

Query ID

lcl|2015

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

2017

Description

Pros28.1B (5'UTR 47 bp and 5'region 228 bp=275bp)

Molecule type

nucleic acid

Subject Length

275

Program

BLASTN 2.2.22



Score = 19.3 bits (20), Expect = 0.11
 Identities = 12/13 (92%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

```

Query 232 CATATTGTTTCAA 244
      |||
Sbjct 121 CATATTGTTTAA 109
  
```

Score = 17.5 bits (18), Expect = 0.37
Identities = 9/9 (100%), Gaps = 0/9 (0%)
Strand=Plus/Minus

```
Query 160 TTATCATAA 168
      ||| ||| ||| |||
Sbjct 86 TTATCATAA 78
```

Score = 15.7 bits (16), Expect = 1.3
Identities = 8/8 (100%), Gaps = 0/8 (0%)
Strand=Plus/Plus

```
Query 222 AAGAAAAA 229
      ||| ||| ||| |||
Sbjct 95 AAGAAAAA 102
```

Score = 15.7 bits (16), Expect = 1.3
Identities = 17/23 (73%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 189 AAATAAAGGATTTTGGACTTCAAA 211
      || ||| | | || ||| |||
Sbjct 107 AATTAAAACAATATGTCTTCAAA 129
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query 207 TCAAAC 213
      |||||
Sbjct 23 TCAAAC 17
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 185 TAGAAAA 191
      |||||
Sbjct 35 TAGAAAA 41
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 108 TAAATAA 114
      |||||
Sbjct 51 TAAATAA 57
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 246 TAAATAA 252
      |||||
Sbjct 51 TAAATAA 57
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query  189  AAATAAA  195
          |||||
Sbjct  52   AAATAAA  58
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Minus

```
Query  216  AAATGTA  222
          |||||
Sbjct  78   AAATGTA  72
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 9/10 (90%), Gaps = 0/10 (0%)
Strand=Plus/Minus

```
Query  152  ACATATTATT  161
          ||||| ||
Sbjct  122  ACATATTGTT  113
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 212 CTTCAAA 218
      |||
Sbjct 123 CTTCAAA 129
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 116 TCAAAAG 122
      |||
Sbjct 125 TCAAAAG 131
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 128 ATTGATT 134
      |||
Sbjct 153 ATTGATT 159
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 55 CAAAGTA 61
      |||
Sbjct 233 CAAAGTA 239
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 9/10 (90%), Gaps = 0/10 (0%)
Strand=Plus/Minus

```
Query 176 ACTATGGTGT 185
      ||| ||| ||
Sbjct 250 ACTATGGAGT 241
```

Score = 13.9 bits (14), Expect = 4.5
Identities = 7/7 (100%), Gaps = 0/7 (0%)
Strand=Plus/Plus

```
Query 213 TTCAAAT 219
      ||| ||| ||
Sbjct 253 TTCAAAT 259
```