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Accession	Sequence	Position
NTDB id 378 SMU RS02690 WP 002263569.1		0
NTDB id 241 SP RS04015 WP 000882523.1		0
NTDB id 281 KZH43 RS03550 WP 000882517.1		0
NTDB id 245 SPD RS03860 WP 000882517.1		0
NTDB id 243 SPR RS03635 WP 000882517.1		0
NTDB id 85 BSU 00860 NP 387967.1	..MMFGRFTERAQKVLALAQEEALRLGHNNIGTEHILLGLVREGEGIAAKALQALGLGSEKIQKEVESLIG.....RGQEMS	75
NTDB id 610 V4T04 RS10165 WP 012897346.1	MKFENIKYTPITLDRILEKAEYYAHQYQYGTIESAHLILAAMATTSGSIAYSLLAGMNVDDSSDLL.....IDLEDLSSHVKVKR	77
NTDB id 287 SP RS11210 WP 001109712.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYSQDET	75
NTDB id 290 KZH43 RS10025 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYSQDET	75
NTDB id 289 SPD RS10700 WP 001109677.1	MNYSKALNECIESAYMVAGHFGARYLESWHLLIAMSNHSYSVAGATLNDYPYEMDRLEE.....VALELTETDYSQDET	75
NTDB id 329 STU RS10020 WP 011225298.1	...MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVPGSVAYLTFTDFEDRIHSEEIETA AAVLAMEKRPKDLSESDII	81
NTDB id 297 STER RS00545 WP 011680614.1	...MTIYSRKMQAIFHRAQLEAERFESPFLTWHVLLAMVEVTGSAVAYLTFTDFEDRIHSEEIETA AAVLAMEKRPKDLSESDII	81
NTDB id 60846 KE3 RS09330 WP 020917567.1	...MSEYSMKMQEVFSIAQYQAARFESPYLESWHVLLAMVAVHDSVAGLTFAEYQNKIAYEEYEAAAVLALGKSPLAD..VKNV	79
NTDB id 377 SMU RS09275 WP 002262344.1	...MTDYSLKMQEVFRLAQFEAARFESSYLESWHVLLAMVEIDSVAAGLSFAEFEADVRFEDYQAAAILAIGKKPKSS..SNDI	79
consensus	*** ** * * **** * **** *	

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NTDB id 281	KZH43 RS03550 WP 000882517.1	MLCQNCCK.INDS	TIH.LYTNLNG.KQKQIDLCQNCYKIIKTD	PNNSLFK	GMTDLNNRDFDP.FGD	FFN	64
NTDB id 245	SPD RS03860 WP 000882517.1	MLCQNCCK.INDS	TIH.LYTNLNG.KQKQIDLCQNCYKIIKTD	PNNSLFK	GMTDLNNRDFDP.FGD	FFN	64
NTDB id 243	SPR RS03635 WP 000882517.1	MLCQNCCK.INDS	TIH.LYTNLNG.KQKQIDLCQNCYKIIKTD	PNNSLFK	GMTDLNNRDFDP.FGD	FFN	64
NTDB id 85	BSU 00860 NP 387967.1	QTIHYTPRAKKVIEL	SMDEARKLGHSYVGTEHILLGLIREGEGVAARVLNN	LGVSL.NKARQVQL..QLL.			142
NTDB id 610	V4T04 RS10165 WP 012897346.1	STLRFSPRAEEVMTAA	SFLAIHNNSSEAVGTEHLLYALLQVEDGFGFLQLLKL	Q.....KINIVSLRK			138
NTDB id 287	SP RS11210 WP 001109712.1	TELPFSRRLQVLFDEAEY	VASVVHAKVLTGEHVLYAILHDSNALATRIL	ER.....AGFSY.EDKKDQVKIAALRR			145
NTDB id 290	KZH43 RS10025 WP 001109677.1	TLPFSRRLQILFDEAEY	VASVVHAKVLTGEHVLYAILHDSNALATRIL	ER.....AGFSY.EDKKDQVKIAALRR			145
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NTDB id 329	STU RS10020 WP 011225298.1	DLRAQSPALEAMLQEA	QGIIASVTGAVEVGSEHVLMAFLLHKDLMVCRLL	EV.....AGFQY.KDDSDKPRIIDLRR			151
NTDB id 297	STER RS00545 WP 011680614.1	DLRAQSPALEAMLQEA	QEIISVTGAVEVGSEHVLMAFLLHKDLMVCRLL	EV.....AGFQY.KDDSDKPRIIDLRR			151
NTDB id 60846	KE3 RS09330 WP 020917567.1	QFLEQSKALKDVLAF	AESICKVTGSTVGTEHVLYAMLNLNLDLFATRL	LEV.....AGFKY.KEDGDSARLLDLRK			149
NTDB id 377	SMU RS09275 WP 002262344.1	MLLEQSHALKRTLAE	AAISQVTHAKEVGTEHVLYAMLLNPNLLATRILEL	VGFHA.KDDGESIRLLDLRK			149
consensus		* * * *	*****!*****	***	* *	* ****	

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NTDB id	378	SMU RS02690 WP 002263569.1	D L N N F R A F N N Q D L P . N T P P T Q A G G G N G N G N . N . R R P G G P Q Q Q A S Q K P N G L E E F G I N L T D I A R K G E I D P V I G R D E E I T R V I E I L	147
NTDB id	241	SP RS04015 WP 000882523.1	D L N N F R P S S N . . T P . P I P P T Q S G G G Y G G N G G Y G S Q N R G S A Q T P P S S Q E K G L L E E F G I N V T E I A R R G D I D P V I G R D D E I I R V I E I L	146
NTDB id	281	KZH43 RS03550 WP 000882517.1	D L N N F R P S S N . . T P . P I P P T Q S G G G Y G G N G G Y G S Q N R G S A Q T P P S S Q E K G L L E E F G I N V T E I A R R G D I D P V I G R D D E I I R V I E I L	146
NTDB id	245	SPD RS03860 WP 000882517.1	D L N N F R P S S N . . T P . P I P P T Q S G G G Y G G N G G Y G S Q N R G S A Q T P P S S Q E K G L L E E F G I N V T E I A R R G D I D P V I G R D D E I I R V I E I L	146
NTDB id	243	SPR RS03635 WP 000882517.1	D L N N F R P S S N . . T P . P I P P T Q S G G G Y G G N G G Y G S Q N R G S A Q T P P S S Q E K G L L E E F G I N V T E I A R R G D I D P V I G R D D E I I R V I E I L	146
NTDB id	85	BSU 00860 NP 387967.1	 G S N E T G S S A A G T N S N A N T P T L D S L A R D L T A I A K E D S L D P V I G R S K E I Q R V I E V L	196
NTDB id	610	V4T04 RS10165 WP 012897346.1	E L E K R T G L K V P E S K K A V T P M S K R K M A K G V A E N S T T P T L D S V S S D L T E E A R L G K L D P M I G R E A E I D R L I H I L	209
NTDB id	287	SP RS11210 WP 001109712.1	N L E E R A G W T R E D L K . A L R Q R H R T . V A D K Q N S M A N M M G M P Q T P S G G L E D Y T H D L T E Q A R S G K L E P V I G R D K E I S R M I Q I L	222
NTDB id	290	KZH43 RS10025 WP 001109677.1	N L E E R A G W T R E D L K . A L R Q R H R T . V A D K Q N S M A N M M G M P Q T P S G G L E D Y T H D L T E Q A R S G K L E P V I G R D K E I S R M I Q I L	222
NTDB id	289	SPD RS10700 WP 001109677.1	N L E E R A G W T R E D L K . A L R Q R H R T . V A D K Q N S M A N M M G M P Q T P S G G L E D Y T H D L T E Q A R S G K L E P V I G R D K E I S R M I Q I L	222
NTDB id	329	STU RS10020 WP 011225298.1	S L E R N A G L S K Q D L K . A I H D L R K P K K S K A S A N F A N M M Q P P Q S S T G E L A D Y T K D L T A L A E S G N L D P I T I G R D E E I S R M I Q V L	229
NTDB id	297	STER RS00545 WP 011680614.1	S L E R N A G L S K Q D L K . A I H D L R K P K K S K A S A N F A N M M Q P P Q S S T G E L A D Y T K D L T A L A E S G N L D P V I G R D E E I S R M I Q V L	229
NTDB id	60846	KE3 RS09330 WP 020917567.1	S L S R N A G F T K E K I K . A I H D L R K P K K A T M G G A F S E M M K P P . S T A G E L S D F T R D L T E L A R Q G K L E P V I G R E K E V S R M V Q V L	226
NTDB id	377	SMU RS09275 WP 002262344.1	V I E R Y A G F S K E D I K . A I F E M R K P K K V K N S S S F S D L M K P P . S V T G E L A D F T R D L T E L A R Q G R L E P V I G R E Q E I S R M V Q I L	226
consensus			* * * * *	

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consensus

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NTDB id 377 SMU RS09275 WP 002262344.1
consensus

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NTDB	id	378	SMU RS02690 WP 002263569.1	KYKEMQSAKLDKENTPVITEKNTEVIVEEKTINIPVGELKEKEEQSQLIHLADDLKRTRVIGQDAAVDVKIAKAIRRNRVGLGTP	477
NTDB	id	241	SP RS04015 WP 000882523.1	KYKEMQKKKITDQDTPISEKTIIEHIIEQKTNIPVGDLKEKEEQSQLIHLEADLKSHVIGQDDAVDVKIAKAIRRNRVGLGTP	476
NTDB	id	281	KZH43 RS03550 WP 000882517.1	KYKEMQKKKITDQDTPISEKTIIEHIIEQKTNIPVGDLKEKEEQSQLIHLEADLKSHVIGQDDAVDVKIAKAIRRNRVGLGTP	476
NTDB	id	245	SPD RS03860 WP 000882517.1	KYKEMQKKKITDQDTPISEKTIIEHIIEQKTNIPVGDLKEKEEQSQLIHLEADLKSHVIGQDDAVDVKIAKAIRRNRVGLGTP	476
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NTDB	id	287	SP RS11210 WP 001109712.1	E..V.PVYKDLVTESDI LTTLSRLSGIPVQKLTQTD AKKYLNLEAE LH KRVIGQQDVASS ISRAIRRNQSGIRSH	538
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consensus				* * **** ** ***** ! * * * * * * * * * * * * * * * * * * *	

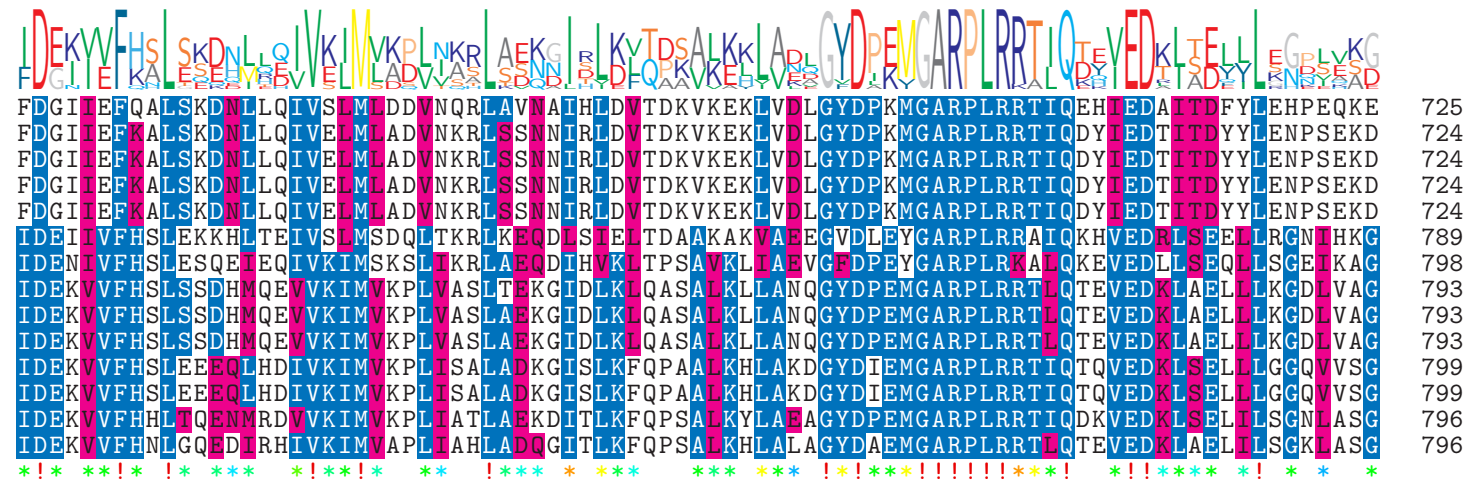
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consensus		

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- ☐ non conserved
- ☒ similar
- ☒ $\geq 50\%$ conserved