```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  MNKTWKRQVFRHTALYTAILMFSHTGGGGAQAQENPYAIVMNSQKLPEVKWGNSYKKGELRPEDRDRKFTFTSTYGIKRN   80
NTDB id 1090 CAA90909.1 1..3114( )           MNKTLKRQVFRHTALYAAILMFSHTGGGGAMAQTHKYAIIMNERNQLEVKGNGQYS..TIKDKDRERKFIYNKDRG..GG   76
consensus                                    !!!! !!!!!!!!!!! !!!!!!!!!!!!!! !! **!!!*!!     *!!!     ! ** *** !!*!!! *     !**
```

```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  TNITFNNTDYLVSEKNGTAVFGAATYLPPYGKVSGFDTDRLTKRGNAVDWINTTHPGLIGYSYQGITCSSSSCPEFGYKT  160
NTDB id 1090 CAA90909.1 1..3114( )           GSVFFDNTDTLVSQQRGTAVFGTATYLPPYGKVSGFDADGLQKRNNAVDWIHTTQAGLAGYAYTDVICRSNQCPQLVYET  156
consensus                                      * ! !!! !!!    !!!!!! !!!!!!!!!!!!!! ! ! !! !!!!!!*!!**!! !! !  * ! !  !!    ! !
```

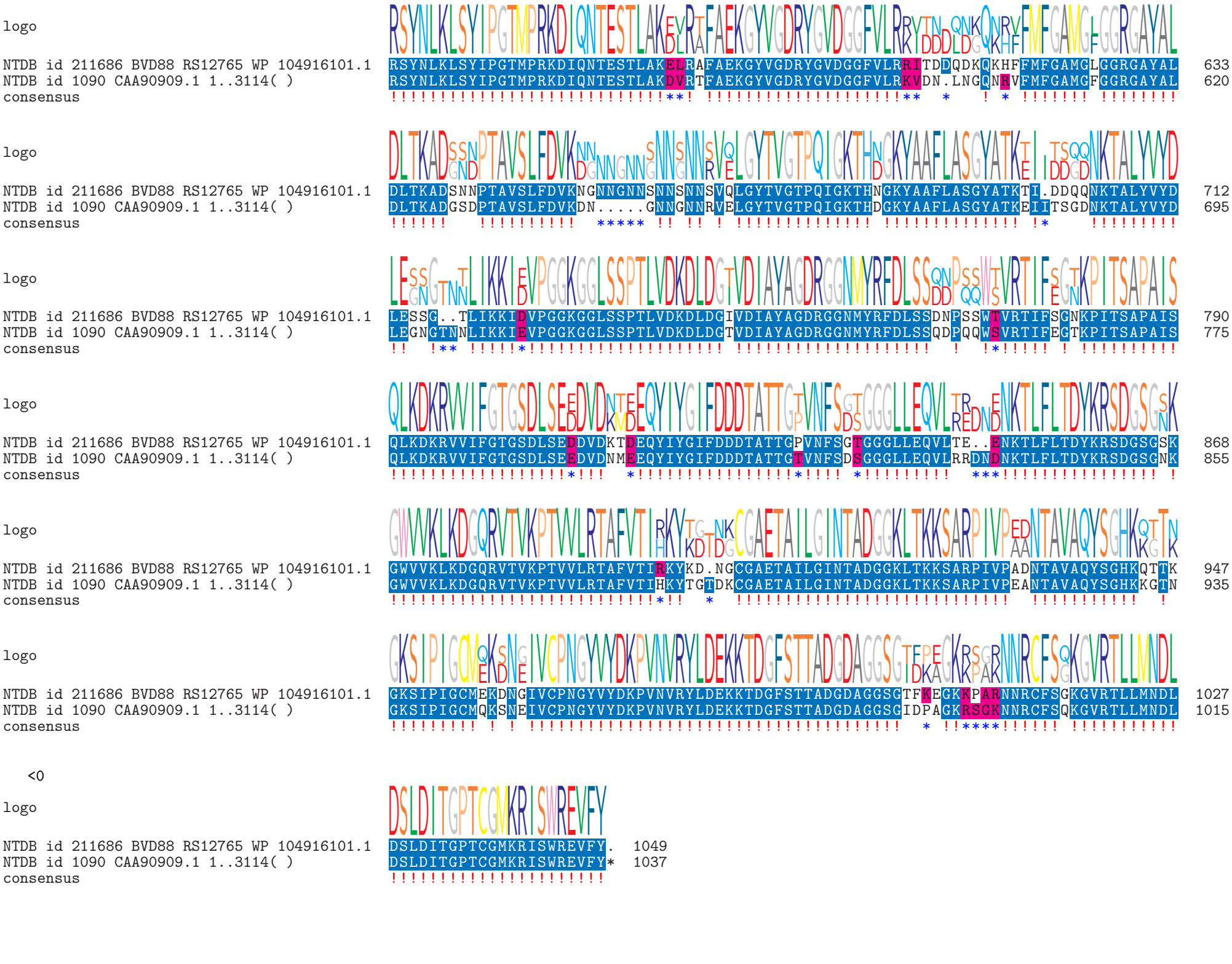
```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  QFTFGNSGLAKKTNSSKLDIYEDKSRDNSPIYKLQDYPWLGVSFNLSSDSYVKQK.RHNSLVSSFSEDVTQSNGTQSPYK  239
NTDB id 1090 CAA90909.1 1..3114( )           KFSFDGIGLAKNA..GSLDRHPDPSRENSPIYKLKDHPWLGVSFNLGSENTVKDGKSFNKLISSFSEGNNNQT.......  227
consensus                                     !*!   !!!!  **  !! **!*!!*!!!!!!! !*!!!!!!!!! !*  !!  * *! !*!!!!!    *  *******
```

```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  DRNLVYRTDDYHNKGNYSHQDAHHAIAFYLNAKLHLLDKKQIKNIAQGSELNLGMLKTHIELPKNFNQRSLVGSVVSWTV  319
NTDB id 1090 CAA90909.1 1..3114( )           ....IVSTTRGHSISLSDWKREHTAMAYYLNAKLHLLDKKGIEDIAQGKTVDLGTLRPRVEAT..VRRGELLNFWATWKI  301
consensus                                    *****  !   !      *   !*!*!*!!!!!!!!!!!!! !  !!!!  * !! !****! ***     !*    *! *
```

```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  KDEGKVSVKLKLPEVKAGRCINKDNPNPKSKAPSPALTAPALWFGPVQNGKVQMYSASVSTYPDSSSSQIFLQNLSRKDD  399
NTDB id 1090 CAA90909.1 1..3114( )           EDKGNITVRLGLPEVKAGRCVNKANPNPNAKAPSPALTAPALWFGPVKDGKAEMYSASVSTYPDSSSSRIYLQNLKRKTD  381
consensus                                     ! ! **!*! !!!!!!!!!*!! !!!!  !!!!!!!!!!!!!!!!!  !!  !!!!!!!!!!!!!!!  !*!!!!  !! !
```

```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  TSKPGRYSLKPLSTSEIKSKEPTFTGRQTVIRLDGGVQQIKLQGNEVT..SFNVNN.GNNTFGIVKDLGVDPDASEWKKV  476
NTDB id 1090 CAA90909.1 1..3114( )           PGKPGRHSLETLTENDIKSREPNFTGRQTIIRLNGGVREIKLDRNNTEVVNFNGNDGNNDTFGIVKDLGVEPDTSEWKKV  461
consensus                                    * !!!!*!! *!*  *!!!*!! !!!!!!*!!! !!!  !!!   !  ** !! ! * ! !!!!!!!!!!*!! !!!!!!
```

```
NTDB id 211686 BVD88 RS12765 WP 104916101.1  LLPWTVRASNDDNQFKTINQQLN.QQKIQYSQRYRIRD..NGNRDLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDK  553
NTDB id 1090 CAA90909.1 1..3114( )           LLPWTVRGFADDNKFKAFNKEENNDNKPKYSQKYRSRDNNKGERNLGDIVNSPIVAVGEYLATSANDGMVHIFKQSGGDK  541
consensus                                    !!!!!!!*  !!! !!  !   !* *!* !!!*!! !!** ! ! !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```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NTDB id 1090 CAA90909.1 1..3114( ) RSYNLKLSYIPGTMPRKDIQNTESTLAKDVRTFAEKGYVGDRYGVDGGFVLRKVDN.LNGQNRVFMFGAMGFGGRGAYAL 620
consensus
logo
NTDB id 211686 BVD88 RS12765 WP 104916101.1 DLTKADSNNPTAVSLFDVKNGNNGNNSNNSNNSVQLGYTVGTPQIGKTHNGKYAAFLASGYATKTI.DDQQNKTALYVYD 712
NTDB id 1090 CAA90909.1 1..3114( ) DLTKADGSDPTAVSLFDVKDN.....GNNGNNRVELGYTVGTPQIGKTHDGKYAAFLASGYATKEIITSGDNKTALYVYD 695
consensus
logo
NTDB id 211686 BVD88 RS12765 WP 104916101.1 LESSG..TLIKKIDVPGGKGGLSSPTLVDKDLDGIVDIAYAGDRGGNMYRFDLSSDNPSSWTVRTIFSGNKPITSAPAIS 790
NTDB id 1090 CAA90909.1 1..3114( ) LEGNGTNNLIKKIEVPGGKGGLSSPTLVDKDLDGTVDIAYAGDRGGNMYRFDLSSQDPQQWSVRTIFEGTKPITSAPAIS 775
consensus
logo
NTDB id 211686 BVD88 RS12765 WP 104916101.1 QLKDKRVVIFGTGSDLSEDDVDKTDEQYIYGIFDDDTATTGPVNFSGTGGGLLEQVLTE..ENKTLFLTDYKRSDGSGSK 868
NTDB id 1090 CAA90909.1 1..3114( ) QLKDKRVVIFGTGSDLSEEDVDNMEEQYIYGIFDDDTATTGTVNFSDSGGGLLEQVLRRDNDNKTLFLTDYKRSDGSGNK 855
consensus
logo
NTDB id 211686 BVD88 RS12765 WP 104916101.1 GWVVKLKDGQRVTVKPTVVLRTAFVTIRKYKD.NGCGAETAILGINTADGGKLTKKSARPIVPADNTAVAQYSGHKQTTK 947
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consensus
logo
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NTDB id 1090 CAA90909.1 1..3114( ) GKSIPIGCMQKSNEIVCPNGYVYDKPVNVRYLDEKKTDGFSTTADGDAGGSGIDPAGKRSGKNNRCFSQKGVRTLLMNDL 1015
consensus
<0
logo
NTDB id 211686 BVD88 RS12765 WP 104916101.1 DSLDITGPTCGMKRISWREVFY. 1049
NTDB id 1090 CAA90909.1 1..3114( ) DSLDITGPTCGMKRISWREVFY* 1037
consensus

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