

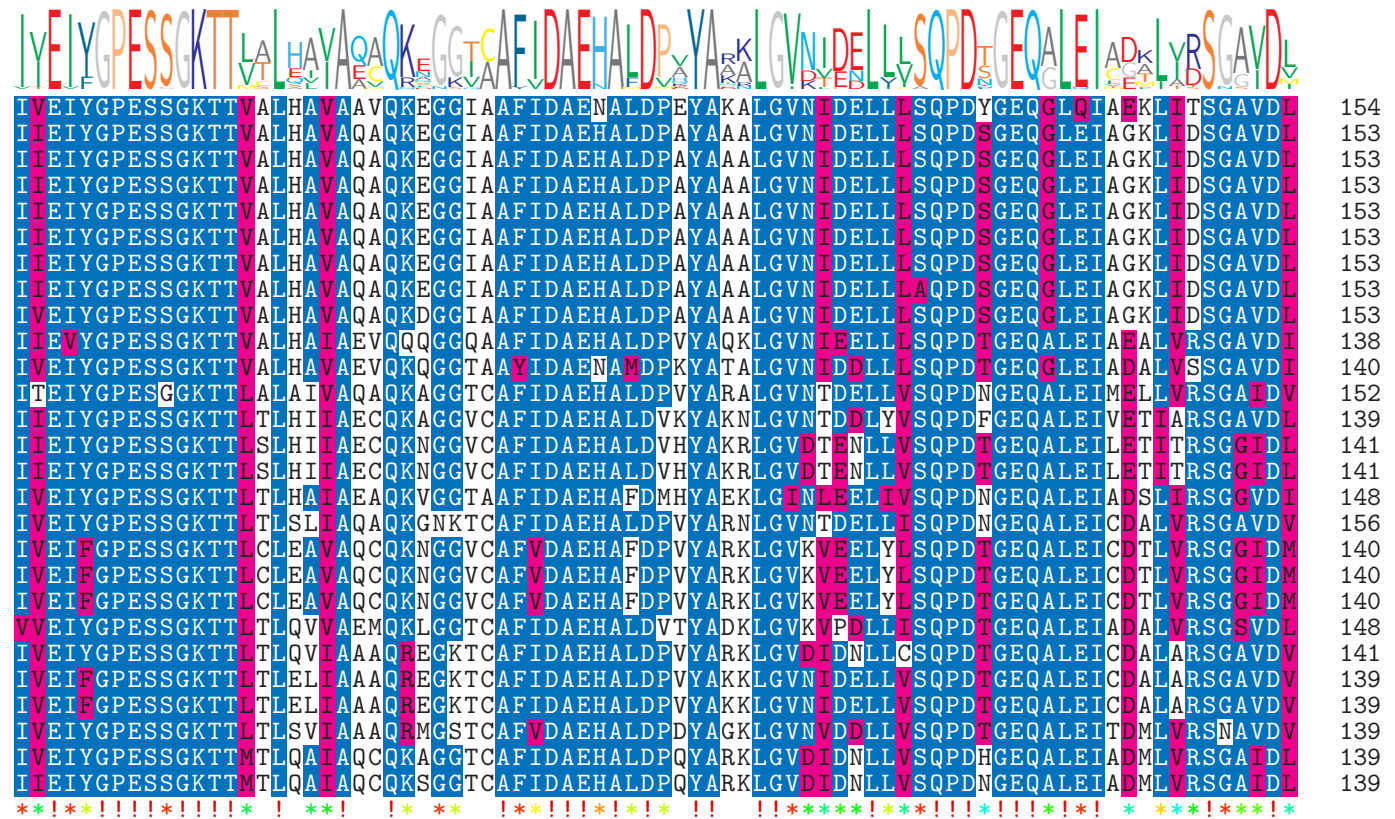
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NTDB id 600 KW2 RS01765 WP 011675413.1	MATKKK....TNFDDITKKYGAERDKALADALALIEKD FGKGSIMRLGEA.ANQKVSVVSSGSLALDIALGAGGYPKGR	74
NTDB id 269 KZH43 RS08665 WP 001085462.1	.MAKKP....KKLEEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
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NTDB id 499 SM12261 RS08315 WP 078228268.1	.MAKKP....KKLDEISKKFGAEREKALNDALKLIEKD FGKGSIMRLGER.AEQKVQVMSSGSLALDIALGSGGYPKGR	73
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NTDB id 453 Spy49 1753c ACI62003.1	.MAKKL....KKNEEITKKFGDERRKALDDALKNIEKD FGKGAVMRLGER.AEQKVQVMSSGSLALDIALGAGGYPKGR	73
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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	MSKDATKEISAPTDAKERSKATETAMSIIEKAFGKGSIMKLGAE.SKLDVQVVSTGSLSLDLALGVGGIPRGR	72
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKRKSLDAALKSLDKT FGKGTILRLGDK.EVEQIDSIGTGSVGLDLALGIGGVPRGR	59
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDEDKQKAIISLAIKQIDKVF GKGA LVRLGDK.QVEKIDAISTGSLGLDLALGIGGVPRGR	61
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NTDB id 355085 CVJ63 RS13620 WP 000963150.1	MAIDENKQKALAAALGQIEKQFGKGSIMRLGED.RSMDVETISTGSLSLDIALGAGGLPMGR	61
NTDB id 1165 A1552VC RS01565 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1142 GTF74 RS11550 WP 000344154.1	MDENKQKALAAALGQIEKQFGKGSIMRLGDN.RAMDVETISTGSLSLDIALGAGGLPMGR	59
NTDB id 1205 PSJM300 05545 AFN77183.1	MDENKKRALAAALGQIEKQFGKGAVMRMGDH.DRQAIPSIISTGSLGLDIALGIGGLPKGR	59
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	MDENKSKALQAALSQIEKQFGKNTVMRLGDN.TVQAVEAVSTGSLTLDIALGIGGLPKGR	59
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consensus

