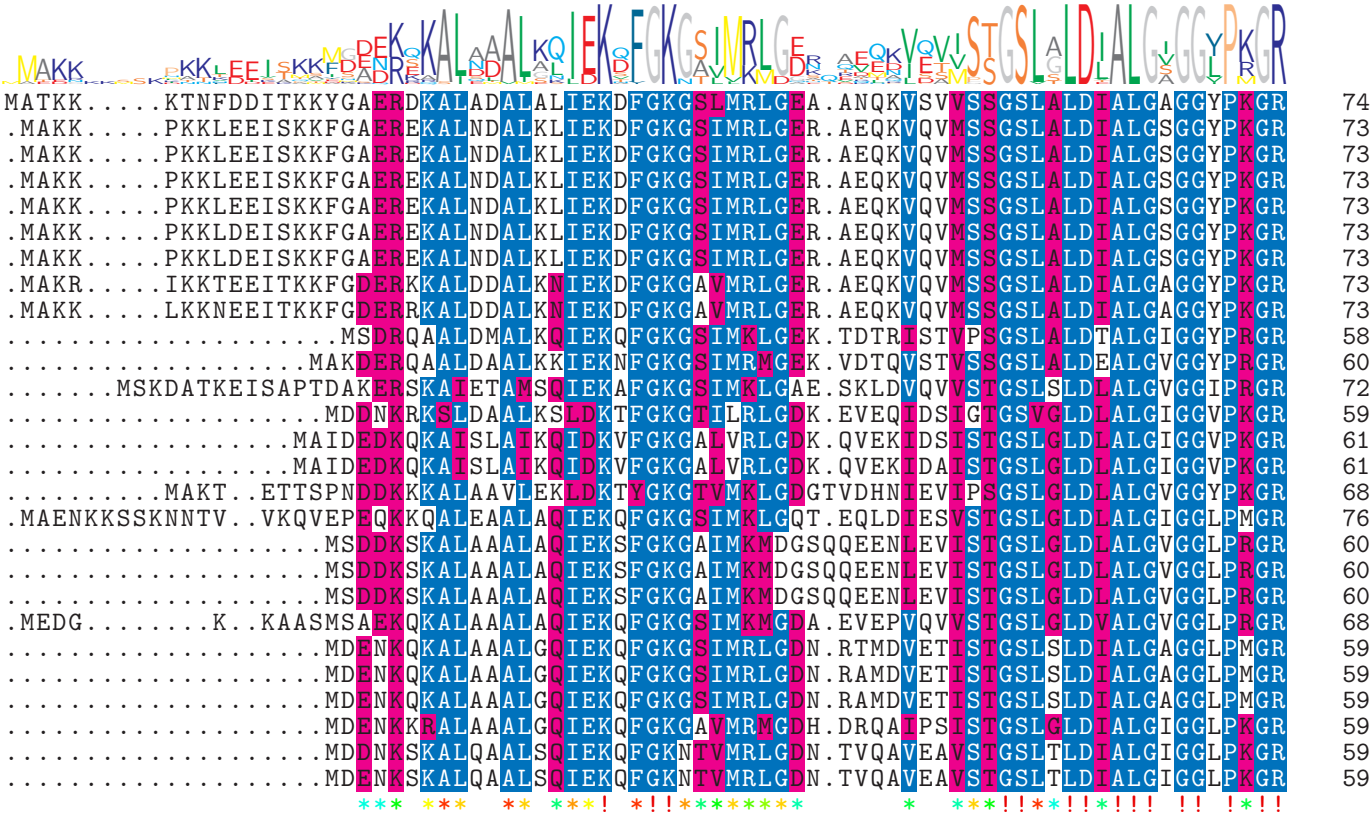
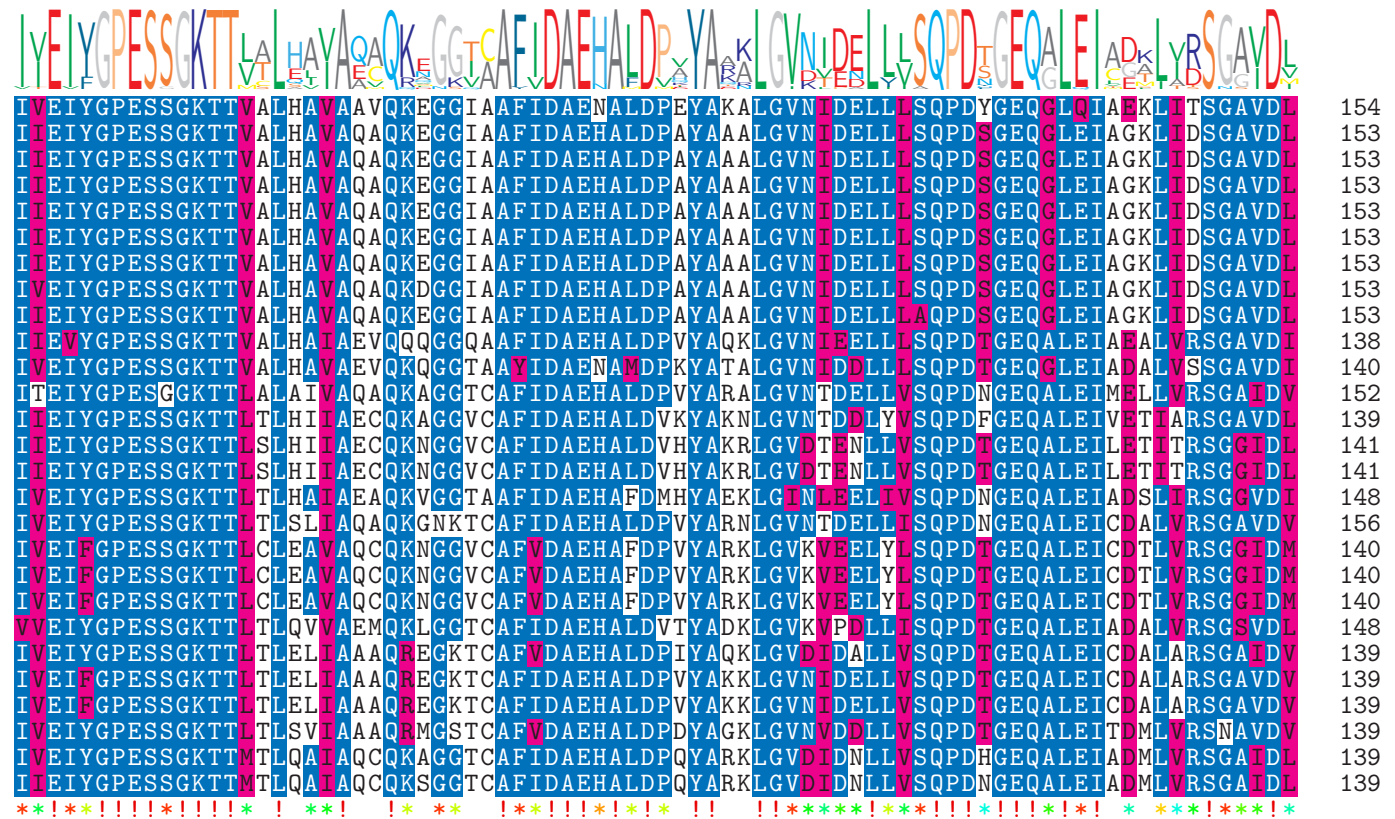


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consensus



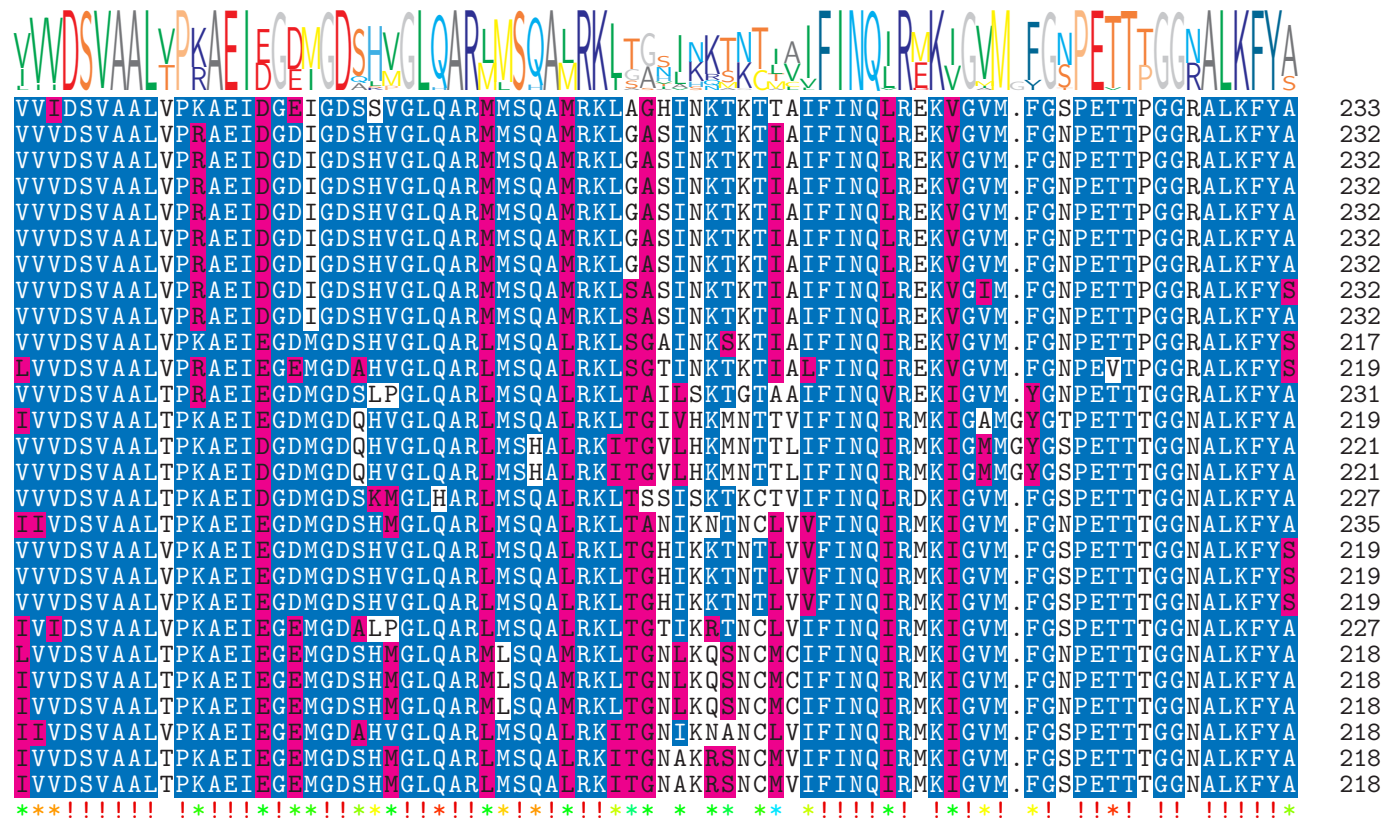
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consensus



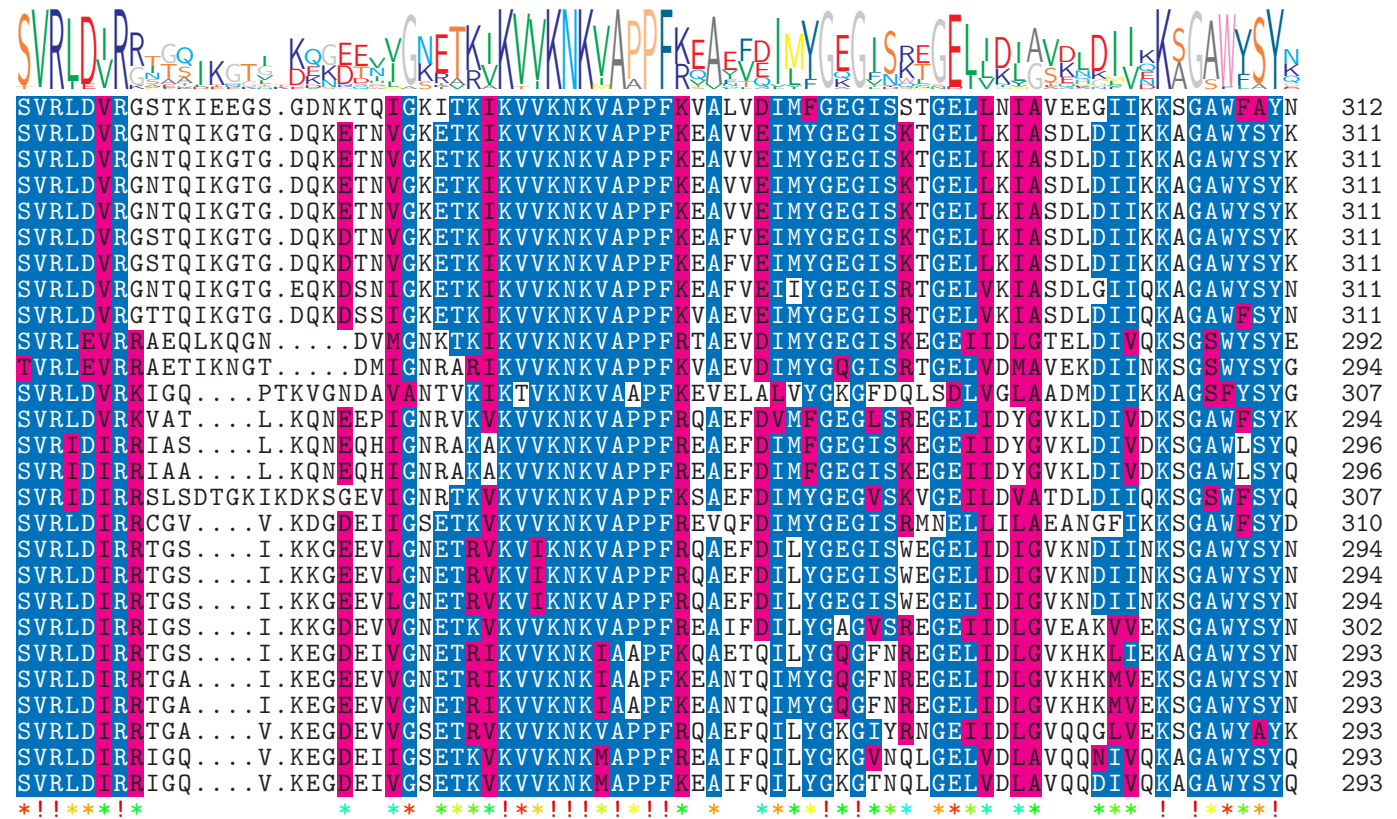
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGS ⁺ ENAKKYLAEHP ⁺ EIFDEIDKQV ⁺ RSKFG ⁺ LIDGEEVSEQDTENKKDE... PKKEEA... VNEEVPLDLGDELEIE 385	385
DEKIGQGS ⁺ ENAKKYLAEHP ⁺ EIFDEIDKQV ⁺ RSKFG ⁺ LIDGEEVSEQDTENKKDE... PKKEEA... VNEEVPLDLGDELEIE 385	385
