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NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 161334 ATN07 RS19455 WP 001283853.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 600 K2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
NTDB id 194 SPR RS08825 WP 001085462.1
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NTDB id 527 SMSK321 RS11065 WP 001085454.1
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NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
NTDB id 1130 NGFG RS03960 WP 003688695.1
NTDB id 1124 NGFG RS03960 WP 003688695.1
NTDB id 1123 OK783 RS03845 WP 003688695.1
NTDB id 1427 RS RS02760 WP 011000510.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 Q5545 AFN77183.1

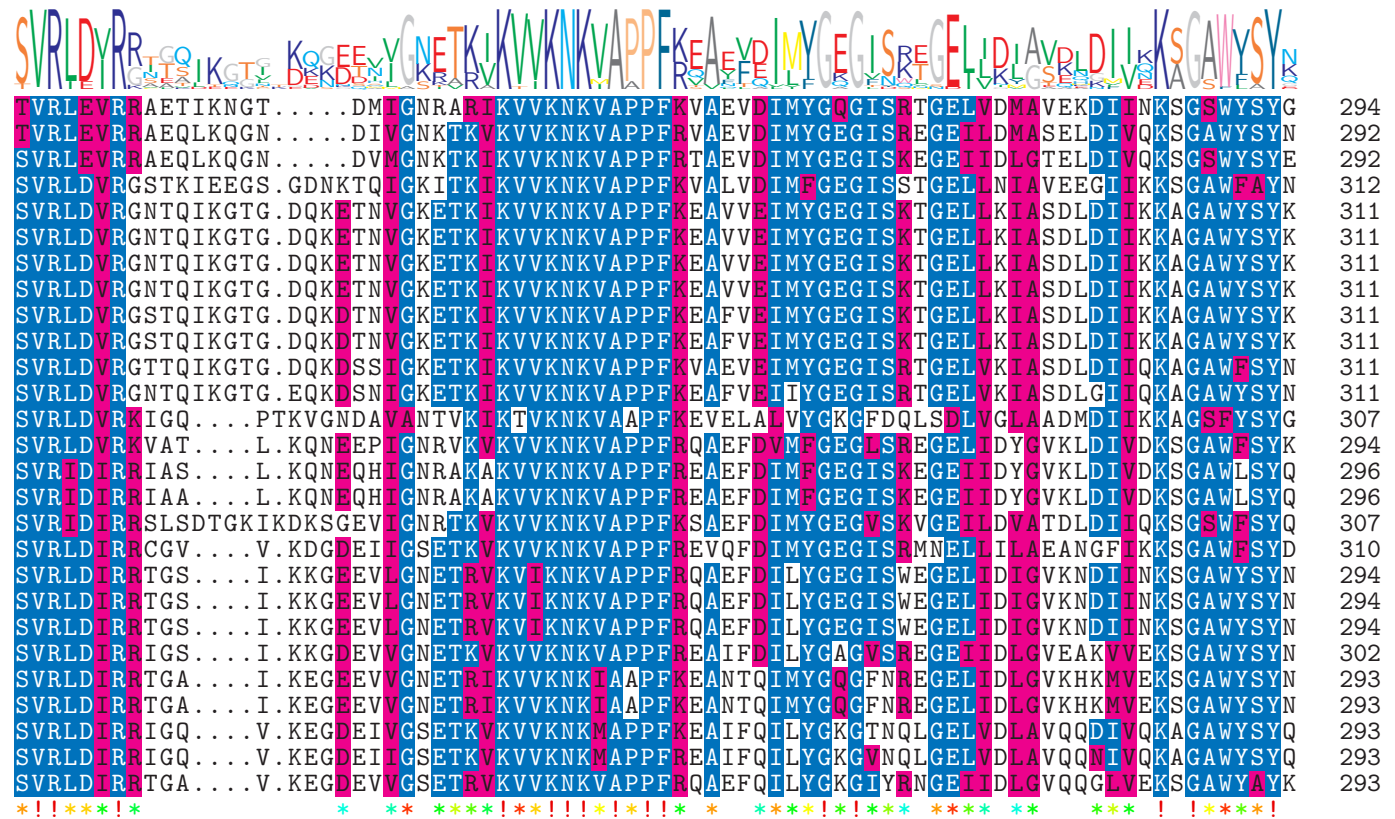
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.....	MAKD	ERQA	ALDA	ALKK	IEKN	FGKS	SIMR	MG	EK	.VDTQ	VST	VSS	SGSL	ALDE	ALGV	GGYP	PRGR						60
.....	MS	DRQA	ALDM	ALKQ	IEKQ	FGKS	SIML	GE	EQ	.AERR	IST	IST	SGSL	ALDV	ALGV	GGYP	PRGR						58
.....	MS	DRQA	ALDM	ALKQ	IEKQ	FGKS	SIML	GE	EK	.TDTRI	ST	VP	SGSL	ALDT	ALGI	GGYP	PRGR						58
MATKK....	KTNF	DDIT	KKYGA	ERD	KALAD	ALAL	IEKD	FGKS	SLMR	LGEA	.ANQK	VSV	VSS	SGSL	ALDI	ALGAGG	YP	PKGR					74
.MAKK....	PKKLEE	ISKKF	GA	ERE	KALND	ALKL	IEKD	FGKS	SIMRL	GER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGSGG	YP	PKGR					73
.MAKK....	PKKLEE	ISKKF	GA	ERE	KALND	ALKL	IEKD	FGKS	SIMRL	GER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGSGG	YP	PKGR					73
.MAKK....	PKKLEE	ISKKF	GA	ERE	KALND	ALKL	IEKD	FGKS	SIMRL	GER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGSGG	YP	PKGR					73
.MAKK....	PKKLEE	ISKKF	GA	ERE	KALND	ALKL	IEKD	FGKS	SIMRL	GER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGSGG	YP	PKGR					73
.MAKK....	PKKLEE	ISKKF	GA	ERE	KALND	ALKL	IEKD	FGKS	SIMRL	GER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGSGG	YP	PKGR					73
.MAKK....	PKKLEE	ISKKF	GA	ERE	KALND	ALKL	IEKD	FGKS	SIMRL	GER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGSGG	YP	PKGR					73
.MAKK....	LKKNEE	ITKKF	GD	ERR	KALDD	ALKN	IEKD	FGKGA	VMR	LGER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGAGG	YP	PKGR					73
.MAKR....	IKKTEE	ITKKF	GD	ERR	KALDD	ALKN	IEKD	FGKGA	VMR	LGER	.AEQK	VQVM	VSS	SGSL	ALDI	ALGAGG	YP	PKGR					73
.....	MSKDAT	KEIS	APTDAK	ERS	KAL	ET	AM	SQIE	KAF	FGKS	SIML	GA	E	.SKLD	VQV	VST	SGSL	SLDL	ALGV	GGIP	PRGR		72
.....	MDDN	KR	KS	SLDA	ALKS	LDKT	FGKGT	ILRL	GD	K	.EVEQ	IDS	IGT	SGV	GLDL	ALGI	GGV	PKGR					59
.....	MAIDE	DKQ	KAL	ISLA	IKQ	IDKV	FGKGA	LVR	LD	GDK	.QVEK	IDS	IST	SGSL	GLDL	ALGI	GGV	PKGR					61
.....	MAIDE	DKQ	KAL	ISLA	IKQ	IDKV	FGKGA	LVR	LD	GDK	.QVEK	ID	IST	SGSL	GLDL	ALGI	GGV	PKGR					61
.....	MAKT	.ETTSPND	DKK	KALAAV	LEK	LDKT	YGKGT	VMKL	GD	GTVDH	NI	EV	IP	SGSL	GLDL	ALGV	GGYP	PKGR					68
.MAENK	KSSKN	NTV	.VKQ	VEPE	KKQ	ALEA	ALAQ	IEKQ	FGKS	SIML	GGT	.EQLD	IES	VST	SGSL	GLDL	ALGI	GGLP	PMGR				76
.....	MSD	DKS	KALAA	ALAQ	IEKS	FGKGA	AIMK	DGS	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	60
.....	MSD	DKS	KALAA	ALAQ	IEKS	FGKGA	AIMK	DGS	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	60
.....	MSD	DKS	KALAA	ALAQ	IEKS	FGKGA	AIMK	DGS	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	60
.MEDG		K	.KAAS	MSA	EKQ	KALAA	ALAQ	IEKQ	FGKS	SIMM	GD	.EVEP	VQV	VST	SGSL	GLDV	ALGV	GGLP	PRGR				68
.....	MDEN	KQ	KALAA	ALGQ	IEKQ	FGKS	SIMRL	GD	N	.RAMD	VET	IST	SGSL	SLDI	ALGAGG	LP	PMGR					59	
.....	MDEN	KQ	KALAA	ALGQ	IEKQ	FGKS	SIMRL	GD	N	.RAMD	VET	IST	SGSL	SLDI	ALGAGG	LP	PMGR					59	
.....	MDEN	KSKAL	QAALS	QIEKQ	FGKNT	VMRL	GD	N	.TVQA	VEAV	ST	SGSL	TLDI	ALGIGG	LP	PKGR</							


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NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

Sequence	Score
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EERLGGGRENASKQFLKENTLREETIAFFVRDHHGIGEDSGVEDTE..DATLQD	343
EERLGGGRENASKQFLKENTLREETIAFFVRDHHGIGEDSGVEDTE..DATLQD	348
DEKIGQGAEKAKNYLKEHQDVFEIDHKKVRAAHGLDDSEVAETEETETASKTKAKAKKEEKAVETEEIELELED	387
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAADNPEIFDEIDHQRVVRVQFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSENAKKYLAADNPEVFAEIDHQRVVRVQFGLIDGEEIAES...KKDE...VAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKRVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKRYLADNPEIFDDIDHKKVRVQYGLIEDNTEEKQSSKE.....ETDEK..ADKNLVLELDDTIEIE	382
DERIGGQKEKTIAYIAIERPEMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA	363
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGM I.....SGSEDDE..GEE.....	343
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGM I.....SGSEDDE..GEE.....	347
DKKLGGGRENASKAFLKENPEIAD EITKAIQNSMGI EGM I.....SGSEDDE..GEE.....	347
DTKLGGGRDTPVKELIKDNPELAEELEAKIREKLQAK	343
GTKIGQGGKNNAVKWLKENPEIADKLEQEIRNTLASNPNS.....VLKATASDSNDESVDVEEF..SEEEL	372
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDET.....GER..PEE.....	348
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GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI.....TEGTQDET.....GER..PEE.....	348
GERIGQGRDNCREFLRNAAELAREIENKVRHGLVTPMG.....AV.TLAEVEED	352
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GDKIGQGGKANACKYLKENPEIAKTLDKKLREMLLNPNEM.....QLIAETSSAADDVEFGAV..PEEF	354
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GSKIGQGGKANAAKYLENPEIQEIEQQIRAKLLVTSAN.....TKATPVAEDLADAD..I.....	347

logo

		IEE	
NTDB id 625 LCA RS02525 WP 011374196.1	...	355	
NTDB id 161334 ATN07 RS19455 WP 001283853.1	...	343	
NTDB id 115 BSU 16940 NP 389576.2	...	348	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
NTDB id 228 SPD RS09265 WP 001085462.1	IEE	388	
NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388	
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388	
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384	
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384	
NTDB id 453 Spy49 1753c ACI62003.1	D..	378	
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383	
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NTDB id 1245 Cj1673c YP 002345041.1	...	343	
NTDB id 1211 C694 RS00795 WP 000963128.1	...	347	
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

- X non conserved
- X similar
- X ≥ 50% conserved