

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:

```
>AP018036.1 Mycobacterium tuberculosis DNA, complete
genome, strain: HN-506
TTGACCGATGACCCGGTTCAGGCTTACCCACAGTGTGGAA
CGCGGTCGTCTCGAACCTAACGGCGACC
CTAAGGTTGACGACGGACCCAGCAGTGATGCTAATCTCAGCG
CTCCGCTGACCCCTCAGCAAAGGGCTTG
GCTCAATCTGTCGCCAGCATTGACCATCGTCGAGGGGTTGC
TCTGTTATCCGTGCCAGCAGCTTGTC
```

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:

```
>AP018035.1 Mycobacterium tuberculosis DNA, complete
genome, strain: HN-321
TTGACCGATGACCCGGTTCAGGCTTACCCACAGTGTGGAA
CGCGGTCGTCTCGAACCTAACGGCGACC
CTAAGGTTGACGACGGACCCAGCAGTGATGCTAATCTCAGCG
CTCCGCTGACCCCTCAGCAAAGGGCTTG
GCTCAATCTGTCGCCAGCATTGACCATCGTCGAGGGGTTGC
TCTGTTATCCGTGCCAGCAGCTTGTC
```

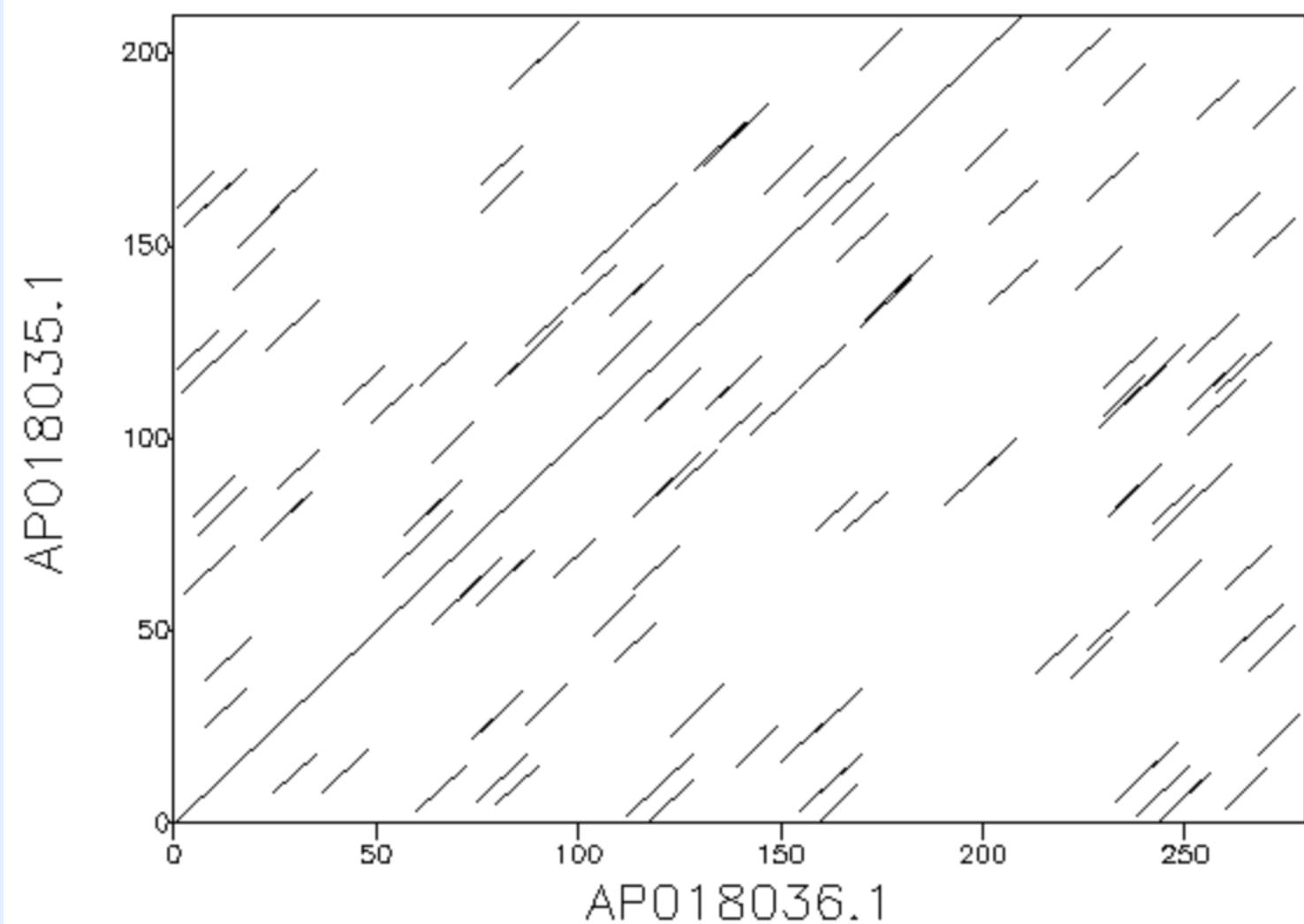
3. To enter the sequence data manually, type here:

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:

Dotmatcher: fasta:::/var/lib/emboss-explorer/output/97925...

(windowsize = 10, threshold = 23.00 11/03/19)



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:

```
>AC073210.8 Homo sapiens BAC clone RP11-460N20 from  
7, complete sequence  
GAATTCTTCAGGTAGCTCTCTAGGGTTCCAAGGCAATACAA  
GAAGAATTGATAGGCAGGAAAATGCA  
TGCTACATACACATATTATTCTGATTTCTTACATGT  
AAAAATTGAAAAATTGCAAATCTGGTC  
TTTCAATTAGCAAAGATTATTTTCAAGCAAAGCAAATAACT  
GTAGAAAATGATGGGGAAACAATGC
```

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  
ACAGTAATTCCTACGTTCTGCATCATTATTACCCATT  
CCCCCTCTTAAATTGCTCTGT  
AAATTCCTACGTTCCAATGACAATCATTCCATTACGTT  
TATCTAAATTACAAACGTTTTCTT  
TCTATATGCCCTAAACTAATTTTCAGATGAAATTAGCAGTGT  
GTCACTTAAACTAGTATTACTTAT
```

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

Matrix file. Use one of the following two fields:

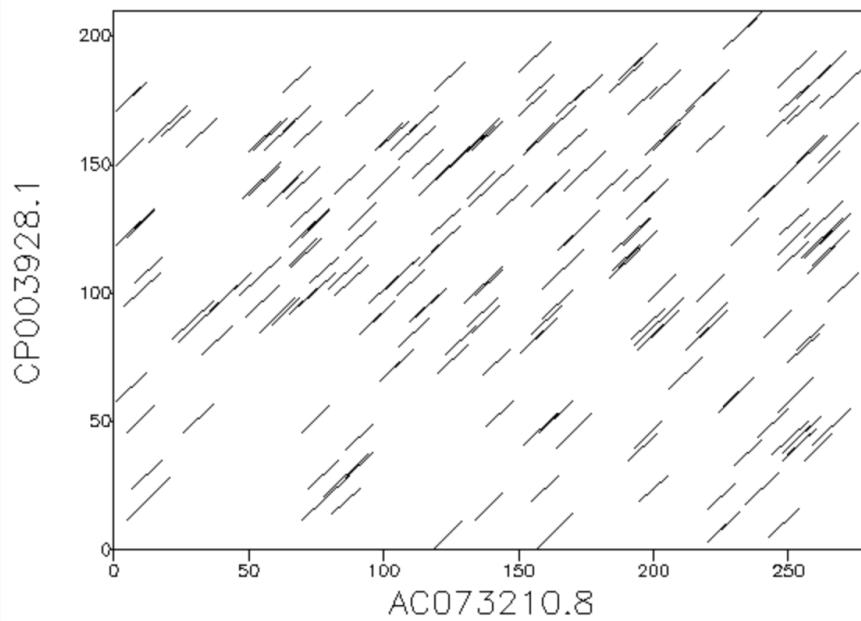
1. To access a standard EMBOSS data file, enter the name here:
(default is EBLOSUM62 for protein, EDNAFULL for nucleic)
2. To upload a data file from your local computer, select it here:



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: No file chosen

```
>AC073210.8 Homo sapiens BAC clone RP11-460N20 from
7, complete sequence
GAATTCTTCAAGGTAGCTTCCTAGGGTTCCAAGGCAATACAA
GAAGAATTGATAGGCAGGAAAATGCA
TGCTACATACACATATTATTCTCTGATTTCCCTTCACATGT
AAAAATTGAAATTGCAAATCTGGTC
TTTCAATTAGCAAAAGATTATTTTCAAGCAAAGCAAATAACT
GTAGAAAAGTATGGGGAAACAATGC
```

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
ACAGTAAATTCTACGTTCTGCATCATTATTACCCCTAATT
CCCCCTCTTAAATTGCTCTGT
AAATTCTACGTTCCAATGACAATCATTCCATTACGTT
TATCTAAATTACAAACGTTTCTT
TCTATATGGCTAAACTAATTTTCAGATGAAATTAGCAGTGT
GTCACTTAAACTAGTATTACTTTAT
```

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:

(.tbl, .dat, EPILOGUE, fms, fna, FNA, FNU, fnd, fnd2)

OUTPUT FILE [outfile](#)

```
#####
# Program: needle
# Rundate: Mon 11 Mar 2019 15:48:49
# Commandline: needle
#   -auto
#   -asequence /var/lib/emboss-explorer/output/012921/.asequence
#   -bsequence /var/lib/emboss-explorer/output/012921/.bsequence
#   -noendweight
#   -brief
#   -outfile outfile
#   -aformat3 srspair
# Align_format: srspair
# Report_file: outfile
#####

=====
#
# Aligned_sequences: 2
# 1: AC073210.8
# 2: CP003928.1
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 632
# Identity: 270/632 (42.7%)
# Similarity: 270/632 (42.7%)
# Gaps: 284/632 (44.9%)
# Score: 467.5
#
#
=====

AC073210.8      0 ----- 0
CP003928.1      1 ACAGTAAATTCTACGTTCTGCATCATTATAACCTAATTCCCCCT 50
AC073210.8      1 ----GAAT---TCT-TCAGGTAGCTCTAGGGTTCCAA-GGCAATACA 41
          .||| .||| ||.||..|||.|||||| .|||||| .|||
CP003928.1      51 CCTTTAATTGTCCTCTGTAAATTCCCTA-CGTTTCCAATGACAAT--- 96
AC073210.8      42 AGAAGAATTGTAGGCAGGAAATGCATGCTACATACACATATTA--T 89
          ||||.||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      97 -----CATTC-----CATTTAACGT 111
AC073210.8      90 TATTCTCT-----GATTTCCTTTC-ACATG---TAAA--AAT 120
          ||||.||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      112 T-TTATCTAAATTACAAACGTTTTCTTCTATATGCCCTAAACTAAT 160
AC073210.8      121 -----TGAATTGCAAATCTGGCTTTCAATTAGCAAAAGATTAT 162
          ||||.||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      161 TTTTCAGATGAAATTAGCA----GTGTGTCACTT--TAAACTAGTAT 202
AC073210.8      163 T--TTTCAGCAAAGCAAATAACT----GTAGAAAACGTATGGGG---- 200
          | .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      203 TACTTTATGC-AACGGTATTACTTGGGTGAA---TATAGGGTATTT 247
AC073210.8      201 -----GAACAAATGCCATTAGCTGCCAAA---ACAGTATGAC--CAGAT 240
          ||||.||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      248 AAGTAGAAAAA---CATTAG-----AAATTACTGTATAACTGGGAG 287
AC073210.8      241 TCAGTAAGTATCTAGTCATGCAAATCACAGCCCAATT-----AAATTA 283
          ||.||.||.||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      288 TTAATTATTACCTA-TAATTAAAT-----TTCTGAAAAATGA 326
AC073210.8      284 AGACCCCATAGGTGCATGTGGAC---AGCATTTCATGCAATGTGGTGCA 330
          ||||.||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      327 ---CCATATGACTAT---ACTAAATCATTTCTATAC----GGT-CA 361
AC073210.8      331 CCTCCACTGGCACCTTCTGCCTGCTTACAGAGATA---CCA---A 373
          | .||| .||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      362 C-----GTCACCTACT-----GATAATGGCGAATTA 387
AC073210.8      374 TTTCCTGAGTGACTCAAGGTGAATACTGGAACTG---AGAATTCT-- 418
          ||||.||.||.||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      388 TTT---TTAGAGTCT-----AT-----AACTGTTAAG-ATTCCTAA 418
AC073210.8      419 --GTGTTCAGAGGGATTACT-GGAAACATGGTTAACACACTTTACCAT- 464
          ||.||.||.||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      419 CAGTTTGAAAGATTAAATAGTAACCTT---TT-----TTTAACTTA 459
AC073210.8      465 ATTAT----AATA-AAATTGTATCTA 490
          .||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
CP003928.1      460 AATATGTGTCATAGTAATCAGACGTATGTT- 490
=====
```

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

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

```
>JZ331708.1 BT1267 Panthera tigris tigris cDNA library  
Panthera tigris tigris cDNA clone BT1267 similar to ferritin  
(FT1), mRNA sequence  
TCGGGGAGACTCGCCGCCGGTTTCTGCTTCAACAGTGCTTG  
AACGGAACCCGGCTGCTCGTCCCCCCCCTC  
ACCCCGGCCGCACTCAGAGCCAGCCTTCGTCACCACTTG  
AC^~~~~~?ACCGGCCAAGGTCCC
```

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

```
CG Input section AGCGCCGCTAGCCGTCGCCGCCAC  
>JZ331707.1 BT1273 Panthera tigris tigris cDNA library  
Panthera tigris tigris cDNA clone BT1273 similar to lamin B  
receptor (LBR), mRNA sequence  
GTTTTGGATGGGGGGTTTGTTCGCCACCCCAATTACTTG  
GGTGATCTCATCATGGCCCTGGCTGGT  
CCCTCCGTGTGGTTCAATCACATTGCCTATTCTATGT  
GATTTATTCACCATCTGCTGGTGCC  
CCGGGAAGCCCGTGACGAGCACCACTGTAGGAAGAAGTATG
```

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 TCGCGGAGAGTCGCCGGTTCTCTGCTTCAACAGTG---CTTGAACGG
                     ||||| .|||..||| .|||..||| .
JZ331707.1      1 -----GTAA-----TTGGATGGTGGGTTTGTTCGC
                     ||||| .|||..||| .|||..||| .
=====
JZ331708.1      47 AACCC-----GGCTG--CTCGTC--CCC-----CCCTCAC
                     .||| | .|||.||| .|||.||| .||| .||| .
JZ331707.1      28 CACCCCCAATTACTTGGGTGATCTCATCATGGCCCTGGCCTGGTCCT---
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331708.1      73 CCCGGCGG--CAACTCAGAGCCA---GCCTT-----C
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331707.1      75 CCCGTGTTGTTCAATCA---CATTGGCTTATTCATGTGATTAT
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331708.1      101 GTCACCA-CTTGACAGCGCCCTCCGACCGGCCAACGGTCCCACGCAC
                     .||||| .||| .||| .||| .||| .||| .||| .
JZ331707.1      121 TTACCATCTTG-----CT-----GGT
                     ||||| .||| .||| .||| .||| .||| .
JZ331708.1      150 TCCAGGCCGCTCAGCGCTCGCCGCCACCACCAACCCGGCCCTTTT
                     .|||..||| .||| .||| .||| .||| .||| .||| .
JZ331707.1      138 ---GCCCGGGAAAC-----CCGTGACGAGCACCACTG-----
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331708.1      200 CAGCCGCCACCATGACGACCGCATTCCCTCTCGAGGTGGCCAGAACATA
                     .|||..||| .|||..||| .|||..||| .|||..||| .
JZ331707.1      168 -----TAGGAAAG-ACTAT-GCCCTGGC---GTGGG---AGAAAGTA
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331708.1      250 CCACCAAG-GACTCGGAGGCCATCAACCG-----CCAGATCAAC
                     .|||..||| .||| .||| .||| .||| .||| .||| .
JZ331707.1      201 CTGCCAGCGAGTC---CC-----CTACCGCATATTTCCCTACATCTAC
                     ||||| .||| .||| .||| .||| .||| .||| .
JZ331708.1      290 CTGGA---GCTCTACGCCCTCTATGTCACCTG-TCCATGTCGACTAT
                     .||| .||| .||| .||| .||| .||| .||| .||| .
JZ331707.1      241 --TGATTTGCTGGGCC---TCTAAATGCTCC-TGCAGTTCTAT
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331708.1      335 TTTGACCGTGTATGTCGCTT---GAAGAACATTGCCAAAATACTTTCTT
                     ||||| .||| .||| .||| .||| .||| .||| .
JZ331707.1      284 TTT---CCG-----TTTACGAAAAA-----AAAAA-----
                     ||||| .||| .||| .||| .||| .||| .||| .
JZ331708.1      383 CACCAATCTCATGAGGGAGGGAAACATGCTGAGAAAATGATGAAGCTGCA
                     .|||..||| .||| .||| .||| .||| .||| .
JZ331707.1      306 -----AAAAAAA-----AAAAA-----
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331708.1      433 GAACCAGCGAGGGCGGCCAATCTCCCTCAGGATATCAAGAAAACCAGACC
                     ||||| .|||..||| .|||..||| .|||..||| .
JZ331707.1      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
ATGAATCCAATCAGAAAAATAACCATGGATCAATCTGTAT
GGTAGTCGGAATAATTAGCCTAATAT
TGCAAATAGGAATATTCTCAATATGGATTAGCCATTCAATT
CAAACCTGGAAGTCAAAACCATACTGG
AATATGCAACCAAAGCATCATTACCTATAAAAATAGCACCTGG
GTAAATCAAACATATGTTAACATTAGC
```

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
ATGAATACAATCAAAAATAACCATGGGTCAATCTGTC
TAATAGTTGGAATAACTAGCCTAATAT
TACAAATAGGAATATACTCAATATGGATTAGCCATTCAATT
CAAACCTAGAGATCAAAACCATTCTGA
AACATGCAACCAAAGCATCATTACCTATGAAAACACACATGG
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 ATGAATCCAATCAGAAAATAAACCATGGATCAATCTGTATGGTAGT
                   |||||..|.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      1 ATGAATACAAATCAAAAATAAACCATGGGTCATCTGTCAAATAGT
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      51 CGGAAATAATTAGCTTAATATTGCAATAGGGAAATTATCTCAATATGGA
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      51 TGGAAATACTAGCTTAATATTCAAATAGGGAAATAATCTCAAATATGGA
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      101 TTAGCCATTCAATTCAAACACTGGAAGTCAAAACCATACTGGAATATGCAAC
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      101 TTAGCCATTCAATTCAAACACTAGAGATCAAACCATCCTGAAACATGCAAC
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      151 CAAAGCATCATTAACCTATAAAAATAGCACCTGGTAAATCAAACATATGT
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      151 CAAAGCATCATTAACCTATAAAAACACATGGTGAATCAAACATATGT
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      201 TAATATTAGCAACACTAACGTTGCTGGAAAAGGCACAACCTTCAGTGAA
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      201 TAACATTAGCAATGCTAACATTGTTGCTGGACAGGATGCAACTTCATGAA
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      251 TATTAGCCGGCAATTCTACCTCTTGTCTATCCGTGGGTGGCTATATAC
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      251 TATTAGCCGGCAATTCTCTCTTTGCCATCAGTAGGTGGCTATATAC
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      301 AGCAAAGATAACCGGCATAAGAATTGGTCCAAAGGAGATGTTTGTCT
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      301 AGCAAAGACAATAGCATAAGAATTGGTCCAAAGGAGACATTTGTCT
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      351 AAGAGAGCCTTTATTCATGTCCTACTTGGAAATGCAGGACTTTTTTC
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      351 AAGAGAACCTTTATTCATGTCCTACTTGGAAATGCAGAACCTTTTC
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250365.2      401 TGACCCAAGGGCCCTGTTG          420
                   .|||||.|||||.|||||.|||||.|||||.|||||.|||||.|||..|||
AF250364.2      401 TGTCTTAAACGGGCTTACTS          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: No file chosen

```
>AP018405.1 Lactobacillus plantarum SN35N DNA,  
complete genome  
CGTAATTACGAACCACCCCCCGCACTAACAGCGTCATCCATC  
ACCCATAGTACTGACTGTGCCCTGCTT  
AAGTTGCACGGTCGCCCTAGCTTGAAACCCGTTGCCATGAC  
ATGTTGGCGAAGAGACAATCAATCATTTAG  
TGGTCATACCGGGCTGTCTGGCAGCGCCCAATCGGCATT  
AGTAAATGGGATTACGGGCCATTAAAGT
```

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

```
>AP018392.1 Lactobacillus paracasei IJH-SONE68 DNA,  
complete genome  
TTATATAGGAATGTCCGTCATCACTCGTCAGCATAGCTATAAG  
CTGGTTTGCTACCGGACATAATTGGAG  
GAGGGCATGAATGCCAATTAGAGGAACTTGGCTTACC  
TGAATGATAAATTCCGTGAAGAATTGAC  
CCCGTCGGTTACAGCACATGGATCCAGACAGCAAAACCG  
TCAAATTAAACCAAAGATAAACTCGAAATT
```

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---CATCACCCATAGTACTGACTGTGCCCTGCT-TAAGTTGC    77
                  ||||||| | .||| .||||| ||||| | |
AP018392.1      16 CGTCATCACTCGTCAGCATA-----GCTATAAG---- 43
AP018405.1      78 ACGGTCGCCCTAGCTTGAAACCCGTTGCCATGACAT-GTTGGCGAACAGC 126
                  ||.|||.|||.||| .||||| .|||||.|||.|||.|
AP018392.1      44 -----CTGGTTTGCTTAC-----GGACATAATTGGAGGGGGG 76
AP018405.1      127 AATCAAT---CATTTAGTGGTCATCACGGGGCTGTCCTGGCAGGCCCA 172
                  .||.||| .|||||.||| .|||...|||||..||| | |
AP018392.1      77 CATGAATGCCAATTAGAGGG--AACTTGGGCTTACCTG-----A 115
AP018405.1      173 ATCGGCATTAG-TAAATGGGATTACGGGCCATTAAAGTCAATTGATCC- 220
                  ||| | | | | | .|||.||| .||| | | | | |
AP018392.1      116 AT-----GATAA-----ATTCCG-----TGAAG--AATTGACCCC 143
AP018405.1      221 -CT-GGTATTGCTAACGATAC-----TGG---CAGTCCAGCTATTAA 259
                  ||| | | | | | | | | | | | | | | | | | | |
AP018392.1      144 GGTCGGT-----TACAGCACATGGATCCA--GACAGCAA--AA 177
AP018405.1      260 CTATGACCG-----TAGCCACA-ATAATTTGATGGTAC---AAATTAGA 299
                  | | | | | | .|||.||| | | | | | | | | | |
AP018392.1      178 C-----CCGTCAAATTAAACCAAAGATAA-----ACTCGAAATTGAA 213
AP018405.1      300 CGATCTGCC--CT---TTTAAACA---TTAT---AAAAAGATT----- 333
                  ||||| | | | | .||| | | | | | | | | | | |
AP018392.1      214 -----GTCCAGCTTCTTTACACAAAGCTTATTGGAAAAGAATCTCGT 257
AP018405.1      334 -----ATTACTGAA---GTAAC---AGTCACT 354
                  .||| | | | | | | | | | | | | | | | | | |
AP018392.1      258 GACCAAGGTAGTCGAAGGCCATTAC-GAATTCCGCAACTTGAACTTGAT 306
AP018405.1      355 ACTGTCAGTAAATCTTTTAT-----ATCATCAGTTAACCTTCATT 399
                  .||.||| | | | | | | | | | | | | | | | | | |
AP018392.1      307 CCCGTCA-----TTATGACCAAGGATGAGT-----TG 333
AP018405.1      400 CAGTGAGCTCGAACGCTAACGAT-----TCATTGGGTATTGATCTGA 444
                  ||||.|||.|| | | | | | | | | | | | | | | |
AP018392.1      334 CAGCCAGCTCCG---GCTACAGATCAACGTCCTGGG-----TTGA 371
AP018405.1      445 A-ATGGCCACTGCCACTC-AACTCTG-CTT-----GATTG 477
                  |||.|||.|| | | | | | | | | | | | | | | | |
AP018392.1      372 AGAAGACGA-----TCAAAATCTGACTTTAAGGCAAAACCCATTAA 414
AP018405.1      478 ACGCCG     483
                  |.||| |
AP018392.1      415 AATCCG     420
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