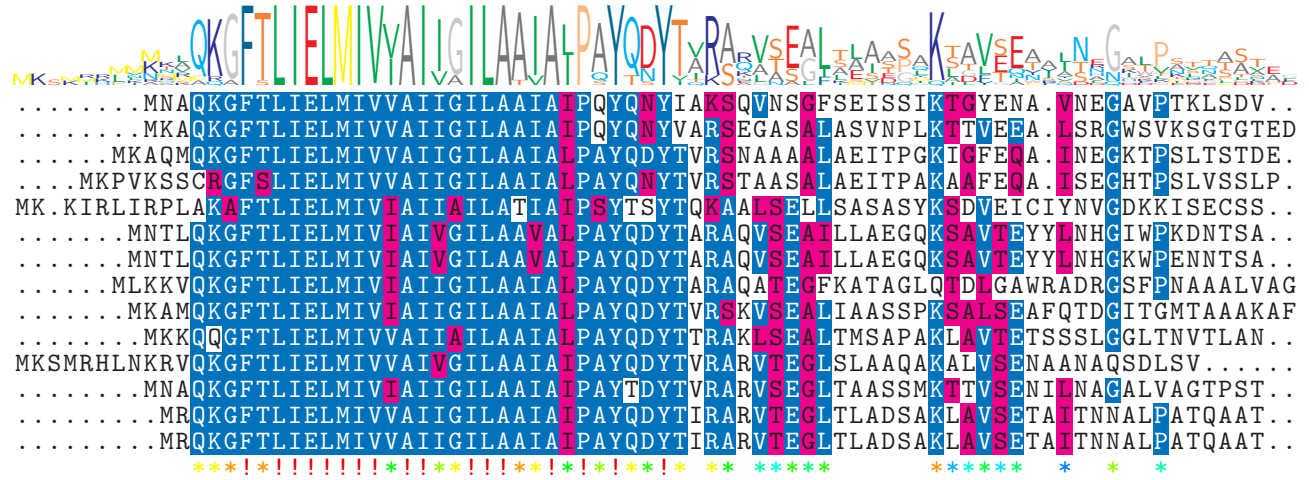


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NTDB id 1119 NGFG RS11465 WP 017147169.1
NTDB id 1191 AAC28468.1 484..945( )
NTDB id 1188 NELON RS01755 WP 003772458.1
NTDB id 263014 COL90 RS17010 WP 053514082.1
NTDB id 1424 RS RS02795 WP 011000517.1
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consensus

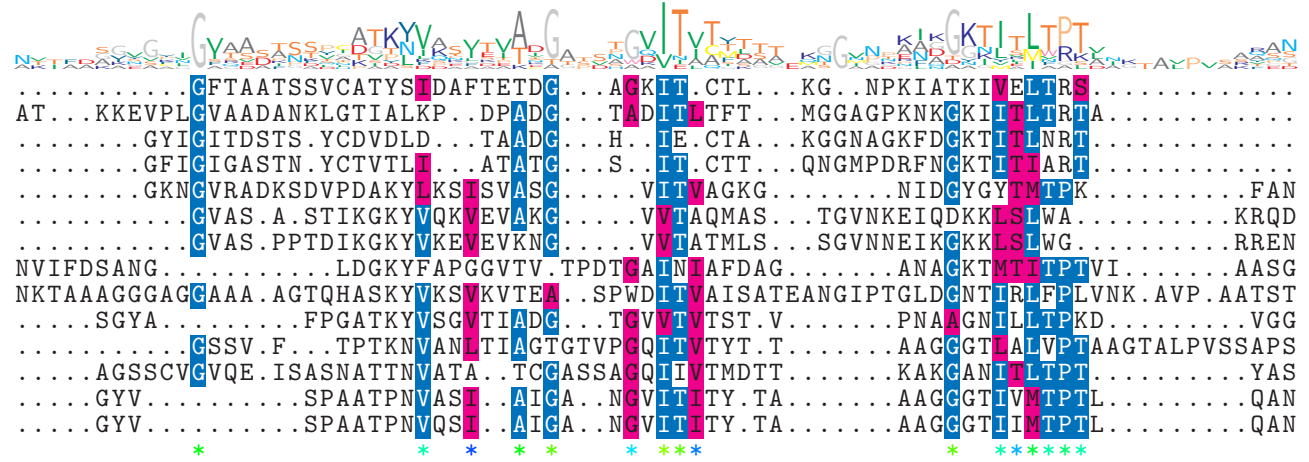
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NTDB id 1274 LPP RS09530 WP 011214168.1
NTDB id 1258 GC085 RS09745 WP 014844212.1
consensus

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logo

|                                             |                                                       |     |
|---------------------------------------------|-------------------------------------------------------|-----|
| NTDB id 1038 HON27 RS01510 WP 000993725.1   | TDGAWTCVSD.....VPTEFLP.KGCTAGTPTEGAITSL               | 149 |
| NTDB id 1192 PAKAF RS23870 WP 024947914.1   | ADGLWKCTSD.....QDEQFIP.KGCSK.....                     | 150 |
| NTDB id 1197 PSJM300 03940 AFN76866.1       | ADGEWSCAST.....LDAKYKP.GKCS.....                      | 139 |
| NTDB id 1204 PSJM300 03935 AFN76865.1       | TDGLWDCTSD.....LDSRYKP.GKCL.....                      | 141 |
| NTDB id 1383 A4U84 RS08530 WP 005711781.1   | NNITWATSCQGAD.....ISLFPANFCGQKATP.....                | 154 |
| NTDB id 1109 OK783 RS10670 WP 157147416.1   | GSVKWFCGQPVTRTGDNDTTVA..DANNAIDTKHLP.STCRDESSAT.....  | 164 |
| NTDB id 1119 NGFG RS11465 WP 017147169.1    | GSVKWFCGQPVTRADDDTVADA..KDGKEIDTKHLP.STCRDKASDAK..... | 166 |
| NTDB id 1191 AAC28468.1 484..945( )         | QISTWTCAPGAAN.....GIETRRLP.TSCQ*.....                 | 153 |
| NTDB id 1188 NELON RS01755 WP 003772458.1   | GAIDWACASAAKETADKRFGTGSGVAVGTLPAKYAP.SECK.....        | 188 |
| NTDB id 263014 COL90 RS17010 WP 053514082.1 | GQLKWTCTSSA.....ILTKYLP.AECRSSGT.....                 | 141 |
| NTDB id 1424 RS RS02795 WP 011000517.1      | GPIMWTCYAQNKAQAASSVAPS...GTMSLAAKYAP.AECR.....        | 168 |
| NTDB id 1002 ACIAD RS15100 WP 004923779.1   | GAVTWKCTTT.....S.DKKYVP.SECRG.....                    | 147 |
| NTDB id 1274 LPP RS09530 WP 011214168.1     | GDVTWTCTGG.....TLLAKYRP.ASCR.....                     | 136 |
| NTDB id 1258 GC085 RS09745 WP 014844212.1   | GDVTWTCTGG.....TLLAKYRP.ASCR.....                     | 136 |
| consensus                                   | * * ! *                                               |     |

- X non conserved
- X similar
- X ≥ 50% conserved