

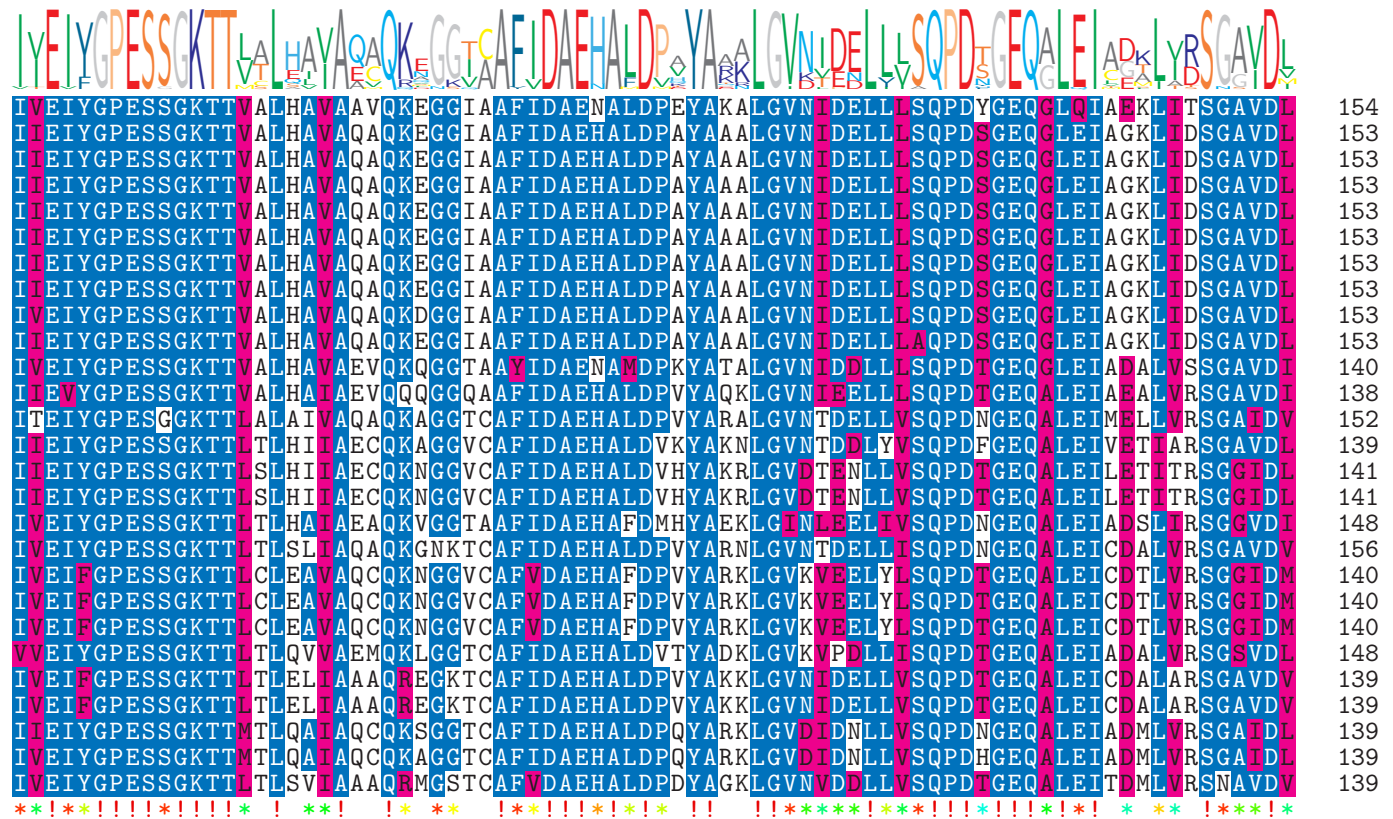
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consensus

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MATKK		KTN	FDD	IT	KKY	GA	ER	KA	LD	AL	AL	IE	DK	FK	SL	MR	LC	EA	AN	QK	VS	VS	SS	GS	SL	AL	LD	AL	GC	GG	YP	PK	GR	
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consensus

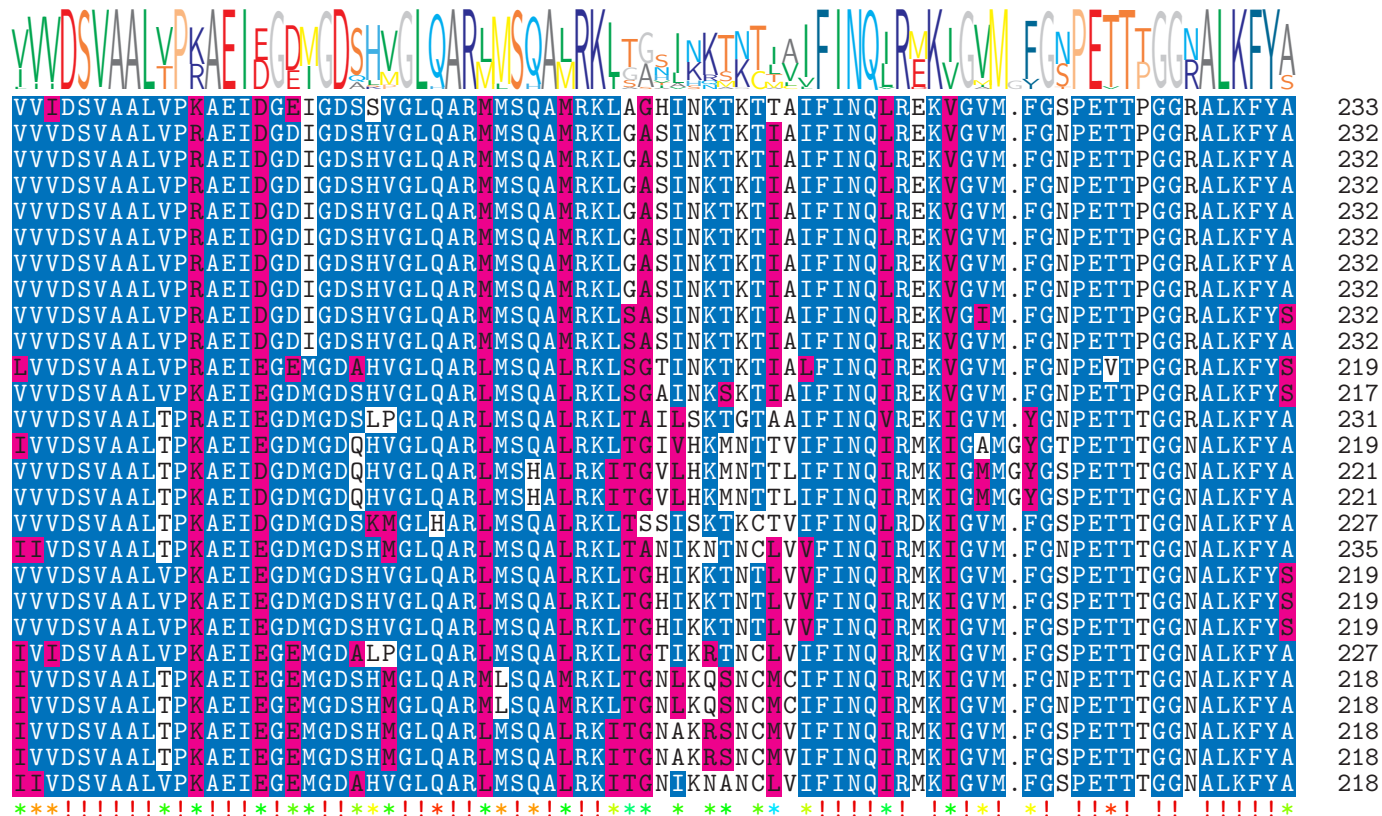
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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


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consensus

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Sequence	Score
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GEKIGGGS E NA K KFL D N P E I F D IDHKVRSVQ F GLIEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
GEKIGGGS E NA K RYL D HP Q L F DEIDRKVRSVQ F GLLESEEEESAMAVASE.....E.....TD D LALDLNNGIEIE	377
SERIGGG R ENAKNYL D H E D V E D EVRLKVR A AY G ISDVPEEDLPTTEDE.QIN.....ILPDDSTEE.	355
EERLGGC R ENAK F L K EN K D I ML I IQ E IR E HY G L D NNGVVQQQA E ET Q EE LFE.E.....	348
DERIGGG K E K TI A Y I A R P E ME Q EIRDRVMAAIRAGNAGEAPALAPAPA E AA E ..A.....	363
DK K LGGG R EN K A F L K EN P E I A D EIT K A I Q N SM G I EGMI....SGSEDDE..GE..E.....	343
DK K LGGG R ENAKALL K ED K AL A D E IT L K I K E S I GS N EEI....MPLPDEP..LE..EM..... E	347
DK K LGGG R ENAKALL K ED K AL A D E IT L K I K E S I GS N EEI....MPLPDEP..LE..EM..... E	347
DTKLGGGRD T V K EL I KN P EL A E E L E A K IREKL Q A.....VLKATASDSND..ES.....DVEEFSEEEEL...	372
GT K IGGG K NN A V K W L KN P E I A D K L E I R N T L AS N P N S....TEGTQDETD.....GERPEE.....	348
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GS K IGGG K AN A AK Y L E EN P E I Q E IE Q Q I RA K LL V TSAN....TKATPVAEDLA..DA.....D..I.....	347

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consensus			

- non conserved
- similar
- ≥ 50% conserved