```
logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  MLASKMRWEIQQPDKEKVKSLTEQLDITPLVASLLVKRGFDTAESARLFLHTKDADFYDPYELKGMREAVDRIKLAVSRG   80
NTDB id 354 BSU 27620 NP 390640.1            MLASKMRWEIQRPDQDKVKSLTEQLHITPLVASLLVKRGFDTAESARLFLHTKDADFYDPFEMKGMKEAADRIKQAISQQ   80
consensus                                    !!!!!!!!!!! !! *!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!*!!!*!! !!!! !*!

logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  EPIMIYGDYDADGVTSTSVMLTALKQLSANVDFYIPDRFTEGYGPNEQAFRSIKERGFSLIITVDTGIAAVHEAEVAKEL  160
NTDB id 354 BSU 27620 NP 390640.1            EKIMIYGDYDADGVTSTSVMLHTLQKLSAQVDFYIPDRFKEGYGPNEQAFRSIKERGFSLIITVDTGIAAVHEAKVAKEL  160
consensus                                    !*!!!!!!!!!!!!!!!!!!!* !  !!!*!!!!!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  GLDVIITDHHEPGPELPDVFAIIHPKQPGCSYPFKELAGVGVAFKLAHALTGSLPEAMLDLAAIGTVADLVPLHDENRLI  240
NTDB id 354 BSU 27620 NP 390640.1            GLDVIITDHHEPGPELPDVRAIVHPKQPGCTYPFKELAGVGVAFKLAHALLGELPDELLDLAAIGTIADLVPLHDENRLI  240
consensus                                    !!!!!!!!!!!!!!!!!!!! !!*!!!!!!!*!!!!!!!!!!!!!!!!!!!! ! !!* *!!!!!!!!*!!!!!!!!!!!!!

logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  ASLGIERLRTTNRPGLKALIKLSGGDIGQADEETIGFQVAPRLNAVGRIEQADPAVHLLMTDDQFEAEELASDIDRLNKE  320
NTDB id 354 BSU 27620 NP 390640.1            ATLGLERLRRTNRLGLKELIKLSGGDIGEANEETVGFQLAPRLNAVGRIEQADPAVHLLMSEDSFEAEELAAEIDQLNKE  320
consensus                                    !*!!*!!!! !!!*!!! !!!!!!!!!! ! !!!*!!!*!!!!!!!!!!!!!!!!!!!!!!**! !!!!!!! *!! !!!!

logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  RQKMVKTMTEEAVEMVQQQGGNPSAIVVAKAGWNPGVVGIVASKLAERFYRPAVVLGIDEEQGIAKGSARSIRGFNLFTS  400
NTDB id 354 BSU 27620 NP 390640.1            RQKMVSKMTDEAIEMVEQQGLDQTAIVVAKAGWNPGVVGIVASKLVDRFYRPAIVLGIDEEKGIAKGSARSIRGFNLFES  400
consensus                                    !!!!!  !!*!!*!!! !!!  **!!!!!!!!!!!!!!!!!!!! *!!!!!!*!!!!!!! !!!!!!!!!!!!!!!!!!!

logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  LSQCRDILPHFGGHPMAAGMTLKAEDVADLRDRLNQMAEETLTEEDFIPVQEVDLVCGVEDITVESITELNMLSPFGMLN  480
NTDB id 354 BSU 27620 NP 390640.1            LSECRDILPHFGGHPMAAGMTLKAEDVPDLRSRLNEIADNTLTEEDFIPVQEVDLVCGVEDITVESIAEMNMLSPFGMLN  480
consensus                                    !! !!!!!!!!!!!!!!!!!!!!!!!!*!!! !!! *!* !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

logo

NTDB id 314038 D2M30 RS13735 WP 125123028.1  PKPHVMVENAVLDEVRLIGANKNHVKMTVKNDSAVLDCVGFNKGELEAGIVPGSTISIVGEMSINEWNNRKKPQLMIKDA  560
NTDB id 354 BSU 27620 NP 390640.1            PKPHVLVENAVLEDVRKIGANKTHVKMTIRNESSQLDCVGFNKGELQEGIVPGSRISIVGEMSINEWNNRKKPQLMIKDA  560
consensus                                    !!!!!*!!!!!!**!! !!!!! !!!!!**!*!  !!!!!!!!!!! !!!!!! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
logo
NTDB id 314038 D2M30 RS13735 WP 125123028.1  AVPEWQLFDIRGKRMWEDTVTALPKEKRVLISFNEKTAQKLRA.ELSGELAEITSESEAEALPLDGKYAVFLDVPPSADR   639
NTDB id 354 BSU 27620 NP 390640.1            AVSEWQLFDLRGKRTWEDTVSALPSAKRAIVSFKEDSTTLLQTEDLRREVHVISSKDQAKAFDLDGAYIVLLDPPPSLDM   640
consensus                                    !!*!!!!!!*!!!! !!!!!*!!!  !! **!! ! *   !  **!  !** !*!   ! ! *!!! ! ! !!*!!! !

logo
NTDB id 314038 D2M30 RS13735 WP 125123028.1  LQRLLDGKKPERIYFVFINHEEHFLSSFPSRNDFKWFYAFLLKRGTFDLGRHGSELARHRGWSIDTINFMTKVFFDLGFV   719
NTDB id 354 BSU 27620 NP 390640.1            LARLLEGKAPERIYFIFLNHEDHFLSTFPARDHFKWYYAFLLKRGAFDVKKHGSELAKHKGWSVETINFMTKVFFDLGFV   720
consensus                                    ! !!!*!! !!!!!!*!*!!!*!!!!*!! ! *!!!*!!!!!!!! !!* *!!!!!!*!*!!!**!!!!!!!!!!!!!!!

logo
NTDB id 314038 D2M30 RS13735 WP 125123028.1  KIEDGVLSVVSGAKKRDLADSQTYQVKQQLMELDQKLNYSAAHELKEWLNKLMNQGSEAYESTRRT   785
NTDB id 354 BSU 27620 NP 390640.1            KIENGVLSVVSGAKKRDLTDSQTYQAKQQLMELDQKLNYSSAEELKEWLNKLMKQDSEAYESTRRT   786
consensus                                    !!! !!!!!!!!!!!!!! !!!!!! !!!!!!!!!!!!!! !*!!!!!!!!!! ! !!!!!!!!!!
```

X non conserved

X similar

X $\geq$ 50% conserved