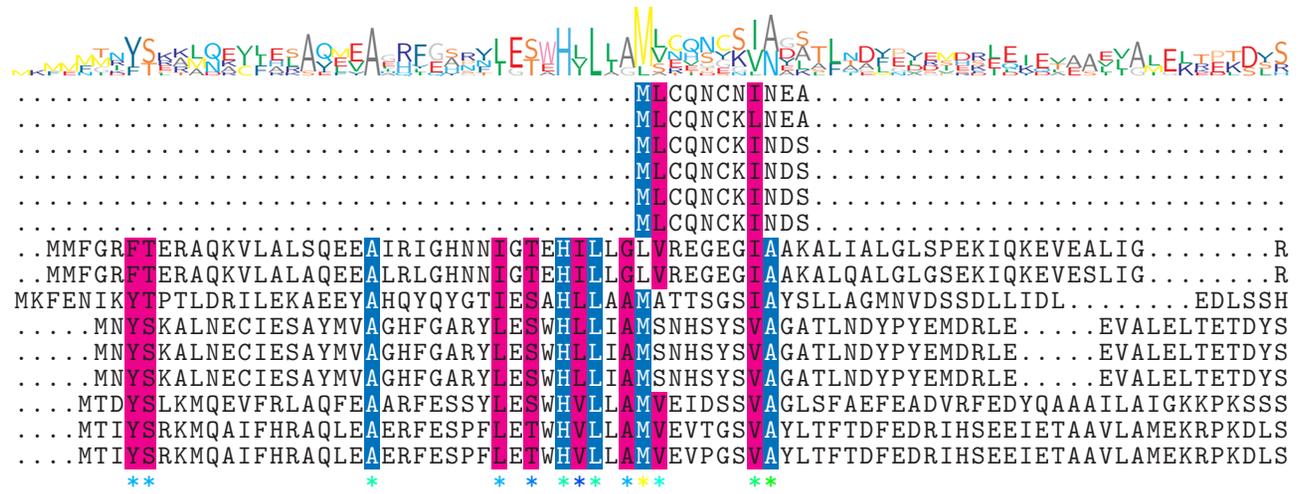


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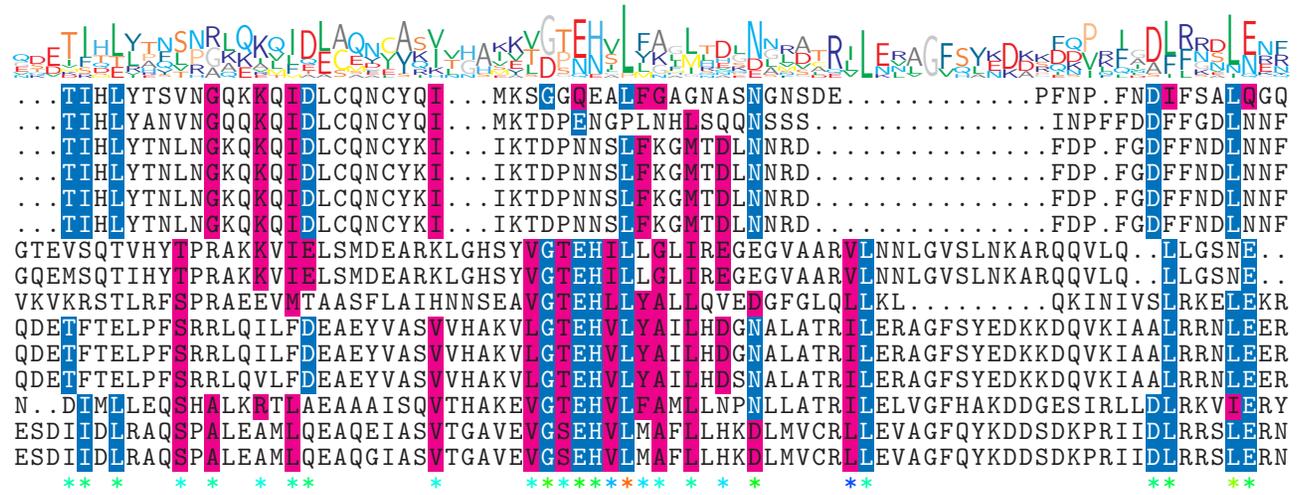
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 NTDB id 377 SMU RS09275 WP 002262344.1
 NTDB id 297 STER RS00545 WP 011680614.1
 NTDB id 329 STU RS10020 WP 011225298.1
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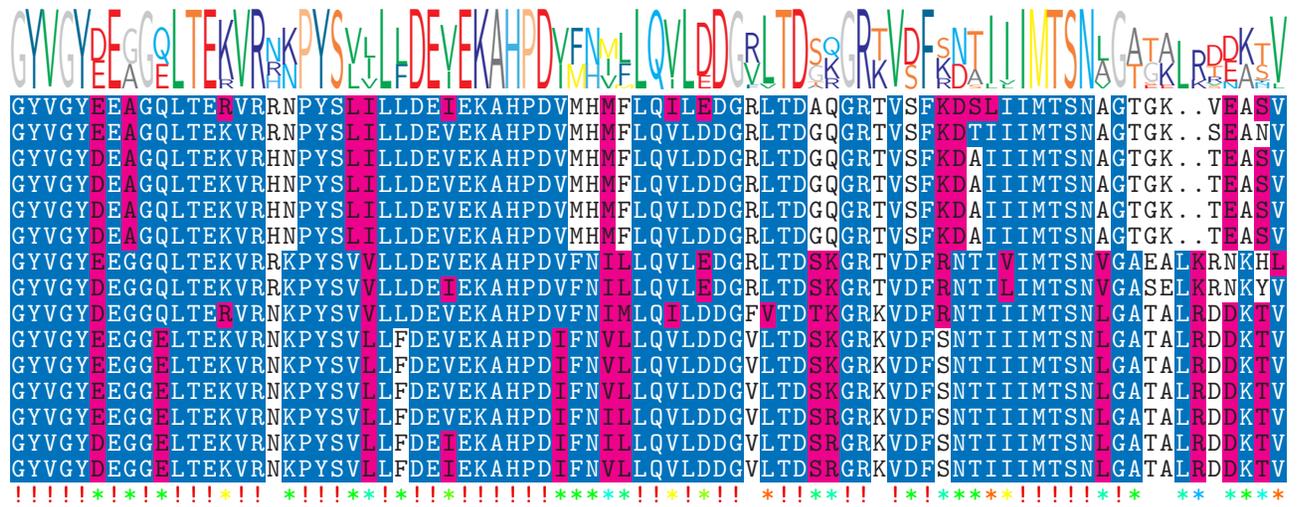
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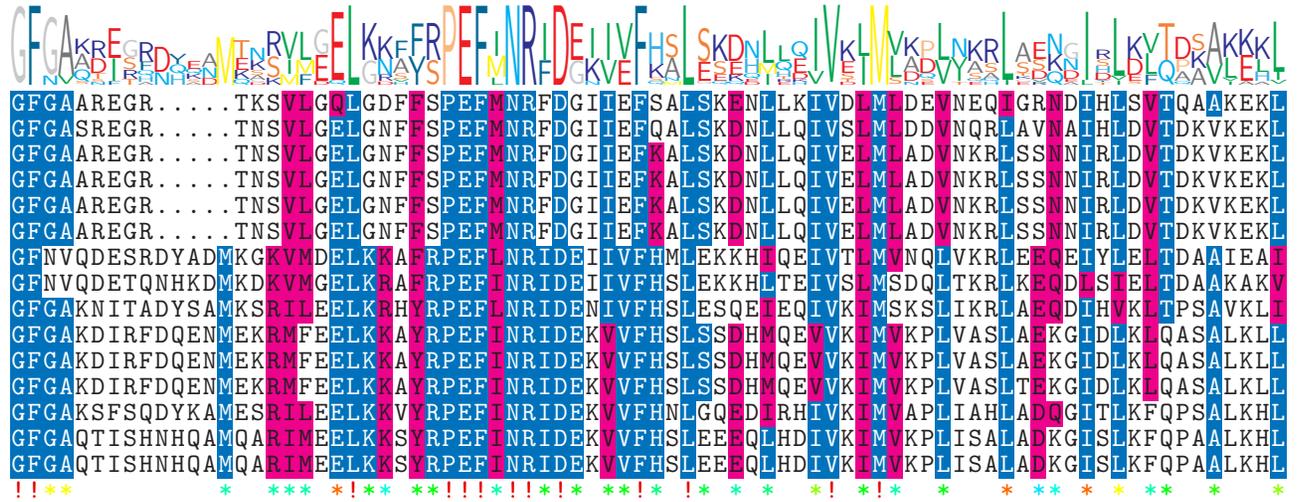
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NTDB id 601 KW2 RS02615 WP 021036805.1
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 NTDB id 377 SMU RS09275 WP 002262344.1
 NTDB id 297 STER RS00545 WP 011680614.1
 NTDB id 329 STU RS10020 WP 011225298.1
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|---|---|----|
| NTDB id 601 KW2 RS02615 WP 021036805.1 | VDLGYNPAMGARPLRRTIQENTIEDSTADFYIEHPEYKQLV.ADLIDDKIVISNQTQETAETTTDEEVP | AE |
