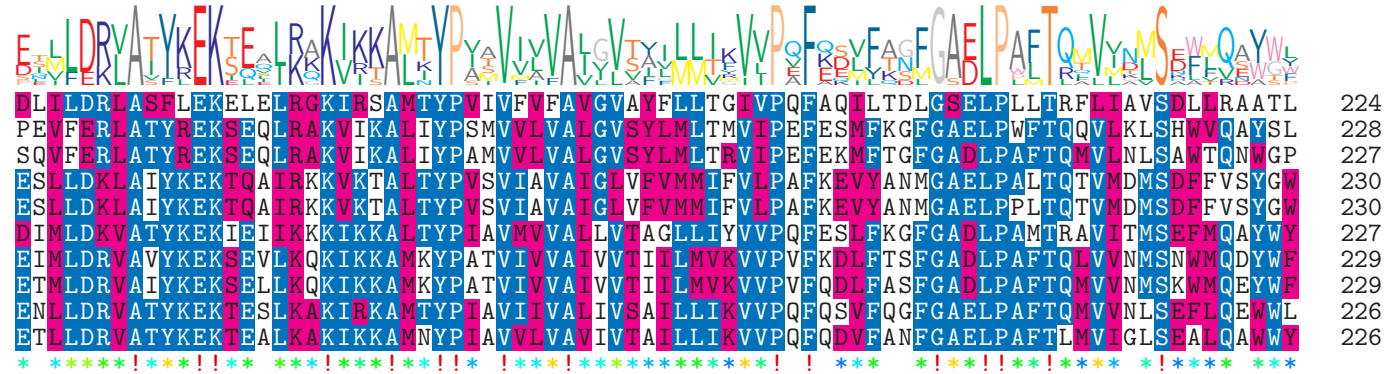
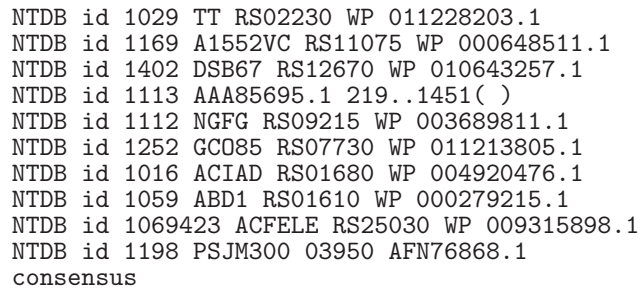
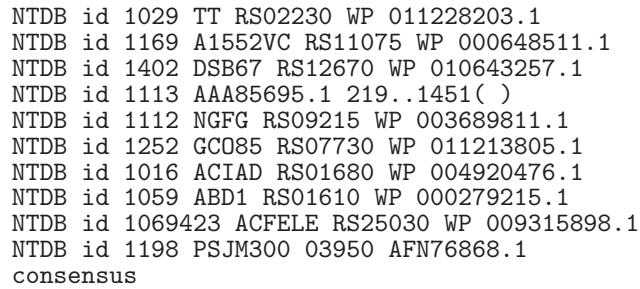


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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1069423 ACFELE RS25030 WP 009315898.1
NTDB id 1198 PSJM300 03950 AFN76868.1
consensus

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NTDB id 1029	TT RS02230 WP 011228203.1	PLLLLAVALLFFAYRWY.YGTPQGRRV	IDRLKLRPLVFGNINRKTAVARFSRTLALLSSSGVNIVEALDITKGTAGNSVVE	303
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NTDB id 1402	DSB67 RS12670 WP 010643257.1	FIGLSFVSLISGKIMSQRSDSFRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSTKTS	SGNMHYQ	307
NTDB id 1113	AAA85695.1 219..1451()	MVLIALGFAIYRFLKLRKRSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE		310
NTDB id 1112	NGFG RS09215 WP 003689811.1	MVLIALGFAIYRFLKLRKRSIKIQRRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE		310
NTDB id 1252	GC085 RS07730 WP 011213805.1	IIIFGALGGVVVSFFYAKNHSLEFAQTTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNI	IIYA	307
NTDB id 1016	ACIAD RS01680 WP 004920476.1	ILILVIGAATAGFLEARKRSKFRFRDQLDRLVLRPLVIGDILVYKAI	IARYSRTLATTFAAGVPLIDALASTAGATNNTVYE	309
NTDB id 1059	ABD1 RS01610 WP 000279215.1	IMIIAIGAVIAAFLEAKRSKFRDGLDKLALKLPIFGDLVYKAI	IARYSRTLATTFAAGVPLIDALESTAGATNNTVYE	309
NTDB id 1069423	ACFELE RS25030 WP 009315898.1	AVIVGVGAIGFTFKELHKRSKKFRDALDRTLILKLPIFGGIVYKSA	VARYARTLSTTFAAGVPLVDALDSVSGATGNIVFK	306
NTDB id 1198	PSJM300 03950 AFN76868.1	VVLAGFVGAAAYAFKQAHTRSEKFRNWFDRMLMKVPVVGDI	LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVR	306
consensus		*****	*****!*****!*	

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NTDB id 1029	TT RS02230 WP 011228203.1	EIVEAAKLKIQQGDPLNLTLAQHPFVFPMPVSSMVAIGEETGALD	TMLSKVADFYEREVDDEAVASLTAAIEPLMITIFLGV	383
NTDB id 1169	A1552VC RS11075 WP 000648511.1	TAINEVYRDTAAGMPMYIAMR.NTEAFPEMVLQVMVIGEESGQLDDMLN	KVATIEFEVDNTVDNLGKILEPLIIVFLGT	387
NTDB id 1402	DSB67 RS12670 WP 010643257.1	LATEEVYRDTAAGMPMYIAMR.HCHVFPELVLMQVMIGEESGRLLDMLNK	IAAIYEFVDNTVDNLGKILEPLIIVFLGV	386
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLN	KAAEFYEVDNAVGWLSAMMEPIIILILGL	389
NTDB id 1112	NGFG RS09215 WP 003689811.1	EATREIRTRVIQGLSMTSGMR.ATELFPNMMLQMSSIGEESGSLDDMLN	KAAEFYEVDNAVGWLSAMMEPIIIVILGL	389
NTDB id 1252	GC085 RS07730 WP 011213805.1	KATDKIREEVATIGQQMFIAE.NTHLFPNMVIQMVVAIGEESGALDEML	SKVADFYEENNAVDALSSILEPIIMSILGI	386
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIREDDVSTGQQLNFAMR.VSNRFPTMAIQMVVAIGEESGALDEML	DKVANYYESEVDHVDGLTSMMEPLIMAILGI	388
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIREDDVATGQQLQFAMR.ISNRFPSMAIQMVVAIGEESGALDEML	DKVATYYENEVDNAVDGLTSMMEPLIMAILGV	388
NTDB id 1069423	ACFELE RS25030 WP 009315898.1	NAVSKIQQDVSTGMLNFSMR.TTSVFPNMAIQMTAIGEESGSLDEMLS	KVASYYEEVDNAVDNLTTLMEPMIMAVLGV	385
NTDB id 1198	PSJM300 03950 AFN76868.1	SATNKKISDVSSGMLNFSMR.TTGTFPSMAVQMTAIGEESGALDEMLS	KVATFYEVDNMVDGLTALMEPMIMAVLGV	385
consensus		* * * * *	*!***** * * * * *	

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NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGTISVQ	406
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVVAMYLPIFNLMSVVG..	408
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NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLVAMYLPLFNLGNVVA..	410
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NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVTAMYLPIFQMGSVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVTAMYLPIFQMGSVV...	408
NTDB id 1069423	ACFELE RS25030 WP 009315898.1	LVGGLIVAMYLPIFQLGNVVG..	406
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLITAMYLPIFQMGSVV...	405
consensus		* * ! * * * * * ! * ! * ! * * * * * *	

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