

logo

|                                             |                                                                                   |    |
|---------------------------------------------|-----------------------------------------------------------------------------------|----|
| NTDB id 1257 GC085 RS04855 WP 163621000.1   | MRKIIAILII..ISASISLAYSKDNSIISVKVLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ    | 78 |
| NTDB id 1284 ACE17W RS12370 WP 010946666.1  | MRKIIAILIL..ISASLSMAYSKDNSIISVKVLPENRVRIDFQFSKPLKQLPASFITQKPPRLVLDFISTDMQIPSDQ    | 78 |
| NTDB id 1408 DSB67 RS13980 WP 010643500.1   | .....                                                                             | 0  |
| NTDB id 408261 GPX87 RS04930 WP 078926717.1 | .....                                                                             | 0  |
| NTDB id 1186 GTF74 RS01320 WP 000788426.1   | .....                                                                             | 0  |
| NTDB id 1175 A1552VC RS12105 WP 000788426.1 | .....                                                                             | 0  |
| NTDB id 1193 PAKAF RS26665 WP 003161249.1   | MNSGLSRLGIALLAA.MFAPALLAADLEKLDVAALPGDRVELKLQFDEPVA.APRGYTIEQPARIALDLPGVQNKLG..T  | 76 |
| NTDB id 1009 ACIAD RS15175 WP 004923730.1   | MKQIIIRQFSIGTVAYAIMQVSAQVAITNVVPMNIPGQGTEIRVMFNGLPP.QPQAYQLEQPARLILDFDKAGQKLA..K  | 77 |
| NTDB id 1039 HON27 RS01460 WP 031993779.1   | MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLILDFDKAQGGLK..Q | 77 |
| NTDB id 1052 ABD1 RS15850 WP 001017033.1    | MNHVFRQFSMGAVAIAIMQAAASAQVSMTNIVPMQIAGQGTEIRVMFNGLPP.QPQAYQLENPSRLILDFDKAQGGLK..Q | 77 |
| consensus                                   | * * * * *                                                                         |    |

logo

|                                             |                                                                                 |     |
|---------------------------------------------|---------------------------------------------------------------------------------|-----|
| NTDB id 1257 GC085 RS04855 WP 163621000.1   | KTKTIIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGTAGSVYSLVLNGKSNDLFENSKEVF.....ITNQV        | 145 |
| NTDB id 1284 ACE17W RS12370 WP 010946666.1  | KTKTIIQLGSLHSYNIVAVGDRVRAILELDRSVSYSGTAGSVYSLVLNGKSNDLFENSKEVF.....ITNQV        | 145 |
| NTDB id 1408 DSB67 RS13980 WP 010643500.1   | .....MKMRHGLTLTPRKLTGLFSLWF....SLLL...APF.....V.AAE                             | 33  |
| NTDB id 408261 GPX87 RS04930 WP 078926717.1 | .....MIKGLNSV..VVRSLRYLCT....GVWTL SAVSV.....V.ASE                              | 32  |
| NTDB id 1186 GTF74 RS01320 WP 000788426.1   | .....MKNGLKTY..VAQTWLT LWV....GLALCASSMV.....F.SAE                              | 32  |
| NTDB id 1175 A1552VC RS12105 WP 000788426.1 | .....MKNGLKTY..VAQTWLT LWV....GLALCASSMV.....F.SAE                              | 32  |
| NTDB id 1193 PAKAF RS26665 WP 003161249.1   | KNREL SVGNTRSVTVVEAKDRTRLIINLTTLSSYTTRVEGNLNFVVVGNSPAGASVASTAPVKASPASYAQPIKPKPY | 156 |
| NTDB id 1009 ACIAD RS15175 WP 004923730.1   | SLIPVTTNEASSIDVSSDDKRARVVVNLKDA GAFTTRVEGNVFILKINNIQSTAT.....PVAT..SA.....      | 138 |
| NTDB id 1039 HON27 RS01460 WP 031993779.1   | SKISVATNEASSVDVTSDDQRSRLTVNLKDTGAFTTRVEGNTFILKINSAQTSNK.....PLPV..VS.....       | 138 |
| NTDB id 1052 ABD1 RS15850 WP 001017033.1    | SKISVATNEASSVDVTSDDQRSRLTVNLKDA GAFTTRVEGNTFILKINSAQTSNK.....PLPV..VS.....      | 138 |
| consensus                                   | * * * * *                                                                       |     |

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|                                             |                                                                                   |     |
|---------------------------------------------|-----------------------------------------------------------------------------------|-----|
| NTDB id 1257 GC085 RS04855 WP 163621000.1   | VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV  | 225 |
| NTDB id 1284 ACE17W RS12370 WP 010946666.1  | VNAKHEIKRIDFRGIEKQGGRLVIDVSDTGIPIDVTQVGKEIVVNFLNTKIPLNLMKRYDVSDFHSPVQIITMQQEGKKV  | 225 |
| NTDB id 1408 DSB67 RS13980 WP 010643500.1   | EVQSNLSKSIDFRTNKDKDAVIVVELVSPAAIVDIKRVQEGLSIDLNTSVKDDQLYLVDVKDFSTVVESVEVFRDTSTT   | 113 |
| NTDB id 408261 GPX87 RS04930 WP 078926717.1 | LTGANQLKNIDFRLNKNKEAVLIVELASPVSTVDVQKKAQGLTIELLNTTEVADDQLYLVDVKDFASAVETIEVFRQEPST | 112 |
| NTDB id 1186 GTF74 RS01320 WP 000788426.1   | SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST | 112 |
| NTDB id 1175 A1552VC RS12105 WP 000788426.1 | SATANQLENIDFRVNKEKA AVLIVELASPSAVVDVQKVQEGLSIELLKTDVADDKLYLLDVKDFSTPVESVEVFRKEPST | 112 |
| NTDB id 1193 PAKAF RS26665 WP 003161249.1   | VPAGRAIRNIDFQRGEKGEKNVVIDLSDPTLSPDIEQGGKIRLDFAKTQLPDALRVRLDVKDFATPVQFVNASAQSDRT   | 236 |
| NTDB id 1009 ACIAD RS15175 WP 004923730.1   | PAPQGGIGNIGFQRGAQGEGLVVIDLQGTNTPVDVQQGSGKVVVRFPGIKIPHTLARRLNTTDFATPVASIDSYNDGSNG  | 218 |
| NTDB id 1039 HON27 RS01460 WP 031993779.1   | .AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSGKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG  | 217 |
| NTDB id 1052 ABD1 RS15850 WP 001017033.1    | .AQPQGVSNIGFQRGSQGEGLVVVDLLGSNTPVDVQQGSGKVVIRTIGTKIPHTLARRLNVNDFATPVSSIDAYNDKGVG  | 217 |
| consensus                                   | * * * * *                                                                         |     |

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NTDB id 1052 ABD1 RS15850 WP 001017033.1
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| Protein        | Sequence       | Score |
|----------------|----------------|-------|
| RTILSKG        | RTILSKG        | 304   |
| RTILSKG        | RTILSKG        | 304   |
| RLVAYIDEDYSHDY | RLVAYIDEDYSHDY | 191   |
| LLEVS          | LLEVS          | 190   |
| QLVTV          | QLVTV          | 190   |
| QLVTV          | QLVTV          | 190   |
| SITIEP         | SITIEP         | 315   |
| VISI           | VISI           | 296   |
| VITI           | VITI           | 295   |
| VITI           | VITI           | 295   |

