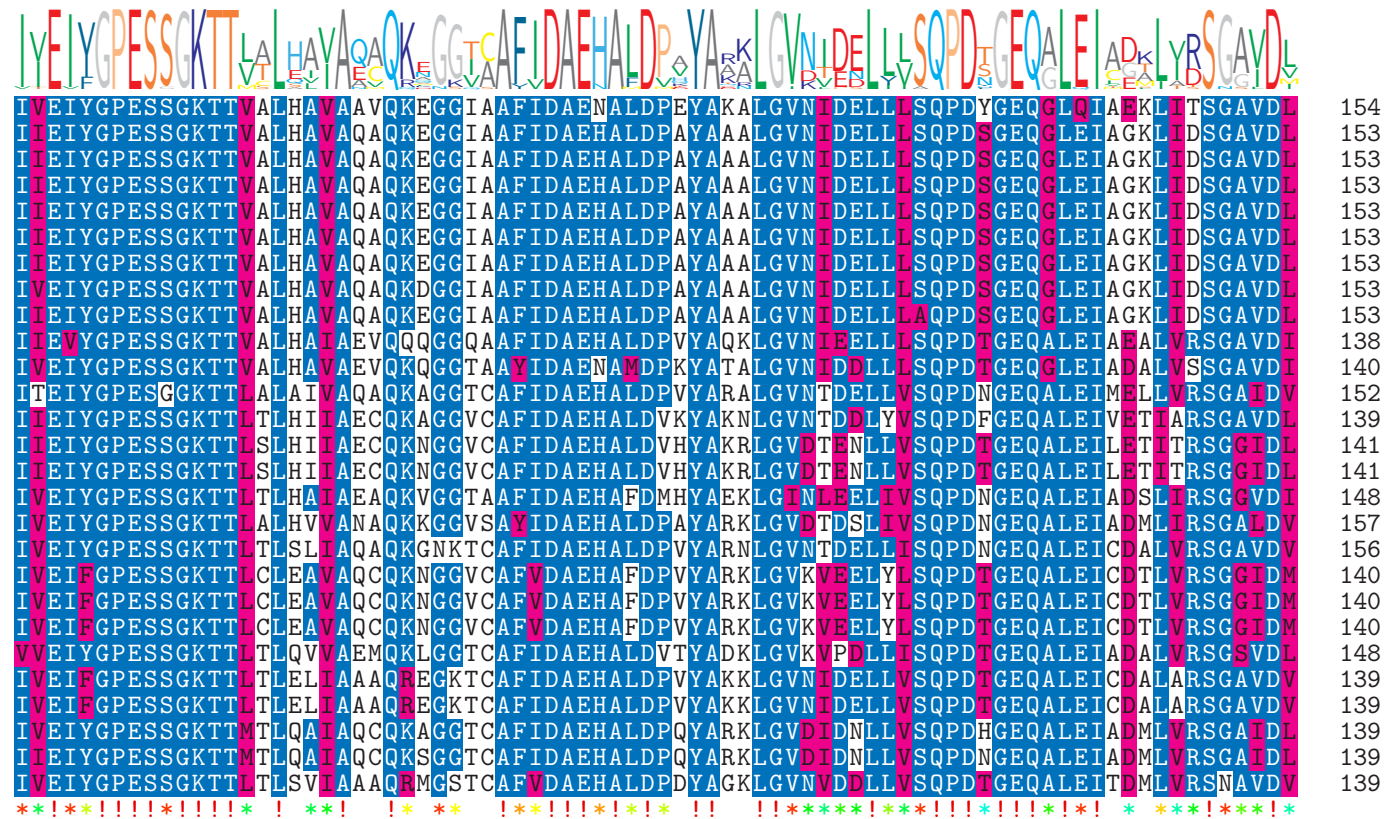


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NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KKRALAAALGQIEKQ	FGKGAVMRMGDH	.DRQA	IPSISTGSLGLD	I	ALGIGGL	PKGR	59
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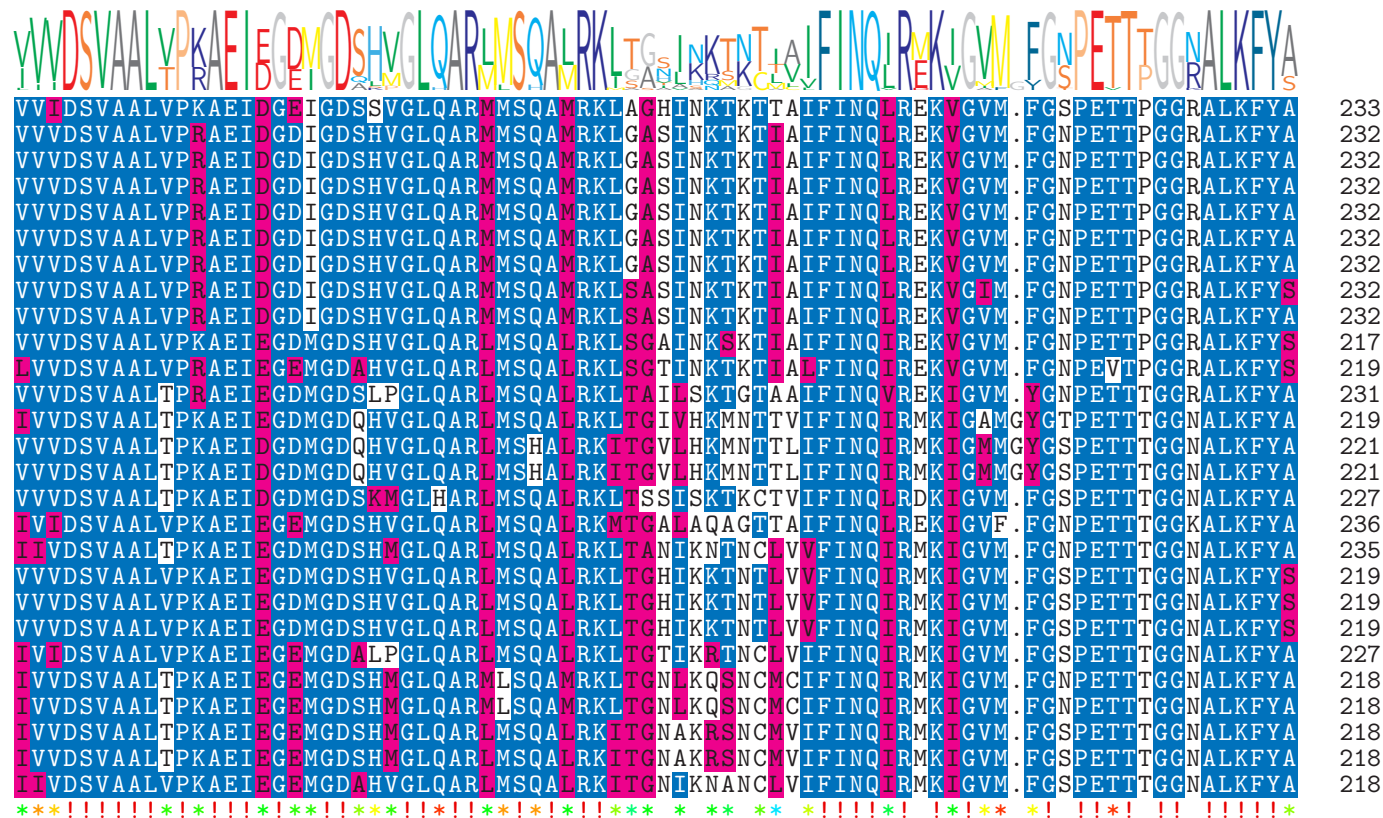
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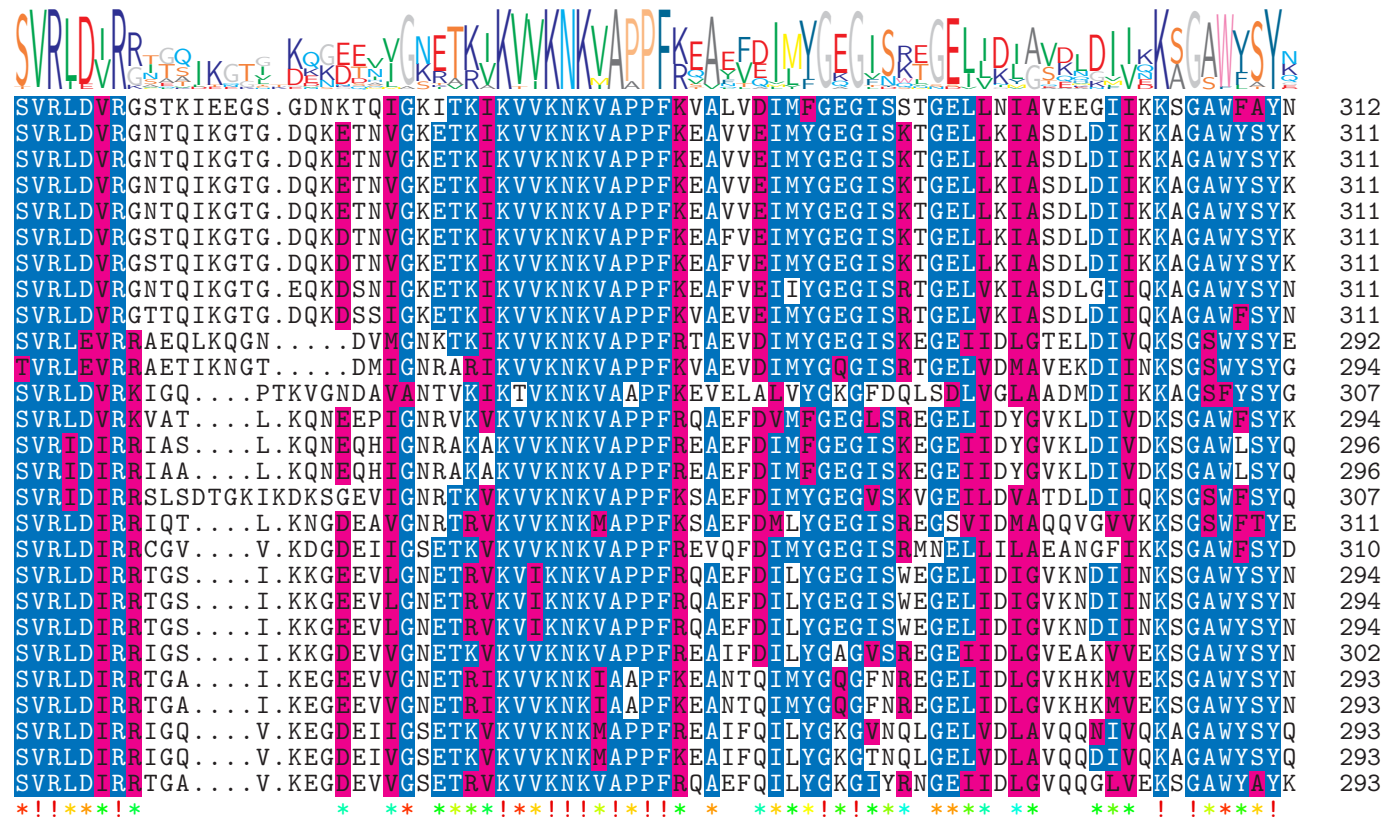
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consensus

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Sequence	Score
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DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEID ⁺ KQV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD..TENKKD ⁺ .E...PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEID ⁺ KQV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD..TENKKD ⁺ .E...PKKEEA..VNEEVPLDLGDEL	382
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GEKIGGGS ⁺ ENAK ⁺ KFLAD ⁺ NP ⁺ EV ⁺ FD ⁺ ID ⁺ HKV ⁺ RVQY ⁺ GL ⁺ IEEDNTEEKQ..SSKEK.....ETDEK..ADKNLVLELDDTI	379
GEKIGGGS ⁺ ENAK ⁺ RYLAD ⁺ HP ⁺ QL ⁺ FD ⁺ ID ⁺ RKV ⁺ RVKF ⁺ GL ⁺ LEESEESAM..AVASE.....E.....TDDLALDLNGI	374
EER ⁺ LGQGR ⁺ ENAK ⁺ QFL ⁺ KEN ⁺ KDIM ⁺ LIQE ⁺ QIRE ⁺ HYGL ⁺ DNNGVVQQQA..EETQEE ⁺ .L.EFE.E.....	348
SERIGGGR ⁺ ENAK ⁺ NYLAD ⁺ HD ⁺ ED ⁺ VE ⁺ VR ⁺ LKV ⁺ RAAY ⁺ GIS ⁺ SDVPEEDLPT..TEDE.Q.I.NILPDDST....EE.....	355
DERIGGG ⁺ KEK ⁺ TIAY ⁺ IA ⁺ ERP ⁺ EME ⁺ QE ⁺ IR ⁺ DRV ⁺ MAAIRAGNAGEAPALAPAPAA.....PEAAEA	363
DKKL ⁺ GGGR ⁺ ENSK ⁺ AF ⁺ LKEN ⁺ PEIAD ⁺ EIT ⁺ KA ⁺ IQNSM ⁺ GI ⁺ EGMISG..SEDDEG..EE.....	343
DKKL ⁺ GGGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALAD ⁺ EIT ⁺ LK ⁺ IKES ⁺ IGS ⁺ NEEIMP..LPDEPL..EEME.....	347
DKKL ⁺ GGGR ⁺ ENAK ⁺ ALL ⁺ KED ⁺ KALAD ⁺ EIT ⁺ LK ⁺ IKES ⁺ IGS ⁺ NEEIMP..LPDEPL..EEME.....	347
DT ⁺ KL ⁺ GGGR ⁺ DR ⁺ TV ⁺ KEL ⁺ IK ⁺ DN ⁺ PE ⁺ LAE ⁺ EEL ⁺ EAK ⁺ IREKLQAK.....	343
GDQL ⁺ GGGR ⁺ EK ⁺ VR ⁺ QFL ⁺ KDN ⁺ PAI ⁺ TE ⁺ IE ⁺ EN ⁺ KV ⁺ AE ⁺ FL ⁺ IGSADQ..FAEDGEAA..AAAAVSEAAAADVAKDSKAAAAPAAK	386
GTKIGGG ⁺ KNN ⁺ AV ⁺ KVL ⁺ KEN ⁺ PEIAD ⁺ KL ⁺ EQE ⁺ IR ⁺ N ⁺ TLASN ⁺ PNSVL..KATASDSNDESDVEEFSEEL..	372
GAKIGGG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALN ⁺ GV ⁺ EMHITE..GTQDET ⁺ DGER.....PEE.....	348
GAKIGGG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALN ⁺ GV ⁺ EMHITE..GTQDET ⁺ DGER.....PEE.....	348
GAKIGGG ⁺ KDN ⁺ VR ⁺ VL ⁺ KEN ⁺ PEIS ⁺ DEID ⁺ AKI ⁺ RALN ⁺ GV ⁺ EMHITE..GTQDET ⁺ DGER.....PEE.....	348
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logo

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consensus

 non conserved
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 ≥ 50% conserved