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piece 1, NC_000913, yijP_ppc+, config: linear, direction: +, begin: 4148259, end: 4148489

Sequence alignment of nine homologous genes (4148260 to 4148330) showing amino acid sequences. The alignment highlights conserved residues with red dots and divergent residues with black dashes. Amino acids are shown below the sequence lines.

... -----] NC_000913.yijP

p10 3.8 bits

p10 2.9 bits

p35 3.1 bits

p35 6.4 bits

p35 2.2 bits

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{-----} p35-(24)-p10 4148308 Gap 2.4 bits  
|-----| p35-p10 4148308 total 4.5 bits  
{-----} ... p35-(22)-p10 4148355 Gap  
|-----| ... p35-p10 4148355 total 6.4  
{-----} p35-(25)-p10 4148329 Gap 4.0 bits  
|-----| p35-p10 4148329 total 5.3 bits
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The diagram illustrates the p10 gene structure across three mRNA strands. The top strand shows the gene name (*4148340 to *4148420) and its orientation (5' to 3'). The middle strand displays the amino acid sequence (fMet-lys-thr-arg-val-leu-glut-gln-lys-tyr-). The bottom strand indicates the reading frame with arrows and labels for start sites (sd), initiation regions (ir), and termination codons (ppc+). Colored boxes highlight specific regions: green for the first reading frame, red for the second, and blue for the third. Red dots mark termination codons.

----- } p35-(22)-p10 4148355 Gap 2-3 bits

... -----| p35-p10 4148355 total 6.4 bits
|-----| sd-ir 4148366 vijp ppct total 5.7 bits

p35 6.5 bits

|-----| p35-p10 4148389 total 10.7 bits

... p10 1.5 bits  p35 5.2 bits <----- ... NC_000913.ppc

{ } p35-(24)-p10 4148479 Gap 2.4 bits
p35-p10 4148479 total 5.5 bits