

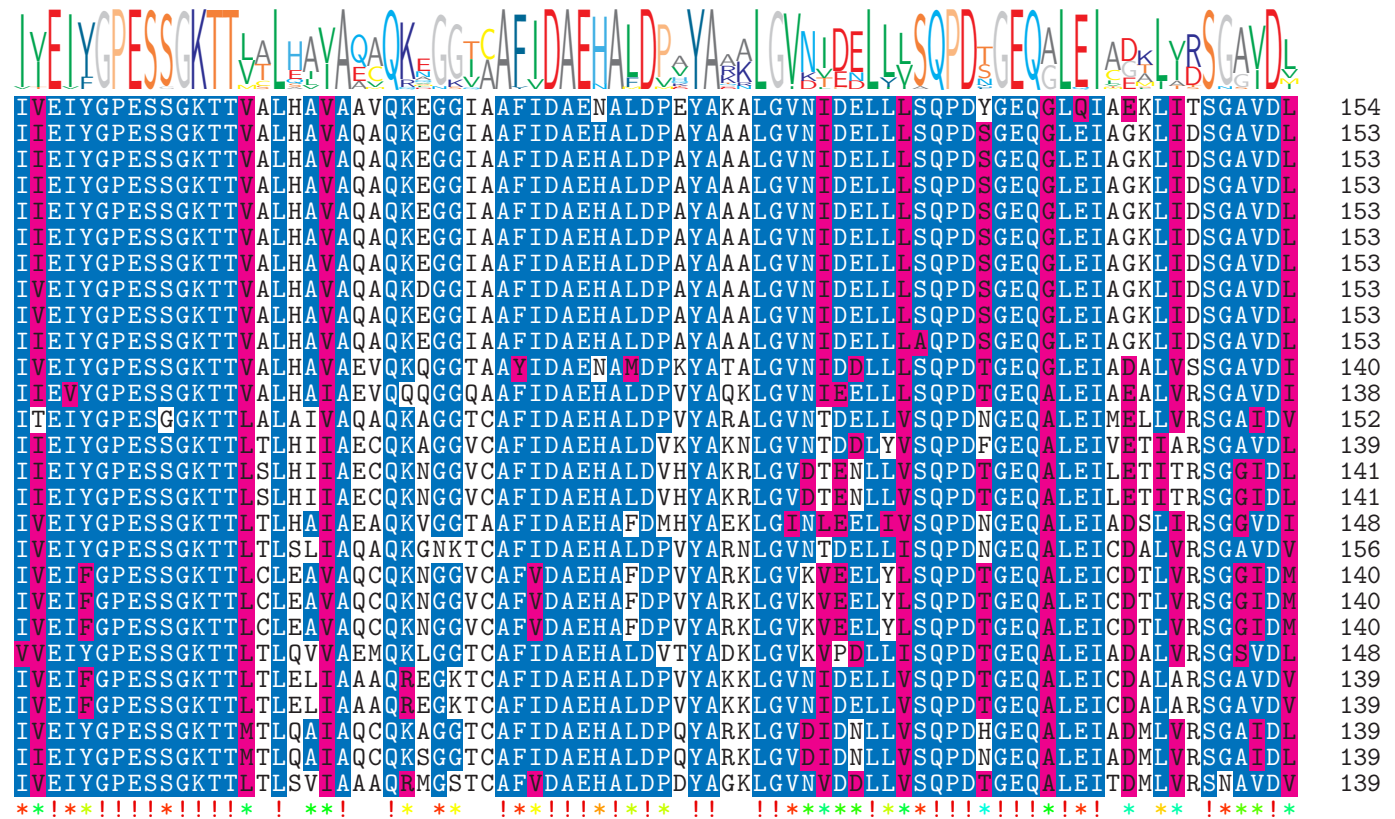
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFGDERKKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 325864 EGX72 RS01580 WP 001085741.1	.MAKK....TKKAEEITKKFGDERRKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFGDERRKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
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NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQIEKQFGKGSIMKLG EK.TDTRISTVPSGSLALDTALGIGGYPGR	58
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTDAKERSKATETAMSQIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDNKRKSLDAALKSLDKTFGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKATISLAIKQIDKVFVGKALVRLGDK.QVEKIDISTGSLGLDLALGIGGVPKGR	61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKATISLAIKQIDKVFVGKALVRLGDK.QVEKIDISTGSLGLDLALGIGGVPKGR	61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTSNDDKKKALAAVLEKLDKTYGKGTVMKLG DGTVDHNIIEVIPSGSLGLDLALGVGGYPKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQKKQALEAALAQIEKQFGKGSIMKLGQT.EQLDIESVSTGSLGLDLALGIGGLPMGR	76
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....K..KAASMSAEKQKALAAALAQIEKQFGKGSIMKMGDA.EVEPVQVVSTGSLGLDVALGVGGLPRGR	68
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDLALGIGGLPKGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSTGSLGLDIALGIGGLPKGR	59
consensus	*** **	

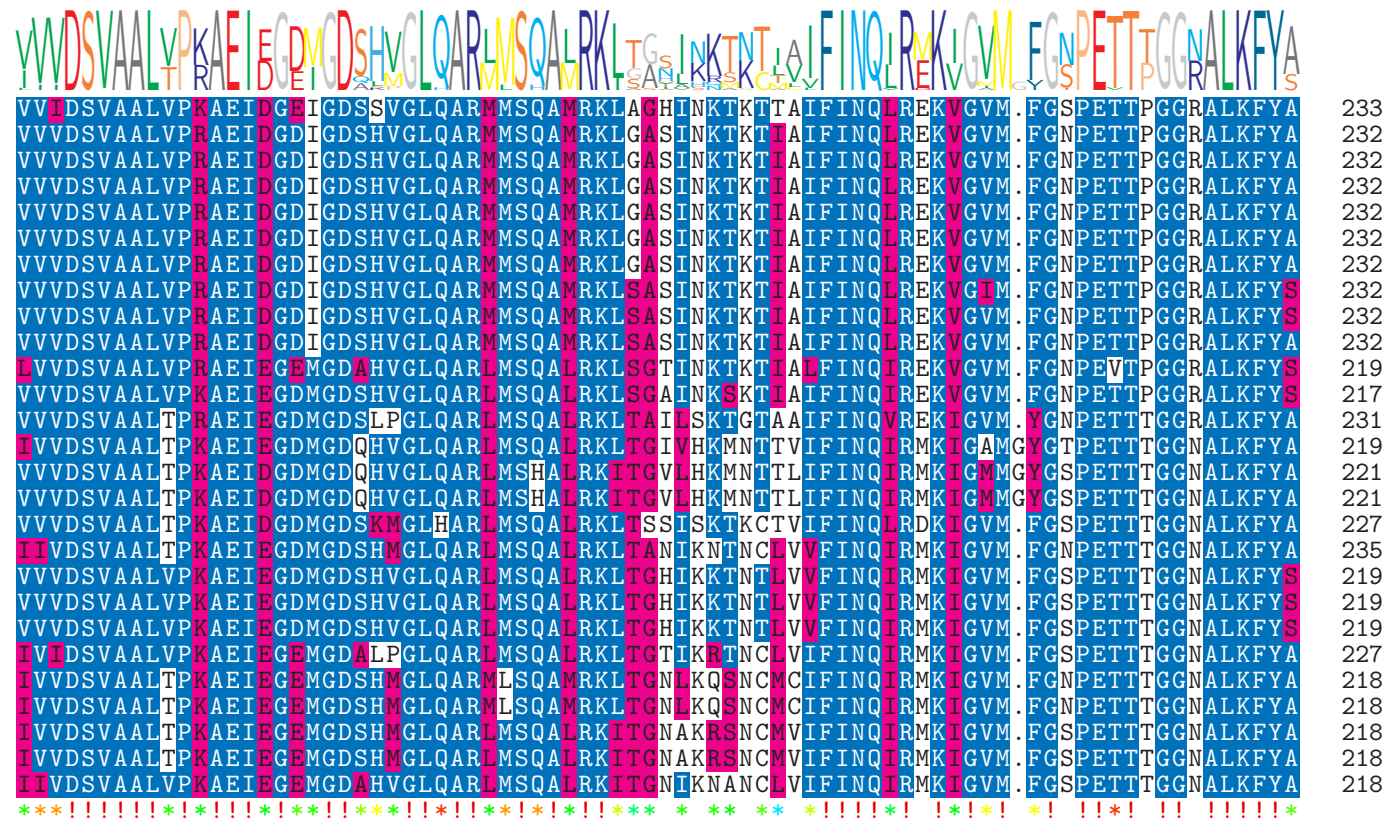
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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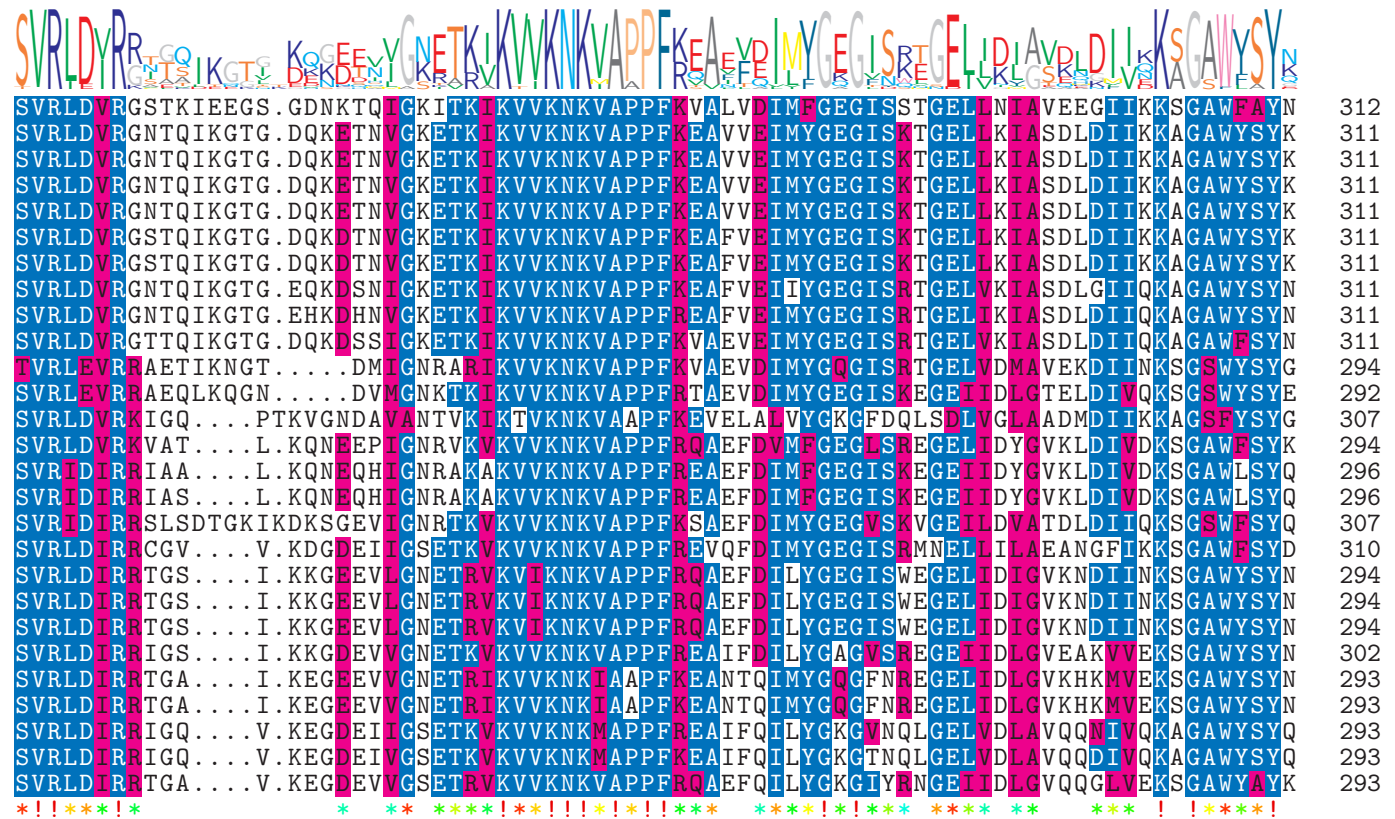
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDEPK...KEE..AVNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTENKKDEPK...KEE..AVNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAHNPEIFDEIDHKVRVQFGLIDGEEIAES...KKDEAA...QVD..SVNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAHNPEIFAEIDHQVRVQFGLIDGEEAAES...KKDEVA...QVD..SVNEEVTLDLGDLEIE	381
GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQFGLIEDNTTEKKSSKEKET.....DE..KADKNLVLELDDTIELE	382
GEKIGQGSSENAKKYLAHNPAIFDEIDHKVRVHFGMTEDDSPVQSELVEE.....K..NEADDLVLDLDNAIEIE	378
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVVKFGLLEESEE..ESAMAVA.....S..EETDDLALDLNGIEIE	377
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAGISDVPEEDLPTTEDE.QIN.....ILPDDSTEE..	355
EERLGGRENAKQFLKENKIDMLMIQEIQIREHYGLDNNGVVQQQAETQEELE.....FE.E.....	348
DERIGQGKEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAPEA.....AEA.....	363
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DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..P.....LEEME	347
DKKLGGGRENKALLKEDKALADEITLKIKESIGSNEEI....MPLPDE..P.....LEEME	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GER.....PEE.....	348
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GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSA.....ADDVEFGAVPEEF....	354
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GNKIGQGGKNNVIRYFEENNQIAEIEIERNIREQLLTTGTN....GAVQ..I..ED.....EEEPDLL..LES.....	349
GSKIGQGGKANAAKYLENPEIQEIEQQIRAKLLVTSAN.....TKATPVAED.....LADADI.....	347

logo

		↓EE	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
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NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388	
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved