Multiple sequence alignment (logo / sequences / consensus)

Block 1

```
logo
NTDB id 1157 A1552VC RS03895 WP 001888250.1   .........MVEDTASVAALYRSYLTPLDIDINIVGTGRDAIESIGRREPDLILLDLRLPDMTGMDVLYAVKEKSPDVPI  71
NTDB id 1045 H0N27 RS16330 WP 168727019.1      MAEQQPLVLLVDDEEDLCLLMQMTLARMGIKTHLAYRVEQAKQLFTQFHYDACLTDLNLPDGSGLDLVKHVSQNYPNTPI  80
NTDB id 370773 FKV23 RS13215 WP 141624266.1    .MTETRSALIVDDERDIRELLVMTLGRMGLRCDTASSVGDARAQLQRNRYDLCLTDMRLPDGSGIELISDISQKYPETPV  79
NTDB id 1473 PAKAF RS24000 WP 003094694.1      ..MSRQKALIVDDEPDIRELLEITLGRMKLDTRSARNVKEARELLAREPFDLCLTDMRLPDGSGLDLVQYIQQRHPQTPV  78
consensus
```

Block 2

```
logo
NTDB id 1157 A1552VC RS03895 WP 001888250.1   VFMTAHGSIDTAVEAMRHGAQDFLIKPCEADRLRVTVNNAIRKASKLKNDVDNKNQNYQGFIGSSQTMQAVYRTIDSAAS  151
NTDB id 1045 H0N27 RS16330 WP 168727019.1      AVLTAYGNMDIAIAALKAGAFDFVSKPVNQVHLDQLLQKALNRQKVEHDTT.ENALENKLLIGRSLPIQQLRIAIKKIAR  159
NTDB id 370773 FKV23 RS13215 WP 141624266.1    AMITAFGNVEAAVEALKAGAFDFVAKPVDLNVLRDLVRHALDLQAARKA...DVDAVASRLYGDSPAMTTLRQTIAKVSR  156
NTDB id 1473 PAKAF RS24000 WP 003094694.1      AMITAYGSIDTAIQALKAGAFDFLTKPVDLGRLRELVATALRLRNPE.A...EEAPVDNRLLGESPPMRALRNQIGKLAR  154
consensus
```

Block 3

```
logo
NTDB id 1157 A1552VC RS03895 WP 001888250.1   SKASIFITGESGTGKEVCAEAIHAASKRGDKPFIAINCAAIPKDLIESELFGHVKGAFTGATERQGAAEAADGGTLFLD  231
NTDB id 1045 H0N27 RS16330 WP 168727019.1      SQAPVFVTGESGTGKEVVANLVHRLSNRSEGPFIAINCGAIPTELMESELFGHKKGSFTGATDKQGLILSAHGGSLFLD  239
NTDB id 370773 FKV23 RS13215 WP 141624266.1    SQAPVYIAGESGVGKELVARTIHAEGARSAGPFVPVNCGAIPSELMESEFFGHKKGSFTGAHADKPGLFQTAEGGTLFLD  236
NTDB id 1473 PAKAF RS24000 WP 003094694.1      SQAPVYISGESGSGKELVARLIHEQGPRIERPFVPVNCGAIPSELMESEFFGHKKGSFTGAIEDKQGLFQAASGGTLFLD  234
consensus
```

Block 4

```
logo
NTDB id 1157 A1552VC RS03895 WP 001888250.1   ELCEMDLDLQTKLLRFIQTGTFQKVGSSKMKSVDVRFVCATNRDPWKEVQEGRFREDLYYRLYVIPLHLPPLRARGDDVI  311
NTDB id 1045 H0N27 RS16330 WP 168727019.1      EIAELPLSMQVKLLRAVQEKKIRPVGSDQEIDVDFRVISASHQDLDLLVRQKFRQDLFFRIHVMDLILPPLRERGEDVL  319
NTDB id 370773 FKV23 RS13215 WP 141624266.1    EVAELPLPMQVKLLRAIQEKSVRAVGANSENPVDVRILSATHKDLSKLVAEGRFRQDLYYRINVIELRVPPLRERLEDLP  316
NTDB id 1473 PAKAF RS24000 WP 003094694.1      EVADLPMAMQVKLLRAIQEKAVRAVGGQQEVAVDVRILCATHKDLAAEVGAGRFRQDLYYRLNVIELRVPPLRERREDIP  314
consensus
```

Block 5

```
logo
NTDB id 1157 A1552VC RS03895 WP 001888250.1   EIAYSLLGFMSKEEGKDFVRLSAEVVERFRQYEWPGNVRQLQNVLRNVVVLNEGREITLDMLPPPLNQMS..API.NRAL  388
NTDB id 1045 H0N27 RS16330 WP 168727019.1      LLANHFIQKICMEWETPPKQLTEAAETYLLQQHFPGNVRELRNMIERAITLSEDATIDISHLHPAPLRANISNPFASAAQ  399
NTDB id 370773 FKV23 RS13215 WP 141624266.1    GLSARILGRLAEAQGRVVPRLDDSAVDALRKYPFPGNVRELENILERALALADDEMLTAGDLHLPRVETDPHNSP.....  391
NTDB id 1473 PAKAF RS24000 WP 003094694.1      LLAERILKRLAGDTGLPAARLTGDAQEKLKNYPFPGNVRELENMLERAYTLCEDDQIQPHDLRLADAPGASQEGA.....  389
consensus
```

Block 6

```
logo
NTDB id 1157 A1552VC RS03895 WP 001888250.1   PL......AHENKVSVHEIFPLWM..TEKQAIEQAIEACDGNIPRAATYLDVSPSTIYRKLQTWNEKVKEKEKER  455
NTDB id 1045 H0N27 RS16330 WP 168727019.1      STQTTVAAPQAVKKLPSEGLERYLENIEKDILLNALNMTHWNRTLAAKKLGMTFRSLRYRLKKFGLDTETEQE.V  473
NTDB id 370773 FKV23 RS13215 WP 141624266.1    .LDPR...TLDPRDTAISALPSYIEEIERAAIQHALQENRYNKTRTAQALGITFRALRYKLKKLGID........  454
NTDB id 1473 PAKAF RS24000 WP 003094694.1      ..........ASLSEIDNLEDYLEDIERKLIMQALEETRWNRTAAAQRLGLTFRSMRYRLKKLGID........  445
consensus
```