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NTDB id 600 KW2 RS01765 WP 011675413.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDYGEQGLEIAGKLTIDSGAVDL	154
NTDB id 269 KZH43 RS08665 WP 001085462.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	153
NTDB id 228 SPD RS09265 WP 001085462.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	153
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NTDB id 159 SP RS09750 WP 001085462.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	153
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NTDB id 408 SMU RS09530 WP 002262392.1	IVEIYGPESGKTTVALHVAQAQKDGGAIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	153
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NTDB id 115 BSU 16940 NP 389576.2	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	138
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NTDB id 1214 NCTC11637 00359 SQJ03206.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	141
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NTDB id 1130 NGFG RS03960 WP 003688695.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	140
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	139
consensus	IVEIYGPESGKTTVALHVAQAQKEGGIAAFDAEHALDPYAAALGVMIDELLV SQPDSGEQGLEIAGKLTIDSGAVDL	

Sequence logo showing amino acid conservation across the protein sequence. The y-axis represents information content, and the x-axis represents the position in the protein. The most conserved residues are highlighted in red and blue.

logo



NTDB id 600 KW2 RS01765 WP 011675413.1	VV	I	D	S	V	A	A	L	V	P	K	A	E	I	D	G	E	I	G	D	S	S	V	G	L	Q	A	R	M	S	Q	A	M	R	K	L	A	C	H	I	N	K	T	K	T	A	I	F	I	N	Q	L	R	E	K	V	G	V	M	.	F	G	S	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	233			
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NTDB id 228 SPD RS09265 WP 001085462.1	V	V	V	D	S	V	A	A	L	V	P	R	A	E	I	D	G	D	I	G	D	S	H	V	G	L	Q	A	R	M	S	Q	A	M	R	K	L	G	A	S	I	N	K	T	K	T	A	I	F	I	N	Q	L	R	E	K	V	G	V	M	.	F	G	N	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	232		
NTDB id 194 SPR RS08825 WP 001085462.1	V	V	V	D	S	V	A	A	L	V	P	R	A	E	I	D	G	D	I	G	D	S	H	V	G	L	Q	A	R	M	S	Q	A	M	R	K	L	G	A	S	I	N	K	T	K	T	A	I	F	I	N	Q	L	R	E	K	V	G	V	M	.	F	G	N	P	E	T	T	P	G	G	R	A	L	K	F	Y	A	232		
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consensus
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 non conserved  
 similar  
 ≥ 50% conserved