

Query ID

lcl|63459

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

63461

Description

Pros28.1 (5'UTR 146 bp and 5'region 129 bp=275bp)

Molecule type

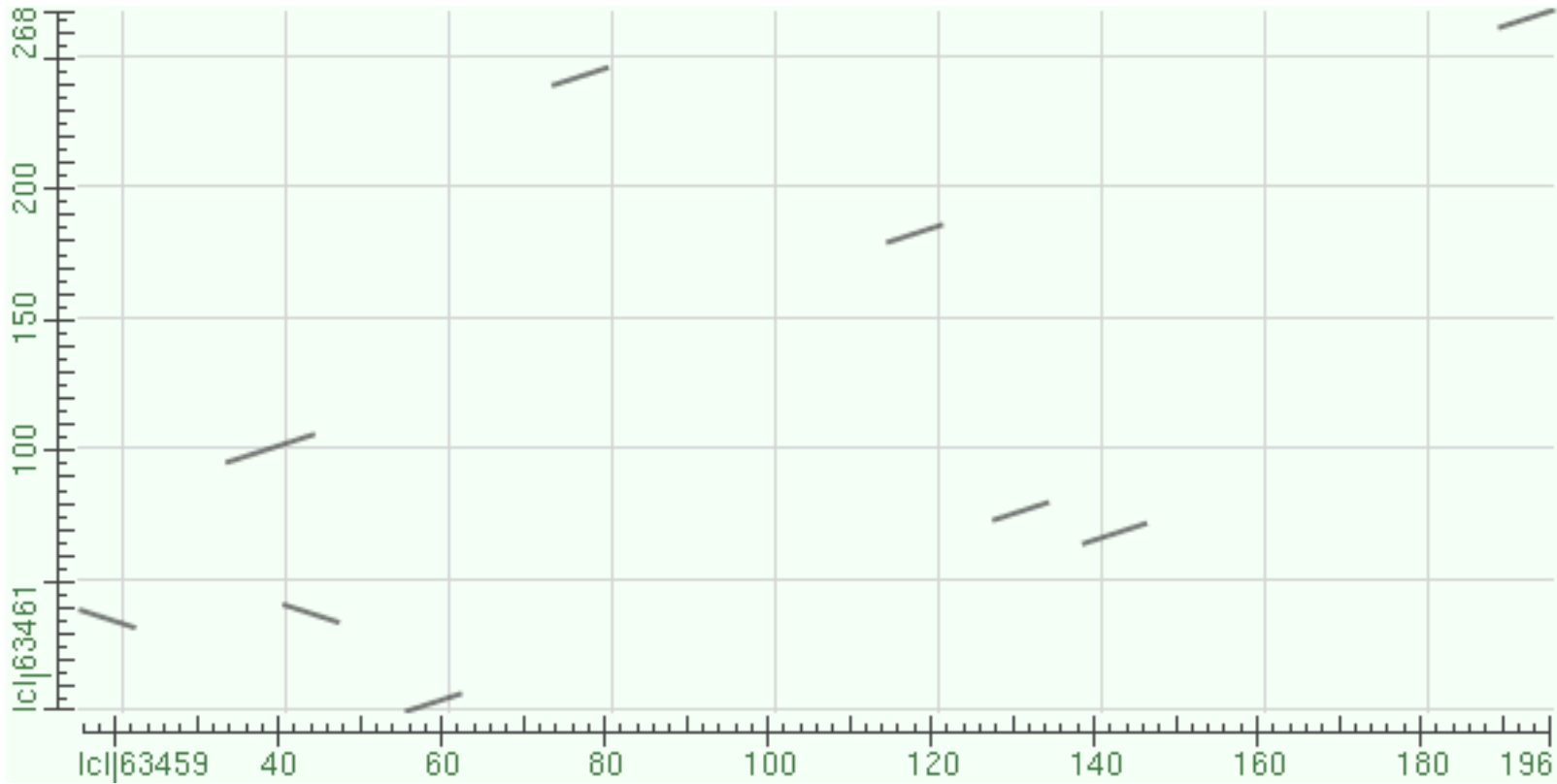
nucleic acid

Subject Length

275

Program

BLASTN 2.2.22



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

```

Query 139 AAGAATTG 146
      |||||
Sbjct 65  AAGAATTG 72
  
```

Score = 15.7 bits (16), Expect = 1.3
Identities = 10/11 (90%), Gaps = 0/11 (0%)
Strand=Plus/Plus

```
Query  34  AGCAACGCTAT  44
      ||| ||| |||
Sbjct  96  AGCAACGATAT  106
```

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

```
Query  56  AAAGTAT  62
      ||| ||| |||
Sbjct  1   AAAGTAT  7
```

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

```
Query  16  ATTCCAT  22
      ||| ||| |||
Sbjct  39  ATTCCAT  33
```

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

```
Query 41 CTATTCC 47
      |||
Sbjct 41 CTATTCC 35
```

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

```
Query 128 ATTGATT 134
      |||
Sbjct 74 ATTGATT 80
```

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

```
Query 115 CTCAAAA 121
      |||
Sbjct 180 CTCAAAA 186
```

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

```
Query 74 TCTGCAA 80
      |||
Sbjct 240 TCTGCAA 246
```

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

Query	190	AATAAAG	196
Sbjct	262	AATAAAG	268