```
logo
NTDB id 1233 CJJ81176 RS04995 WP 002853564.1  MRCINCGAFALLCFCELCELELSEFSLNVRKLDNNFKVYSFYKYHEIQHLLHSKHYFYGYFVYKMLAKLSFAKFKDFFDP   80
NTDB id 31690 HPG27 RS07305 WP 001203590.1    MRCLTCLKLSFKPLCPNCLNDLP.LSLKVRV.LEGVSVYSFYAYSEIEELIKSKYALIGSRILPLLSQKAGAEFVRILQE   78
NTDB id 1221 C694 RS07590 WP 001203580.1      MRCLTCLKLSFKPLCPNCLNDLP.LSLKVRV.LEGVSVYSFYAYSEIEELIKSKYALIGSRILPLLSQKAGAEFVKILQE   78
consensus                                     !!!**!********!**!***!* *!!*!!* *****!!!!*!*!!**!**!****!******!*****!*!********

logo
NTDB id 1233 CJJ81176 RS04995 WP 002853564.1  ...RMTINVIALDDKVEDMLYSHSAILARYLKTKFVKPVFNVLKAQNHIKYSGKSLEFRQKHKRNYKLLKTIHEPVILVD   157
NTDB id 31690 HPG27 RS07305 WP 001203590.1    QGLNTPLYGIAIDDKIK.SFYSHSAALLKGFCQGNLKPTYGTLRATNTISYAGKSLEFRANNPRGFTFKGDKNLDYFLLD   157
NTDB id 1221 C694 RS07590 WP 001203580.1      QGLNIPLYGIAIDDKIK.SFYSHSAALLKGFCQGNLKPTYGRLRANNAVSYAGKSLEFRANNPRNFTFKGDESLDYFLLD   157
consensus                                     ******!****!!*!!!** **!!!!!*!*********!!*** !*!*! **!*!!!!!!!****!*******  ****!*!

logo
NTDB id 1233 CJJ81176 RS04995 WP 002853564.1  DIVTTGSSLLEAKKVLEENKISVLFALVLADAKV   191
NTDB id 31690 HPG27 RS07305 WP 001203590.1    DIITTGTTLKEALKYLKALNIKAHFAIALCSADE   191
NTDB id 1221 C694 RS07590 WP 001203580.1      DIITTGTTLKEALKYLKTLNIKVHFAIALCSADE   191
consensus                                     !!*!!!**!*!!*!*!* **!***!!**!**!**
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X non conserved

X similar

X ≥ 50% conserved