

# BLASTx Search Outputs of the 5' End Border Sequences against GenBank Non-redundant Protein Sequences "nr"

BLASTX 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= Region\_1  
(1852 letters)

Database: /usr/local/blast/db/blastlibs/nr  
10,862,569 sequences; 3,701,345,023 total letters

Searching..... done

Sequences producing significant alignments:	Score	E
	(bits)	Value
ref XP_368121.2  hypothetical protein MGG_01123 [Magnaporthe gri...	38	3.8
ref XP_958911.1  hypothetical protein NCU09139 [Neurospora crass...	37	6.5

>ref|XP\_368121.2| hypothetical protein MGG\_01123 [Magnaporthe grisea 70-15]  
gb|EDK02191.1| hypothetical protein MGG\_01123 [Magnaporthe grisea 70-15]  
Length = 1179

Score = 38.1 bits (87), Expect = 3.8  
Identities = 19/56 (33%), Positives = 30/56 (53%)  
Frame = +2

Query: 785 KGREGEDRWHERGVDDHDDASEEERVATTQGRKERDARSVKGVGEGRVGGMKDD 952  
KG G+ +W +++G DD DD+ + E + +RDA +G G GR G + D  
Sbjct: 1084 KGLRGKWKWSNKKGRDDEDEMDDGEEVAVALKGRDAGRGRGGGGGRGRGGRPD 1139

>ref|XP\_958911.1| hypothetical protein NCU09139 [Neurospora crassa OR74A]  
gb|EAA29675.1| conserved hypothetical protein [Neurospora crassa OR74A]  
Length = 584

Score = 37.4 bits (85), Expect = 6.5  
Identities = 18/45 (40%), Positives = 26/45 (57%), Gaps = 1/45 (2%)  
Frame = +2

Query: 809 WHERGVDDHDDASEEERVATTQGRKERDARSVKGVG-EGRVGG 940  
W G DDHD D+SE+E + + R++ DA S+ G G+ GG

Sbjct: 508 WDPVGGFDDHDGDSSEDEEIEAERERRQDDAASLAGTSIAGKKGG 552

Database: /usr/local/blast/db/blastlibs/nr  
Posted date: Apr 19, 2010 11:58 AM  
Number of letters in database: 3,701,345,023  
Number of sequences in database: 10,862,569

Lambda	K	H
0.318	0.134	0.401

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 10862569

Number of Hits to DB: 11,843,195,143

Number of extensions: 260090038

Number of successful extensions: 598890

Number of sequences better than 10.0: 2

Number of HSP's gapped: 597235

Number of HSP's successfully gapped: 2

Length of query: 617

Length of database: 3,701,345,023

Length adjustment: 143

Effective length of query: 474

Effective length of database: 2,147,997,656

Effective search space: 1018150888944

Effective search space used: 1018150888944

Neighboring words threshold: 12

Window for multiple hits: 40

X1: 16 ( 7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 33 (17.3 bits)