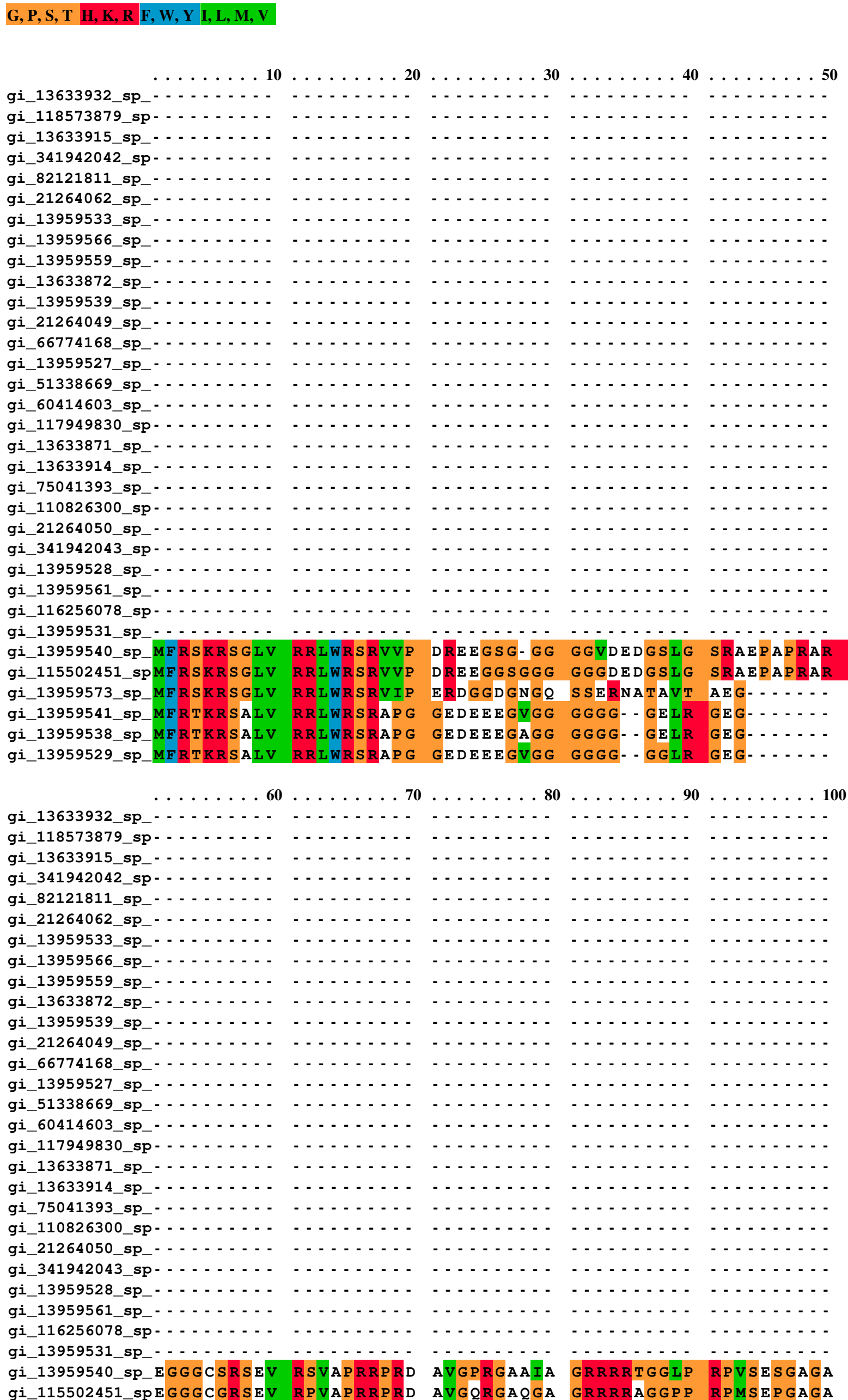


Results colour-coded according to the CLUSTALX residue colour scheme

The current colour scheme of the alignment is by **residue**.

