$\square$ DAMKAAMALEKKLNQALLD HALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFERLTLRH

DAMKAAMALEKKLNQALLD HALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRLGGPEAGLGEYLFERLTLKH

DAMKAAMALEKKLNQALLD HALGSARTDPHLCDFLETHFLDEEVKLIKKMGDHLTNLHRGGPEAGLGEYLFERLTLKH

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DAMKAAMALEKKLNQALDHANGANLH

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DAMKAAMALTH AAVNS LVNLYL ÇASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AAVNS LVNLYL QASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AAVNS LVNLYL QASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AAVNS LVNLYLQASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AANNS LVNLYLQASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AANNS LVNLYLQASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AANNS LVNLYLQASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKPAEDEWGKTP
AANNS LVNLYLQASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKFPAEDEWGKTP
AANNS LVNLYLQASYTYLSLGFYFDRDDVALEGVSHIFRELAEEKREGYERLIKMONORGGRALFODIKKFPAEDEWGKTP QFGGPAGLSLASTVFGRNRSGDSLPASDRPPISSPLATSGTIFSAISCFWDLPAPFLWLAPSCQPTWSSQIRQNVSTDWE

OFFICE OF THE STATE OF THE Feedback Resubmission Submission Details TGNSHPQFEKLKGGSSRGGGGGGGGGGGGGGGG 261 : Decsessessessessess Copy Result Files mview-I20250609-141846-0845-98449036-p1m Reference sequence (1):  $6MX6\_A$  Identities normalised by aligned length. Colored by: identity pid **161**  $\vdash$ 81 cov pid **241** 100.0% 100.0% H EMBL-EBI home 100.0% 98.9% 98.9% 98.9% 98.9% 73.4% 99.4% 100.0% 98.9% 98.9% pid 100.0% 98.9% 98.9% 98.9% 98.9% 73.4% 99.4% pid 98.9% 98.9% 73.4% 99.4% 98.9% 100.0% 1 77.1% 77.1% 77.1% 100.0% 77.1% 77.1% 77.1% 77.1% 91.2% 77.1% 77.1% 100.0% 1 77.1% 77.1% 77.1% 77.1% 91.2% 77.1% 77.1% 77.1% 77.1% 91.2% 77.1% 77.5% COV 000 Job Dispatcher Help & Privacy Your Jobs Input form consensus/100% consensus/90% consensus/80% consensus/70% consensus/100% consensus/90% consensus/80% consensus/70% consensus/90% consensus/100% 5 CAG32996.1 6 AIC54405.1 7 CAE11873.1 8 NP\_000137.2 9 AAP36762.1 10 2FG4\_A 1 6WX6\_A 2 AKI70338.1 3 AAA35831.1 4 AKI70336.1 5 CAG32996.1 6 AIC54405.1 7 CAE11873.1 8 NP\_000137.2 9 AAP36762.1 10 2FG4\_A 8 NP\_000137.2 9 AAP36762.1 10 2FG4\_A 1 6WX6\_A 2 AKI70338.1 3 AAA35831.1 4 AKI70336.1 5 CAG32996.1 6 AIC54405.1 7 CAE11873.1 6WX6\_A AKI70338.1 AAA35831.1 AKI70336.1 6WX6 A Multiple Sequence Alignment (MSA) 08 0 1 2 8 4 240 160 MView **Tool Output** Mview Results for Job ID **Tool output** Download

%6.86	%6.86	98.9%	%6.86	%6.86	73.4%	99.4%	%6.86	99.4%				
77.1%	77.1%	77.1%	77.1%	77.1%	91.2%	77.1%	77.5%	76.7%				
2 AKI70338.1	3 AAA35831.1	4 AKI70336.1	5 CAG32996.1	6 AIC54405.1	7 CAE11873.1	8 NP_000137.2	9 AAP36762.1	10 2FG4_A	consensus/100%	consensus/90%	consensus/80%	consensus/70%

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