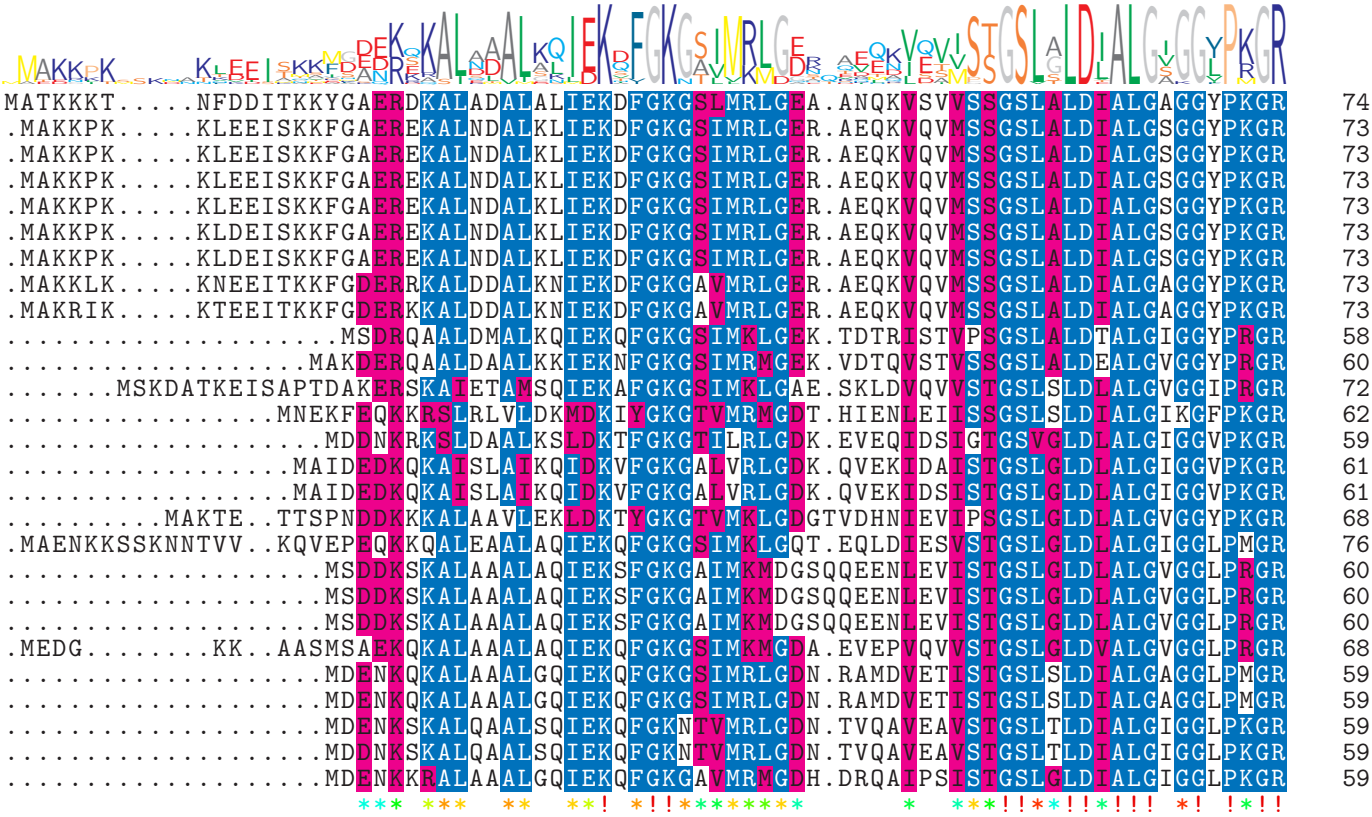


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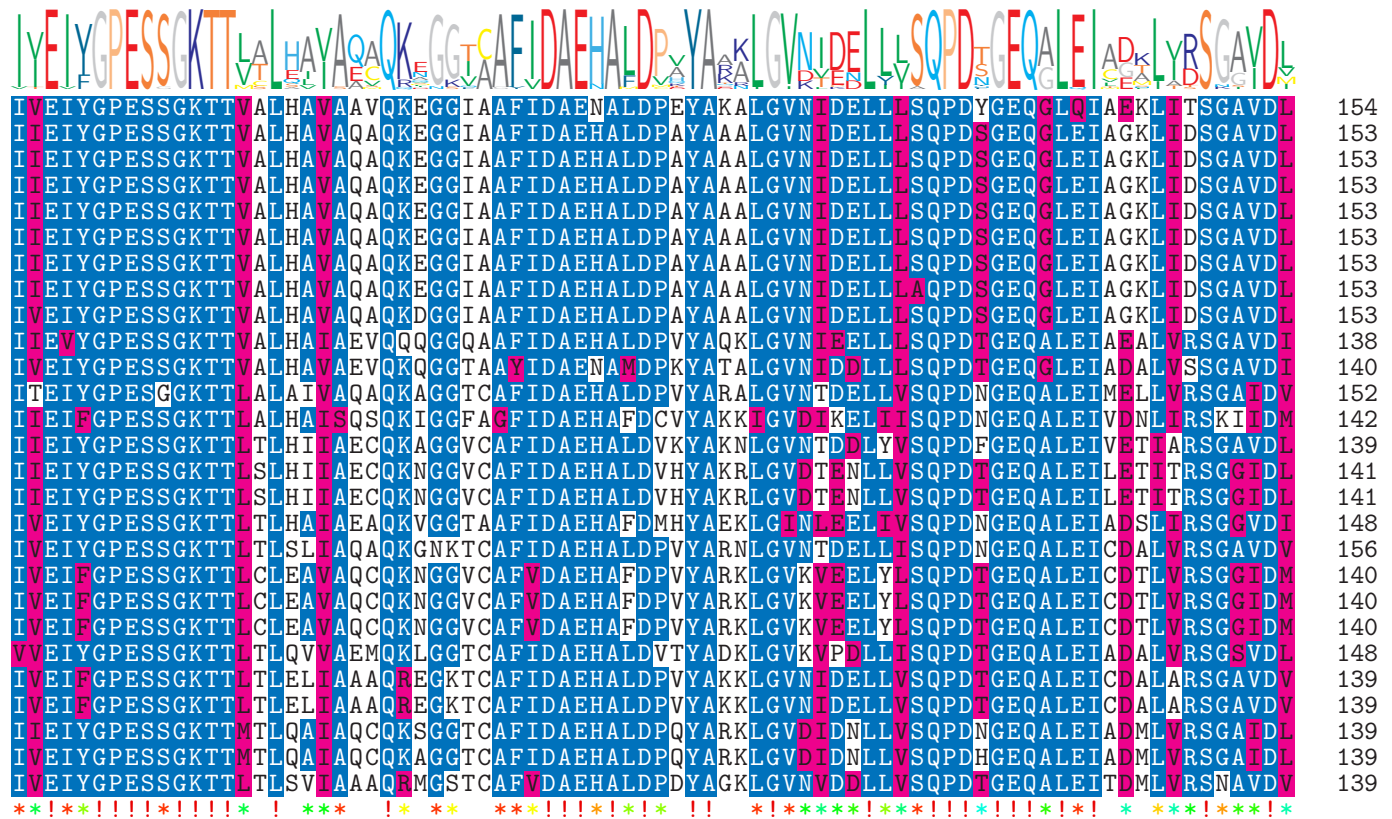
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consensus



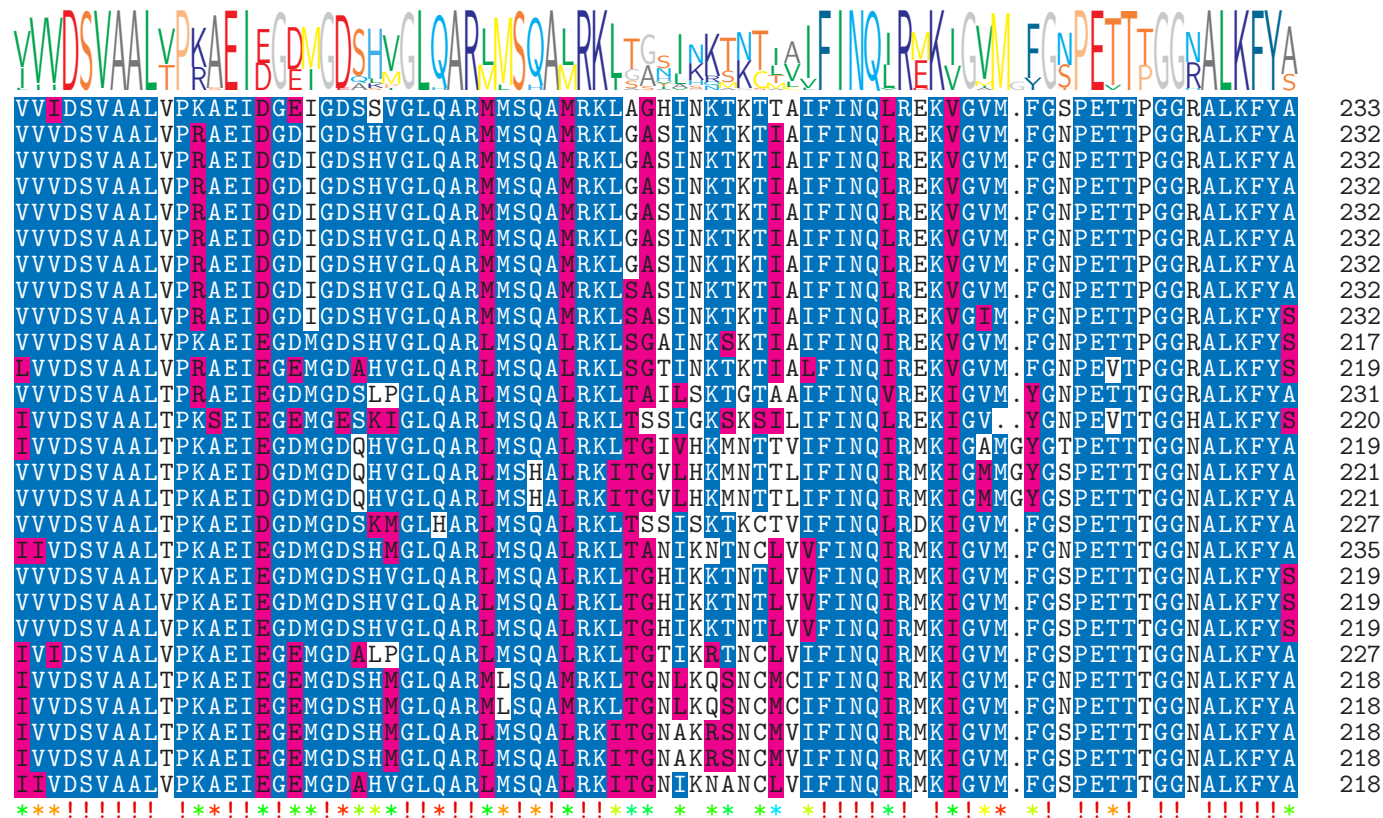
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consensus

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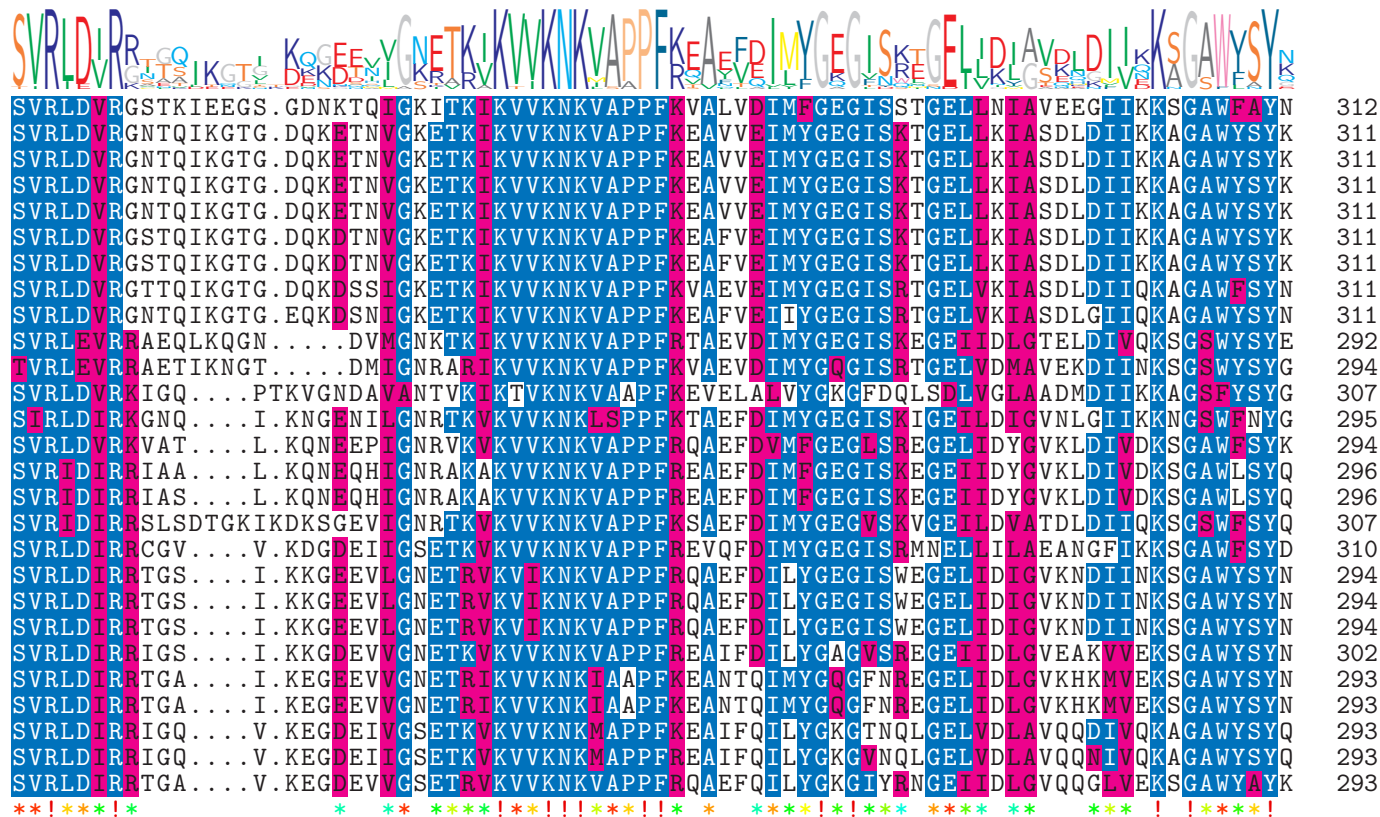
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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Sequence	Score
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DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFD ⁺ EID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFD ⁺ EID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFD ⁺ EID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IFD ⁺ EID ⁺ DKQ ⁺ VR ⁺ SKF ⁺ CLIDGEEVSEQDTE ⁺ NKKDE....PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGGGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ IFD ⁺ EID ⁺ DHQ ⁺ VR ⁺ VQF ⁺ CLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGGGS ⁺ ENAK ⁺ KYLAD ⁺ NPE ⁺ IFD ⁺ EID ⁺ DHQ ⁺ VR ⁺ VQF ⁺ CLIDGEEIAES....KKDE....VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGGGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ Q ⁺ IFD ⁺ EID ⁺ DRK ⁺ VR ⁺ VKF ⁺ CLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGGGS ⁺ ENAK ⁺ KKFLAD ⁺ NPE ⁺ IFD ⁺ DD ⁺ IDHK ⁺ VR ⁺ VQY ⁺ CLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EE ⁺ RL ⁺ GGGREN ⁺ AK ⁺ QFL ⁺ KEN ⁺ KD ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ CLDNNGVVQQQA ⁺ EETQEEL.EFE.E.....	348
SERIGGGR ⁺ ENAK ⁺ NYLAD ⁺ HED ⁺ VED ⁺ EVRL ⁺ KV ⁺ RAAY ⁺ CI ⁺ SDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGGQKE ⁺ KTIAY ⁺ IAER ⁺ PE ⁺ ME ⁺ Q ⁺ IERD ⁺ RVMAAIRAGNAGEAPALAPAPAAPEAAAAE.....	363
DMK ⁺ LGQRDSV ⁺ KE ⁺ FL ⁺ KE ⁺ KN ⁺ IIN ⁺ EM ⁺ QKN ⁺ IINQHF ⁺ K.....	330
DKKL ⁺ GGGREN ⁺ SKA ⁺ FL ⁺ KEN ⁺ PE ⁺ IA ⁺ DE ⁺ ITKA ⁺ IQNSM ⁺ CI ⁺ EGMI....SGSEDDE..GEE.....	343
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITLK ⁺ IKES ⁺ GSNEEI....MPLPDEP..LEEME.....	347
DKKL ⁺ GGGREN ⁺ AK ⁺ ALL ⁺ KED ⁺ KALADE ⁺ ITLK ⁺ IKES ⁺ GSNEEI....MPLPDEP..LEEME.....	347
DTKL ⁺ GGGRD ⁺ TV ⁺ KE ⁺ L ⁺ IKDN ⁺ PE ⁺ LA ⁺ EELAK ⁺ IREKLQAK.....	343
GTKIGGQK ⁺ NNAV ⁺ KW ⁺ LKEN ⁺ PE ⁺ IA ⁺ DK ⁺ LE ⁺ Q ⁺ IRNTLA ⁺ SNPNS....VLKATASDSNDESD..VEEFSEEEEL.....	372
GAKIGGQK ⁺ DN ⁺ VR ⁺ VWLKEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIRAL ⁺ NGVEMHI....TEGTQDETD.....GERPEE.....	348
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GAKIGGQK ⁺ DN ⁺ VR ⁺ VWLKEN ⁺ PE ⁺ IS ⁺ DE ⁺ IDA ⁺ KIRAL ⁺ NGVEMHI....TEGTQDETD.....GERPEE.....	348
GE ⁺ RIGGGRD ⁺ NCREF ⁺ LN ⁺ AE ⁺ LARE ⁺ EN ⁺ KV ⁺ REHL ⁺ CVTPMG....AV.TLAEVEEED.....	352
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GNKIGGQK ⁺ NNVIR ⁺ YFE ⁺ ENN ⁺ QIA ⁺ EIE ⁺ IRNI ⁺ REQLLT ⁺ TGTN....GAVQ.I.EDEEEEPD....LLES.....	349
GNKIGGQK ⁺ NNVIR ⁺ YLE ⁺ EN ⁺ PQI ⁺ STE ⁺ IEA ⁺ VIRE ⁺ QLLT ⁺ TKASD....QTAA.HDETEEEEPD....LLES.....	349
GSKIGGQK ⁺ ANA ⁺ AKY ⁺ LE ⁺ EN ⁺ PE ⁺ IG ⁺ IE ⁺ EQ ⁺ IRAK ⁺ LLY ⁺ TSAN....TKATPVAEDLADAD....I.....	347

logo

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consensus

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 ≥ 50% conserved