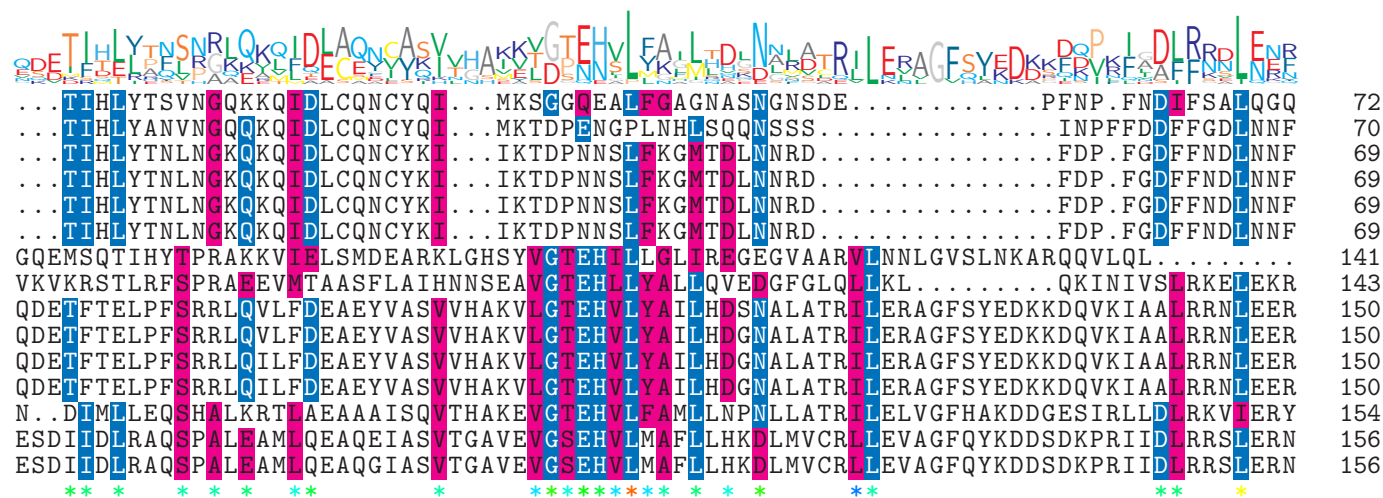
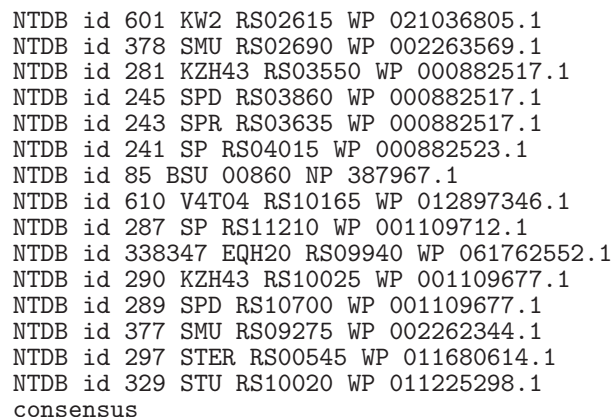


