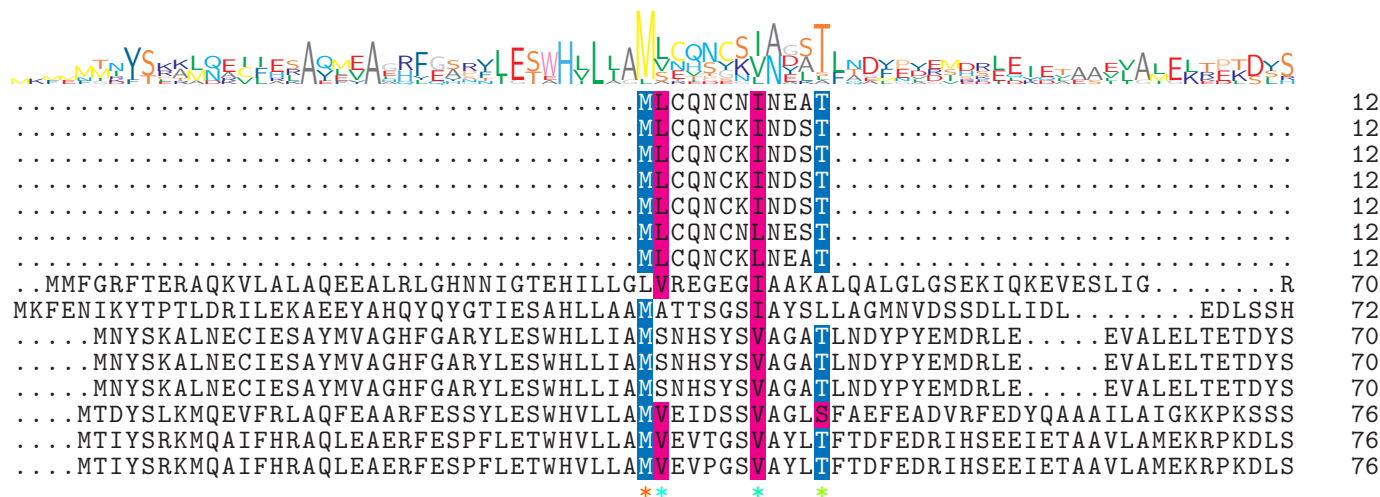


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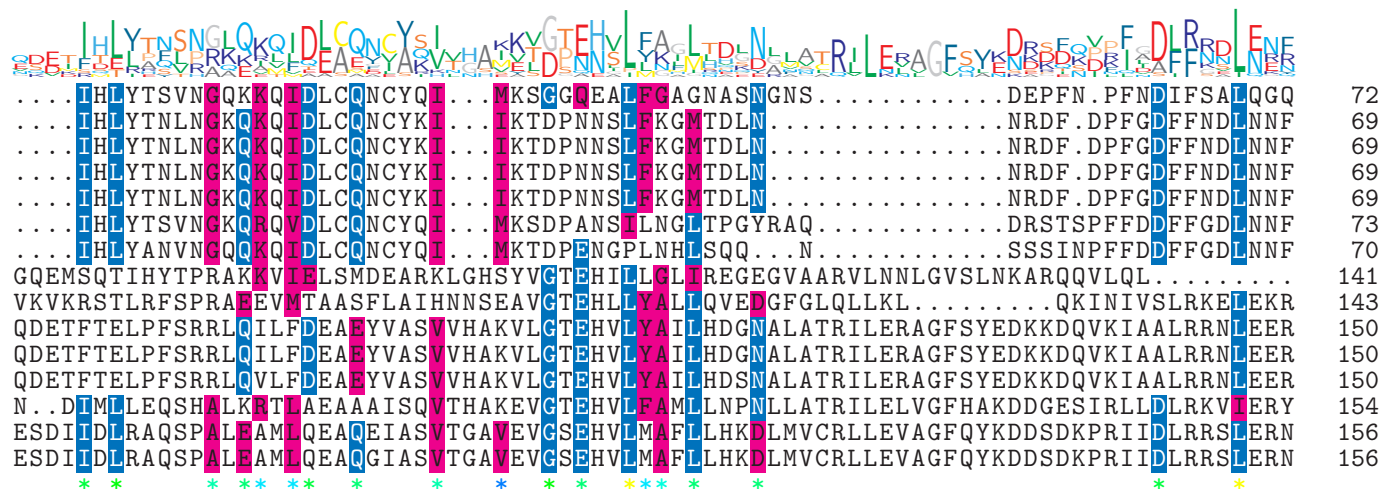


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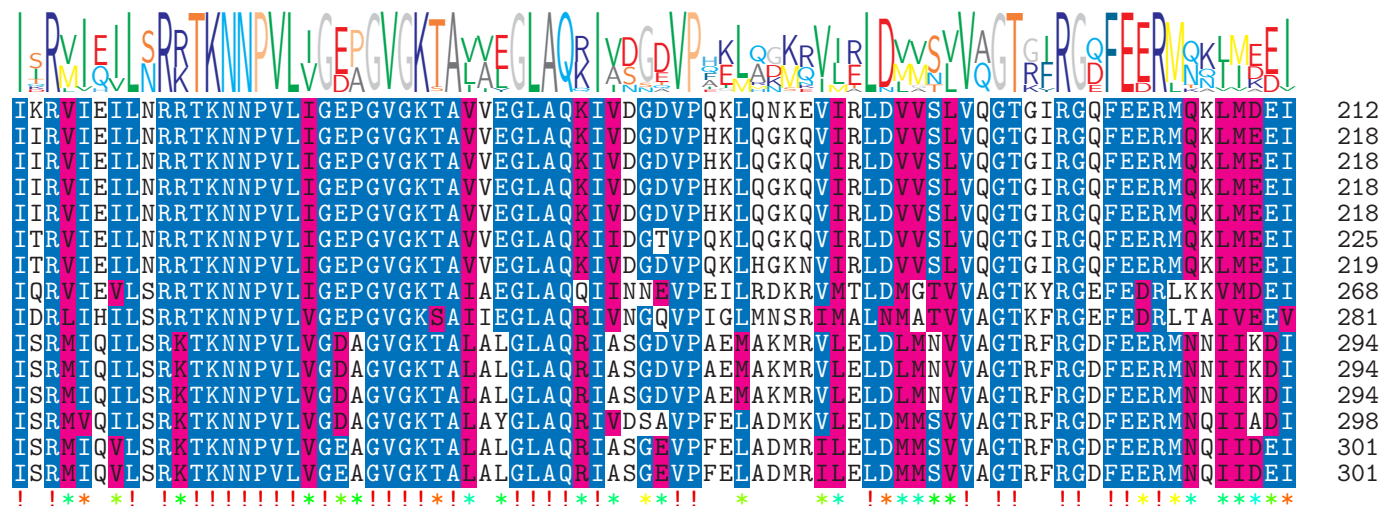
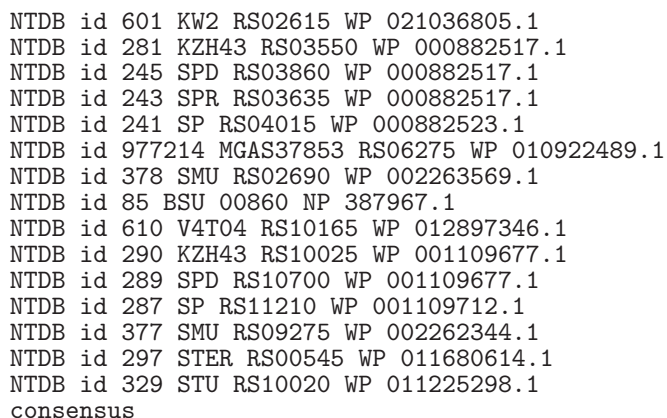
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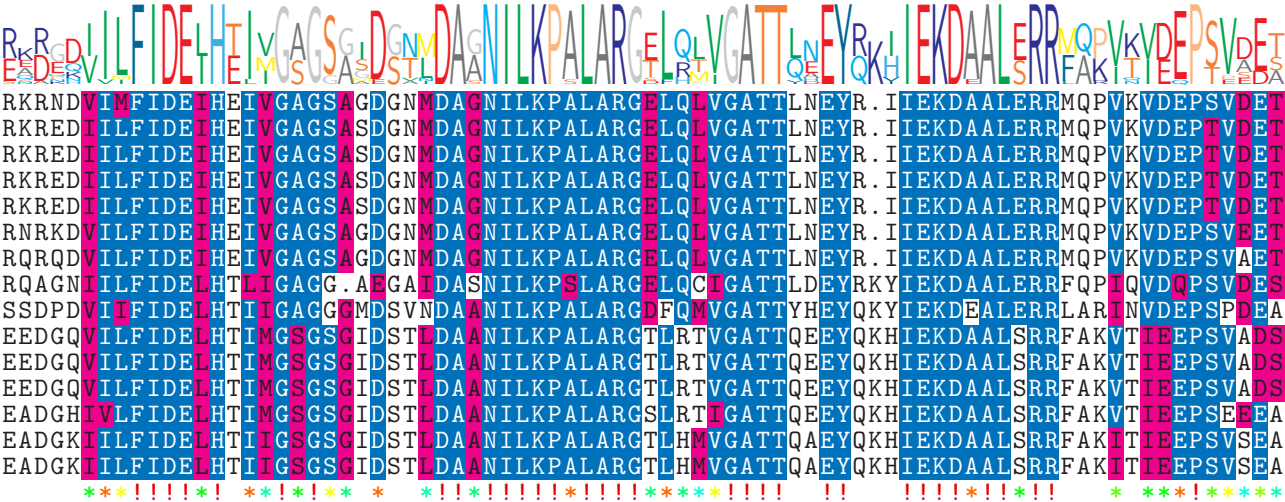
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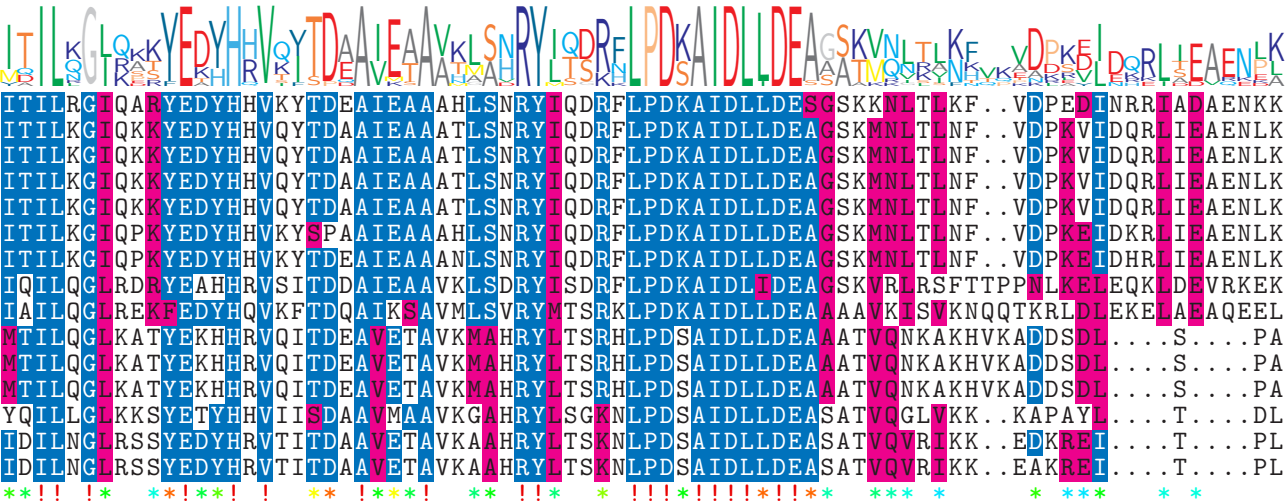
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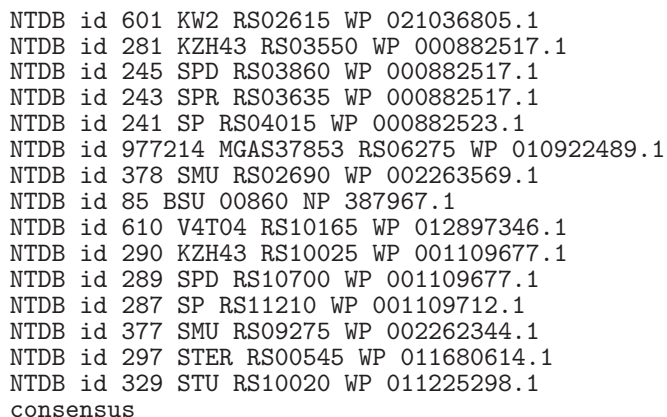


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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
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|-----------|--------|-----------|---------|----|-------------|-----------------------------------------------------------------------------------|-----|
| NTDB id   | 601    | KW2       | RS02615 | WP | 021036805.1 | GAPPGYVGYDEAGQLTEKVRNKPYSLLILLDEVEKAHPDVMMFLQLLEDGRLTDAQGRTVSFKDSLIIIMTSNAGTGK..V | 601 |
| NTDB id   | 281    | KZH43     | RS03550 | WP | 000882517.1 | GAPPGYVGYDEAGQLTEKVRHNPKYSLLILLDEVEKAHPDVMMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..T | 607 |
| NTDB id   | 245    | SPD       | RS03860 | WP | 000882517.1 | GAPPGYVGYDEAGQLTEKVRHNPKYSLLILLDEVEKAHPDVMMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..T | 607 |
| NTDB id   | 243    | SPR       | RS03635 | WP | 000882517.1 | GAPPGYVGYDEAGQLTEKVRHNPKYSLLILLDEVEKAHPDVMMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..T | 607 |
| NTDB id   | 241    | SP        | RS04015 | WP | 000882523.1 | GAPPGYVGYDEAGQLTEKVRHNPKYSLLILLDEVEKAHPDVMMFLQVLDDGRLTDGQGRTVSFKDAIIIMTSNAGTGK..T | 607 |
| NTDB id   | 977214 | MGAS37853 | RS06275 | WP | 010922489.1 | GAPPGYIGYDEAGQLTEQVRRNPKYSLLILLDEVEKAHPDVMMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..S | 614 |
| NTDB id   | 378    | SMU       | RS02690 | WP | 002263569.1 | GAPPGYVGYDEAGQLTEKVRNPKYSLLILLDEVEKAHPDVMMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGK..S  | 608 |
| NTDB id   | 85     | BSU       | 00860   | NP | 387967.1    | GSPPGYVGYDEAGQLTEKVRNPKYSVLLDETEKAHPDVFNILLQVLDDGRLTDSKGRTVDFRNTIIMTSNVGASELKR    | 667 |
| NTDB id   | 610    | V4T04     | RS10165 | WP | 012897346.1 | GAPPGYVGYDECGQLTEKVRNPKYSVLLDEVEKAHPDVFNIMLQILDDGFVTDTKGRKVDFRNTIIIMTSNLGATALRD   | 676 |
| NTDB id   | 290    | KZH43     | RS10025 | WP | 001109677.1 | GAPPGYVGYDEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRD  | 671 |
| NTDB id   | 289    | SPD       | RS10700 | WP | 001109677.1 | GAPPGYVGYDEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRD  | 671 |
| NTDB id   | 287    | SP        | RS11210 | WP | 001109712.1 | GAPPGYVGYDEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSKGRKVDFSNTIIIMTSNLGATALRD  | 671 |
| NTDB id   | 377    | SMU       | RS09275 | WP | 002262344.1 | GAPPGYVGYDEGGELTEKVRNKPYSVLLFDEVEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRD  | 674 |
| NTDB id   | 297    | STER      | RS00545 | WP | 011680614.1 | GAPPGYVGYDEGGELTEKVRNKPYSVLLFDETEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRD  | 677 |
| NTDB id   | 329    | STU       | RS10020 | WP | 011225298.1 | GAPPGYVGYDEGGELTEKVRNKPYSVLLFDETEKAHPDIFNVLLQVLDDGVLTDSRGRKVDFSNTIIIMTSNLGATALRD  | 677 |
| consensus |        |           |         |    |             | !*!!!!*!!*!*!*!!!!*!! !!!**!*!!*!!!!!!* * !!*!*!! *!! !!! !* ***!!!!!! !          |     |

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|-----------|--------|-----------|---------|----|-------------|------------------------------------------------------------------------------------|-----|
| NTDB id   | 601    | KW2       | RS02615 | WP | 021036805.1 | EASVGFGAAREG.....RTKSVLGGLGDFFSPEFMNRFDGITIEFSALSKENLLKIVDLMIDEVNEQIGRNDTHLSVTQAA  | 676 |
| NTDB id   | 281    | KZH43     | RS03550 | WP | 000882517.1 | EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGITIEFKALSNDLLQIVELMLADVNRKLSSNNIRLDVTDKV   | 682 |
| NTDB id   | 245    | SPD       | RS03860 | WP | 000882517.1 | EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGITIEFKALSNDLLQIVELMLADVNRKLSSNNIRLDVTDKV   | 682 |
| NTDB id   | 243    | SPR       | RS03635 | WP | 000882517.1 | EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGITIEFKALSNDLLQIVELMLADVNRKLSSNNIRLDVTDKV   | 682 |
| NTDB id   | 241    | SP        | RS04015 | WP | 000882523.1 | EASVGFGAAREG.....RTNSVLGELGNFFSPEFMNRFDGITIEFKALSNDLLQIVELMLADVNRKLSSNNIRLDVTDKV   | 682 |
| NTDB id   | 977214 | MGAS37853 | RS06275 | WP | 010922489.1 | EASVGFGAAREG.....RTSSVLGELSNFFSPEFMNRFDGITIEFKALSKEHLLHIVDLMIEDVNERLGYNGIHLDVTDKV  | 689 |
| NTDB id   | 378    | SMU       | RS02690 | WP | 002263569.1 | EANVGFGASREG.....RTNSVLGELGNFFSPEFMNRFDGITIEFQALSNDLLQIVSLMLDDVNQRRLAVNAIHLDVTDKV  | 683 |
| NTDB id   | 85     | BSU       | 00860   | NP | 387967.1    | NKYVGFNVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSTELTDAA   | 747 |
| NTDB id   | 610    | V4T04     | RS10165 | WP | 012897346.1 | DKTVGFGAKNITADYSAMKSRILEELKRHYRPEFINRIDEINIVFHSLESQETIEQIVKIMSKSLIKRLAEQDIHVKLTPSA | 756 |
| NTDB id   | 290    | KZH43     | RS10025 | WP | 001109677.1 | DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSDDHMQEVVKIMVKPLVASLAEKGIDLKLQASA   | 751 |
| NTDB id   | 289    | SPD       | RS10700 | WP | 001109677.1 | DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSDDHMQEVVKIMVKPLVASLAEKGIDLKLQASA   | 751 |
| NTDB id   | 287    | SP        | RS11210 | WP | 001109712.1 | DKTVGFGAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVVFHSLSDDHMQEVVKIMVKPLVASLAEKGIDLKLQASA   | 751 |
| NTDB id   | 377    | SMU       | RS09275 | WP | 002262344.1 | DKTVGFGAKSFSQDYKAMESRIEELKKVYRPEFINRIDEKVVFNHNGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSA    | 754 |
| NTDB id   | 297    | STER      | RS00545 | WP | 011680614.1 | DKTVGFGAQTISHNHQAMQARIMEELKKSYPPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAA   | 757 |
| NTDB id   | 329    | STU       | RS10020 | WP | 011225298.1 | DKTVGFGAQTISHNHQAMQARIMEELKKSYPPEFINRIDEKVVFHSLEEEQLHDIVKIMVKPLISALADKGISLKFQPAA   | 757 |
| consensus |        |           |         |    |             | * *!!!!* * ** *! * !!!*!! ! * ! !* * * *! *!* * * * * * * * * * * * * *            |     |

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NTDB id 601 KW2 RS02615 WP 021036805.1
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NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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KKKLA<sup>Y</sup>LD<sup>Y</sup>PE<sup>Y</sup>MGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>EN<sup>Y</sup>ED<sup>Y</sup>SIAD<sup>Y</sup>FY<sup>Y</sup>TEHP<sup>Y</sup>EYKQL<sup>Y</sup>.VAD<sup>Y</sup>LID<sup>Y</sup>DKI<sup>Y</sup>VIS<sup>Y</sup>NQT<sup>Y</sup>QETA<sup>Y</sup>ETT<sup>Y</sup>DEE<sup>Y</sup>VPAE 748  
 KEKLV<sup>Y</sup>DLGYD<sup>Y</sup>PKMGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>DY<sup>Y</sup>IED<sup>Y</sup>TIT<sup>Y</sup>DY<sup>Y</sup>LEN<sup>Y</sup>PSEKDL<sup>Y</sup>.KAV<sup>Y</sup>MTSK<sup>Y</sup>GN<sup>Y</sup>IQ<sup>Y</sup>IKS<sup>Y</sup>AKKA<sup>Y</sup>EVK<sup>Y</sup>SS<sup>Y</sup>EKEK<sup>Y</sup>.. 752  
 KEKLV<sup>Y</sup>DLGYD<sup>Y</sup>PKMGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>DY<sup>Y</sup>IED<sup>Y</sup>TIT<sup>Y</sup>DY<sup>Y</sup>LEN<sup>Y</sup>PSEKDL<sup>Y</sup>.KAV<sup>Y</sup>MTSK<sup>Y</sup>GN<sup>Y</sup>IQ<sup>Y</sup>IKS<sup>Y</sup>AKKA<sup>Y</sup>EVK<sup>Y</sup>SS<sup>Y</sup>EKEK<sup>Y</sup>.. 752  
 KEKLV<sup>Y</sup>DLGYD<sup>Y</sup>PKMGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>DY<sup>Y</sup>IED<sup>Y</sup>TIT<sup>Y</sup>DY<sup>Y</sup>LEN<sup>Y</sup>PSEKDL<sup>Y</sup>.KAV<sup>Y</sup>MTSK<sup>Y</sup>GN<sup>Y</sup>IQ<sup>Y</sup>IKS<sup>Y</sup>AKKA<sup>Y</sup>EVK<sup>Y</sup>SS<sup>Y</sup>EKEK<sup>Y</sup>.. 752  
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 KAKVA<sup>Y</sup>E<sup>Y</sup>EGV<sup>Y</sup>DL<sup>Y</sup>EY<sup>Y</sup>GARPLRR<sup>Y</sup>AI<sup>Y</sup>QKH<sup>Y</sup>VED<sup>Y</sup>RLSE<sup>Y</sup>ELL<sup>Y</sup>RG<sup>Y</sup>NIH<sup>Y</sup>KGQH<sup>Y</sup>IV<sup>Y</sup>LD<sup>Y</sup>VED<sup>Y</sup>GEF<sup>Y</sup>VVK<sup>Y</sup>TTAKTN<sup>Y</sup>..... 810  
 VKLIA<sup>Y</sup>AE<sup>Y</sup>Y<sup>Y</sup>FD<sup>Y</sup>PEY<sup>Y</sup>GARPLRR<sup>Y</sup>AI<sup>Y</sup>QKEV<sup>Y</sup>ED<sup>Y</sup>LLSE<sup>Y</sup>QL<sup>Y</sup>SGE<sup>Y</sup>IKAGNH<sup>Y</sup>VS<sup>Y</sup>IGAS<sup>Y</sup>NNK<sup>Y</sup>IKIA<sup>Y</sup>QIV<sup>Y</sup>..... 816  
 LKLLAN<sup>Y</sup>QGYD<sup>Y</sup>PEMGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>TEV<sup>Y</sup>ED<sup>Y</sup>KLA<sup>Y</sup>ELL<sup>Y</sup>LK<sup>Y</sup>GD<sup>Y</sup>LVAGS<sup>Y</sup>ILK<sup>Y</sup>IGV<sup>Y</sup>KAG<sup>Y</sup>QLK<sup>Y</sup>FDIA<sup>Y</sup>..... 810  
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 LKHLA<sup>Y</sup>LALAGYD<sup>Y</sup>AE<sup>Y</sup>MGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>TEV<sup>Y</sup>ED<sup>Y</sup>KLA<sup>Y</sup>ELL<sup>Y</sup>SGK<sup>Y</sup>LASG<sup>Y</sup>QTLK<sup>Y</sup>IGI<sup>Y</sup>QKEK<sup>Y</sup>LK<sup>Y</sup>FDIV<sup>Y</sup>..... 813  
 LKHLAKD<sup>Y</sup>GYD<sup>Y</sup>IE<sup>Y</sup>MGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>TQV<sup>Y</sup>ED<sup>Y</sup>KLSE<sup>Y</sup>ELL<sup>Y</sup>GGQ<sup>Y</sup>VVSG<sup>Y</sup>QTLK<sup>Y</sup>IGCSK<sup>Y</sup>DKL<sup>Y</sup>TFTV<sup>Y</sup>..... 816  
 LKHLAKD<sup>Y</sup>GYD<sup>Y</sup>IE<sup>Y</sup>MGARPLRR<sup>Y</sup>TIQ<sup>Y</sup>TQV<sup>Y</sup>ED<sup>Y</sup>KLSE<sup>Y</sup>ELL<sup>Y</sup>GGQ<sup>Y</sup>VVSG<sup>Y</sup>QTLK<sup>Y</sup>IGCSK<sup>Y</sup>DKL<sup>Y</sup>TFTV<sup>Y</sup>..... 816

- X non conserved
- X similar
- X  $\geq 50\%$  conserved