```
NTDB id 1121109 EL143 RS11400 WP 126326787.1  MYRIERCLPAWVLGVAASFALPAVPAWYVTAAAGTGLLLVARRSGVAVVLLAALLGMAYGIWRTELALANQWPVGRFAAD  80
NTDB id 1128 NGFG RS01490 WP 020997305.1      .MFRRWFLPCWVVGVAVSFALSVVPHWPFWLAAFAVLAVLARRFAFAGLMLCVLAGAAYGVFRTEAALSSQWRAEAVSGV  79
consensus                                     *      *!!*!!*!!! !!!!* !!*!*    !!    !  **!!! * ! **!* ! ! !!!**!!! !!  !!*      *
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```
NTDB id 1121109 EL143 RS11400 WP 126326787.1  TLTLKVTGLPQREERRVRFEAQVQDAGGRQRRVQLSDYSLRDWPVGSVWRANVRLRAPVGEVNLRGFNREAWALANGLDA  160
NTDB id 1128 NGFG RS01490 WP 020997305.1      PLTVEVTDMPRSDGRRVQFAAKAVDSGGRTFDLLLSDYKRREWAVGSRWRITARVHPVVGELNLRGLNREAWALSNGVGG  159
consensus                                     *!!* !! *!  * !!! ! !   ! !!!   * !!!!  !*!*!!! !!   !****!!!*!!!! !!!!!!! !!* *
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```
NTDB id 1121109 EL143 RS11400 WP 126326787.1  LGTVGKARFQVGQDPAGGVLGLRVAISGNWQQV...QGFEQGVALMRALSIGEQGALPNRAWQAFRPLGLTHLVSISGLH  237
NTDB id 1128 NGFG RS01490 WP 020997305.1      VGTVGADRVLLHGGSGWGIAVWRSRISRNWRQADADGGLSDGIGLMRALSVGEQSALRPGLWQAFRPLGLTHLVSISGLH  239
consensus                                     *!!!!  !  **  ** !*   !  !! !! ! *** !   !**!!!!!!*!!! !!**  !!!!!!!!!!!!!!!!!!!
```

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NTDB id 1121109 EL143 RS11400 WP 126326787.1  VSMVGLMAAWLARLVLRRLPFSFKRPRTVVLAAGLAAAACLYALLAGFGVPTQRTVLMLAAFAWIWHSRKGQSVWFAWWAA  317
NTDB id 1128 NGFG RS01490 WP 020997305.1      VTMVAVIFAWLAKRLLACSPRLPARPRAWVLAAGCAGALFYALLAGFSVPTQRSVLMLAAFAWAWRRG.RLSAWATWWQA  318
consensus                                     !*!!*** !!!!* *! * !  * !!!  !!!!!*!*!* !!!!!!! !!!!!*!!!!!!!!! !*  *  ! !  !! !
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```
NTDB id 1121109 EL143 RS11400 WP 126326787.1  LSAVLLFDPLAVLGVGTWLSFGLVAALLWISAWRLEEKGWRVFWRGQYALLLVSLVALGFMFAALPLISPLVNLLAVPWF  397
NTDB id 1128 NGFG RS01490 WP 020997305.1      LAAVLLFDPLAVLGVGTWLSFGLVAALIWACAGRLYEGKRQTAVRGQWAASVLSLVLLGYLFASLPLVSPLVNAVSIPWF  398
consensus                                     ! !!!!!!!!!!!!!!!!!!!!!!!!!!!*! *! !! !          !!!*!  **!!! !!**!! !!!*!!!!! * *!!!
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```
NTDB id 1121109 EL143 RS11400 WP 126326787.1  SWVLVPLALAASAFPFIPLQTFAAGAGQQYTMHALFWLGDRAPEWSVAAAPAGLLWLAAAAVSAALLPRGMGLRPWAFIVL  477
NTDB id 1128 NGFG RS01490 WP 020997305.1      SWVLTPLALLGSVVPFAPLQQAGAFLAEYTLRFLVWLADVSPEFAVAAAPLPLLVLAVCAALLLLLPRGLGLRPWAVLLL  478
consensus                                     !!!! !!!! *!  !! !!!  *!  * !!** ! !!*!  !!* !!!!! *!! !! *!    !!!!!*!!!!!! **!
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```
NTDB id 1121109 EL143 RS11400 WP 126326787.1  AGFVFYRPPAVPHGAVKITVWDVGQGLAVSFHTASKTLLFDTGTEAAAQTQLIPSLRAMGVRRLDAAVFSHHDNDHDGGA  557
NTDB id 1128 NGFG RS01490 WP 020997305.1      AGFVSYRPEAVPENEAAVTVWDAGQGLSVLVRTANRHLLFDTGTVAAAQTGIVPSLNAAGVRRLDKLVLSHHDSDHDGGF  558
consensus                                     !!!! !!!*!!!*    *!!!! !!!! !  *!! **!!!!!!! !!!!! **!!! ! !!!!!!  ! !!!! !!!!!
```

logo

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NTDB id 1121109 EL143 RS11400 WP 126326787.1   ELIRQAFSPTVVWAGQPGFYPNARPCHEGKAWNWDGVHFEWLSLSEKS.DDDNEQSCILRVVAAEKALLVTGDLSRRGEQ   636
NTDB id 1128 NGFG RS01490 WP 020997305.1       QAVGK.IPNGGIYAGQPEFYEGARHCAE.QRWQWDGVDFEFLRPSERKNIDDNGKSCVLRVVAGGAALLVTGDLDTKGEE   636
consensus                                        *  * **  **!!!! !!* !! !*!*  !*!!!!*!!*! *!!* * !!!  !!*!!!!!*  !!!!!!!!  *!!
```

logo

```
NTDB id 1121109 EL143 RS11400 WP 126326787.1   SLVGQYGEDLYSHVLVLGHHGSNSASSSAFLNVVAPQYAIASSGFANAYGHPAEAVKNRLRAHGIRLMRTDLHGVQQFWF   716
NTDB id 1128 NGFG RS01490 WP 020997305.1       SLVGKYGGNLYSQVLVLGHHGSNTSSSGVFLNAVSPEYAVASSGYANAYKHPTEAVQNRVRAHGIKLLRTDLSGALQFGL   716
consensus                                      !!!! !!  !!!*!!!!!!!!!!* !!  !!! ! ! !!*!!!!*!!!! !! !!! !!*!!!!!*!*!!!!*!  !!
```

logo

```
NTDB id 1121109 EL143 RS11400 WP 126326787.1   VKKEERSSDLEPDSSKPYWQKKPFKHE   743
NTDB id 1128 NGFG RS01490 WP 020997305.1       GRGGVKAQR..LRVYKFYWQKKPFE..   739
consensus                                       *   *   ***   !*!!!!!!!  **
```

X non conserved

X similar

X ≥ 50% conserved