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consensus

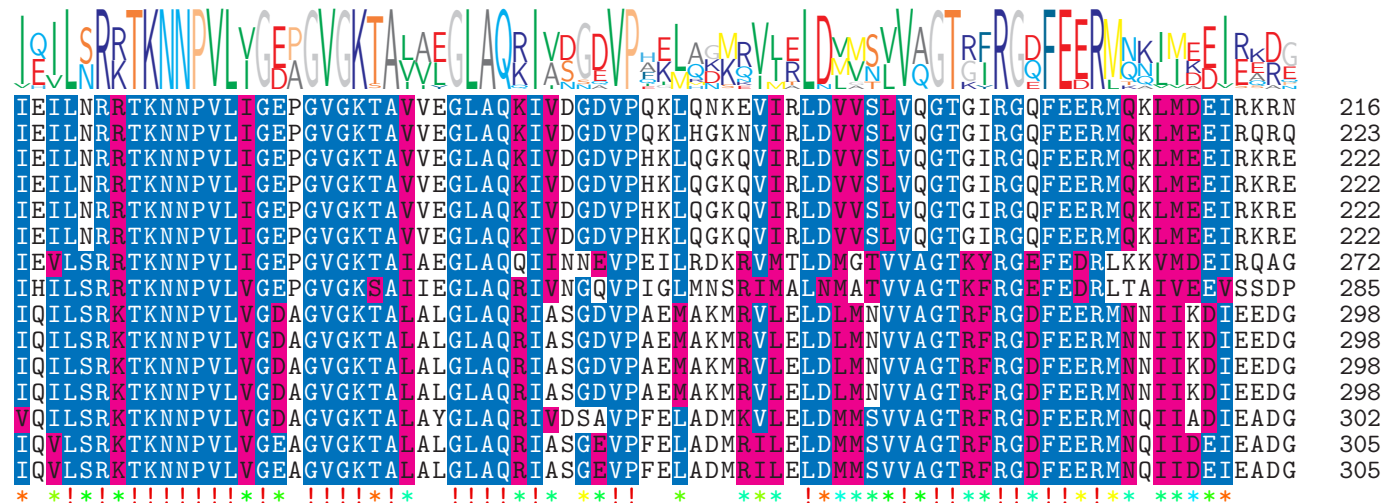
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consensus

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Sequence	Position
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REEDFEKAAAYFRDQIAKYKEMQKK.....KITDQDTP ⁸ IISEKTEHIEIEQKTNIPVGD ⁹ LKEKEQSQLIHLAEDLKSHVI	453
REEDFEKAAAYFRDQIAKYKEMQKK.....KITDQDTPS ¹⁰ ISEKTEHIEIEQKTNIPVGD ¹¹ LKEKEQSQLIHLAEDLKSHVI	453
QSQE ¹² FEKAAASLRDTEQRLREQVEDTKKSWKEKQGENSEVTVDDIAMV ¹³ VSSWTVGPVSKIAQTETDKLLNMENILHSRVI	511
IKLD ¹⁴ IKASRTKEKA ¹⁵ VEKIADKIYKF.....SVKEDKRQEVTDQAVVAVASTLTGVPITQMTKSESDRLINLEKELHKR ¹⁶ VI	520
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MDGKWKQAAQLIAKE.....E.....EVPV.YKDLV ²³ TESDILTTLSRLSGIPVQKLTQTD ²⁴ AKKYNLEAELHKRVI	515
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logo

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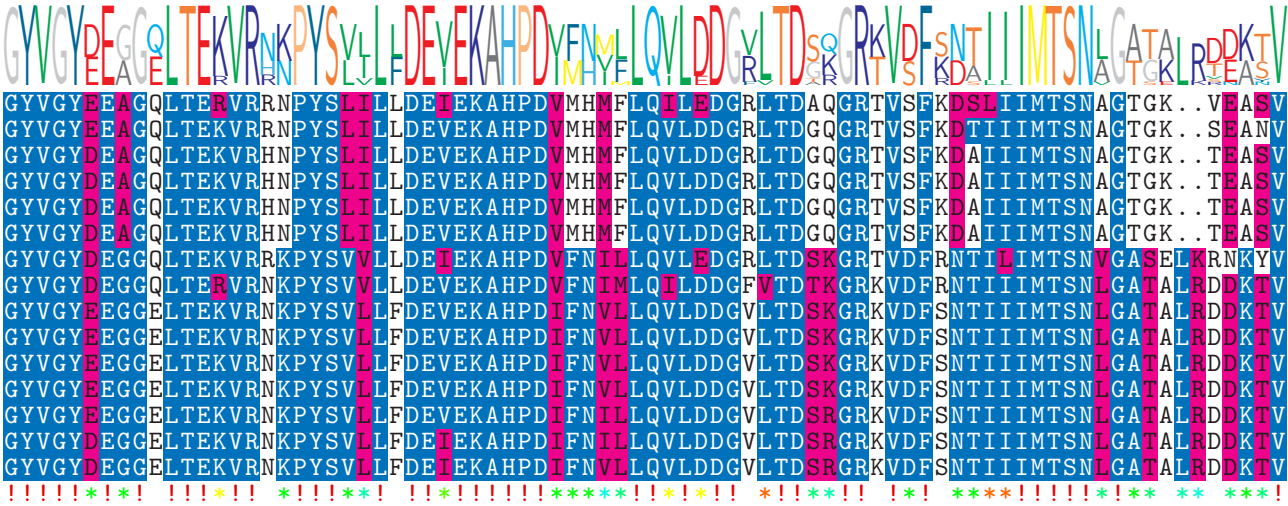
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consensus

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QD	AV	SK	SR	RR	RS	G	RT	PK	PI	GS	F	FL	GP	TV	GK	TE	AK	AL	AL	EV	LE	FG	DE	SS	MI	RE	DM	SE	ME	KE	HS	AA	SR	LN	GA	PP		
QD	EAV	DK	ISK	AIRR	SRV	GL	GKPN	RP	IGS	F	LV	GP	TG	VG	KTEL	AQ	LAK	EL	FG	SS	ES	MIR	FD	MSE	YME	KHSV	AK	LIG	APP						527			
QD	AAV	DK	IAK	AIRR	NRV	GL	GTPN	RP	IGS	F	LV	GP	TG	VG	KTEL	SK	Q	LA	IE	LF	GS	ED	S	MIR	FD	MSE	YME	KH	AV	AK	LV	GAPP				534		
QD	DAV	DK	IAK	AIRR	NRV	GL	GTPN	RP	IGS	F	LV	GP	TG	VG	KTEL	SK	Q	LA	IE	LF	GS	ADS	MIR	FD	MSE	YME	KHSV	AK	LV	GAPP						533		
QD	DAV	DK	IAK	AIRR	NRV	GL	GTPN	RP	IGS	F	LV	GP	TG	VG	KTEL	SK	Q	LA	IE	LF	GS	ADS	MIR	FD	MSE	YME	KHSV	AK	LV	GAPP						533		
QD	DAV	DK	IAK	AIRR	NRV	GL	GTPN	RP	IGS	F	LV	GP	TG	VG	KTEL	SK	Q	LA	IE	LF	GS	ADS	MIR	FD	MSE	YME	KHSV	AK	LV	GAPP						533		
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QD	EAV	VA	AK	AV	RR	AR	AG	LK	DP	KR	PI	GS	F	FL	GP	TG	VG	KTEL	AR	AL	AE	S	I	F	G	DE	ES	MIR	ID	MSE	YME	KH	ST	SR	LV	GS	PP	
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consensus



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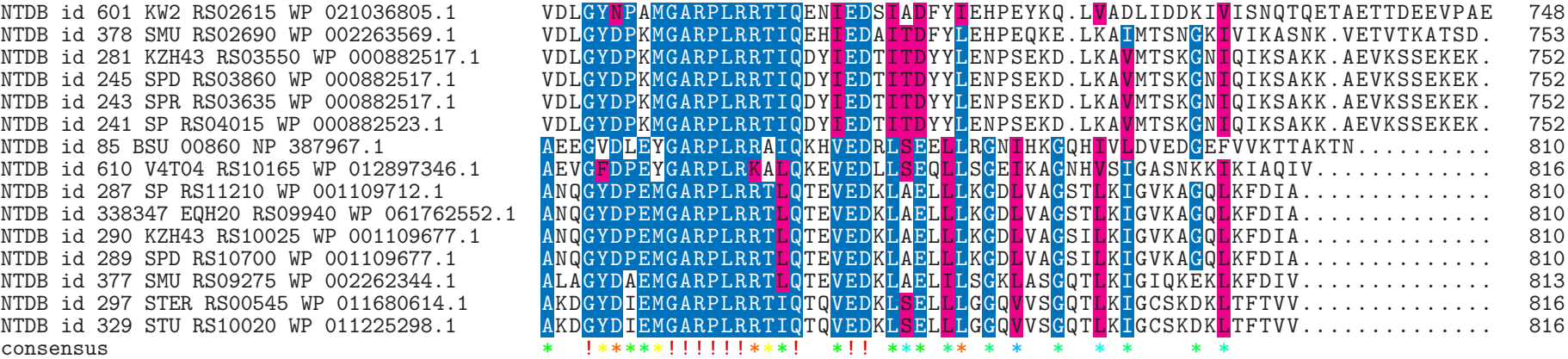
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consensus



680
687
686
686
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751
760
755
755
755
755
758
761
761

logo



☐ non conserved
☒ similar
☒ ≥ 50% conserved