```
logo
                                                  MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE
NTDB id 258 KZH43 RS03475 WP 000590640.1          ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE  82
NTDB id 217 SPD RS03775 WP 000590640.1            ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE  82
NTDB id 183 SPR RS03560 WP 000590640.1            ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE  82
NTDB id 147 SP RS03905 WP 000590640.1             ..MIKILLVEDDLGLSNSV.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE  82
NTDB id 49584 SSGZ1 RS04965 WP 014637852.1       ..MIKILLVEDDLSLSNSV.FDFLDDFADVMQVFDGEEGIYEAETGVYDLILLDLMLPEKDGFQVLKELREKGVTTPVLITTAKE  82
NTDB id 362 SMU RS05200 WP 002262214.1           ..MIKLLLVEDDLSLSNSI.FDFLDDFADVMQVFDGEEGLYEAESGVYDLILLDLMLPEKNGFQVLKELREKGITTPVLIMTAKE  82
NTDB id 374 SMU RS06885 WP 002262930.1           ..MKKILIVDDEKPISDIIKFNLAKEGYDTITAFDGREALSKYEEENPDLIILDLMLPELDGLEVAKEVRKN.SHVPIIMLSAKD  82
NTDB id 606 V4T04 RS01910 WP 003130756.1         MTSKKILIIEDEKNLARFVSLELEHEGYATEIKDNGRSGLEEATSKDYDLILLDLMLPELDGFEVARRLRKE.KDTPIIMMTARD  84
NTDB id 471 HSISS4 RS01430 WP 002883757.1        .MSKRILIVEDEKNLARFVSLELQHEGYDVVTADNGREGLEMALEKDFDLILLDLMLPEMDGFEVTRRLQQE.KDTYIMMMTARD  83
consensus                                          ****!***!** ***** ***************!************!!!*!!!!!!!**!**!*****************!**
```

```
logo
                                                  SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE     NT     LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL
NTDB id 258 KZH43 RS03475 WP 000590640.1          SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL  157
NTDB id 217 SPD RS03775 WP 000590640.1            SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL  157
NTDB id 183 SPR RS03560 WP 000590640.1            SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL  157
NTDB id 147 SP RS03905 WP 000590640.1             SLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NT.....LTYGNIVVNLSTNTVKVEDTPVELLGKEFDL  157
NTDB id 49584 SSGZ1 RS04965 WP 014637852.1       SLEDKGHGFELGADDYLTKPFYLEELKMRIQALLKRAGKFNE.....NT.....LTYGDVTVDLSTNSTTVNGEEVELLGKEFDL  157
NTDB id 362 SMU RS05200 WP 002262214.1           GLDDKGHGFELGADDYLTKPFYLEELKMRIQALLKRSGKFNE.....NN.....LTYGELTVDTATNTTMVNGKEVELLGKEFDL  157
NTDB id 374 SMU RS06885 WP 002262930.1           SEFDKVIGLEIGADDYVTKPFSNRELLARVKAHLRRTENIESAVAEENASGIPEIIIGDLQILPDAFVAKKRGTEVELTHREFEL  167
NTDB id 606 V4T04 RS01910 WP 003130756.1         STMDRVAGLDIGADDYITKPFAIEELLARVRAFFRREEHGHAV.ERAENTSFRDLV.....IDKTNRTVHRGKKVIDLTRREYDL  163
NTDB id 471 HSISS4 RS01430 WP 002883757.1        SIMDIVAGLDRGADDYIVKPFAIEELLARIRATFRRQDIEAAKNAPAKASTYRDLK.....LDVQNRTVVRGDEAIPLTKREFDL  163
consensus                                        ***!***!***!!!!!**!!!***!!**!**!***!******     **      **** * * ******** ** **!***!**!
```

```
logo
                                                  LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ
NTDB id 258 KZH43 RS03475 WP 000590640.1          LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ  224
NTDB id 217 SPD RS03775 WP 000590640.1            LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ  224
NTDB id 183 SPR RS03560 WP 000590640.1            LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ  224
NTDB id 147 SP RS03905 WP 000590640.1             LVYFLQNQNVILPKTQIFDRLWGFDSDTTISVVEVYVSKVRKKLKGT.TFAENLQTLRSVGYLLKDVQ  224
NTDB id 49584 SSGZ1 RS04965 WP 014637852.1       LVYFLQNQNVILPKTQIFDRIWGFDSDTTISVVEVYVSKIRKKLKGT.TFGENLQTLRSVGYILKNA.  223
NTDB id 362 SMU RS05200 WP 002262214.1           LVYFLQNQNVILPKSQIFDRIWGFDSDTTISVVEVYVSKIRKKLKDT.TFGKNLQTLRSVGYILKDAN  224
NTDB id 374 SMU RS06885 WP 002262930.1           LHHLATHTGQVMTREHLLETVWGYDYFGDVRTVDVTVRRLREKIEDTPSRPEYILTRRGVGYYMKSYD  235
NTDB id 606 V4T04 RS01910 WP 003130756.1         LLTLMQNVGDVVTREHLVSQVWGYEEGTETNVVDVYIRYLRNKID.VEGQDSYIQTVRGLGYVMRERK  230
NTDB id 471 HSISS4 RS01430 WP 002883757.1        LNTLLSNMNQVMTREELLLQVWKYDDAIETNVVDVYIRYLRGKID.VPGKESYIQTVRGMGYVIREK.  229
consensus                                        !*********************!**********!*!*****!*!**** *******!*!**!!**** *
```

X non conserved

X similar

X $\geq$50% conserved