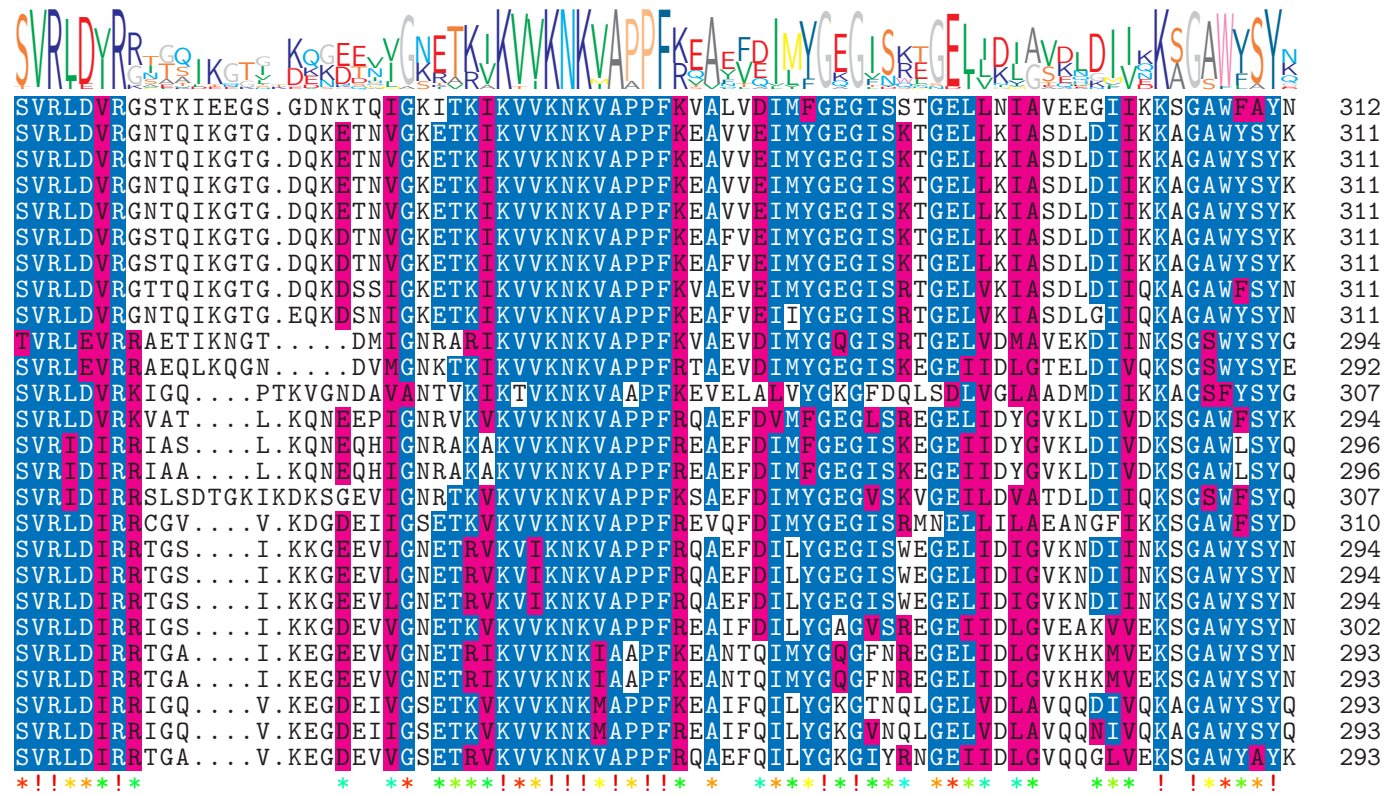


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NTDB id 408 SMU RS09530 WP 002262392.1	.MAKR.....IKKTEEITKKFGD	ERRKALDDALKN	IEKDFGKG	AVMRLGER	.AEQKVQV	MSSGSL	ALD	I	ALGAGGY	PKGR	73				
NTDB id 625 LCA RS02525 WP 011374196.1	MAKD	ERQAALDAALKK	IEKNFGKGS	SIMRMGEK	.VDTQVST	VSSGSL	ALDE	ALGVGGY	PRGR	60					
NTDB id 115 BSU 16940 NP 389576.2	MS	DRQAALDMALKQ	IEKQFGKGS	SIMKLGEK	.TDTRIST	VPSGSL	ALD	TALGIGGY	PRGR	58					
NTDB id 1313 DR RS12030 WP 010888966.1	MSKDATKEISAPTD	AKERSKATETAMSQ	IEKAFGKGS	SIMKLGAE	.SKLDVQVV	STGSL	SLDL	ALGVGGI	PRGR	72					
NTDB id 1245 Cj1673c YP 002345041.1	MDDN	KRKS	SLDA	AALKS	LDK	TFGKGT	ILRLGDK	EVEQ	IDS	IGTGS	VGLDL	ALGIGGV	PKGR	59	
NTDB id 1211 C694 RS00795 WP 000963128.1	MAIDE	DKQK	AI	SLA	IKQ	ID	KVFGK	GALVRLGDK	QVEK	IDS	ISTGSL	GLDL	ALGIGGV	PKGR	61
NTDB id 1214 NCTC11637 00359 SQJ03206.1	MAIDE	DKQK	AI	SLA	IKQ	ID	KVFGK	GALVRLGDK	QVEK	IDA	ISTGSL	GLDL	ALGIGGV	PKGR	61
NTDB id 1334 RAOC RS04870 WP 004918236.1	MAKT	ETTS	PND	DKK	KALAAVLEK	LDKT	YGKGT	VMKLG	DGTVD	HNIEV	IPSGSL	GLDL	ALGVGGY	PKGR	68
NTDB id 1389 A4U84 RS07560 WP 021112712.1	.MAENKKSSKNNTV..VKQVEPEQ	KKQ	ALEA	AALAQ	IEKQFGKGS	SIMKLG	QT	EQ	LDIES	VSTGSL	GLDL	ALGIGGL	PMGR	76	
NTDB id 1130 NGFG RS03960 WP 003688695.1	MSD	DK	SKALAA	AALAQ	IEKS	FGKG	AIMKMDGS	QREENLEV	ISTGSL	GLDL	ALGVGGL	PRGR	60		
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NTDB id 1123 OK783 RS03845 WP 003688695.1	MSD	DK	SKALAA	AALAQ	IEKS	FGKG	AIMKMDGS	QREENLEV	ISTGSL	GLDL	ALGVGGL	PRGR	60		
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NTDB id 1205 PSJM300 05545 AFN77183.1	MDEN	KK	RALAA	ALGQ	IEKQFGKG	AVMRMDH	DRQA	IPS	ISTGSL	GLD	I	ALGIGGL	PKGR	59	
consensus															

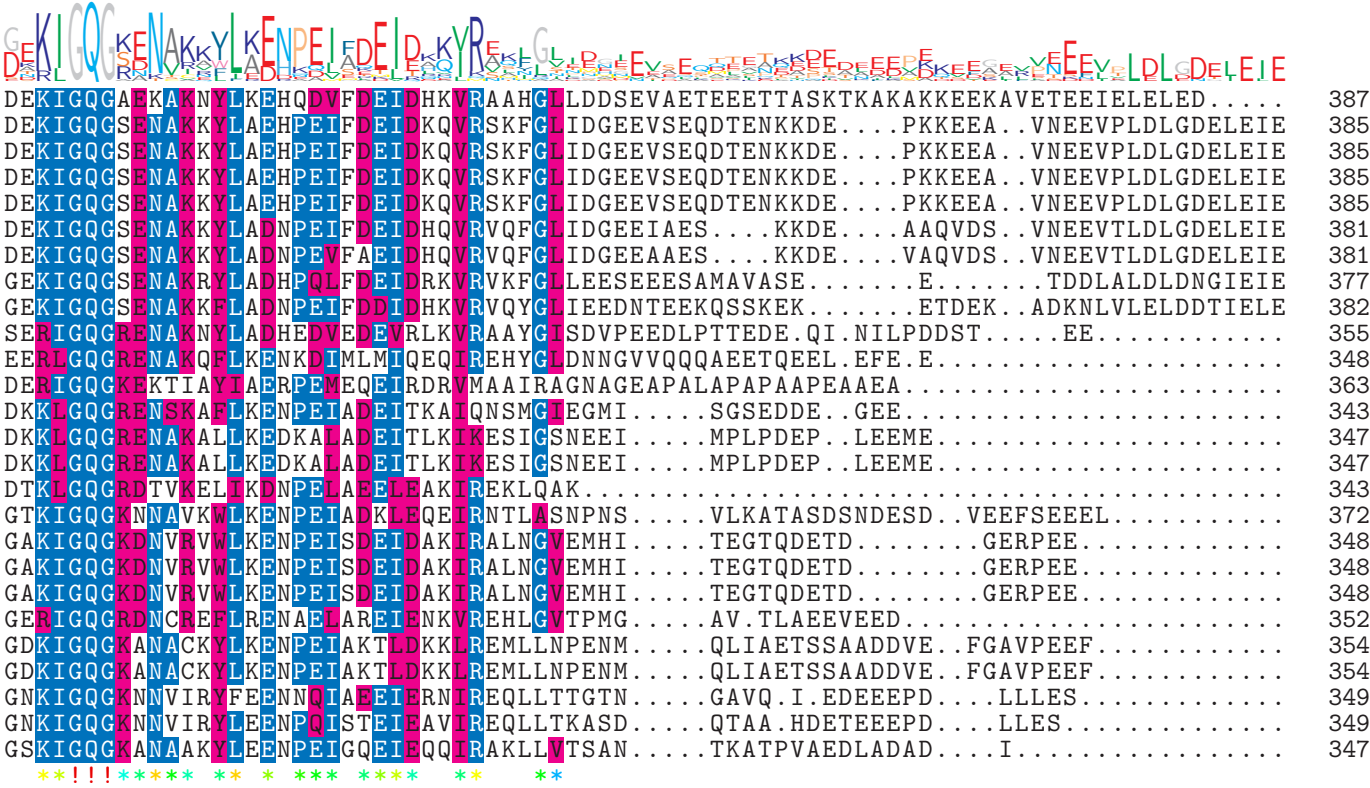


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NTDB id 1313 DR RS12030 WP 010888966.1
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consensus



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NTDB id 600 KW2 RS01765 WP 011675413.1
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NTDB id 228 SPD RS09265 WP 001085462.1
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consensus



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consensus

 non conserved
 similar
 ≥ 50% conserved