logo

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consensus

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| Sequence                                                                                                                                                        | Position |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|
| G N I T L R L D V P W D Q A L D I I L T T Q G L D K R R K G N V M L I D T K A S M D K M E E E Q L K S Q Q T I E K L E P I R S D L I Q N Y A K A A D I A V L     | 384      |
| G D I T L R L N D I P W D Q A L D I I L T T Q G L D K R R K G N V M L I D T K A S M D K M E E E Q L K S Q Q T I E K L E P I R S D L I Q N Y A K A A D I A V L   | 384      |
| G N I T L R L D G V P W Q Q V L D I I L Q V K G L D K R V D G N V I L V A P K E E L D L R E K Q Q L E K Q K L E K I G E L S E I K V I F A K A S D I A E M       | 271      |
| G N I T L R L D G V P W Q Q V L D I I L Q V K G L D K R V D G N V I L V A P K E E L D L R E K Q Q L E K A R L A E E L C D L R S D I I K V H F A K A S D I A E M | 270      |
| G N I T L R L D G V P W Q Q V L D I I L Q V K G L D K R V D G N V I L V A P K E E L D L R E K Q Q L E K A R L A E E L C D L K S E I I K I N F A K A S D I A A M | 270      |
| G N I T L R L D G V P W Q Q V L D I I L Q V K G L D K R V D G N V I L V A P K E E L D L R E K Q Q L E K A R L A E E L C D L K S E I I K I N F A K A S D I A A M | 270      |
| G N I T L R L Q N V P W D Q A L D I I L K T K N L D K R R K G N V I L V A P A D E T A A R R E Q L E A Q K Q I A E L A P L R E L I Q N Y A K A A D I A K L       | 395      |
| G N I T L H L K D V P W D Q A L D I I L K T K N L D K R R R G N V I W I A P V S E L I K S E E D E A K A I A Q S T K L A P L Q T E Y I L K Y A K A A D I E K L   | 376      |
| G N I T L R L K D V P W D Q A L D I I L K T K N L D K R R R G N V I W I A P V A E L I K A E E E A K A V A Q S V K L A P L Q T E Y I Q L K Y A K A G D I M G L   | 375      |
| G N I T L R L K D V P W D Q A L D I I L K T K N L D K R R R G N V I W I A P V A E L I K A E E E A K A V A Q S V K L A P L Q T E Y I Q L K Y A K A G D I M G L   | 375      |

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| Protein                                                           | Sequence                                                                                                                                                                                                                                                                        | Length |
|-------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------|
| ITKDKQ                                                            | ...NSLLS <sup>+</sup> DRGK <sup>+</sup> IS <sup>+</sup> VDARTNT <sup>+</sup> IWIQDTG <sup>+</sup> TK <sup>+</sup> IEE <sup>+</sup> VEL <sup>+</sup> IKQ <sup>+</sup> LDIPVKQ                                                                                                    | 433    |
| ITKDKQ                                                            | ...NSLLS <sup>+</sup> DRGK <sup>+</sup> IS <sup>+</sup> VDARTNT <sup>+</sup> IWIQDTG <sup>+</sup> TK <sup>+</sup> IEE <sup>+</sup> VEL <sup>+</sup> IKQ <sup>+</sup> LDIPVKQ                                                                                                    | 433    |
| INGEGN                                                            | ...IS <sup>+</sup> MS <sup>+</sup> LS <sup>+</sup> DRGS <sup>+</sup> MT <sup>+</sup> IDERTNS <sup>+</sup> LL <sup>+</sup> IREL <sup>+</sup> PEN <sup>+</sup> IE <sup>+</sup> VIRE <sup>+</sup> IE <sup>+</sup> IES <sup>+</sup> LDIPVKQ                                         | 321    |
| IGGSGT                                                            | ...VN <sup>+</sup> ML <sup>+</sup> SERGS <sup>+</sup> IS <sup>+</sup> IDERTN <sup>+</sup> ALL <sup>+</sup> IREL <sup>+</sup> PEN <sup>+</sup> IK <sup>+</sup> VIRE <sup>+</sup> IE <sup>+</sup> IES <sup>+</sup> LDIPVKQ                                                        | 320    |
| IGGEGN                                                            | ...VN <sup>+</sup> ML <sup>+</sup> SERGS <sup>+</sup> IS <sup>+</sup> IDERTNS <sup>+</sup> LL <sup>+</sup> IREL <sup>+</sup> PON <sup>+</sup> IA <sup>+</sup> VIRE <sup>+</sup> IE <sup>+</sup> IES <sup>+</sup> LDIPVKQ                                                        | 320    |
| IGGEGN                                                            | ...VN <sup>+</sup> ML <sup>+</sup> SERGS <sup>+</sup> IS <sup>+</sup> IDERTNS <sup>+</sup> LL <sup>+</sup> IREL <sup>+</sup> PON <sup>+</sup> IA <sup>+</sup> VIRE <sup>+</sup> IE <sup>+</sup> IES <sup>+</sup> LDIPVKQ                                                        | 320    |
| FQSVTSDGGQEG                                                      | ...KEGG <sup>+</sup> RGS <sup>+</sup> IT <sup>+</sup> VDR <sup>+</sup> TNS <sup>+</sup> IIAYQP <sup>+</sup> QER <sup>+</sup> LDE <sup>+</sup> LR <sup>+</sup> IV <sup>+</sup> SQ <sup>+</sup> LDIPV <sup>+</sup> BQ                                                             | 449    |
| ITQGRNSGTSNSN                                                     | ...TNGSATVEPLGDSV <sup>+</sup> G <sup>+</sup> TLLS <sup>+</sup> PRG <sup>+</sup> TIS <sup>+</sup> LD <sup>+</sup> PRTNT <sup>+</sup> LI <sup>+</sup> IND <sup>+</sup> TSQ <sup>+</sup> K <sup>+</sup> ID <sup>+</sup> Q <sup>+</sup> IRK <sup>+</sup> MID <sup>+</sup> LLDIPVKQ | 447    |
| ITQGSNNSNGLQHTSGGGTSTSTNLNTGVD <sup>+</sup> SLGNNV <sup>+</sup> G | ...SLLS <sup>+</sup> PRG <sup>+</sup> TI <sup>+</sup> IQD <sup>+</sup> DRNT <sup>+</sup> LI <sup>+</sup> IND <sup>+</sup> TAQS <sup>+</sup> ID <sup>+</sup> Q <sup>+</sup> IRK <sup>+</sup> MID <sup>+</sup> LLD <sup>+</sup> VQVKQ                                             | 455    |
| ITQGSNNSNGLQHTSGGGTSTSTNLNTGVD <sup>+</sup> SLGNNV <sup>+</sup> G | ...SLLS <sup>+</sup> PRG <sup>+</sup> TI <sup>+</sup> IQD <sup>+</sup> DRNT <sup>+</sup> LI <sup>+</sup> IND <sup>+</sup> TAQS <sup>+</sup> ID <sup>+</sup> Q <sup>+</sup> IRK <sup>+</sup> MID <sup>+</sup> LLD <sup>+</sup> VQVKQ                                             | 455    |

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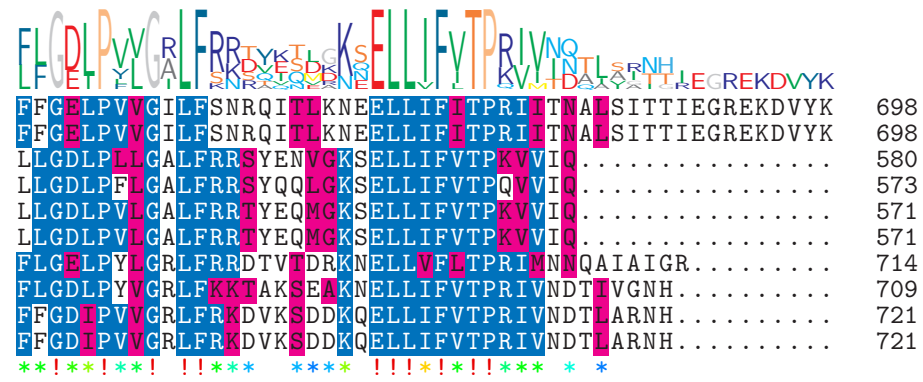


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-  non conserved
-  similar
-   $\geq 50\%$  conserved