

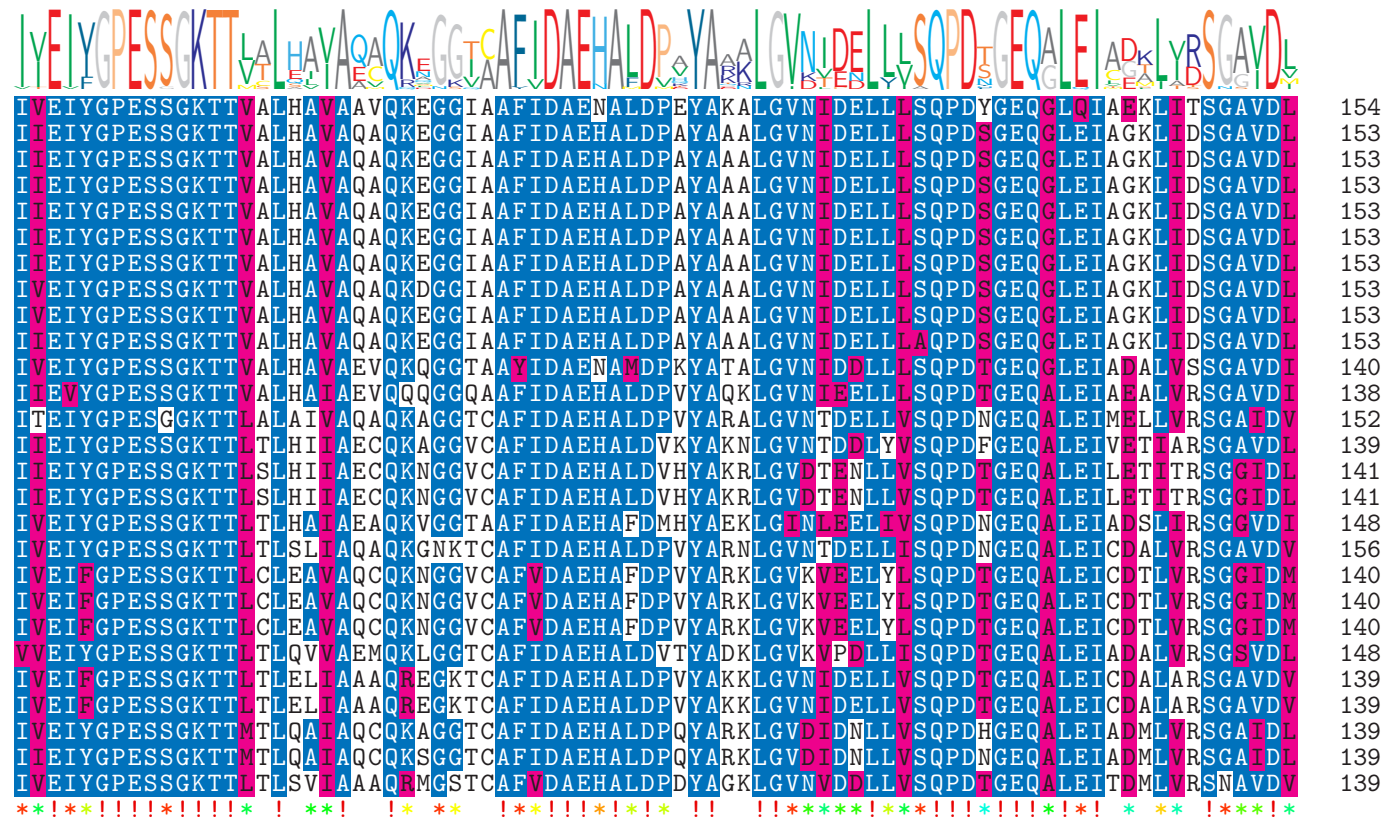
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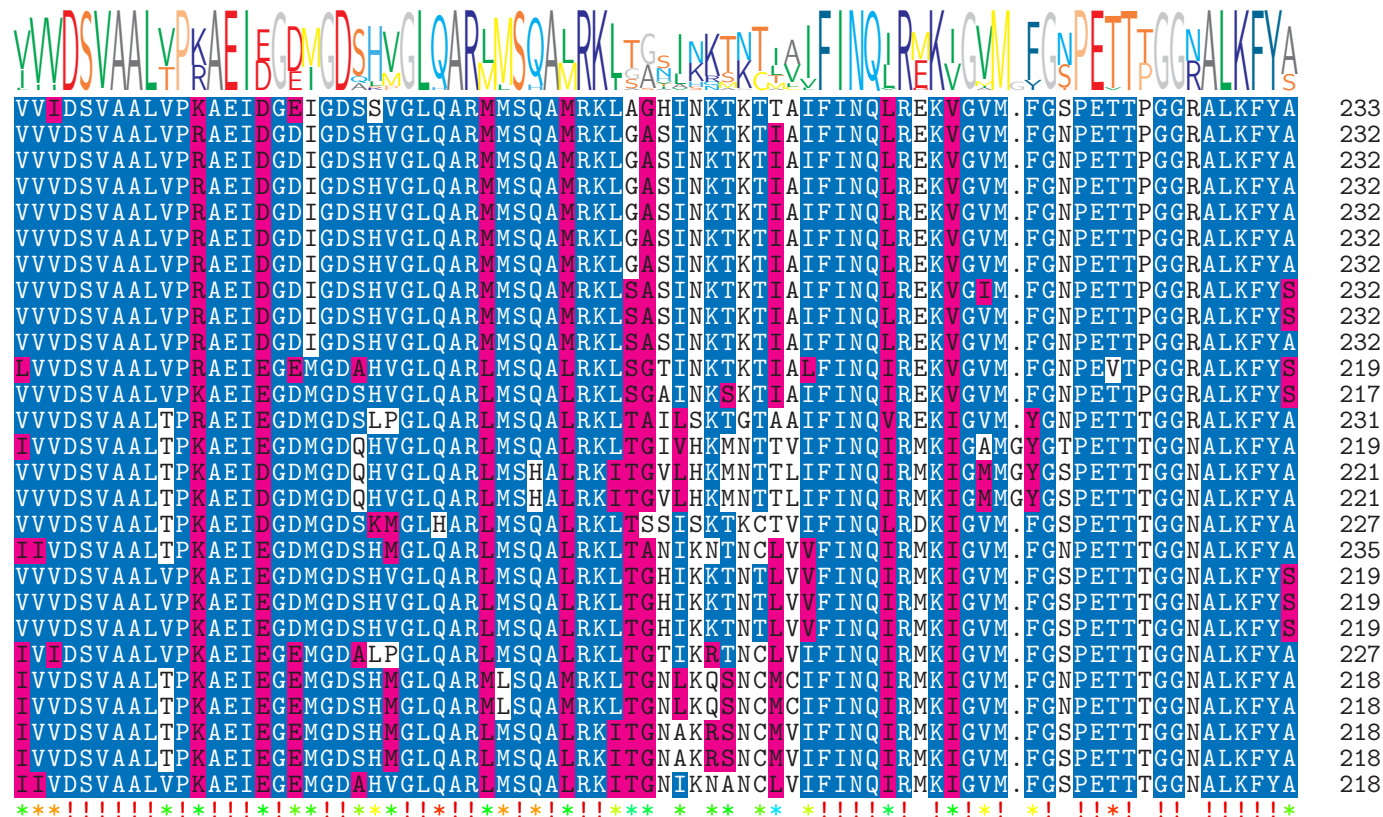
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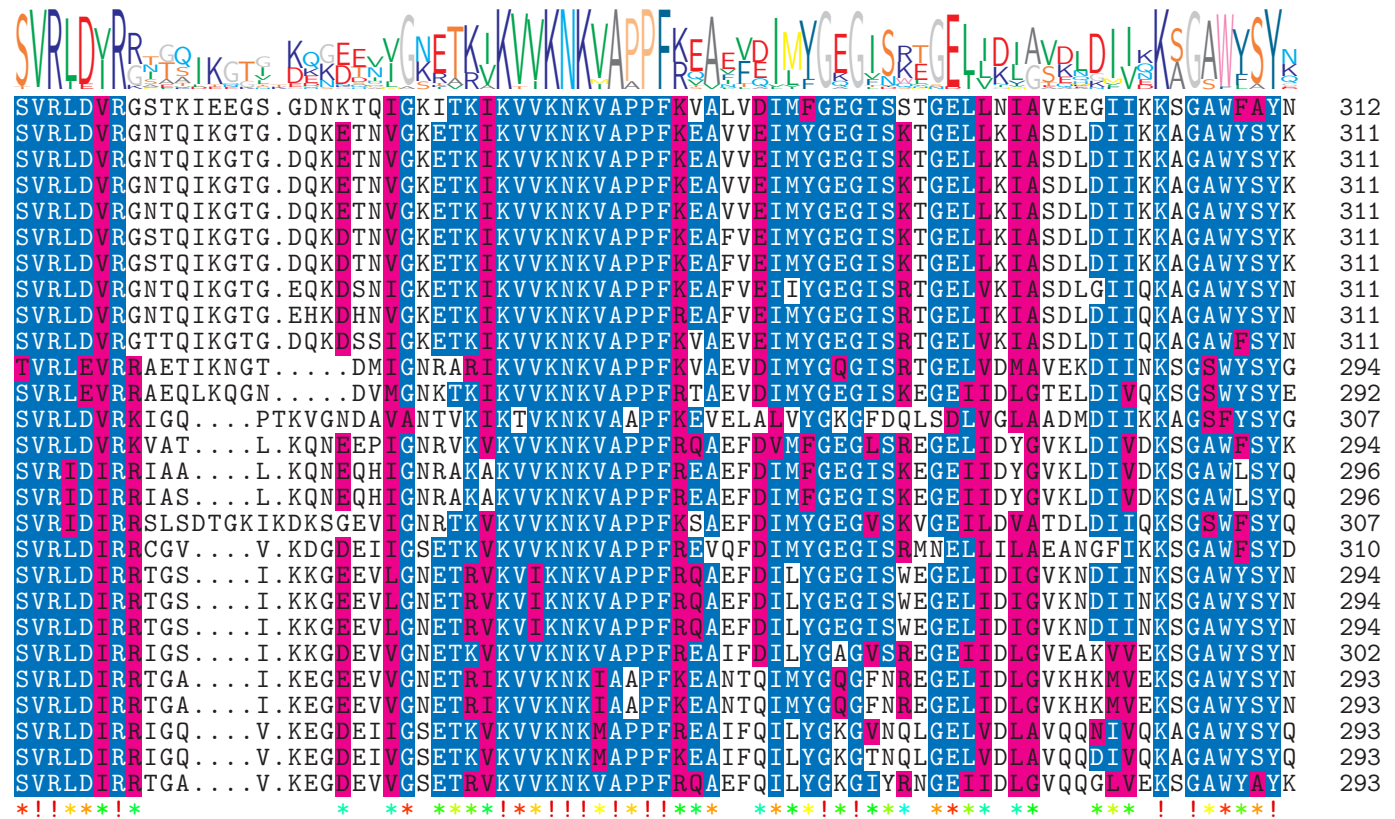
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TEN ⁺ KK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TEN ⁺ KK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TEN ⁺ KK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPE ⁺ IF ⁺ DEID ⁺ KQ ⁺ VR ⁺ SKF ⁺ GL ⁺ IDGEEVSEQD ⁺ TEN ⁺ KK ⁺ DEPK ⁺ ...KEE ⁺ ..AVNEE ⁺ VPLDL ⁺ GDELE ⁺ IE	385
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GEKIGQGS ⁺ ENAK ⁺ KLAD ⁺ NPE ⁺ IF ⁺ DDID ⁺ HK ⁺ VR ⁺ VQY ⁺ GL ⁺ IEEDNTEEEK ⁺ QSSKEK ⁺ E...DE ⁺ ..KADKNL ⁺ VLELD ⁺ DDTIE ⁺ LE	382
GEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPA ⁺ IF ⁺ DEID ⁺ HK ⁺ VR ⁺ VHF ⁺ GMTEDD ⁺ SPVQSELVEE ⁺ ...K ⁺ ..NEAD ⁺ DLVLDL ⁺ DNAIE ⁺ IE	378
GEKIGQGS ⁺ ENAK ⁺ KRYLA ⁺ DHPQL ⁺ FDEID ⁺ RV ⁺ RVK ⁺ FGL ⁺ LEESEE ⁺ ..ESAMAVA ⁺ ...S ⁺ ..EETD ⁺ DLALDL ⁺ NGIE ⁺ IE	377
SERIGQGR ⁺ ENAK ⁺ NFLAD ⁺ HD ⁺ VE ⁺ DEV ⁺ RLK ⁺ VR ⁺ AAY ⁺ GISDVPEEDLPTTEDE ⁺ ..QIN ⁺ ...ILPDD ⁺ STEE ⁺ ..	355
EERLGG ⁺ RENAK ⁺ NFLAD ⁺ ENK ⁺ IMLM ⁺ IQEQ ⁺ IREHY ⁺ GL ⁺ DNNGVVQQAAETQEELE ⁺ ...FE ⁺ ..E ⁺ ..	348
DERIGQG ⁺ KEKTI ⁺ AIY ⁺ IAER ⁺ PEME ⁺ Q ⁺ EIRDRV ⁺ MAAIR ⁺ AGNAGEAPALAPAPA ⁺ AEAE ⁺ ...AEA ⁺ ...	363
