

logo

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NTDB id 626 LCA RS04960 WP 011374694.1
NTDB id 599 KW2 RS05940 WP 021037268.1
NTDB id 525 SMSK321 RS06295 WP 000705298.1
NTDB id 267 KZH43 RS05590 WP 000705306.1
NTDB id 226 SPD RS05990 WP 000705306.1
NTDB id 192 SPR RS05715 WP 000705306.1
NTDB id 157 SP RS06205 WP 000705306.1
NTDB id 497 SM12261 RS05565 WP 000705318.1
NTDB id 188616 BBP08 RS03850 WP 001015245.1
NTDB id 407 SMU RS04605 WP 002262865.1
consensus

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MKITNYEIYKL KKSGLTNQQILKVLEYGEN VDQELLGDIADISGCR NPAVFMERYFQIDDA HLSKEFQKFPSFS MLTKNQLLKVHLAAGFGTISELRLAAWLTSTSHNWALSALETAQTARLPERYWPTFQASFQSTTLQRQCIDEVRTTYLI MITNFDLFRW KKAGMTNLGNKLKFFRK YDRKISLRQMQVAQVK SIPNFIEQYKNQDVK KLRADYKKFSSFS MKITNYEIYKL KKSGLTNQQILKVLEYGEN VDQELLGDIADISGCR NPAVFMERYFQIDDA HLSKEFQKFPSFS MKITNYEIYKL KKSGLTNQQILKVLEYGEN VDQELLGDIADISGCR NPAVFMERYFQIDDA HLSKEFQKFPSFS MKITNYEIYKL

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ILD	DD	YP	WD	SE	IV	DA	PV	LL	FY	KG	GN	DL	LL	KF	PK	VA	WG	SR	NA	CS	KQ	GA	KS	VE	KY	IQ	GL	EN	EL	VI	VS	GL	AK	GI	DT	AA	HL	MA	AL																																					
IL	LD	KD	YP	QR	LL	ET	YL	P	PV	LL	FY	R	G	D	L	LL	K	Q	P	C	L	A	V	G	A	R	Q	A	T	H	S	K	Q	S	L	E	Q	L	L	Q	L	T	A	.	T	T	I	S	G	L	A	G	C	A	D	A	M	A	T	H	E	V	A	L	159											
IL	LD	LD	Y	P	E	R	L	E	I	T	Y	N	P	P	V	L	FY	Q	G	N	I	D	L	L	K	N	P	K	L	A	F	V	G	S	R	L	A	G	Q	S	G	I	K	S	Q	K	I	V	E	L	N	Q	S	F	T	I	V	S	G	L	A	G	I	D	T	A	H	L	S	A	I	154				
IL	LD	D	C	Y	P	W	L	S	E	I	D	A	P	V	L	L	FY	Q	G	N	L	D	L	L	K	F	P	K	V	A	V	G	S	R	A	C	S	K	Q	G	A	K	S	V	E	K	V	I	Q	G	L	E	N	E	L	V	I	V	S	G	L	A	G	I	D	T	A	A	H	M	A	A	L	155		
IL	LD	D	C	Y	P	W	L	S	E	I	D	A	P	V	L	L	FY	Q	G	N	L	D	L	L	K	F	P	K	V	A	V	G	S	R	A	C	S	K	Q	G	A	K	S	V	E	K	V	I	Q	G	L	E	N	E	L	V	I	V	S	G	L	A	G	I	D	T	A	A	H	M	A	A	L	155		
IL	LD	D	C	Y	P	W	L	S	E	I	D	A	P	V	L	L	FY	Q	G	N	L	D	L	L	K	F	P	K	V	A	V	G	S	R	A	C	S	K	Q	G	A	K	S	V	E	K	V	I	Q	G	L	E	N	E	L	V	I	V	S	G	L	A	G	I	D	T	A	A	H	M	A	A	L	155		
IL	LD	D	C	Y	P	W	L	S	E	I	D	A	P	V	L	L	FY	Q	G	N	L	D	L	L	K	F	P	K	V	A	V	G	S	R	A	C	S	K	Q	G	A	K	S	V	E	K	V	I	Q	G	L	E	N	E	L	V	I	V	S	G	L	A	G	I	D	T	A	A	H	M	A	A	L	155		
IL	LD	D	C	Y	P	W	L	S	E	I	D	A	P	V	L	L	FY	Q	G	N	L	D	L	L	K	F	P	K	V	A	V	G	S	R	A	C	S	K	Q	G	A	K	S	V	E	K	V	I	Q	G	L	E	N	E	L	V	I	V	S	G	L	A	G	I	D	T	A	A	H	M	A	A	L	155		
IL	LD	D	C	Y	P	W	L	S	E	I	D	A	P	V	L	L	FY	Q	G	N	L	D	L	L	K	F	P	K	V	A	V	G	S	R	A	C	S	K	Q	G	A	K	S	V	E	K	V	I	Q	G	L	E	N	E	L	V	I	V	S	G	L	A	G	I	D	T	A	A	H	M	A	A	L	155		
IL	D	S	N	Y	P	L	E	L	K	E	I	Y	N	P	P	V	L	FY	Q	G	N	I	E	L	L	S	K	P	K	L	A	V	G	A	R	Q	A	S	Q	I	G	C	Q	S	V	K	K	I	I	K	E	T	N	N	Q	F	V	I	V	S	G	L	A	R	D	I	D	T	A	A	H	V	S	A	L	154
IL	D	L	K	E	Y	P	L	E	L	K	N	I	Y	N	P	P	V	L	FY	Q	G	N	D	L	D	L	A	R	P	K	L	A	V	G	S	R	N	A	S	Q	M	G	V	A	A	V	K	K	I	I	Q	D	L	S	K	Q	F	V	I	S																

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QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE

K R K E F P F C G S T N G A E E E K T E V S K E L L V K S K A R R Y S E K E K S R S T M Y K R K A N

QRGLAPIGVIGTGLINCSYPPQNEHLQQVVAEKGLLSEYALGTPARRYQFPARNKI IAGLC HSLIVTEARHKSGSLITAN 239

KTKPTTIAVIGTGLDIFYPLENRRKIQEYLAQYLV LSEYSLGKPLKYHFPERNRI IAGLCRGVIVAEAKMRSGLITCE 234

QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE 235

QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE 235

QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE 235

QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE 235

QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE 235

QNGGKTI AVIGTGLDVFYPKANKRLQDYIGNDHLV LSEYGPGEQPLKFHFPARNRI IAGLCRGVIVAEAKMRSGLITCE 235

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KSGGATIAVIGTGLDVIHYPKENRRRLQDYIAKNHLL LSEYEAQSQPLKYHFPERNRI IAGLSQGVIVAEAKITRSGLITCE 233

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consensus

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X	non conserved
X	similar
X	$\geq 50\%$ conserved