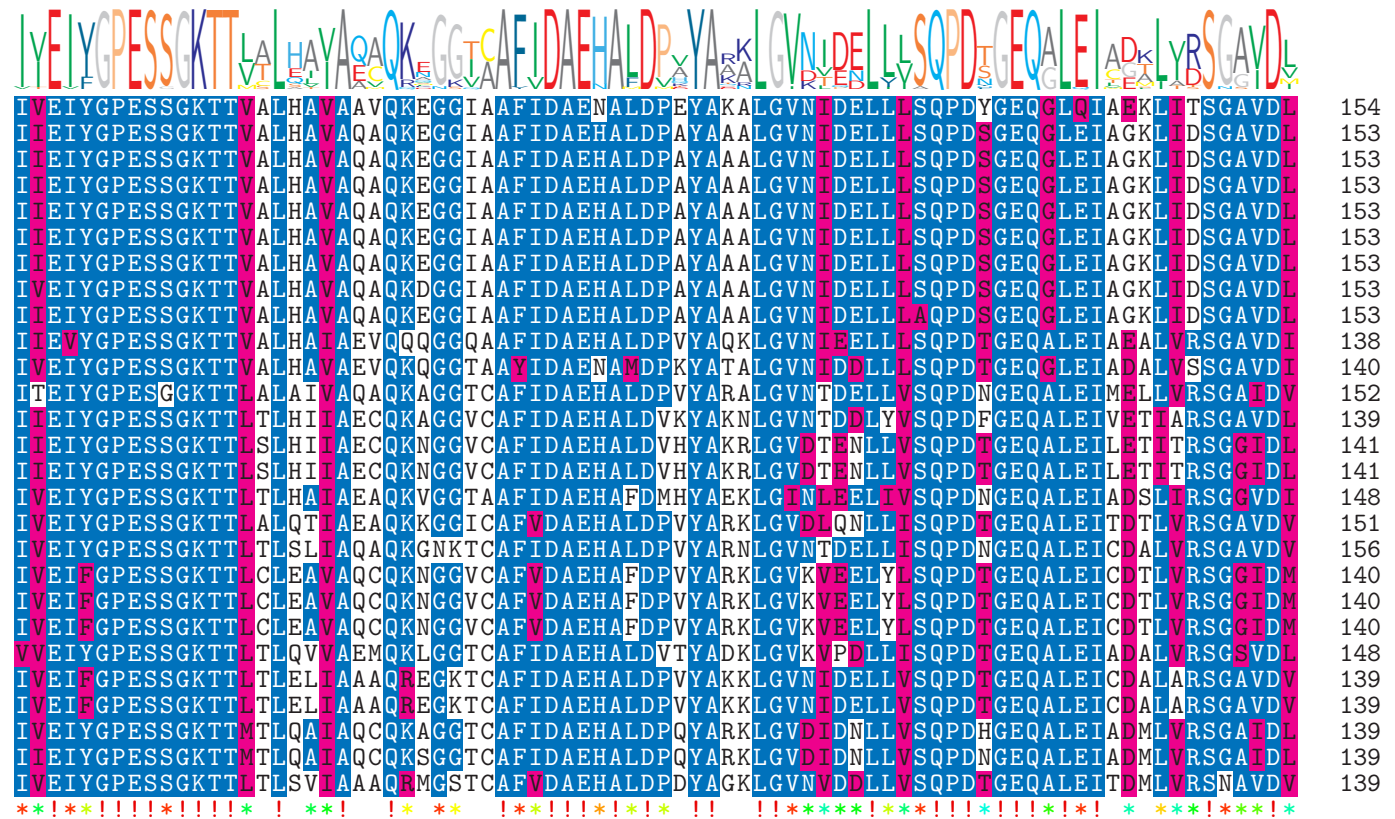


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NTDB id 228 SPD RS09265 WP 001085462.1	.MAKKPK....KLEEISKKFGA	ERE	KAL	NDAL	KL	IEKD	FGKGS	SIMRLGER	.AEQK	VQVM	SSGSL	ALDI	I	ALGSGGY	PKGR	73																
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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKKRIK....KTEEITKKFGD	ERR	KAL	DDAL	KN	IEKD	FGKGA	VMRLGER	.AEQK	VQVM	SSGSL	ALDI	I	ALGAGGY	PKGR	73																
NTDB id 453 Spy49 1753c ACI62003.1	.MAKKLK....KNEEITKKFGD	ERR	KAL	DDAL	KN	IEKD	FGKGA	VMRLGER	.AEQK	VQVM	SSGSL	ALDI	I	ALGAGGY	PKGR	73																
NTDB id 115 BSU 16940 NP 389576.2	MSDRQAAL	DALK	KQ	IEK	QFGKGS	IM	KLGEK	.TDTR	IST	VP	SSGSL	ALD	I	ALGIGGY	PRGR	58																
NTDB id 625 LCA RS02525 WP 011374196.1	MAKDERQAAL	DAAL	KK	IEKN	F	GKGS	IMRMGEK	.VDTQ	VST	VSSGSL	ALDE	ALGV	GGY	PRGR	60																	
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAP	TDAK	ERS	KA	TETAM	SQ	IEKA	F	GKGS	IM	KLGA	E.SKLD	VQV	VST	GSLSLD	I	ALGV	GGI	PRGR	72												
NTDB id 1245 Cj1673c YP 002345041.1	MDDNKR	KSL	DAAL	KS	LD	KT	F	GKGT	ILRL	GDK	.EVEQ	IDS	IG	TGS	VGLD	I	ALGI	GGV	PKGR	59												
NTDB id 1214 NCTC11637 00359 SQJ03206.1	M..AIDEDK	QKA	ISLA	TK	ID	KV	F	GKGA	LVRL	GDK	.QVEK	IDA	IST	GSL	GLD	I	ALGI	GGV	PKGR	61												
NTDB id 1211 C694 RS00795 WP 000963128.1	M..AIDEDK	QKA	ISLA	TK	ID	KV	F	GKGA	LVRL	GDK	.QVEK	IDS	IST	GSL	GLD	I	ALGI	GGV	PKGR	61												
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NTDB id 186547 BA011 RS08565 WP 012757658.1	MSQNSRLR	LVE..DKSV	DK	S	KALEA	ALS	Q	IERS	F	GKGS	IM	KLGS	N	V	VE	IET	IST	GSL	GLD	I	ALGV	GGL	PRGR	71								
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NTDB id 1130 NGFG RS03960 WP 003688695.1	MSDDK	S	KAL	AA	LAQ	IEK	S	F	GKGA	IM	K	M	D	G	S	Q	Q	EEN	LEV	IST	G	S	L	G	L	D	I	ALGV	GGL	P	RGR	60
NTDB id 1124 NGFG RS03960 WP 003688695.1	MSDDK	S	KAL	AA	LAQ	IEK	S	F	GKGA	IM	K	M	D	G	S	Q	Q	EEN	LEV	IST	G	S	L	G	L	D	I	ALGV	GGL	P	RGR	60
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NTDB id 1427 RS RS02760 WP 011000510.1	.MEDG.....KKA	A..SMSA	E	KK	QAL	AA	LAQ	IEK	Q	F	GKGS	IM	K	M	G	DA	.EVEP	VQV	V	T	G	S	L	G	L	D	I	ALGV	GGL	P	RGR	68
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consensus

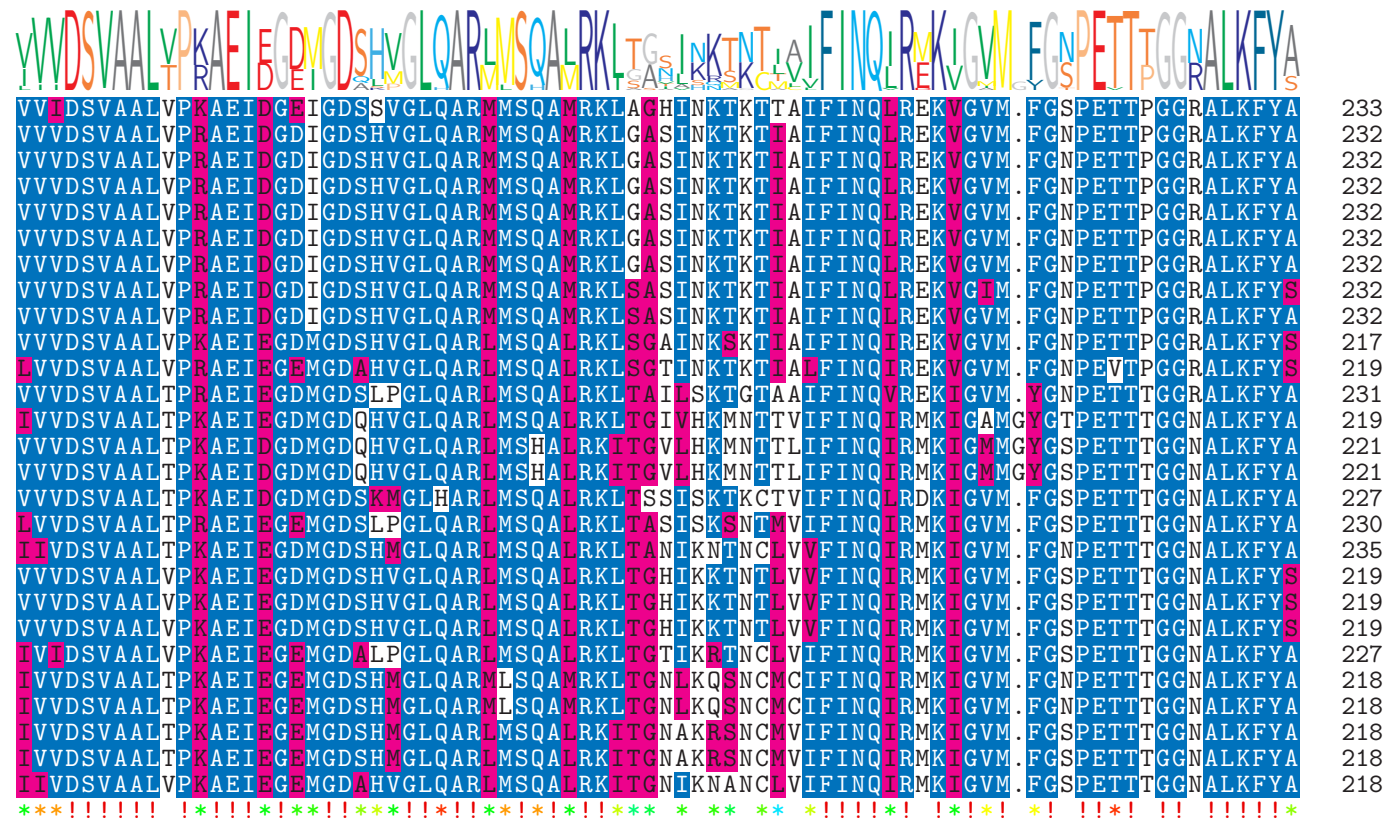
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consensus

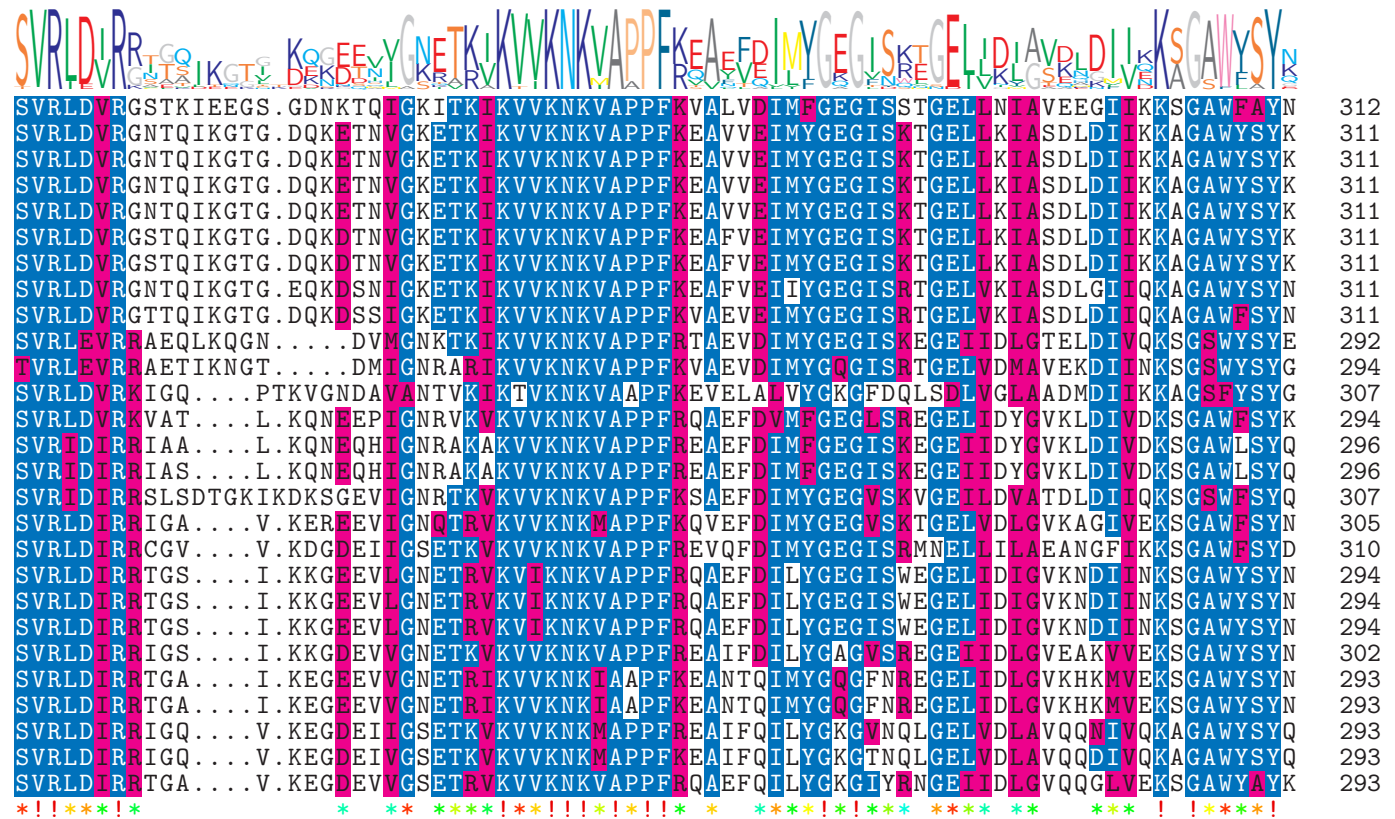
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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
DEKIGQGA ⁺ AKAK ⁺ NYLKEHQ ⁺ DV ⁺ FDEIDHKV ⁺ RAAH ⁺ GLDDSEVAETEEETTAS ⁺ KTAKAKKE ⁺ EKAVETEEIELELED.....	387
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEIDKQ ⁺ VRSKF ⁺ GLIDGEEVSEQDTENKKD ⁺ E....PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEIDKQ ⁺ VRSKF ⁺ GLIDGEEVSEQDTENKKD ⁺ E....PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ EHPEIF ⁺ DEIDKQ ⁺ VRSKF ⁺ GLIDGEEVSEQDTENKKD ⁺ E....PKKEEA ⁺ ..VNEEVPLDLGDELEIE	385
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPEIF ⁺ DEIDHQ ⁺ VRVQF ⁺ GLIDGEEIAES....KKD ⁺ E....AAQVDS ⁺ ..VNEEVPLDLGDELEIE	381
DEKIGQGS ⁺ ENAK ⁺ KYLA ⁺ DNPEVFA ⁺ IEDHQ ⁺ VRVQF ⁺ GLIDGEAAES....KKD ⁺ E....VAQVDS ⁺ ..VNEEVPLDLGDELEIE	381
GEKIGQGS ⁺ ENAK ⁺ KFLADNPEIF ⁺ DDIDHK ⁺ VRVQF ⁺ GLIEDNTTEEKQSSKEK.....ETDEK ⁺ ..ADKNLVLELDDTIELE	382
GEKIGQGS ⁺ ENAK ⁺ RYLADHPQLF ⁺ DEIDRK ⁺ VRVKF ⁺ GLLEESEESAMAVASE.....E.....TDDLALDLNGLIEIE	377
EE ⁺ RLGQGR ⁺ ENAK ⁺ QFLKEN ⁺ KDIMLMIQEQ ⁺ IREHYGLDNNGVVQQQAETQEEL.EFE.E.....	348
SERIGQGR ⁺ ENAK ⁺ NYLADHEDVE ⁺ DEVRLK ⁺ VRAAYG ⁺ ISDVPEEDLPTTEDE.QI.NILPDDST.....EE.....	355
DERIGQG ⁺ KEKTIAYIA ⁺ ERP ⁺ MEQEIRDRVMAAIRAGNAGEAPALAPAPAAP ⁺ E.....AAEA.....	363
DKKLGGGREN ⁺ AKSKAF ⁺ LKENPEIA ⁺ DEITKAIQNSMG ⁺ IEGMISGSEDDEG.....E.....	343
DKKLGGGREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPL.....E.....EME.....	347
DKKLGGGREN ⁺ AKALLKEDKALADEITLKIKESIGSNEEIMPLPDEPL.....E.....EME.....	347
DTKLGGGRD ⁺ TVKELIK ⁺ DNPELA ⁺ EEL ⁺ EAKIREKLQAK.....	343
SRL ⁺ KGQGR ⁺ ENAK ⁺ TLFLRDN ⁺ PLAR ⁺ EIELSLRQNA ⁺ GLIADRFLQNGGPEPDGD.....GDASAE.....M.....	364
GTKIGQGK ⁺ NNAVKWLKENPEIA ⁺ DKLEQ ⁺ EIRNTLASPNNSVLKA..TASDSND.....ESDVVEEFSEEL.....	372
GAKIGQGK ⁺ DNVRVWLKENPEIS ⁺ DEIDAK ⁺ IRALNGVEMHITEGT..QDET ⁺ DGE.....R.....PEE.....	348
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GAKIGQGK ⁺ DNVRVWLKENPEIS ⁺ DEIDAK ⁺ IRALNGVEMHITEGT..QDET ⁺ DGE.....R.....PEE.....	348
GE ⁺ RIGQGR ⁺ DNCR ⁺ REFL ⁺ RNAELAR ⁺ EIENK ⁺ VR ⁺ REHLGVTPMGA ⁺ VTL..A.EEVEE.....D.....	352
GDKIGGQK ⁺ ANACKYLKENPEIA ⁺ KTLDKKLREMLLNPNENMQLIA..ETSSAAD.....DVEFGAVPEEF.....	354
GDKIGGQK ⁺ ANACKYLKENPEIA ⁺ KTLDKKLREMLLNPNENMQLIA..ETSSAAD.....DVEFGAVPEEF.....	354
GNKIGQGK ⁺ NNVIRYLEENPQISTEIEAVIREQLLTKASDQTAA..HDETEE.....EPDLL..ES.....	349
GNKIGQGK ⁺ NNVIRYFEENNQIA ⁺ EIEIERNIREQLLTGTNGAVQ...I.EDEE.....EPDLL..LES.....	349
GSKIGQGA ⁺ KANAAKYLEENPEIGQEIEQQIRAKLLVTSANTKAT..PVAEDLA.....DADI.....	347

logo

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NTDB id 600 KW2 RS01765 WP 011675413.1	...		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE		388
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved