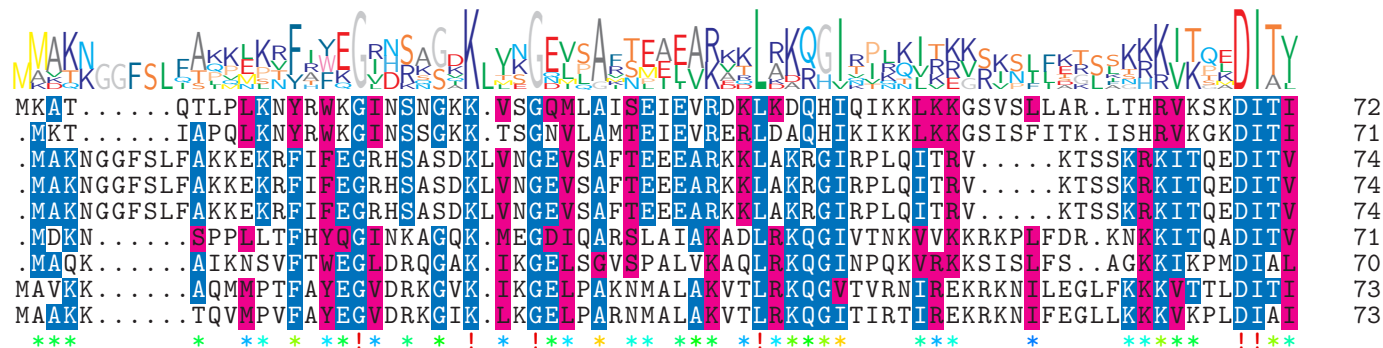


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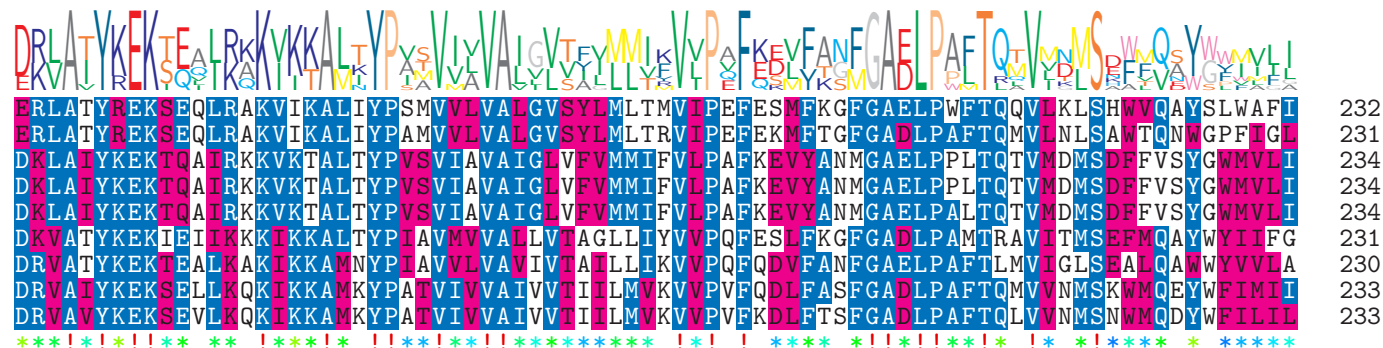
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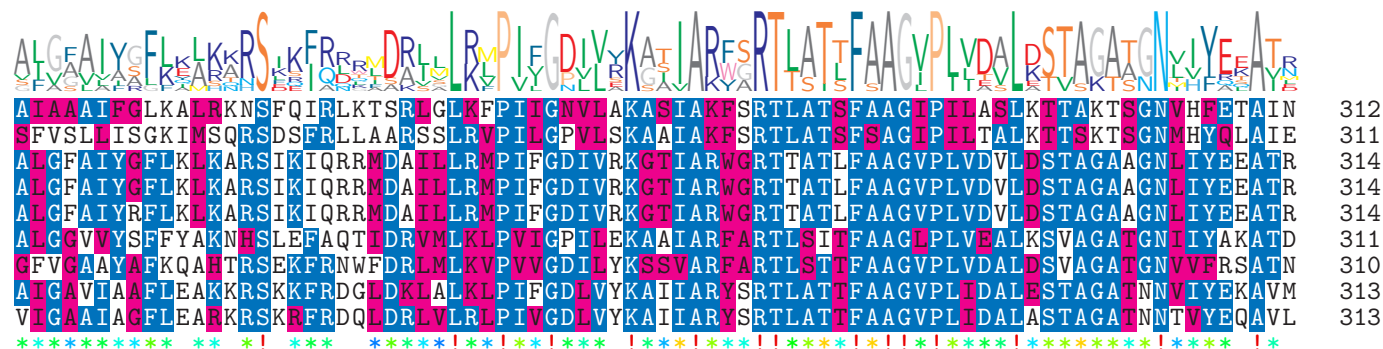
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consensus

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Sequence 6	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	F	Y	E	F	E	D	V	N	A	V	G	R	L	S	A	M	M	E	P	I	I	I	V	F	L	G	V	I	G	T	L																								
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Sequence 9	K	I	K	S	D	V	S	S	G	M	Q	L	N	F	S	M	R	T	T	G	T	F	P	S	M	A	V	Q	M	T	A	G	E	E</																																																																		

VYAMYLPIFNLGSA
LTIAMYLPIFNLMALG

	V	T	L	V	L	V	V	I	V	V	I	*				
408	V	A	M	Y	L	P	I	F	N	L	M	S	V	L	G	.
407	V	T	A	M	Y	L	P	I	F	N	L	M	S	V	L	G
410	L	V	A	M	Y	L	P	I	F	N	L	G	N	V	V	A
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405	I	I	A	M	Y	L	P	I	F	Q	M	G	S	V	V	.
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408	V	I	A	M	Y	L	P	I	F	Q	M	G	S	V	V	.

* * * * ! ! ! ! * * ! ! * * * * * *

-  non conserved
-  similar
-  > 50% conserved