

dotmatcher

Draw a threshold dotplot of two sequences ([read the manual](#))

Unshaded fields are optional and can safely be ignored. ([hide optional fields](#))

Input section

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here: No file chosen

```
>AP018036.1 Mycobacterium tuberculosis DNA, complete
genome, strain: HN-506
TTGACCGATGACCCCGGTT CAGGCTTCACCACAGTGTGGAA
CGCGGTCGTCTCCGAACTTAACGGCGACC
CTAAGGTTGACGACGGACCCAGCAGTGATGCTAATCTCAGCG
CTCCGCTGACCCCTCAGCAAAGGGCTTG
GCTCAATCTCGTCCAGCCATTGACCATCGTCGAGGGGTTTGC
TCTGTTATCCGTGCCGAGCAGCTTTGTC
```

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here: No file chosen

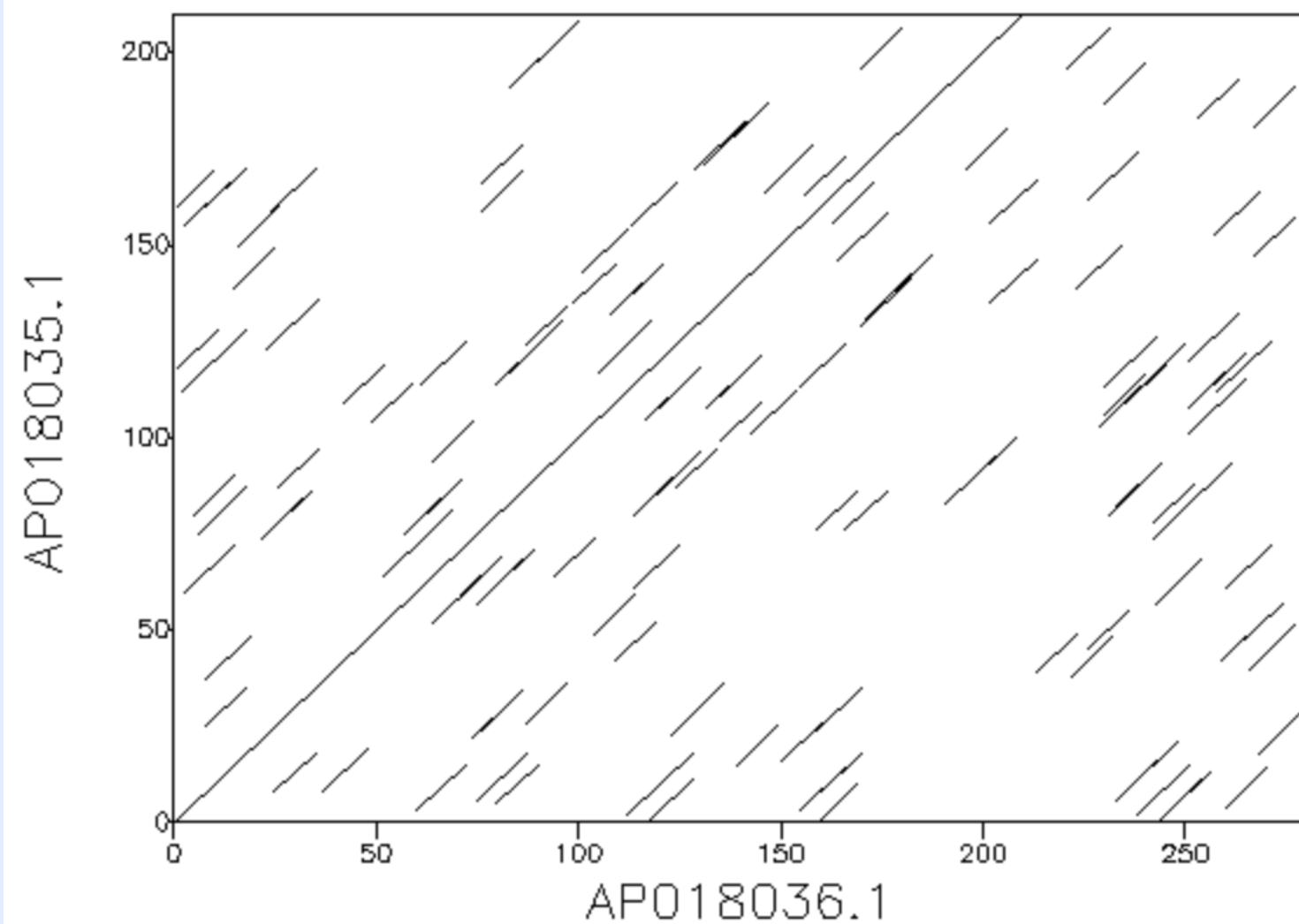
```
>AP018035.1 Mycobacterium tuberculosis DNA, complete
genome, strain: HN-321
TTGACCGATGACCCCGGTT CAGGCTTCACCACAGTGTGGAA
CGCGGTCGTCTCCGAACTTAACGGCGACC
CTAAGGTTGACGACGGACCCAGCAGTGATGCTAATCTCAGCG
CTCCGCTGACCCCTCAGCAAAGGGCTTG
GCTCAATCTCGTCCAGCCATTGACCATCGTCGAGGGGTTTGC
TCTGTTATCCGTGCCGAGCAGCTTTGTC
```

3. To enter the sequence data manually, type here:

Matrix file. Use one of the following two fields:

1. To access a standard EMBOSS data file, enter the name here:
(default is *EBLOSUM62* for protein, *EDNAFULL* for nucleic)
2. To upload a data file from your local computer, select it here: No file chosen

Dotmatcher: fasta::/var/lib/emboss-explorer/output/97925...
(windowsize = 10, threshold = 23.00 11/03/19)



dotmatcher

Draw a threshold dotplot of two sequences ([read the manual](#))

Unshaded fields are optional and can safely be ignored. ([hide optional fields](#))

Input section

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here: No file chosen

```
>AC073210.8 Homo sapiens BAC clone RP11-460N20 from
7, complete sequence
GAATTCTTCAGGTAGCTTCCTAGGGTTTCCAAGGCAATACAA
GAAGAATTTTGATAGGCAGGAAATGCA
TGCTACATACACATATTATTATTCTCTGATTTCCCTTTCACATGT
AAAAATTGAAAATTGCAATCTGGTC
TTTCAATTAGCAAAAGATTATTTTTCAGCAAAGCAAATAACT
GTAGAAAAC TGATGGGGGAACAAATGC
```

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here: No file chosen

```
>CP003928.1 Sulfolobus islandicus LAL14/1, complete
genome
ACAGTAAATTCCTACGTTTCTGCATCATTATTATACCCTAATT
CCCCCTCCTTTAATTGTCTCTCTGT
AAATTCCTACGTTTCCAATGACAATCATTCCATTTTACGTTT
TATCTAAATTATACAAACGTTTTTCTT
TCTATATGGCCTAAACTAATTTTTCAGATGAAATTAGCAGTGT
GTCACTTTAAACTAGTATTACTTTAT
```

