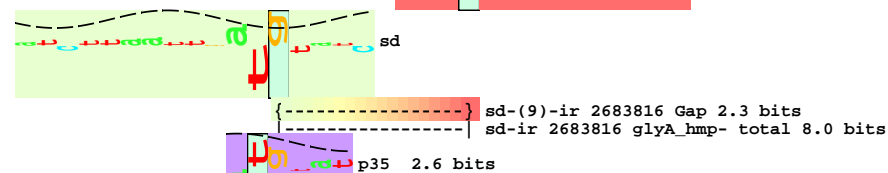


piece 1, NC_000913, glyA_hmp-, config: linear, direction: -, begin: 2683886, end: 2683510

* 2683880 * 2683870 * 2683860 * 2683850 * 2683840 * 2683830 * 2683820 * 2683810
 5' t a c t g t a g c g a t g g t t t g a g c g t c a a g c a t a t g g t c t t c c t t t t t t g c a t c t t a a t t g a t c t c a a a t g c a t c t t a t 3'
 - tyr - cys - ser - asp - gly - leu - ser - val - lys - his - met - val - phe - leu - phe - leu - his - leu - asn - fMet - his - leu - ile
 - thr - val - ala - met - val - leu -
 - leu -

NC_000913.hmp



* 2683800 * 2683790 * 2683780 * 2683770 * 2683760 * 2683750 * 2683740 * 2683730 *
 5' a a a a a a t a g c c c t g c a a t g t a a a t g g t t c t t t g g t g t t t t c a g a a a g a a t g t g a t g a a g t g a a a a a t t t g c a t c a c a a a c 3'
 - lys - asn - ser - pro - ala - met - fMet - val - leu - trp - cys - phe - ser - glu - arg - met - fMet - lys - asn - leu - his - his - lys - pro -

ir glyA_hmp-

orf 11 codons

p35 4.3 bits

ir glyA_hmp-

orf 3 codons

p10 3.8 bits

sd-(7)-ir 2683751 Gap 3.7 bits
sd-ir 2683751 glyA_hmp- total 7.8 bits

p35-(23)-p10 2683803 Gap 1.4 bits

p35-p10 2683803 total 4.9 bits

sd-(8)-ir 2683746 Gap 2.4 bits
sd-ir 2683746 glyA_hmp- total 6.8 bits
p35-(24)-p10 2683742 Gap 2.4 bits
p35-p10 2683742 total 5.7 bits

* 2683720 * 2683710 * 2683700 * 2683690 * 2683680 * 2683670 * 2683660 * 2683650 *
 5' c t g a a a a g a a a t c c g t t t c c g g t t g c a a g c t c t t t a t t c t c c a a a g c c t t g o g t a g c o t g a a g g t a a t c g t t t g c g t a a a t 3'
 - glu - lys - lys - ser - val - ser - gly - cys - lys - leu - phe - ile - leu - phe - gln - ser - leu - ala - fMet - arg - lys - val - phe -
 - fMet - gln - ala - leu - tyr - ser - pro - lys - pro - cys - val - ala -

p35 4.8 bits

orf 26 codons

p10

p10 3.4 bits

p35-(21)-p10 2683670 Gap 3.3 bits
p35-p10 2683670 total 4.9 bits

p35 2.1 bits

p35-(23)-p10 2683647 Gap 1.4 bits

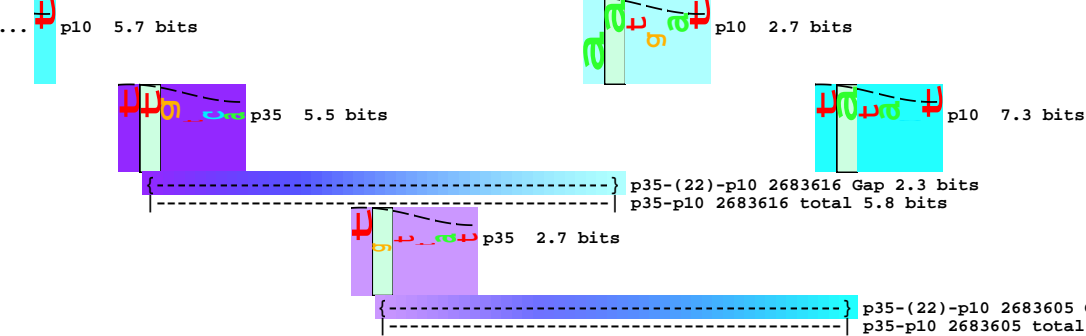
*2683640 * *2683630 * *2683620 * *2683610 * *2683600 * *2683590 * *2683580 * *2683570 *

5' t c c t t t g t c a a g a c c t g t t a t c g c a c a a t g a t t c g g t t a t a c t g t t c g c c g t t g t c c a a c a g g a c c g c c t a t a a a g g c c a a 3'

- ser - phe - val - lys - thr - cys - tyr - arg - thr - met - ile - arg - leu - tyr - cys - ser - pro - leu - ser - asn - arg - thr - ala - tyr - lys - gly - gln -

-fMet - ser - arg - pro - val - ile - ala - gln -

- leu - cys - gln - asp - leu - leu - ser - his - asn - asp - ser - val - ile - leu - phe - ala - val - val - gln - gln - asp - arg - leu -



*2683560 * *2683550 * *2683540 * *2683530 * *2683520 * *2683510 *

5' a a a t t t t a t t g t t a g c t g a g t c a g g a g a t g c g g a t g t t a a a g c g t g a a a t g a a 3'

- lys - phe - tyr - cys - - - -fMet - arg - met - leu - lys - arg - glu - met -

- - - -fMet - leu - ala - glu - ser - gly - asp - ala - asp - val - lys - ala - - -

