

logo

NTDB id 1361 HI 0985 AAC22646.1	MNDITVITLRLIMQVPKLGGVGTIDKILSNITLNEILNYDV.....AFRQMCWGA.IQIRRWFKPEAKFIIPALV...WS	70
NTDB id 626 LCA RS04960 WP 011374694.1	MLTKNQQLLLKVHLAAGFGTISELR.....LAAMLSTSHWALSALEIAQTARLPERYWPTFQASFQSTTLQRQCID	71
NTDB id 599 KW2 RS05940 WP 021037268.1	.MITNFDLFRW.KKACMTNLGVNK.....LLKFFRK.YDRKISLRQMCQVAQVK..SIPNFIQYKIQDVK..KLR	65
NTDB id 525 SMSK321 RS06295 WP 000705298.1	MKITNYEYIKL.KKSGLTNQIILK.....VLEYGEN.VDQELLGDIADISGCR..NPAVFMERYFQIDDA.HLEK	66
NTDB id 267 KZH43 RS05590 WP 000705306.1	MKITNYEYIKL.KKSGLTNQIILK.....VLEYGEN.VDQELLGDIADISGCR..NPAVFMERYFQIDDA.HLSK	66
NTDB id 226 SPD RS05990 WP 000705306.1	MKITNYEYIKL.KKSGLTNQIILK.....VLEYGEN.VDQELLGDIADISGCR..NPAVFMERYFQIDDA.HLSK	66
NTDB id 192 SPR RS05715 WP 000705306.1	MKITNYEYIKL.KKSGLTNQIILK.....VLEYGEN.VDQELLGDIADISGCR..NPAVFMERYFQIDDA.HLSK	66
NTDB id 157 SP RS06205 WP 000705306.1	MKITNYEYIKL.KKSGLTNQIILK.....VLEYGEN.VDQELLGDIADISGCR..NPAVFMERYFQIDDA.HLSK	66
NTDB id 497 SM12261 RS05565 WP 000705318.1	MKITNYEYIKL.KKSGLTNQVLA.....VLEYGEN.VDQELLGDIADISGCR..NPAVFMERYFQIDDA.HLEK	66
NTDB id 1119518 EL071 RS08320 WP 001015250.1	..MNHFELFKL.KKAGLTNLNINN.....IINYLKKNSLTSLSVRNMAVVSKCK..NPTFFFIENYKQIDDLK..KLRQ	65
NTDB id 407 SMU RS04605 WP 002262865.1	..MDNFQLFKL.KKAGLTNLNIN.....IIDYEER.TQKSLSLRDMMAVVSKNK..KPLIFMEHYKNIDSK..ALRK	64
consensus	*****	

logo

NTDB id 1361 HI 0985 AAC22646.1	QKEGNHLVNYFSPFYPLLKQTASFPLLFGKNTALISQRQMAMVGSRYCTTYCEYWAKIFATELSLAGFTITSGLALG	150
NTDB id 626 LCA RS04960 WP 011374694.1	HEVBTTYLTILDKDYPQRILLETLPPVLLFYRCDLRLLLKQPCIAVVGARQATHYSKQSTLEQLLQGLT.A.TTITSGLAQG	149
NTDB id 599 KW2 RS05940 WP 021037268.1	DYKKFSSFSILDDLYPERLREIYNPPVLLFYQGNIDLLKNPKLAFVGSRLAGQSGIKSVGKIVTELN.QSFTIVSGLAKG	144
NTDB id 525 SMSK321 RS06295 WP 000705298.1	EFKKIPFSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRSCSKQGAKSVEKVIQGLE.NELVIVSGLAKG	145
NTDB id 267 KZH43 RS05590 WP 000705306.1	EFQKFPFSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKG	145
NTDB id 226 SPD RS05990 WP 000705306.1	EFQKFPFSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKG	145
NTDB id 192 SPR RS05715 WP 000705306.1	EFQKFPFSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKG	145
NTDB id 157 SP RS06205 WP 000705306.1	EFQKFPFSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKG	145
NTDB id 497 SM12261 RS05565 WP 000705318.1	EFQKFPFSFSILDDCYPWDLSEIYDAPVLLFYKGNLDLLKFPKVAVVGSRACSKQGAKSVEKVIQGLE.NELVIVSGLAKG	145
NTDB id 1119518 EL071 RS08320 WP 001015250.1	EFKKFPVLSILDSNYPLELKEIYNPPVLLFYQGNIELLSKPKTAVVGARQASQIGCQSVKKTIKETN.NQFVIVSGLARG	144
NTDB id 407 SMU RS04605 WP 002262865.1	EFNRFPSSLILDKEYPLELKNIYNPPVLLFYQCDLDDLARPKLAVVGSRNASQMCVAIVKKTIQDLS.KQFVITSGLARG	143
consensus	*****!!!!!!	

logo

NTDB id 1361 HI 0985 AAC22646.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQDYISNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	230
NTDB id 626 LCA RS04960 WP 011374694.1	ADAMAHEVALQRGLAPIGVIGTGINC SYPPQNEHLQ.QVVAEKGLLSEYALGTPARRYQFPARNKIIAGLCNLSIVTEA	228
NTDB id 599 KW2 RS05940 WP 021037268.1	IDTASHLSATIKTKTPTIAVIGTGLDIFYPLENRKIQ.EYLAQYQLVLSEYSLGEKPLKYHFPERNRIIAGLSRGVVVEA	223
NTDB id 525 SMSK321 RS06295 WP 000705298.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQ.DYISNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	224
NTDB id 267 KZH43 RS05590 WP 000705306.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQ.DYICNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	224
NTDB id 226 SPD RS05990 WP 000705306.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQ.DYICNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	224
NTDB id 192 SPR RS05715 WP 000705306.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQ.DYICNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	224
NTDB id 157 SP RS06205 WP 000705306.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQ.DYICNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	224
NTDB id 497 SM12261 RS05565 WP 000705318.1	IDTAAHMAALQNGGKTIAVIGTGLDVFYYPKANKRLQ.DYICNDHVLVSEYGPGEQPLKFHFPARNRIIAGLCRGVIVAEA	224
NTDB id 1119518 EL071 RS08320 WP 001015250.1	IDTAAHVSALKNGGSSIAVIGSGLDVYYP TENKKLQ.EYMSYNHVLVSEYFTGEQPLKFHFPERNRIIAGLCQGVIVAEA	223
NTDB id 407 SMU RS04605 WP 002262865.1	IDTA AHLASIKSGGATIAVIGTGLDVHYPKENRLQ.DYIAKNHVLVSEYEAQSQPLKYHFPERNRIIAGLSQGVIVAEA	222
consensus	*!!!!	

logo

NTDB id 1361 HI 0985 AAC22646.1	TEKSGSLITARYALECNRVFAVPCNIQKSSQGCHRLIKGAMLVENAKDILETLYQHSIHSQTEIDFDQIAVPNYTPP	310
NTDB id 626 LCA RS04960 WP 011374694.1	RHKSGSLITANLALQANRNVYAIPGRIDQSLSQGCNQLIAAGATPILDKNILEELRYFD.....	288
NTDB id 599 KW2 RS05940 WP 021037268.1	KLRSGSLITCERALEEGRDIFAIPGNIADGTSDCGNHLIQGAKLVYQAQDILEEVLN.....	282
NTDB id 525 SMSK321 RS06295 WP 000705298.1	KMRSGSLITCERAMEEGRDVFIPAIGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.....	282
NTDB id 267 KZH43 RS05590 WP 000705306.1	KMRSGSLITCERAMEEGRDVFIPAIGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.....	282
NTDB id 226 SPD RS05990 WP 000705306.1	KMRSGSLITCERAMEEGRDVFIPAIGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.....	282
NTDB id 192 SPR RS05715 WP 000705306.1	KMRSGSLITCERAMEEGRDVFIPAIGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.....	282
NTDB id 157 SP RS06205 WP 000705306.1	KMRSGSLITCERAMEEGRDVFIPAIGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.....	282
NTDB id 497 SM12261 RS05565 WP 000705318.1	KMRSGSLITCERAMEEGRDVFIPAIGSILDGLSDGCHHLIQEGAKLVTSGQDVLAEFEF.....	282
NTDB id 1119518 EL071 RS08320 WP 001015250.1	KMRSGSLITCERALEEGRVFAIPGNIIDGKSDGCHHLIQEGAKCITSGKDILSEYQ.....	280
NTDB id 407 SMU RS04605 WP 002262865.1	KIRSGSLITCERAMEEGRDVFVPCNILDGQSEGCHHLIQEGAKCITSGFDILNEFNF.....	280
consensus	***!!!!!!***!*****!*****!?!*****!*!!*!!*!!*!!*****	

logo

NTDB id 1361 HI 0985 AAC22646.1	PDPRRLVEAPSHPKLYSRIGYTPVSIDDLAEEFNLSVDVLLVQLLDLELQDLIISENGLYKRV	373
NTDB id 626 LCA RS04960 WP 011374694.1		288
NTDB id 599 KW2 RS05940 WP 021037268.1		282
NTDB id 525 SMSK321 RS06295 WP 000705298.1		282
NTDB id 267 KZH43 RS05590 WP 000705306.1		282
NTDB id 226 SPD RS05990 WP 000705306.1		282
NTDB id 192 SPR RS05715 WP 000705306.1		282
NTDB id 157 SP RS06205 WP 000705306.1		282
NTDB id 497 SM12261 RS05565 WP 000705318.1		282
NTDB id 1119518 EL071 RS08320 WP 001015250.1		280
NTDB id 407 SMU RS04605 WP 002262865.1		280
consensus		

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