

logo

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NTDB id 216293 BWR56 RS00355 WP 076984227.1
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 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus



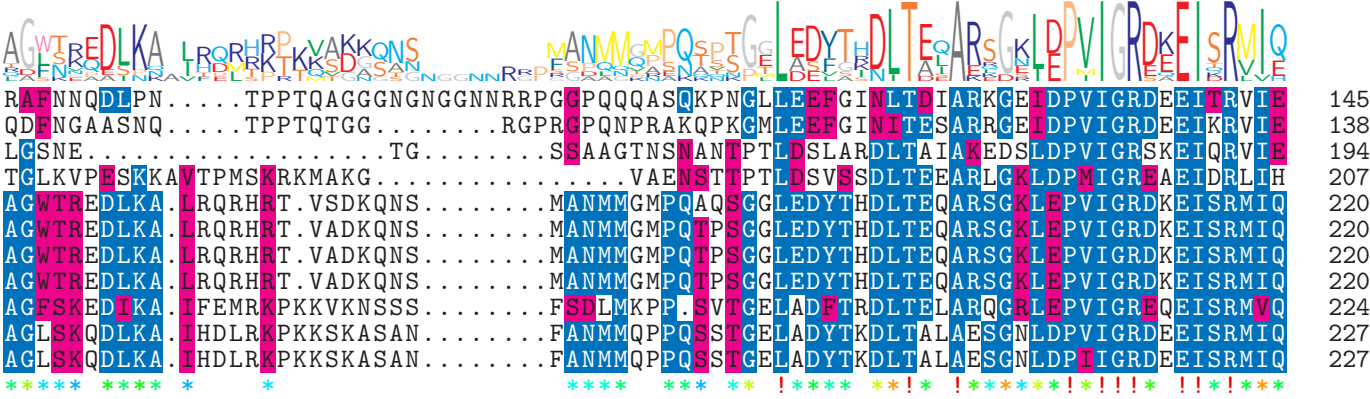
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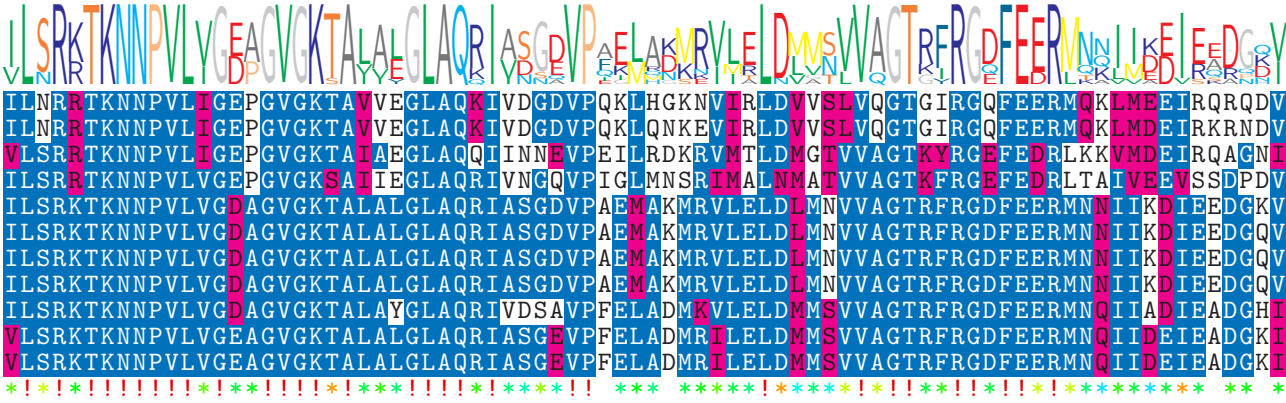
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logo

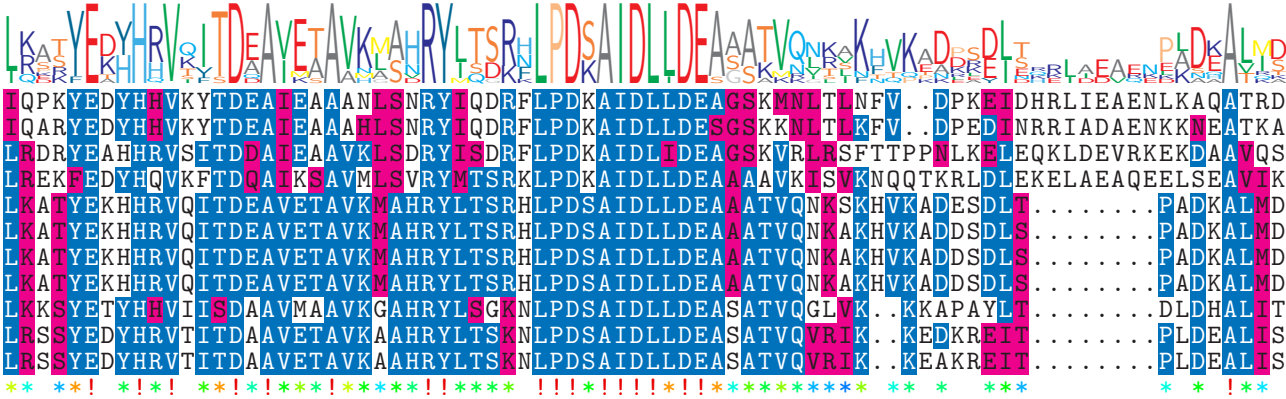
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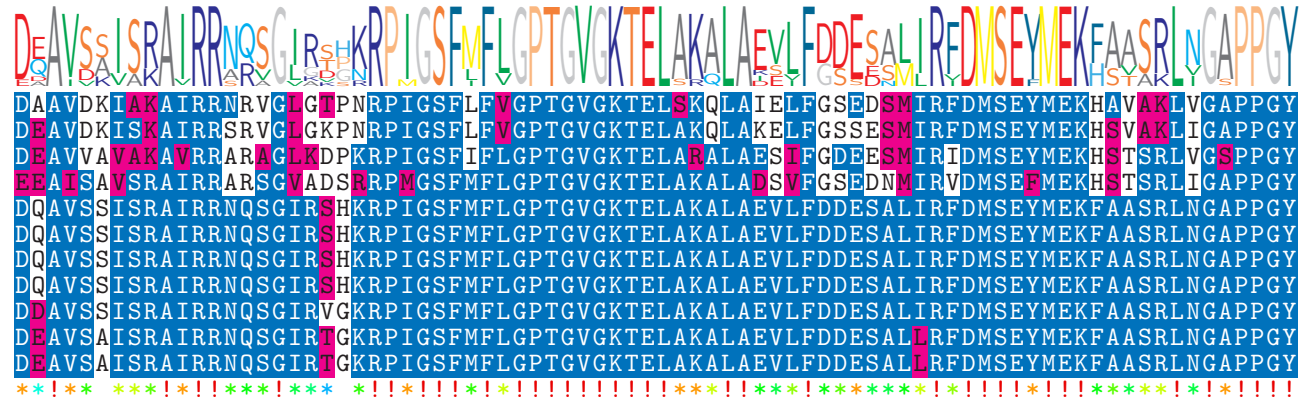
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NTDB id 378 SMU RS02690 WP 002263569.1	GAKDIRFDQENMEKRIFEELKKAYRPEFINRIDEKVFHSLSSSEHLCSEIVKIMVKPLVASLAKEGIDLKLQASALKLLA	689
NTDB id 601 KW2 RS02615 WP 021036805.1	GASREG....RTNSVIGELGNFISPEFMNRFDGITIEFQALSKDNLLQIVSLMLDDVNQRLAVNAIHLDDVTDKVKKEKLVD	682
NTDB id 85 BSU 00860 NP 387967.1	GAAREG....RTKSVLGGQLGDFISPEFMNRFDGITIEFSALSKENLLKIVDLMDEVNEQIGRNDIHLSTQAAKEKLVD	753
NTDB id 610 V4T04 RS10165 WP 012897346.1	NVQDETQNHKDMKDKVMGELKRAFRPEFINRIDEIVFHSLEKKHLTEIVSLMSDQLTKRLKEQDLSIELTDAAKAKVAE	762
NTDB id 216293 BWR56 RS00355 WP 076984227.1	GAKNITADYSAMKSRILEELKRHYRPEFLNRIDENIVFHSLESQEIEQIVKIMSKSLTKRLAEQDIHVKLTPSAVKLTAE	757
NTDB id 290 KZH43 RS10025 WP 001109677.1	GAKDIRFDQENMEKRIFEELKKAYRPEFINRIDEKVFHSLSSDHMQEVVKIMVKPLVASLAKEGIDLKLQASALKLLAN	757
NTDB id 289 SPD RS10700 WP 001109677.1	GAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVFHSLSSDHMQEVVKIMVKPLVASLAKEGIDLKLQASALKLLAN	757
NTDB id 287 SP RS11210 WP 001109712.1	GAKDIRFDQENMEKRMFEELKKAYRPEFINRIDEKVFHSLSSDHMQEVVKIMVKPLVASLTEKGIDLKLQASALKLLAN	760
NTDB id 377 SMU RS09275 WP 002262344.1	GAKSFSQDYKAMESRILEELKKVYRPEFINRIDEKVFHNLGQEDIRHIVKIMVAPLIAHLADQGITLKFQPSALKHLAL	763
NTDB id 297 STER RS00545 WP 011680614.1	GAQTISHNHQAMQARIMEELKKSYPREFINRIDEKVFHSLSEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAK	763
NTDB id 329 STU RS10020 WP 011225298.1	GAQTISHNHQAMQARIMEELKKSYPREFINRIDEKVFHSLSEEEQLHDIVKIMVKPLISALADKGISLKFQPAALKHLAK	763
consensus	*** * * * * *****! * * * * ! ! ! ! ! * * * * ! *	

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NTDB id 378 SMU RS02690 WP 002263569.1	GYDPENMGARPLRRTLQTEVEDKLAELLKGLVAGQTLKIGVSAGKLKFDIA	753
NTDB id 601 KW2 RS02615 WP 021036805.1	LGYNPAMGARPLRRTIQENIEDSIADFYIEHPEYKQ.LVADLIDDKIVISNQTQET...AETTDEEVPAE	748
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NTDB id 290 KZH43 RS10025 WP 001109677.1	QGYDPENMGARPLRRTLQTEVEDKLAELLKKGDLVAGSILKIGVKAGQLKFDIA.....	810
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consensus	! * * * * * ! ! ! ! ! * * * * ! *	

- ☒ non conserved
- ☒ similar
- ☒ ≥ 50% conserved