DEKIGQGS ⁺ ENAKKYLAEHP ⁺ EIFDEIDKQV ⁺ RSKFG ⁺ LIDGEEVSEQDTENKKDE... PKKEEA... VNEEVPLDLGDELEIE 385	385
DEKIGQGS ⁺ ENAKKYLADNPEV ⁺ FAEIDHQV ⁺ RVVQFGLIDGEEAAE... SKKDE... VAQVDS... VNEEVTLDLGDELEIE 381	381
DEKIGQGS ⁺ ENAKKYLADNPEIF ⁺ DEIDHQV ⁺ RVVQFGLIDGEEIAE... SKKDE... AAQVDS... VNEEVTLDLGDLEIE 381	381
GEKIGQGS ⁺ ENAKKFLADNPEIF ⁺ DDIDHKV ⁺ RVVQGLIEEDNTEEEKQSSKEK... ETDEK... ADKNLVLELDDTIELE 382	382
GEKIGQGS ⁺ ENAKRYLADHP ⁺ QLFDEIDRKV ⁺ RVKFG ⁺ LLEESEESAMAVASE... E... TDDLALDLNGIEIE 377	377
EERLGGGRENAKQFLKENK ⁺ DI ⁺ MLMIQE ⁺ QIREHYGLDNGGVVQQAEETQEEL ⁺ EFE... E... 348	348