The colour assignments have been adapted from the defaults in CLUSTALX (Thompson *et al*, 1997) Abstract :



[illegible]

	210.	220.	230.	240.	250
gi_13633932_sp	LVKKLKKKKG	AMEELEKALS	CPG-QPSNCV	TIP-	-	-	-	-	-	-
gi_118573879_sp	LVKKLKKKKG	AMEELEKALS	CPG-QPSNCV	TIP-	-	-	-	-	-	-
gi_13633915_sp	LVKKLKKKKG	AMEELEKALS	CPG-QPSNCV	TIP-	-	-	-	-	-	-
gi_341942042_sp	LVKKLKKKKG	AMEELEKALS	CPG-QPSNCV	TIP-	-	-	-	-	-	-
gi_82121811_sp	LVKKLKKKKG	AMEELEKALS	SPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_21264062_sp	LVKKLKKKKG	AMEDLEKALS	SPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_13959533_sp	LVKKLKKKKG	AMEELEKALS	SPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_13959566_sp	LVKKLKKKKG	AMEELEKALS	SPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_13959559_sp	LVKKLKKKKG	AMEELEKALS	SPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_13633872_sp	LVKKLKKKKG	AMEELEKALS	CPG-QPSNCV	TIP-	-	-	-	-	-	-
gi_13959539_sp	LVKKLKKKKG	AMDELERALS	CPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_21264049_sp	LVKKLKKKKG	AMEELERALS	CPG-QPSNCV	TIP-	-	-	-	-	-	-
gi_66774168_sp	LVKKLKKKKG	AMDELERALS	CPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_13959527_sp	LVKKLKKKKG	AMDELERALS	CPG-QPSKCV	TIP-	-	-	-	-	-	-
gi_51338669_sp	LVKKLKK-TG	QLDELEKAIT	TQN-VNTKCI	TIP-	-	-	-	-	-	-
gi_60414603_sp	LVKKLKK-TG	QLDELEKAIT	TQN-INTKCI	TIP-	-	-	-	-	-	-
gi_117949830_sp	LVKKLKK-TG	RLDELEKAIT	TQN-CNTKCV	TIPSTCSEIW	GLSTANTVDQ	-	-	-	-	-
gi_13633871_sp	LVKKLKK-TG	RLDELEKAIT	TQN-CNTKCV	TIPSTCSEIW	GLSTANTVDQ	-	-	-	-	-
gi_13633914_sp	LVKKLKK-TG	RLDELEKAIT	TQN-CNTKCV	TIPSTCSEIW	GLSTPNTIDQ	-	-	-	-	-
gi_75041393_sp	LVKKLKK-TG	RLDELEKAIT	TQN-CNTKCV	TIPSTCSEIW	GLSTPNTIDQ	-	-	-	-	-
gi_110826300_sp	LVKKLKK-TG	RLDELEKAIT	TQN-CNTKCV	TIPSTCSEIW	GLSTPNTIDQ	-	-	-	-	-
gi_21264050_sp	LVKKLKK-TG	QLDELEKAIT	TQN-RNTKCV	TIPSNCSSEIW	GLSTPNTIEQ	-	-	-	-	-
gi_341942043_sp	LVKKLKEKKD	ELDSLITAIT	TNGAHPSKCV	TIQ-	-	-	-	-	-	-
gi_13959528_sp	LVKKLKEKKD	ELDSLITAIT	TNGAHPSKCV	TIQ-	-	-	-	-	-	-
gi_13959561_sp	LVKKLKEKKD	ELDSLITAIT	TNGAHPSKCV	TIQ-	-	-	-	-	-	-
gi_116256078_sp	LVKKLKEKKD	ELDSLITAIT	TNGAHPSKCV	TIQ-	-	-	-	-	-	-
gi_13959531_sp	LVKKLKEKKD	ELDSLITAIT	TNGAHPSKCV	TIQ-	-	-	-	-	-	-
gi_13959540_sp	LLKRLKE--R	SLDTLLEAVE	SRGGVPGGCV	LVP-	-	-	-	-	-	-
gi_115502451_sp	LLKRLKE--R	SLDTLLEAVE	SRGGVPGGCV	LVP-	-	-	-	-	-	-
gi_13959573_sp	LLKRLKE--R	SLHSLQLAVE	SRGGTPGGCV	LVA-	-	-	-	-	-	-
gi_13959541_sp	VLKKLKE--R	QLELLQLAVE	SRGGTRTACL	LLP-	-	-	-	-	-	-
gi_13959538_sp	VLKKLKE--R	QLELLQLAVE	SRGGTRTACL	LLP-	-	-	-	-	-	-
gi_13959529_sp	VLKKLKE--R	QLELLQLAVE	SRGGTRTACL	LLP-	-	-	-	-	-	-
	260.	270.	280.	290.	300
gi_13633932_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_118573879_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13633915_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_341942042_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_82121811_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_21264062_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13959533_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13959566_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13959559_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13633872_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13959539_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_21264049_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_66774168_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13959527_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_51338669_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_60414603_sp	-	RS	LDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_117949830_sp	WDTTGLYSFS	EQ	TRSLDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13633871_sp	WDTTGLYSFS	EQ	TRSLDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_13633914_sp	WDTTGLYSFS	EQ	TRSLDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_75041393_sp	WDTTGLYSFS	EQ	TRSLDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_110826300_sp	WDTTGLYSFS	EQ	TRSLDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_21264050_sp	WDTSGLYSYP	DQ	TRSLDGRL	-	-	QVS-	HRKGL	PH	-	-
gi_341942043_sp	-	RT	LDGRL	-	-	QVA-	GRKGF	PH	-	-
gi_13959528_sp	-	RT	LDGRL	-	-	QVA-	GRKGF	PH	-	-
gi_13959561_sp	-	RT	LDGRL	-	-	QVA-	GRKGF	PH	-	-
gi_116256078_sp	-	RT	LDGRL	-	-	QVA-	GRKGF	PH	-	-
gi_13959531_sp	-	RT	LDGRL	-	-	QVA-	GRKGF	PH	-	-
gi_13959540_sp	-	-	RADL	-	-	RL	GGQPAP	PQ	-	-
gi_115502451_sp	-	-	RADL	-	-	RL	GGQPAP	PQ	-	-
gi_13959573_sp	-	-	RGEL	-	-	RL	GAAARRPP	PH	-	-
gi_13959541_sp	-	GR	LDGRL	GPGAPASAQP	AQP	PSSYS	SL	P	-	-
gi_13959538_sp	-	GR	LDGRL	-	-	GP	GAPAGA	QPAQPPSSYS	-	-
