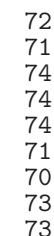


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NTDB id 1059 ABD1 RS01610 WP 000279215.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

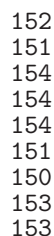
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NTDB id 1016 ACIAD RS01680 WP 004920476.1
consensus

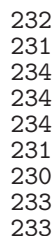
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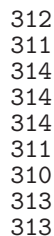
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consensus
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consensus

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logo

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consensus

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Sequence 1	E	I	R	V	A	T	S	A	S	M	S	A	R	A	T	E	L	F	P	N	M	L	Q	M	V	A	G	E	E	S	G	L	D	M	L	N	K	V	A	T	I	F	E	V	D	N	A	V	D	L	S	A	M	M	E	P	L	I	V	L	G	W	V	G	L																																			
Sequence 2	K	V	R	E	R	T	S	A	S	L	P	L	N	F	S	E	S	N	R	E	L	A	V	S	S	M	G	E	E	S	G	L	D	M	L	N	K	V	A	T	I	F	E	V	D	N	A	V	D	L	S	A	M	M	E	P	L	I	V	L	G	W	V	G	L																																			
Sequence 3	E	V	Y	R	D	T	A	A	G	M	P	M	Y	I	A	M	R	N	T	E	A	F	F	E	M	V	L	Q	M	V	A	G	E	E	S	G	L	D	D	M	L	N	K	V	A	T	I	F	E	V	D	N	T	V	D	N	L	S	K	I	L	E	P	L	I	I	V	F	L	G	T	V	V	G	L																									
Sequence 4	E	I	R	T	R	V	I	Q	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	S	S	I	G	E	E	S	G	S	L	D	D	M	L	N	K	A	A	E	F	Y	E	D	E	V	D	N	A	V	G	W	L	S	A	M	M	E	P	I	I	I	L	G	L	V	I	G	T	L																								
Sequence 5	E	I	R	T	R	V	I	Q	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	S	S	I	G	E	E	S	G	S	L	D	D	M	L	N	K	A	A	E	F	Y	E	D	E	V	D	N	A	V	G	R	L	S	A	M	M	E	P	I	I	I	V	I	L	G	L	V	I	G	T	L																						
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Sequence 7	K	I	R	E	V	A	T	G	Q	Q	M	F	I	A	M	E	N	T	H	L	F	P	N	M	V	I	Q	M	V	A	G	E	E	S	G	A	L	E	K	M	L	S	K	V	A	T	F	Y	E	E	V	D	N	A	V	D	L	S	S	L	L	E	P	I	I	M	S	I	L	G	I	L	V	G	L																									
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Sequence 9	K	I	R	E	D	V	A	T	G	Q	Q	L	Q	F	A	M	R																																																																																			

VVMAYLPIFNLSVLG . 408
VTAMYLPIFNLSVLG . 407
LVAMYLPIFNLNVA* 410
LVAMYLPIFNLNVA . 410
LVAMYLPIFNLNVA . 410
VVAMYLPIFKLGSAV . 406
ITAMYLPIFQMGSVV . 405
VTIAMYLPIFQMGSVV . 408
VIAMYLPIFQMGSVV . 408

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