

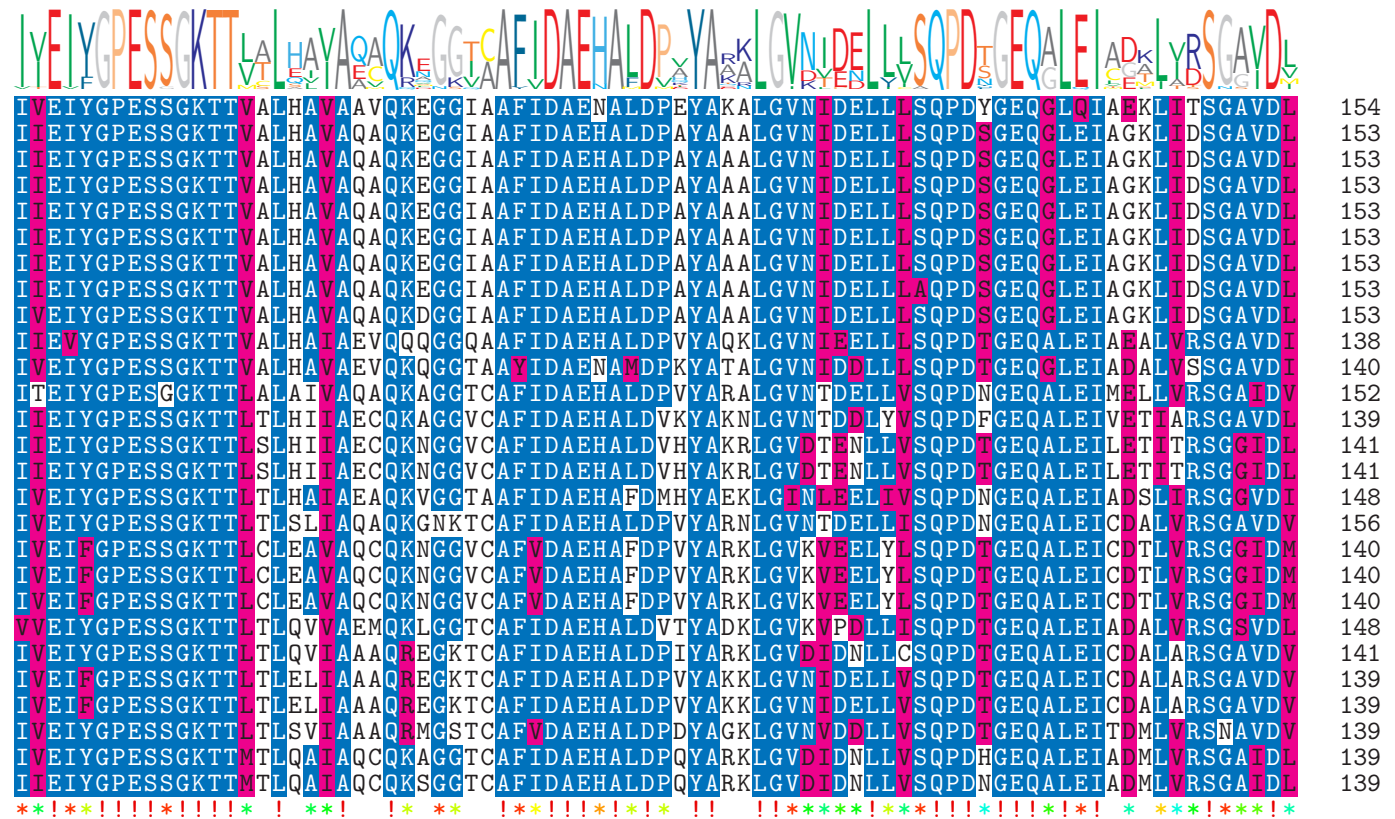
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKKL....KKNEEITKKFG	DERRKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQVM	SSGSLALD	I	ALGAGGYPKGR	73
NTDB id 408 SMU RS09530 WP 002262392.1	.MAKRI....KKTEEITKKFG	DERKKALDDALKNIEKD	FGKGAVMRLGER	.AEQKVQVM	SSGSLALD	I	ALGAGGYPKGR	73
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQFGKGSIMKLGEK	.TDTRI	STVPSGSLALD	TALGIGGYPRGR			58
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAALDAALK	KIEKNFGKGSIMRMGEK	.VDTQVSTV	SSGSLALDEALGVGGYPRGR				60
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAM	SQIEKAFGKGSIMKLGAE	.SKLDVQVV	STGSLSLDLALGVGGIPRGR			72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKS	LDKTFGKGTILRLGDK	.EVEQIDS	IGTGSVGLDLALGIGGVPRGR				59
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NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDEDKQKAI	SLAIKQIDKVF	FGKGALVRLGDK	.QVEKIDS	ISTGSLGLDLALGIGGVPRGR			61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT..ETTS	PNDDKKKALAAVLEK	LDKTYGKGTVMKLG	DGTVDHNI	EVIPSGSLGLDLALGVGGYPRGR			68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQ	VEPEQKKQALEAALA	QIEKQFGKGSIMKLGQT	.EQLDIES	VSTGSLGLDLALGIGGLPMGR			76
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NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDKSKALAAALA	QIEKSFGKGAIMKMDGSQ	QEEENLEVISTGSLGLDLALGVGGLPRGR					60
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NTDB id 1427 RS RS02760 WP 011000510.1	.MED.....GK..KAAS	MSAEKQKALAAALA	QIEKQFGKGSIMKMDA	.EVEPVQVV	STGSLGLDVALGVGGLPRGR			68
NTDB id 253173 COG37 RS07185 WP 000963143.1	MAIDENKQKALAAAL	GQIEKQFGKGSIMRLGED	.RSMDVET	ISTGSLSLDIALGAGGLPMGR				61
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAAAL	GQIEKQFGKGSIMRLGDN	.RAMDVET	ISTGSLSLDIALGAGGLPMGR				59
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAAL	GQIEKQFGKGSIMRLGDN	.RAMDVET	ISTGSLSLDIALGAGGLPMGR				59
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	MDDNKSKALQAALS	QIEKQFGKNTVMRLGDN	.TVQAVEAV	STGSLTLDIALGIGGLPKGR				59
NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALS	QIEKQFGKNTVMRLGDN	.TVQAVEAV	STGSLTLDIALGIGGLPKGR				59
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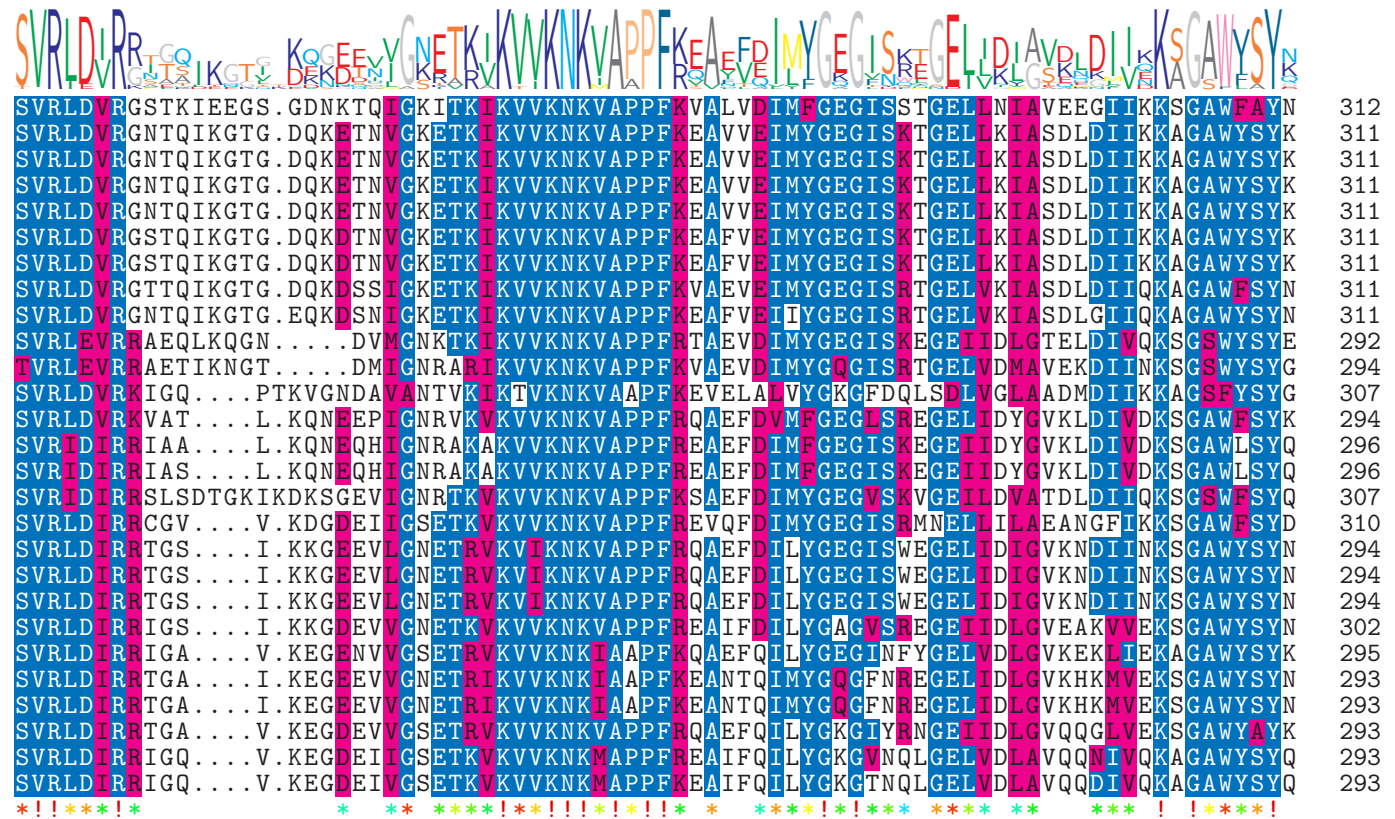
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consensus

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NTDB id 527 SMSK321 RS11065 WP 001085454.1	DEKIGQGS	ENAKKYLADNPEVFA	DEIDHQVRVQFGL	IDGEEAAES....KK	DE....VAQVDS	.VNEEVTLDLGDELEIE		381
NTDB id 453 Spy49 1753c ACI62003.1	GEKIGQGS	ENAKRYLADHPQLF	DEIDRKVRVKFGL	LEESEEEESAMAVASE	E.....	TDDLALDLDN	GIEIE	377
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NTDB id 1142 GTF74 RS11550 WP 000344154.1	GDKIGQGS	KANACKYLLKENPEIA	KTLDKKLREMLLN	PNEN.....MQLIAETSSAA	...DDVEFGAVPEEF			354
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NTDB id 159 SP RS09750 WP 001085462.1	IEE	388
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consensus

 non conserved
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 ≥ 50% conserved