

Query ID

lcl|64049

Description

Pros28.1Amel (246 bp 5' region intron and part of exon of CG42322 +26bp 5'UTR = 272bp of the construct)

Molecule type

nucleic acid

Query Length

272

Subject ID

64051

Description

Pros28.1ADyak (5'UTR and 5'region intron of GE25683 = 289 bp)

Molecule type

nucleic acid

Subject Length

289

Program

BLASTN 2.2.22


```
Query 236 TTG---TTTCAAGTAAATAACTTGT CACAAGCAA 266
      ||      ||||| ||| ||||| ||| |||||
Sbjct 221 TTTACTTTTCAAATAACTAACTGGTCGCAAGCAA 254
```

Score = 24.7 bits (26), Expect = 0.003
Identities = 16/18 (88%), Gaps = 0/18 (0%)
Strand=Plus/Plus

```
Query 240 TTCAAGTAAATAACTTGT 257
      || || ||||| |||||
Sbjct 47 TTAAATTAAATAACTTGT 64
```

Score = 17.5 bits (18), Expect = 0.39
Identities = 9/9 (100%), Gaps = 0/9 (0%)
Strand=Plus/Plus

```
Query 108 TAAATAACT 116
      ||||| |||
Sbjct 53 TAAATAACT 61
```

Score = 15.7 bits (16), Expect = 1.4
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Plus

```
Query 123 AAATTATT 130
      ||||| |||
Sbjct 33 AAATTATT 40
```

Score = 15.7 bits (16), Expect = 1.4
Identities = 21/27 (77%), Gaps = 2/27 (7%)
Strand=Plus/Minus

```
Query 103 TTTTGTAAT-AACTCAA-AGAAATT 127
          ||||| | | ||| ||| |||||
Sbjct 113 TTTTGTTACTTAACGCAATCAGAAATT 87
```

Score = 15.7 bits (16), Expect = 1.4
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Plus

```
Query 261 AAGCAAAT 268
          |||||
Sbjct 136 AAGCAAAT 143
```

Score = 15.7 bits (16), Expect = 1.4
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Plus

```
Query 109 AAATAACT 116
          |||||
Sbjct 231 AAATAACT 238
```

Score = 13.9 bits (14), Expect = 4.7
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 98 GGGAGTT 104
```

Sbjct 12 |||||
 GGGAGTT 18

Score = 13.9 bits (14), Expect = 4.7
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 189 AAATAAA 195
 |||||
Sbjct 71 AAATAAA 65

Score = 13.9 bits (14), Expect = 4.7
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 16 ATTCCAT 22
 |||||
Sbjct 128 ATTCCAT 122

Score = 13.9 bits (14), Expect = 4.7
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

Query 78 CAAAATA 84
 |||||
Sbjct 149 CAAAATA 143

Score = 13.9 bits (14), Expect = 4.7

Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query  243  AAGTAAA  249
          ||| |||
Sbjct  227  AAGTAAA  221
```

Score = 13.9 bits (14), Expect = 4.7
Identities = 13/16 (81%), Gaps = 3/16 (18%)
Strand=Plus/Plus

```
Query  51  GTCGCA---AAGTATA  63
          ||| ||| ||| |||
Sbjct  244  GTCGCAAGCAAGTATA  259
```

Score = 13.9 bits (14), Expect = 4.7
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query  32  CTAGCAA  38
          ||| |||
Sbjct  274  CTAGCAA  280
```