

```

NTDB id 624 LCA RS00040 WP 011373726.1
NTDB id 113 BSU 40900 NP 391970.1
NTDB id 597 KW2 RS01935 WP 021036727.1
NTDB id 1136184 DQM44 RS00810 WP 003053955.1
NTDB id 498 SM12261 RS01980 WP 000282464.1
NTDB id 526 SMSK321 RS08825 WP 000282440.1
NTDB id 268 KZH43 RS08520 WP 000282467.1
NTDB id 227 SPD RS09110 WP 000282467.1
NTDB id 193 SPR RS08685 WP 000282467.1
NTDB id 158 SP RS09595 WP 000282442.1
NTDB id 409 SMU RS08940 WP 002263454.1
NTDB id 583 DLJ51 RS09560 WP 002962590.1
consensus

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Sequence	Score
MINRVVLVGRLTDRVLDLRYTSSGAAVGTFMAVNRQFTNANGDREADFTNCVTVWRKSAENFANFTKKGSLVGVDRGLQTR	80
MLNRVVLVGRLTGDKPELRYTPNGAAVATFTLAVNRFTTNQSGEREADFTNCVTVWRQEAENVANFLKKGSLAGVDGRGLQTR	80
MNKTMLIGRLTINAPEISKTTNNKSYVRVTLAVNRFFKNQSGEREADFTSLTWGKSAETLVSYAKKGSLISVEGELRTR	79
MYNKVIAIGRLVAKPELVKTATDKHVARLSLAVNRFFKNASGEREADFTSVVWCKLAETLVSYASKGSLMSIDGELRTR	80
MYNKVIMIGRLTSTPELHKTNNDKSVARATIAVNRRYKDNQGEREADFVNMVLWCKLAESLSASYATKGSLISVDGELRTR	80
MYNKVILIGRLTSTPELHKTNNDKSVARATIAVNRRYKDNQGEREADFVNMVLWGRLAETLASYATKGSLISVDGELRTR	80
MYNKVIMIGRLTSTPELHKTNNDKSVARATIAVNRRYKDNQGEREADFVNMVLWGRLAETLASYATKGSLISVDGELRTR	80
MYNKVIMIGRLTSTPELHKTNNDKSVARATIAVNRRYKDNQGEREADFVNMVLWGRLAETLASYATKGSLISVDGELRTR	80
MYNKVIMIGRLTSTPELHKTNNDKSVARATIAVNRRYKDNQGEREADFVNMVLWGRLAETLASYATKGSLISVDGELRTR	80
MYNKVILIGRLTSTPELHKTNNDKSVARATIAVNRRYKDNQGEREADFVNMVLWGRLAETLASYATKGSLISVDGELRTR	80
MYNKVILIGRLVATPEMVKTPKDKSVTRVTLAVNRFFKSDQGERQADFVNMVLWGRLAETLASYAGSKGSLISLDGELRTR	80
MYNKVILIGRLTAAPEMVKTPSNKSVTHITLAVNRFFKTDQGERQADFVNMVFWCKLAESLVSYAKKGSLVSLDGEIRTR	80

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RYE.KNGQMNYVTEVLVTG.FQLLESRAQRAMRENNAG
K.FNDEVFIAIAAGYB.KTLEESRAQSSONYNENRSGSQYFGGGQNDSEFESNQGSPBRNANFESRDP
NYENQGGQRVYVTEVVVDNFSLLESRTTTEQRQG.DGASQNFNSNQSNQSQ.....QSGFTSPQQTGNAPAAANNTQADP 153
NYENQGGQRVFVTEVQAESVQFLEPKNGGCSGS.....GGYNEGNSGGGQYFGGGQNDNPFGGNQNNQRRNQNSFNDDP 155
NYTDKNEQKHYITEILGLSYDLLESRA TLALRESAVK..... 116
KYD.KDGQVHYVTEVLCQS.FQLLESRAQRAMRENNVT..... 116
RFE.KNGQMNYVTEVLVTGFQLLESRAQRAMRENNAG..... 116
RFE.KNGQMNYVAEVLVTGFQLLESRAQRAMRENNAG..... 116
RFE.KNGQMNYVTEVLVTGFQLLESRAQRAMRENNAG..... 116
RFE.KNGQMNYVTEVLVTGFQLLESRAQRAMRENNAG..... 116
RFE.KNGQMNYVTEVLVTGFQLLESRAQRAMRENNAG..... 116
RFE.KNGQMNYVTEVLVTGFQLLESRAQRAMRENNAG..... 116
RFE.KNGQMNYVTEVLVTGFQLLESRAQRAMRENNAG..... 116
KYE.KDGVTHFVTEVLGHS.FQLLESRAQRAMRENNSE..... 116
HYE.KDGQTHYVTEILAQSFQLLESRAQRALRENNGA..... 116
*** **** * ! * * * * ! ! * * * * * * * * * * * * * * * * *

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consensus

```



- ☐ non conserved
- ☒ similar
- ☒ $\geq 50\%$ conserved