

logo

		MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVEGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVEGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAAL	79
NTDB id 1168	A1552VC RS11070 WP 000957200.1	0
NTDB id 1293	VP RS12240 WP 005479695.1	0
NTDB id 1401	DSB67 RS12665 WP 010643259.1	0
NTDB id 1251	GCO85 RS07725 WP 011946523.1	0
NTDB id 1110	NGFG RS09235 WP 003689817.1	0
NTDB id 377070	FRC97 RS13300 WP 011796722.1	0
NTDB id 1018	ACIAD RS01685 WP 004920473.1	0
NTDB id 1058	ABD1 RS01615 WP 001274986.1	0
consensus			

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		ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDPLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEIYVPSGA	158
NTDB id 1028	TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDPLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLLEIYVPSGA	158
NTDB id 1306	DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPFAL..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLLEIYVPSGA	157
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NTDB id 1018	ACIAD RS01685 WP 004920473.1	0
NTDB id 1058	ABD1 RS01615 WP 001274986.1	0
consensus			

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1028	TT RS08215 WP 011173991.1	SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237
NTDB id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGRLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237
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NTDB id 1401	DSB67 RS12665 WP 010643259.1	0
NTDB id 1251	GCO85 RS07725 WP 011946523.1	0
NTDB id 1110	NGFG RS09235 WP 003689817.1	0
NTDB id 377070	FRC97 RS13300 WP 011796722.1	0
NTDB id 1018	ACIAD RS01685 WP 004920473.1	0
NTDB id 1058	ABD1 RS01615 WP 001274986.1	0
consensus			

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 consensus



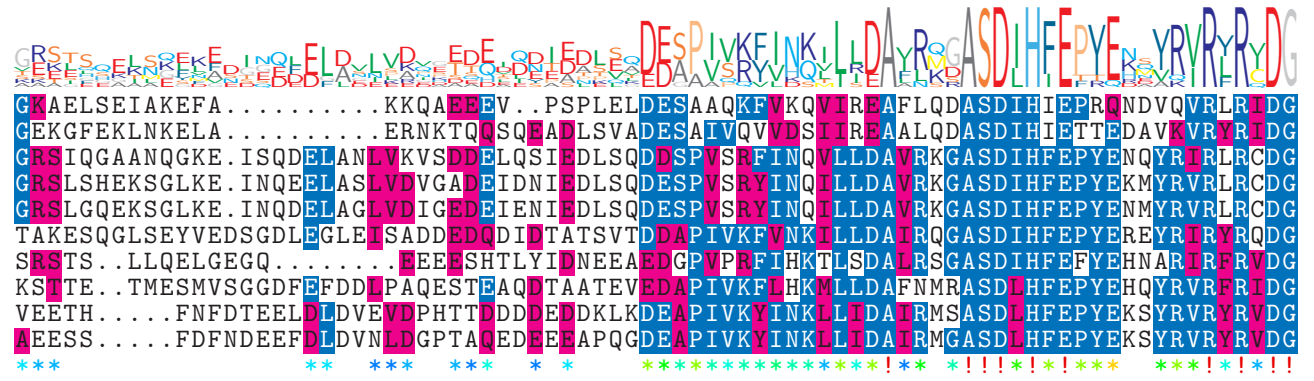
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 consensus



543
540
218
218
218
227
208
231
222
222

logo

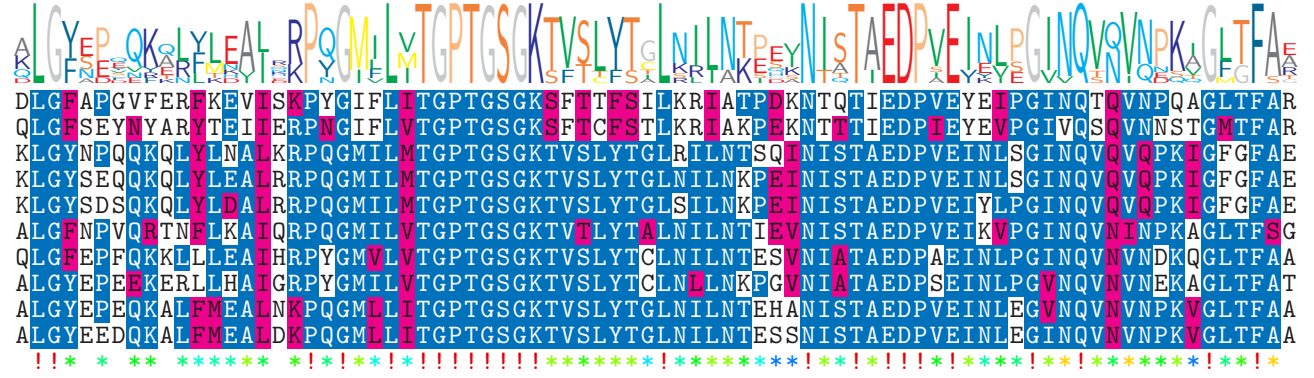
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 consensus



621
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logo

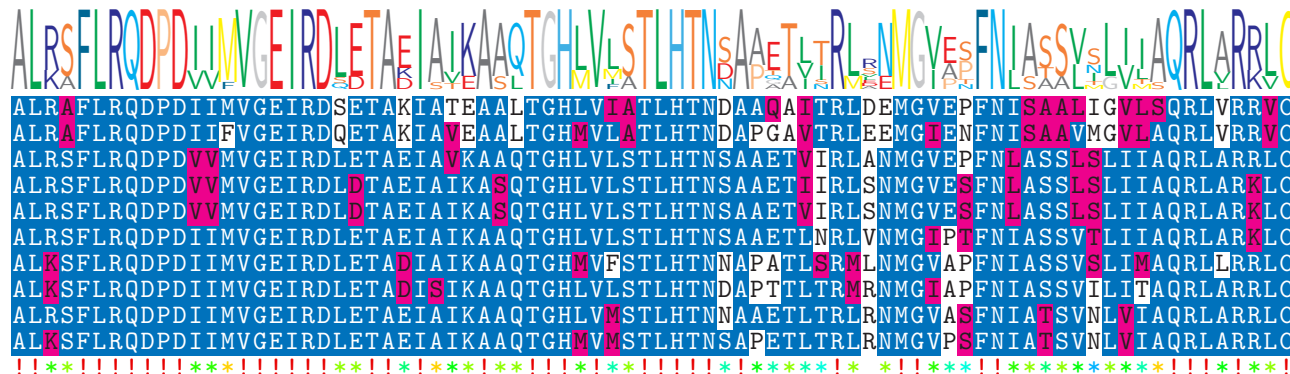
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 consensus



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368
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logo

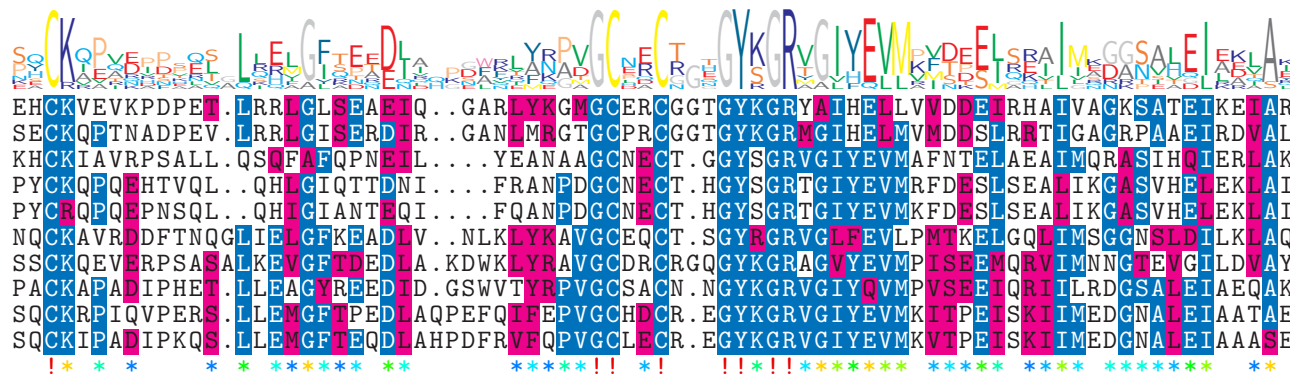
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 NTDB id 1058 ABD1 RS01615 WP 001274986.1



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562
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570

- non conserved
- similar
- ≥ 50% conserved