

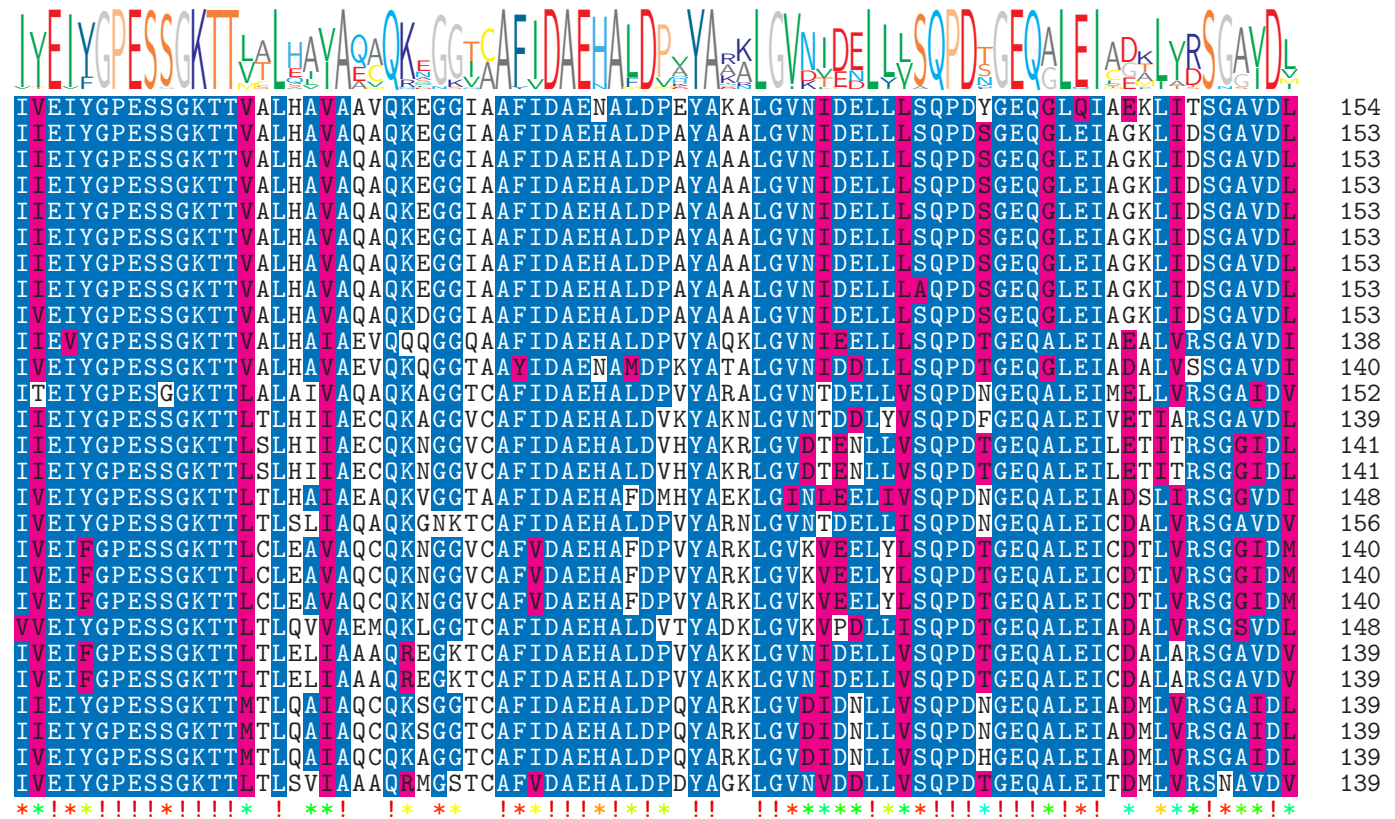
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFG	DERKKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQ	VMSGSLALD	I	ALGAGGY	PKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTR	I	STVPSGSLALD	T	ALGIGGY	PRGR	58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKK	IEKNFGKGSIMRMGEK	.VDTQVST	VSSGSLALDE	ALGVGGY	PRGR			60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	SQIEKAFGKGSIMKLGAE	.SKLDVQ	VSTGSLSLDL	ALGVGGI	PRGR		72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKS	LDKTFGKGTILRLGDK	.EVEQ	I	DSIGTGSVGLDL	ALGIGGV	PKGR		59
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQA	ALSQIEKQFGKNTVMRLG	DN.TVQ	AVEAVSTGSLTLD	I	ALGIGGL	PKGR		59
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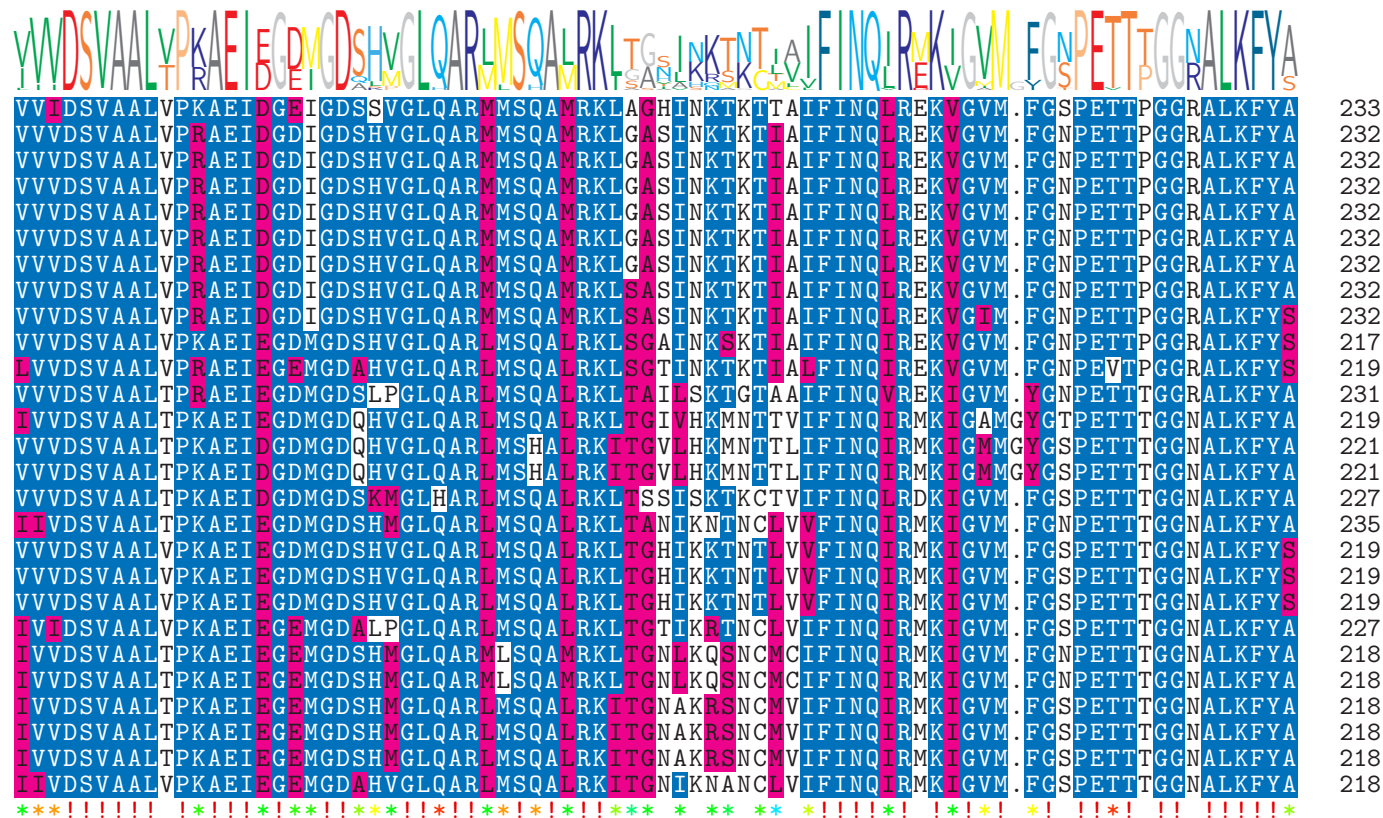
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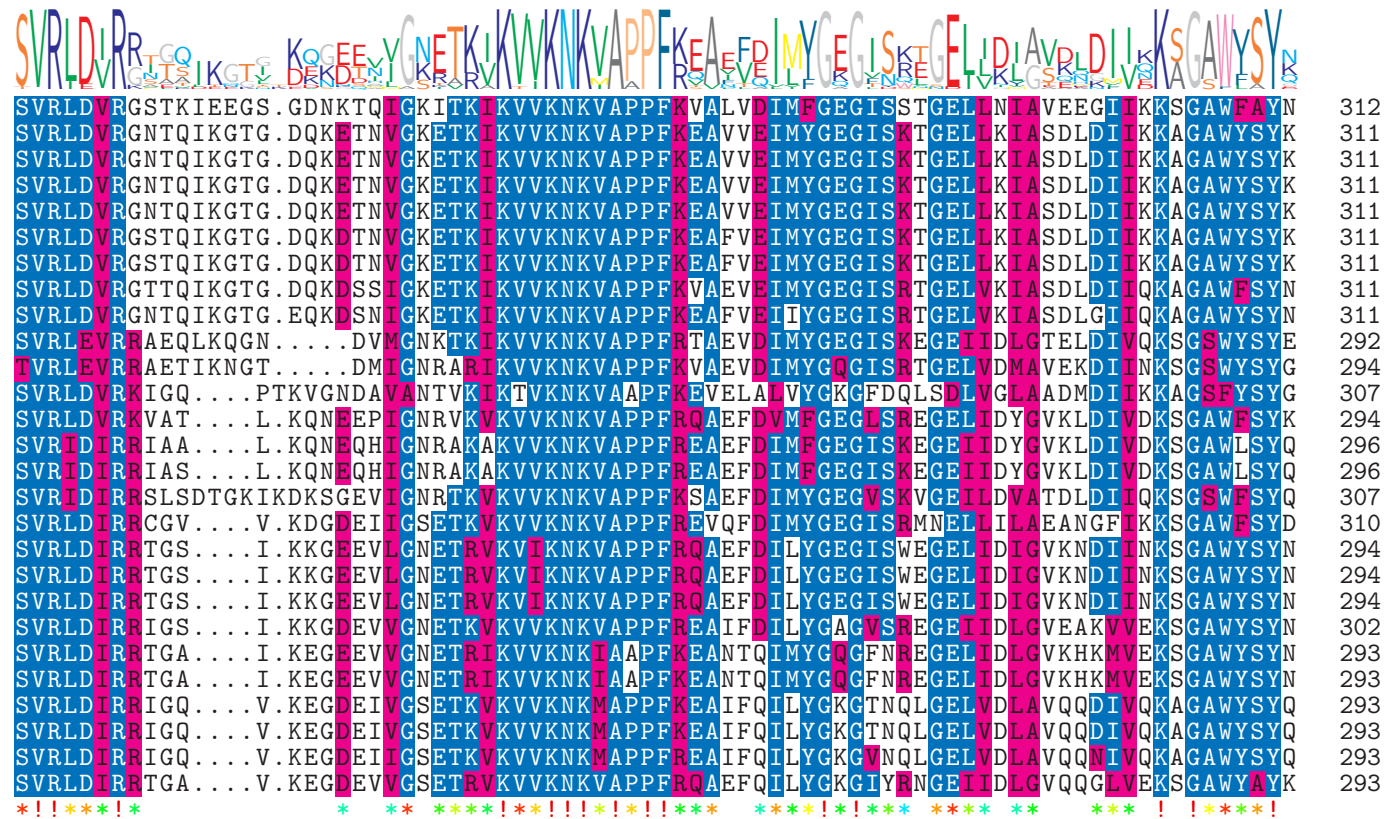
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GEKIGGGS E NA K KFLADNP E IF D DI D H K V R V Q YGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EE R LG Q Q G RENA K Q F L K EN K DI M L I Q E Q I REHYGLDNNGVVQQQAEE.TQEEL.E..FE.E.....	348
SERIGG G RENA K NYLAD H ED V ED V RL K VRAAY G ISDVPEEDLP T TE.DE.QI.N..ILPDDST.....EE.....	355
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DKKL G Q G RENA K ALL K ED K ALADEIT L K I ES I GSNEEIMPL..PDEPLE..E M E.....	347
DKKL G Q G RENA K ALL K ED K ALADEIT L K I ES I GSNEEIMPL..PDEPLE..E M E.....	347
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GT K IG Q Q K NNAV K VLKEN P E I AD K LE Q EIR N TLASNPNSVLK..ATASDSND E SDVEEFSE.....EEL.....	372
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logo

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved