

logo

		MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	80
NTDB id 1028	TT RS08215 WP 011173991.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL	79
NTDB id 1306	DR RS10060 WP 027479822.1		0
NTDB id 1410	SGL RS13950 WP 010873519.1		0
NTDB id 1366	NTHI RS01950 WP 011271972.1		0
NTDB id 1355	HI 0298 AAC21962.1		0
NTDB id 1384	A4U84 RS08525 WP 010787006.1		0
NTDB id 1468	ASU2 RS05090 WP 014991734.1		0
NTDB id 78197	IT63 RS03695 WP 000650606.1		0
NTDB id 1436	BW25113 RS00530 WP 001025145.1		0
NTDB id 1168	A1552VC RS11070 WP 000957200.1		0
NTDB id 1401	DSB67 RS12665 WP 010643259.1		0
NTDB id 1293	VP RS12240 WP 005479695.1		0
NTDB id 1251	GC085 RS07725 WP 011946523.1		0
NTDB id 1018	ACIAD RS01685 WP 004920473.1		0
NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
consensus			

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		ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLD T L S L E E V E D L T G L V V E P Y Q T T K S A F L Y A L A K H Y P E L G L P V P P P . . P	158
NTDB id 1028	TT RS08215 WP 011173991.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
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NTDB id 1410	SGL RS13950 WP 010873519.1		0
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NTDB id 1058	ABD1 RS01615 WP 001274986.1		0
consensus			

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NTDB	id	Accession	Protein	Score	Length	Gap	Consensus
NTDB	id 1028	TT RS08215 WP 011173991.1	SGEGQKDKLKGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	237	237	0	
NTDB	id 1306	DR RS10060 WP 027479822.1	SDAGRTGGKLGGERLITHGYITDAQLQVALDAQQQTGEALGATLISQRAITEDQLYEVLAEQEGTTFLPNPSGFHPGEEVL	237	237	0	
NTDB	id 1410	SGL RS13950 WP 010873519.1		0	0	0	
NTDB	id 1366	NTHI RS01950 WP 011271972.1		0	0	0	
NTDB	id 1355	HI 0298 AAC21962.1		0	0	0	
NTDB	id 1384	A4U84 RS08525 WP 010787006.1		0	0	0	
NTDB	id 1468	ASU2 RS05090 WP 014991734.1		0	0	0	
NTDB	id 78197	IT63 RS03695 WP 000650606.1		0	0	0	
NTDB	id 1436	BW25113 RS00530 WP 001025145.1		0	0	0	
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NTDB	id 1018	ACIAD RS01685 WP 004920473.1		0	0	0	
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consensus							

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NTDB	id	Accession	Species	Protein	Sequence	Score
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NTDB	id 1306	DR RS10060	WP 027479822.1	GSMLRADALRLLA	VPVDETEQGVTVLTSDPRKRPDIDALIGRPVQLMLTRPRDIERLIEQFYPQGRGLGEQLVQEGTLSR	317
NTDB	id 1410	SGL RS13950	WP 010873519.1	MTS		
NTDB	id 1366	NTHI RS01950	WP 011271972.1			
NTDB	id 1355	HI 0298	AAC21962.1			
NTDB	id 1384	A4U84 RS08525	WP 010787006.1			
NTDB	id 1468	ASU2 RS05090	WP 014991734.1			
NTDB	id 78197	IT63 RS03695	WP 000650606.1			
NTDB	id 1436	BW25113 RS00530	WP 001025145.1			
NTDB	id 1168	A1552VC RS11070	WP 000957200.1			
NTDB	id 1401	DSB67 RS12665	WP 010643259.1			
NTDB	id 1293	VP RS12240	WP 005479695.1			
NTDB	id 1251	GC085 RS07725	WP 011946523.1			
NTDB	id 1018	ACIAD RS01685	WP 004920473.1			
NTDB	id 1058	ABD1 RS01615	WP 001274986.1			
consensus						