DKKLGG ⁺ GRENS ⁺ KA ⁺ FL ⁺ KNPE ⁺ IA ⁺ DEIT ⁺ KAI ⁺ QNSM ⁺ G ⁺ IEGMI ⁺ ...SGSEDD ⁺ ..E ⁺ ...GEE ⁺ ...	343
DKKLGG ⁺ GRENA ⁺ KALL ⁺ KED ⁺ KALA ⁺ DEIT ⁺ LK ⁺ IKES ⁺ IG ⁺ SNEEI ⁺ ...MPLPDE ⁺ ..P ⁺ ...LEEME ⁺ ...	347
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GKIGQG ⁺ KNN ⁺ AVK ⁺ WL ⁺ KNPE ⁺ IA ⁺ DKLE ⁺ QEIR ⁺ N ⁺ TLASNPNS ⁺ ...VLKATASDS ⁺ ...NDES ⁺ DVEEFSEEL ⁺ ...	372
GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KNPE ⁺ IS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMHI ⁺ ...TEGTQDET ⁺ ...GER ⁺ ...PEE ⁺ ...	348
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GAKIGQG ⁺ KDN ⁺ VR ⁺ VL ⁺ KNPE ⁺ IS ⁺ DEID ⁺ AK ⁺ IRAL ⁺ NGVEMHI ⁺ ...TEGTQDET ⁺ ...GER ⁺ ...PEE ⁺ ...	348
GERIGQG ⁺ GRDN ⁺ CREFL ⁺ ENAE ⁺ LARE ⁺ IE ⁺ ENK ⁺ VR ⁺ REHL ⁺ GVTPMG ⁺ ...AVTLA ⁺ EEV ⁺ ...EED ⁺ ...	352
GDKIGQG ⁺ KANACK ⁺ YL ⁺ KNPE ⁺ IA ⁺ KTLD ⁺ KKL ⁺ REMLLN ⁺ PNEM ⁺ ...QLIAETSSA ⁺ ...ADDVEFGAVPEEF ⁺ ...	354
GDKIGQG ⁺ KANACK ⁺ YL ⁺ KNPE ⁺ IA ⁺ KTLD ⁺ KKL ⁺ REMLLN ⁺ PNEM ⁺ ...QLIAETSSA ⁺ ...ADDVEFGAVPEEF ⁺ ...	354
GNKIGQG ⁺ KNN ⁺ VIRY ⁺ LEEN ⁺ PQISTE ⁺ IEAV ⁺ IREQLLT ⁺ TKASD ⁺ ...QTAA ⁺ HD ⁺ ET ⁺ ...EEEPDLL ⁺ ..ES ⁺ ...	349
GNKIGQG ⁺ KNN ⁺ VIRY ⁺ FEENN ⁺ QIA ⁺ IE ⁺ IEIRN ⁺ IREQLLT ⁺ TGTN ⁺ ...GAVQ ⁺ ..I ⁺ ED ⁺ ...EEEPDLL ⁺ ..LES ⁺ ...	349
GSKIGQG ⁺ KANA ⁺ AK ⁺ YL ⁺ ENPE ⁺ IG ⁺ IEEQ ⁺ IRAK ⁺ LV ⁺ TSAN ⁺ ...TKATPVAED ⁺ ...LADAD ⁺ I ⁺ ...	347

logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved