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logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  MRAWYNKVSIFLILVSLVYVTYLTYISSSKLLVGAAVAKNHDNEVVVTDIEEFSTAYYSGLQKGDVIKSINNHKVKRPLE   80
NTDB id 91 BSU 31690 NP 391047.2               MKNLIKKFTIAVIVLSILYISYTTYISMNGIIIGTKIHKNDKSQFMIEEISESSYGQFVGLRQGDIILKINKEKPSDKHL   80
consensus                                      !*    ! *! *!**!**!**! !!!!   ***!  **!!*    ** *! ! ! * * !!  !!*!  !! *!*  **

logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  VQKYNSNHVTSIVVERDGEKVKVKPD....LMNDGNFSTFIIPLIFYIACLFCCFFVLKINESKKLFSALILIIFLLSAS  156
NTDB id 91 BSU 31690 NP 391047.2               KWGY.LSHINSLDILRSGKKIHLKDFDLVTLNRPYSFFLFVLPLFFYFLSIICIFYILKVNKKRRSFAAYILILLLDIS  159
consensus                                         !*  !* !* * ! ! !***!* ****!  *  !  !**!! !!  ** !*!**!!*!  ** ! ! !!!* !!  !

logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  LAYLSAGGSAKGDLLSRCIMVFTLTSVMLNYLLFLYQYFKELGTVLFNKKVFILYSIPFLNLVFELFRTQLFFR.HYVPK  235
NTDB id 91 BSU 31690 NP 391047.2               IAYISAGGPFRGHIINRYINLFTFISSPILYLQFIQRYLGEIGKTFLNRIS.FLYIIPIFNLGIEFFQDYLQVDIDFLAT  238
consensus                                      *!!*!!!!* *!*** !*! *!!  ! ** !! !*  !  !*!    !*  * !! !!  !! ! !  !   *****

logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  INLLSFFISF..IIVSVYFGSILIKSKDTEQAHIIKVLTIINILSFSPFLFLYIIPYVFLGTDGISSFLAASFMFLIPFS  313
NTDB id 91 BSU 31690 NP 391047.2               LNLVSFATLTLFSFSAIYL..HLNKYKYAEHSFILKLLILTNTLSFAPFLIFFVLPIIFTGNYIFPALASASLLVLIPFG  316
consensus                                      *!!*!!    **    *! ***! ! !  !* *!*!*! * ! !!! !!!  ***! *! !    *    !! * !!!!

logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  LVYQFMTNKIYNVDFILSRLKYYGILALTPTIILVTVFELMGSPAGDYYYFRLAILMYIIMVAVFYYKEVLDFRFRLKRV  393
NTDB id 91 BSU 31690 NP 391047.2               LVYQFVANKMFDIEFILGRMRYYALLAMIPTLLIVGALVLFDVMDIQMNPVRQTVFFFVVMFAVFYFKEVMDFKFRLKRF  396
consensus                                      !!!!!* !!** **!!! !**!!**!!* !!***!    !   *    * !  *  ***! !!!!*!!!*!!*!!!!!

logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  SEKFNYQDSIYKFTQLIRDSISLNQVFEELKNTILEVSLVSRAHVYEVSADGSIKLYNGEPVNSFEKVYQKEFRKVTPEI  473
NTDB id 91 BSU 31690 NP 391047.2               SEKFNYQDSIFKYTQLMRGVTSLQQVFKELKNTILDVLLVSKAYTFEVTPDHKVIFLDKHEVGPDWNFYQEEFENVTSEI  476
consensus                                      !!!!!!!!!!*!*!!!*!   !!*!!! !!!!!!!*! !!!*!* *!!**!* *     **! *    !! !!   !!*!!

logo
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1  GKIVEFNKGFVMKIGERGGKSFVILCLSKMNTPRLTLEELSWLKTLAFYTNVSIENVMKIEELMSHLEEIKQQESNPVWL  553
NTDB id 91 BSU 31690 NP 391047.2               GKIIEVNQGFLMKVGERGGSSYVLLCLSNINTPRLTRDEISWLKTLSFYTSVSMENVLHIEELMEHLKDLKQEGTNPIWL  556
consensus                                      !!!*! ! !!*!!*!!!!! !*!*!!!! *!!!!!! *!*!!!!!! !!! !!*!!!**!!!!! !! **!!  *!!*!!
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logo
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NTDB id 1090337 ABFT42 RS15970 WP 268471514.1   KKLMYTIEEKQRSDLARDLHDSVLQDLISLKRQCELFLADFKKDNNPCQEEVQDKLVQMNEQMSDVISMTRETCHELRPQ   633
NTDB id 91 BSU 31690 NP 391047.2                KKLMFAIEEKQRSGLARDLHDSVLQDLISLKRQCELFLGDFKKDDNPCREEVQDKLVQMNEQMSDVISMTRETCHELRPQ   636
consensus                                       !!!!* !!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!*!!!!! !!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
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logo
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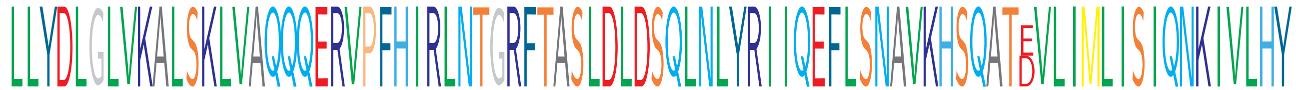

```
NTDB id 1090337 ABFT42 RS15970 WP 268471514.1   LLYDLGLVKALSKLVAQQQERVPFHIRLNTGRFTASLDLDSQLNLYRIIQEFLSNAVKHSQATEVLIMLISIQNKIVLHY   713
NTDB id 91 BSU 31690 NP 391047.2                LLYDLGLVKALSKLVAQQQERVPFHIRLNTGRFTASLDLDSQLNLYRIIQEFLSNAVKHSQATDVLIMLISIQNKIVLHY   716
consensus                                       !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!
```

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logo
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NTDB id 1090337 ABFT42 RS15970 WP 268471514.1   EDDGVGFDQEKTNEHSMSMGLSGIKERVRALDGRLRIETSEGKGFKADIEMEL   766
NTDB id 91 BSU 31690 NP 391047.2                EDDGVGFDQEKNTEHSMSMGLSGIKERVRALDGRLRIETSEGKGFKADIEIEL   769
consensus                                       !!!!!!!!!!!  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!
```

X non conserved

X similar

X ≥ 50% conserved