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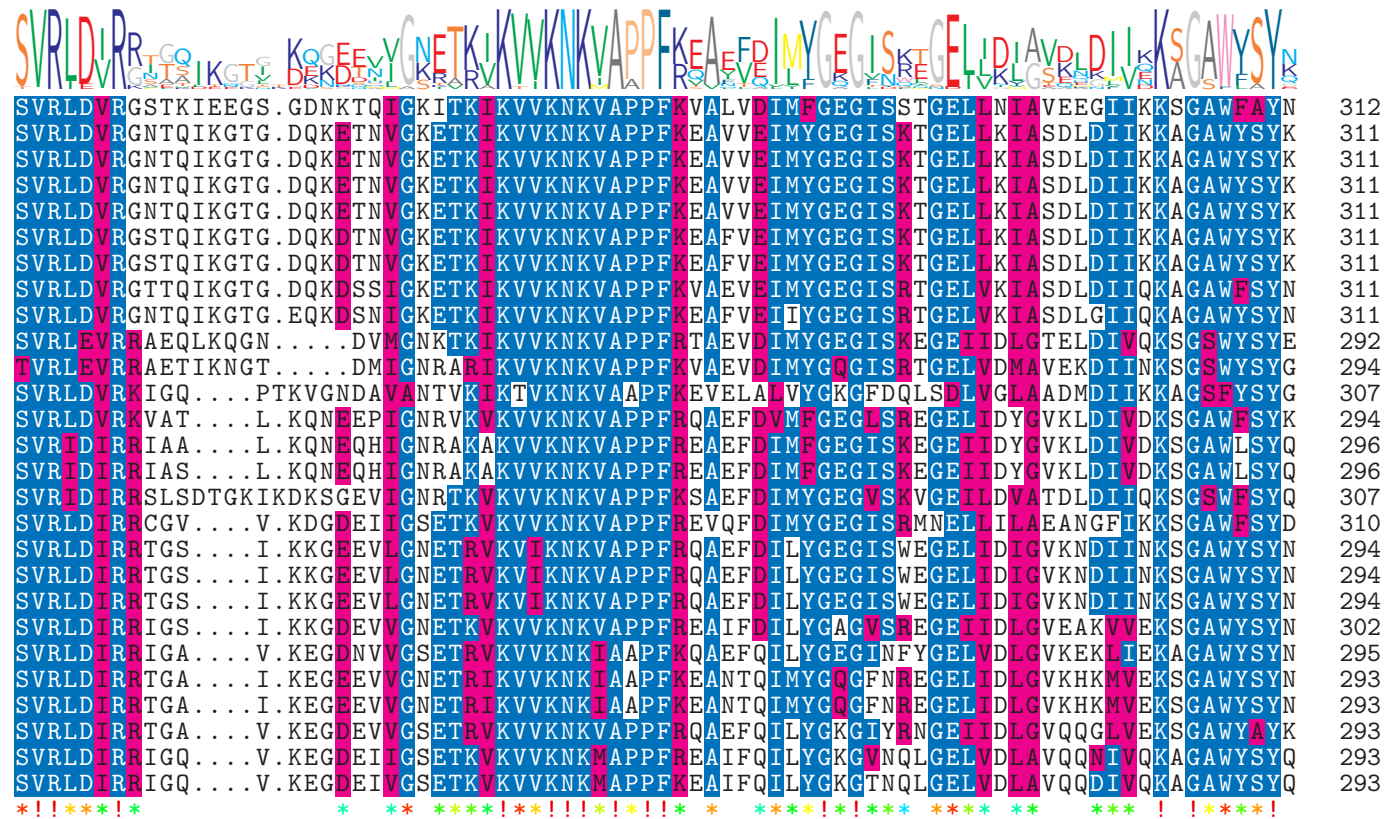
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consensus

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Sequence	Score
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
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DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAADNPVFDEIDHQVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAADNPVFDEIDHQVRVQFGLIDGEEIAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
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GERIGQGRDNCREFLRENAELAREIENKVRHLGVTPM.....GAVTLAE.EVE...ED...	352
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GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPN.....MQLIAETSSAA..DDVEFGAVPEEF...	354
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPN.....MQLIAETSSAA..DDVEFGAVPEEF...	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSA.....NTKATPVAEDL...ADADI.....	347
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GNKIGQGGKNNVIRIFYENNQIAEIEIRNIREQLLTGT.....NGAVQ.I.EDE...EEPDLLES...	349

logo

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

-  non conserved
-  similar
-  ≥ 50% conserved