

F54D10.10

RID: 4SB0ZCJX016

Job Title:TRINITY_DN3074_c0_g1_i1.p1

TRINITY_DN3074_c0_g1~~TRINITY_DN3074_c0_g1_i1.p1...

Program: BLASTP

Query: TRINITY_DN3074_c0_g1_i1.p1

TRINITY_DN3074_c0_g1~~TRINITY_DN3074_c0_g1_i1.p1 ORF type:5prime_partial

len:138 (+),score=20.44 TRINITY_DN3074_c0_g1_i1:3-416(+) ID:

lcl|Query_74750(amino acid) Length: 138

Database: nr All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples from
WGS projects

Sequences producing significant alignments:

Scientific Acc. Description Name	Common Taxid	Score Score	cover	Max Value	Total Query Ident	E Len	Per. Name
hypothetical protein GCK72_007074 [Caenorhabditis remanei]							
Caenorhabdit... NA		31234		76.3	76.3 80%	1e-14	39.02
123	KAF1767116.1						

Alignments:

>hypothetical protein GCK72_007074 [Caenorhabditis remanei]

Sequence ID: KAF1767116.1 Length: 123

Range 1: 1 to 122

Score:76.3 bits(186), Expect:1e-14,

Method:Compositional matrix adjust.,

Identities:48/123(39%), Positives:70/123(56%), Gaps:13/123(10%)

Query 26 MGNLHSTIMERLPQIAQIFNKNWISNLIVKVGQLRVELTTRMlnlfqklqfqqlPVRQRM
85

MGNLHS I +R+ Q + F+KNW S +I ++ +LR E+ R L + QFQQ P + +
Sbjct 1 MGNLHSNITQRIQQF-EFFDKNWFSGIIGRLRLREEIVERAYALVRNFQFQQEPAHRHI
59

Query 86 VRVG---PVEEAPG-----AEWVEYQDRIELYNTNEMKLIYFVCAMNILFLGVFLR
133

G PV + +++ QDRIE+YN NEMKL+YFVC +N+L L
Sbjct 60 ASTGTGGPVTRSRSRSNVAIENPSDFGVLQDRIEVYNNNEMKLVYFVCVNVNLLVLAFLFN
119

Query 134 YLF 136
++F

Sbjct 120 WVF 122

PTA-2

RID: 4S9P5447016

Job Title:TRINITY_DN5476_c0_g2_i1.p1
 TRINITY_DN5476_c0_g2~~TRINITY_DN5476_c0_g2_i1.p1...
 Program: BLASTP
 Query: TRINITY_DN5476_c0_g2_i1.p1
 TRINITY_DN5476_c0_g2~~TRINITY_DN5476_c0_g2_i1.p1 ORF type:5prime_partial
 len:155 (+),score=11.72 TRINITY_DN5476_c0_g2_i1:3-467(+) ID:
 lcl|Query_75995(amino acid) Length: 120
 Database: nr All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF excluding environmental samples from
 WGS projects

Sequences producing significant alignments:

Scientific Acc.	Common	Max	Total Query	E	Per.
Description					Name
Name	Taxid	Score	Score cover	Value	Ident Len
Accession					
hypothetical protein CRE_00743 [Caenorhabditis remanei]					
Caenorhabdit... NA		31234	130	130	75% 3e-36 80.22
125 XP_003117941.1					
Protein CBG14648 [Caenorhabditis briggsae]					
Caenorhabdit... NA		6238	125	125	75% 2e-34 76.92
125 XP_002644667.1					
hypothetical protein B9Z55_024276 [Caenorhabditis nigoni]					
Caenorhabdit... NA		1611254	125	125	75% 2e-34 78.02
125 PIC18352.1					
hypothetical protein L3Y34_011972 [Caenorhabditis briggsae]					
Caenorhabdit... NA		6238	125	125	75% 3e-34 76.92
115 ULT82378.1					
hypothetical protein GCK72_024394 [Caenorhabditis remanei]					
Caenorhabdit... NA		31234	117	117	56% 3e-31 75.00
102 KAF1747928.1					

Alignments:

Query	30		
MNFllllialyllvtltvaFPLLMISVFIGIFVYKNSVTPEVHQDVLNFGNSINAIQKT	89		
XP_003117941.1			
1 ...V.....I.....AL...R.....H..M...EQ.L...RQ.	60		
XP_002644667.1			
1SI.....M....I..AL.A.Y.....M...EK.MD..RQ.	60		
PIC18352.1			
1S.....M....I..AL...Y...A.....M...EK.MD..RQ.	60		
ULT82378.1			
1SI.....M....I..AL.A.Y.....M...EK.MD..RQ.	60		
KAF1747928.1			
1AL...R.Y.....H..M...EQ.L...RQ.	37		
Query	90	LTPSSPEDDSMTRSGIDRARRQYMDHCNGIN	120
XP_003117941.1	61	CA...V..T.....E.....V.	91
XP_002644667.1	61	CS..T.V..T.....E.....	91
PIC18352.1	61	CS..T.V..T.....E.....	91
ULT82378.1	61	CS..T.V..T.....E.....	91

KAF1747928.1 38 CA....V..T.....E.....V. 68