SERIGQGR ⁺ ENAKNYLADHED ⁺ VEDEVRLK ⁺ VRAAYGISDVPEEDLPTTEDE.QI.NILPD ⁺ DST... EE... 355	355
DERIGGQKEKTIAY ⁺ IAERP ⁺ EMEQEID ⁺ RD ⁺ RVMAAIRAGNAGEAPALAPAPAAPEAAE... A... 363	363
DKKLGGGREN ⁺ SKAFILKENPEIA ⁺ DEITKAIQNSM ⁺ GIEGMISG... SEDDE... GE... E... 343	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMP... LPDEP... LE... E... ME... 347	347
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIMP... LPDEP... LE... E... ME... 347	347
DTKLGGGRD ⁺ TVKELIKDNPELAE ⁺ ELEAKIREKLQAK... 343	343
GTKIGQGKNNNAV ⁺ WLKENPEIA ⁺ DKLEQEI ⁺ RNTLASNPNSVL... KATASDSND... ESDVEEFSEEL... 372	372
GAKIGGQKDNVRVWLKENPEIS ⁺ DEIDAKIRALNGVEMHITE... G... TQ... DETDGERPEE... 348	348
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GAKIGGQKDNVRVWLKENPEIS ⁺ DEIDAKIRALNGVEMHITE... G... TQ... DETDGERPEE... 348	348
GERIGGGRDNCREFLRENAELAREIENK ⁺ VREHLGVTPMGAV... TL.AEEVEE... D... 352	352
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GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLN ⁺ PNM ⁺ QL... IAETSSAAD... DVEFGAVPEEF... 354	354
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logo

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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