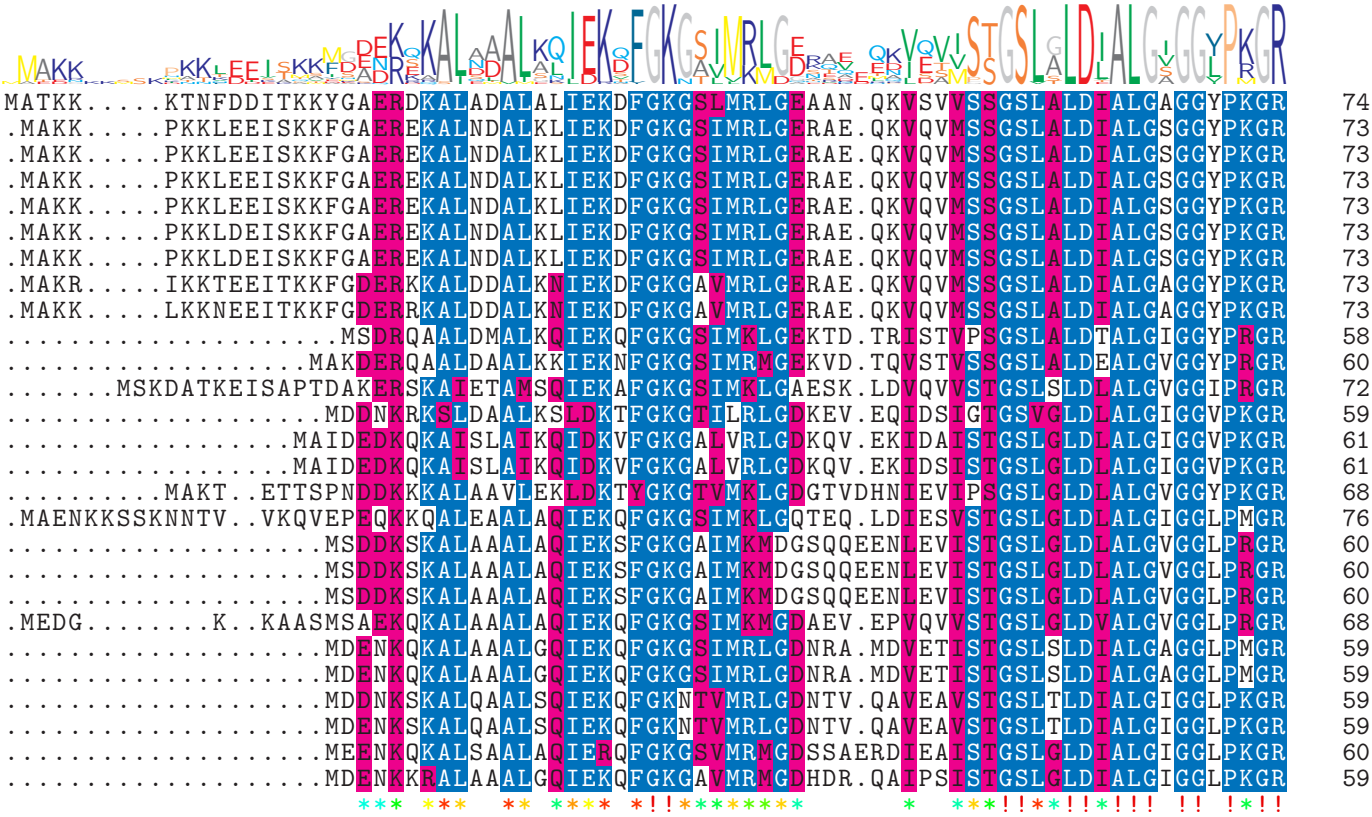


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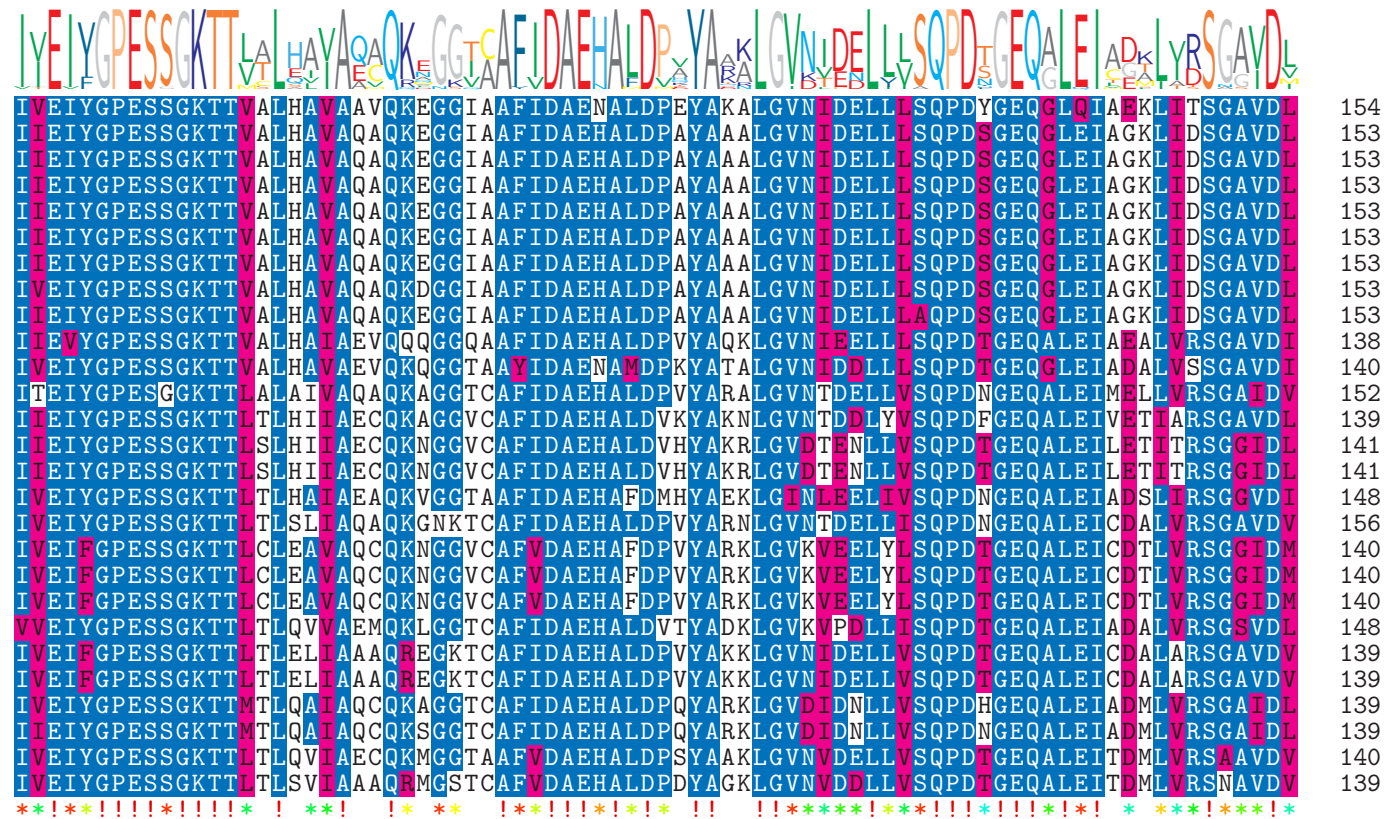
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consensus

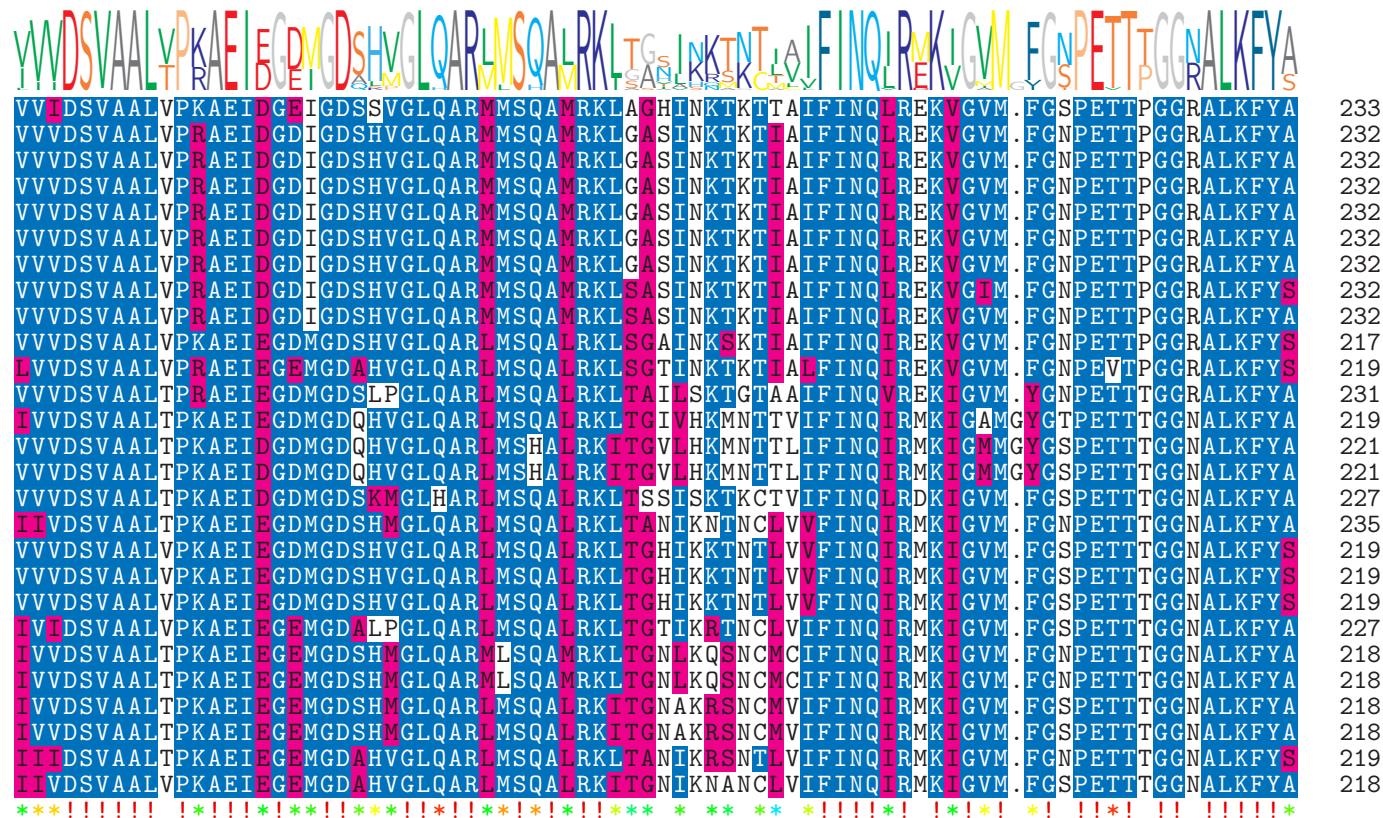
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consensus

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NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVVKNKVAPPFKSAEFD	DIMYGGEGVSKVGEILDVATDL	DIIQKSGSWFSYQ	307
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NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVKVVKNKVAPPFRQAEFQILYGGKIYRNGEIIDLG	VQQGLVEKSGAWYAYK	293	
consensus	*!!**!* *	* ** *****!*****!*****!*	* *****!***** ***** *	*** ! !*****!	


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consensus

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Sequence	Score
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DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEID ⁴ KQV ⁵ RSKF ⁶ GLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEID ⁴ KQV ⁵ RSKF ⁶ GLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ¹ ENAKKYLA ² EHPEIF ³ DEID ⁴ KQV ⁵ RSKF ⁶ GLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGS ¹ ENAKKYLA ² DNPEIF ³ DEID ⁴ HQV ⁵ RVVQF ⁶ GLIDGEEAAE...SKKDE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGS ¹ ENAKKFLADNPEIF ² DD ³ ID ⁴ HKV ⁵ RVVQF ⁶ GLIEEDNTEEEKSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGQGS ¹ ENAKRYLA ² DHPQLF ³ DEID ⁴ RKV ⁵ RVKQF ⁶ GLLEESEESAMAVASE.....E.....TD ¹ D ² LALDLN ³ GIEIE	377
EE ¹ RLGQGR ² ENAKQFL ³ KNKD ⁴ IMLM ⁵ IQEQ ⁶ IREHY ⁷ GLD ⁸ NNGVV ⁹ QQAEET ¹⁰ QEEL ¹¹ .EFE.E.....	348
SERIGQGR ¹ ENAKNYLA ² DHED ³ VE ⁴ RLK ⁵ VRAAY ⁶ GISD ⁷ VPEEDLPTTEDE.QI.NILPDDST.....EE	355
DERIGQG ¹ KEKTI ² AI ³ AE ⁴ RP ⁵ MEQE ⁶ IE ⁷ DRV ⁸ MAA ⁹ IRAGNAGEAPALAPAPAAP..EAA.....EA.....	363
DKKL ¹ GGGREN ² AKFL ³ KNPEIA ⁴ DEIT ⁵ KA ⁶ IQNSM ⁷ GIEGMISGSEDDEGEE.....	343
DKKL ¹ GGGREN ² AKALL ³ KED ⁴ KALADEIT ⁵ LK ⁶ IKESIG ⁷ SNEEIMPLPDEPLEEM.....E.....	347
DKKL ¹ GGGREN ² AKALL ³ KED ⁴ KALADEIT ⁵ LK ⁶ IKESIG ⁷ SNEEIMPLPDEPLEEM.....E.....	347
DTKL ¹ GGGRD ² TV ³ KEL ⁴ IKDN ⁵ PELA ⁶ ELEAK ⁷ IREKLQAK.....	343
GTKIGQG ¹ KNNNAV ² KL ³ KNPEIA ⁴ DKLE ⁵ QEIR ⁶ NTL ⁷ ASN ⁸ PNSVLKATASDSNDES.DVEEF.....SEEL.....	372
GAKIGQG ¹ KDNVRV ² WL ³ KNPEIS ⁴ DEID ⁵ AK ⁶ IRALN ⁷ GVEMHITEGTQDET.....DGER.....PEE.....	348
GAKIGQG ¹ KDNVRV ² WL ³ KNPEIS ⁴ DEID ⁵ AK ⁶ IRALN ⁷ GVEMHITEGTQDET.....DGER.....PEE.....	348
GAKIGQG ¹ KDNVRV ² WL ³ KNPEIS ⁴ DEID ⁵ AK ⁶ IRALN ⁷ GVEMHITEGTQDET.....DGER.....PEE.....	348
GERIGQGR ¹ DNCR ² REFL ³ RENA ⁴ ELAR ⁵ EI ⁶ ENK ⁷ VREHL ⁸ GVTPMGAVTLAAEEVE.....ED.....	352
GDKIGQG ¹ KANACKYL ² KNPEIA ³ AKT ⁴ L ⁵ DKKL ⁶ REMLLN ⁷ PENMQLIAETSSAADV.EFGAV.....PEEF.....	354
GDKIGQG ¹ KANACKYL ² KNPEIA ³ AKT ⁴ L ⁵ DKKL ⁶ REMLLN ⁷ PENMQLIAETSSAADV.EFGAV.....PEEF.....	354
GNKIGQG ¹ KNNVIR ² YLEENP ³ QIST ⁴ EIEAV ⁵ IREQLLT ⁶ TKASDQTAAHDE.....TEEE.....PDLLS.....	349
GNKIGQG ¹ KNNVIR ² YFEENN ³ QIA ⁴ EIEI ⁵ ERN ⁶ IREQLLT ⁷ TGTNGAVQI.E.....DEEE.....PDLLS.....	349
QEKIGQG ¹ KDNVRV ² YL ³ KNPEIA ⁴ AKT ⁵ LE ⁶ QQI ⁷ RAELLEKKLPVAAVEEE.....VETV.....DD.....	346
GSKIGQG ¹ KANAAKY ² LEENPEI ³ GQ ⁴ EIEQ ⁵ IRAKLL ⁶ VTSANTKATPVA.....EDLA.....DADI.....	347

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved