

logo

		MSXLSIGDRRLGAALLDRLDNLQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK	
NTDB id 1410 SGL RS13950 WP 010873519.1			0
NTDB id 1028 TT RS08215 WP 011173991.1	MSVLTIGDKRLGAALLDAGLLTDEELQRALERHREVGGSLAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPKVK		80
NTDB id 1306 DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNLDLQRALERHSEVGGRLADVLLIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAL		79
NTDB id 1168 A1552VC RS11070 WP 000957200.1			0
NTDB id 1293 VP RS12240 WP 005479695.1			0
NTDB id 1401 DSB67 RS12665 WP 010643259.1			0
NTDB id 1110 NGFG RS09235 WP 003689817.1			0
NTDB id 1251 GC085 RS07725 WP 011946523.1			0
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NTDB id 1058 ABD1 RS01615 WP 001274986.1			0
NTDB id 1018 ACIAD RS01685 WP 004920473.1			0
consensus			0

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		SLTPAEKAKELRAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP	
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NTDB id 1028 TT RS08215 WP 011173991.1	ALLPAEKAKELKAIPFALDEEAGVVRVAFLNPLDLSLEEVEDLTGLVVEPYQTTKSAFLYALAKHYPELGLPVPPP..P		158
NTDB id 1306 DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIIVVPSGA		157
NTDB id 1168 A1552VC RS11070 WP 000957200.1			0
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consensus			0

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		SGEGQKDLKLGELLQKGWISREALEEALVEQEKTGDLLGRILV.RKGLPEEALYRALAEQKGLEFLESTEGIVPDPSAA	
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NTDB id 1306 DR RS10060 WP 027479822.1	SDAGRTGGKLGERLITHGYITDAQLQVALDAQQTGEALGATLISQRAITEDQLYEVLAEEQEGTTFLPNPSGFHPGEEVL		237
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consensus			0

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NTDB id 1410 SGL RS13950 WP 010873519.1	MTS	3
NTDB id 1028 TT RS08215 WP 011173991.1	LLLLRSDALRYGAVPIGFQNGEVEVVLSDPRHKEAVAQLLNRPARYLALPQAWHEELFRRAYPQKNRLGEVLVQEGKLSR	317
NTDB id 1306 DR RS10060 WP 027479822.1	GSMLRADALRLLAVPVDETEQGVTVLTS DPRKRDPIDALIGRPVQLMLTRPRDIERLIEQFYPPQRGRLLGEQLVQEGTLSR	317
NTDB id 1168 A1552VC RS11070 WP 000957200.1		0
NTDB id 1293 VP RS12240 WP 005479695.1		0
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NTDB id 1110 NGFG RS09235 WP 003689817.1		0
NTDB id 1251 GC085 RS07725 WP 011946523.1		0
NTDB id 349059 EZZ78 RS05540 WP 003112841.1		0
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consensus		

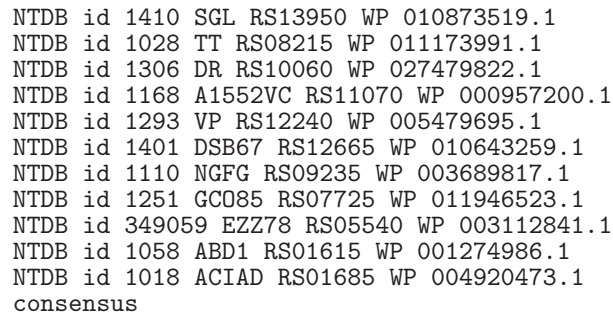
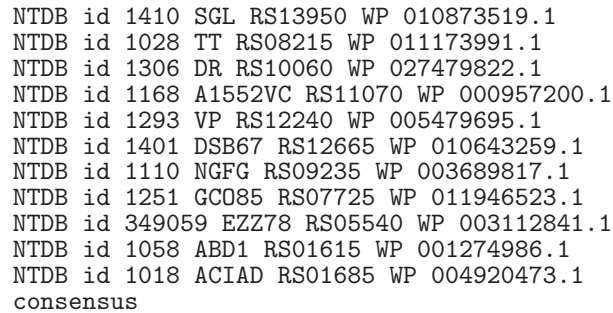
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NTDB id 1306 DR RS10060 WP 027479822.1	DQLREALQVQAREGKVKPLGGEVITELGFASPDVEVDSALQKQNVGGRIEDTLVQ..SGKLSPEMLARSL.....AAQL	388
NTDB id 1168 A1552VC RS11070 WP 000957200.1	MLTNLVA ILRQAE LISATQEAVVTQVSASGTSVPEALLE..LSIFHAQELTEQL.....SHIF	57
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NTDB id 349059 EZZ78 RS05540 WP 003112841.1	MNDSIQLSGLSRQLVQANLLDEKTAVQAQAQAQRNKL SLVTHLVQ..SKLVSGLALAE LS.....AEQF	62
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFTGFFRRLVEEKHVS AATMQTALDAAKRAKQDTVAYLIE..EVHLSPSLLAETI.....SAEF	65
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQALEKAKKFKQDTPYPLID..NFSISPLTIAEII.....SLEF	65
consensus	* * * * *	

