Multiple sequence alignment

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NTDB id 1045 H0N27 RS16330 WP 168727019.1      ..........MAEQQPLVLLVDDEEDLCLLMQMTLARMGIKTHLAYRVEQAKQLFTQFHYDACLTDLNLPDGSGLDLVKHV   71
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   MSLGKAERRPRGELARVLVVDDEADIRELLDLTVARMGLSADCAATVAQARQLLEQHRYQLCLTDMRLPDGEGLEIVRLI   80
NTDB id 1473 PAKAF RS24000 WP 003094694.1      ...........MSRQKALIVDDEPDIRELLEITLGRMKLDTRSARNVKEARELLAREPFDLCLTDMRLPDGSGLDLVQYI   69
consensus

logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1      SQNYPNTPIAVLTAYGNMDIAIAALKAGAFDFVSKPVNQVHLDQLLQKALNRQKVEH..DTTENALENKLLIGRSLPIQQ  149
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   GERYGETPVAVITAFGSAQNAVAALKAGAFDYLAKPVALDQLRSLIKSALSLPTRSGSSEAGQPSGAAAQLIGESNAIAQ  160
NTDB id 1473 PAKAF RS24000 WP 003094694.1      QQRHPQTPVAMITAYGSLDTAIQALKAGAFDFLTKPVDLGRLRELVATALRLRNPEAE.....EAPVDNRLLGESPPMRA  144
consensus

logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1      LRIAIKKIARSQAPVFVTGESGTGKEVVANLVHRLSNRSEGPFIAINCGAIPTELMESELFGHKKGSFTGATQDKQGLIL  229
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   VRQMIEKLARSQAPLYVSGESGTGKELAARLIHDHSARRTAPFVPVNCGAIPENLMESEFFGYRKAFTGADSDRAGFFQ   240
NTDB id 1473 PAKAF RS24000 WP 003094694.1      LRNQIGKLARSQAPVYISGESGSGKELVARLIHEQGPRIERPFVPVNCGAIPSELMESEFFGHKKGSFTGAIEDKQGLFQ  224
consensus

logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1      SAHGGSLFLDEIAELPLSMQVKLLRAVQEKKIRPVGSDQEIDVDFRVISASHQDLDLLVRQGKFRQDLFFRIHVMDLILP  309
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   AATGGTLFLDEVADLPLLMQVKLLRAIQEKKVRKVGSTVEEAVDVRIISATHRMLKDCVDAGSFRQDLYYRLNVIELRMP  320
NTDB id 1473 PAKAF RS24000 WP 003094694.1      AASGGTLFLDEVADLPMAMQVKLLRAIQEKAVRAVGGQQEVAVDVRILCATHKDLAAEVGAGRFRQDLYYRLNVIELRVP  304
consensus

logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1      PLRERGEDVLLLANHFIQKICMEWETPPKQLTEAAETYLLQHFPGNVRELRNMIERAITLSEDATIDISHLHPAPLRAN   389
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   PLRERQEDVEPLVAALLVRICGA...QPPRVEAAAMRALKAYSFPGNVRELENVLERATALCSNDTVLIDDLQLAPVMAV  397
NTDB id 1473 PAKAF RS24000 WP 003094694.1      PLRERREDIPLLAERILKRIAGDTGLPAARLTGDAQEKLKNYRFPGNVRELENMLERAYTLCEDDQIQPHDLRLADAPGA  384
consensus

logo
NTDB id 1045 H0N27 RS16330 WP 168727019.1      ISNPFASAAQSIQTTVAAPQAVKKLPSEGLERYLENIEKDILLNALNMTHWNRTLAAKKLGMTFRSLRYRLKKFGLDTET  469
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   SDS.................V...GRDGETLDDYINRVEKQAIVEALTKTDFNRTAAARLLGVTFRSLRYRIERLGIEE..  456
NTDB id 1473 PAKAF RS24000 WP 003094694.1      SQE................GAASLSEIDNLEDYLEDIERKLIMQALEETRWNRTAAAQRLGLTFRSMRYRLKKLGID...  445
consensus
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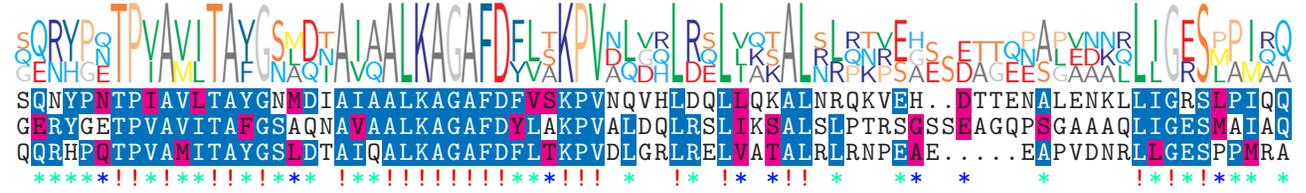
logo

EQEV

NTDB id 1045 H0N27 RS16330 WP 168727019.1   EQEV   473
NTDB id 35146 CAP2UW1 RS03855 WP 015765361.1   456
NTDB id 1473 PAKAF RS24000 WP 003094694.1   445
consensus

☐X non conserved
X similar
X ≥ 50% conserved