3. To enter the sequence data manually, type here:

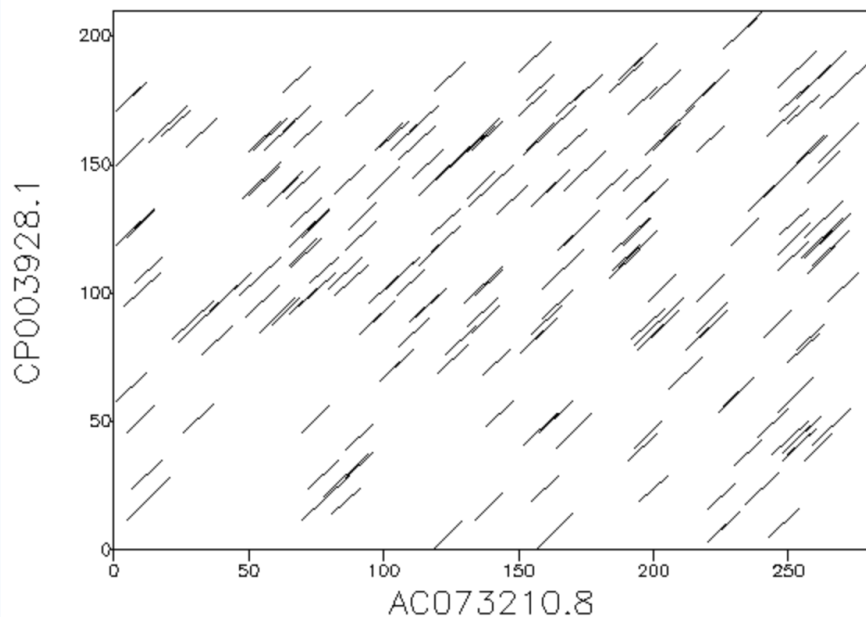
Matrix file. Use one of the following two fields:

1. To access a standard EMBOSS data file, enter the name here:
(default is *EBLOSUM62* for protein, *EDNAFULL* for nucleic)
2. To upload a data file from your local computer, select it here: No file chosen

Created dotmatcher.1.png

IMAGE FILE [dotmatcher.1.png](#)

```
Dotmatcher: fasta::/var/lib/emboss-explorer/output/12732...
                (windowsize = 10, threshold = 23.00 11/03/19)
```



needle

Needleman-Wunsch global alignment of two sequences ([read the manual](#))

Unshaded fields are optional and can safely be ignored. ([hide optional fields](#))

Input section

Input section

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:

```
>AC073210.8 Homo sapiens BAC clone RP11-460N20 from
7, complete sequence
GAATTCTTCAGGTAGCTTCCTAGGGTTTCCAAGGCAATACAA
GAAGAATTTTGATAGGCAGGAAAATGCA
TGCTACATACACATATTATTCTCTGATTTCCTTTACATGT
AAAAATTGAAAATTGCAAACTCTGGTC
TTTCAATTAGCAAAAGATTATTTTCAGCAAAGCAAATAACT
GTAGAAAACCTGATGGGGGAACAAATGC
```

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:

```
>CP003928.1 Sulfolobus islandicus LAL14/1, complete
genome
ACAGTAAATTTCTACGTTTCTGCATCATTATTATACCCTAATT
CCCCCTCCTTTAATTTGTCTCTCTGT
AAATTTCTACGTTTCCAATGACAATCATTCCATTTTACGTTT
TATCTAAATTATACAAACGTTTTTCTT
TCTATATGGCCCTAACTAATTTTCAGATGAAATTAGCAGTGT
GTCACTTTAAACTAGTATTACTTTAT
```

3. To enter the sequence data manually, type here:

Matrix file. Use one of the following two fields:

1. To access a standard EMBOSS data file, enter the name here:

#-----
#-----

needle

Needleman-Wunsch global alignment of two sequences ([read the manual](#))

Unshaded fields are optional and can safely be ignored. ([hide optional fields](#))

Input section

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:

```
>JZ331708.1 BT1267 Panthera tigris tigris cDNA library
Panthera tigris tigris cDNA clone BT1267 similar to ferritin
(FT1), mRNA sequence
TCGCGGAGAGTCGCCGCGTTTCCTGCTTCAACAGTGCTTG
AACGGAACCCGGCTGCTCGTCCCCCCTC
ACCCCGGCCGGCCACTCAGAGCCAGCCTTCGTCACCACTTG
AC*CCCCCTCCGACCCGGCCCAAGGTCCC
CG Input section AGCGCCGCTCAGCCGTCGCCGCCGCCAC
```

