

logo

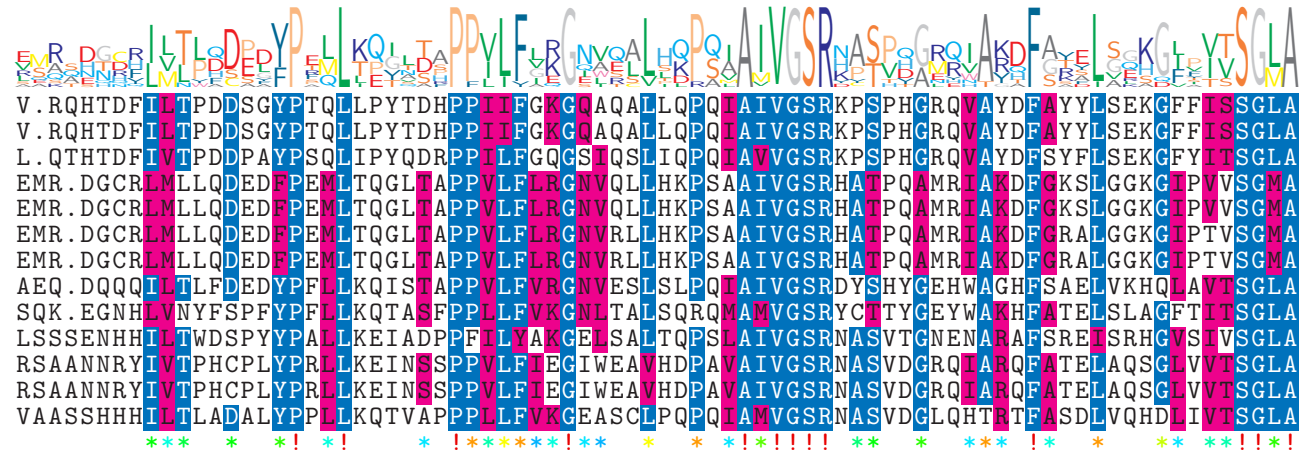
NTDB id 1073 ABD1 RS00865 WP 015451369.1
 NTDB id 1043 HON27 RS16615 WP 168727007.1
 NTDB id 1021 ACIAD RS00975 WP 004930462.1
 NTDB id 1094 KZH42 RS01320 WP 002224767.1
 NTDB id 1089 NMB RS00600 WP 002224767.1
 NTDB id 1122 OK783 RS09595 WP 003705341.1
 NTDB id 1120 NGFG RS10355 WP 020997408.1
 NTDB id 1388 A4U84 RS04945 WP 062924099.1
 NTDB id 1361 HI 0985 AAC22646.1
 NTDB id 1250 GC085 RS13065 WP 027219989.1
 NTDB id 1062803 ACG4IX RS00175 WP 000654772.1
 NTDB id 1152 A1552VC RS00200 WP 000654772.1
 NTDB id 1399 DSB67 RS15600 WP 010645755.1
 consensus



