

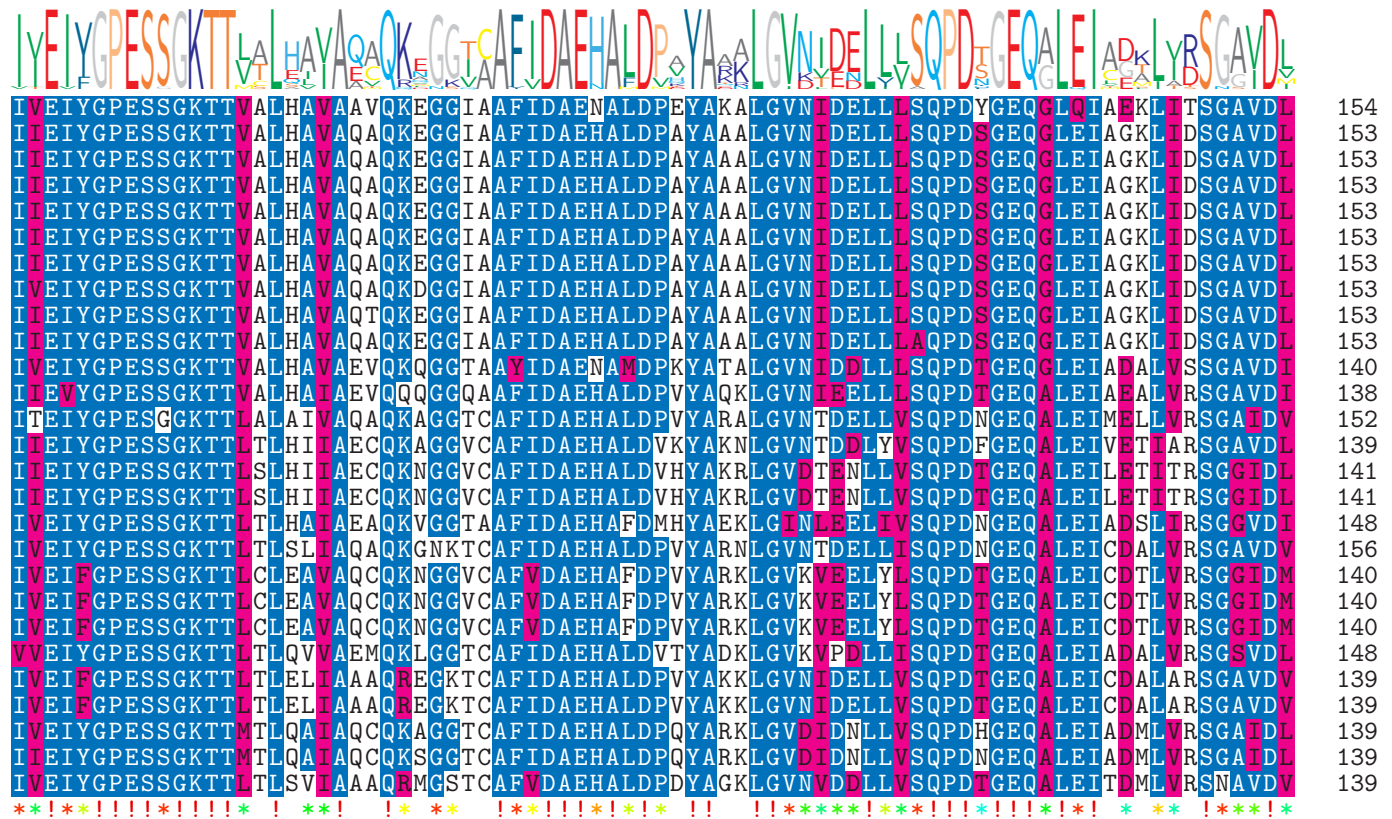
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consensus	*** **	

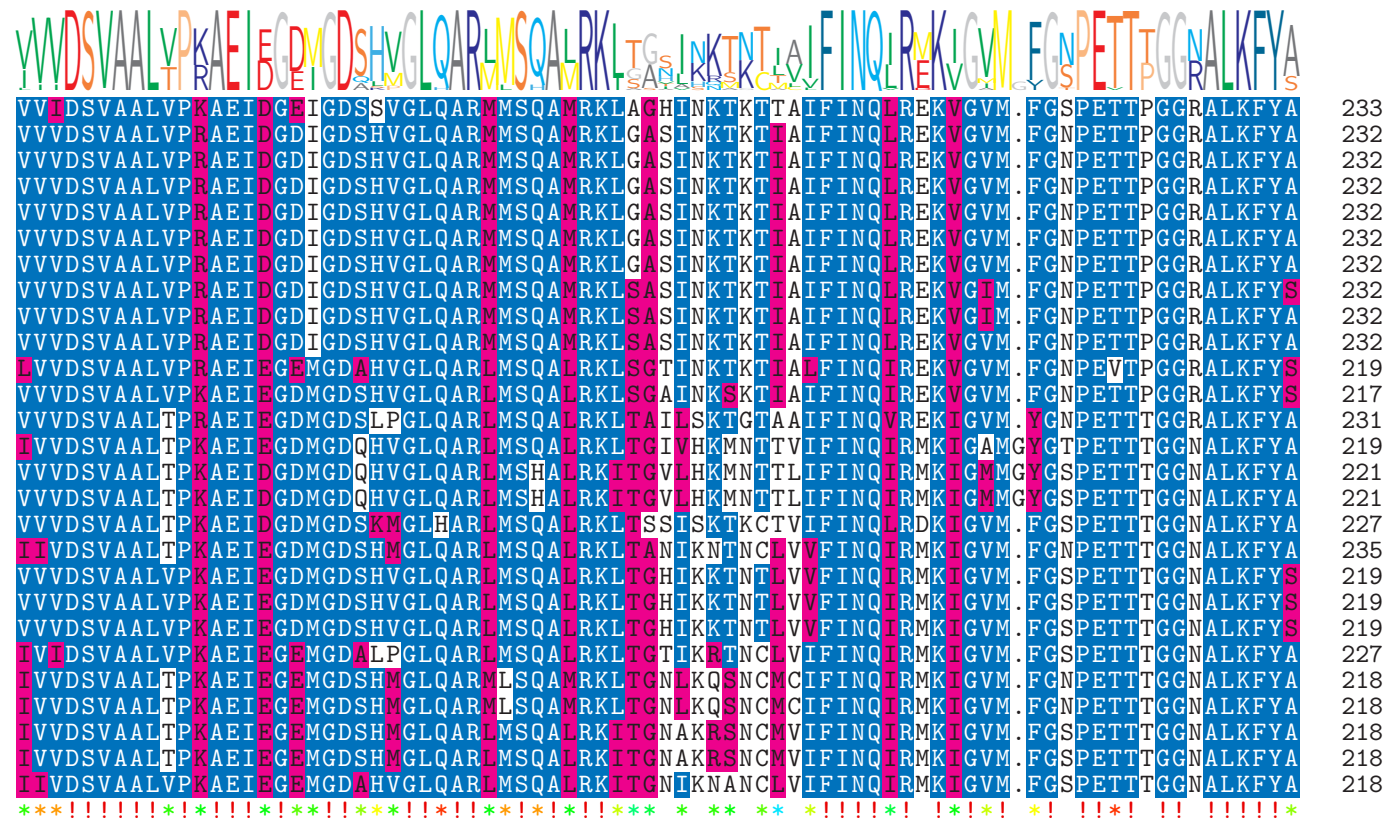
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consensus

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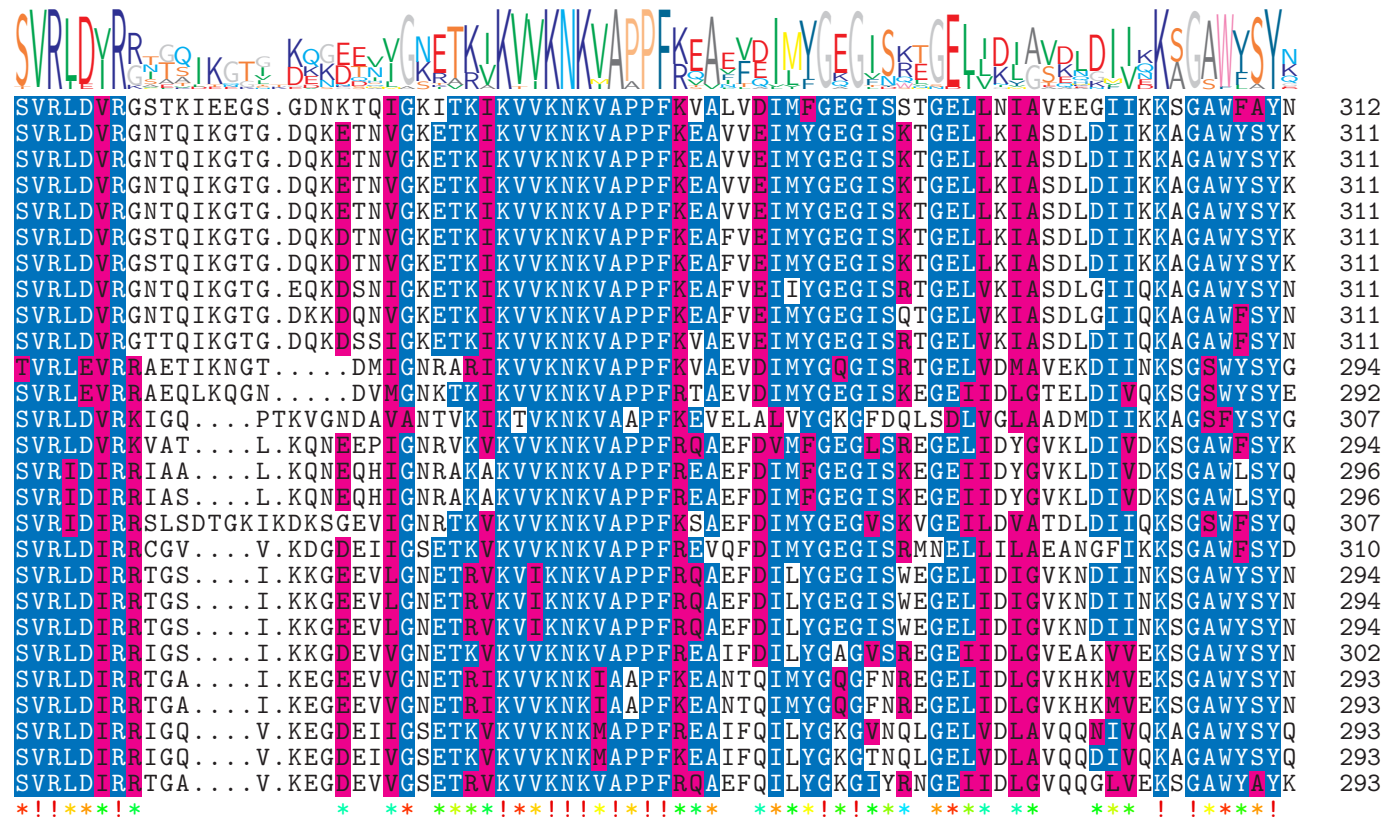
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGGGS E NAKKYLA E HP E IF D EIDKQVRSKF G LIDGEEVSEQDTENKKDEPKK...EE..AVNEEVPLDLGDELEIE	385
DEKIGGGS E NAKKYLA E HP E IF D EIDKQVRSKF G LIDGEEVSEQDTENKKDEPKK...EE..AVNEEVPLDLGDELEIE	385
DEKIGGGS E NAKKYLA D N P E I F D EIDHQRV V Q F LIDGEEIAES...KKDEAAQ...VD..SVNEEVTLDLGDELEIE	381
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GEKIGGGS E NAKKYLA D H P D I F E IDHKKVR V Q F GLIEPDEEDIV E EAQ.....VE..ETSD E LVLDLDSTIEIE	378
GEKIGGGS E NAKRYLA D H P Q L F D EIDRKVR V K F GLLEESSEESAMAV.....AS..EETD E LALDLNGIEIE	377
SERIGGGS E NAKNYLA D H D V E DEVRLK V RAAY G ISDVPEEDLPTTEDE.QIN.....ILPDDSTEE.	355
EE R LGGGREN A K N FL E ND K IM L MI Q E I RE H Y G L D NNGVVQQQAET E QEELE.....FE.E.....	348
DERIGGG E K T I A Y I A E R P E M E G E I RDRV M A I RAGNA E APALAP A PA A PE AAE A	363
DKKLGGGREN S K A FL K EN P E I A D EIT K AI Q NS M G I EG M I.....SGSEDD..E.....GEE.....	343
DKKLGGGREN A K A LL K ED K AL A D E IT L K I ES I GS N EEI.....MPLPDE..P.....LEEM E	347
DKKLGGGREN A K A LL K ED K AL A D E IT L K I ES I GS N EEI.....MPLPDE..P.....LEEM E	347
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GTKIGGGK N NA V K L KEN P E I A D K L E Q E I R N T L AS N PN SVLKATASDS.....NDES D VEEFSEEE L ...	372
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GNKIGGGK N NA V IR Y LE E N P Q I ST E IE A VI R E Q LL T KAS DQTAA.HDET.....EEEPD L L..ES.....	349
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GS K IGGGK A NA A K Y LE E NN P E I G E IE Q Q I R A KL L Y T SA NTKATPVAED.....LAD A D I	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved