

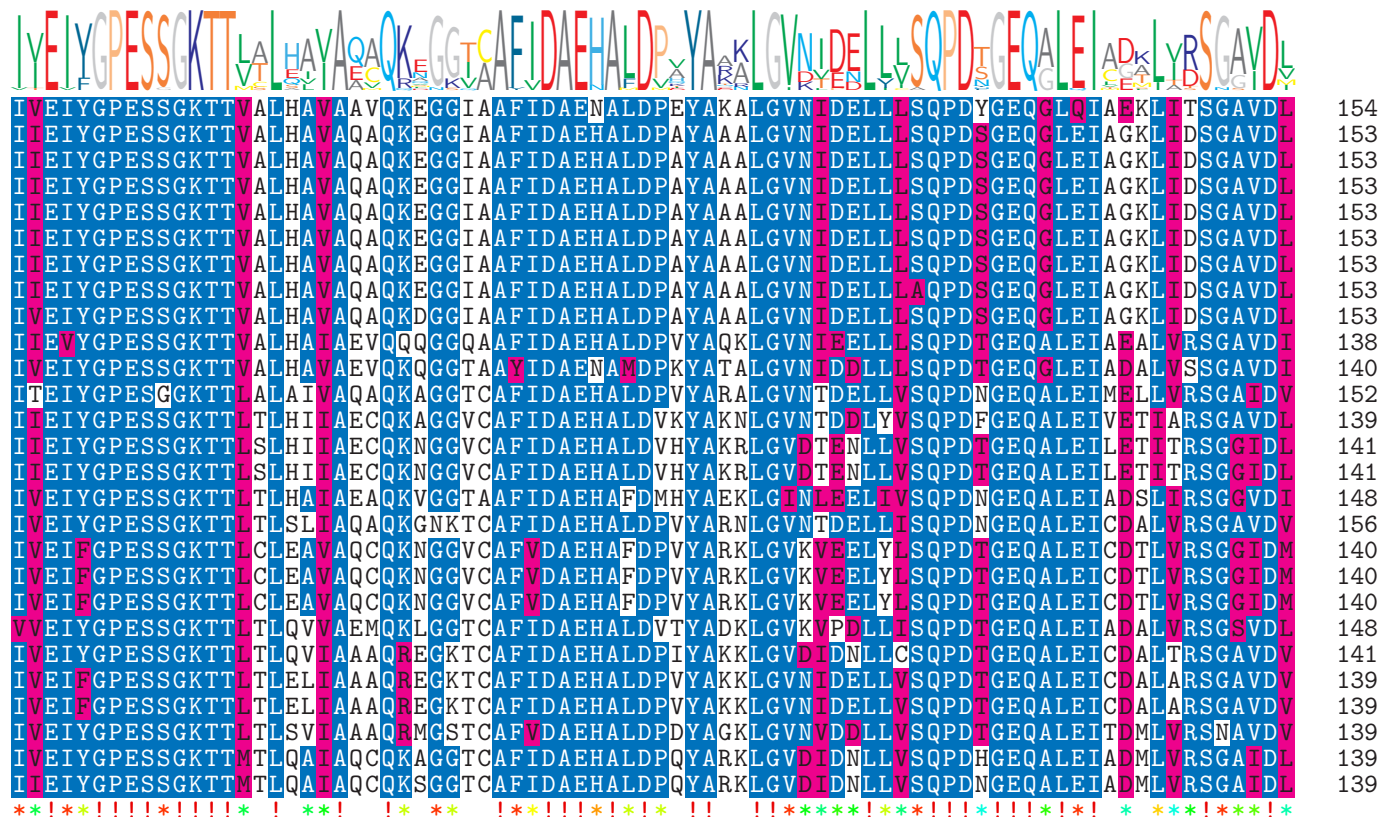
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKK....KTNFDDITKKYGAERDKALADALALIEKD FGKGSIMRLGEA.ANQKVS	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKK....PKKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
NTDB id 228 SPD RS09265 WP 001085462.1	.MAKK....PKKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKK....LKKNEEITKKFGDERRKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR....IKKTEEITKKFGDERKKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALKQIEKQFGKGSIMKLGEK.TDTRISTVPSGSLALDTALGIGGYPRGR	58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALKKIEKNFGKGSIMRMGEK.VDTQVSTVSSGSLALDEALGVGGYPRGR	60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTDAKERSKATETAMSQIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPRGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDNKRKSLDAALKSLDKT FGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPKGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAIISLAIKQIDKVF GKGA LVRLGDK.QVEKIDAISTGSLGLDLALGIGGVPKGR	61
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKAIISLAIKQIDKVF GKGA LVRLGDK.QVEKIDSISTGSLGLDLALGIGGVPKGR	61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTSNPDDKKKALAAVLEKLDKT YGKGTVMKLGDTVDHNIIEVIPSGSLGLDLALGVGGYPKGR	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 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSI	59
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
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NTDB id 159 SP RS09750 WP 001085462.1
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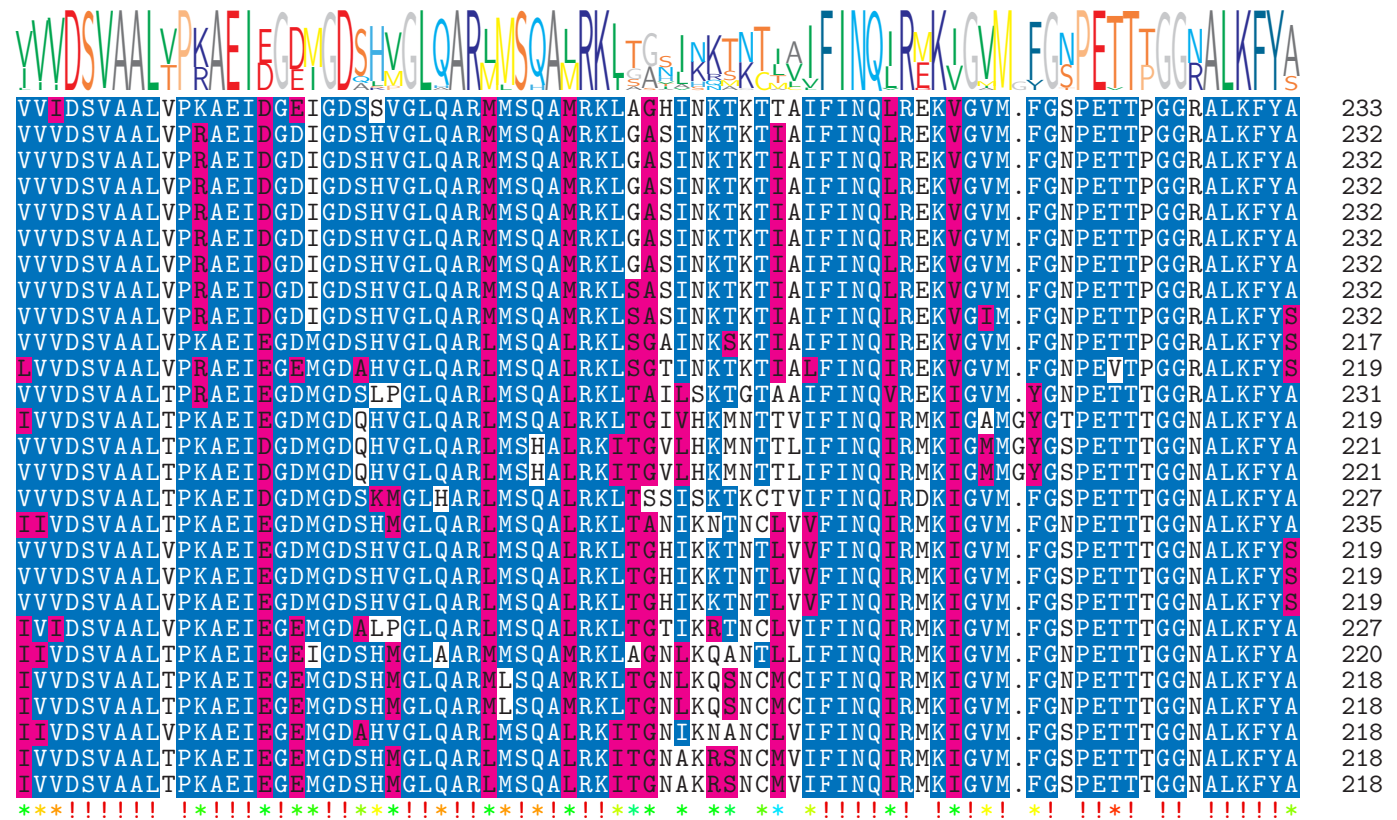
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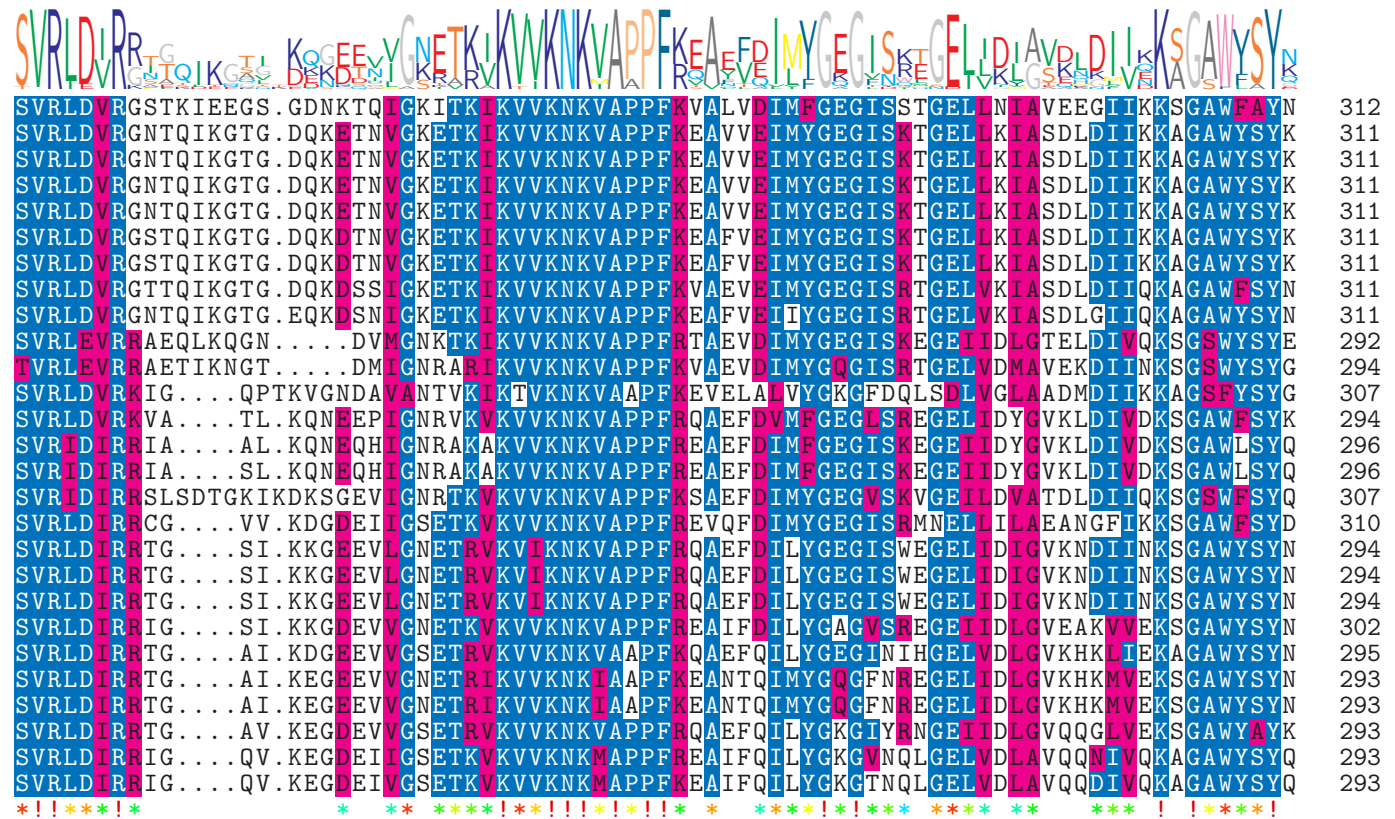
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIFDEIDKQVRSKFLIDGEEVSEQDTEN...KKDE...PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ENAKKYLAHNPEVFAEIDHQVRVQFLIDGEEAAE...S...KKDE...VAQVDS..VNEEVTLDLGDEL	378
DEKIGQGS ENAKKYLAHNPEIFDEIDHQVRVQFLIDGEEIAE...S...KKDE...AAQVDS..VNEEVTLDLGDEL	378
GEKIGQGS ENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVA..SE.....E.....TDDLALDLNGI	374
GEKIGQGS ENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSK..EK.....ETDEK..ADKNLVLELDDTI	379
EERLGGG RENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAAET...QEEL.EFE.E.....	348
SERIGQGS RENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTED...E.QI.NILPDDST.....EE.....	355
DERIGQG KETTIAYTIAERPMEQETIDRVMAAIRAGNAGEAPALAPAPAPEAAEA	363
DKKLGGG RENSKAFLKENPEIADEITKAIQNSMGTIEGMISGS...EDD..EGEE.....	343
DKKLGGG RENAKALLKEDKALADEITLKIKESIGSNEEIMPL...PDE..PLEEME.....	347
DKKLGGG RENAKALLKEDKALADEITLKIKESIGSNEEIMPL...PDE..PLEEME.....	347
DTKLGGGRD TVKELIKDNPELAELEAKIREKLQAK	343
GTKIGQG KNNNAVKWLKENPEIADKLEQIRNTLASNPNSVLK...ATASDSNDESDVEEF...SEEL	372
GAKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEG...TQDETGDGE...RPEE	348
GAKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEG...TQDETGDGE...RPEE	348
GAKIGQGD NVRVWLKENPEISDEIDAKIRALNGVEMHITEG...TQDETGDGE...RPEE	348
GERIGQGRD NCREFLRENAELAREIENKVRHGLVTPMGAVT...L...AEEVEED	352
GDKIGQGD KANACNFLKENSATIAAELDKKLREMLLHKGNELTP...AAGVNSHDEDEFAGE...GNEEF	357
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GDKIGQGD KANACKYLKENPEIAKTLDDKKLREMLLNPNENMQLI...AETSSAADVEFGA...VPEEF	354
GSKIGQGD KANAAYLEENPEIGQETIEQQIRAKLLVTSANTKA...TPVAEDLADADI	347
GNKIGQGD KNNVIRYLEENPQISTEIEAVIREQLLTKASDQTA...A.HDETEEEPDLLES	349
GNKIGQGD KNNVIRYFENNQIAEIERNIREQLLTTGTNGAV...Q.I.EDEEEPDLLE...S	349

logo

	E	I	E	E	E	
NTDB id 600 KW2 RS01765 WP 011675413.1						387
NTDB id 269 KZH43 RS08665 WP 001085462.1	EIEIEE					388
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consensus						

-  non conserved
-  similar
-  ≥ 50% conserved