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:

```
>JZ331707.1 BT1273 Panthera tigris tigris cDNA library
Panthera tigris tigris cDNA clone BT1273 similar to lamin B
receptor (LBR), mRNA sequence
GTTTTTGGATGGTGGGGTTTTGTTCCGCCACCCAATTACTTG
GGTGATCTCATCATGGCCCTGGCCTGGT
CCCTCCCGTGTGTTTCAATCACATTTTGCCTTATTTCTATGT
GATTTATTTCAACATCTTGCTGGTGCC
CCGGGAAGCCCGTGACGAGCACCCTGTAGGAAGAAGTATG
```

3. To enter the sequence data manually, type here:

Matrix file. Use one of the following two fields:

1. To access a standard EMBOSS data file, enter the name here:

OUTPUT FILE [outfile](#)

```
#####
# Program: needle
# Rundate: Mon 11 Mar 2019 15:52:05
# Commandline: needle
# -auto
# -asequence /var/lib/emboss-explorer/output/225112/.asequence
# -bsequence /var/lib/emboss-explorer/output/225112/.bsequence
# -noendweight
# -brief
# -outfile outfile
# -aformat3 srspair
# Align_format: srspair
# Report_file: outfile
#####

#=====
#
# Aligned_sequences: 2
# 1: JZ331708.1
# 2: JZ331707.1
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 558
# Identity:      192/558 (34.4%)
# Similarity:    192/558 (34.4%)
# Gaps:          303/558 (54.3%)
# Score: 259.5
#
#
#=====

JZ331708.1      1 TCGCGGAGAGTCGCGCGGTTTCCTGCTTCAACAGTG---CTTGAACGG      46
                        |||| |...||| .|||.||
JZ331707.1      1 -----GTTT----TTGGATGGTGGGTTTGTTCGC      27

JZ331708.1     47 AACCC-----GGCTG--CTCGTC---CCC-----CCCTCAC      72
      .|||| |.|| |||.|| ||| ||||
JZ331707.1     28 CACCCCAATTACTTGGGTGATCTCATCATGGCCCTGGCCTGGTCCCT---      74

JZ331708.1     73 CCCGGCCGG--CCACTCAGAGCCA---GCCTT-----C      100
      |||...|||.|||.|| | ||||
JZ331707.1     75 CCCGTGTGGTTTCAATCA---CATTTGCCTTATTCTATGTGATTTAT      120

JZ331708.1    101 GTCACCA-CTTGACAGCGCCCTCCGACCGGCCAAGGTCCCGCGCCAC      149
      .||||| |||| | |||
JZ331707.1    121 TTCACCATCTG-----CT-----GGT-----      137

JZ331708.1    150 TCCAGCGCCGCTCAGCCGTCGCGCGCCGCCACCACCACCGCCCTTTT      199
      |||.||...||| |||..|.|.|||||.|
JZ331707.1    138 ---GCCCGGAAGC-----CCGTGACGAGCACCAC TG-----      167

JZ331708.1    200 CAGCCGCCACCATGACGACCGCATCCCCCTCGCAGGTGCGCCAGAACTA      249
      .|.|||.|.|.|||.|.|.|||.|||.|||.||
JZ331707.1    168 -----TAGGAAGA-AGTAT--GGCCTGGC--GTGGG--AGAAGTA      200

JZ331708.1    250 CCACCAG-GACTCGGAGGCCGCCATCAACCG-----CCAGATCAAC      289
      |.|||||.|||.|| | |.|||||.|||.|||.||
JZ331707.1    201 CTGCCAGCGAGTC-----CC-----CTACCGCATATTTCCCTACATCTAC      240

JZ331708.1    290 CTGGA---GCTCTACGCCTCCTATGTCTACCTG-TCCATGTCGTACTAT      334
      .|| ||||..|||.|| ||||..|| | | |..|||.|||
JZ331707.1    241 --TGATTTGCTCTGGGCCCCC---TCTAAATGCTCC-TGCAGTTCTAT      283

JZ331708.1    335 TTTGACCGTGATGATGTGGCTTT--GAAGAACTTTGCCAAATACTTTCTT      382
      ||| ||| | | |.|||.|||.|||.||
JZ331707.1    284 TTT--CCG-----TTTACGAAAAA-----AAAAA-----      305

JZ331708.1    383 CACCAATCTCATGAGGAGAGGGAACATGCTGAGAAACTGATGAAGCTGCA      432
      |..|.||..|||.|||.|||.||
JZ331707.1    306 -----AAAAAAAAA-----AAAAA-----      323

JZ331708.1    433 GAACCAGCGAGGCGGCCGAATCTTCCTTCAGGATATCAAGAAACCAGACC      482

JZ331707.1    323 -----      323

JZ331708.1    483 GTGATGAC      490

JZ331707.1    323 -----      323

#-----
#-----
```


water

Smith-Waterman local alignment of sequences ([read the manual](#))

Unshaded fields are optional and can safely be ignored. ([hide optional fields](#))

Input section

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here: No file chosen

```
>AF250365.2 Influenza A virus (A/Weiss/43 (H1N1))  
neuraminidase (NA) gene, complete cds  
ATGAATCCAAATCAGAAAATAATAACCATTGGATCAATCTGTAT  
GGTAGTCGGAATAATTAGCCTAATAT  
TGCAAATAGGGAATATTATCTCAATATGGATTAGCCATTCAATT  
CAAACTGGAAGTCAAAACCATACTGG  
AATATGCAACCAAGCATCATTACCTATAAAAATAGCACCTGG  
GTAAATCAAACATATGTTAATATTAGC
```

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here: No file chosen

```
>AF250364.2 Influenza A virus (A/Swine/Iowa/30 (H1N1))  
neuraminidase (NA) gene, complete cds  
ATGAATACAAATCAAAAAATAATAACCATTGGGTCAATCTGTC  
TAATAGTTGGAATAACTAGCCTAATAT  
TACAAATAGGGAATATAATCTCAATATGGATTAGCCATTCAATT  
CAAACTAGAGATCAAAACCATCCTGA  
AACATGCAACCAAGCATCATTACCTATGAAAACAACACATGG  
GTGAATCAAACATATGTTAACATTAGC
```

3. To enter the sequence data manually, type here:

Matrix file. Use one of the following two fields:

1. To access a standard EMBOSS data file, enter the name here:

OUTPUT FILE [outfile](#)

```
#####
# Program: water
# Rundate: Mon 11 Mar 2019 15:55:32
# Commandline: water
# -auto
# -asequence /var/lib/emboss-explorer/output/888673/.asequence
# -bsequence /var/lib/emboss-explorer/output/888673/.bsequence
# -brief
# -outfile outfile
# -aformat3 srspair
# Align_format: srspair
# Report_file: outfile
#####

#=====
#
# Aligned_sequences: 2
# 1: AF250365.2
# 2: AF250364.2
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 420
# Identity:      371/420 (88.3%)
# Similarity:    371/420 (88.3%)
# Gaps:          0/420 ( 0.0%)
# Score: 1659.0
#
#
#=====

AF250365.2      1 ATGAATCCAAATCAGAAAATAATAACCATGGATCAATCTGTATGGTAGT      50
  |||||.|||||.|||||||||||||||.|||||||.||.|||
AF250364.2      1 ATGAATACAAATCAAAAATAATAACCATGGGTCAATCTGTCTAATAGT      50
  |||||.|||||.|||||||||||||||.|||||||.||.|||
AF250365.2     51 CGGAATAATTAGCCTAATATTGCAAAATAGGGAATATTATCTCAATATGGA      100
  .|||||.|||||.|||||||||||||||.|||||||.||.|||
AF250364.2     51 TGGAATAACTAGCCTAATATTACAAATAGGGAATATAATCTCAATATGGA      100
  |||||.|||||.|||||||||||||||.|||||||.||.|||
AF250365.2    101 TTAGCCATTCAATTCAAACCTGGAAGTCAAACCATACTGGAATATGCAAC      150
  |||||.|||||.|||||||||||||||.|||||||.||.|||
AF250364.2    101 TTAGCCATTCAATTCAAACCTAGAGATCAAACCATCCTGAAACATGCAAC      150
  |||||.|||||.|||||||||||||||.|||||||.||.|||
AF250365.2    151 CAAAGCATCATTACCTATAAAAAATAGCACCTGGGTAAATCAAACATATGT      200
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250364.2    151 CAAAGCATCATTACCTATGAAACAACACATGGGTGAATCAAACATATGT      200
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250365.2    201 TAATATTAGCAACACTAACGTTGTTGCTGGAAAAGGCACAACCTCAGTGA      250
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250364.2    201 TAACATTAGCAATGCTAACATTGTTGCTGGACAGGATGCAACTTCAATGA      250
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250365.2    251 TATTAGCCGCAATTCATCTCTTTGTCCTATCCGTGGGTGGGCTATATAC      300
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250364.2    251 TATTAGCCGCAATTCCTCTCTTTGCCCTATCAGTAGGTGGGCTATATAC      300
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250365.2    301 AGCAAAGATAACGGCATAAGAATTGGTTCCAAAGGAGATGTTTTGTCAT      350
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250364.2    301 AGCAAAGACAATAGCATAAGAATTGGTTCCAAAGGAGACATTTTTGTCAT      350
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250365.2    351 AAGAGAGCCTTTTATTTCATGTTCTCACTTGGAAATGCAGGACTTTTTTTC      400
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250364.2    351 AAGAGAACCCTTTATTTCATGCTCTCACTTGGAAATGCAGAACCTTTTTTC      400
  |||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||
AF250365.2    401 TGACCCAAGGCGCCCTGTTG      420
  |||||.|||||.|||||.|||||
AF250364.2    401 TGACTCAAGGCGCTTGCTG      420
  |||||.|||||.|||||.|||||
```

#-----
#-----

Unshaded fields are optional and can safely be ignored. ([hide optional fields](#))

Input section

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:

```
>AP018405.1 Lactobacillus plantarum SN35N DNA,
complete genome
CGTAATTACGAACCAACCCCGCACTAACAGCGTCATCCATC
ACCCATAGTACTGACTGTCGCCCTGCTT
AAGTTGCACGGTCGCCCTAGCTTGAAACCCGTTGCCATGAC
ATGTTGGCGAAGAGCAATCAATCATTTAG
TGGTCATCACCGGGCTGTCCTGGCAGCGCCCAATCGGCATT
AGTAAATGGGGATTACGGGCCATTAAAGT
```

3. To enter the sequence data manually, type here:

Select an input sequence. Use one of the following three fields:

1. To access a sequence from a database, enter the USA here:
2. To upload a sequence from your local computer, select it here:

```
>AP018392.1 Lactobacillus paracasei IJH-SONE68 DNA,
complete genome
TTATATAGGAATGTCCGTCATCACTCGTCAGCATAGCTATAAG
CTGGTTTGCTACCGGACATAATTGGAG
GAGGGGCATGAATGCCCAATTTAGAGGAACTTTGGGCTTACC
TGAATGATAAATTCGCTGAAGAATTGAC
CCCGGTGGTTACAGCACATGGATCCAGACAGAAAACCCG
TCAAATTAACCAAAGATAAACTCGAAATT
```

3. To enter the sequence data manually, type here:

Matrix file. Use one of the following two fields:

1. To access a standard EMBOSS data file, enter the name here:

OUTPUT FILE [outfile](#)

```
#####
# Program: water
# Rundate: Mon 11 Mar 2019 15:59:56
# Commandline: water
# -auto
# -asequence /var/lib/emboss-explorer/output/507941/.asequence
# -bsequence /var/lib/emboss-explorer/output/507941/.bsequence
# -brief
# -outfile outfile
# -aformat3 srspair
# Align_format: srspair
# Report_file: outfile
#####

#=====
#
# Aligned_sequences: 2
# 1: AP018405.1
# 2: AP018392.1
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 556
# Identity:      240/556 (43.2%)
# Similarity:    240/556 (43.2%)
# Gaps:          255/556 (45.9%)
# Score: 382.0
#
#
#=====

AP018405.1      32 CGTCATC---CATCACCCATAGTACTGACTGTGCGCCCTGCT-TAAGTTGC      77
      ||| ||| | | . | | | . | | | | | | | | | |
AP018392.1      16 CGTCATCACTCGTCA-GCATA-----GCTATAAG----      43

AP018405.1      78 ACGGTCGCCCTAGCTTGAAACCCGTTGCCATGACAT-GTTGGCGAAGAGC      126
      || . | | | . . | | | | | | | | | | . | | | .
AP018392.1      44 -----CTGGTTTGCTACC-----GGACATAATTGGAGGAGGGG      76

AP018405.1      127 AATCAAT---CATTTAGTGGTCATCACGGGGCTGTCCTGGCAGCGCCCA      172
      . | | | | | | | | | | | | | | | | | | | | | |
AP018392.1      77 CATGAATGCCCAATTTAGAGG--AACTTTGGGCTTACCTG-----A      115

AP018405.1      173 ATCGGCATTAG-TAAATGGGGATTACGGGCCATTAAAGTCAATTGATCC-      220
      || | | | | | | | | | | | | | | | | | | | |
AP018392.1      116 AT-----GATAA-----ATTCCG-----TGAAG--AATTGACCCC      143

AP018405.1      221 -GT-GGTATTTGCTAACGATAC-----TGG---CAGTGCCAGCTATTAA      259
      || | | | | | | | | | | | | | | | | | | | |
AP018392.1      144 GGTCCGT-----TACAGCACATGGATCCA--GACAGCAA--AA      177

AP018405.1      260 CTATGACCG-----TAGCCACA-ATAATTTGATGGTAC---AAATTAGA      299
      | | | | | | | | | | | | | | | | | | | | |
AP018392.1      178 C-----CCGTCAAATTACCAAAGATAA-----ACTCGAAATTGAA      213

AP018405.1      300 CGATCTGTCCC--CT--TTTAAACA----TTAT---AAAAAGATT-----      333
      || | | | | | | | | | | | | | | | | | | | |
AP018392.1      214 -----GTCCCAGCTTCTTTACACAAAGCTTATTGGGAAAAGAATCTCGT      257

AP018405.1      334 -----ATTACTGAA-----GTAAC----AGTCACT      354
      . | | | | | | | | | | | | | | | | | | | |
AP018392.1      258 GACCAAGGTAGTCGAAGCGTTTAC-GAATTGCGGCAACTTGAAGTTGAT      306

AP018405.1      355 ACTGTCAGTAATAATCTTTTAT----ATCATCAGTTTAATTTTCATT      399
      . | . | | | | | | | | | | | | | | | | | |
AP018392.1      307 CCCGTC-----TTATGACCAAGGATGAGT-----TG      333

AP018405.1      400 CAGTGAGCTTCGAACGCTAACGAT----TCATTGGGTATTGATCTTGA      444
      || | . . | | | | | | | | | | | | | | | |
AP018392.1      334 CAGCCAGCTCCG--GCTACAGATCAACGTCTGCGG-----TTGA      371

AP018405.1      445 A-ATGCCCACTGCCACTC-AACTCTG-CTT-----GATTTG      477
      | | . | . | | | | | | | | | | | | | | |
AP018392.1      372 AGAAGACGA-----TCAAAATCTGACTTTTAAGGCAAAACCCATTTA      414

AP018405.1      478 ACGCCG      483
      | . | | |
AP018392.1      415 AATCCG      420

#-----
#-----
```