| NTDB id 378 SMU RS02690 WP 002263569.1 | VDLGYDPKMGARPLRRTIQEHIEDAITDFYLEHPEQKELK.AIMTSNGKIVIKASNK.VETVTKATSD. | AE |
| NTDB id 241 SP RS04015 WP 000882523.1 | VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSACK.AEVKSSEKEK. | AE |
| NTDB id 281 KZH43 RS03550 WP 000882517.1 | VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSACK.AEVKSSEKEK. | AE |
| NTDB id 245 SPD RS03860 WP 000882517.1 | VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSACK.AEVKSSEKEK. | AE |
| NTDB id 243 SPR RS03635 WP 000882517.1 | VDLGYDPKMGARPLRRTIQDYIEDTITDYYLENPSEKDLK.AVMTSKGNIQIKSACK.AEVKSSEKEK. | AE |
| NTDB id 251947 CG481 RS00525 WP 011983220.1 | ADKGFDRREYGARPLRRAIQKHVEDRLSEELLKGVIEKGGKVIIFDKERESFVIRSAEKVK..... | AE |
| NTDB id 85 BSU 00860 NP 387967.1 | AEEGVLDLEYGARPLRRAIQKHVEDRLSEELLRGNIHKGQHIVLDVEDGEFVVKTTAKTN..... | AE |
| NTDB id 610 V4T04 RS10165 WP 012897346.1 | AEEGVLDPEYGARPLRKALQKEVEDLLSEQLLSGETKAGNHVSI GASNKKIKIAQIV..... | AE |
| NTDB id 290 KZH43 RS10025 WP 001109677.1 | ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA..... | AE |
| NTDB id 289 SPD RS10700 WP 001109677.1 | ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSILKIGVKAGQLKFDIA..... | AE |
| NTDB id 287 SP RS11210 WP 001109712.1 | ANQGYDPEMGARPLRRTLQTEVEDKLAELLLKGDLVAGSTLKIIGVKAGQLKFDIA..... | AE |
| NTDB id 377 SMU RS09275 WP 002262344.1 | ALAGYDAEMGARPLRRTLQTEVEDKLAELILSGKLASGQTLKIIGIQKEKIKFDIV..... | AE |
| NTDB id 297 STER RS00545 WP 011680614.1 | AKDGYDIEMGARPLRRTIQTQVEDKLSSELLGGQVVSQGTLKIGCSKDKLTFTVV..... | AE |
| NTDB id 329 STU RS10020 WP 011225298.1 | AKDGYDIEMGARPLRRTIQTQVEDKLSSELLGGQVVSQGTLKIGCSKDKLTFTVV..... | AE |
| consensus | ** !*****!!!!** *!! *** ** * * * * * * * * * * * * | |

- X non conserved
- X similar
- X ≥ 50% conserved