

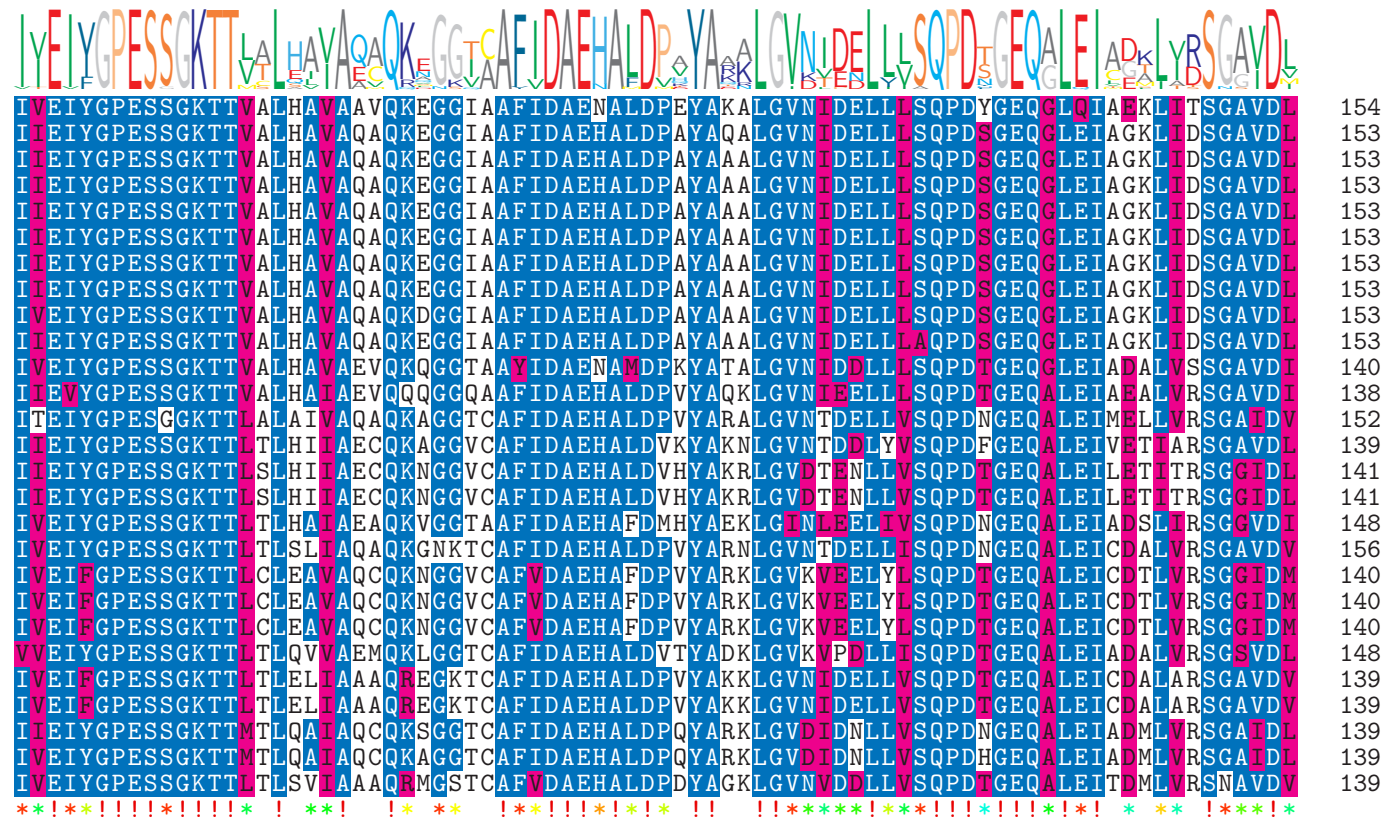
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NTDB id 527 SMSK321 RS11065 WP 001085454.1	.MAKK.....PKKLDEISKKKFGAEREKALNDALKLIEKDFGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKK.....LKKNEEITKKKFGDERRKALDDALKNIEKDFGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	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	MSKDATKEISAPTD AKERSKATETAMSQIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDNKRKSLDAALKSLDKTFGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKATISLAIKQIDKVFVGK GALVRLGDK.QVEKIDAI STGSLGLDLALGIGGVPKGR	61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKATISLAIKQIDKVFVGK GALVRLGDK.QVEKIDSISTGSLGLDLALGIGGVPKGR	61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTSPNDDKKKALAAVLEKLDKTYGKGTVMKLGDGTVDHNI EVIPSGSLGLDLALGVGGYPKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQKKQALEAALAQIEKQFGKGSIMKLGQT.EQLDIESVSTGSLGLDLALGIGGLPMGR	76
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSI STGSLGLDIALGIGGLPKGR	59
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NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
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consensus

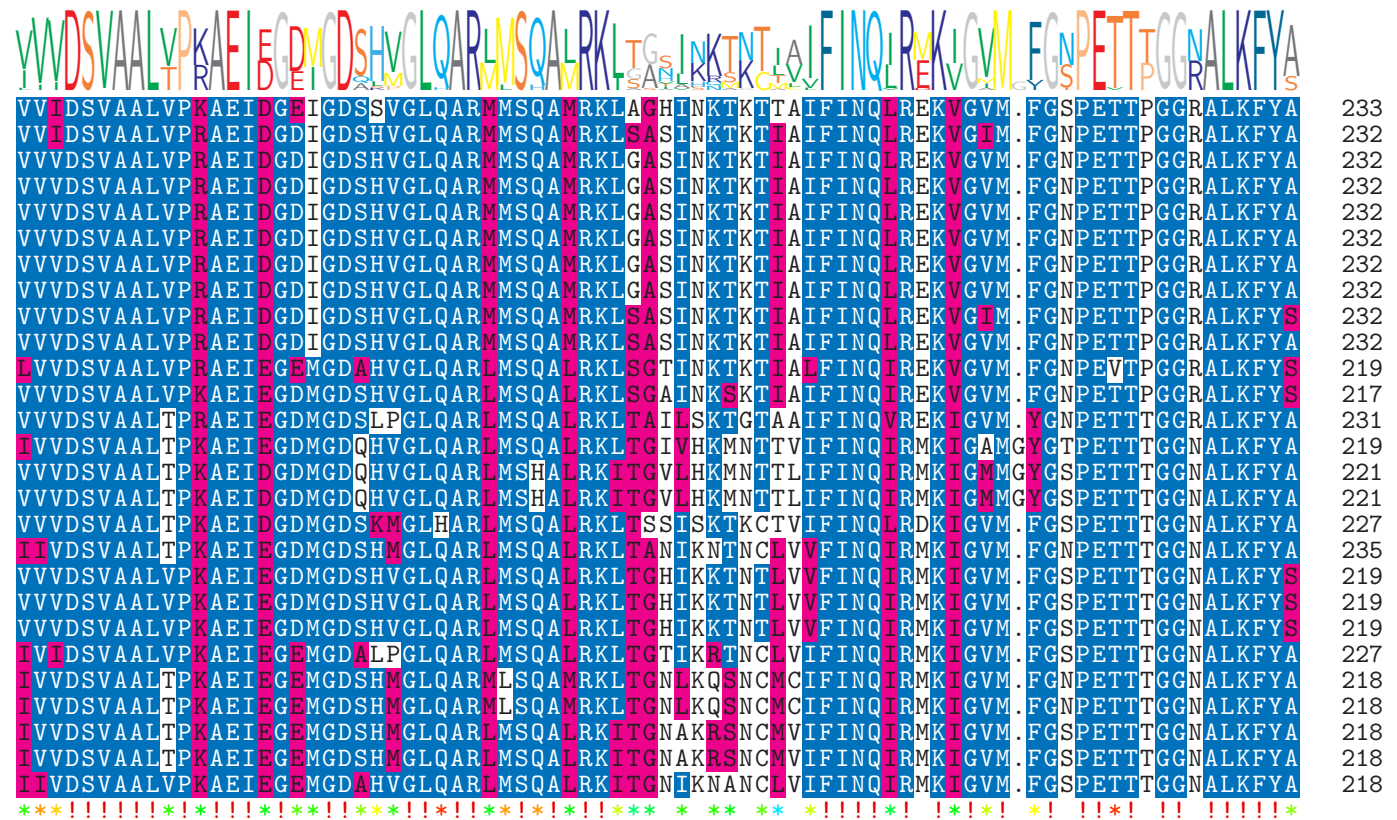
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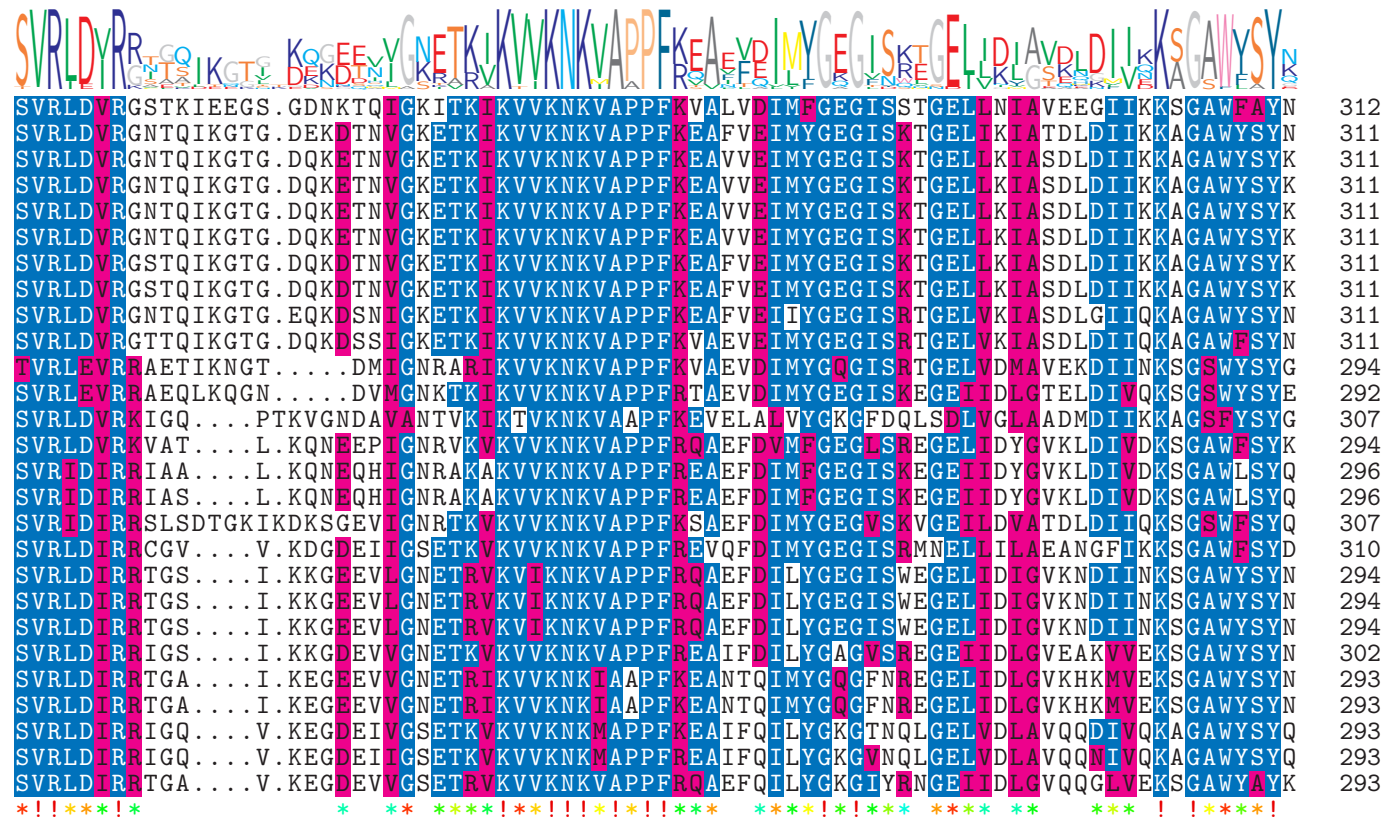
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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DEKIGQGSSENAKKYLAHPHPEIFDEIDKQVRSKFGLIDGEEVSEQDNTENKKDEP...KKEEAV..NEEVPLDLGDELEIE	385
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DEKIGQGSSENAKKYLAHPHPEIFDEIDKQVRSKFGLIDGEEVSEQDNTENKKDEP...KKEEAV..NEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAES...KKDEA...AQVDSV..NEEVTLDLGDELEIE	381
DEKIGQGSSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEAAES...KKDEV...AQVDSV..NEEVTLDLGDELEIE	381
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SERIGQGRENAKNYLADHEDVEVRLKVRAAAGISDVPEEDLPTTEDE.QIN.....ILPDDSTEE.	355
EERLGGQRENAKQFLKENDIMLMIQEQIREHYGLDNNGVVQQAAETQEELE.....FE.E.....	348
DERIGQGKEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEA.....AEA.....	363
DKKLGQGSRENSKAFLENPEIADAITKAIQNSMGTIEGMI.....SGSEDDE.....GEE.....	343
DKKLGQGSRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP.....LEEME	347
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GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GERPEE....	348
GAKIGQGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GERPEE....	348
GERIGQGRDNCREFLENARIEIENKVRHLGVTPMG....AV.TLAEV.....EED.....	352
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GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM....QLIAETSSA.....ADDVEFGAVPEEF....	354
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GSKIGQGGKANAAKYLEENPEIQEIEQQIRAKLLVTSAN.....TKATPVAED.....LADAD...I.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1 ... 387
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consensus

 non conserved
 similar
 ≥ 50% conserved