

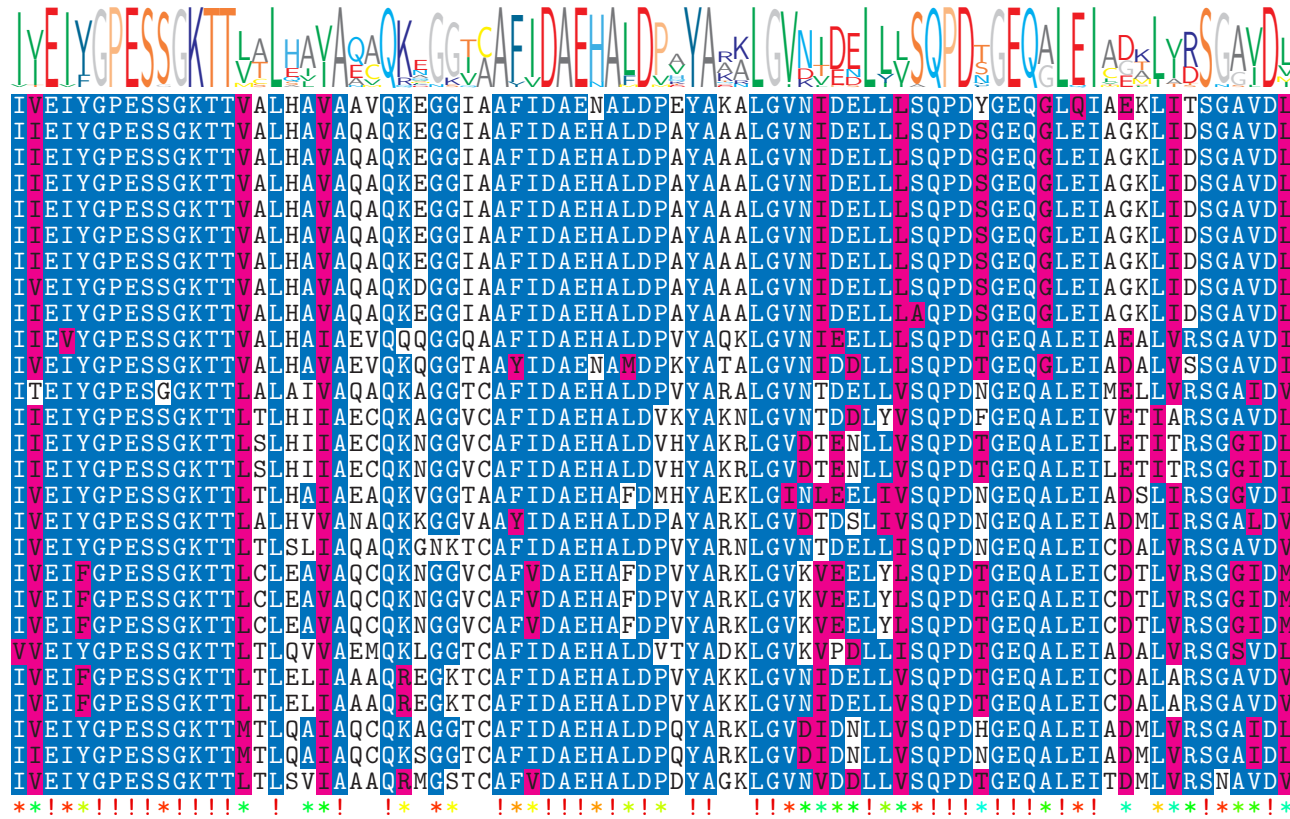
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NTDB id 1245 Cj1673c YP 002345041.1	MDDN	KRKSLDAALKSLDKT	FGKGTILRLGDK	.EVEQ	IDSIGTGSVGLDL	ALG	IGGV	PKGR	59
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDE	DKQKAIISLAIKQID	KVFGKGALVRLGDK	.QVEK	IDSISTGSLGLDL	ALG	IGGV	PKGR	61
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDE	DKQKAIISLAIKQID	KVFGKGALVRLGDK	.QVEK	IDAISTGSLGLDL	ALG	IGGV	PKGR	61
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NTDB id 419193 GTQ89 RS06630 WP 007052644.1	.MALETKPAKDPAA.EDKH	ELDPKRKAALDTALAQ	VEKSF	FGKGSAMRLGDQ	.PEQNV	EVIP	TGSLALD	MALGIGGLPKGR	77
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDEN	KQKALAAALGQIEKQ	FGKGSIMRLGDN	.RAMDVET	ISTGSLSLD	I	ALGAGGL	PMGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDN	KSKALQAALSQIEKQ	FGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGL	PKGR	59
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KKRALAAALGQIEKQ	FGKGAVMRMGDH	.DRQA	IPSISTGSLGLD	I	ALGIGGL	PKGR	59
consensus		*** **	***	***!	***!	***!	***!	***!	

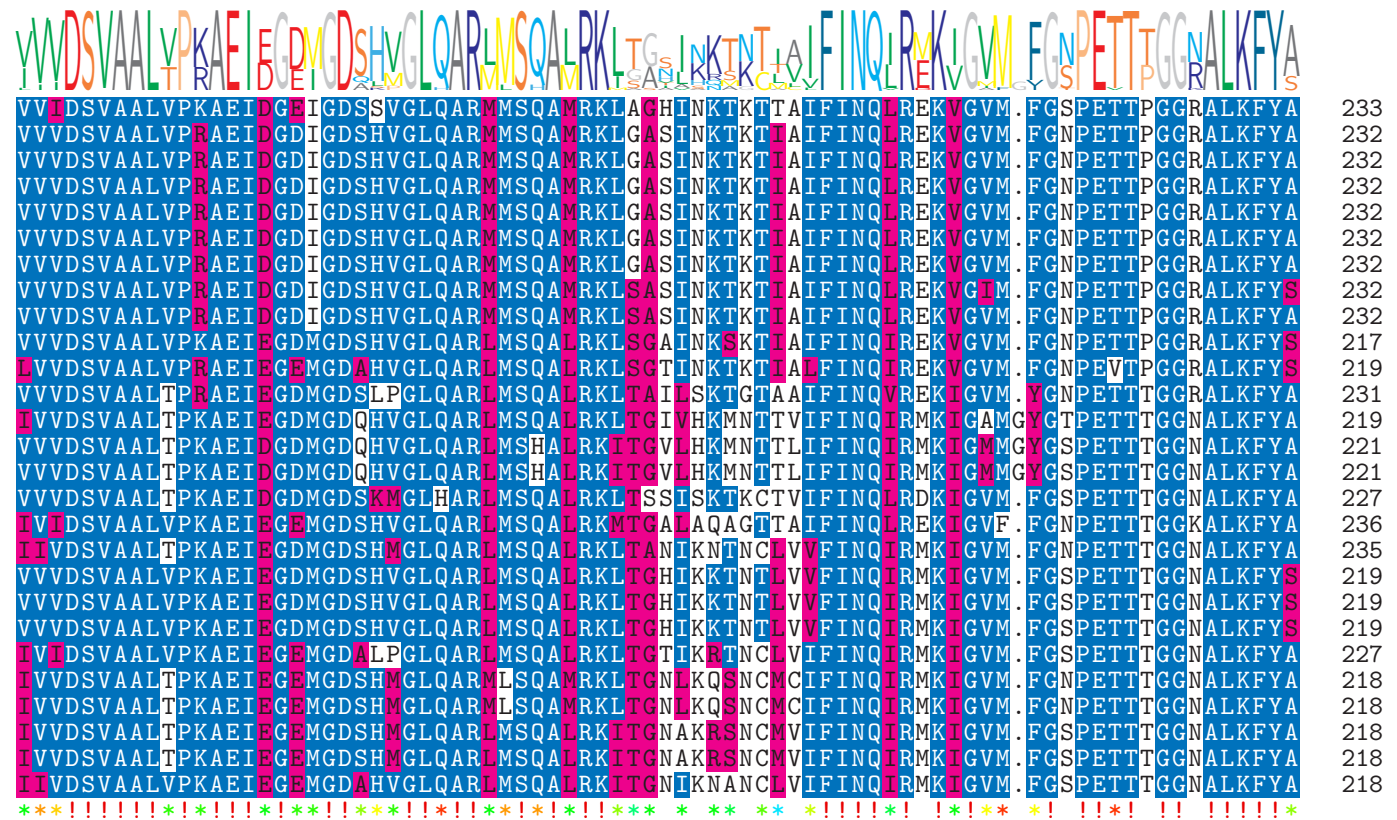
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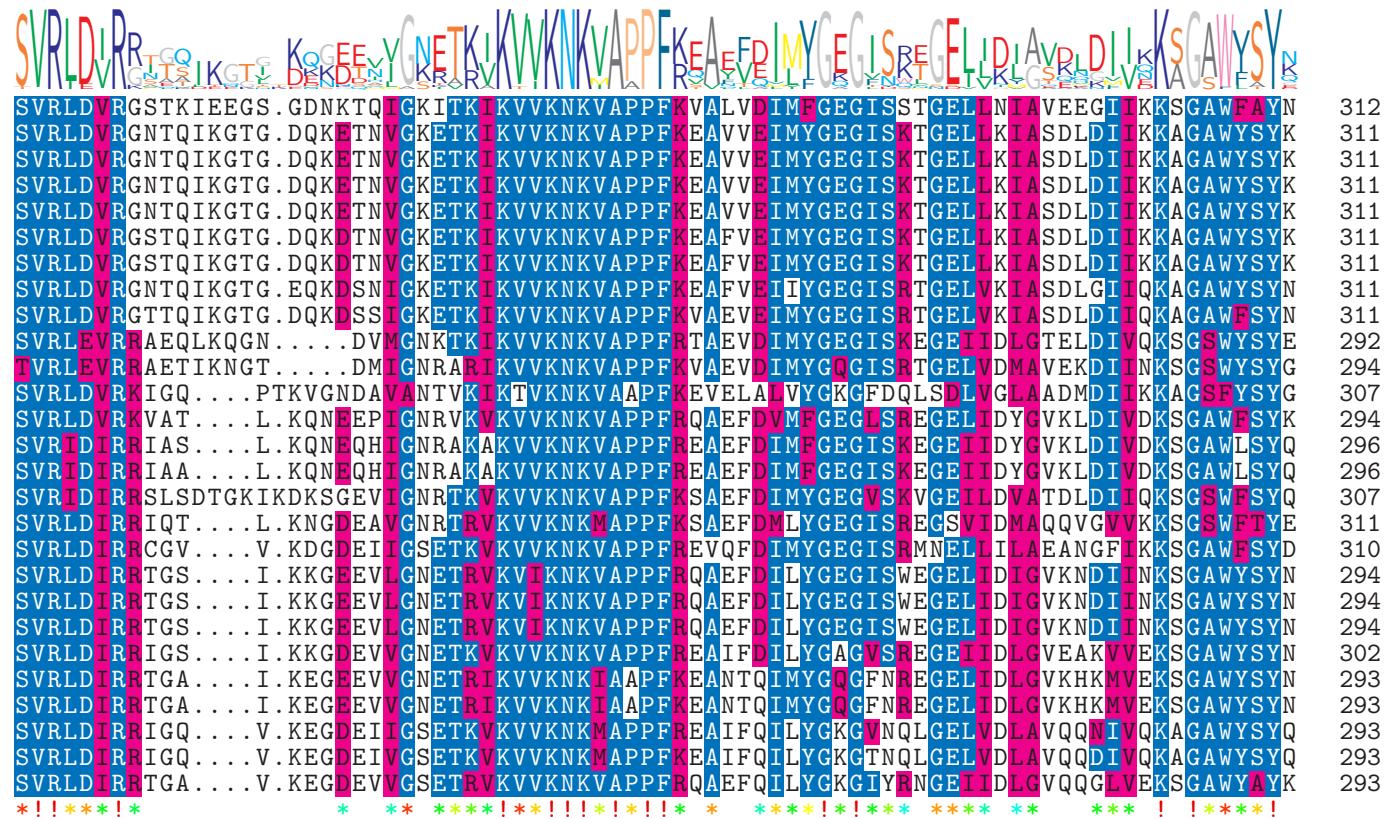
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEID ⁺ KQV ⁺ RSKF ⁺ GL ⁺ IDGEEVSEQD..TENKKD.E...PKKEEA..VNEEVPLDLGDEL	382
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ DNPEIF ⁺ DEID ⁺ HKV ⁺ RVQF ⁺ GL ⁺ IDGEEIAES.....KKD.E...AAQVDS..VNEEVTLDLGDEL	378
DEKIGGGS ⁺ ENAK ⁺ KYLA ⁺ DNPEIF ⁺ FAID ⁺ HQV ⁺ RVQF ⁺ GL ⁺ IDGEEAAES.....KKD.E...VAQVDS..VNEEVTLDLGDEL	378
GEKIGGGS ⁺ ENAK ⁺ KFLAD ⁺ NP ⁺ EV ⁺ FD ⁺ ID ⁺ HKV ⁺ RVQY ⁺ GL ⁺ IEEDNTEEKQ..SSKEK.....ETDEK..ADKNLVLELDDTI	379
GEKIGGGS ⁺ ENAK ⁺ RYLA ⁺ DHP ⁺ QL ⁺ FDEID ⁺ RKV ⁺ RVKF ⁺ GL ⁺ LEESEESAM..AVASE.....E.....TDDLALDLNGI	374
EE ⁺ RL ⁺ GQG ⁺ REN ⁺ AQ ⁺ FL ⁺ KEN ⁺ KDIM ⁺ LI ⁺ QEQ ⁺ IRE ⁺ HY ⁺ GL ⁺ DNNGVVQQQA..EETQEE.L.EFE.E.....	348
SERIGGQ ⁺ REN ⁺ AK ⁺ NYLA ⁺ DH ⁺ ED ⁺ VE ⁺ DEV ⁺ RLK ⁺ VRAAY ⁺ GIS ⁺ SDVPEEDLPT..TEDE.Q.I.NILPDDST....EE.....	355
DERIGQG ⁺ KEKT ⁺ IAY ⁺ IA ⁺ ERP ⁺ EME ⁺ QE ⁺ IR ⁺ DRV ⁺ MAA ⁺ IRAG ⁺ NAGEAPALAPAPAA.....PEAAEA	363
DKKL ⁺ GQG ⁺ RENS ⁺ KA ⁺ FL ⁺ KEN ⁺ PEI ⁺ ADE ⁺ IT ⁺ KA ⁺ IQNS ⁺ MG ⁺ IEGMISG..SEDDEG..EE.....	343
DKKL ⁺ GQG ⁺ REN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IKES ⁺ IG ⁺ SNEEIMP..LPDEPL..EEME.....	347
DKKL ⁺ GQG ⁺ REN ⁺ AK ⁺ ALL ⁺ KED ⁺ KAL ⁺ ADE ⁺ IT ⁺ LK ⁺ IKES ⁺ IG ⁺ SNEEIMP..LPDEPL..EEME.....	347
DT ⁺ KL ⁺ GQGR ⁺ DTV ⁺ KEL ⁺ IK ⁺ DN ⁺ PE ⁺ LAE ⁺ EEL ⁺ EAK ⁺ IRE ⁺ KLQAK.....	343
GDQL ⁺ GQGR ⁺ EK ⁺ VR ⁺ QFL ⁺ KN ⁺ PA ⁺ ITE ⁺ IE ⁺ EN ⁺ KV ⁺ AE ⁺ FL ⁺ IGSADQ..FAEDGEAA..AAAAVSEAAAADVAKDSKAAAAPAAK	386
GTKIGGQ ⁺ KNN ⁺ AV ⁺ KVL ⁺ KEN ⁺ PEI ⁺ AD ⁺ KL ⁺ EQ ⁺ IR ⁺ NTLA ⁺ SNP ⁺ NSVL..KATASDSNDESDVEEFSEEL..	372
GAKIGGQ ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NG ⁺ VEMHITE..GTQDET ⁺ DGER.....PEE.....	348
GAKIGGQ ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NG ⁺ VEMHITE..GTQDET ⁺ DGER.....PEE.....	348
GAKIGGQ ⁺ KDN ⁺ VR ⁺ VWL ⁺ KEN ⁺ PEI ⁺ SD ⁺ EID ⁺ AK ⁺ IRAL ⁺ NG ⁺ VEMHITE..GTQDET ⁺ DGER.....PEE.....	348
GE ⁺ RIGQ ⁺ GRDN ⁺ CRE ⁺ FL ⁺ RENA ⁺ EL ⁺ AR ⁺ IE ⁺ EN ⁺ KV ⁺ REHL ⁺ GVTPMGAV..TLA.EEVEED..	352
GDKIGGQ ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DK ⁺ KL ⁺ REML ⁺ LN ⁺ PEN ⁺ MQL..IAETSSAADVVEFGAVPEEF..	354
GDKIGGQ ⁺ KAN ⁺ ACK ⁺ YL ⁺ KEN ⁺ PEI ⁺ AK ⁺ TL ⁺ DK ⁺ KL ⁺ REML ⁺ LN ⁺ PEN ⁺ MQL..IAETSSAADVVEFGAVPEEF..	354
GNKIGGQ ⁺ KNN ⁺ VIR ⁺ YLE ⁺ EN ⁺ PQ ⁺ IST ⁺ EIE ⁺ AV ⁺ IRE ⁺ QLLT ⁺ TKASDQT..AA.HDETEEEPDLL..ES.....	349
GNKIGGQ ⁺ KNN ⁺ VIR ⁺ YFE ⁺ ENN ⁺ QIA ⁺ EIE ⁺ ERN ⁺ IRE ⁺ QLLT ⁺ TGTNGA..VQ.I.EDEEEPDLL..LES.....	349
GS ⁺ KIGQ ⁺ QKANA ⁺ AK ⁺ YL ⁺ EN ⁺ PEI ⁺ IG ⁺ EIE ⁺ EQ ⁺ IR ⁺ AKLL ⁺ VTSANTK..ATPVAEDLADADI.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE.....	388
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved