

logo

NTDB id 1419 SGL RS12550 WP 010873252.1	MKEILKTLTEAMTLPEDSYSEQDAEFLEIFIEEIEEIFVDLQPLINKWMQSENIATLTEIRRHFTLKGSGRMIGAKSSAELAWT	0
NTDB id 413 AAK55817.1 141..845()		0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	MKEILKTLTEAMTLPEDSYSEQDAEFLEIFIEEIEEIFVDLQPLINKWMQSENIATLTEIRRHFTLKGSGRMIGAKSSAELAWT	85
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	VEDTLNLRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQQLQQQSLEPALEELLQLSHTLMAETVTG	0
NTDB id 413 AAK55817.1 141..845()		0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	VEDTLNLRVINQSLQLTPTIQSYVQLVFKFYFLKLVDNFKQKRAHTLDFRPLILLGQQQLQQQSLEPALEELLQLSHTLMAETVTG	170
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	LELDYIEQDSLAEPIIQATHTEIEINLDETTLTFMEEAEEHLATIHQFLDQELHQYDSYNALIRALHTLRGSSAMAQVETIFEAS	0
NTDB id 413 AAK55817.1 141..845()		0
NTDB id 374 SMU RS06885 WP 002262930.1		0
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consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	TKVEHLFKILLQEELSSHSEEILLQLQEYREFVRDLSLELLSRYSSSEQLEARLLQFNQSWDAYVEQHGDRTDPLMPSHGLVSQQLQ	0
NTDB id 413 AAK55817.1 141..845()		0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	TKVEHLFKILLQEELSSHSEEILLQLQEYREFVRDLSLELLSRYSSSEQLEARLLQFNQSWDAYVEQHGDRTDPLMPSHGLVSQQLQ	340
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	LDVSELDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMLGLHEYTSQLKESYEVLLDKPALLQSDYIFEIYQKAHQQLI	0
NTDB id 413 AAK55817.1 141..845()		0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	LDVSELDAELDFEKGIRNEFPDYLERLSEQADLLLQHTHSQAMLGLHEYTSQLKESYEVLLDKPALLQSDYIFEIYQKAHQQLI	425
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	QLFDALAAGQVRGVVKQHQSI	LEELKLYTQYTPDISNDLPQQDSTSFEPIYNIEPEPEV	MTSDPN	6
NTDB id 413 AAK55817.1 141..845()				0
NTDB id 374 SMU RS06885 WP 002262930.1				0
NTDB id 1046 HON27 RS03130 WP 168726941.1	QLFDALAAGQVRGVVKQHQSI	LEELKLYTQYTPDISNDLPQQDSTSFEPIYNIEPEPEV	MTSDPN	510
NTDB id 1417 SGL RS04200 WP 014407071.1				0
NTDB id 1047 HON27 RS03110 WP 000389061.1				0
consensus				0

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NTDB id 1419 SGL RS12550 WP 010873252.1	ISSTQVNRNFDADLLDIFLEEAEELLE	GTAAQAFETFEEL	DAFNNLYR	HTLKGGANMVQATYLG	LIAHELES	IYERLIQK	31
NTDB id 413 AAK55817.1 141..845()							0
NTDB id 374 SMU RS06885 WP 002262930.1							0
NTDB id 1046 HON27 RS03130 WP 168726941.1	ISSTQVNRNFDADLLDIFLEEAEELLE	GTAAQAFETFEEL	DAFNNLYR	HTLKGGANMVQATYLG	LIAHELES	IYERLIQK	595
NTDB id 1417 SGL RS04200 WP 014407071.1							0
NTDB id 1047 HON27 RS03110 WP 000389061.1							0
consensus							0

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NTDB id 1419 SGL RS12550 WP 010873252.1	QLVVTSDLIDFIRLVQDDLADRLQIMREQQLDYAAPYTINALKRAEQ	NSNLP	LVVLF	ESTV	SSQKYS	SEIIDEIPVEL	60
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consensus							0

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NTDB id 374 SMU RS06885 WP 002262930.1				0
NTDB id 1046 HON27 RS03130 WP 168726941.1	EPALAELETHHDQVFD	ASCELRTPVEMITTVTSQENEVAANEQDIEAVVEQTFLEEATELLEMAESLLKQWFEQRTNR	ALFTDEDAPTTAIDPFESSSWLEIDQMMEADPLA	759
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NTDB id 1047 HON27 RS03110 WP 000389061.1				0
consensus				0

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NTDB id 1419 SGL RS12550 WP 010873252.1	SIPETNAPAYQTAGGLDDNDLAE	LQDLLGVGDVEPAITNPGLHSFAGADRVTPLTNEVLL	FA	AIDDLG	LINAPVL	194
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NTDB id 374 SMU RS06885 WP 002262930.1						0
NTDB id 1046 HON27 RS03130 WP 168726941.1	S		ILL	QLQRAVHSLKGGARMVGLEAVQAIAYQLENAFEQFALHHFNSNIYDHLL		812
NTDB id 1417 SGL RS04200 WP 014407071.1						0
NTDB id 1047 HON27 RS03110 WP 000389061.1						0
consensus						0

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NTDB id 1419 SGL RS12550 WP 010873252.1	EEFASWDEAFALFKDAIFNHNYSFEDGLTDSLANKSFATFEHPPFSTPTALEEAREDEFKSLERALLEQADSSYMTFISGMGTETPLMREAWES	266
NTDB id 413 AAK55817.1 141..845()	DEEFSF.....TELETLIDTPAPKSFATISHPPFRLPVAMEEDEDEFKDLEALLEQADSSLGGGIAGMGGARLPARP...R	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	ESAIAWLKDAIFNHNYSQHFDGLQSSLENIQF..FETTIQIPTKLTRA.DLFSS.EP.....VMTFIQGDGTEPPPPMGAWEQ	885
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NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	TYREBSNNQTMRVPAKSCHEMSTNLSCEMYNRNRLESDREBSSTLYMMLNQRLSDQLRMVBSLEYETTLEGALLASRSTNSR	351
NTDB id 413 AAK55817.1 141..845()	QVKSRSFEQTMRVPIKQLDNLSNLIGELVVKRNRLEQDQERLRQFLDNLLNQAQNLSDVGGRMQDLYERTLLEGALLASRSTNSR	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
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consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	HHSSKTTYPDARITAKSSSTSRYSCTDLEMDSTSHNPLSRMEEAYBYVESKSTISYKYBETESYARTSRYSYJAEQEOMR	436
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NTDB id 1046 HON27 RS03130 WP 168726941.1	IAKHGIEHSRYTDFDPLEMDQYSSLNQLSKSLAESASDLVDFKNTLSDKIRDTESLLLQQSRIQAEIQEGLMR	1029
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consensus		

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consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	EQGTSYMYYSDDGQGLNENVRQKAYEKGLIRMEAQSLQSEYYSLLFHAQFSTKEISBSISGRGVGLDWBSISYKSTSGHYS	606
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NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	RQGTDVVVVVSDDGQIDVEKVRQKALLAGLIKP..EQDLEQQDILQLIFHPGLSTAEQVTQISGRGVGLDVVQSDIKSLGGHVS	1197
NTDB id 1417 SGL RS04200 WP 014407071.1		0
NTDB id 1047 HON27 RS03110 WP 000389061.1		0
consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	YESYVGRGTTFTIRYPETYSYEBALMCKYABBSFAFPMQCYEBTRBYEPKSTYEQYFESGQKLYEYENEAALLLKRYPLRYLENYMR	690
NTDB id 413 AAK55817.1 141..845()	IESTVGKGTTFITIRLPLTLISICKALCCLSDRARIAAFPMGDGVEDTRDYLPKDIVTD.EDGQKCVKYGKEALLLPLYPLKDLLNYNR	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	VESVYGQGTTFITIRVPTTVAVSDALMVKVADQQFAIPLAQIDRIIRVSPASLEQYFESPQELFEYEN.....KRYPLRYLSEFVG	1277
NTDB id 1417 SGL RS04200 WP 014407071.1		0
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consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	RLPFRRLNGGCKQEEEDSLFVIMARANSGRITVALPYDQYLGEEQIVVKP EGPFRSPES AGATYRCDGSYMP ADYNTARETAQS	774
NTDB id 413 AAK55817.1 141..845()	QLSRGSSVYGGKQEEEDVVRVIIARGSSGNLLALQIDQVLGEEE.IVIKQIEGPPIPKPPGIAGATVRGDGSIMPIADVLELIEIAQG	0
NTDB id 374 SMU RS06885 WP 002262930.1		0
NTDB id 1046 HON27 RS03130 WP 168726941.1	NQPIPRLNG...VMYSLPVLMIKANNGQTVALLVDQLIGSRAQIVVKPIGQQFSSIGAIAGATILGDGQVCLILDGQNIARQIQS	1359
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consensus		

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NTDB id 1419 SGL RS12550 WP 010873252.1	RLRTHKDESEAYVRKTLTPRVEDBENCAIMYIEFESVSRKLETPDAVESTEPENFQWQKAAKRCIMXYLELEEN	858
NTDB id 413 AAK55817.1 141..845()	MKKILIVDDEKPTSDIIFKNMTKEGYEVVTAFNGREALEQFEAEQP.DIIILDLMLEID	59
NTDB id 374 SMU RS06885 WP 002262930.1	MKKILIVDDEKPTSDIIFKNLAKEGYDTITAFDGREALSKYEEENP.DLIILDLMLEID	59
NTDB id 1046 HON27 RS03130 WP 168726941.1	TQRHKQLSEAVY.....RQRESDERRLLIMIVDDSVTVRKVTSRLLERQGYDVTAKDGVDAIEQENIKP.DLMLLDIEMPRMD	1437
NTDB id 1417 SGL RS04200 WP 014407071.1	MNAVILVEDSSSQREMTSGILKDHGQVTTIACDGVAELEKIQNFSP.DLVVLDIVMPRMN	59
NTDB id 1047 HON27 RS03110 WP 000389061.1	MEDAFQNLKVMVIVDDSKTIRRTAETLLQREGCEVITAVDGFELSKIAEANP.DIVFVDIMPRMD	65
consensus	*****! * **** * * !*****! *! *!*** * ! !*****!***!***	

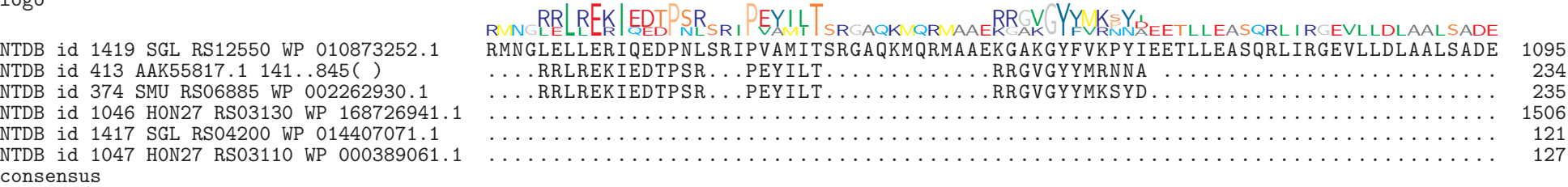
logo

NTDB id 1419 SGL RS12550 WP 010873252.1	GLEVLKELIRK...TSSVPILMLSSKDSEFDKVLGELGADYVTKPFSNR...ELLARIKALLRR...ESMPVSYBENSKPSR...I	942
NTDB id 413 AAK55817.1 141..845()	GLEVLSETQADEELSSIPVALLTSRGADRHKKVAAKTGATGYFTKPYTEKDIIDAANRMINGEVLLPGSTRKTNSI.LSRFKKAR	138
NTDB id 374 SMU RS06885 WP 002262930.1	GLEVAKEVRK...NSHVPIIMLSAKDSEFDKVLGELGADYVTKPFSNR...ELLARVKAHLRRTENIESAVAEENASGIPEI..II	139
NTDB id 1046 HON27 RS03130 WP 168726941.1	GFEVLNLVRHHDMMHQYMPITIMTSRTGEKHRERAFSLGVSQYMGKPFQEEELLENIDALLVAFESEVKS.....	1506
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NTDB id 1047 HON27 RS03110 WP 000389061.1	GYTCALIKNSQNYQNIPVIMLSSKDGLFDQAKGRVGSDEYTKPFSKDELLNAIRNHVSS.....	127
consensus	! ** ** *!***** ** * *! ** !*!!** ** * *	

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NTDB id 1419 SGL RS12550 WP 010873252.1	GNFSEEAPTIVRSNPGTL.....R.....STVLIIDDSVMVREMLSMTFKKADYHTETARDGQDAWEKLSGLPCDLILCDIEMP	1017
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NTDB id 374 SMU RS06885 WP 002262930.1	GDQLILPDFAVAKKRGTEVELTHREFELLHHLATHGTQVMTREHLLT.....VWGYDYFG...DVRTVDVTV.	204
NTDB id 1046 HON27 RS03130 WP 168726941.1		1506
NTDB id 1417 SGL RS04200 WP 014407071.1		121
NTDB id 1047 HON27 RS03110 WP 000389061.1		127
consensus		

logo



 non conserved
 similar
 ≥ 50% conserved