logo

```
NTDB id 356826 E5093 RS01785 WP 177155284.1  MPNSPVHPAPIYRVRVAVPVYLYDGFDYMLSAAEYQQAAVGARVLVSFGRQNLVGIIIEKLPPDHPLDPKIKLKAISELL  80
NTDB id 1072 ABD1 RS01805 WP 000156662.1      MTITPKPDSVVYRVRVAVPVHLYDTFDYTLTQAQYERAHVGSRVAISFGRQNLIGIITEKVDPSESFTGTFQLKAISDLL  80
consensus                                    !* *!  * **!!!!!!!!!*!!! !!! !* ! !  !*!! !! *!!!!!!!*!!! !!**! **  *   !!!!!*!!
```

logo

```
NTDB id 356826 E5093 RS01785 WP 177155284.1  DQQPILDQKVLTLLTWSAQYYQFPIGEVMHSALPSLLRQGRPYNLLARMWKLLD.DQAEAKLKRSEKQQEAYKVLKLHPS  159
NTDB id 1072 ABD1 RS01805 WP 000156662.1      DEQPILDEQVLSLLTWSAQYYQFPIGEVMQTALPALLRQGKPMDVLFHLWKITPCDNVEALLKRSGKQQDAYQILKLHPA  160
consensus                                    ! !!!!!  !!*!!!!!!!!!!!!!!!!!**!!! !!!!!*!  *! **!!* **!* !! !!!! !!!*!! *!!!!! 
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logo

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NTDB id 356826 E5093 RS01785 WP 177155284.1  GTSENILNLAGIETATLKALEKKQICYCDLEQQDFSPVPMTLAQMPLTPNSDQKRAIETVLKAQHRYQAFLLDGLTGSGK  239
NTDB id 1072 ABD1 RS01805 WP 000156662.1      GTTENILNLSGVETATLKALQKKGLVDCTLEPHDFSPSPVQLAQMPLTLNEDQKKATQYVVNAQHQYQAFLLDGLTGSGK  240
consensus                                    !!*!!!!!! !*!!!!!!!! !! ** ! !!**!!!! !* !!!!!!!*! !!!*!   !* !!! !!!!!!!!!!!!!!
```
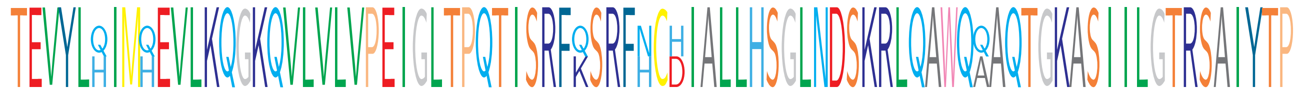

logo



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NTDB id 356826 E5093 RS01785 WP 177155284.1  TEVYLQIMQEVLKQGKQVLVLVPEIGLTPQTISRFQSRFHCHIALLHSGLNDSKRLQAWQAAQTGKASIILGTRSAIYTP  319
NTDB id 1072 ABD1 RS01805 WP 000156662.1      TEVYLHIMHEVLKQGKQVLVLVPEIGLTPQTISRFKSRFNCDIALLHSGLNDSKRLQAWQQAQTGKASIILGTRSAIYTP  320
consensus                                    !!!!!*!!*!!!!!!!!!!!!!!!!!!!!!!!!!! !!!*!*!!!!!!!!!!!!!!!!!! !!!!!!!!!!!!!!!!!!!
```

logo

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NTDB id 356826 E5093 RS01785 WP 177155284.1  LPNLGLIILDEEHDLSFKQQEGFRYHARDVALYRAHLEHCPVILGSATPSIDSYALTEQGKMIRLELNQRAGPALMPKIH  399
NTDB id 1072 ABD1 RS01805 WP 000156662.1      LPRLGLIILDEEHDLSYKQQEGFRYHARDVALYRGHLQGCPVLLGSATPSIDSYHLVETGKLTALQLNQRAGHALLPKMH  400
consensus                                    !! !!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!*!! *!!!*!!!!!!!!!!!*! ! !!*  ! !!!!!! !!*!!*!
```
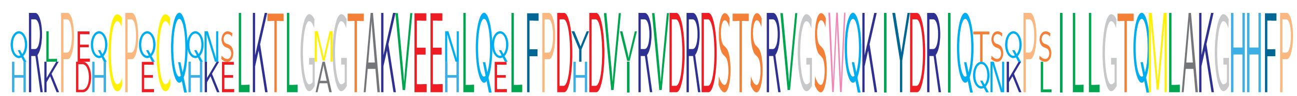

logo

```
NTDB id 356826 E5093 RS01785 WP 177155284.1  IIDLKVAQKQQGLSLLLIQEIKKRLQKKEQVLIFLNRRGYAPVLVCDSCGWQAQCPHCDANFTLHHSPYTHLHCHHCGTI  479
NTDB id 1072 ABD1 RS01805 WP 000156662.1      LIDLKIVKKQHGISQPLIEQIKNTLARKEQVLIFLNRRGYAPVLVCESCGWQANCPHCDAHFTLHTQPYSYLHCHHCGTV  480
consensus                                    *!!!!*  !!*!*! *!!  !!  ! *!!!!!!!!!!!!!!!!!!!*!!!!!!*!!!!!!*!!!!* !!**!!!!!!!!*
```

logo



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NTDB id 356826 E5093 RS01785 WP 177155284.1  QRKPEQCPQCQHNELKTLGMGTAKVEENLQQLFPDYDVVRVDRDSTSRVGSWQKIYDRIQTSQPLILLGTQMLAKGHHFP  559
NTDB id 1072 ABD1 RS01805 WP 000156662.1      HRLPDHCPECQQKSLKTLGAGTAKVEEHLQELFPDHDVIRVDRDSTSRVGSWQKIYDRIQQNKPSILLGTQMLAKGHHFP  560
consensus                                    *! !**!! !!*  !!!!! !!!!!!!*!! !!!!*!!*!!!!!!!!!!!!!!!!!!!!!   ! !!!!!!!!!!!!!!!
```

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logo

NTDB id 356826 E5093 RS01785 WP 177155284.1  YVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGDVYLQTLRPDHPLLSTLVEQDYRAFARQTLKERQAAL  639
NTDB id 1072 ABD1 RS01805 WP 000156662.1     HVTLVAILDIDAGLLSVDIRAPERTAQLIVQVAGRAGRGEHKGHVYLQTLRPDHPLLTTLIEKDYRAVAKQTLAERKVAL  640
consensus                                    *!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!*!!*! !!!! !*!!! !!  !!

logo

NTDB id 356826 E5093 RS01785 WP 177155284.1  LPPFRYTALIRCESKSQEQNQQFLQQHAQWLRENSEQLIDIWGPIPAPMERKAGRYQAHLVLLSQDRARLHFYLRAWWQN  719
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LPPYRYAVLIRAESKDRDYTLHFLNEAAEQLRQIAGDIVDIWGPIPAPMERKAGRYRAHMVILSADRARLHFYLRQWWAQ  720
consensus                                    !!!*!!  !!!*!!!  *   *!!* *!  !!     **!!!!!!!!!!!!!!!!!! !!*!*!! !!!!!!!!!! !! *

logo

NTDB id 356826 E5093 RS01785 WP 177155284.1  MLYH.KPSNMKLSLDIDPQEFS   740
NTDB id 1072 ABD1 RS01805 WP 000156662.1     LVHAPRQHQLRLSIDVDPQEFS   742
consensus                                    ***********!!*!*!!!!!!
```

X non conserved
X similar
X ≥ 50% conserved