gi_13959529_sp	-	GR	LDGRL	GPGAPASAQP	AQP	PSSYS	SL	P	-	-
	310.	320.	330.	340.	350
gi_13633932_sp	-	VI	YCRVWR	WPD	LQSHHEL	KPLECCE	-FP	FGSKQKEVCI	NPYHYKRVES	-
gi_118573879_sp	-	VI	YCRVWR	WPD	LQSHHEL	KPLECCE	-FP	FGSKQKEVCI	NPYHYKRVES	-
gi_13633915_sp	-	VI	YCRVWR	WPD	LQSHHEL	KPLECCE	-FP	FGSKQKEVCI	NPYHYKRVES	-
gi_341942042_sp	-	VI	YCRVWR	WPD	LQSHHEL	KPLECCE	-FP	FGSKQKEVCI	NPYHYKRVES	-

gi_82121811_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	D	I	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	K	R	V	E	S
gi_21264062_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	E	V	C	E	-	Y	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	K	R	V	E	S
gi_13959533_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	D	I	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	K	R	V	E	S
gi_13959566_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	D	I	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	K	R	V	E	S
gi_13959559_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	D	I	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	K	R	V	E	S
gi_13633872_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	E	C	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	K	R	V	E	S
gi_13959539_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	E	C	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	R	R	V	E	T
gi_21264049_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	A	L	E	C	C	E	-	F	P	F	G	S	K	Q	K	D	V	C	I	N	P	Y	H	Y	K	R	V	D	S
gi_66774168_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	E	C	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	R	R	V	E	T
gi_13959527_sp_-	-	V	I	Y	C	R	V	W	R	W	P	D	L	Q	S	H	H	E	L	K	P	L	E	C	C	E	-	F	P	F	G	S	K	Q	K	E	V	C	I	N	P	Y	H	Y	R	R	V	E	T
gi_51338669_sp_-	-	V	I	Y	C	R	L	W	R	W	P	D	L	H	S	H	H	E	L	R	A	M	E	L	C	E	-	F	A	F	N	M	K	K	D	E	V	C	V	N	P	Y	H	Y	Q	R	V	E	T
gi_60414603_sp_-	-	V	I	Y	C	R	L	W	R	W	P	D	L	H	S	H	H	E	L	R	A	M	E	M	C	E	-	Y	A	F	N	M	K	K	D	E	V	C	V	N	P	Y	H	Y	Q	R	V	E	T
gi_117949830_sp-	-	V	I	Y	C	R	L	W	R	W	P	D	L	H	S	H	H	E	L	K	A	I	E	N	C	E	-	Y	A	F	N	L	K	K	D	E	V	C	V	N	P	Y	H	Y	Q	R	V	E	T
gi_13633871_sp_-	-	V	I	Y	C	R	L	W	R	W	P	D	L	H	S	H	H	E	L	K	A	I	E	N	C	E	-	Y	A	F	S	L	K	K	D	E	V	C	V	N	P	Y	H	Y	Q	R	V	E	T
gi_13633914_sp_-	-	V	I	Y	C	R	L	W	R	W	P	D	L	H	S	H	H	E	L	K	A	I	E	N	C	E	-	Y	A	F	N	L	K	K	D	E	V	C	V	N	P	Y	H	Y	Q				

	360	370	380	390	400
gi_13633932_sp	PVLPPVLVPR	HSEYNPQHSL	LAQFRNL	G	QNEPHMPHN
gi_118573879_sp	PVLPPVLVPR	HSEYNPQHSL	LAQFRNL	G	QNEPHMPLN
gi_13633915_sp	PVLPPVLVPR	HSEYNPQHSL	LAQFRNL	G	QNEPHMPLN
gi_341942042_sp	PVLPPVLVPR	HSEYNPQHSL	LAQFRNL	G	QNEPHMPLN
gi_82121811_sp	PVLPPVLVPR	HSEFNPQHSL	LVQFRNL	S	HNEPHMPHN
gi_21264062_sp	PVLPPVLVPR	HSEFNPQHSL	LVQFRNL	S	HNEPHMPLN
gi_13959533_sp	PVLPPVLVPR	HNEFNPQHSL	LVQFRNL	S	HNEPHMPQN
gi_13959566_sp	PVLPPVLVPR	HNEFNPQHSL	LVQFRNL	S	HNEPHMPQN
gi_13959559_sp	PVLPPVLVPR	HNEFNPQHSL	LVQFRNL	S	HNEPHMPQN
gi_13633872_sp	PVLPPVLVPR	HSEYNPQHSL	LAQFRNL	G	QNEPHMPLN
gi_13959539_sp	PVLPPVLVPR	HSEYNPQLSL	LAKFRSA	S	LHSEPLMPHN
gi_21264049_sp	PVLPPVLVPR	NSEFNAKLSM	LPRFRNP	L	HQTEPPMPQN
gi_66774168_sp	PVLPPVLVPR	HSEYNPQLSL	LAKFRSA	S	LHSEPLMPHN
gi_13959527_sp	PVLPPVLVPR	HSEYNPQLSL	LAKFRSA	S	LHSEPLMPHN
gi_51338669_sp	PVLPPVLVPR	HTEIPAEFPP	LDDY		SHSIPEN
gi_60414603_sp	PVLPPVLVPR	HTEIPAEFPP	LDDY		SHSIPEN
gi_117949830_sp	PVLPPVLVPR	HTEILTELPP	LDDY		THSIPEN
gi_13633871_sp	PVLPPVLVPR	HTEILTELPP	LDDY		THSIPEN
gi_13633914_sp	PVLPPVLVPR	HTEILTELPP	LDDY		THSIPEN
gi_75041393_sp	PVLPPVLVPR	HTEILTELPP	LDDY		THSIPEN
gi_110826300_sp	PVLPPVLVPR	HTEILTELPP	LDDY		THSIPEN
gi_21264050_sp	PVLPPVLVPR	HTEILTELPP	LDDY		TNSIPEN
gi_341942043_sp	PGIDL SGLTL	QSN- APSMLV	KDEYVHDFEG	QPSLPTEGHS	IQT IQHPPSN
gi_13959528_sp	PGIDL SGLTL	QSNAPPSMLV	KDEYVHDFEG	QPSLPTEGHS	IQT IQHPPSN
gi_13959561_sp	PGIDL SGLTL	QSNAPSSMMV	KDEYVHDFEG	QPSLSTEGHS	IQT IQHPPSN
gi_116256078_sp	PGIDL SGLTL	QSNAPPSMLV	KDEYVHDFEG	QPSLSTEGHS	IQT IQHPPSN
gi_13959531_sp	PGIDL SGLTL	QSNAPSGMLV	KDEYVHDFEG	QPSLATEGHS	IQT IQHPPSN
gi_13959540_sp	PESPP	YSRLSPP			DQYKP
gi_115502451_sp	PESPP	YSRLSPR			DEYKP
gi_13959573_sp	PESPP	YSRLSPN			DEQKP
gi_13959541_sp	LESPP	YSRYPMD			FLKPT
gi_13959538_sp	LESPP	YSRYPMD			FLKPT
gi_13959529_sp	LESPP	YSRYPMD			FLKPT

	410	420	430	440	450
gi_13633932_sp_AT	T	F	P	D	S
gi_118573879_sp	A	T	F	P	D
gi_13633915_sp_AT	T	F	P	D	S
gi_341942042_sp	A	T	F	P	D
gi_82121811_sp_AT	T	F	P	D	S
gi_21264062_sp_AT	T	F	P	E	S
gi_13959533_sp_AT	T	F	P	D	S
gi_13959566_sp_AT	T	F	P	D	S
gi_13959559_sp_AT	T	F	P	D	S

gi_13633872_sp	ATFPDSFQQP	HSHPFAQYPN	SSYP	NSPGSSSSSTY	PHSPTS
gi_13959539_sp	ATYPDSFQQP	PCSA LPPSPS	HAFS	QSPC--TASY	PHSPGS
gi_21264049_sp	ATFPDSFPQQ	PANALPFTPN	SPTNSYPSSP	NSGTGSTATF	PHSPSS
