

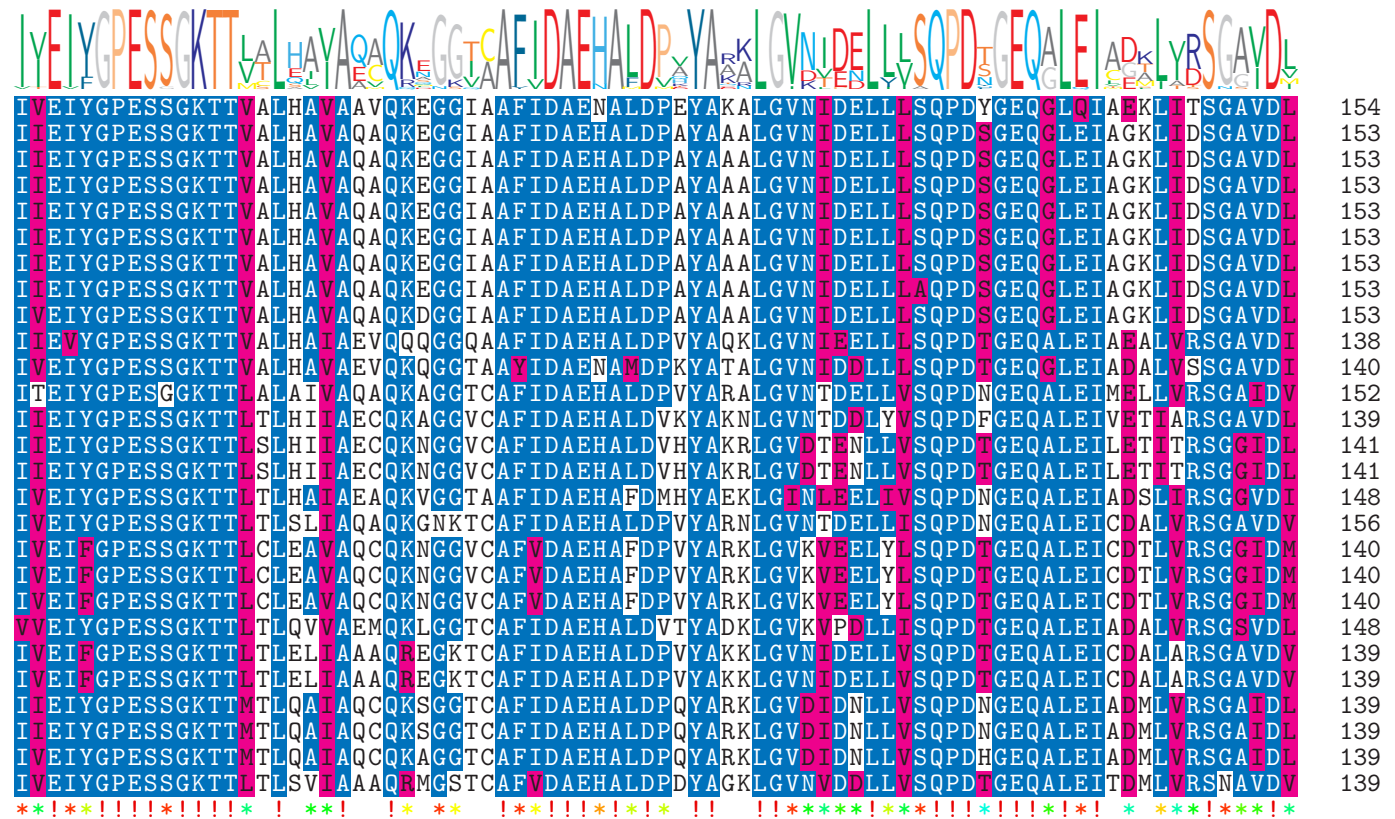
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NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK.....PKKLEEISKKFGA	EREKALNDALKLIEKD	FGKGSIMRLGER	.AEQKVQV	MSSGSLALD	I	ALGSGGY	PKGR	73		
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR.....IKKTEEITKKFG	DERKKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQV	MSSGSLALD	I	ALGAGGY	PKGR	73		
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTRI	STVPSGSLALD	T	ALGIGGY	PRGR		58		
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDA	ALKKIEKNFGKGSIMRMGEK	.VDTQV	STVSSGSLALDE	A	LGVGGY	PRGR		60		
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	SQIEKAFGKGSIMKLGAE	.SKLDVQV	VSTGSLSLD	I	ALGVGGI	PRGR	72		
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDA	ALKSLDKTTFGKGTILRLGDK	.EVEQIDS	IGTGSVGLD	I	ALGIGG	VPKGR		59		
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAI	SLAIKQIDKVF	FGKGALVRLGDK	.QVEKIDA	ISTGSLGLD	I	ALGIGG	VPKGR	61		
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NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTS	PNDDKKKALA	AVLEKLDKTYGKGTVMKLG	DGTVDHNI	EVIPS	GS	LGLD	I	ALGVGGY	PKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQ	VEPEQKKQALEA	AALQIEKQFGKGSIMKLG	QT.EQLDIES	VSTGSLGLD	I	ALGIGGL	PMGR		76	
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAAS	MSAEKQKALAA	AALQIEKQFGKGSIMKMD	A.EVEPVQV	VSTGSLGLD	V	ALGVGGL	PRGR		68	
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAA	ALGQIEKQFGKGSIMRLG	DN.RAM	D	VETISTG	SLSLD	I	ALGAGGL	PMGR	59	
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQA	ALSQIEKQFGKNTVM	RLGDN.TVQ	A	VEAVSTG	SLTL	D	I	ALGIGGL	PKGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQA	ALSQIEKQFGKNTVM	RLGDN.TVQ	A	VEAVSTG	SLTL	D	I	ALGIGGL	PKGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAA	ALGQIEKQFGKGAVMR	MDH.DRQA	I	PSISTG	SLGLD	I	ALGIGGL	PKGR	59	
consensus	***	***	*	***!	***!	***!	*	***!	***!	***!	

