

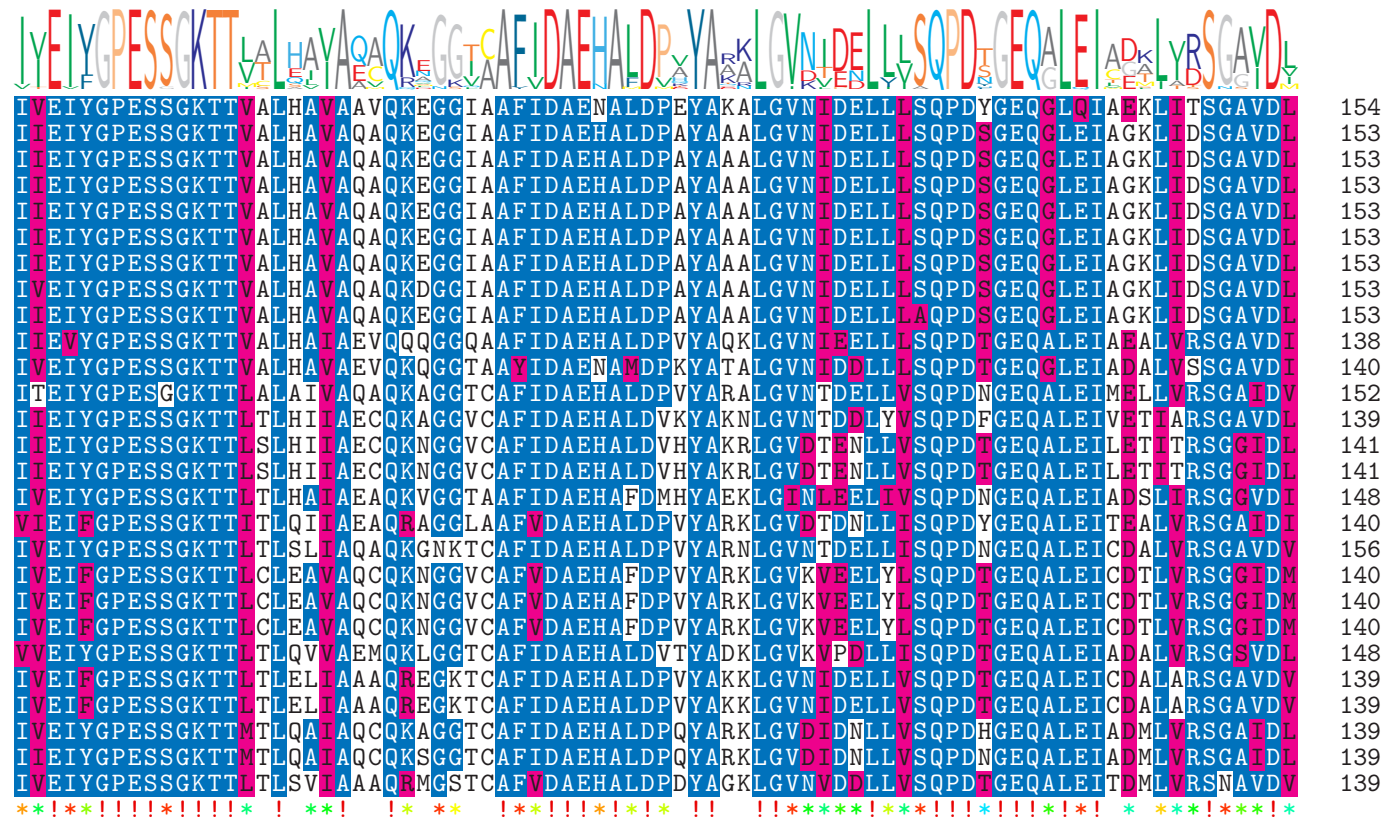
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NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAK.....KPKKLEEISKKFGA	EREKALNDALKL	IEKD	FGKGSIMRLGER	.AEQKVQVMSSGSLALD	I	ALGSGGYPKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAK.....KPKKLEEISKKFGA	EREKALNDALKL	IEKD	FGKGSIMRLGER	.AEQKVQVMSSGSLALD	I	ALGSGGYPKGR	73
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NTDB id 159 SP RS09750 WP 001085462.1	.MAK.....KPKKLEEISKKFGA	EREKALNDALKL	IEKD	FGKGSIMRLGER	.AEQKVQVMSSGSLALD	I	ALGSGGYPKGR	73
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NTDB id 453 Spy49 1753c ACI62003.1	.MAK.....KLKKNEEITKKFG	DERKKALDDALKN	IEKD	FGKGAVMRLGER	.AEQKVQVMSSGSLALD	I	ALGAGGYPKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQ	IEKQFGKGSIMKLGEK	.TDTRI	ISTVPSGSLALD	TALGIGGYPRGR			58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKK	IEKNFGKGSIMRMGEK	.VDTQV	STVSSGSLALDEAL	GVGGYPRGR			60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTDAKERSKA	TETAM	SQIEKA	FGKGSIMKLGAE	.SKLDVQVVSTGSLSLDL	ALGVGGIPRGR		72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKS	LDKT	FGKGTILRLGDK	.EVEQID	ISTGTSVGLDL	ALGIGGVPRGR		59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAIISLAIKQ	IDKV	FGKGALVRLGDK	.QVEKIDA	ISTGSLGLDL	ALGIGGVPRGR		61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKAIISLAIKQ	IDKV	FGKGALVRLGDK	.QVEKIDS	ISTGSLGLDL	ALGIGGVPRGR		61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAK..TETTTSPNDDKKK	KALAAVLEK	LDKT	YGKGTVMKLG	DGTVDHNI	IEVIPSGSLGLDL	ALGVGGYPRGR	68
NTDB id 39627 ACIPR4 RS03440 WP 013567257.1	MADDRGKATIELALAG	IEKQFGKGSIMRLGAKDA	IVPISV	ISTGSI	SFIDL	ALGVGGVPRGR		60
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNT..VVKQVEP	EKKKQALEAALAQ	IEKQFGKGSIMKLQQT	.EQLDIES	VSTGSLGLDL	ALGIGGLPMGR		76
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NTDB id 1123 OK783 RS03845 WP 003688695.1	MSDDKSKALAAALAQ	IEKSFGKGAIMKMDGSQ	QEENLEVI	ISTGSLGLDL	ALGVGGLPRGR			60
NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....KKAASMSAEKQ	KALAAALAQ	IEKQFGKGSIMKMGDA	.EVEPVQVVSTGSLGLD	VALGVGGLPRGR			68
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQ	IEKQFGKGSIMRLGDN	.RAMDVET	ISTGSLSLD	I	ALGAGGLPMGR		59
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQ	IEKQFGKNTVMRLGDN	.TVQAVEA	VSTGSLTLD	I	ALGIGGLPKGR		59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQ	IEKQFGKGAVMRMGDH	.DRQAIPS	ISTGSLGLD	I	ALGIGGLPKGR		59
consensus	*** **	*	***	*****	*	*****!!!!!!	!!!!!!	

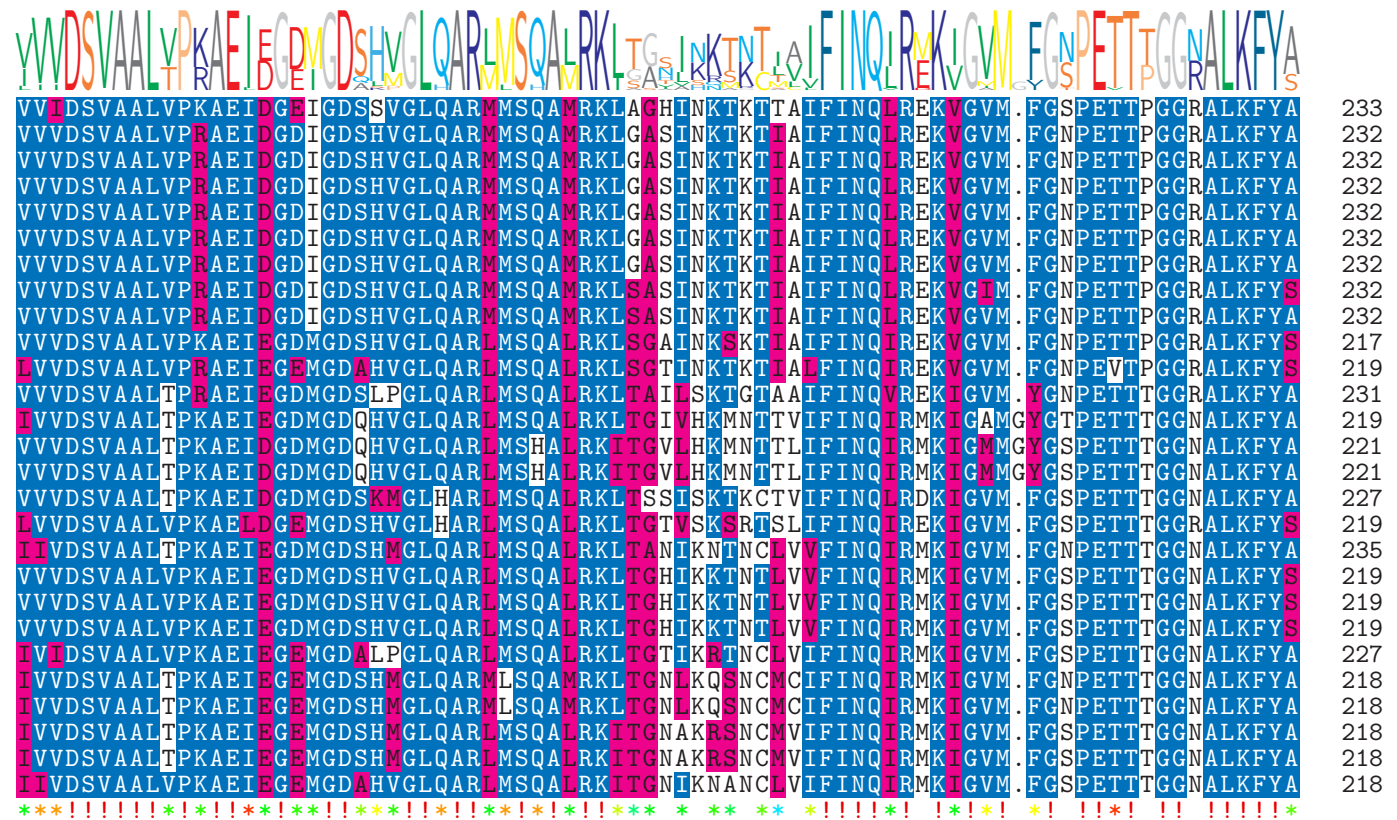
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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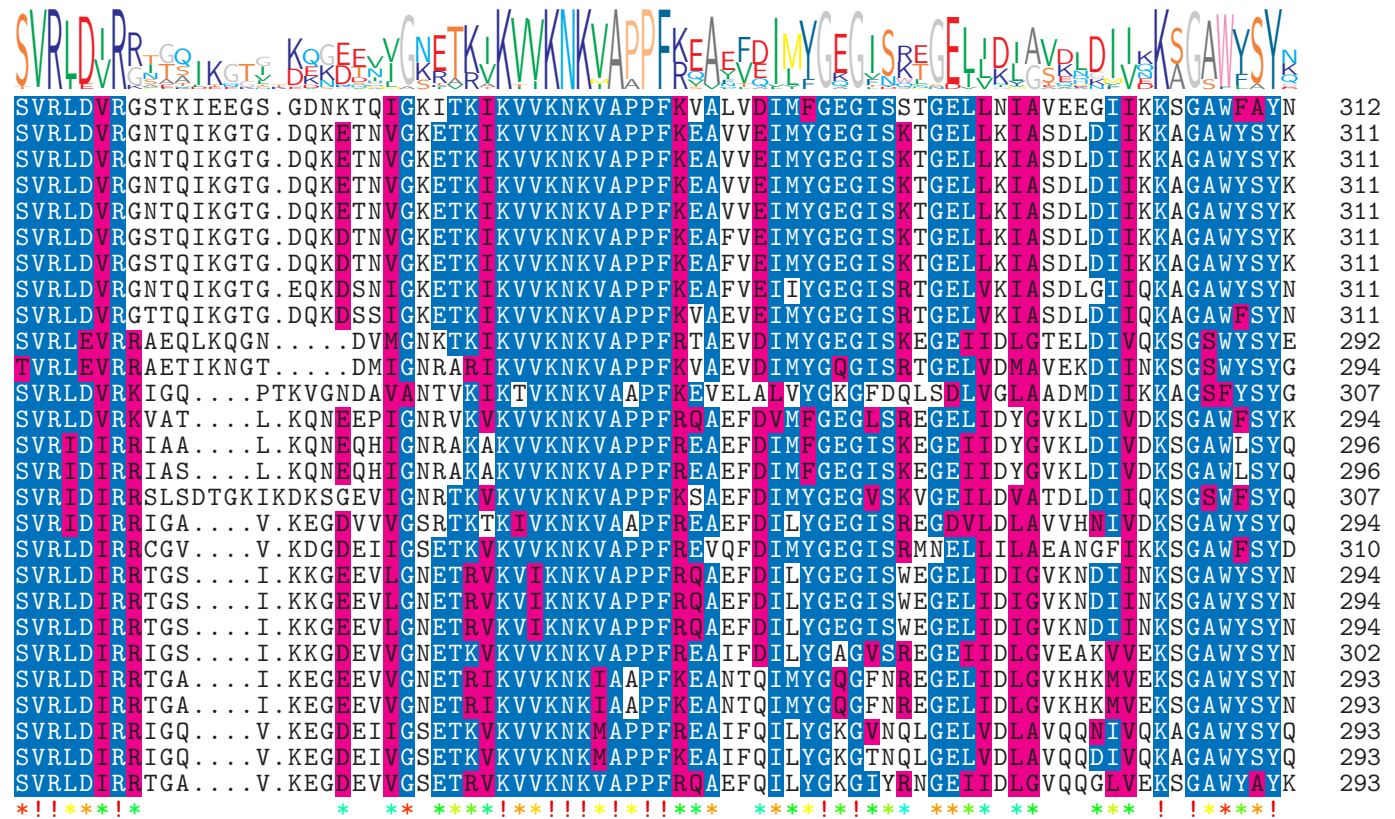
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGS E NAKKYLAEHPEIF F DEIDKQVRSKF G LIDGEEVSEQD..TENKKDE...PKKEEA..VNEEVPLDLGDELE	383
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DEKIGQGS E NAKKYLAHNPEIF F DEIDHQVRVQF G LIDGEEIAES.....KKDE...AAQVDS..VNEEVPLDLGDELE	379
DEKIGQGS E NAKKYLAHNPEIF F DEIDHQVRVQF G LIDGEEIAES.....KKDE...VAQVDS..VNEEVPLDLGDELE	379
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GEKIGQGS E NAKRYLADHPQLF F DEIDRKVRVKG G LLEESEESAM..AVASE.....E.....TDDLALDLNNGIE	375
EE R LGQGR E NAKQFLKENKDIMLMIQE Q IREHY G LDNNGVVQQA..EETQE E L.EFE.E.....	348
SERIGQGR E NAKNYLAHDH D VE V DEVR L KVRAAY G ISDVPEEDLPT..TEDE.QI.NILPDDST.....EE.....	355
DERIGQG E KEKTIA Y IAERP E MEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAA.EA.....	363
DKKLGGGR E NSKAF L KENPEIA D DEITKAIQNSM G IEGMIS..GSEDDEG..EE.....	343
DKKLGGGR E NAKALLKEDKALA D DEITLKIKESIGSNEEIM..PLPDEPL..EEM.E.....	347
DKKLGGGR E NAKALLKEDKALA D DEITLKIKESIGSNEEIM..PLPDEPL..EEM.E.....	347
DTKLGGGR D TVKEL I KDNPELA E EEL E AKI R EKLQAK.....	343
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GTKIGGQKN N AVKVLKENPEIA D KLEQEIRNTLASNPNSV..LKATASDSNDES.DVE.....EFSEEL.....	372
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GE R IGQGR D NCREFL N ENAE L ARIENK V REHL G VTPMGA..VTLA.EEEVEE.....	352
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GSKIGGQKANAAKYLEENPEI G EEEQIRAKLLVTSANT..KATPVAEDLADA.DI.....	347

logo

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

-  non conserved
-  similar
-  ≥ 50% conserved