

**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: 7032555437

Effective search space used: 7032555437

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)