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NTDB	id	1028	TT	RS08215	WP	011173991.1	EALKEALEVQKGLPRAKPLGEI	VELGLARPEDVEEALQKQRRGGGR	LEDTLVQS..GKLRPEAL	LAQA.....VATQL	388				
NTDB	id	1306	DR	RS10060	WP	027479822.1	DQLREALQVQAREGKVKPLGEVI	ITELGFASPDEVDLSALQKQNVGGGR	LEDTLVQS..GKLSPEML	LARS.....LAAQL	388				
NTDB	id	1410	SGL	RS13950	WP	010873519.1	SSSSKKSRAVALRNYFSPFGNKI	VAGGHVDAEQLRQALVQVKKTGRS	LPEELKAVTGRELSPEL	LRQYKKNQLFELKVL	83				
NTDB	id	1366	NTHI	RS01950	WP	011271972.1			MTSYA.....LLHTQR	VTAAQ.....NGEI	20				
NTDB	id	1355	HI	0298	AAC21962.1				MTSYA.....LLHTQR	VTAK.....NGEV	20				
NTDB	id	1384	A4U84	RS08525	WP	010787006.1			MSQYT.....ICEQQ	TERI	15				
NTDB	id	1468	ASU2	RS05090	WP	014991734.1			MQYS.....VCDMN	SQQV	14				
NTDB	id	78197	IT63	RS03695	WP	000650606.1					0				
NTDB	id	1436	BW25113	RS00530	WP	001025145.1					0				
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NTDB	id	1401	DSB67	RS12665	WP	010643259.1		MLTNLSTV	LRQAG	ILTFSQEESSL	LEQVKASGISMPEAL	LSS..GFFQSHE	ITEH.....LSSV	57	
NTDB	id	1293	VP	RS12240	WP	005479695.1		MHSNLSTI	LRQKGL	LTF	SQEE	SLIEQVKASGISMPEAL	LSS..GFFTSS	ELAEH.....LSSI	57
NTDB	id	1251	GC085	RS07725	WP	011946523.1		MALATEEY	RLQGIGQL	LVLEKLLDKTKA	IELHKLAAAEKIS	LLQYIVKN..KILSAEQ	IALT.....AAQN	65	
NTDB	id	1018	ACIAD	RS01685	WP	004920473.1		MSAFTTPPK	FSGFIRRL	VEEGYVNAQNM	MQQALEKAKKFKQD	IVPYLIDN..FSISPLT	IAEI.....ISLE	65	
NTDB	id	1058	ABD1	RS01615	WP	001274986.1		MSALHTSPK	FTGFFRR	LVEEKHVS	AATMTALDAAKRAKQD	TVAYLIEE..VHLSPSL	LAET.....ISAE	65	
consensus							*	*	*	*	*	*	*		

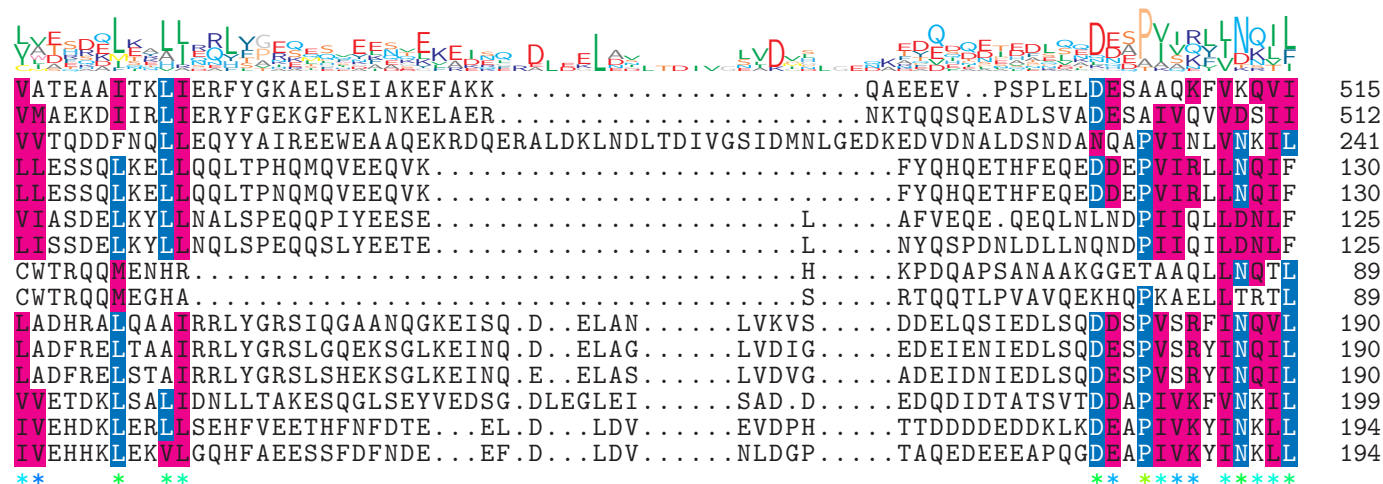
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NTDB	id	1306	DR	RS10060	WP	027479822.1	CYEFLDPIQN....PPDPKVALMIPEATARRVVVPVRLQ...GNSLVVAMKDPRNVFALDDLKLITG....KEILPA	455
NTDB	id	1410	SGL	RS13950	WP	010873519.1	GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRFKFLPLAQEGDPPSVLVMVDPDNLAQAQDELNRILRVKG..FELRR	161
NTDB	id	1366	NTHI	RS01950	WP	011271972.1	TI.....SPDLWERNQQQSLLLRYPALPLKEE...NNRLWLGVDSLNSLSACETIAFI...TG.KPVEPI	79
NTDB	id	1355	HI	0298	AAC21962.1		TI.....SPDLWERNQQQSLLLRYPALPLKEE...NNRLWLGVDSLNSLSACETIAFI...TG.KPVEPI	79
NTDB	id	1384	A4U84	RS08525	WP	010787006.1	DI.....SPSRWQKNCEEKQLLLRYLAVPVQET...EHKLWLAVDDENNLTACEIFAFAFM...TH.KQIEPV	74
NTDB	id	1468	ASU2	RS05090	WP	014991734.1	DI.....SESLWQKNCDEKHILLRYLAIPIQEN...DDTLWLAIIDMNNLSACEIFAFAFI...AH.KTIEPV	73
NTDB	id	78197	IT63	RS03695	WP	000650606.1	MKDAQNLNTLCQRHQAVLINSA...SNSITVAVVDAPSHALLDALHFA...TQ.KQIDIIV	52
NTDB	id	1436	BW25113	RS00530	WP	001025145.1	MNIPQLTALCLRYHGVLLDAS...EEVHVHAVVDAPSHELLDALHFA...TT.KRIEIT	52
NTDB	id	1168	A1552VC	RS11070	WP	000957200.1	CLPETDLTRY....DYANLCQQLGLRELITRYDALPTIAKQ...GNLLLAVSDPTTLQAEEEFRAFA...TG.LQVELA	124
NTDB	id	1401	DSB67	RS12665	WP	010643259.1	GLSCTSLNQY....EYASLCQQLGLRDLITRHNAIPLNRT...SSTLILAVADPTNLQAEDDFRFA...TG.LQVELV	124
NTDB	id	1293	VP	RS12240	WP	005479695.1	GLSQPELSQY....EYASLCQQLGLRELITRHNAIPLHRT...PSTLLLAVADPTNQQAEDDFRFA...TG.LQVELV	124
NTDB	id	1251	GCO85	RS07725	WP	011946523.1	GVPMLDINCI....DVGTIPVNLVNEKLIKRRHAMVPLFSR...GTNLYLATDPSKQASLKEIQFH...TG.LNTHAI	132
NTDB	id	1018	ACIAD	RS01685	WP	004920473.1	GEPLLDLGVF....DPALFLKDKIDEKLIQKYRIMPLVHR...GHVLYVATSNPNTTEAMDAIRFN...SK.LKV EPI	132
NTDB	id	1058	ABD1	RS01615	WP	001274986.1	AEPYFDLDVY....DTSQIPKDLVDQKLIKLRHILPLIQR...GQILYVATSNPNTTEAMDAIRFN...SK.LLVEPV	132
consensus							* ** ***** ***** * *** *	

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consensus

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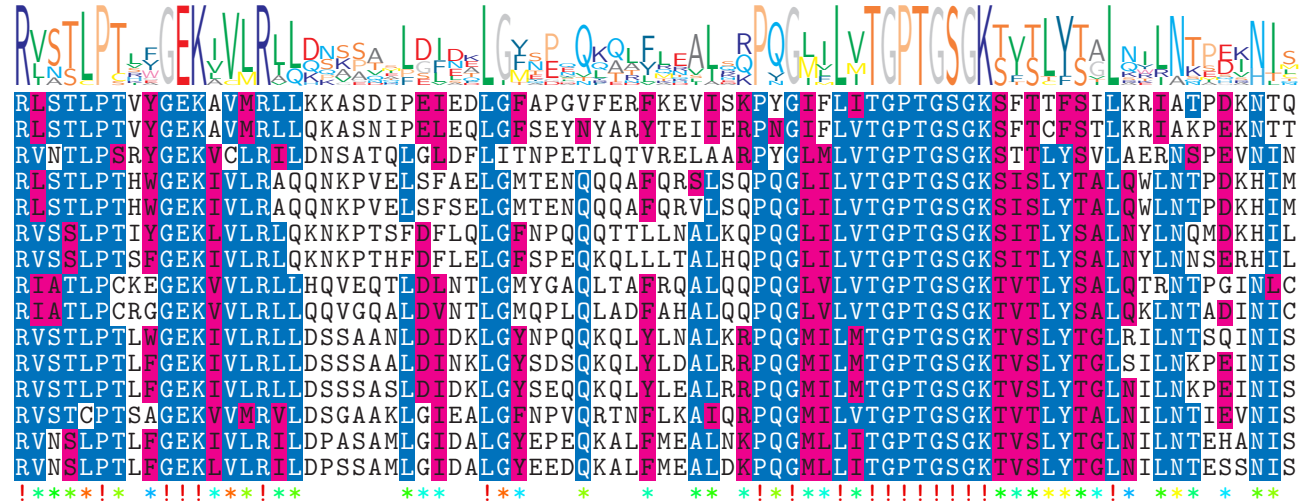
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consensus

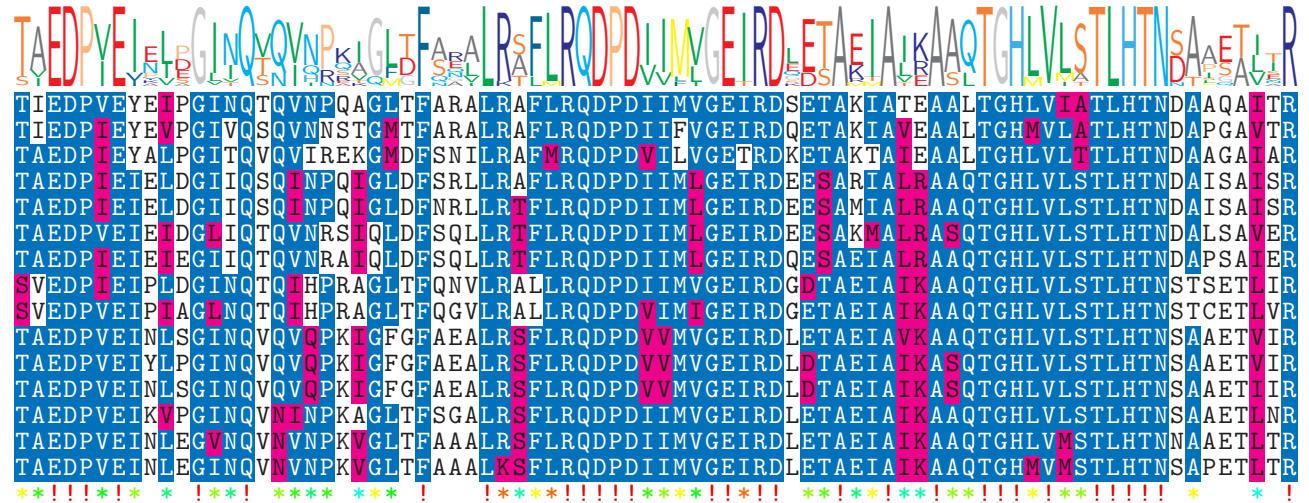
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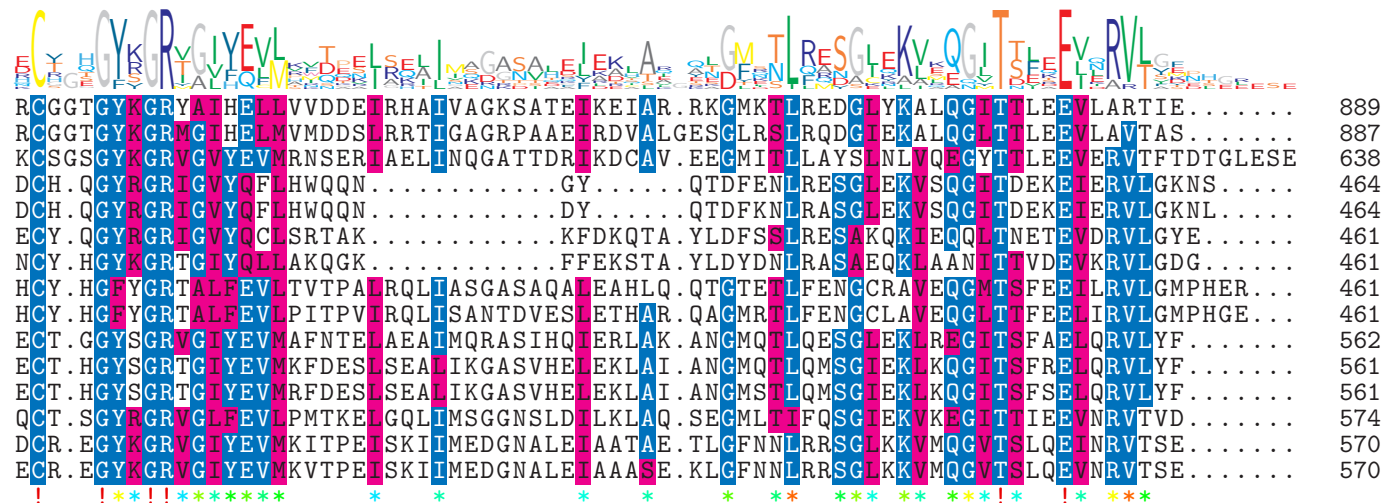
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consensus

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved