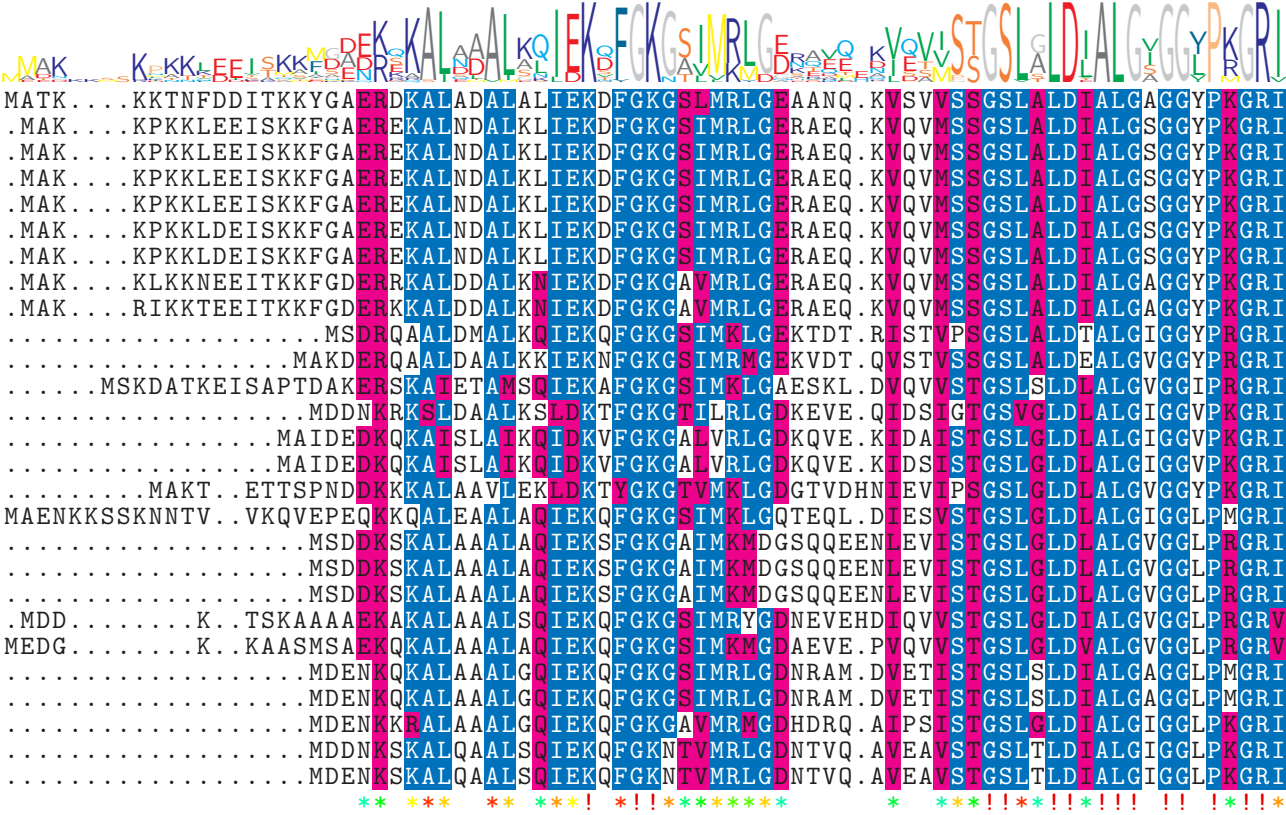


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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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consensus



logo

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NTDB id 1427 RS RS02760 WP 011000510.1	VR	L	D	I	R	R	I	G	S	.	.	.	.	.	.	.	.	.	.	I	.	K	K	G	.	D	E	V	V	G	N	E	T	K	V	K	V	V	K	N	K	V	A	P	P	F	R	E	A	I	F	D	I	L	Y	G	A	G	V	S	R	E	G	E	I	I	D	L	G	V	E	A	K	V	V	E	K	S	G	A	W	Y	S	Y	N	G	303
NTDB id 1165 A1552VC RS01565 WP 000344154.1	VR	L	D	I	R	R	T	G	A	.	.	.	.	.	.	.	.	.	.	I	.	K	E	G	.	E	E	V	V	G	N	E	T	R	I	K	V	V	K	N	K	I	A	A	P	F	K	E	A	N	T	Q	I	M	Y	G	Q	G	F	N	R	E	G	E	L	I	D	L	G	V	K	H	K	M	V	E	K	S	G	A	W	Y	S	Y	N	G	294
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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EKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLDIGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGLDIGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLAHNPEVFAEIDHQVRVQFGLDIGEEAAE.....SKKDE...VAQVDS..VNEEVPLDLGDELEI	380
EKIGQGSENAKKYLAHNPEIFDEIDHQVRVQFGLDIGEEIAE.....SKKDE...AAQVDS..VNEEVPLDLGDELEI	380
EKIGQGSENAKKRYLAHPQIFDEIDRKVRVKFGLLEESEES..AMAVASE.....E.....TDDLALDLNGIEI	376
EKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEE..KQSSKEK.....ETDEK..ADKNLVLEDDTIEL	381
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KKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP....DEPLE.EME.....	347
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ERIGGGKDNCREFLRENAELAREIENKVREHLGVTPMGA..V.TLAEVEED.....	352
DKIGGGKANACKYILKENPEIAKTLDDKKIREMLLNPNMQ..LIAETSSAADV.EFGAV.....PEEF.....	354
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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved