

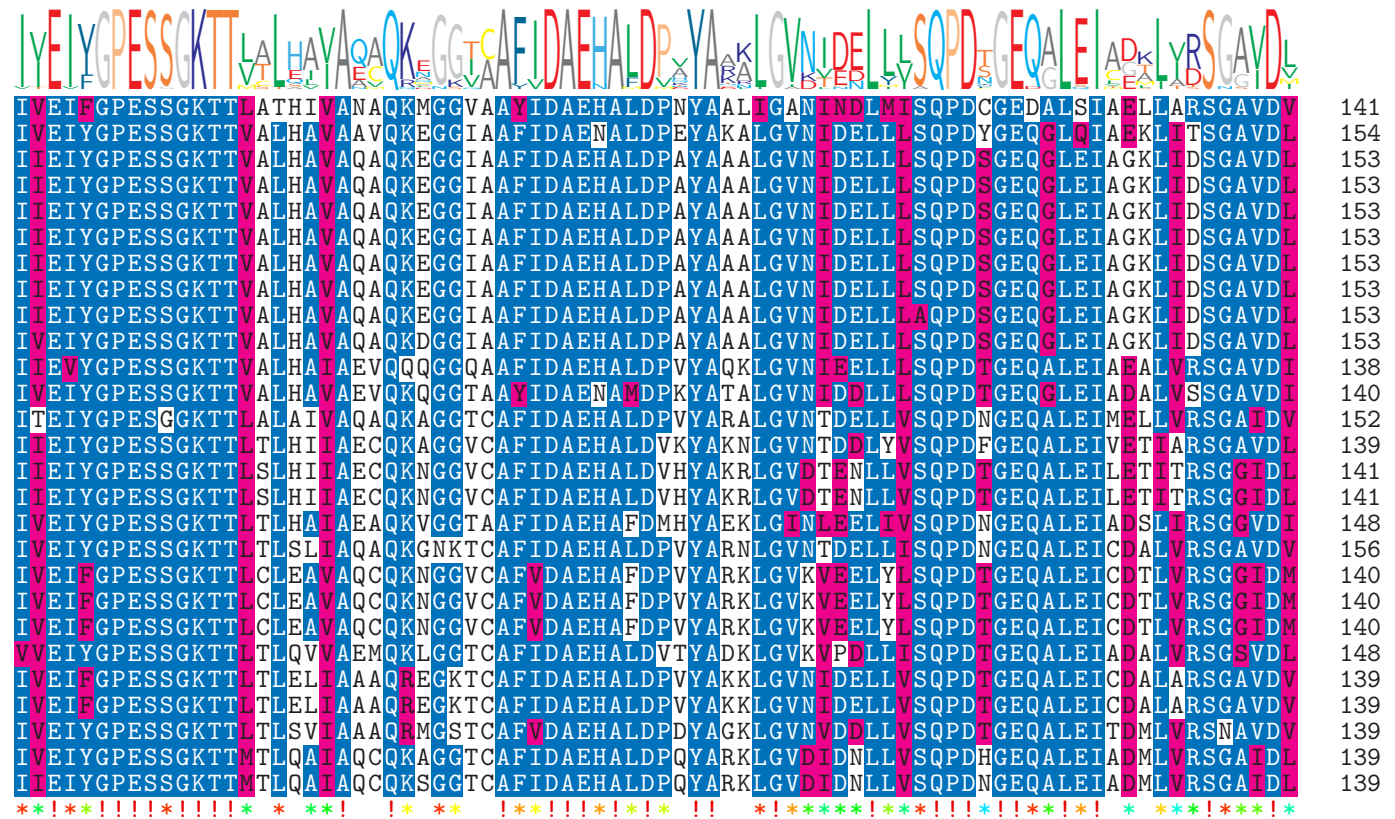
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFGD	ERRKALDDALKNIEKDFGKGAVMRLGER	.AEQKVQV	MSSGSLALDIALGAGGY	PKGR	73	
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFGD	ERKKALDDALKNIEKDFGKGAVMRLGER	.AEQKVQV	MSSGSLALDIALGAGGY	PKGR	73	
NTDB id 115 BSU 16940 NP 389576.2	MS	DRQAALDMALKQIEKQFGKGSIMKLGEK	.TDTRIST	VPSSGSLALDTALGIGGY	PKGR	58	
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NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAMSQIEKAFGKGSIMKLGA	E.SKLDVQV	VSTGSLSLDIALGVGGI	PKGR	72	
NTDB id 1245 Cj1673c YP 002345041.1	MDDN	KRKSLDAALKSLDKTTFGKGTILRLGDK	.EVEQID	ISTGSGVGLDIALGIGGV	PKGR	59	
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDE	DKQKATISLAIKQIDKVFVGKGA	LVR LGDK.QVEKID	ISTGSLGLDIALGIGGV	PKGR	61	
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDE	DKQKATISLAIKQIDKVFVGKGA	LVR LGDK.QVEKID	ISTGSLGLDIALGIGGV	PKGR	61	
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTSPND	DKKKALAAVLEKLDKTYGKGTVMKLG	DGTVDHNI	IEVIPS	GSLGLDIALGVGGY	PKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQ	KKQALEAALAQIEKQFGKGSIMKLQ	QT.EQLDIE	SVSTGSLGLDIALGIGGL	PMGR	76	
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAASMSA	EKQKALAAALAQIEKQFGKGSIMKMG	DA.EVEPVQV	VSTGSLGLDIALGVGGL	PKGR	68	
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDEN	KQKALAAALGQIEKQFGKGSIMRLG	DN.RAMDVET	ISTGSLSLDIALGAGGL	PMGR	59	
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDEN	KQKALAAALGQIEKQFGKGSIMRLG	DN.RAMDVET	ISTGSLSLDIALGAGGL	PMGR	59	
NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KKRALAAALGQIEKQFGKGAVMRMG	DH.DRQAIP	SISTGSLGLDIALGIGGL	PKGR	59	
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDN	KSKALQAALSQIEKQFGKNTVMRLG	DN.TVQAVE	AVSTGSLTLDIALGIGGL	PKGR	59	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDEN	KSKALQAALSQIEKQFGKNTVMRLG	DN.TVQAVE	AVSTGSLTLDIALGIGGL	PKGR	59	
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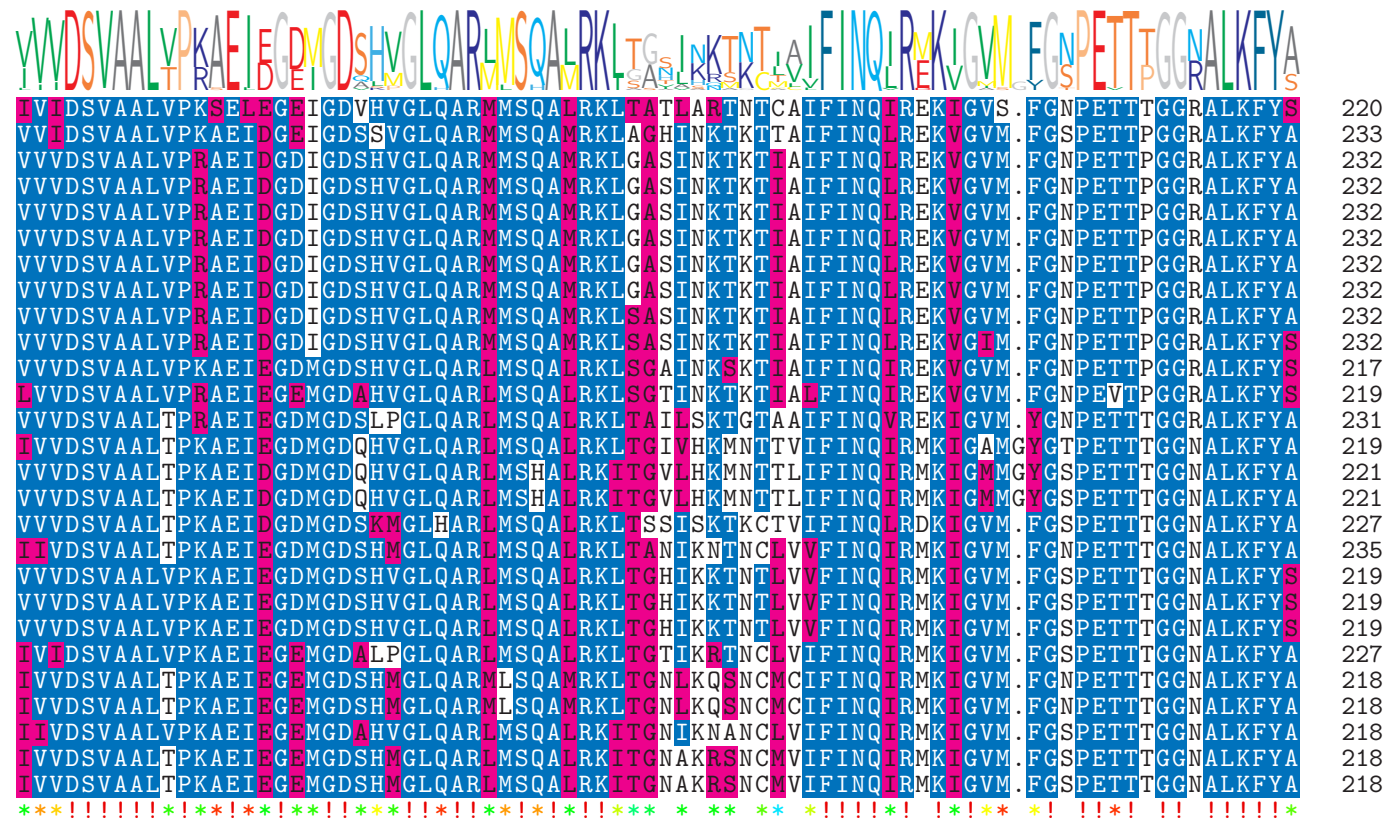
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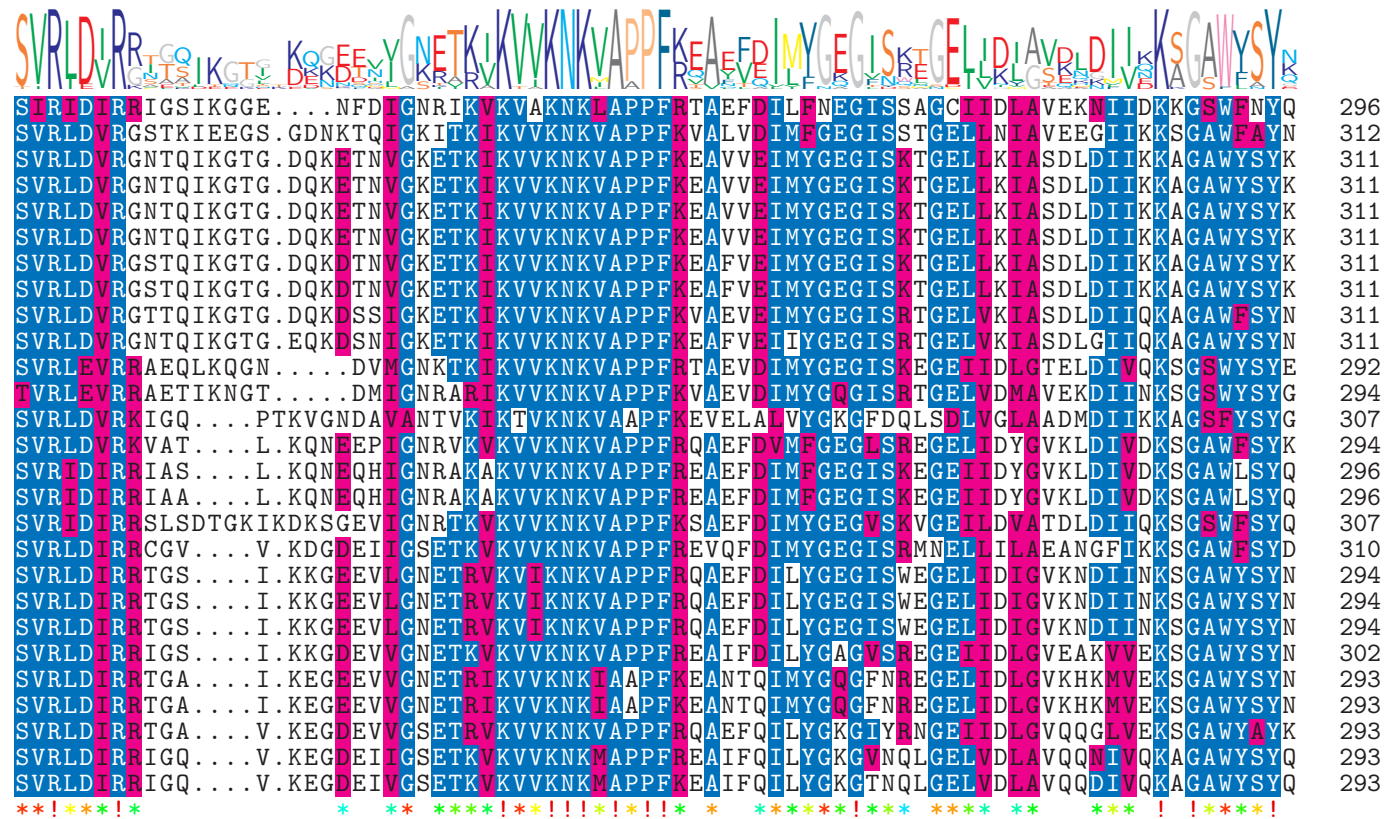
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGSSENAKKYLAENPEVFAEIDHKQVRVQFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGGRENAAKQFLKENKDIMLMIQEIRHYGLDNNGVVQQAAETQEEL.EFE.E.....	348
SERIGQGGRENAAKNYLADHEDVEVLKVRVRAAYGISDVPEEDLPTTEDE.QI.NILPDST.....EE.....	355
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DKKLGQGGRENAAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LE..EME.....	347
DKKLGQGGRENAAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LE..EME.....	347
DTKLGGGRDITVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGGKNNAVKWLKENPEIADKLEQEIINTLASNPNS....VLKATASDSND..ESDVVEEFSEEEEL..	372
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETDERPEE.....	348
GERIGQGGKDNCRFLRENAELAREIENKVRHLGVTPMG....AV.TLAEVEVE..D.....	352
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GDKIGQGGKANACKYFLKENPEIAKTLDDKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
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logo

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consensus			

- X non conserved
- X similar
- X ≥ 50% conserved