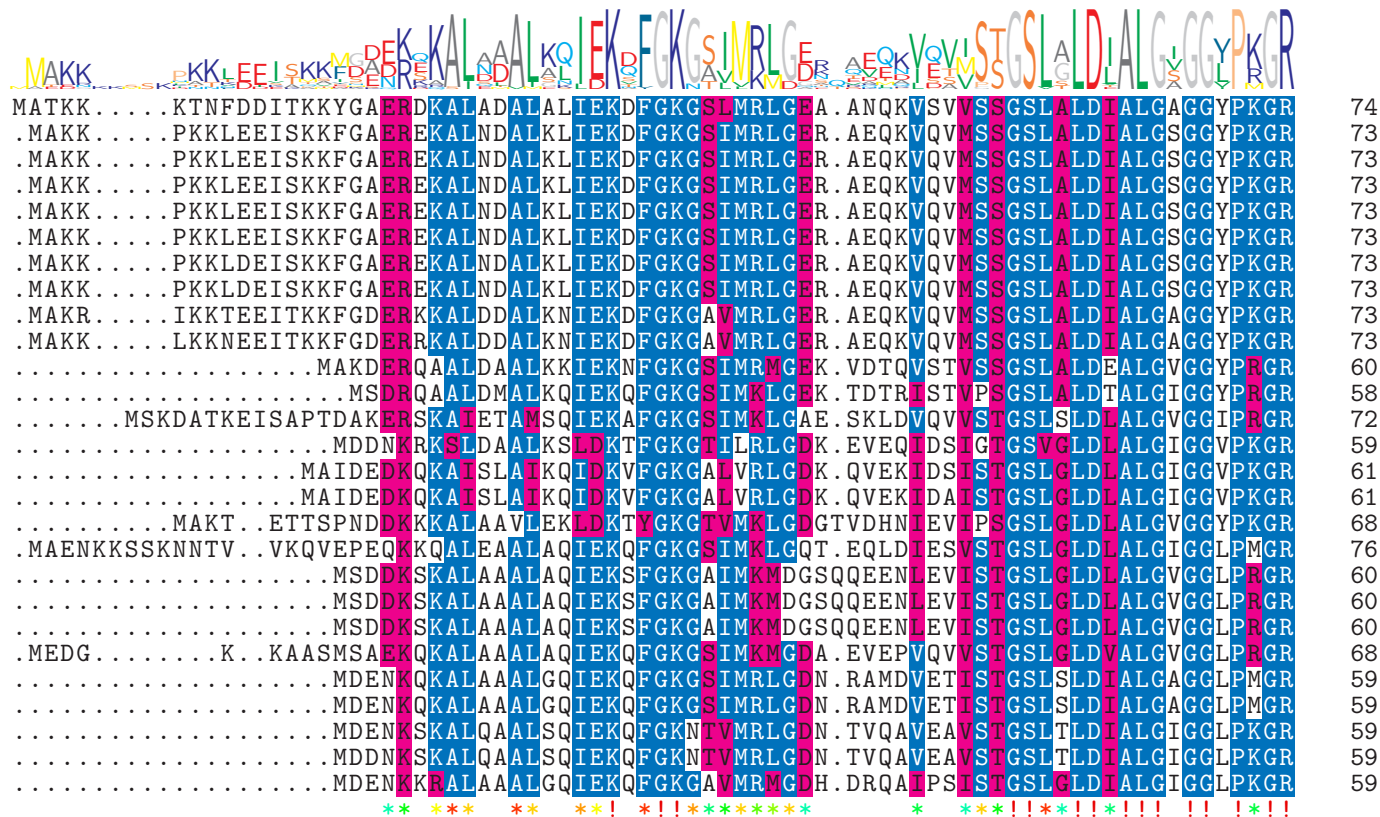


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consensus

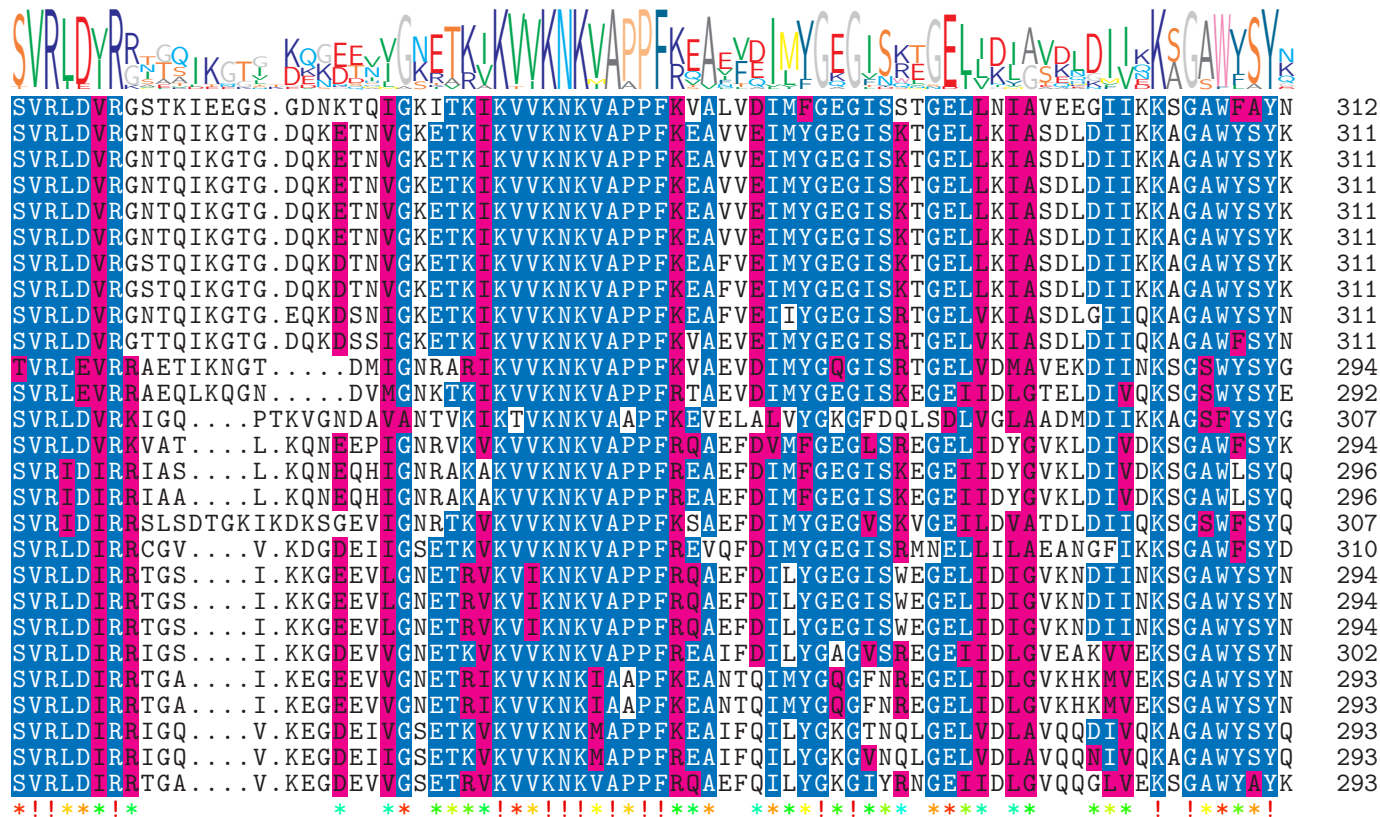
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DEKIGQGS	ENAKKYLAEHP	PEIF	DEIDK	QVRSK	FG	LIDGEEV	SEQD	TENKK	DEP	...	KKEEA	..VNEE	VTLDL	GDELE	E						385
DEKIGQGS	ENAKKYLAEHP	PEIF	DEIDK	QVRSK	FG	LIDGEEV	SEQD	TENKK	DEP	...	KKEEA	..VNEE	VPLDL	GDELE	E						385
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DEKIGQGS	ENAKKYLADN	PEIF	DEIDH	QV	RVQ	FLIDGEE	IAES	...	KKDEA	...	AQVDS	..VNEE	VTLDL	GDELE	E						381
DEKIGQGS	ENAKKYLADN	PEVFAE	IDH	QV	RVQ	FLIDGEE	AAES	...	KKDEV	...	AQVDS	..VNEE	VTLDL	GDELE	E						381
GEKIGQGS	ENAKKFLADN	PEIFD	IDH	KV	RVQ	GLIEED	NTEEK	QSSKEK		ETDEK	..ADKNL	VLEL	DDT	I	E						382
GEKIGQGS	ENAKRYLADHP	QLF	DEIDR	KV	RVK	FLLEE	SEES	SAMAVASE		E		TD	L	ALD	L	NG	I	E			377
SERIGQG	RENAKNYLADH	EDVE	EVRLK	V	RAAY	GISDV	PEED	LPTTEDE	.QIN			ILPDD	S	T	E						355
EE	RLGG	RENAKQFL	KNKD	IMLM	IQE	IREHY	GLD	NNGV	VQQQA	EETQ	EELE		FE	E							348
DERIGQG	EKTIAYIA	IERPEME	QEIR	DRV	MAA	IRAGN	AGEA	PALAP	APAPAA	PEAAE	..A										363
DKKLGG	RENSKAF	LKENPEI	AD	EIT	KAI	QNSM	G	IEGMI		SGS	EDDE	..GE	..E								343
DKKLGG	RENAKALL	KEDKAL	AD	EIT	LK	IKES	IGS	NEEI		MPL	PDEP	..LE	..EM								347
DKKLGG	RENAKALL	KEDKAL	AD	EIT	LK	IKES	IGS	NEEI		MPL	PDEP	..LE	..EM								347
DTKLGG	RD	TVKELIK	DNP	ELAE	E	LEAKI	REKLQ	AK													343
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GERIGQ	RDCN	REFL	RNA	ELAR	E	ENK	VREHL	GVT	PMG	...	AV	TLA	EEVEE	..D							352
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GDKIGQG	KANACKYL	LKENPEI	AKT	L	DKK	REML	LN	PENM	...	QLIA	ETSSA	AD	..DV								354
GNKIGQG	KNNVIRY	FE																			

logo

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consensus			

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