

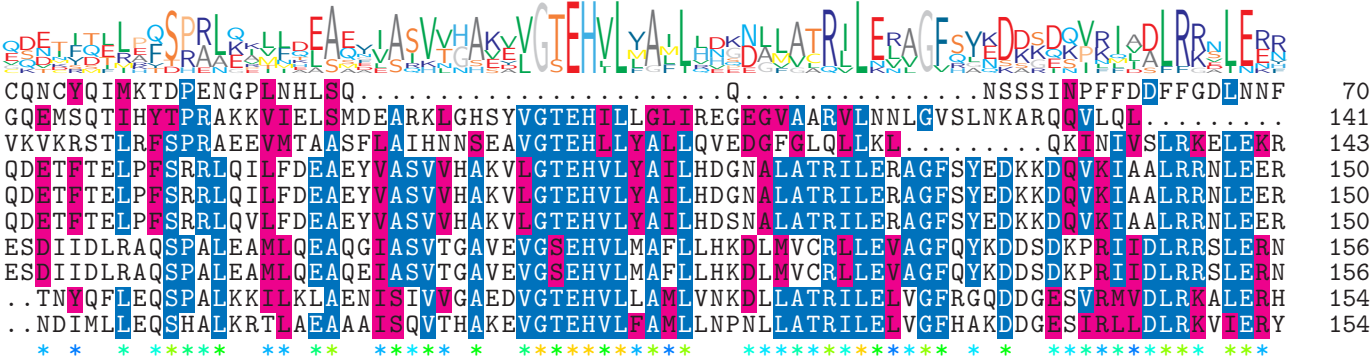
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NTDB id 85 BSU 00860 NP 387967.1
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NTDB id 290 KZH43 RS10025 WP 001109677.1
NTDB id 289 SPD RS10700 WP 001109677.1
NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 329 STU RS10020 WP 011225298.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 222968 A6J68 RS10720 WP 000020286.1
NTDB id 377 SMU RS09275 WP 002262344.1
consensus



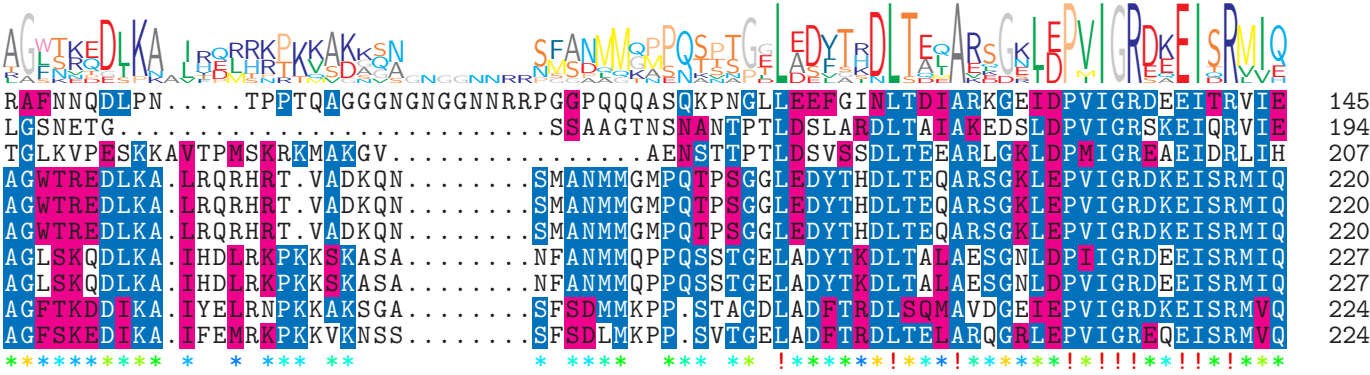
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[illegible]

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ILFIDELHTILGAGG.AEAGTDAANILKPSLARGELQCIGATTLDEYRKYIEKDAALERRFQIIVDQPSVDESIQILQG	353
ILFIDELHTIILGAGGMDSVNDAANILKPALARGDFQMGVATTYHIEYQKYIEKDEALERRLARINVDQPSVDEAIAILQG	367
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ILFIDELHTIILGSGSGIDSTLDAANILKPALARGTLHMVGATTQAEYQKHIEKDAALSRRFQKVTIEEPSVSEADITILNG	387
ILFIDELHTIMGSGSGIDSTLDAANILKPALARGTLRTIGATTQEEYQKHIEKDAALSRRFQKVLVEEPNLEADAYEILLG	384
ILFIDELHTIMGSGSGIDSTLDAANILKPALARGSLRTIGATTQEEYQKHIEKDAALSRRFQKVTIEEPSVEEAYQILLG	384

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Sequence	Position
LKATYEDYHRVITDAEAVETAVKMAHRYLTSRNLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKALMD	382
LRDRYEAHHRVSTITDAEAAVKLSDRYISDRFLDPDKAIDLIDEAGSKVRLSFTTTPNKLKELEKLDEVRKEKDAAVQS	433
LRKEFEDYHQVKFTDAEAKTSAVMLSVRYMTSRKLPDKAIDLLDEAAAVKISVKNQKTRLDEKLEAEAESEAVIK	447
LKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKALMD	452
LKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKALMD	452
LKATYEKHHRVQITDEAVETAVKMAHRYLTSRHLPDSAIDLLDEAAATVQNKAKHVKAADSDS...S...PADKALMD	452
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LRSSYEDYHRVTITDAAVETAVKMAHRYLTSRKNLPDSADILLDEASATVQVRIKK..EDKREI...T...PLDEALIS	457
LKPAYEAFHNVTISDEAVMTAVKVAHRYLTSRKNLPDSADILLDEASATVQVRIKK..NAPSL...T...EVDQATIT	454
LKKSSETYHHVITSDAAVMAAVKGAHRYLSGKNLPDSADILLDEASATVQGLVKK..KAPAYL...T...DLHALIT	454

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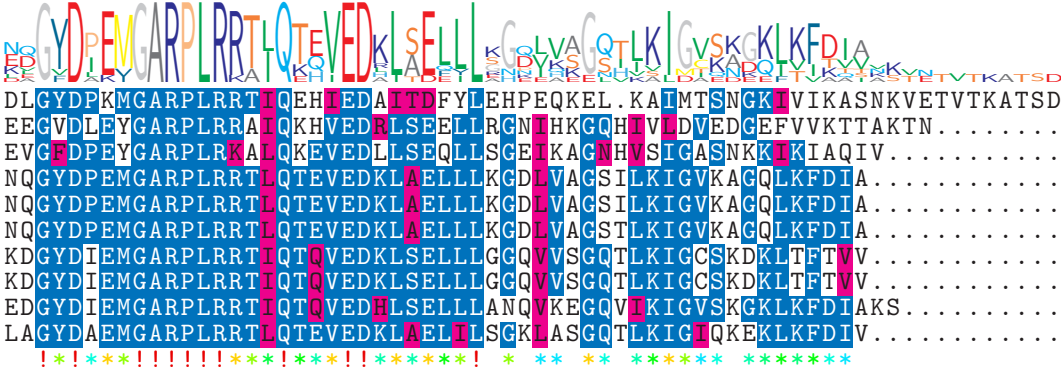
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688
752
761
756
756
756
762
762
759
759

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consensus



753
810
816
810
810
810
816
816
815
813

[X] non conserved
[X] similar
[X] ≥ 50% conserved