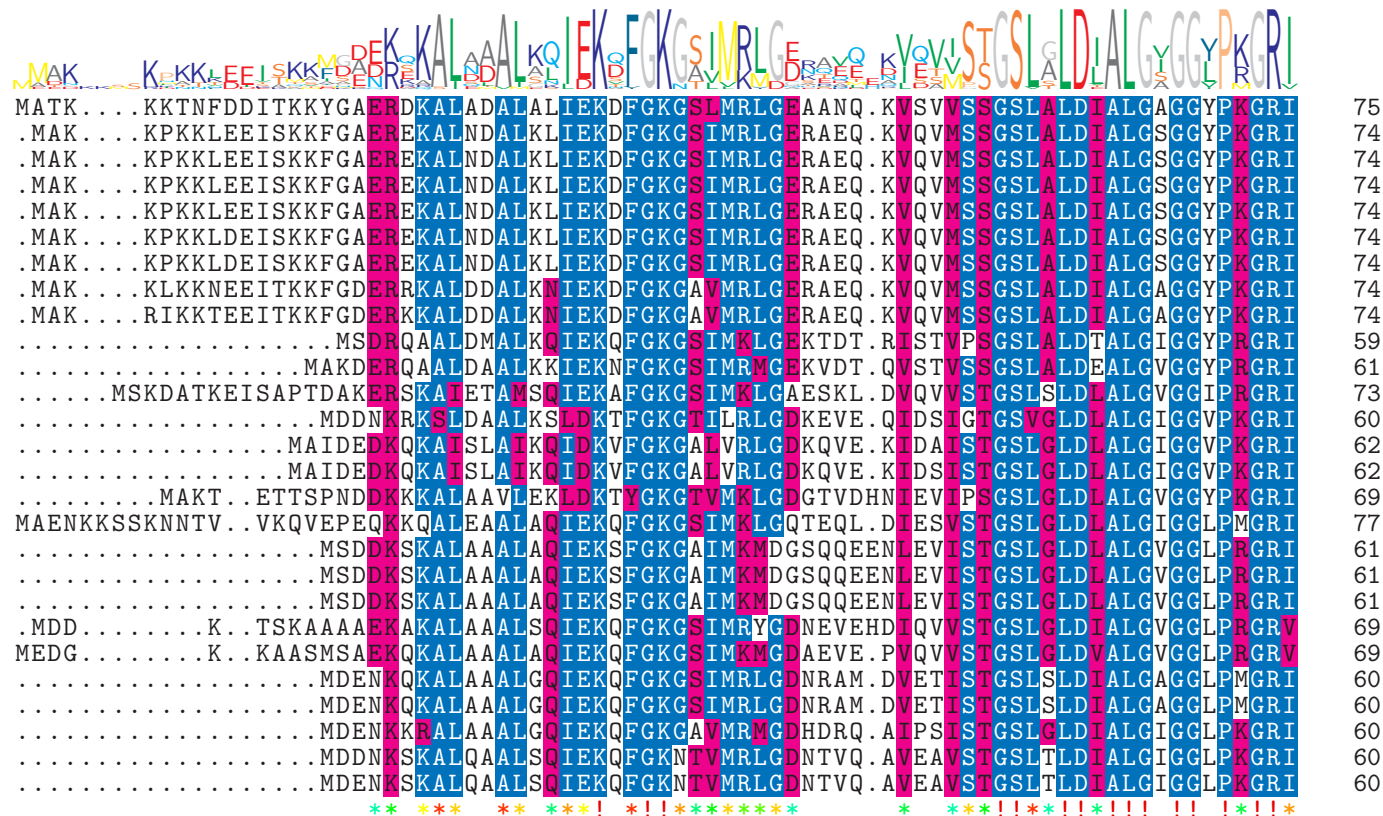


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consensus

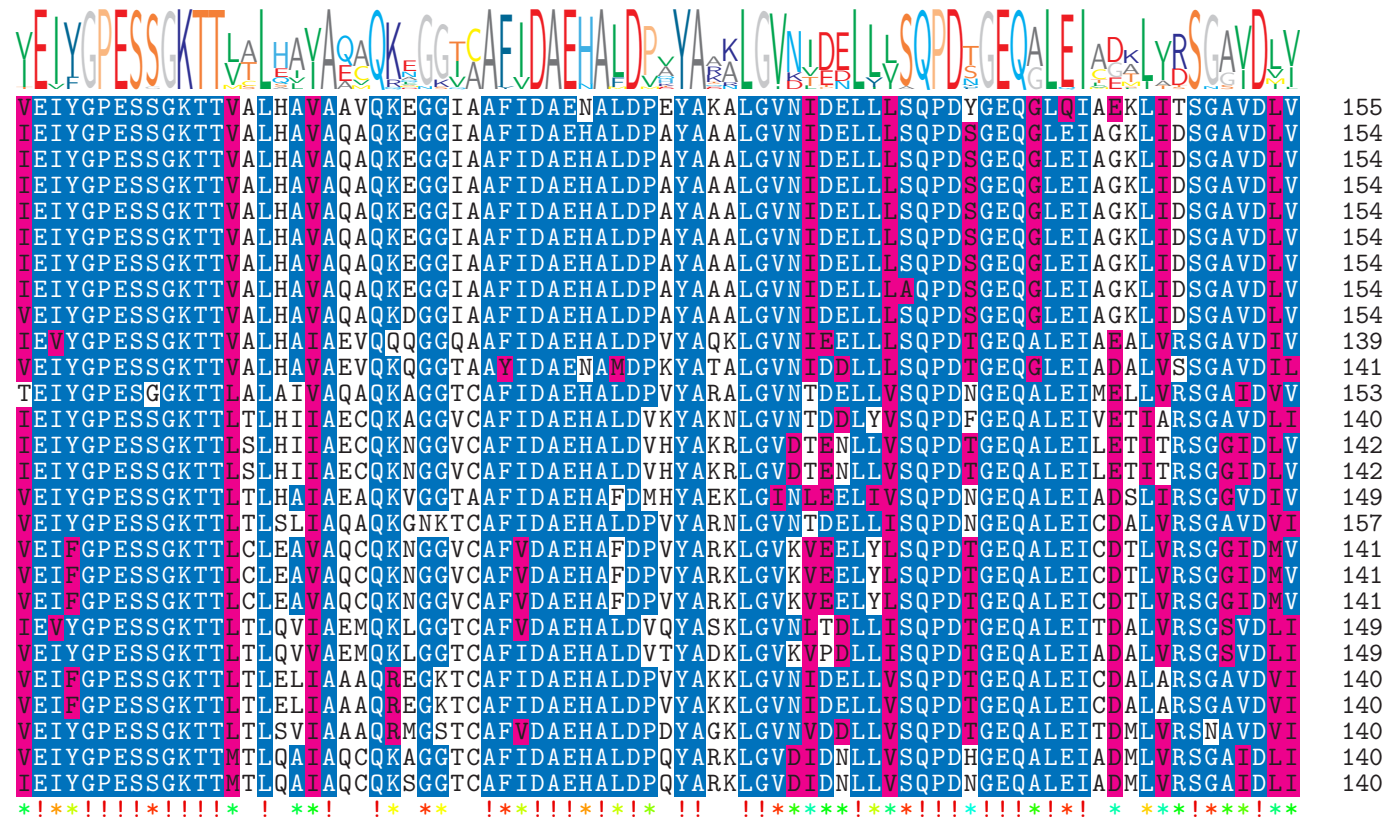
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consensus

