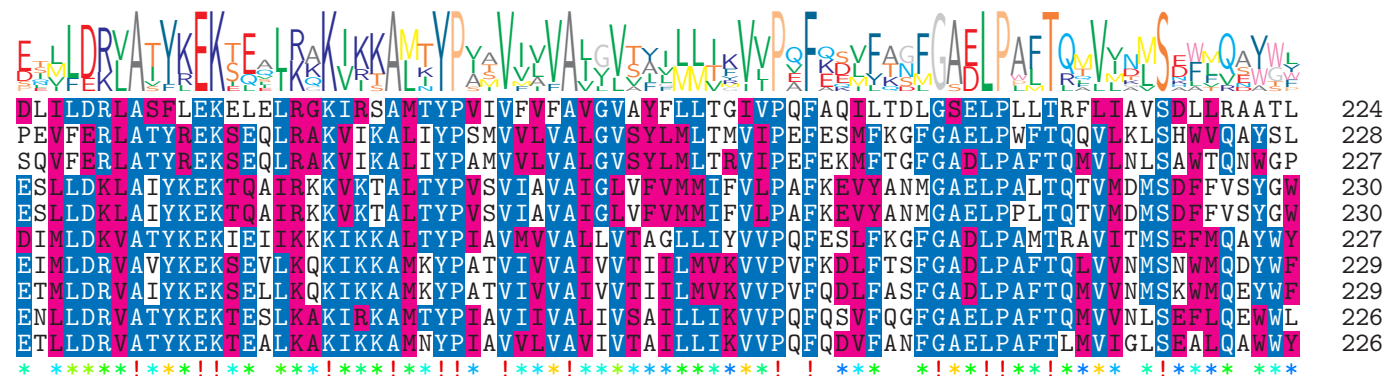
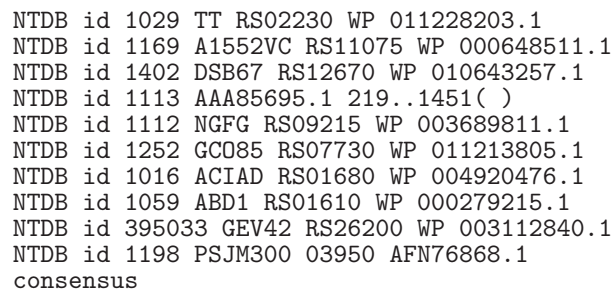
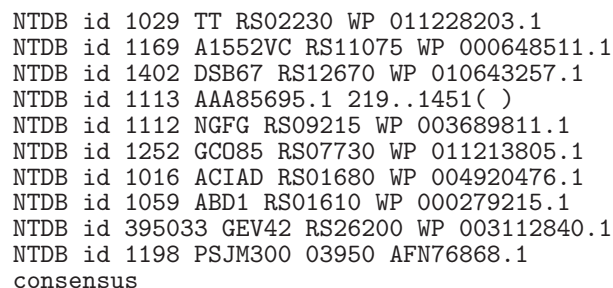


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NTDB id 1029 TT RS02230 WP 011228203.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1112 NGFG RS09215 WP 003689811.1
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 395033 GEV42 RS26200 WP 003112840.1
NTDB id 1198 PSJM300 03950 AFN76868.1
consensus

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NTDB id 1029	TT RS02230 WP 011228203.1	PLLLILAVALFFAYRWY.YGTPQGRRV	IDRLKLRLPVFGNINRKTAVARFSRTLALLLSSGVNIVEALDITKGTAGNSVVE	303
NTDB id 1169	A1552VC RS11075 WP 000648511.1	WAFIAIAAAIFGLKALRKN	SFQIRLKT SRLGLKFPITIGNVLA KASIAKFSRTLATSFAAGIPILASLKTTAKTSGNVHFE	308
NTDB id 1402	DSB67 RS12670 WP 010643257.1	FIGLSFVSLISGKIMSQRSDS	FRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSKTSGNMHYQ	307
NTDB id 1113	AAA85695.1 219..1451()	MVLIALGFAYIRFLKLRKARS	IKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1112	NGFG RS09215 WP 003689811.1	MVLIALGFAYIGFLKLRKARS	IKIQRMDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1252	GC085 RS07730 WP 011213805.1	IIIFGALGGVVVSFFYAKN	HSLEFAQTIDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIYA	307
NTDB id 1016	ACIAD RS01680 WP 004920476.1	ILILVIGAAIAGFLEARKRSK	RFRDQLDRLVLRLPVIGDLVYKAIARIYSRTLATTFAAGVPLIDALASTAGATNNTVYE	309
NTDB id 1059	ABD1 RS01610 WP 000279215.1	IMIIAIGAVIAAFLEAKRSK	KFRDGLDKLALKLPFGDLVYKAIARIYSRTLATTFAAGVPLIDALESTAGATNNVIYE	309
NTDB id 395033	GEV42 RS26200 WP 003112840.1	AVIVGVGAIGFTFKELHKRSK	KFRDRTLDRITLKLPIFGGIVYKSAVARYARTLSTTFAAGVPLVDALDSVSGATGNIVFK	306
NTDB id 1198	PSJM300 03950 AFN76868.1	VVLAGFVGAAYAFKQAHTRSE	KFRNWFDRMLMKVPVVGDI LYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVR	306
consensus		*****	*****!*****!*****!*****!*****!*****!*****!*****	

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NTDB id 1029	TT RS02230 WP 011228203.1	EIVEAAKLKIQGDPLNLT	LAQHPFVFPMPVSSMVAIGEETGALDTMLS	SKVADFYEREVDEAVASLTAAIEPLMITFLGV	383				
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NTDB id 1402	DSB67 RS12670 WP 010643257.1	LAIEEVYRD	TAAAGMPMYIAMR.HCHVFPELVLQ	VMVIGEESGRLLDDMLNKIAAIYEF	EVNDNTVDNLGKILEPLIIVFLGV	386			
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTR	VIQGLSMTSGMR.ATELFPNMMLQMS	SIGEESGLDDMLNKA	AEFYEDVDNAV	GWLSAMMEPTIILILGL	389		
NTDB id 1112	NGFG RS09215 WP 003689811.1	EATREIRTR	VIQGLSMTSGMR.ATELFPNMMLQMS	SIGEESGLDDMLNKA	AEFYEDVDNAV	GRLSAMMEPTIIVILGL	389		
NTDB id 1252	GC085 RS07730 WP 011213805.1	KATDKIRE	EVATGQQMFIAME.NTHLFPNMV	IQMVAIGEESGAL	EKMLS	SKVADFYEEV	NNAVDALSSLLEPTIIMSILGI	386	
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIRE	DVSTGQQLNFAMR.VSNRFPTMA	IQMVAIGEESGAL	DEMLDKVAN	YYESEVD	HAVDGLTSMMEPLIMAILGI	388	
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIRE	DVATGQQLQFAMR.ISNRFPSMA	IQMVAIGEESGAL	SMLDKVAT	YYENEVD	NAV	DGLTSMMEPLIMAILGV	388
NTDB id 395033	GEV42 RS26200 WP 003112840.1	NAVSKI	KQDVSTGQQLNFAMR.TTSVFPNMA	IQMTAIGEESGL	DEMLSKVAS	YYEEVD	NAV	DGLTSMMEPLIMAILGV	385
NTDB id 1198	PSJM300 03950 AFN76868.1	SATN	KIKSDVSSGMQLNFAMR.TTGT	FPSMAVQMTAIGEESGAL	DEMLSKVAT	FYEDVDNM	VDGLTALMEPMIMAVLGV	385	
consensus		*****	*****	*****	*****	*****	*****	*****	*****

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NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIIVACMFLPLFKIIGT	LSVQ	406				
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVVAMYLP	PIFNLM	SVLG..	408			
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NTDB id 1113	AAA85695.1 219..1451()	VIGTLLV	AMYLP	PIFN	LG	NVVA*	410	
NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLV	AMYLP	PIFN	LG	NVVA..	410	
NTDB id 1252	GC085 RS07730 WP 011213805.1	LVGGLVV	AMYLP	PIFK	LG	SAV...	406	
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLV	I	AMYLP	PIFQ	MG	SVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLV	I	AMYLP	PIFQ	MG	SVV...	408
NTDB id 395033	GEV42 RS26200 WP 003112840.1	LVGGLI	V	AMYLP	PIFQ	LG	NVVG..	406
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLI	I	AMYLP	PIFQ	MG	SVV...	405
consensus		***!*****	***!*****	***!*****	***!*****	***!*****	***!*****	

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