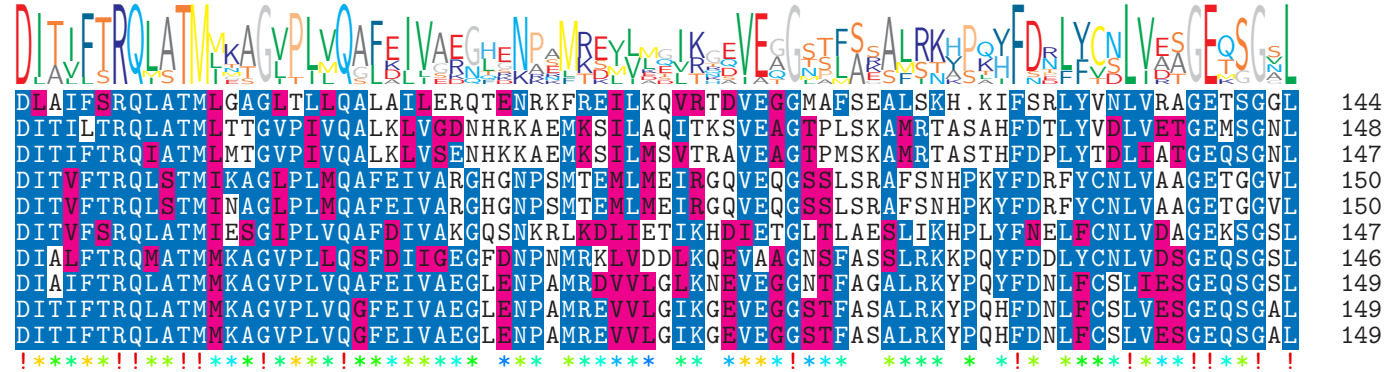


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NTDB id 1029 TT RS02230 WP 011228203.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NCFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1014659 ABV836 RS17190 WP 000279216.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

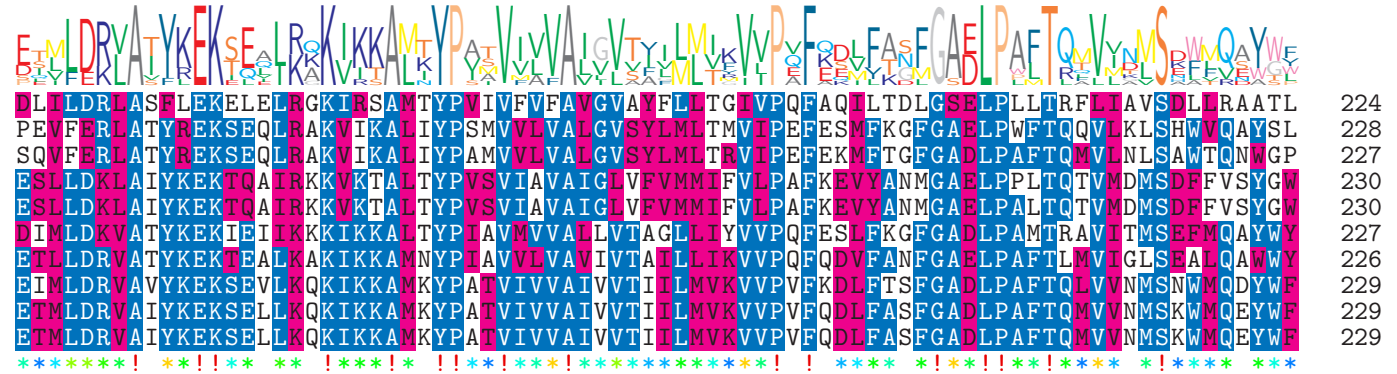
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NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1014659 ABV836 RS17190 WP 000279216.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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NTDB id 1029	TT RS02230 WP 011228203.1	PLLLLAVALFFAYRW.YYGTPQGRRV	IDRLKLRPLVFGNINRKTAVARFSRTLALLSSSGVNIVEALDITKGTAGNSVVE	303
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NTDB id 1402	DSB67 RS12670 WP 010643257.1	FIGLSFVSLISGKIMSQRSDS	FRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ	307
NTDB id 1112	NGFG RS09215 WP 003689811.1	MVLIALGFATYGFKLKARSIKI	QRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1113	AAA85695.1 219..1451()	MVLIALGFATYRFLKLKARSIKI	QRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1252	GC085 RS07730 WP 011213805.1	IIIFGALGGVVVSFFYAKNHS	LEFAQTTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNNIYA	307
NTDB id 1198	PSJM300 03950 AFN76868.1	VVLAGFVGAAAYAFKQAHTR	SEKFRNWFDRMLMKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNNVFR	306
NTDB id 1016	ACIAD RS01680 WP 004920476.1	ILILVIGAATAGFLEARKRSKR	FRDQLDRLVLRPLVIGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE	309
NTDB id 1014659	ABV836 RS17190 WP 000279216.1	IMITATGAVIAAFLEAKKRSK	KFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE	309
NTDB id 1059	ABD1 RS01610 WP 000279215.1	IMITATGAVIAAFLEAKKRSK	KFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATNNVIYE	309
consensus		*****	*****!*****!*	

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NTDB id 1029	TT RS02230 WP 011228203.1	EIVEAAKLKIQGGDP	NLTLAQHPFVFPPMVSSMVAIGEETGALDMLSKVADFYEREVDEAVASLTAAIEPLMITIFLGV	383
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NTDB id 1402	DSB67 RS12670 WP 010643257.1	LAIEEVYRDTAAGMPMYIAMR	.HCHVFPELVLMQVMIGEESGRLDDMLNKIAAIYEFVDNTVDNLGKILEPLIIVFLGV	386
NTDB id 1112	NGFG RS09215 WP 003689811.1	EATREIRTRVIQGLSMTSGMR	.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEVDNAVGRLSAMMEPIIIVILGL	389
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTRVIQGLSMTSGMR	.ATELFPNMMLQMSSIGEESGSLDDMLNKAAEFYEVDNAVGRLSAMMEPIIILILGL	389
NTDB id 1252	GC085 RS07730 WP 011213805.1	KATDKIREEVATGQQMFIAME	.NTHLFPNMVIQMVVAIGEESGALDEKMLSKVADFYEVEVNNAVDALSSLEPIIMSILGI	386
NTDB id 1198	PSJM300 03950 AFN76868.1	SATNKIKSDVSSGMQLNFSMR	.TTGTFPSPMAVQMTAIGEESGALDEMLSKVATFYEDEVDNMVDGLTALMEPMIMAVLGV	385
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIREDVSTGQQLNFAMR	.VSNRFPTMAIQMVAIGEESGALDEMLDKVANYYESEVDHVDGLTSMMEPLIMAILGI	388
NTDB id 1014659	ABV836 RS17190 WP 000279216.1	KAVMKIREDVATGQQLQFAMR	.VSNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV	388
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIREDVATGQQLQFAMR	.ISNRFPSMAIQMVAIGEESGALDSMLDKVATYYENEVDNAVDGLTSMMEPLIMAILGV	388
consensus		* * * * *	*****!***** * * * * *	

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NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGTISVQ	406
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVAMYLPIFNLMSVLG..	408
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NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLVAMYLPLFNLGNVVA..	410
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NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLIIAMYLPIFQMGSVV...	405
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVIAMYLPIFQMGSVV...	408
NTDB id 1014659	ABV836 RS17190 WP 000279216.1	LVGGLVIAMYLPIFQMGSVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVIAMYLPIFQMGSVV...	408
consensus		* * ! * * * * * ! * ! ! * ! * * * * *	

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