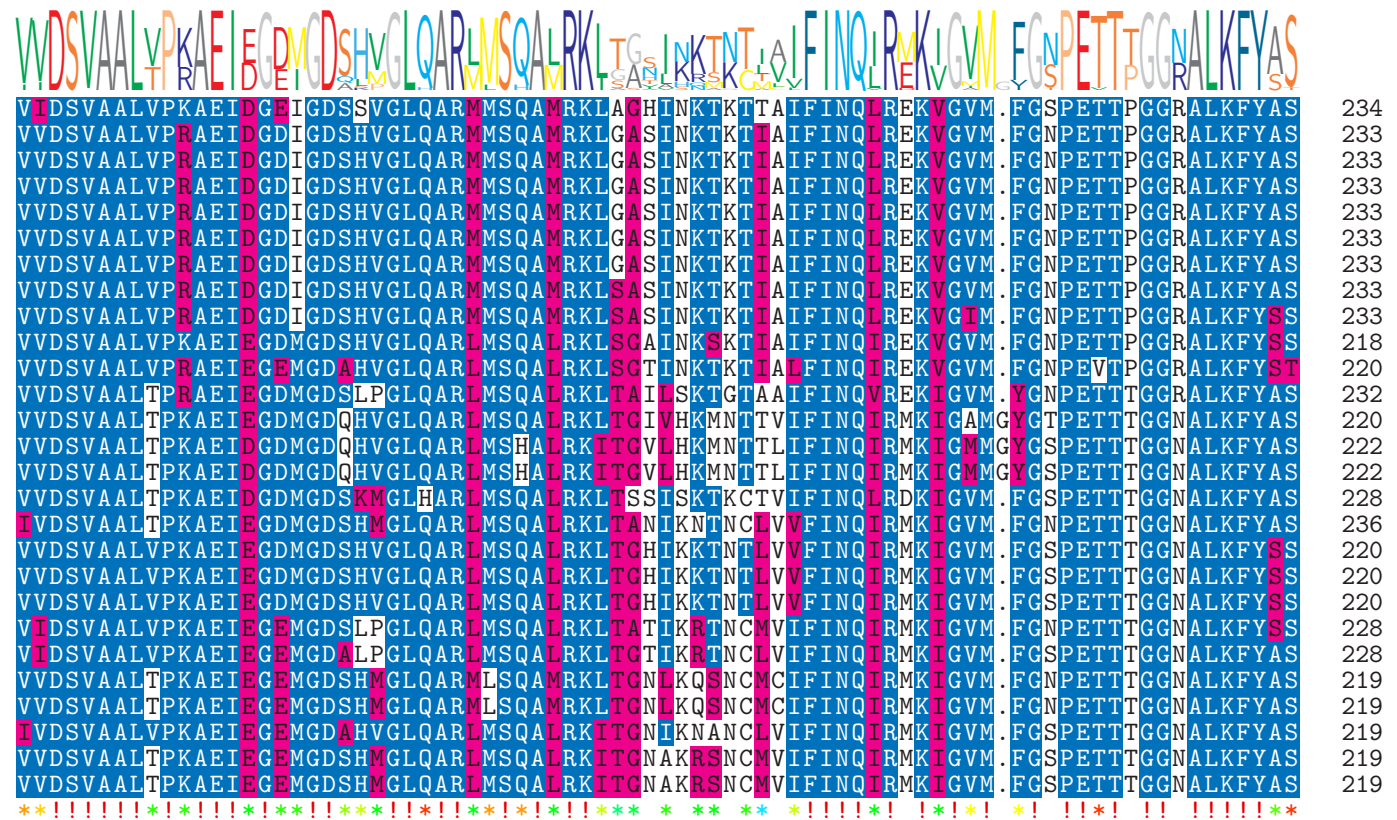
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consensus

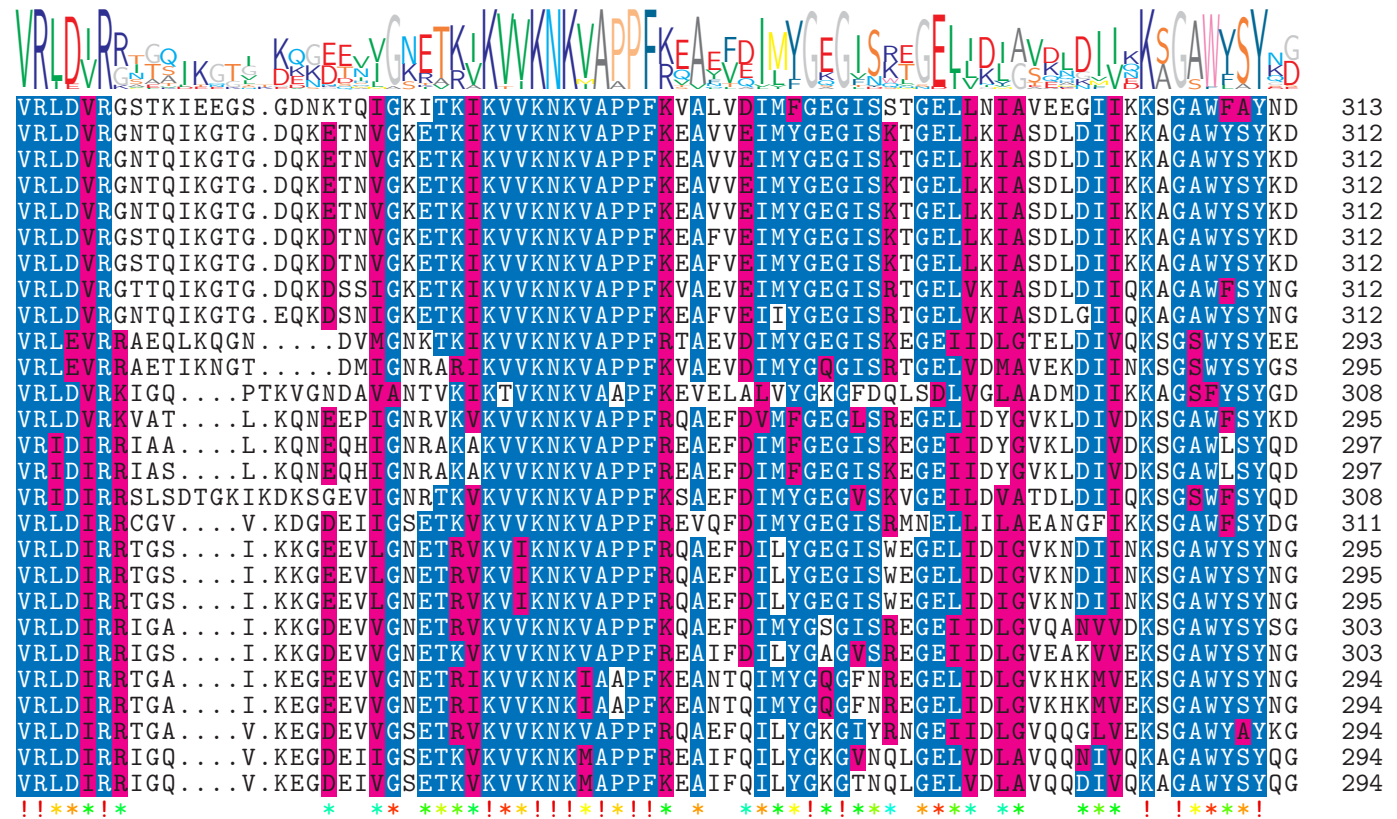
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consensus

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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EKIGQGSENAKKYLA EHP E I FDEIDKQVRSKFG LIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
EKIGQGSENAKKYLA EHP E I FDEIDKQVRSKFG LIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI	384
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EKIGQGSENAKRYLA DHPQLFDEIDRKVRVKFGLIEESEES..AMAVASE.....ETDE..TDDLALDLNGIEI	376
EKIGQGSENAKKFLADNPEI FDDIDHKVRVQYGLIEEDNTEE..KQSSKEK.....ETDEK..ADKNLVLELDDTIEL	381
ERLGGGR ENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQ..QAETQEEL.EFE.E.....	348
ERIGGGRENAKNYLADHEDVEDEVRLKVRAAYGISDVPEEDL..PTTEDE.QI.NILPDDST.....EE.....	355
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KKLGGGRENKAF LKENPEIADEITKAIQNSMGIEGMIS..GSE...DDEGE.E.....	343
KKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP...DEPLE.EME.....	347
KKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP...DEPLE.EME.....	347
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ERIGGGRDNCREFLR ENAELARIENKVRHGLVTPMGA..V.TLAEVEED.....	352
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SKIGQKANAACKYLEENPEIGQEIEQQIRAKLLVTSANT..KATPVAEDLADA.DI.....	347
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NKIGQGNNVIRYFEEFNQIAEIERNI REQLLTGTNG..AVQ.I.EDEEEP.DLL.....LES.....	349

logo

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NTDB	id	600	KW2	RS01765	WP 011675413.1	 387
NTDB	id	269	KZH43	RS08665	WP 001085462.1	EIEE 388
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NTDB	id	204136	BG534	RS07030	WP 003812760.1	 353
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NTDB	id	1022	ACIAD	RS06390	WP 004925639.1	 349
NTDB	id	1074	ABD1	RS10195	WP 000344167.1	 349
consensus						

-  non conserved
-  similar
-  ≥ 50% conserved