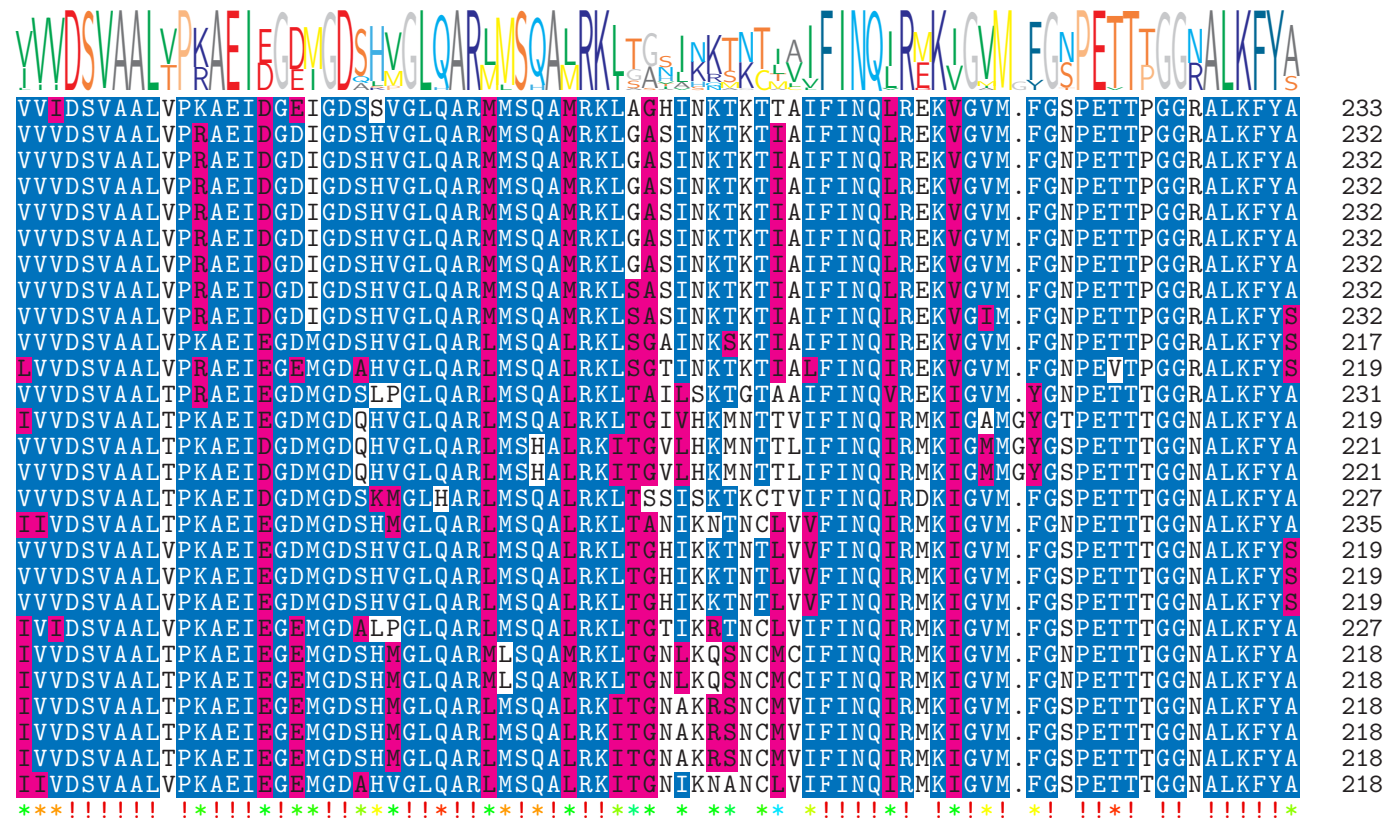
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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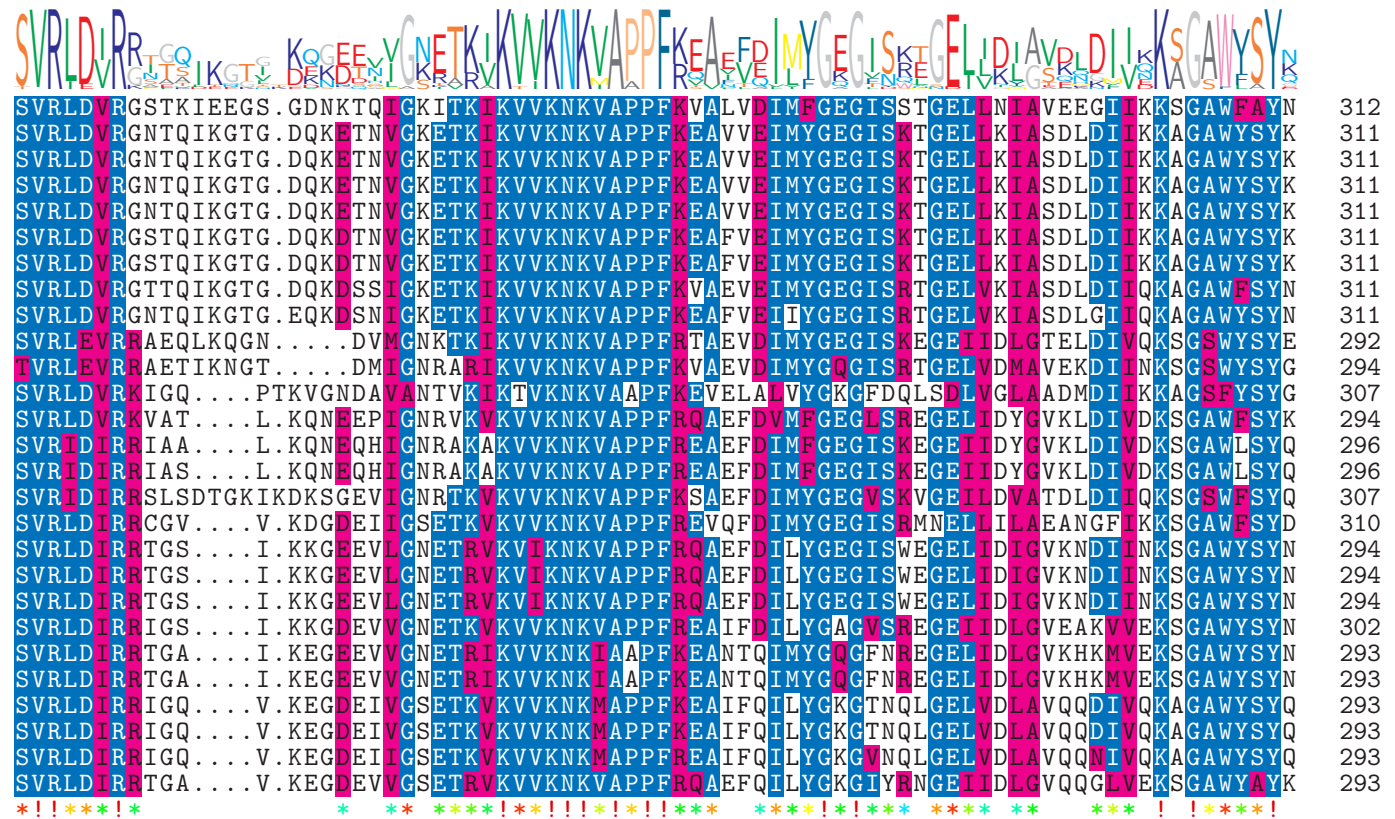
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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DEKIGQGSENAKKYLAADNPVFAEIDHQVRVQFGLIDGEEAAE.....SKKDE.....VAQVDS..VNEEVPLDLGDEL	378
DEKIGQGSENAKKYLAADNPVFEIDHQVRVQFGLIDGEEIAE.....SKKDE.....AAQVDS..VNEEVPLDLGDEL	378
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGSENAKKFLADNPVFEIDHKVVRVQGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGGRENAAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAE.TQEEL.E..FE.E.....	348
SERIGGGRENAAKNYLADHEDVEDEVRLKVRVQGLSDVPEEDLPSTE.DE.QI.N..ILPDDST.....EE.....	355
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DKKLGGGRENKAFLENPEIADEITKAIQNSMGTGEMISGS..EDDEGE..E.....	343
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGRENAAKALLKEDKALADEITLKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK	343
GTKIGQGKNNNAVKWLKENPEIADKLEQIRNTLASNPNSVLK..ATASDSNDESDVEEFSE.....EEL.....	372
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHITEG..TQDET.....GERPE.....E.....	348
GERIGGGRDNCREFLRENAELAREIENKVRHGLVTPMGAV..TLAEEVEED.....	352
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logo

	E	I	E	E	E	
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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved