Multiple sequence alignment (logo / sequences / consensus)

```
Block 1
logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1   MAEQQPLVLLVDDEEDLCLLMQMTLARMGIKTHLAYRVEQAKQLFTQFHYDACLTDLNLPDGSGLDLVKHVSQNYPNTPLI   80
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1 .MSENRSALIVDDEHDIRELLVLTLGRMGLRTDTAPNLAAAREMLATVAYDLCLTDMRLPDGSGLELVGEIGTRFPGTPV   79
NTDB id 1473 PAKAF RS24000 WP 003094694.1   ..MSRQKALIVDDEPDIRELLEITLGRMKLDTRSARNVKEARELLAREPFDLCLTDMRLPDGSGLDLVQYIQQRHPQTPV   78
consensus

Block 2
logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1   AVLTAYGNMDIAIAALKAGAFDFVSKPVNQVHLDQLLQKALNRQKVEHDTTENALENKLLIGRSLPIQQLRIAIKKIARS  160
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1 AVITAYGNVEAAVEALKAGAFDFVSKPVDIHVLRGLVRQALELGERARRTS..EEQSSRLLGASDAMVTLRNTIAKVARS  157
NTDB id 1473 PAKAF RS24000 WP 003094694.1   AMITAYGSLDTAIQALKAGAFDFLTKPVDLGRLRELVATALRLRNPEAE.E...APVDNRLLGESPPMRALRNQIGKLARS  155
consensus

Block 3
logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1   QAPVFVTGESGTGKEVVANLVHRLSNRSEGPFIAINCGAIPTELMESELFGHKKGSFTGATQDKQGLILSAHGGSLFLDE  240
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1 QAPVYINGESGTGKELVARTIHAQGARAGGPFVPVNCGAIPTELMESEFFGHKKGSFTGAHSDKPGLFQAADGGTLFLDE  237
NTDB id 1473 PAKAF RS24000 WP 003094694.1   QAPVYISGESGSGKELVARLIHEQGPRIERPFVPVNCGAIPSELMESEFFGHKKGSFTGAIEDKQGLFQAASGGTLFLDE  235
consensus

Block 4
logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1   IAELPLSMQVKLLRAVQEKKIRPVGSDQEIDVDFRVISASHQDLDLLVRQGKFRQDLFFRIHVMDLILPPLRERGEDVLL  320
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1 VAELPLPMQVKLLRAIQEKCIRPVGASAEVQVDVRLLSATHKDLGALVSDGRFRHDLYYRINVIGLNVPPLRERTGDLPL  317
NTDB id 1473 PAKAF RS24000 WP 003094694.1   VADLPMAMQVKLLRAIQEKAVRAVGGQQEVAVDVRILCATHKDLAAEVGAGRFRQDLYYRLNVIELRVPPLRERREDIIPL  315
consensus

Block 5
logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1   LANHFIQKICMEWETPPKQLTEAAETYLLQQHFPGNVRELRNMIERAITLSEDATIDISHLHPAPLRA..NISNPFAS.A  397
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1 LSNAILQRLAQAMHRAPPMLDDDAVAALEAYPFPGNVRELENVLERALAMADGDRITADDLHLPAPPGAPRTQSPVITGT  397
NTDB id 1473 PAKAF RS24000 WP 003094694.1   LAERILKRLAGDTGLPAARLTGDAQEKLKNYRFPGNVRELENMLERAYTLCEDDQIQPHDLRLADAPGASQEGAASLS..  393
consensus

Block 6
logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1   AQSIQTTVAAPQ...AV..KKLPSEGLERYLENIEKDILLNALNMTHWNRTLAAKKLGMTFRSLRYRLKKFGLDTETEQE  472
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1 HPALPPSSAAPRDPRTVSPYETAGTALPSFIEDIERAAIQQALQENRYNKTKTAAALGITFRALRYKLKKLGID......  471
NTDB id 1473 PAKAF RS24000 WP 003094694.1   ...................EIDNLEDYLEDIERKLIMQALEETRWNRTAAAQRLGLTFRSMRYRLKKLGID......  445
consensus
```

logo

```
                                                V
NTDB id 1045 H0N27 RS16330 WP 168727019.1       V    473
NTDB id 1060271 ACF3M1 RS03350 WP 394003925.1   .    471
NTDB id 1473 PAKAF RS24000 WP 003094694.1       .    445
consensus
```

X non conserved
X similar
X ≥ 50% conserved