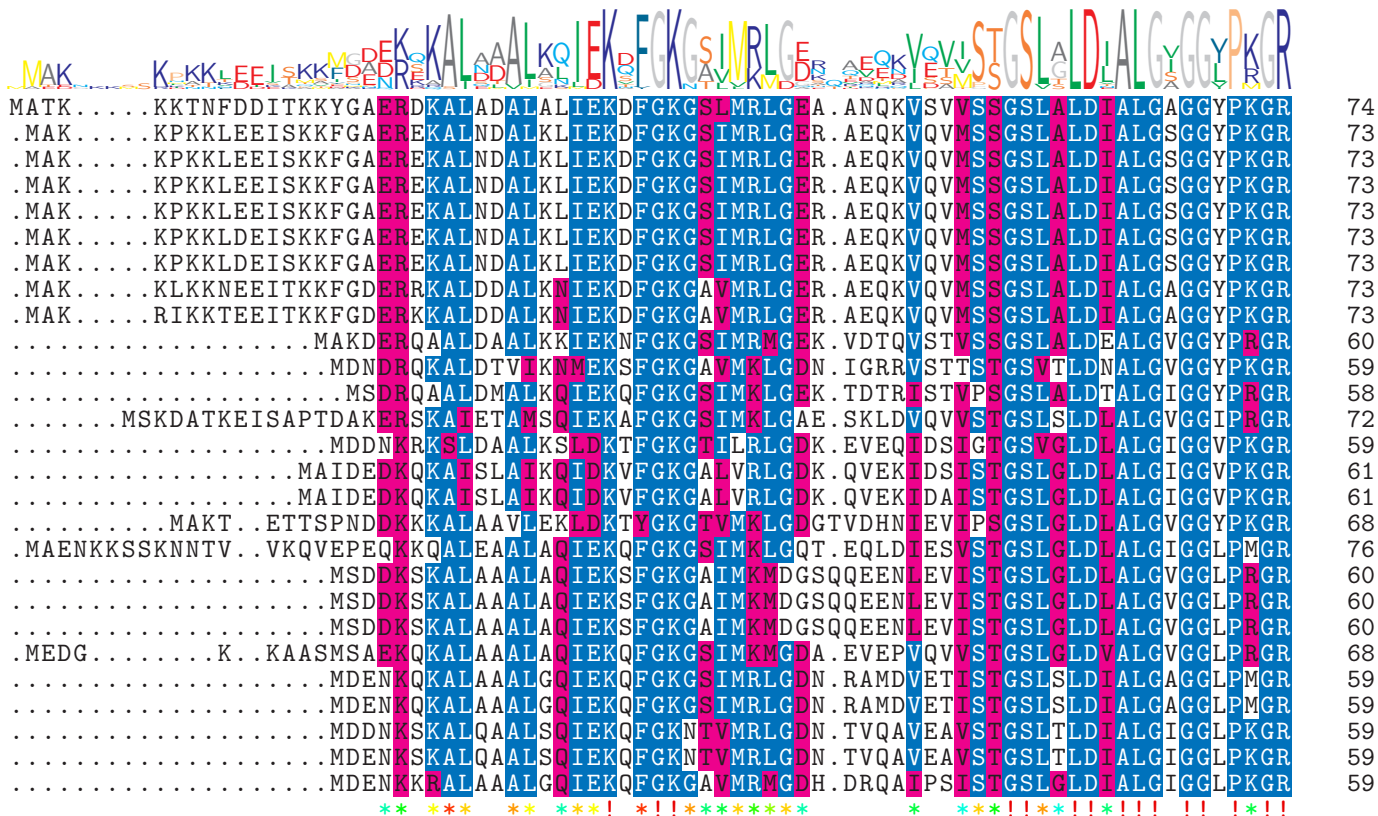


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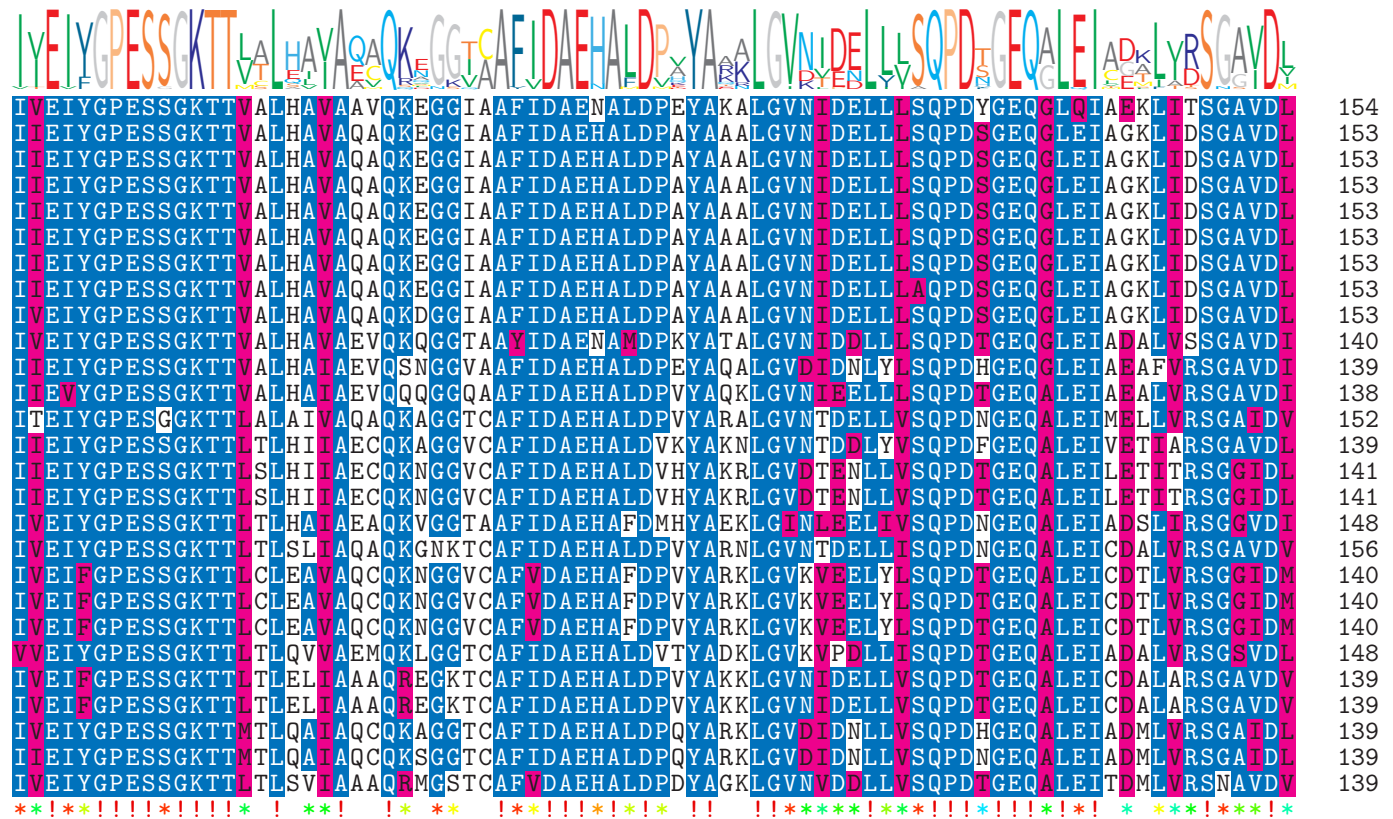
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consensus

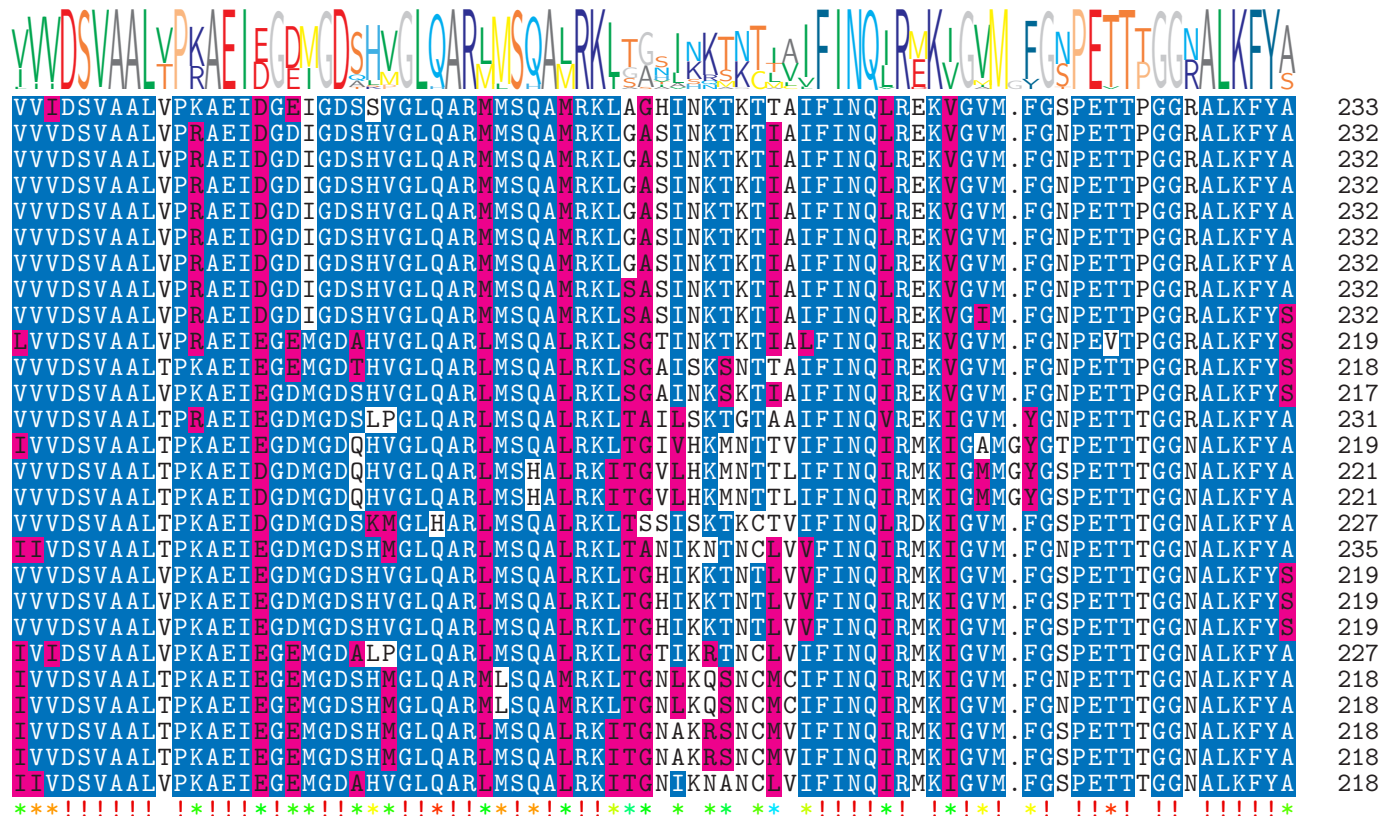
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consensus

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logo

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consensus	*!!	*****!	*	*	*	*	*	*****!	*!!	!!	*!!	!!	*	*	*	*****!	*!!	*****	*****	*****	*****	*****	*****	*****	*****!	!!	*****!

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
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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 ⁺ HQ ⁺ VR ⁺ VQ ⁺ FG ⁺ LIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
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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
SERIGQGR ⁺ EN ⁺ AK ⁺ NYLA ⁺ DH ⁺ ED ⁺ VE ⁺ EVRLK ⁺ VRAAYG ⁺ ISDVPEEDLPTTEDEQINILPDDSTEE.....	355
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EERLQCG ⁺ REN ⁺ AK ⁺ QFL ⁺ KEN ⁺ DK ⁺ IM ⁺ LI ⁺ QE ⁺ IR ⁺ EHYGLDNNGVVQQQAETQEELFEFE.....	348
DERIGQG ⁺ KEKT ⁺ IAY ⁺ IA ⁺ ERPE ⁺ MEQE ⁺ IRDRVMAAIRAGNAGEAPALAPAPAPEAEAE.....	363
DKKLGGG ⁺ RENS ⁺ KA ⁺ FL ⁺ KEN ⁺ PE ⁺ IA ⁺ DE ⁺ IT ⁺ KA ⁺ IQNSMG ⁺ ITEGMI....SGSEDD..EGEE.....	343
DKKLGGG ⁺ RENA ⁺ KALL ⁺ KE ⁺ DKALA ⁺ DE ⁺ IT ⁺ LK ⁺ IKESIGSNEEI....MPLPDE..PLEEME.....	347
DKKLGGG ⁺ RENA ⁺ KALL ⁺ KE ⁺ DKALA ⁺ DE ⁺ IT ⁺ LK ⁺ IKESIGSNEEI....MPLPDE..PLEEME.....	347
DTKLQGRD ⁺ TV ⁺ KE ⁺ L ⁺ IK ⁺ DN ⁺ PE ⁺ LA ⁺ EELAK ⁺ IREKLQAK.....	343
GTKIGQG ⁺ KNN ⁺ AV ⁺ KWL ⁺ KEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ QEI ⁺ RNTLA ⁺ SNPNS....VLKATASDSNDESD..VEEFSEEL.....	372
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIRALN ⁺ GVEMHI....TEGTQDETDGER.....PEE.....	348
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIRALN ⁺ GVEMHI....TEGTQDETDGER.....PEE.....	348
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GDKIGQG ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PE ⁺ IA ⁺ AK ⁺ TLD ⁺ KKL ⁺ REMLLN ⁺ PENM....QLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGQG ⁺ KNN ⁺ VIR ⁺ Y ⁺ LEEN ⁺ PQ ⁺ ISTE ⁺ IE ⁺ AV ⁺ IREQLLT ⁺ TKASD....QTAA.HDETEEEDPD..LL..ES.....	349
GNKIGQG ⁺ KNN ⁺ VIR ⁺ Y ⁺ FEEN ⁺ NQ ⁺ IA ⁺ E ⁺ EI ⁺ ERN ⁺ IREQLLT ⁺ VTGTN....GAVQ.I.EDEEEDPD..LL..LES.....	349
GSKIGQG ⁺ KANA ⁺ AK ⁺ YL ⁺ EN ⁺ PE ⁺ IG ⁺ QE ⁺ IE ⁺ QQ ⁺ IRAK ⁺ LL ⁺ VT ⁺ SAN....TKATPVAEDLADAD..I.....	347

logo

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NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

- non conserved
- similar
- ≥ 50% conserved