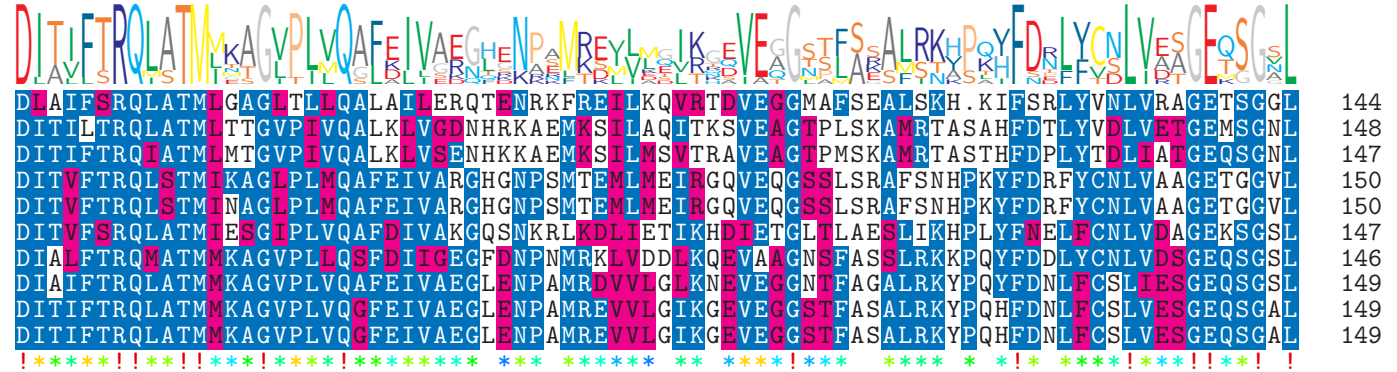


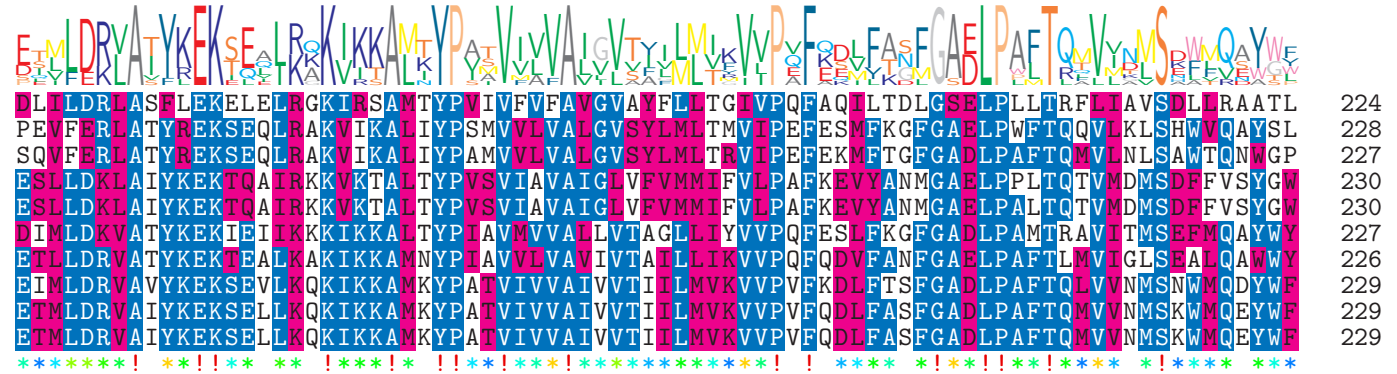
```
NTDB id 1029 TT RS02230 WP 011228203.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1061100 ACGTHP RS09725 WP 000279218.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus
```



```

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 NFGF 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 1061100 ACGTHP RS09725 WP 000279218.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

```



logo

NTDB id 1029	TT RS02230 WP 011228203.1	PLLLLAVALFFAYRW.YYGTIPQGRRV	IDRLKLRPLVFGNINRKTAVARFSRTLALLSSSGVNIVEALDITKGTAGNSVVE	303
NTDB id 1169	A1552VC RS11075 WP 000648511.1	WAFIAIAAAIFGLKALRKN	SFQIRLKT SRLGLKFPITIGNVLAKASIAKFSRTLATSFAAGIPILASLKT	308
NTDB id 1402	DSB67 RS12670 WP 010643257.1	FIGLSFVSLISGKIMSQRSDS	FRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTT	307
NTDB id 1112	NGFG RS09215 WP 003689811.1	MVLIALGFATYGFKLKARSIKI	QRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLD	310
NTDB id 1113	AAA85695.1 219..1451()	MVLIALGFATYRFLKLKARSIKI	QRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLD	310
NTDB id 1252	GC085 RS07730 WP 011213805.1	IIIFGALGGVVVSFFYAKN	HSLEFAQTTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSV	307
NTDB id 1198	PSJM300 03950 AFN76868.1	VVLAGFVGAAAYAFKQAHTR	SEKFRNWFDRMLMKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDAL	306
NTDB id 1016	ACIAD RS01680 WP 004920476.1	ILILVIGAATAGFLEARKRSKR	FRDQLDRLVLRPLVIGDLVYKAIIARYSRTLATTFAAGVPLIDALASTAGATN	309
NTDB id 1061100	ACGTHP RS09725 WP 000279218.1	IMIATIGAVIAAFLEAKKRSK	KFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATN	309
NTDB id 1059	ABD1 RS01610 WP 000279215.1	IMIATIGAVIAAFLEAKKRSK	KFRDGLDKLALKLPIFGDLVYKAIIARYSRTLATTFAAGVPLIDALESTAGATN	309
consensus		*****	*****!*****!*	

logo

NTDB id 1029	TT RS02230 WP 011228203.1	EIVEAAKLKIQQGDPLNLT	LTAQHPFVFPMPVSSMVAIGEETGALD	TMLSKVADFYEREVDEAVASLTAAIEPLMIT	383
NTDB id 1169	A1552VC RS11075 WP 000648511.1	TAINEVYRDTAAGMPMYIAMR	.NTEAFPEMVLQVMVIGEESGQLDD	MNLKVATIIYEFVDNTVDNLGKILEPLI	387
NTDB id 1402	DSB67 RS12670 WP 010643257.1	LAIEEVYRDTAAGMPMYIAMR	.HCHVFPELVLMQVMIGEESGRLLD	MNLKIAAIYEFVDNTVDNLGKILEPLI	386
NTDB id 1112	NGFG RS09215 WP 003689811.1	EATREIRTRVIQGLSMTSGMR	.ATELFPNMMLQMSSIGEESGLDD	MNLKAAEFYEVDNAVGRLSAMMEPII	389
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTRVIQGLSMTSGMR	.ATELFPNMMLQMSSIGEESGLDD	MNLKAAEFYEVDNAVGRLSAMMEPII	389
NTDB id 1252	GC085 RS07730 WP 011213805.1	KATDKIREEVATGQQMFIA	ME.NTHLFPNMVIQMVAIIGEESGAL	EKMLSKVADFYEVEVNNAVDALSSLEPI	386
NTDB id 1198	PSJM300 03950 AFN76868.1	SATNKKISDVSSGMQLNFS	SMR.TTGTFPMAVQMTAIGEESGAL	DEMLSKVATFYEDEVDNMVDGLTALMEP	385
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIREEDVSTGQQLNFAMR	.VSNRFPTMAIQMVAIGEESGAL	DEMLDKVANYYESEVDHVDGLTSMMEPLI	388
NTDB id 1061100	ACGTHP RS09725 WP 000279218.1	KAVMKIREEDVATGQQLQFAMR	.VSNRFPTMAIQMVAIGEESGAL	DEMLDKVANYYENEVDNAVVDGLTSMMEPLI	388
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIREEDVATGQQLQFAMR	.ISNRFPTMAIQMVAIGEESGAL	DEMLDKVANYYENEVDNAVVDGLTSMMEPLI	388
consensus		* * * * *	*****!*****	* * * * *	

<0

logo

NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGT	ISVQ	406
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVIVAMYLPIFNLMS	VLG..	408
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VVGGLVIVAMYLPIFNLMS	VLG..	407
NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLVAMYLPLFNLGN	VVVA..	410
NTDB id 1113	AAA85695.1 219..1451()	VIGTLLVAMYLPLFNLGN	VVVA*.	410
NTDB id 1252	GC085 RS07730 WP 011213805.1	LVGGLVIVAMYLPIFKLGS	AV...	406
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLVIVAMYLPIFQMGS	VV...	405
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVIVAMYLPIFQMGS	VV...	408
NTDB id 1061100	ACGTHP RS09725 WP 000279218.1	LVGGLVIVAMYLPIFQMGS	VV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVIVAMYLPIFQMGS	VV...	408
consensus		* * ! * * * * * ! * ! ! * ! * * * * *		

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