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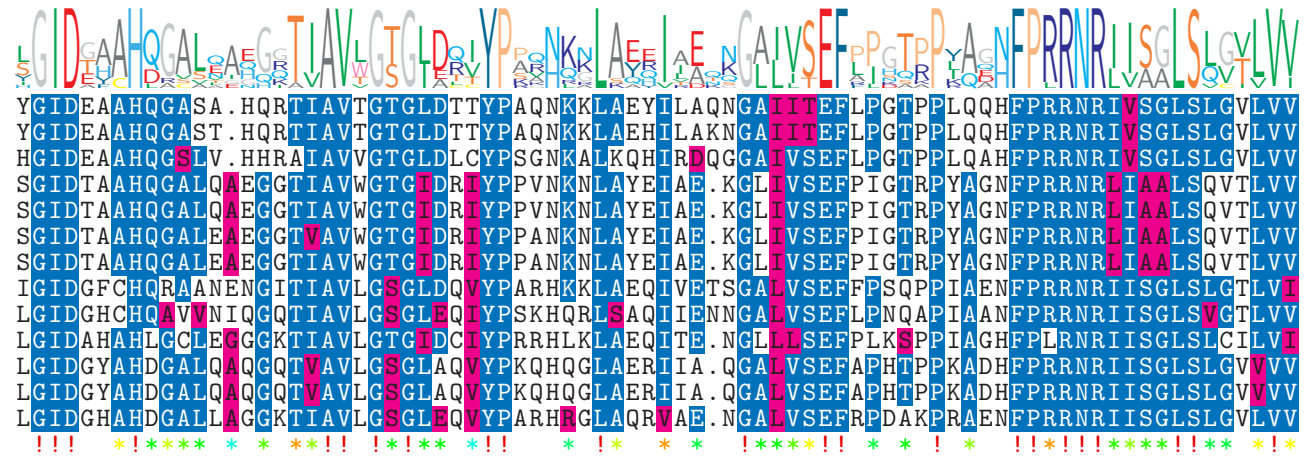
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EATLKSGSLITANKAAEQGKTVFAIPGHYSEFHQGCHQLIREGAILIDHPEQIIEEDIALPTQWQSQQQNQT..... 309
 EATLKSGSLITANKAAEQGKTVFAIPGHYSEFHQGCHQLIREGAILIDHPEQIIEEDIALPTQWQSQQQNQT..... 309
 EATLKSGSLITANKAAEQGKTVFAIPGHYSEFHQGCHQLIREGAILIDHPEQIIEEDIALPTQWQSQSTASGEANAD... 314
 EAALESGLLITARLAAEMGREVMVAVPGSIDNPHSKGCHKLKIDGAKLVECLDDILNECPGLLQNTGASSYSINKGIPEKR 314
 EAALESGLLITARLAAEMGREVMVAVPGSIDNPHSKGCHKLKIDGAKLVECLDDILNECPGLLQNTGASSYSINKGIPEKR 314
 EAALESGLLITAGLAAEMGREVMVAVPGSIDNPHSKGCHKLKIDGAKLVECLDDILNECPGLLQNTGASSYSINKDTPDTG 314
 EAALESGLLITAGLAAEMGREVMVAVPGSIDNPHSKGCHKLKIDGAKLVECLDDILNECPGLLQNTGASSYSINKDTPDTG 314
 EATVNSGSLITARYALEQGREVFALPNSVQNPYSEGGCHKLKEGALLVENVEDILEATAWQRQSVHIQPSL.FDTK.... 302
 EATEKSGSLITARYALEQNRVFAVPGNIQNKSSQGCHRLIKQGAMLVENAKDILETLTYQHS.IHSQTEIDFDQI.... 302
 EAAIKSGSLITARMALEQNRDVLAIIPGSIHNPARGCHYLLQQGAKLVTSVADVLDLDELKIEHHQ..... 292
 EAAEKSGSLITARYAAEQGREVFVAVPGSIFNAASQGSNQLIRQGACLVQSVQQIHQELKNALTWS..... 294
 EAAEKSGSLITARYAAEQGREVFVAVPGSIFNAASQGSNQLIRQGACLVQSVQQIHQELKNALTWS..... 294
 EAAEKSGSLITARYALEQGREVFALPASINAPNASGGNQLIQNGACLVQNTQEVLEIQLSLLDWS..... 296

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.....EEANT.....NTP EIREHLIDLYQSLDWVGNIDQLVVHNNIPVSELTSSLMELELLGLCMQSSGLYLRC 374
EETNT.....NTP EIPHEHLIDLYQSLDWVGNIDQLVVHNNIPVSELTSSLMELELLGLCMQSSGLYLRC 374
DSGKT.....DDADLPDDLPLLYQLLDWQQQLDQLAQHYQGSTAELTAQLMELELLGVCIIQSSGRYLRC 379
 ITAVQTASDQLSLPEGKMPSEKTENRPVGGSIIDRMGFDPVHPDVLAGQLAMPAADLYAALLELELDGVAAMPGGRYQR 394
 ITAVQTASDQLSLPEGKMPSEKTENRPVGGSIIDRMGFDPVHPDVLAGQLAMPAADLYAALLELELDGVAAMPGGRYQR 394
 RRAVQTAY..APPPAAKMPSEGAAGGTAVGGIIDKMGFDPVHPDVLAGQLAMPAADLYAALLELELDGVAAMPGGRYQR 392
 RRTVQTAY..APPPAAKMPSEGAAGGTAVGGIIDKMGFDPVHPDVLAGQLAMPAADLYAALLELELDGVAAMPGGRYQR 392
P..KQAVKSEPKFAKNLPELTACQQQLFEQISLEPISVDDLAKATDMAVETALIELLNLELLGKVQVIRGGYVIT 375
AVPNYTPPPDPR...RL.VEAPSHPKLYSRIQYTPVSIIDLAEEFNLSVDVLLVQLLDLELQDLTIISENGLYKRV 373
FTSNKPIFSLASGK....ENLVKFIGFETTIDQLIDRSGYGMQVTSGLAELELKGAVIIVPGGYIRK 357
LSEQVPYQATLFSVQSDDEELPFPELLANVGIETPIDILASRTQIPVQDIMMQLLELELLGHVVAVPGGYIRK 368
LSEQVPYQATLFSVQSDDEELPFPELLANVGIETPIDILASRTQIPVQDIMMQLLELELLGHVVAVPGGYIRK 368
INQSL....DLFSAPIDEEELPFQQLLANVGNIEATPVDILASRTNIPVQEVMMQLLELELLSGHVAVVSGGYIRK 366

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RS.. 376
 RS.. 376
 RSPY 383
 IRT. 397
 IRT. 397
 IRT. 395
 IRT. 395
 375
 373
 EYER 361
 GRG. 371
 GRG. 371
 GRG. 369

consensus

 non conserved
 similar
 $\geq 50\%$ conserved