

logo

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NTDB id 1029 TT RS02230 WP 011228203.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
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 1069560 ACFACP RS24220 WP 016253888.1
NTDB id 1198 PSJM300 03950 AFN76868.1
consensus
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[illegible]

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NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1112 NGCF RS09215 WP 003689811.1
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consensus
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E	L	D	R	V	A	Y	K	E	K	E	L	R	A	K	I	K	K	A	M	T	Y	P	Y	A	V	V	A	V	L	L	L	V	V	P	F	Q	S	V	F	A	G	F	G	A	E	L	P	A	E	T	V	M	S	W	Q	Y	W	E																			
D	L	I	D	R	L	A	S	F	L	E	K	E	L	R	G	K	I	R	S	A	M	T	Y	P	V	I	V	F	V	F	A	G	V	A	F	L	L	T	G	I	V	P	Q	F	A	Q	I	L	T	D	L	G	S	E	L	P	L	L	T	R	F	L	I	A	V	S	D	L	L	R	A	A	T	L			
S	Q	V	F	E	R	L	A	T	Y	R	E	K	S	E	Q	L	R	A	K	I	V	P	A	M	V	L	V	A	L	G	V	S	Y	L	M	L	T	R	V	I	P	E	F	E	K	M	T	G	F	G	A	D	L	P	A	F	T	Q	M	V	N	L	S	A	W	T	Q	N	W	G	P						
P	E	V	F	E	R	L	A	T	Y	R	E	K	S	E	Q	L	R	A	K	I	V	P	A	M	V	L	V	A	L	G	V	S	Y	L	M	L	T	M	V	I	P	E	F	E	S	M	F	K	G	F	G	A	E	L	P	W	F	T	Q	Q	V	L	K	L	S	H	W	V	Q	A	Y	S	L				
E	S	L	D	K	L	A	I	Y	K	E	K	T	Q	A	I	R	K	K	V	K	T	A	L	T	Y	P	S	V	I	A	V	A	I	G	L	V	F	V	M	M	I	F	V	L	P	A	F	K	E	V	Y	A	N	M	G	A	E	L	P	A	L	T	Q	T	V	M	D	M	S	D	F	F	V	S	Y	G	W
E	S	L	D	K	L	A	I	Y	K	E	K	T	Q	A	I	R	K	K	V	K	T	A	L	T	Y	P	S	V	I	A	V	A	I	G	L	V	F	V	M	M	I	F	V	L	P	A	F	K	E	V	Y	A	N	M	G	A	E	L	P	A	L	T	Q	T	V	M	D	M	S	D	F	F	V	S	Y	G	W
D	I	M	L	D	K	V	A	T	Y	K	E	K	T	I	E	I	K	K	I	K	K	A	L	T	Y	P	I	A	M	V	V	A	L	L	I	Y	V	V	P	F	Q	S	F	E	L	F	K	G	F	G	A	D	L	P	A	M	T	R	A	V	I	T	S	E	F	M	Q	A	Y	W							
E	I	M	L	D	R	V	A	Y	K	E	K	S	E	L	K	Q	K	I	K	K	A	M	K	Y	P	A	T	V	I	V	A	I	V	T	I	I	L	M	V	K	V	V	P	V	F	Q	D	L	F	T	S	F	G	A	D	L	P	A	F	T	Q	M	V	N	S	M	S	N	W	M	Q	D	Y	W			
E	T	M	L	D	R	V	A	Y	K	E	K	S	E	L	K	Q	K	I	K	K	A	M	K	Y	P	A	T	V	I	V	A	I	V	T	I	I	L	M	V	K	V	V	P	V	F	Q	D	L	F	A	S	F	G	A	D	L	P	A	F	T	Q	M	V	N	S	M	S	K	W	M	Q	E	Y	W			
E	N	L	D	R	V	A	T	Y	K	E	K	T	E	S	L	K	A	K	I	K	K	A	M	T	Y	P	I	A	V	I	V	A	L	I	V	S	A	I	L	L	I	K	V	V	P	Q	F	Q	S	V	F	E	G	F	G	A	E	L	P	A	F	T	Q	M	I	V	N	L	S	E	F	M	Q	E	W	W	
E	T	L	D	R	V	A	T	Y	K	E	K	T	E	A	L	K	A	K	I	K	K	A	M	N	T	Y	P	I	A	V	L	V	A	I	V	T	A	I	L	L	I	K	V	V	P	Q	F	Q	D	V	F</																										

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NTDB id 1029	TT RS02230 WP 011228203.1	PLLLLAVALFFAYRW.YYGTIPQGRRV	IDRLKLRPLVFGNINRKTAVARFSRTLALLSSSGVNIVEALDITKGTAGNSVVE	303
NTDB id 1402	DSB67 RS12670 WP 010643257.1	FIGLSFVSLISGKIMSQRSDS	FRLLAARSSLRVPILGPVLSKAAIAKFSRTLATSFSAGIPILTALKTTSTKTSGNMHYQ	307
NTDB id 1169	A1552VC RS11075 WP 000648511.1	WAFIAIAAAIFGLKALKRNSFQIRLKT	SRIGLKFPPIIGNVLAKASIAKFSRTLATSFAAGIPILASLKTAKTSGNVHFE	308
NTDB id 1113	AAA85695.1 219..1451()	MVLIALGFAIYRFLKLRKRSIKIQR	MDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1112	NGFG RS09215 WP 003689811.1	MVLIALGFAIYGFLLKLRKRSIKIQR	MDAILLRMPIFGDIVRKGTIARWGRTTATLFAAGVPLVDVLDSTAGAAGNLIYE	310
NTDB id 1252	GC085 RS07730 WP 011213805.1	IIFGALGGVVYSFFYAKNHSLEFAQT	IDRVMLKLPVIGPILEKAAIARFARTLSITFAAGLPLVEALKSVAGATGNIYA	307
NTDB id 1016	ACIAD RS01680 WP 004920476.1	ILILVIGAAIAGFLEARKRSKFRDQ	LDRLVLRPLVIGDILVYKAIARYSRTLATTFAAGVPLIDALASTAGATNNTVYE	309
NTDB id 1059	ABD1 RS01610 WP 000279215.1	IMIIAIGAVIAAFLEAKRSKFRDGL	DKLALKLPIFGDLVYKAIARYSRTLATTFAAGVPLIDALESTAGATNNTVYE	309
NTDB id 1069560	ACFACP RS24220 WP 016253888.1	FIILAIIFGFAPKELHKRSQKFRDT	LDRTLKLPIFGGIVYKSAVARYARTLSTTFAAGVPLVDALDSVSGATGNIVFK	306
NTDB id 1198	PSJM300 03950 AFN76868.1	VVLAGFVGAAAYAFKQAHTRSEKFR	NWFDRLMLKVPVVGDIYKSSVARFARTLSTTFAAGVPLVDALDSVAGATGNVVR	306
consensus		*****	*****!*****!*	

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NTDB id 1029	TT RS02230 WP 011228203.1	EIVEAAKLKIQQGDPLNLTLAQHPFV	FPPMVSSMVAIGEETGALDMLSKVADFYEREVDNAVSLTAAIEPLMITIFLGV	383
NTDB id 1402	DSB67 RS12670 WP 010643257.1	LAIEEYVRDIAAGMPMYIAMR.HCHV	FPPELVLMQVMIGEESGRLLDMLNKIAAIYEFVDNTVDNLSTILEPLIIVFLGV	386
NTDB id 1169	A1552VC RS11075 WP 000648511.1	TAINEYVRDIAAGMPMYIAMR.NTEA	FPPELVLMQVMIGEESGRLLDMLNKVATIEFEVDNTVDNLGKILEPLIIVFLGT	387
NTDB id 1113	AAA85695.1 219..1451()	EATREIRTRVIQGLSMTSGMR.ATEL	FPNMMLQMSSIGEESGRLLDMLNKAAEFYEVDNAVGLSAMMEPIIILILGL	389
NTDB id 1112	NGFG RS09215 WP 003689811.1	EATREIRTRVIQGLSMTSGMR.ATEL	FPNMMLQMSSIGEESGRLLDMLNKAAEFYEVDNAVGLSAMMEPIIIVILGL	389
NTDB id 1252	GC085 RS07730 WP 011213805.1	KATDKIREEVATGQGMFIAME.NTHL	FPNMVIQMV AIGEESGALEKMLSKVADFYEEVNNAVDALESSILEPIIMSILGI	386
NTDB id 1016	ACIAD RS01680 WP 004920476.1	QAVLKIREDDVSTGQQLNFAMR.VSNR	FPTMAIQMV AIGEESGALDEMLDKVANYYESEVDHVDGLTSMMEPLIMAILGI	388
NTDB id 1059	ABD1 RS01610 WP 000279215.1	KAVMKIREDDVATGQQLQFAMR.ISNR	FPSMAIQMV AIGEESGALDSMLDKVATYYENEVDNAVGLTSMMEPLIMAILGV	388
NTDB id 1069560	ACFACP RS24220 WP 016253888.1	NAVSKIQQDVSTGMLNFSMR.TTST	VFPNMAIQMTAIGEESGRLLDEMLSKVASYYEEVDNAVDNLTTLMEPMIMAVLGV	385
NTDB id 1198	PSJM300 03950 AFN76868.1	SATNKKISDVSSGMLNFSMR.TTGT	FPSMAVQMTAIGEESGALDEMLSKVATFYEVDNMVDGLTALMEPMIMAVLGV	385
consensus		***	***!*!!!!!!*!!!!!!*!!!!!!*!!!!!!*!!!!!!*!!!!!!*!!!!!!*	

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NTDB id 1029	TT RS02230 WP 011228203.1	IVGMIVAGMFLPLFKIIGTISVQ	406
NTDB id 1402	DSB67 RS12670 WP 010643257.1	VVGGLVTIAMYLPIFNLMSVLG..	407
NTDB id 1169	A1552VC RS11075 WP 000648511.1	VVGGLVVAMYLPIFNLMSVLG..	408
NTDB id 1113	AAA85695.1 219..1451()	VIGTLLVAMYLPLFNLGNVVA*	410
NTDB id 1112	NGFG RS09215 WP 003689811.1	VIGTLLVAMYLPLFNLGNVVA..	410
NTDB id 1252	GC085 RS07730 WP 011213805.1	LVGGLVVAMYLPIFKLGSAV...	406
NTDB id 1016	ACIAD RS01680 WP 004920476.1	LVGGLVTIAMYLPIFQMGSVV...	408
NTDB id 1059	ABD1 RS01610 WP 000279215.1	LVGGLVTIAMYLPIFQMGSVV...	408
NTDB id 1069560	ACFACP RS24220 WP 016253888.1	LVGGLIVAMYLPIFQLGNVVG..	406
NTDB id 1198	PSJM300 03950 AFN76868.1	LVGGLITIAMYLPIFQMGSVV...	405
consensus		***!*****!***!*****	

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