

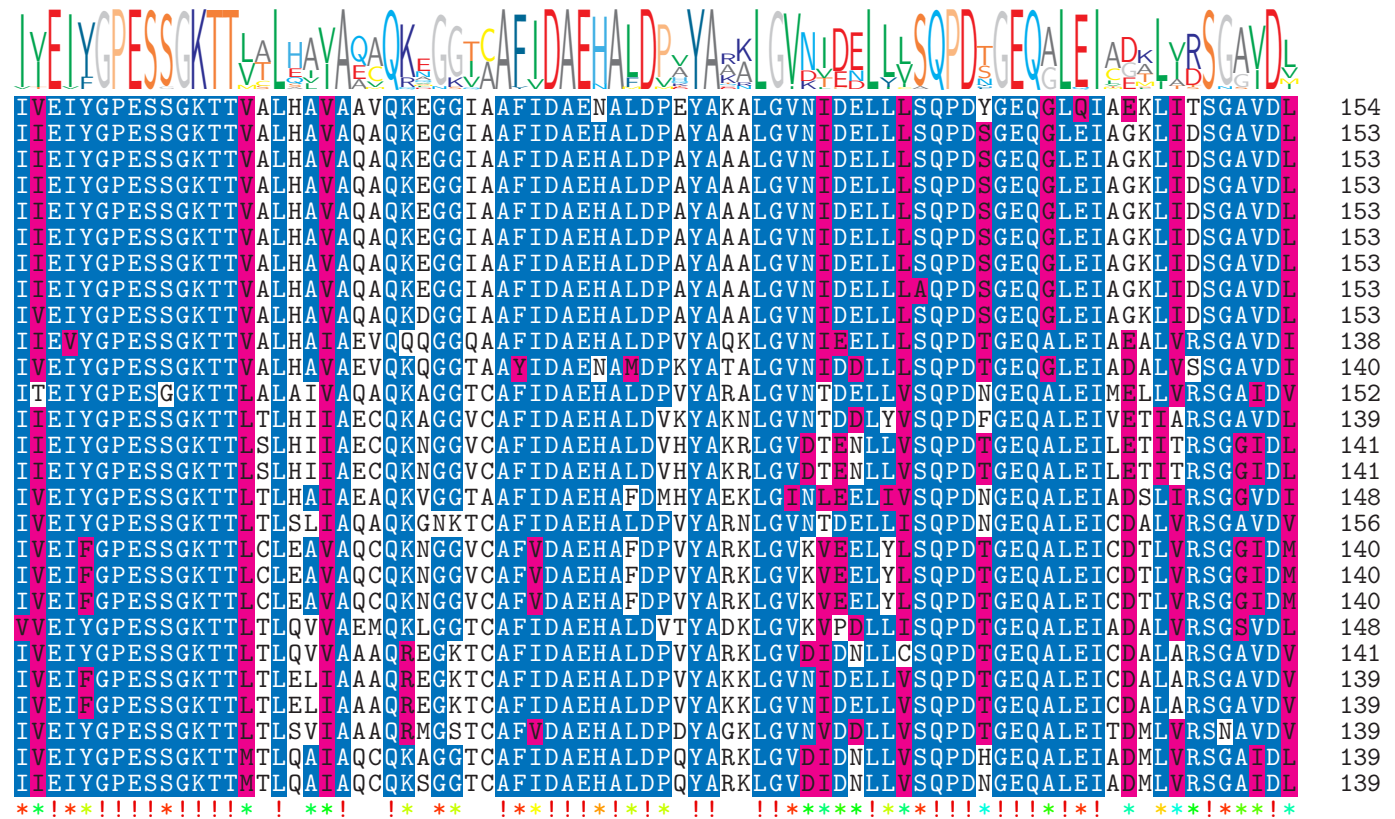
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NTDB id 115 BSU 16940 NP 389576.2	MSDRQAALDMALK	QIEKQ	FGKGSIMKLGE	K	TDTRI	STVPS	GSLALD	TALGI	GGY	PRGR		58		
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NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERS	KATETAMS	QIEKA	FGKGSIMKLGAE	SKLDVQVV	STGSL	SLDL	LALGV	GGI	PRGR	72		
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NTDB id 58461 NGJ45 RS18830 WP 015571667.1	MAIDENKQ	KALAAALG	QIEKQ	FGKGSIMRLGED	RSMDVET	IST	GSLSLD	I	ALGAGGL	PMGR		61		
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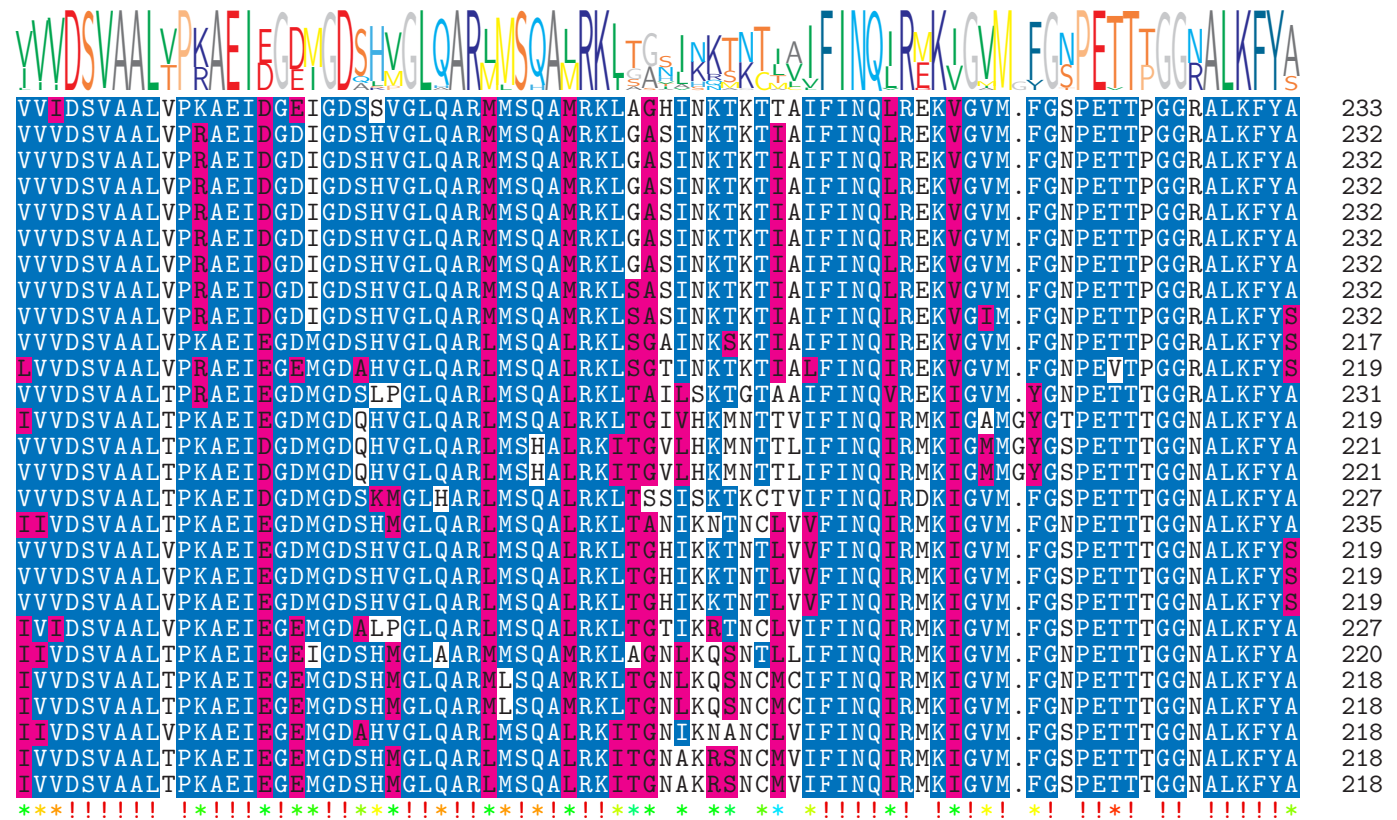
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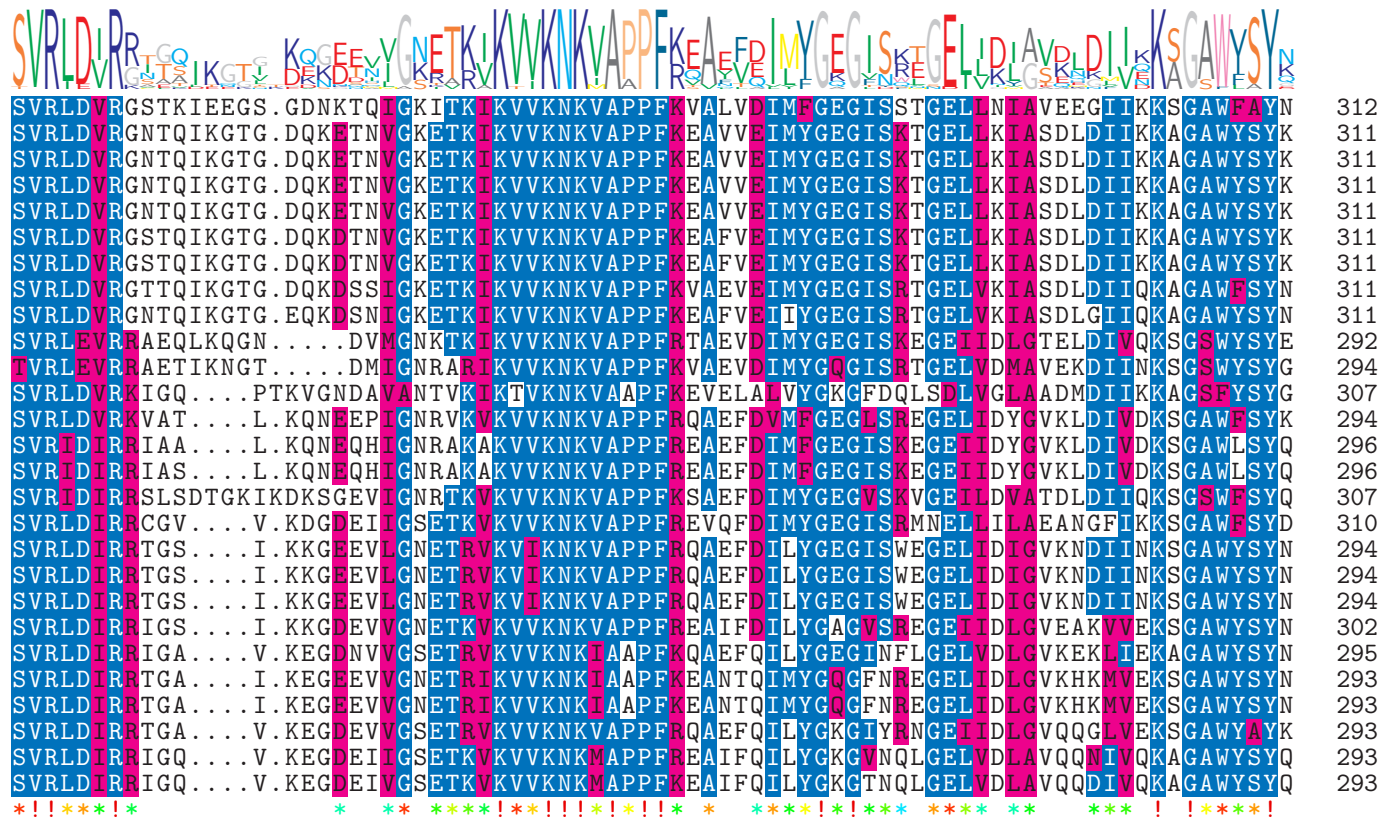
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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

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Sequence	Score
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DEKIGQGS ¹ ENAKKYL ² LAHPEIF ³ DEID ⁴ KQVRSKF ⁵ GL ⁶ IDGEEVSEQDTENKKDE PKKEEA . . VNEEVPLDLGDELEIE	385
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DEKIGQGS ¹ ENAKKYL ² ADNPEIF ³ DEID ⁴ HQVRVQF ⁵ GL ⁶ IDGEEIAE SKKDE AAQVDS . . VNEEVTLDLGDLEIE	381
GEKIGQGS ¹ ENAKRYL ² ADHPQLF ³ DEID ⁴ RKVRVKF ⁵ GL ⁶ LEESEEEESAMAVASE E TDDLALDLNGIEIE	377
GEKIGQGS ¹ ENAKKFL ² ADNPEIF ³ DDID ⁴ HKVRVQY ⁵ GL ⁶ IEEDNTEEKQSSKEK ETDEK ADKNLVLELDDTIELE	382
EE ¹ RLGQGR ² ENAKQFL ³ KENKDIMLMIQE ⁴ QIREHY ⁵ GL ⁶ DNNGVVQQAEETQEEL . EFE . E	348
SERIGQGR ¹ ENAKNYL ² ADHEDVE ³ DEVRLK ⁴ VRAAY ⁵ GIS ⁶ SDVPEEDLPTTEDE . QI . NILPDDST EE	355
DERIGQG ¹ KEKTIA ² YIAER ³ PEMEQEIRDRV ⁴ MAAIRAGNAGEAPALAPAPAAPEAA EA	363
DKKLGGGREN ¹ SKAF ² ILKENPEIAD ³ EITKAIQNSM ⁴ GIEGMI SGSEDD GEE	343
DKKLGGGREN ¹ AKALLKED ² KALADEIT ³ LKIKESIG ⁴ SNEEI MPLPDEP LEEME	347
DKKLGGGREN ¹ AKALLKED ² KALADEIT ³ LKIKESIG ⁴ SNEEI MPLPDEP LEEME	347
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GERIGQGRD ¹ NCREFL ² RENAEL ³ AREIENK ⁴ VREHL ⁵ GVTPMG AVTL . AEEVE ED	352
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GDKIGGQK ¹ ANACKYLKENPEIAKT ² LDKKLREMLLNPNEM QLIAETSSAA DDVEFGAVPEEF	354
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GSKIGGQK ¹ ANAACKYLEENPEIG ² QIEEQ ³ IRAKLL ⁴ ITSAN TKATPVAEDL ADADI	347
GNKIGQGK ¹ NNVIRYLEENP ² QISTEIEAV ³ IREQLLTKASD QTA . . HDTE EEPDLLES	349
GNKIGQGK ¹ NNVIRYLEENP ² QIAEIEIR ³ IREQLLTGTN GAVQ . I . EDE EEPDLLES	349

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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved