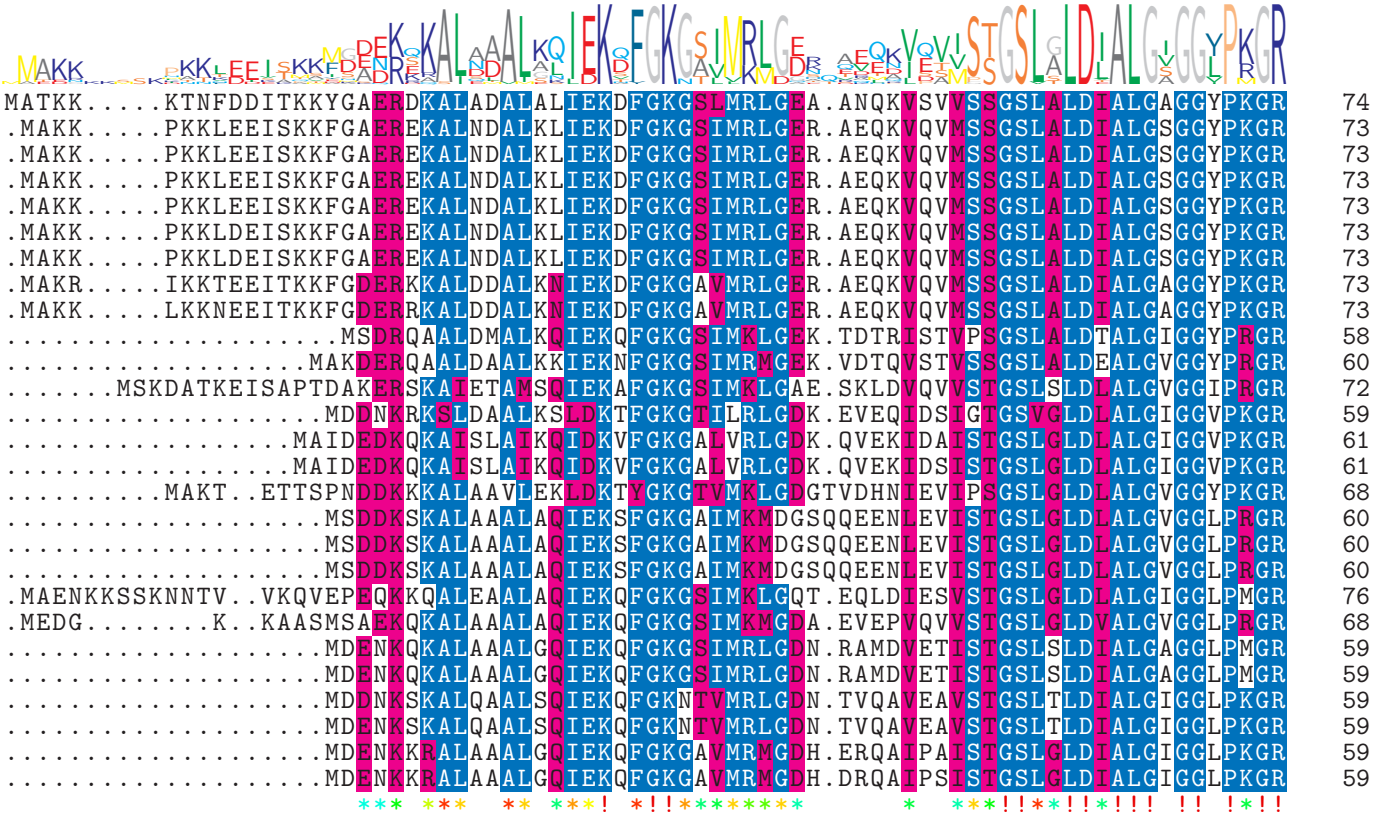


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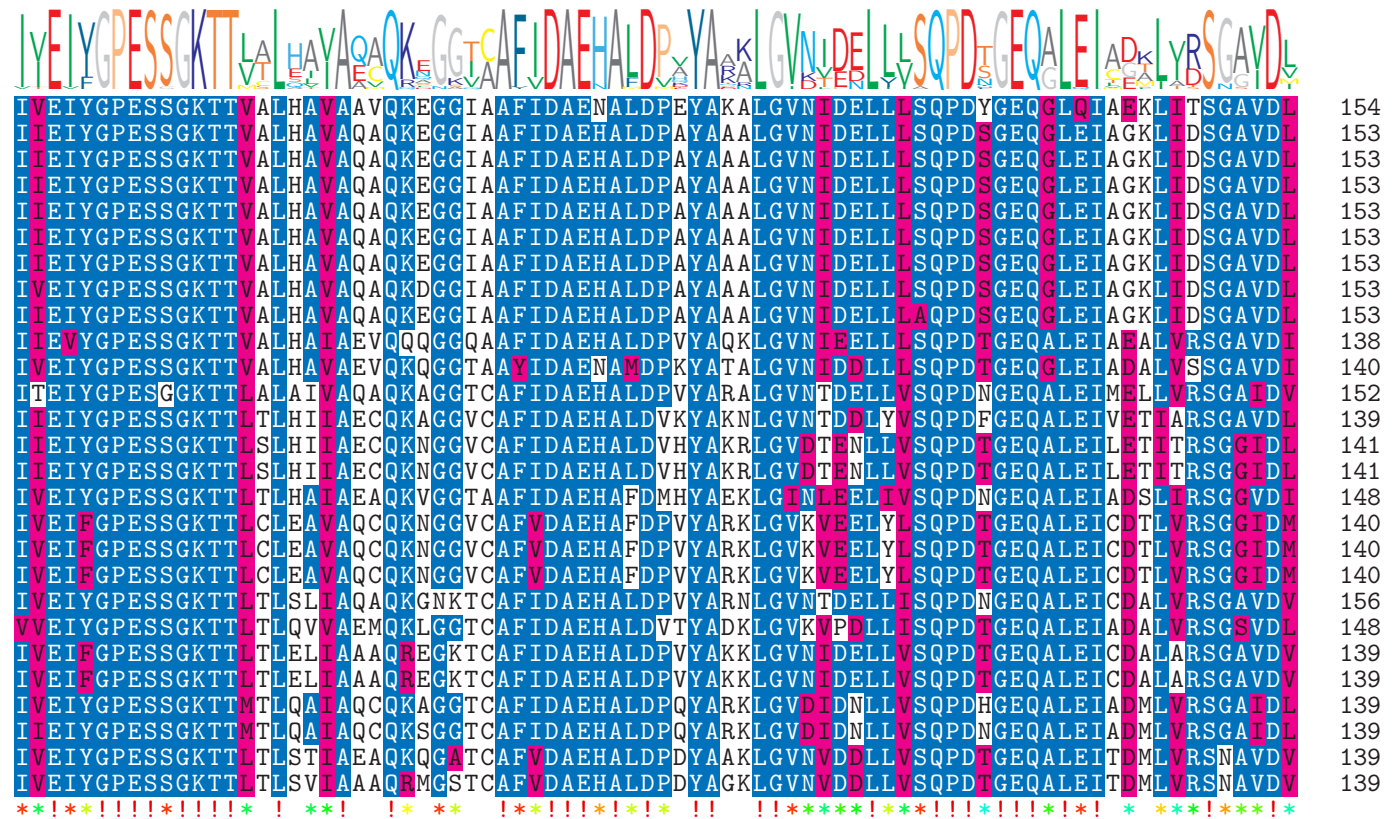
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consensus



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consensus

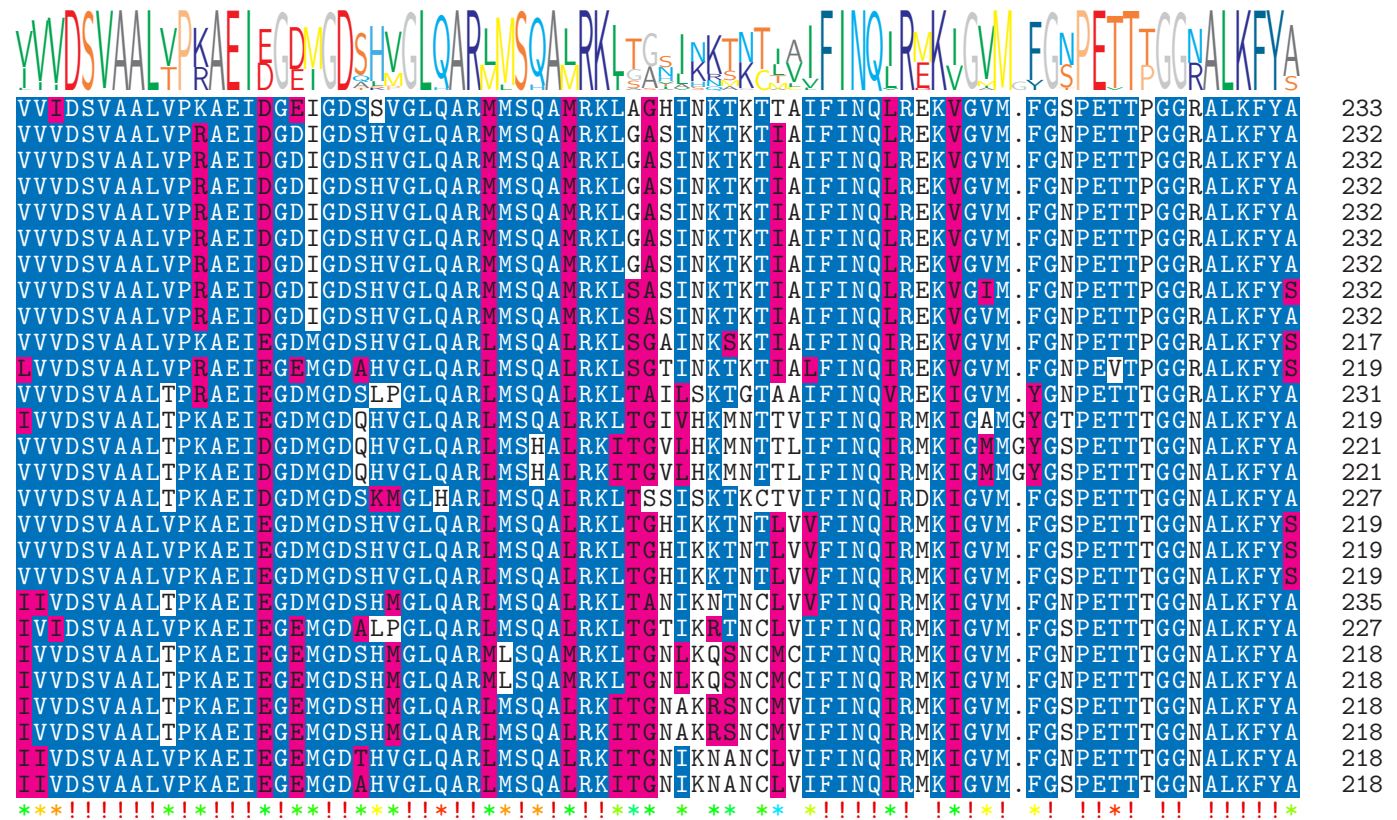
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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logo

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NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVEIMY	GEGISKTGELLKIASDLDIKKAGAW	SYK	311	
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NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRAETIKNGT.....DMIGN	RARIKVVKNKVAPPFKVAEVDIMY	GQGISRTGELVDMAVEKDI	INKSGSWYSYG	294	
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NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRSLSDTGKIKDKSGEV	IGNRTKVKVVKNKVAPPFKSAEFD	DIMYGEGVSKVGEILDVATDL	DIQKSGSWFSYQ	307	
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEV	VGNETRIKVVKNKIAAPFKEANTQ	IMYGGGFNRREGELIDLG	VKHKMVEKSGAWSYN	293	
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	VGSETKVKVVKNKMAPPFK	EAI	FIQILYGGKGTNRNLGELVD	LAVQQDIVQKAGAWSYQ	293
NTDB id 136982 Achr RS05890 WP 039802691.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVKVVKNKVAPPFRQAE	FIQILYGGKGIYRNGE	IIDLGVQQLLEKSGAWSYQ	293	
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVKVVKNKVAPPFRQAE	FIQILYGGKGIYRNGE	IIDLGVQQLLVEKSGAWYAYK	293	
consensus	*!!***!* *	** *****!*****!!*!!*!!* *	*****!*!*** ***** **	*** ! !*****!		


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GEKIGQGSENAKFLADNPEIFDDIDHKVRVQFGLIEEDNTEEEKSSKEK...ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNNGIEIE	377
EERLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGGQKEKTIATYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPE.....AA.EA.....	363
DKKLGGGRENKSKAFLKENPEIADIEITKATIQNSMGIEMGIS.....GSEDDEG.....EE.....	343
DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEIM....PLPDEPL.....EEME.....	347
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DTKLGGGRDITVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT.....EGTQDE.....TDGERPEE.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHIT.....EGTQDE.....TDGERPEE.....	348
GTKIGGQKNNAVKWLKENPEIADKLEQEIRNTLASNPNSV....LKATASD.....SNDESDVEEFSEEE.L.....	372
GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMGA....VTLA.E.....EVEED.....	352
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQ....LIAETSS....AA..DDVEFGAVPEEF.....	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNMQ....LIAETSS....AA..DDVEFGAVPEEF.....	354
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKASDQ....TAAHD.E.....TEEEPDLLES.....	349
GNKIGGQKNNVIRYFEENNQIAEEIERNIREQLLTGTNG....AVQI..E.....DEEPPDLLLES.....	349
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GSKIGGQKANAAKYLENPEIQEIEQIRAKLLVTSANT....KATPVAE.....DLADADI.....	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved