YSTOVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFRELAEEKREGYERLLKMQNQRGGRALFQDTKKPAED
YSTOVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFRELAEEKREGYERLKMQNQRGGRALFQDTKKPAED
YSTOVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLKMQNQRGGRALFQDTKKPAED
YSTOVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLKMQNQRGGRALFQDTKKPAED
YSTOVEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEEKREGYERLKMQNQRGGRALFQDTKKPAED EWGYTPDAMKAAMALEKKLNQALLDHALGSARTDPHLCDFLETHFLDEEVKLTKKMGDHLTNLHRLGGFEAGLGEYLFE
EWGYTPDAMKAAMALEKKLNQALUDHALGSARTDPHLCDFLETHFLDEEVKLTKKMGDHLTNLHRLGGFEAGLGEYLFE
EWGYTPDAMKAAMALEKKLNQALUDHALGSARTDPHLCDFLETHFLDEEVKLTKKMGDHLTNLHRLGGFEAGLGEYLFE
EWGYTPHLOTHUNDHALGGFEAGLGEYLFE Feedback NOZUCSKS-----NOZUCKON ------BSQIRQN
-----QEGPAGLSLASTVFGRNRSGDSLPASDRPPISSPLATSGTIFSAISCFWDLPAPFLWLAPSCQPTESQURQN
------SSQIRQN SSQURQN

SSQURQN

SSQURQN

SSQURQN

MSSQURQN Resubmission Submission Details TGUSH POTEKLIKG---GSSRGGGGGGGGGS 267 . RLTLRHDGGSGGSGGSGGASGGS Copy Result Files mview-I20250609-140455-0131-70717827-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% 99.4% 98.9% 98.9% 98.9% 98.9% 76.3% 100.0% 99.4% 98.9% 98.9% pid 100.0% 99.4% 98.9% 98.9% 98.9% 98.9% 89.2% 76.3% pid 98.9% 98.9% 98.9% 89.2% 76.3% 100.0% 1 77.1% 77.1% 77.1% 100.0% 1 77.1% 77.1% 77.1% 77.1% 77.1% 77.1% 77.5% 88.5% 100.0% 1 77.1% 77.1% 77.1% 77.1% 77.1% 77.1% 77.5% 88.5% 76.7% 77.1% 77.1% 77.1% 77.5% 88.5% 76.7% COV 000 Job Dispatcher Help & Privacy Your Jobs Input form consensus/100% consensus/100% consensus/100% consensus/80% consensus/90% consensus/90% consensus/90% 1 6WX6\_A 2 NP\_000137.2 3 AIC54405.1 4 AAA35831.1 5 CAG32996.1 6 AKI70338.1 7 AKI70336.1 8 AAP36762.1 9 CAE11873.1 1 6WX6\_A 2 NP\_000137.2 3 AIC54405.1 4 AAA35831.1 5 CAG32996.1 6 AKI70338.1 7 AKI70336.1 8 AAP36762.1 9 CAE11873.1 6WX6\_A NP\_000137.2 AIC54405.1 AAA35831.1 5 CAG32996.1 6 AKI70338.1 7 AKI70336.1 8 AAP36762.1 9 CAE11873.1 10 2FG4\_A 6WX6 A Multiple Sequence Alignment (MSA) 08 1 2 8 4 1 4 4 240 MView **Tool Output** Mview Results for Job ID **Tool output** Download

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99.4%	%6.86	%6.86	%6.86	%6.86	%6.86	89.2%	76.3%	99.4%				
77.1%	77.1%	77.1%	77.1%	77.1%	77.1%	77.5%	88.5%	76.7%				
2 NP_000137.2	3 AIC54405.1	AAA35831.1	CAG32996.1	6 AKI70338.1	7 AKI70336.1	8 AAP36762.1	9 CAE11873.1	10 2FG4_A	consensus/100%	consensus/90%	consensus/80%	consensus/10%
7	m	4	2	9	7	ω	6	10				

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