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NTDB id 1410 SGL RS13950 WP 010873519.1	GVDSVDPEVAPIATQQMAELIGRFFPLDTCRRFKFLPLAQQEGDPPSVLVAMVDPDNLAAQDELNRILRVKGF..ELRRL	161
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NTDB id 1306 DR RS10060 WP 027479822.1	GYEFLDPIQNPPD....PKVALMIP EATARRV VVPVRLQG...NSLVVAMKDPNRNVFALDDLKLITG....KEILPA	455
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NTDB id 1293 VP RS12240 WP 005479695.1	GLSQPELSQYEYA.....SLCQQGLGLRELITRHNALPLHRT...STLLLAVADPTNQQAEDDFRFATG.....LQVELV	124
NTDB id 1401 DSB67 RS12665 WP 010643259.1	GLSCTSLNQYEYA.....SLCQTLGLRDLITRHNALPLNRTS...STLILAVADPTNLQAEDDFRFATG.....LQVELV	124
NTDB id 1110 NGFG RS09235 WP 003689817.1	SYSILDLRHYPRH.....RVLMLGVLTEEQMV E FHCVPVFRRG...DKVFFAVSDPTQMPQIQKTVSAAG.....I AVELV	123
NTDB id 1251 GC085 RS07725 WP 011946523.1	GVPMLDINCIDVG.....TIPVNLVNEKLIK RHAMVPLFSRG...TNLYLATDDPSKQASLKEIQFHTG.....LNTHAI	132
NTDB id 349059 EZZ78 RS05540 WP 003112841.1	GIAYCDLNSLDKE.....SFPRDAISEKLVQRHVIPLWRRG...NKL FVGISDPANHQAINDVQFSTG.....LTTEAI	129
NTDB id 1058 ABD1 RS01615 WP 001274986.1	AEPYFDLDVYDTS.....QIPKDLVDQKLILKHRILPLIQRG...QILYVATSNPSNIEAIDAIRFN SK.....LKV EPI	132
NTDB id 1018 ACIAD RS01685 WP 004920473.1	GEPLIDLGVFDPA.....LFLKDKID EKLIQKYRIMPLVHRG...HVLVYVATSNPTNIEAMDAIRFN SK.....LKV EPI	132
consensus	* * * * *	

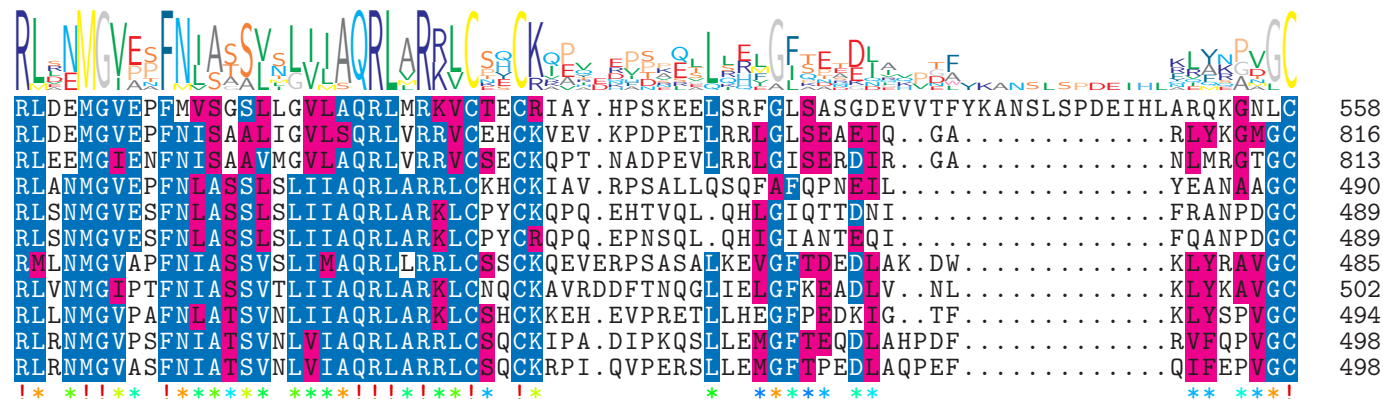
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consensus
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consensus

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NTDB id 1058 ABD1 RS01615 WP 001274986.1
NTDB id 1018 ACIAD RS01685 WP 004920473.1
consensus

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NTDB id 1410 SGL RS13950 WP 010873519.1	EMRAKRRKSALTCRTCAAELQQEWLDCPYCMTSRFS	672
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved