

NTDB id 1111 NGFG RS09220 WP 00368984.1	MSDI...VLSPEAV.PLAALVLGLLVGSFLNVVIYRVPVMMERGWTVFAKEHLNPLTDD	ESRTFNLMKPDSSCPKCRVP	76
NTDB id 1028109 AB4W10 RS22680 WP 002888947.1	MTTLAALS.LHFPVFWYGFLLFGLGALGSFYNNVVIYRLPRMLTQT.....ADDERITLSTP	GSSPCQCRQP	65
NTDB id 1080 FDQ49 RS18305 WP 022575844.1	MQDIIAYFIQNLTALYIAVALVSLCIGSFLNVVIYRTPRMMEQDWQQECQMLLNPEQPIIDHEKLTLTSKP	PASSCCPACHQP	80
NTDB id 1061 ABD1 RS18470 WP 001152280.1	MQDIIAYFIQNLTALYIAVALVSLCIGSFLNVVIYRTPKMMEQDWQQECQMLLNPEQPIIDHERLTLNKPA	SSCPACQQP	80
NTDB id 1170 A1552VC RS11080 WP 000418747.1	.MELFFYFY...PWLFPPVLATLFGLIVGSFLNVVIYRLPKIMEREWRAECAASFPEYGITPPEGKLTLSLPR	STCPHCQT	76
NTDB id 1403 DSB67 RS12675 WP 010643256.1	.MEVFQYY...PWLFVVVFATIFGLIVGSFLNVVIYRLPKIMELEWRRECAESFPEYKIEPPKETLTLSPR	SSCQCCTQ	76
consensus	* * * * *	* * * * *	*

NTDB id 1111	NGFG RS09220 WP 003689814.1	IRAWQ	NIPIVSYLLLRGK	CAS	CQT	KIS	IRYPLIELLT	GVLFGLVAWQ	YGWSWIT	LGGLILTAFLIS	LTFFIDADTQYL	PDS	156	
NTDB id 1028109	AB4W10 RS22680 WP 002888947.1	IARWD	NIPILSFWLGR	RARC	CQA	PI	AWSYPLTE	LATGLFILTALLA	APGLAGLVL	LSFLLI	LARIADARTQLLP	DR	145	
NTDB id 1080	FDQ49 RS18305 WP 022575844.1	IRWYQ	NIPILSWLVLRG	KCGH	CHQ	HPS	IRYPATIELLT	TMLCSLVVVMV	FGPTIQM	LFGLVLTWVLIA	LTFIDFTDQLLP	DR	160	
NTDB id 1061	ABD1 RS18470 WP 001152280.1	IRWYQ	NIPVISWLVRG	KCGH	CHQ	HPS	IRYPAIELLT	TMLCSLVVVMV	FGPTIQM	LFGLVLTWVLIA	LTFIDFTDQLLP	DR	160	
NTDB id 1170	A1552VC RS11080 WP 000418747.1	IRVID	NIPILSWALRG	QC	SHCK	APIS	ARYPLIELLT	ALMSLVIA	THFPFGVF	AVALLFFSYV	LIAATFIDDL	TL	156	
NTDB id 1403	DSB67 RS12675 WP 010643256.1	IRIRD	NIPVISWLVRG	KCGH	CQA	PI	NARYPLIELLT	AFCSGFIAFH	FGFSYFT	VALVFFTF	VLIAATFIDL	DTMLLP	DR	156
consensus		!!*	!!!!*!*	*!!!!**	**!	*	*****!	****	*****	*****	*****!	***!!!	!!	

[illegible]

NTDB id 1111	NGFG RS09220 WP 003689814.1	L I G L V A A I V M R V A K G R H F A F G P A L T V S G W I I F T A N D S V W R A V N W L T H P V R . . .	286
NTDB id 1028109	AB4W10 RS22680 WP 002888947.1	A S G L V W T L L Q R L W T R Q S L Q Q P L A F G P W L A L A G S I F L W Q Q M V	266
NTDB id 1080	FDQ49 RS18305 WP 022575844.1	L L G A I I G I I L L X L R N D . . N Q P F A F G P Y I A I A G W V A F L W G D Q I . . . M K I Y L G G	286
NTDB id 1061	ABD1 RS18470 WP 001152280.1	L L G A I I G I I L L X L R N D . . N Q P F A F G P Y I A I A G W V A F L W G D Q I . . . M K I Y L G G	286
NTDB id 1170	A1552VC RS11080 WP 000418747.1	V V G V I F G L I Q L R Q Q K K G I D M A F P F G P Y L A I A G W F A L L W G D K V . . . I D W Y F T T W V G Q P L	291
NTDB id 1403	DSB67 RS12675 WP 010643256.1	V V G V I F G L I Q L R L Q K Q G I E K A F P F G P Y L A I A G W V S L I W G H Q I . . . L N W Y F T S I L G V . .	289
consensus		** ! * * ** *	* * ! ! ! * * * * ! * * * * * *

Sequence	Position
IRAWQNIPIVSYLLLRGKCASQTKISIRYPLIELLTGVLFGLVAWQYQGSWITLGLILTAFLISLTFIDADTQYLPDS	156
IAWRDNIPLLSFLWLGRARCCQAPIAWSYPLTELATGLLFTLAGALLAPGIPLAGGLVLSFLILARIDARTQLLPDR	145
IRWYQNIPLISWLVLRGKCGHCQHPISIRYPAIELLTMLCSLVVMVFGPTIQMLFGLVLTWVLIALTFIDFDTQLLPDR	160
IRWYQNIPIVISWLVLRGKCGHCQHPISIRYPAIELLTMLCSLVVMVFGPTIQMLFGLVLTWVLIALTFIDFDTQLLPDR	160
IRVIDNIPLLSWLALRGQCSHCKAPISARYPLIELLTALMSLVIAITHFPFGFVAVALLFFSVYLIAATFIDFDTLLLPDQ	156
IRIRDNIPVISWLVLRGKCHNCQAPINARYPLIELLTAFCSGFIATFHFGFSYFTVALVFFTEVLIAATFIDLDTMLLPDQ	156

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