Mview

Multiple Sequence Alignment (MSA)

Results for Job ID mview-I20250609-141852-0861-96387037-p1m Copy

Resubmission

Tool Output | Result Files | Submission Details

Tool output

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MView


   Reference sequence (1): 2FG4_A
   Identities normalised by aligned length.
   Colored by: identity

                      cov    pid   1 [       .        .        .        .        :        .        .        .
80
 1 2FG4_A          100.0% 100.0%     ------------------------------------------------------------------------SSQIRQN
 2 6WX6_A          100.0%  76.2%     TGWSHPQFEKLKGGSSRGGGGGSGGS----------------------------------GGSGGSMSSQIRQN
 3 AAA35831.1      100.0%  98.9%     ------------------------------------------------------------------------MSSQIRQN
 4 AAP36762.1      100.0%  98.9%     ------------------------------------------------------------------------MSSQIRQN
 5 AIC54405.1      100.0%  98.9%     ------------------------------------------------------------------------MSSQIRQN
 6 AKI70336.1      100.0%  98.9%     ------------------------------------------------------------------------MSSQIRQN
 7 AKI70338.1      100.0%  98.9%     ------------------------------------------------------------------------MSSQIRQN
 8 CAE11873.1      100.0%  72.2%     ------QFGGPAGLSLASTVFGRNRSGDSLPASDRPPISSPLATSGTIFSAISCFWDLPAPFLWLAPSCQPTMSSQIRQN
 9 CAG32996.1      100.0%  98.9%     ------------------------------------------------------------------------MSSQIRQN
10 NP_000137.2     100.0%  99.4%     ------------------------------------------------------------------------MSSQIRQN
   consensus/100%                    ........................................................................SSQIRQN
   consensus/90%                     ........................................................................MSSQIRQN
   consensus/80%                     ........................................................................MSSQIRQN
   consensus/70%                     ........................................................................MSSQIRQN

                      cov    pid  81        .        1        .        .        .        .        :        .
160
 1 2FG4_A          100.0% 100.0%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 2 6WX6_A          100.0%  76.2%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 3 AAA35831.1      100.0%  98.9%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 4 AAP36762.1      100.0%  98.9%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 5 AIC54405.1      100.0%  98.9%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKXPAED
 6 AKI70336.1      100.0%  98.9%     YSTDVEAAVNSLVNLYLQASYIYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 7 AKI70338.1      100.0%  98.9%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 8 CAE11873.1      100.0%  72.2%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
 9 CAG32996.1      100.0%  98.9%     YSTDVEAAANSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
10 NP_000137.2     100.0%  99.4%     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
   consensus/100%                    YSTDVEAAsNSLVNLYLQASYhYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIK.PAED
   consensus/90%                     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
   consensus/80%                     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED
   consensus/70%                     YSTDVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAED

                      cov    pid 161        .        .        .        2        .        .        .        .
240
 1 2FG4_A          100.0% 100.0%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 2 6WX6_A          100.0%  76.2%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 3 AAA35831.1      100.0%  98.9%     EWGKTPDAMKAAMTLEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 4 AAP36762.1      100.0%  98.9%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 5 AIC54405.1      100.0%  98.9%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 6 AKI70336.1      100.0%  98.9%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 7 AKI70338.1      100.0%  98.9%     EWGKTPDTMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 8 CAE11873.1      100.0%  72.2%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
 9 CAG32996.1      100.0%  98.9%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
10 NP_000137.2     100.0%  99.4%     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
   consensus/100%                    EWGKTPDsMKAAMsLEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
   consensus/90%                     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
   consensus/80%                     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE
   consensus/70%                     EWGKTPDAMKAAMALEKKLNQALLDLHALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFE

                      cov    pid 241        :        .     ] 267
 1 2FG4_A          100.0% 100.0%     RLTLKHD-------------------
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```
 2 6WX6_A         100.0%  76.2%    RLTLRHDGGSGGSGGSGGSGGGASGGS
 3 AAA35831.1     100.0%  98.9%    RLTLKHD--------------------
 4 AAP36762.1     100.0%  98.9%    RLTLKHDL-------------------
 5 AIC54405.1     100.0%  98.9%    RLTLKHD--------------------
 6 AKI70336.1     100.0%  98.9%    RLTLKHD--------------------
 7 AKI70338.1     100.0%  98.9%    RLTLKHD--------------------
 8 CAE11873.1     100.0%  72.2%    RLTLKHD--------------------
 9 CAG32996.1     100.0%  98.9%    RLTLKHD--------------------
10 NP_000137.2    100.0%  99.4%    RLTLKHD--------------------
   consensus/100%                  RLTL+HD.....................
   consensus/90%                   RLTLKHD.....................
   consensus/80%                   RLTLKHD.....................
   consensus/70%                   RLTLKHD.....................
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If you use this service, please consider citing the following publication: The EMBL-EBI Job Dispatcher sequence analysis tools framework in 2024. More information about this bioinformatics application can be found in its bio.tools record.

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