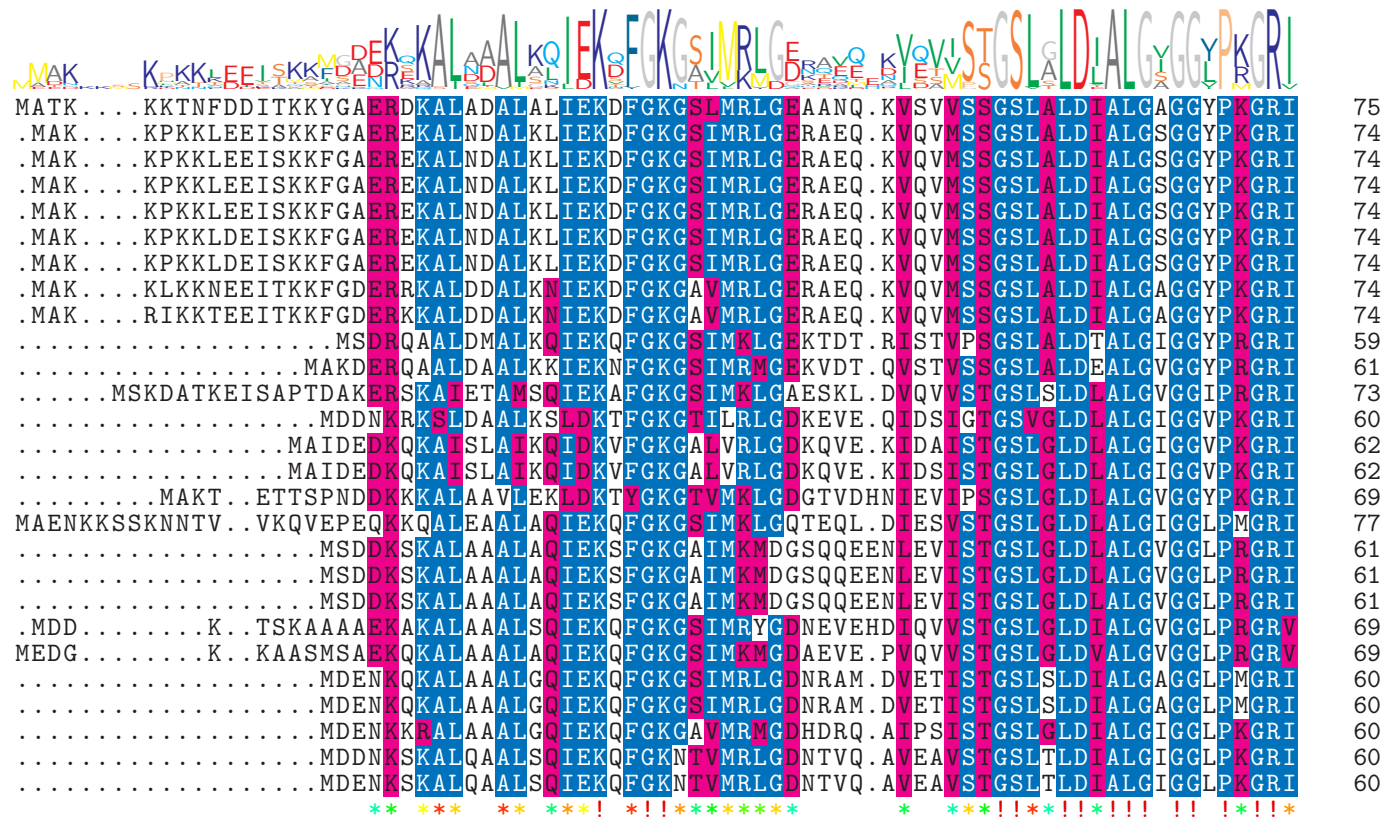


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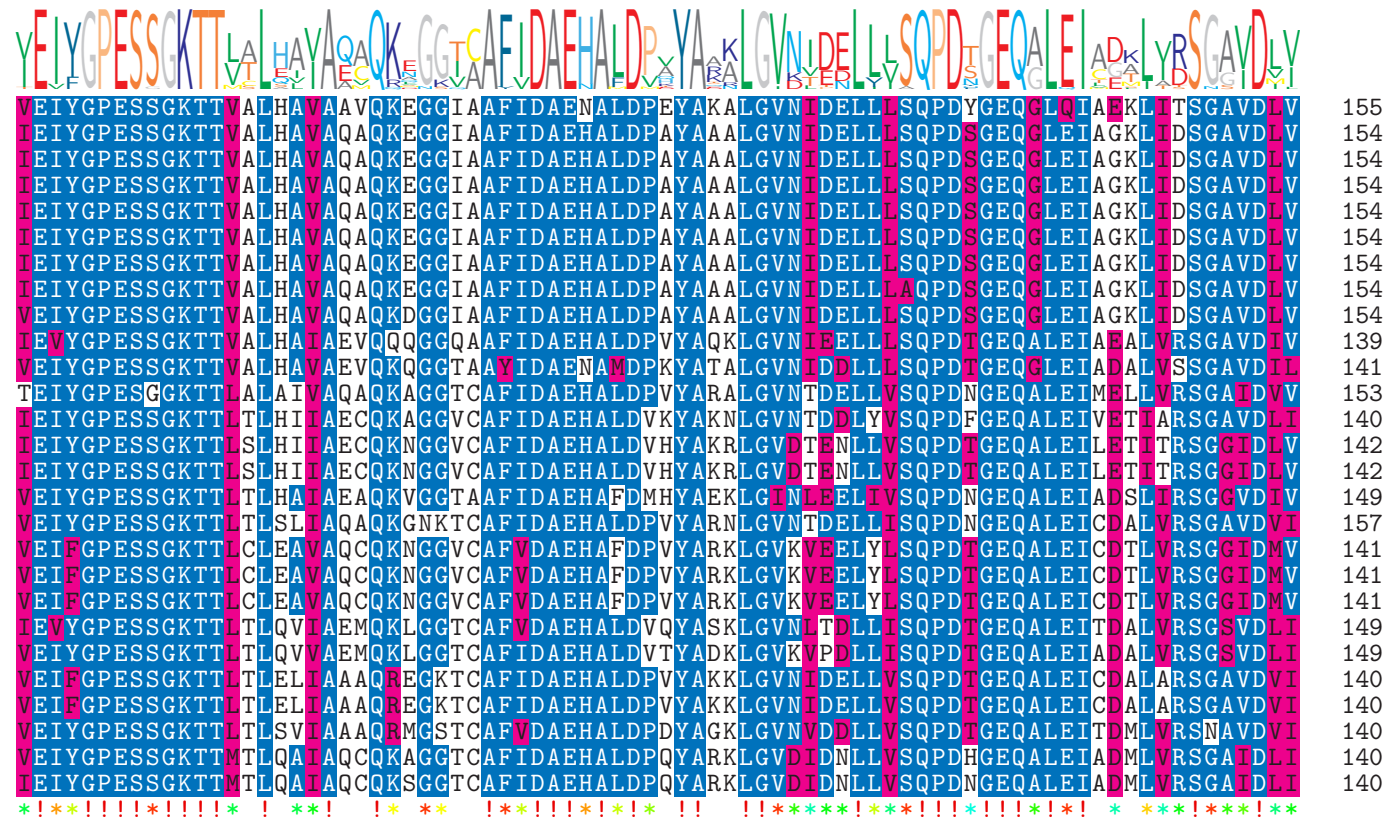
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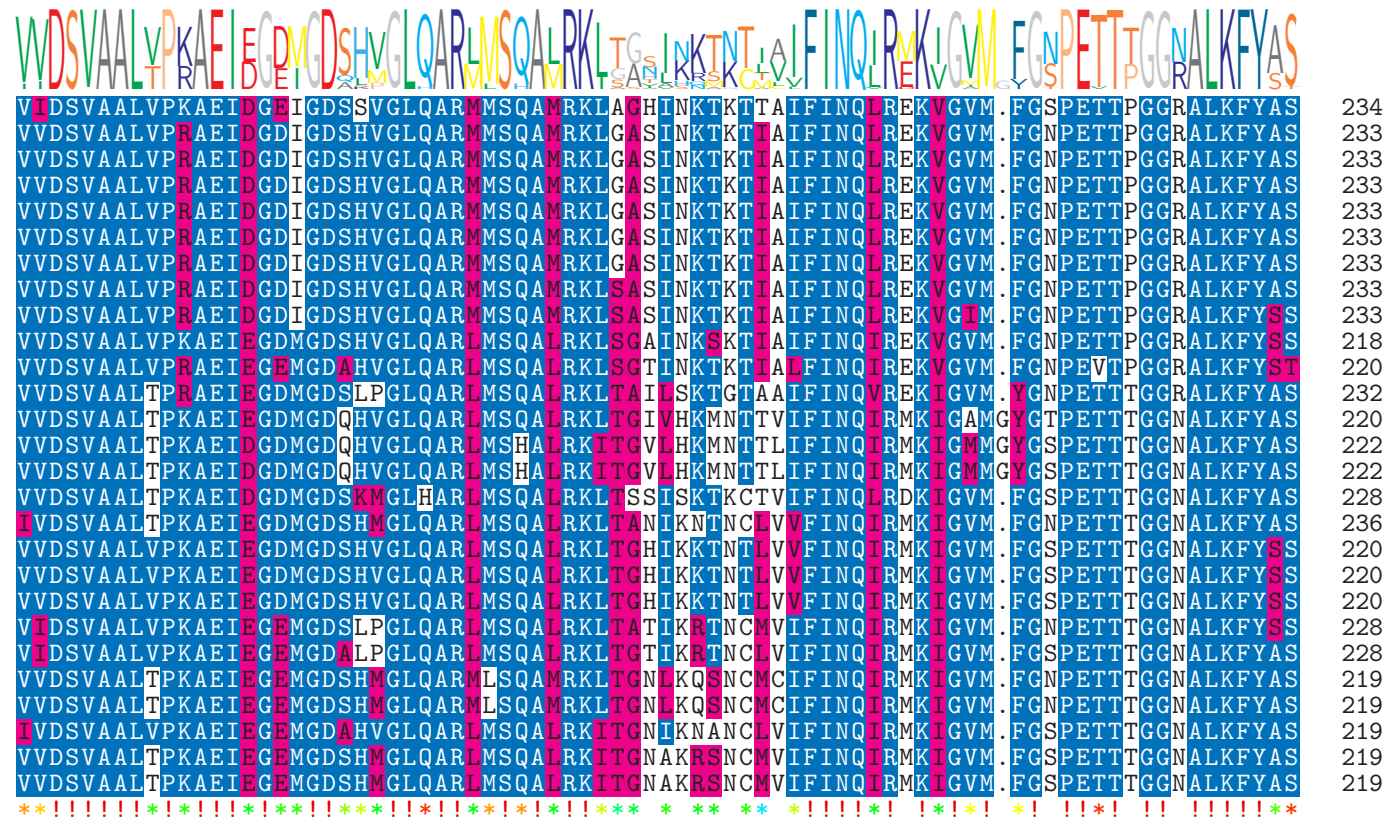
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consensus

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Sequence	Score
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EKIGQGSENAKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSK ⁺ FLIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI 384	384
EKIGQGS ⁺ ENAKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSK ⁺ FLIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI 384	384
EKIGQGS ⁺ ENAKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSK ⁺ FLIDGEEVSE..QDTENKKDE...PKKEEA..VNEEVPLDLGDELEI 384	384
EKIGQGS ⁺ ENAKKYLA ⁺ DNPEVFA ⁺ EID ⁺ HQVRVQ ⁺ FLIDGEEAAE.....SKKDE...VAQVDS..VNEEVPLDLGDELEI 380	380
EKIGQGS ⁺ ENAKKYLA ⁺ DNPEIF ⁺ DEID ⁺ HQVRVQ ⁺ FLIDGEEIAE.....SKKDE...AAQVDS..VNEEVPLDLGDELEI 380	380
EKIGQGS ⁺ ENAKRYLADHPQLF ⁺ DEID ⁺ RKVRVK ⁺ FLIGEESEES..AMAVASE.....ETDEK..ADKNLVLELDDTIEL 376	376
EKIGQGS ⁺ ENAKKFLADNPEIFDD ⁺ IDHKVRVQ ⁺ GLIEEDNTEE..KQSSKEK.....ETDEK..ADKNLVLELDDTIEL 381	381
ERLGGGR ⁺ ENAKQFLKENKD ⁺ IMLMIQEQIREHYGLD ⁺ NNGVVQQ..QAETQE ⁺ EL ⁺ EFE ⁺ .E..... 348	348
ERIGQGR ⁺ ENAKNYLADHEDVE ⁺ DEVRLK ⁺ VRAAYGIS ⁺ SDVPEEDL..PTTEDE.QI.NILPDDST.....EE..... 355	355
ERIGQGKEKTIAYIA ⁺ ERPMEIQE ⁺ ITDRVM ⁺ AAIRAGNAGEAPALAPAPAAPEAA.EA..... 363	363
KKLGGGR ⁺ ENSKAFLKENPEIA ⁺ DEITKAIQNSMGIEGMIS..GSE....DDEGE.E..... 343	343
KKLGGGR ⁺ ENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP....DEPLE.EME..... 347	347
KKLGGGR ⁺ ENAKALLKEDKALADEITLKIKESIGSNEEIM..PLP....DEPLE.EME..... 347	347
TKLGGGRD ⁺ TVKELIKDNPELAE ⁺ ELEAKIREKLQAK..... 343	343
TKIGQGNNA ⁺ VKWLKENPEIAD ⁺ KLQEIRNTLASNPNSV..LKATASDSND ⁺ ES ⁺ .DVEEF.....SEEL..... 372	372
AKIGQKDNVRVWLKENPEIS ⁺ DEIDAKIRALNGVMHIT..E.....GTQDE.TDGER.....PEE..... 348	348
AKIGQKDNVRVWLKENPEIS ⁺ DEIDAKIRALNGVMHIT..E.....GTQDE.TDGER.....PEE..... 348	348
AKIGQKDNVRVWLKENPEIS ⁺ DEIDAKIRALNGVMHIT..E.....GTQDE.TDGER.....PEE..... 348	348
NRIGQKDNVREYLKEHKEMAI ⁺ EIENKVRENQ ⁺ IVSRAA..T.FPASEAEDGE..... 353	353
ERIGQGRDNCREFLRENA ⁺ ELAREIENKVREHLGVTPMGA..V.TLAEVEED..... 352	352
DKIGQKKANACKYLKENPEIAKTLDKKLREMLLNPNMQ..LIAETSSAADV.EFGAV.....PEEF..... 354	354
DKIGQKKANACKYLKENPEIAKTLDKKLREMLLNPNMQ..LIAETSSAADV.EFGAV.....PEEF..... 354	354
SKIGQKKANAACKYLEENPEIGQ ⁺ EIEQQIRAKLLVTSANT..KATPVAEDLADA.DI..... 347	347
NKIGQGNNVIRYLEENPQISTEIEAVIREQLLTKASDQ..TAA.HDETEEEP.DLL.....ES..... 349	349
NKIGQGNNVIRYFEENNQIAE ⁺ IERNI ⁺ REQLLTGTNG..AVQ.I.EDEEEP.DLL.....LES..... 349	349

logo

		ELEE	
NTDB id 600 KW2 RS01765 WP 011675413.1		387	
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEE	388	
NTDB id 228 SPD RS09265 WP 001085462.1	EIEE	388	
NTDB id 194 SPR RS08825 WP 001085462.1	EIEE	388	
NTDB id 159 SP RS09750 WP 001085462.1	EIEE	388	
NTDB id 527 SMSK321 RS11065 WP 001085454.1	EIEE	384	
NTDB id 499 SM12261 RS08315 WP 078228268.1	EIEE	384	
NTDB id 453 Spy49 1753c ACI62003.1	ED..	378	
NTDB id 408 SMU RS09530 WP 002262392.1	ED..	383	
NTDB id 115 BSU 16940 NP 389576.2		348	
NTDB id 625 LCA RS02525 WP 011374196.1		355	
NTDB id 1313 DR RS12030 WP 010888966.1		363	
NTDB id 1245 Cj1673c YP 002345041.1		343	
NTDB id 1214 NCTC11637 00359 SQJ03206.1		347	
NTDB id 1211 C694 RS00795 WP 000963128.1		347	
NTDB id 1334 RAOC RS04870 WP 004918236.1		343	
NTDB id 1389 A4U84 RS07560 WP 021112712.1		372	
NTDB id 1130 NGFG RS03960 WP 003688695.1		348	
NTDB id 1124 NGFG RS03960 WP 003688695.1		348	
NTDB id 1123 OK783 RS03845 WP 003688695.1		348	
NTDB id 260533 CXD89 RS06780 WP 003812760.1		353	
NTDB id 1427 RS RS02760 WP 011000510.1		352	
NTDB id 1165 A1552VC RS01565 WP 000344154.1		354	
NTDB id 1142 GTF74 RS11550 WP 000344154.1		354	
NTDB id 1205 PSJM300 05545 AFN77183.1		347	
NTDB id 1022 ACIAD RS06390 WP 004925639.1		349	
NTDB id 1074 ABD1 RS10195 WP 000344167.1		349	
consensus			

-  non conserved
-  similar
-  ≥ 50% conserved