

BLASTp Search Outputs of the Putative Reading Frames Spanning the Junctions between the Insert and Its Flanking Borders in Maize Event DAS-40278-9 against GenBank Non Redundant Protein Sequences “nr”

RF_1_+1

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) “Protein database searches using compositionally adjusted substitution matrices”, FEBS J. 272:5101-5109.

Query= RF_1_+1
(97 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.316 | 0.134 | 0.407 |

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: 733,641,133

Number of extensions: 26006184

Number of successful extensions: 49370

Number of sequences better than 1.0: 0

Number of HSP's gapped: 49446

Number of HSP's successfully gapped: 0

Length of query: 97
Length of database: 3,701,345,023
Length adjustment: 66
Effective length of query: 31
Effective length of database: 2,984,415,469
Effective search space: 92516879539
Effective search space used: 92516879539
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.6 bits)
S2: 83 (36.6 bits)

RF_1_+2

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_1_+2
(63 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.319 | 0.127 | 0.379 |

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: 414,133,728
Number of extensions: 10700990
Number of successful extensions: 30730
Number of sequences better than 1.0: 0
Number of HSP's gapped: 30755
Number of HSP's successfully gapped: 0
Length of query: 63
Length of database: 3,701,345,023
Length adjustment: 35
Effective length of query: 28
Effective length of database: 3,321,155,108
Effective search space: 92992343024
Effective search space used: 92992343024
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 83 (36.6 bits)

RF_1_-1

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_1_-1
(69 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.330 | 0.146 | 0.435 |

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: 460,835,964

Number of extensions: 14027875

Number of successful extensions: 30752

Number of sequences better than 1.0: 0

Number of HSP's gapped: 30773

Number of HSP's successfully gapped: 0

Length of query: 69

Length of database: 3,701,345,023

Length adjustment: 41

Effective length of query: 28

Effective length of database: 3,255,979,694

Effective search space: 91167431432

Effective search space used: 91167431432

Neighboring words threshold: 11

Window for multiple hits: 40

X1: 15 (7.1 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 40 (21.8 bits)

S2: 83 (36.6 bits)

RF_1_-2

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis,

Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_1_-2
(13 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.362 | 0.162 | 0.621 |

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: 56,544,655
Number of extensions: 206820
Number of successful extensions: 412
Number of sequences better than 1.0: 0
Number of HSP's gapped: 412
Number of HSP's successfully gapped: 0
Length of query: 13
Length of database: 3,701,345,023
Length adjustment: 0
Effective length of query: 13
Effective length of database: 3,701,345,023
Effective search space: 48117485299
Effective search space used: 48117485299
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 14 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 37 (22.0 bits)

S2: 81 (35.8 bits)

RF_1_-3

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_1_-3
(26 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.316 | 0.128 | 0.379 |

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: 146,783,749

Number of extensions: 1580604

Number of successful extensions: 1786

Number of sequences better than 1.0: 0

Number of HSP's gapped: 1787

Number of HSP's successfully gapped: 0

Length of query: 26

Length of database: 3,701,345,023

Length adjustment: 1
Effective length of query: 25
Effective length of database: 3,690,482,454
Effective search space: 92262061350
Effective search space used: 92262061350
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 16 (7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.6 bits)
S2: 83 (36.6 bits)

RF_2_+1

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_2_+1
(38 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.325 | 0.143 | 0.417 |

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: 261,613,575
Number of extensions: 5101555
Number of successful extensions: 12518
Number of sequences better than 1.0: 0
Number of HSP's gapped: 12518
Number of HSP's successfully gapped: 0
Length of query: 38
Length of database: 3,701,345,023
Length adjustment: 12
Effective length of query: 26
Effective length of database: 3,570,994,195
Effective search space: 92845849070
Effective search space used: 92845849070
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 15 (7.0 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.6 bits)
S2: 83 (36.6 bits)

RF_2_+2

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_2_+2
(19 letters)

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

Searching..... done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.340 | 0.153 | 0.504 |

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: 126,776,404

Number of extensions: 1167500

Number of successful extensions: 2068

Number of sequences better than 1.0: 0

Number of HSP's gapped: 2068

Number of HSP's successfully gapped: 0

Length of query: 19

Length of database: 3,701,345,023

Length adjustment: 0

Effective length of query: 19

Effective length of database: 3,701,345,023

Effective search space: 70325555437

Effective search space used: 70325555437

Neighboring words threshold: 11

Window for multiple hits: 40

X1: 15 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 39 (21.9 bits)

S2: 82 (36.2 bits)

RF_2_+3

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_2_+3
(39 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.323 | 0.144 | 0.431 |

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: 259,602,545
Number of extensions: 4934052
Number of successful extensions: 8052
Number of sequences better than 1.0: 0
Number of HSP's gapped: 8058
Number of HSP's successfully gapped: 0
Length of query: 39
Length of database: 3,701,345,023
Length adjustment: 13
Effective length of query: 26
Effective length of database: 3,560,131,626
Effective search space: 92563422276
Effective search space used: 92563422276
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 16 (7.5 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.9 bits)
S2: 83 (36.6 bits)

RF_2_-1

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_2_-1
(39 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.330 | 0.149 | 0.450 |

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: 287,699,643

Number of extensions: 6355977

Number of successful extensions: 24150

Number of sequences better than 1.0: 0

Number of HSP's gapped: 24153

Number of HSP's successfully gapped: 0

Length of query: 39

Length of database: 3,701,345,023

Length adjustment: 13
Effective length of query: 26
Effective length of database: 3,560,131,626
Effective search space: 92563422276
Effective search space used: 92563422276
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 83 (36.6 bits)

RF_2_-2

BLASTP 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.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= RF_2_-2
(39 letters)

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

Searching.....done

***** No hits found *****

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 |
|--------|-------|-------|
| 0.328 | 0.138 | 0.462 |

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: 274,192,558
Number of extensions: 4977462
Number of successful extensions: 17497
Number of sequences better than 1.0: 0
Number of HSP's gapped: 17498
Number of HSP's successfully gapped: 0
Length of query: 39
Length of database: 3,701,345,023
Length adjustment: 13
Effective length of query: 26
Effective length of database: 3,560,131,626
Effective search space: 92563422276
Effective search space used: 92563422276
Neighboring words threshold: 11
Window for multiple hits: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 83 (36.6 bits)