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NTDB id 1306 DR RS10060 WP 027479822.1	MSXLSIGDRLGAALLDQGYLGDNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLLAVQPDPAAL	79
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
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NTDB id 1401 DSB67 RS12665 WP 010643259.1		0
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NTDB id 193153 BE844 RS01170 WP 011215550.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
consensus		

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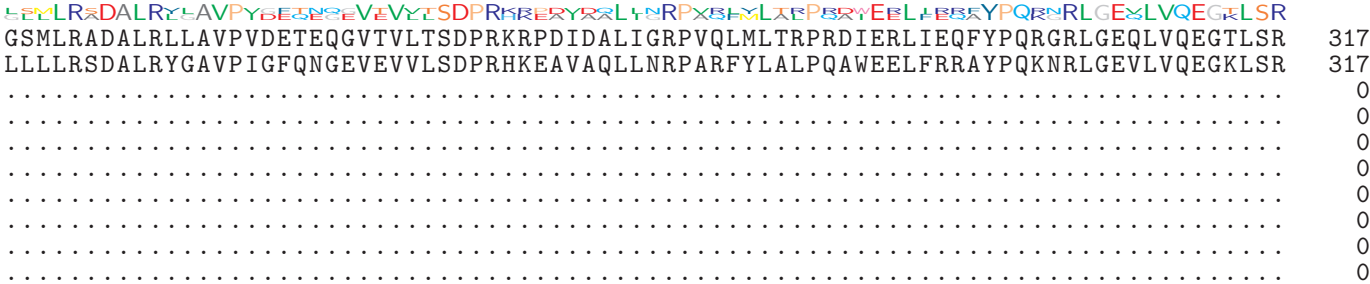
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NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDRTLSEEEVDTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P	158
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NTDB id 1018 ACIAD RS01685 WP 004920473.1		0
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
NTDB id 1028 TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKQWISREALEEALVEQKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
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NTDB id 1251 GC085 RS07725 WP 011946523.1		0
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consensus



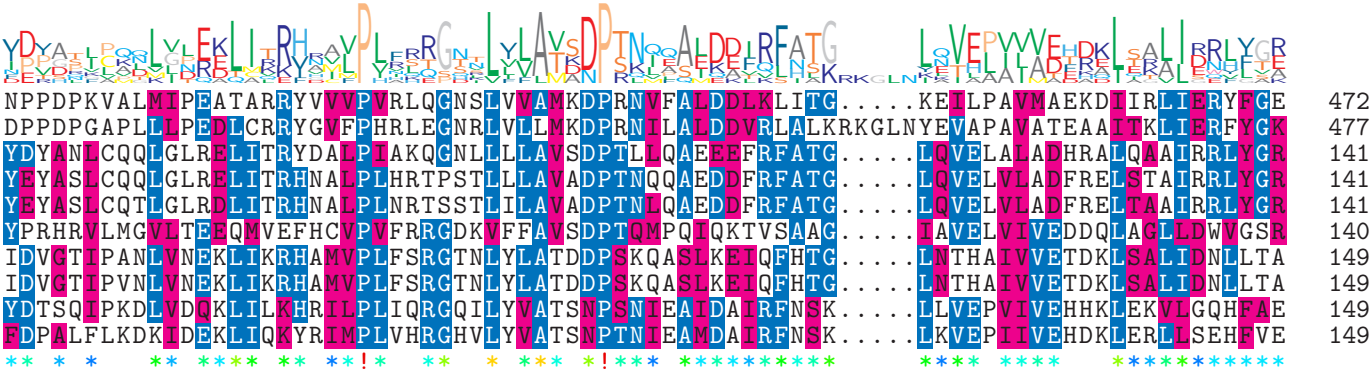
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Sequence 1	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 2	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 3	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 4	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
Sequence 5	L	R	E	Y	A	P	P	L	S	R	L	A	R	K	M	S	L	D	S	E	R	R	P	Q	D	G	R	K	K	S	K	S	T	A	I	F	R	V	S	T	L	P	T	L	E	G	E	K	V	M	R	L	D	S	S	A	L	L	P	E	A																																							
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consensus



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782
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449
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consensus



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consensus



887
889
562
561
561
558
574
574
570
570

☒ non conserved
☒ similar
☒ ≥ 50% conserved