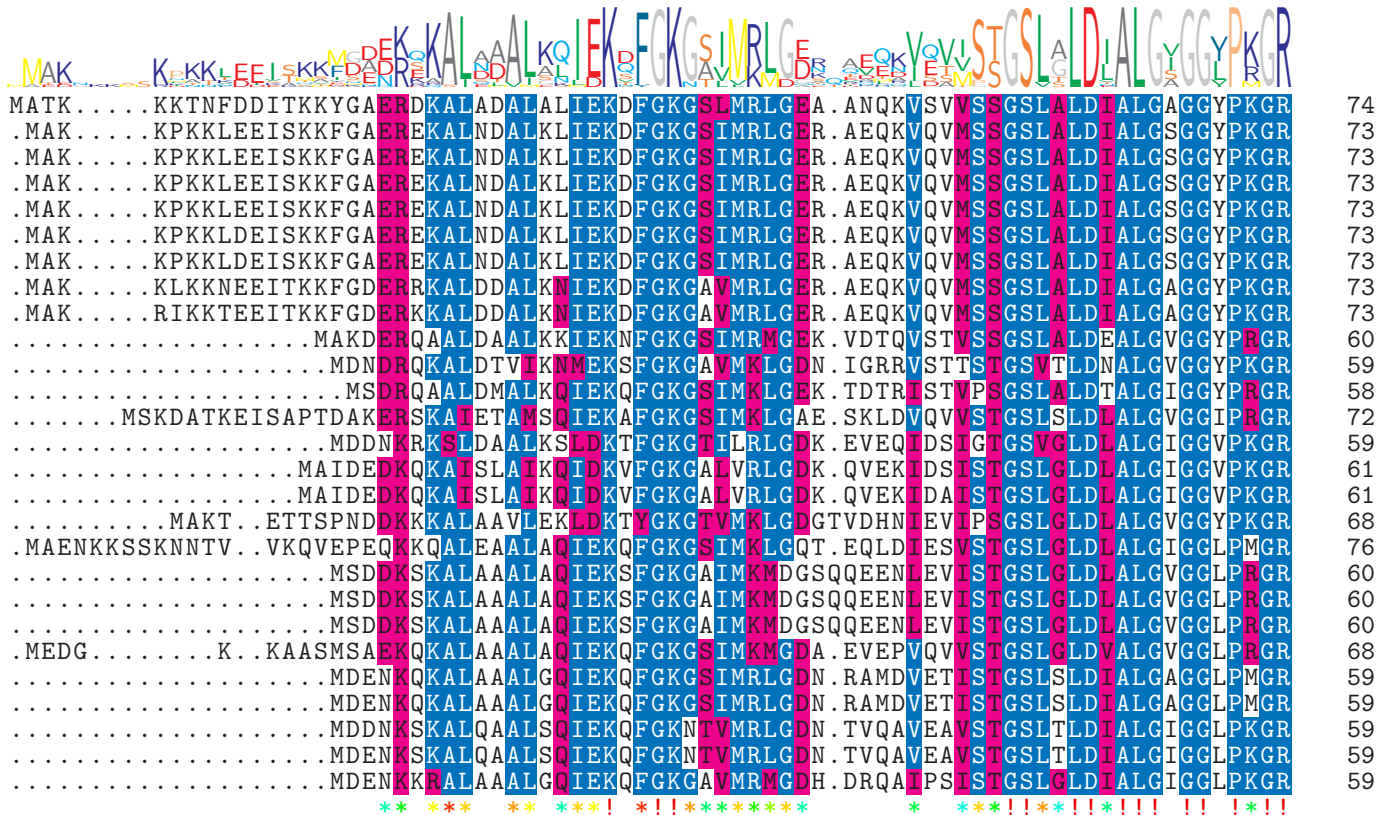


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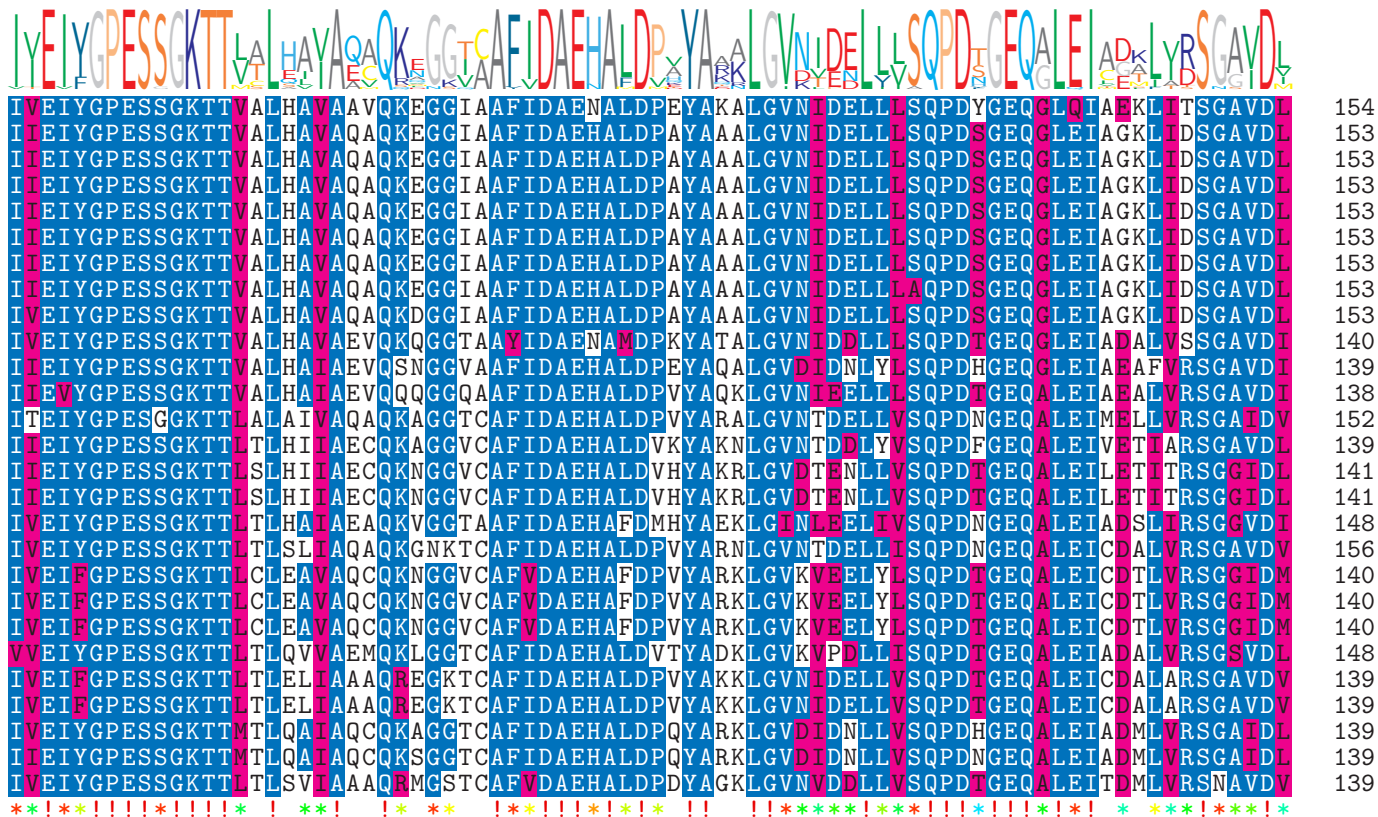
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consensus

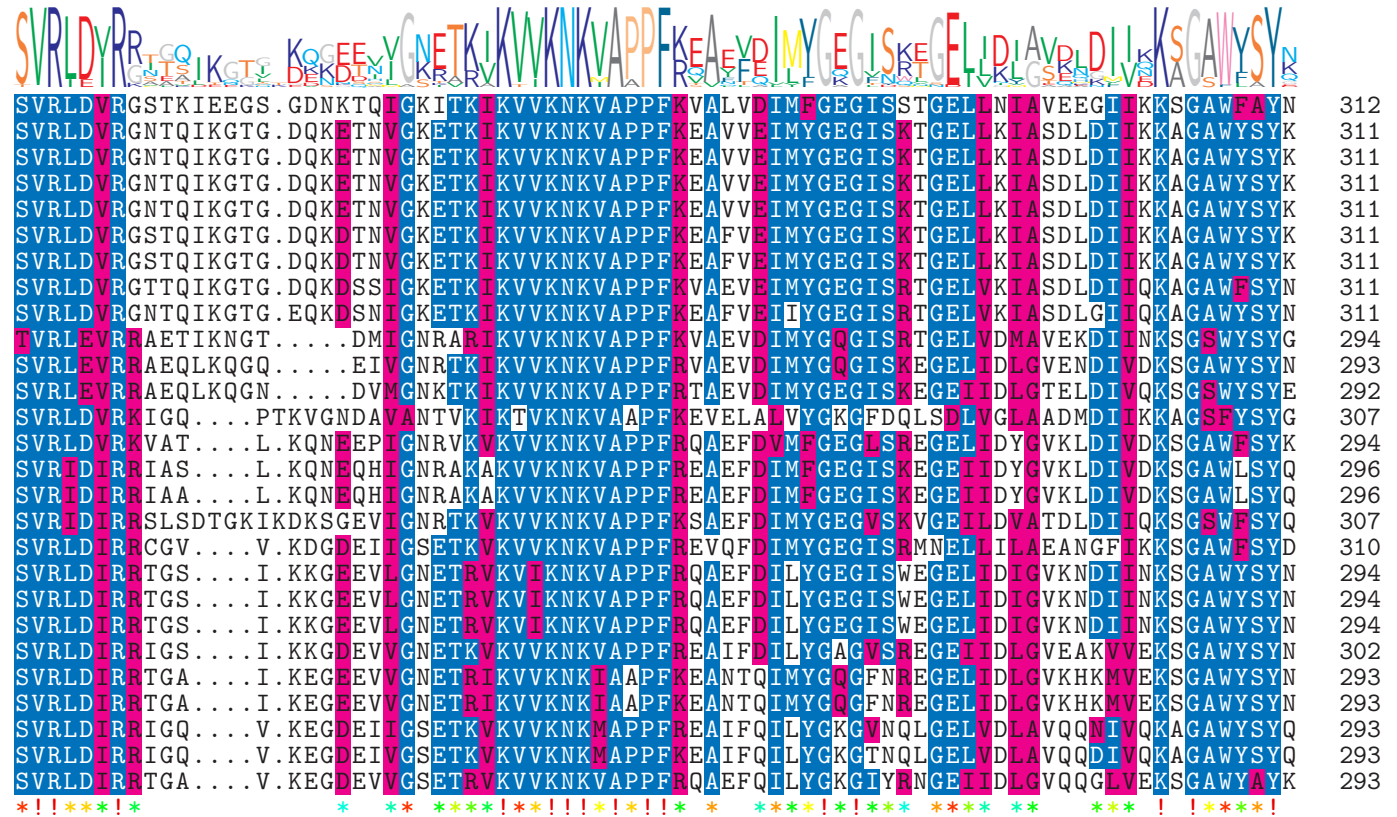
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NTDB id 1313 DR RS12030 WP 010888966.1	VV	DSVAAL	TPRAEIE	GDMGDS	LPGLQAR	MSQAL	RKLT	AIL	SKTGT	A	IFINQ	VREK	IGVM	Y	CNP	PETTT	GGRALKFYA	231		
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NTDB id 1165 A1552VC RS01565 WP 000344154.1	I	V	V	DSVAAL	TPKAEIE	GEMGDS	HMGLQAR	MSQAM	RKLTG	NL	KQSN	CMC	IFINQ	IRMKI	IGVM	FGNP	PETTT	TGGNALKFYA	218	
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consensus	***	!!!!!!	!*	!!!!	*!	***!	***!	***!	***!	***!	***!	***!	***!	*	*	*	!!!!!!	*!	!!!!!!	***

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consensus



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consensus

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Sequence	Score
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DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ EN ⁺ AK ⁺ KYLA ⁺ EH ⁺ PE ⁺ IF ⁺ DE ⁺ ID ⁺ KQ ⁺ VR ⁺ SK ⁺ FG ⁺ LIDGEEVSEQD ⁺ TENKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
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GEKIGQGS ⁺ EN ⁺ AK ⁺ RYLA ⁺ DHP ⁺ QL ⁺ F ⁺ DE ⁺ ID ⁺ RK ⁺ VR ⁺ VK ⁺ FG ⁺ LLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ⁺ EN ⁺ AK ⁺ KFLA ⁺ DN ⁺ PE ⁺ IF ⁺ DD ⁺ ID ⁺ HK ⁺ VR ⁺ VQ ⁺ YGLIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
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DERIGQG ⁺ KE ⁺ KT ⁺ IA ⁺ Y ⁺ IA ⁺ ER ⁺ PE ⁺ ME ⁺ QE ⁺ IRDRVMAAIRAGNAGEAPALAPAPAPEAAEA.....	363
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DK ⁺ KL ⁺ GQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KE ⁺ DKA ⁺ LAD ⁺ E ⁺ IT ⁺ LK ⁺ IKESIGSNEEI....MPLPDE..PLEEME.....	347
DK ⁺ KL ⁺ GQGR ⁺ EN ⁺ AK ⁺ ALL ⁺ KE ⁺ DKA ⁺ LAD ⁺ E ⁺ IT ⁺ LK ⁺ IKESIGSNEEI....MPLPDE..PLEEME.....	347
DTKL ⁺ GQGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LAE ⁺ LEAK ⁺ IREKLQAK.....	343
GTKIGQG ⁺ KNN ⁺ AV ⁺ KWL ⁺ KEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QEI ⁺ RNTLA ⁺ SNPNS....VLKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHI....TEGTQDET ⁺ DGER....PEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHI....TEGTQDET ⁺ DGER....PEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ ID ⁺ AK ⁺ IRALN ⁺ GVEMHI....TEGTQDET ⁺ DGER....PEE.....	348
GE ⁺ RIGQGRD ⁺ NC ⁺ REF ⁺ LRENA ⁺ E ⁺ LARE ⁺ IE ⁺ KN ⁺ VR ⁺ HL ⁺ GVTPMG....AVTLA.EEEVED.....	352
GDKIGQG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ AK ⁺ TLD ⁺ KKL ⁺ REMLLN ⁺ PENM....QLIAETSSAADDVE..FGAVPEEF.....	354
GD ⁺ KIGQG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ AK ⁺ TLD ⁺ KKL ⁺ REMLLN ⁺ PENM....QLIAETSSAADDVE..FGAVPEEF.....	354
GN ⁺ KIGQG ⁺ KNN ⁺ VIR ⁺ Y ⁺ LEEN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IREQLLT ⁺ TKASD....QTAA.HDETEEEP ⁺ PD..LL..ES.....	349
GN ⁺ KIGQG ⁺ KNN ⁺ VIR ⁺ Y ⁺ FEEN ⁺ NQ ⁺ IA ⁺ E ⁺ EI ⁺ ERN ⁺ IREQLLT ⁺ VTGTN....GAVQ.I.EDEEEEP ⁺ PD..LL..LES.....	349
GS ⁺ KIGQG ⁺ KANA ⁺ AK ⁺ YL ⁺ EN ⁺ PE ⁺ IG ⁺ QE ⁺ IE ⁺ QQ ⁺ IRAKLL ⁺ YTSAN....TKATPVAEDLADAD..I.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE 388
NTDB id 228 SPD RS09265 WP 001085462.1	IEE 388
NTDB id 194 SPR RS08825 WP 001085462.1	IEE 388
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consensus	

-  non conserved
-  similar
-  ≥ 50% conserved