BLAST ® » tblastn-2sequences » results for RID-K5BCK3BR114

Job Title	cds.comp144315 ...
RID	K5BCK3BR114 Search expires on 08-12 22:39 pm
Program	Blast 2 sequences
Query ID	lcl|Query_35091 (amino acid)
Query Descr	cds.comp144315 ...
Query Length	2501
Subject ID	lcl|Query_35093 (dna)
Subject Descr	PGEN_.00g070040-vv0.74.a ...
Subject Length	32079

Descriptions

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PGEN_.00g070040-vv0.74.a	67.4	146	13%	1e-13	27.04%	Query_35093

Graphic Summary

Distribution of the top 4 Blast Hits on 1 subject sequences

Alignments

Alignment view [Pairwise]   ☐ CDS feature   [Restore defaults]

PGEN_.00g070040-vv0.74.a
Sequence ID: Query_35093 Length: 32079 Number of Matches: 4
Range 1: 5104 to 5649

Score	Expect	Method	Identities	Positives	Gaps	Frame
67.4 bits(163)	1e-13()	Compositional matrix adjust.	53/196(27%)	99/196(50%)	24/196(12%)	+1

```
Query  630   KTLLLPLFFDRKQPEEMRMIAYLTSILARPSRPELEMIAKSLEDEPSTNVGTLVW---TS   686
             K+ ++ +F D+++  E+R+ AY T I+  PS   L + +L  E    VG+ VW    T+
Sbjct  5104  KSRIMQIFTDQEEDSEVRIAAYKT-IMECPSDDILRKVKYTLAKEEVNQVGSYVWSHLTN   5280

Query  687   LVASSNKMPKCDCIKSLARNSTMA-------MRFAQKSEGGLQHSNYMYRSSYDKKTRLG   739
             L+ SS+ P    IKS+ ++T+        +F++  EG +        + +K   G
Sbjct  5281  LMESSD--PHKQAIKSILEDATLQKDFDMDKRKFSRNYEGSI---------FLEKINTG   5424

Query  740   HSYEQVLLHSAKERFPRAFAMQYTATLMGKTVDLFELGYKAKGVDTIVDRMYGVLGDTSM   799
              + E  ++ S+K   PR+  + T  L G  ++LFE+G +A+G++  ++   +G  G  S
Sbjct  5425  ATVEGDMIWSSKSFIPRSAMLNLTVDLFGSAINLFEIGGRAEGLEYFLESYFGPNGYFS-   5601

Query  800   TNIVRKLFDTKFMKTV   815
              N V+    D   ++T+
Sbjct  5602  ENDVQAAADETAVQTI   5649
```

Range 2: 5853 to 6131

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.9 bits(63)	0.053()	Compositional matrix adjust.	28/109(26%)	45/109(41%)	16/109(14%)	+3

```
Query  841    GHVYMKLFGQELIYFDLPSMLGPSLTSSPDGSDGSQPNDLKLTKILPELMNVVISLNRLL  900
              G +YM++FG EL Y +    +   SL S                 L  LMN+   N
Sbjct  5853   GSLYMRVFGNELRYMNFQGL--DSLISQNS------------FNFLDMLMNLAKE-NDYQ  5987

Query  901    KTQKSAFFPLMSTMLPTETGLPLRFGIDKVAALKIDGDVKFEKEKDPNT  949
              TQ + F   S ++PT +G PL   ++  + + +   K +  K  N+
Sbjct  5988   FTQSTLFLD-SSIIIPTSSGFPLNLTVNGTSTVDMKASGKMDIMKLKNS  6131
```

Range 3: 20134 to 20214

Score	Expect	Method	Identities	Positives	Gaps	Frame
25.8 bits(55)	0.52()	Compositional matrix adjust.	9/27(33%)	19/27(70%)	0/27(0%)	+1

```
Query  2154   KRDNKWADVEIKTPYETMKMHNLRTPQ  2180
              R++  ADV + TP+E+++  NL++ +
Sbjct  20134  NRNSMNADVSLVTPFESLRQFNLKSKE  20214
```

Range 4: 22907 to 22945

Score	Expect	Method	Identities	Positives	Gaps	Frame
24.3 bits(51)	1.4()	Composition-based stats.	8/13(62%)	9/13(69%)	0/13(0%)	+2

```
Query  2427   QRTCFSKTPVKSC  2439
              QR CFSK P + C
Sbjct  22907  QRLCFSKIPSRHC  22945
```

Taxonomy

Reports
- ° **Lineage**
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Dot Plot

Plot of lcl|Query_35091 vs lcl|Query_35093

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