

logo

NTDB id 1073 ABD1 RS00865 WP 015451369.1
 NTDB id 1043 HON27 RS16615 WP 168727007.1
 NTDB id 1021 ACIAD RS00975 WP 004930462.1
 NTDB id 1094 KZH42 RS01320 WP 002224767.1
 NTDB id 1089 NMB RS00600 WP 002224767.1
 NTDB id 1122 OK783 RS09595 WP 003705341.1
 NTDB id 1120 NGFG RS10355 WP 020997408.1
 NTDB id 1250 GC085 RS13065 WP 027219989.1
 NTDB id 1399 DSB67 RS15600 WP 010645755.1
 NTDB id 1009840 ABFV67 RS13710 WP 187985339.1
 NTDB id 1152 A1552VC RS00200 WP 000654772.1
 NTDB id 1388 A4U84 RS04945 WP 062924099.1
 NTDB id 1361 HI 0985 AAC22646.1

consensus

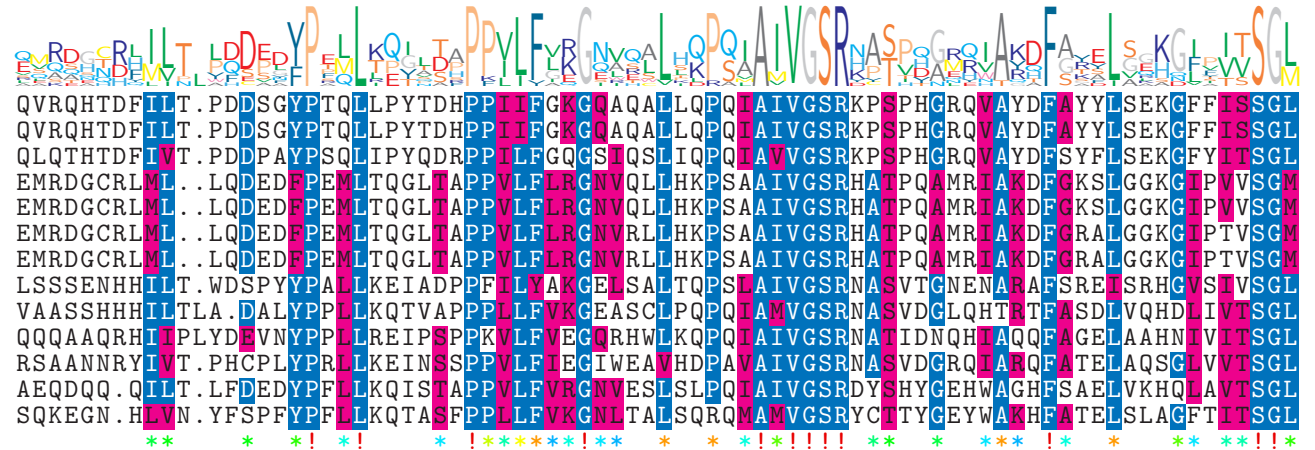


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VEATLKSGSLITANKAAEQGKTVFATPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDIALPTQWQSQQNQNT....EE 311
 VEATLKSGSLITANKAAEQGKTVFATPGHIYSEFHQGCHQLIREGAILIDHPEQIIEDIALPTQWQSQQNQNT....EE 311
 VEATLKSGSLITANKAAEQGKVFATPGHIYSEFHQGCHQLIREGAILVDHPEQIIEDIALPTHWHSQSTASGEANADDS 316
 VEAAL ESGSLITARLAAEMGREVMVAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGASSYSINKGIPEK 313
 VEAAL ESGSLITARLAAEMGREVMVAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGASSYSINKGIPEK 313
 VEAAL ESGSLITAGLAAEMGREVMVAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGASSYSINKDTPDT 313
 VEAAL ESGSLITAGLAAEMGREVMVAVPGSIDNPHSKGCHKLIKDGAKLVECLDDILNECPGLLQNTGASSYSINKDTPDT 313
 IEAALKSGSLITARMALQNRDVLAIQPSIHNPLARGCHYLQQGAKLVTSVADVDELKIEHHQFTSN..... 296
 VEAALKSGSLITARYALEQGREVFALPASINAPNASGGNLIQNGACLVTQTEVLNEIQSLLDWSINQS..... 300
 VEAALKSGSLITARYAIEQGRDVFVIVPGPITSTNSQGSNQLIRQGACLVQTVEDILAEVENLLNWKDSP..... 301
 VEAALKSGSLITARYAAEQGREVFVAVPGSIFNAASQGSNQLIRQGACLVQSVQQIHQELKNALTWSLSEQ..... 298
 IEATVNSGSLITARYALEQGREVFALPNSVQNPYSEGCHKLIKEGALLVENVEDILEATAWQRQSVHIQPSL.FDTKP.. 303
 VEATEKSGSLITARYALEQNREVFVAVPGNIQNKSSQGCHRLIKQGAMLVENAKDILETLYQHS..IHSQTEIDFDQIAVP 305

consensus

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.....AN...TNTPEIREHLIDLYQSLDWVGGNIDQLVVHNNIPVSELTSSLMELELLGLCMQQSGLYLRL 373
TN...TNTPEIPEHLIDLYQSLDWVGGNIDQLVVHNNIPVSELTSSLMELELLGLCMQQSGLYLRL 373
GK...TDDADLPDDLPLLYQLLDWGGQDLQDLAQHYQGSTAELTAQLMELELLGVCIIQQSGRYLR 378
 RITAVQTASDQLSLPEGKMPSEKTENRPVGGSIIDRMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGRYQ 393
 RITAVQTASDQLSLPEGKMPSEKTENRPVGGSIIDRMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGRYQ 393
 GRRVAVQTAY..APPPAAKMPSEGAAGGTAVGGIILDKMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGRYQ 391
 GRRTVAVQTAY..APPPAAKMPSEGAAGGTAVGGIILDKMGFDPVHPDVLAGQLAMPAADLYAALLELELDGSVAAMPGGRYQ 391
KPIFSL....ASGKENVLKFIFGFTTTIDQIIDRSYGMQVTSGLAELELKGAVTAVPGGYIR 356
LDLFSAPIDEEELFPFQLLANVGNVATPVVILASRTNIPVQEVMMQLLELELGHVVAVSAGGYIR 365
SSTQELFFCPNDEEQLPFPELLANVGVVATPVVILASRTNIPVQEVMMQLLELELGHVVAVSAGGYIR 370
VPYQATLFSAVQSDDEELPFPELLANVGVVATPVVILASRTNIPVQEVMMQLLELELGHVVAVSAGGYIR 367
KQAVKSEPKFAKNLPELTACQQQLFEQISLEPISVDDLAKATDMAVETALIELLNLELLGVVKQVRGGYVI 374
NYTPPPDPR...RL.VEAPSHPKLYSRIGYTPVSIIDLAEEFNLSVDVLLVQLLDLELQDLIISENGLYKRL 372

consensus

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CRS... 376
 CRS... 376
 CRSPY. 383
 RIRT.. 397
 RIRT.. 397
 RIRT.. 395
 RIRT.. 395
 CEYER. 361
 KGRG.. 369
 KGRGKL 376
 KGRG.. 371
 T..... 375
 V..... 373

consensus

 non conserved
 similar
 $\geq 50\%$ conserved