

# BLAST ®

## Basic Local Alignment Search Tool

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### TCAG

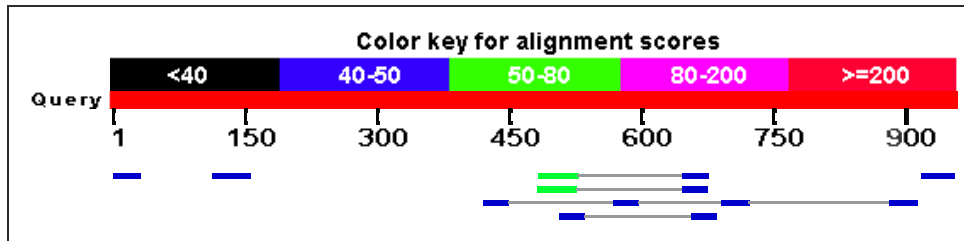
**RID** [Y0V0JVXS015](#) (Expires on 08-06 13:30 pm)

**Query ID** lc|18059  
**Description** None  
**Molecule type** nucleic acid  
**Query Length** 952

**Database Name** nr  
**Description** Nucleotide collection (nt)  
**Program** BLASTN 2.2.29+

### [Graphic Summary](#)

Distribution of 14 Blast Hits on the Query Sequence





51.8 bits(56) 0.015() 37/43(86%) 0/43(0%) Plus/Plus

Features:  
18 bp at 5' side: conserved hypothetical protein73 bp at 3' side: hypothetical protein; putative CmpX-like domain

Query 481 CGCGCGAGAGCAATGCGCGCGAGAGCAGTAGGCGCGAGAGCAG 523  
Sbjct 6060725 CGCGCGAGAGCAGAACGCGCGAGAGCAGAACGCGCGAGAACAG 6060767

Range 2: 6060725 to 6060752

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	26/28(93%)	0/28(0%)	Plus/Plus	

Features:  
18 bp at 5' side: conserved hypothetical protein88 bp at 3' side: hypothetical protein; putative CmpX-like domain

Query 644 CGCGCGAGAGCAGTAGGCGCGAGAGCAG 671  
Sbjct 6060725 CGCGCGAGAGCAGAACGCGCGAGAGCAG 6060752

Pyrenophora teres f. teres 0-1 hypothetical protein, mRNA  
Sequence ID: **ref|XM\_003305062.1|** Length: 6999 Number of Matches: 4  
Range 1: 3928 to 3957

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:  
Query 877 CGCGAGAGCAGGTGTGACGCATGTGATGCG 906  
Sbjct 3957 CGCGACAGCAGGTGTGACGCATGTGAAGCG 3928

Range 2: 3928 to 3957

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:  
Query 689 CGCGAGAGCAGGTGTGACGCATGTGATGCG 718  
Sbjct 3957 CGCGACAGCAGGTGTGACGCATGTGAAGCG 3928

Range 3: 3928 to 3957

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:  
Query 566 CGCGAGAGCAGGTGTGACGCATGTGATGCG 595  
Sbjct 3957 CGCGACAGCAGGTGTGACGCATGTGAAGCG 3928

Range 4: 3928 to 3957

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	28/30(93%)	0/30(0%)	Plus/Minus	

Features:  
Query 419 CGCGAGAGCAGGTGTGACGCATGTGATGCG 448  
Sbjct 3957 CGCGACAGCAGGTGTGACGCATGTGAAGCG 3928

PREDICTED: Pundamilia nyererei zinc finger protein 536-like (LOC102211462), mRNA  
Sequence ID: **ref|XM\_005726452.1|** Length: 8083 Number of Matches: 1  
Range 1: 7257 to 7285

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	28/30(93%)	1/30(3%)	Plus/Plus	

Features:  
Query 5 GCAGACACACAGTGTGTGATTGACGCAG 34

