logo 

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NTDB id 1390 A4U84 RS00055 WP 021115958.1           MAGVNKVIIVGNLGNDPDMRTMPNGDAVATLSVATSESWNDKMTGERREVTEWHRIVFFRRQAEVAGQYLRKGSKVYVEG   80
NTDB id 624 LCA RS00040 WP 011373726.1              ..MINRVVLVGRLTRDVDLRYTSSGAAVGTFSMAVNRQFTNANG.D..READFINCVIWRKSAENFANFTKKGSLVGVDG   75
NTDB id 112 BSU 36310 NP 391512.2                   ..MFNQVMLVGRLTKDPDLRYTSAGAAVAHVTLAVNRSFKNASG.E..IEADYVNCTLWRKTAENTALYCQKGSLVGVSG   75
NTDB id 35093 LMOSLCC2378 RS00270 WP 003721668.1    ..MMNRVVLVGRLTKDPELRYTPAGVAVATFTLAVNRTFTNQQG.E..READFINCVVWRKPAENVANFLKKGSMAGVDG   75
NTDB id 113 BSU 40900 NP 391970.1                   ..MLNRVVLVGRLTKDPELRYTPNGAAVATFTLAVNRTFTNQSG.E..READFINCVTWRRQAENVANFLKKGSLAGVDG   75
consensus                                             **!*!**!!*!**!***!*** !*!!*****!*******  * *  ***********!* !!* *****!!!***!*!
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logo 

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NTDB id 1390 A4U84 RS00055 WP 021115958.1           KLKTRKWQDQNGQDRYTTEIQGDVLQMLDSRSSGGDFGGNQGSGWNQAPAQTNYNQGGYS..DNYAQNNNFNGG.....N  153
NTDB id 624 LCA RS00040 WP 011373726.1              RLQTRNYENQQGQRVYVTEVVVDNFSLLESRTTTEQRQGDGASQNF....NSNQS........NGSQQSGFTSPQQTGNA  143
NTDB id 112 BSU 36310 NP 391512.2                   RIQTRSYENEEGVNVYVTEVLADTVRFMDPKPREKAAD..........................................  113
NTDB id 35093 LMOSLCC2378 RS00270 WP 003721668.1    RVQTRNYEGNDGKRVYVTEIVAESVQFLEPRNSNGGGNNYQSGNN....NNNYNSGGNNFGQAPTNNGGFGQDQQQSQN  151
NTDB id 113 BSU 40900 NP 391970.1                   RLQTRNYENQQGQRVFVTEVQAESVQFLEPKNGGGSGSGGYNEGNS....GG.....GQYFGG.GQNDNPFGGNQNNQRR  145
consensus                                           ***!!******!*****!!************ * * * *   ***     * *    *        **  *   **
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logo 

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NTDB id 1390 A4U84 RS00055 WP 021115958.1           ATRPQPAQKPAAQAEPPMDNFDDDIPF  180
NTDB id 624 LCA RS00040 WP 011373726.1              PAANNTQADPFANNGQAIDISDDDLPF  170
NTDB id 112 BSU 36310 NP 391512.2                   ...........................  113
NTDB id 35093 LMOSLCC2378 RS00270 WP 003721668.1    QNYQSTNNDPFASDGKPIDISDDDLPF  178
NTDB id 113 BSU 40900 NP 391970.1                   NQGNSFNDDPFANDGKPIDISDDDLPF  172
consensus                                              *  * ***** * ***********
```

X non conserved

X similar

X ≥50% conserved