

Additional File 3. Discontinuous sequence identity between Accession JN606867 and clone TrVe61FuB1_8246

“Align Sequences Nucleotide BLAST” was performed with the default setting of blastn.

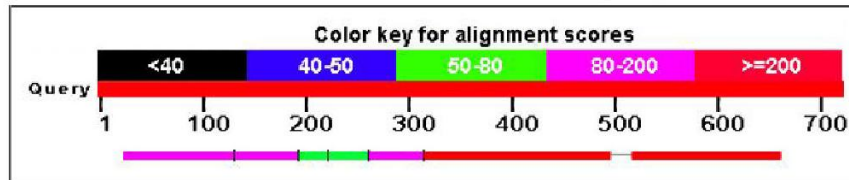
Blast 2 sequences

TrVe61FuB1_8246: Length -- 513 bp | protein...

Query ID	icl 56675	Subject ID	56677
Description	TrVe61FuB1_8246: Length -- 513 bp protein binding other cellular components other biological processes	Description	JN606867
Molecule type	nucleic acid	Molecule type	nucleic acid
Query Length	716	Subject Length	2295
		Program	BLASTN 2.2.26+

Graphic Summary

Distribution of 7 Blast Hits on the Query Sequence



<u>Accession</u>	<u>Description</u>	<u>Max score</u>	<u>Total score</u>	<u>Query coverage</u>	<u>E value</u>	<u>Max ident</u>	<u>Links</u>
56677	JN606867	335	1171	85%	2e-05	100%	

Alignments

>lcl|56677 JN606867
Length=2295

Sort alignments for this subject seq
E value Scores Percent identity
Query start position Subject start

Score = 335 bits (181), Expect = 2e-95
Identities = 184/186 (99%), Gaps = 0/186 (0%)
Strand=Plus/Minus

```
Query 308 CCTGCCAATGCTTCTTCTTACAAGTGCACCATCGCCCTCGGACTGGGACTTGGCCAAGAT 367
      |||
Sbjct 186 CCTGCCAATGCTTCTTCTTACAAGTGCACCATCGCCCTCGGACTGGGACTTGGCCAAGAT 127

Query 368 CTTCTGGCAACTAGTCTGGGCTGTGGAAACTGGACATGATGATATAACGTCGAGAAGA 427
      |||
Sbjct 126 CTTCTGGCAACTAATCTGGGCTGTGGAAACTGGACATGATGATATAACGTCGAGAAGA 67

Query 428 CGGGTTTTTTTATTATTGKGGGATTTGATGTTTTATGAGGAATGAAAGTTTAGTAGATACAGA 487
      |||
Sbjct 66 CGGGTTTTTTTATTATTGKGGGATTTGATGTTTTATGAGGAATGAAAGTTTAGTAGATACAGA 7

Query 488 GATCAT 493
      |||
Sbjct 6 GATCAT 1
```

Score = 265 bits (143), Expect = 2e-74
Identities = 143/143 (100%), Gaps = 0/143 (0%)
Strand=Plus/Plus

```
Query 514 CACGGTCCGTTTGTGATGAATACGCACGCTGAGATTGACAAAAAATGGAAGACTATTAC 573
      |||
Sbjct 1988 CACGGTCCGTTTGTGATGAATACGCACGCTGAGATTGACAAAAAATGGAAGACTATTAC 2047

Query 574 TATGGCAAGAATGGTTTCGAGCTGGCaaaaaaTGGAAATCTAAATGAGCTACATATAAG 633
      |||
Sbjct 2048 TATGGCAAGAATGGTTTCGAGCTGGCaaaaaaTGGAAATCTAAATGAGCTACATATAAG 2107

Query 634 CAACTGCTTAGGGCCCCAAAAGA 656
      |||
Sbjct 2108 CAACTGCTTAGGGCCCCAAAAGA 2130
```

Score = 196 bits (106), Expect = 9e-54
Identities = 106/106 (100%), Gaps = 0/106 (0%)
Strand=Plus/Minus

```
Query 25 TTTTGTCTTGGGAAGAGAGATTGATCCACAATTGAGACCAGTGTGAGTGCCTTCTCCGG 84
      |||
Sbjct 1511 TTTTGTCTTGGGAAGAGAGATTGATCCACAATTGAGACCAGTGTGAGTGCCTTCTCCGG 1452

Query 85 CGGGCATTTCTGAGTGAACAATACCTCTGCCGGCAGTCATCCACTG 130
      |||
Sbjct 1451 CGGGCATTTCTGAGTGAACAATACCTCTGCCGGCAGTCATCCACTG 1406
```

Score = 121 bits (65), Expect = 5e-31
Identities = 65/65 (100%), Gaps = 0/65 (0%)
Strand=Plus/Minus

```
Query 128 CTGCAGTCCACCAGCACCTATGGTGCCTTATGACCGGCAAAATCTTGATGTGTGACGCC 187
      |||
Sbjct 1136 CTGCAGTCCACCAGCACCTATGGTGCCTTATGACCGGCAAAATCTTGATGTGTGACGCC 1077

Query 188 TCCCT 192
      |||
Sbjct 1076 TCCCT 1072
```

Score = 115 bits (62), Expect = 3e-29
Identities = 62/62 (100%), Gaps = 0/62 (0%)
Strand=Plus/Minus

```
Query 251 AGGTGTAACAGCAAATTCATCTAGCAAGAGAAATGGATCTAGGGACTTCAACTCAGGCCT 310
      |||
Sbjct 412 AGGTGTAACAGCAAATTCATCTAGCAAGAGAAATGGATCTAGGGACTTCAACTCAGGCCT 353

Query 311 GC 312
      ||
Sbjct 352 GC 351
```

Score = 76.8 bits (41), Expect = 1e-17
Identities = 41/41 (100%), Gaps = 0/41 (0%)
Strand=Plus/Minus

```
Query 219 CCTCGGTGAGGATGGTCAGGAAATCCAGCAGGAGGTGTAAC 259
      |||
Sbjct 878 CCTCGGTGAGGATGGTCAGGAAATCCAGCAGGAGGTGTAAC 838
```

Score = 60.2 bits (32), Expect = 1e-12
Identities = 32/32 (100%), Gaps = 0/32 (0%)
Strand=Plus/Minus

```
Query 190 CCTGCAACATATATGTAAACAGTCTCAAAGCCT 221
      |||
Sbjct 993 CCTGCAACATATATGTAAACAGTCTCAAAGCCT 962
```