gi_66774168_sp	ATYPDSFQQS	LCPAP			
gi_13959527_sp	ATYPDSFQQS	LGPAP			
gi_51338669_sp	TNFPAGI-EP	QSNIPETTP	PGYL	SEDG--ETSD	HQMNHS
gi_60414603_sp	TNFPAGI-EP	QSNYIPETTP	PGYL	SEDG--ETSD	HQMNPS
gi_117949830_sp	TNFPAGI-EP	QSNYIPETTP	PGYI	SEDG--ETSD	QQLNQS
gi_13633871_sp	TNFPAGI-EP	QSNYIPETTP	PGYI	SEDG--ETSD	QQLNQS
gi_13633914_sp	TNFPAGI-EP	QSNYIPETTP	PGYI	SEDG--ETSD	QQLNQS
gi_75041393_sp	TNFPAGI-EP	QSNYIPETTP	PGYI	SEDG--ETSD	QQLNQS
gi_110826300_sp	TNFPAGI-EP	QSNYIPETTP	PGYI	SEDG--ETSD	QQLNQS
gi_21264050_sp	TNFP TGI-EP	PNNYIPETTP	PGYI	SEDG--EASD	QQMNQS
gi_341942043_sp	RASTETYSAP	ALLAPAESNA	TSTTNFPNIP	VASTSQPAS I	LAGSHSEGLL
gi_13959528_sp	RASTETYSAP	ALLAPSESNA	TSTTNFPNIP	VASTSQPAS I	LAGSHSEGLL
gi_13959561_sp	RASTETYSTP	ALLAPSESNA	TSTANFPNIP	VASTSQPAS I	LGGSHSEGLL
gi_116256078_sp	RASTETYSTP	ALLAPSESNA	TSTTNFPNIP	VASTSQPAS I	LAGSHSEGLL
gi_13959531_sp	RASTETYSTP	ALLAPSESNA	TSTTNFPNIP	VASTSQPAS I	LAGSHSEGLL
gi_13959540_sp	LDLSDSTLSY	TETEATNSL			
gi_115502451_sp	LDLSDSTLSY	TETEATNSL			
gi_13959573_sp	LDLSDSTLSY	TETEATNSP			
gi_13959541_sp	AGCPDAVPSS	AETGGTN--			
gi_13959538_sp	ADCPDAVPSS	AETGGTN--			
gi_13959529_sp	ADCPDAVPSS	DETGGTN--			

	460	470	480	490	500
gi_13633932_sp_	SDPGSPF	QMPADTPPPA	YLPPEDQMT	HTSDTSQPM	DTNMMAPGIHP
gi_118573879_sp_	SDPGSPF	QMPADTPPPA	YLPPEDPMTQ	DGSQPM	DTNMMAPSLPS
gi_13633915_sp_	SDPGSPF	QMPADTPPPA	YLPPEDPMTQ	DGSQPM	DTNMMAPPLPS
gi_341942042_sp_	SDPGSPF	QMPADTPPPA	YLPPEDPMAQ	DGSQPM	DTNMMAPPLPA
gi_82121811_sp_	SGPSSPF	QLPADTPPPA	YMPDDQMGQ	DNSQSMDTS	NTMIPQIMP
gi_21264062_sp_	SGPSSPF	QLPADTPPPA	YMPDDEQMGQ	DGSQSMETG	SSLAPQ
gi_13959533_sp_	SGPGSPF	QLPADTPPPA	YMPDDQMGQ	DNSQPM	DTNNMIPQIMP
gi_13959566_sp_	SGPGSPF	QLPADTPPPA	YMPDDQMGQ	DNSQPM	DTNNMIPQIMP
gi_13959559_sp_	SGPGSPF	QLPADTPPPA	YMPDDQMAP	DNSQPM	DTNSNMIPQTMP
gi_13633872_sp_	SDPGSPF	QMPADTPPPA	YLPPEDPMAQ	DGSQPM	DTNMTAPTLP
gi_13959539_sp_	PSEPESPY	QHSVDTPPLP	YHATEASETQ	SGQP	VDA-TADRHVVL
gi_21264049_sp_	SDPGSPF	QMP-ETPPA	YMPPEEPMTQ	DCPQPM	DTNLLAPNLPLE
gi_66774168_sp_	PSSPG	HVFPQSPCPT	SYPHSPGSPS	ESDSPYQH	
gi_13959527_sp_	PSSPG	HVFPQSPCPT	SYPQSPGSPS	ESDSPYQH	
gi_51338669_sp_	MDAGSPN	LSPNPMSPA	HNN		
gi_60414603_sp_	MDAGSPN	LSPNPMSPA	HNN		
gi_117949830_sp_	MDTGSPA	ELSP TTLSPV	NHS		
gi_13633871_sp_	MDTGSPA	ELSP TTLSPV	NHS		
gi_13633914_sp_	MDTGSPA	ELSP TTLSPV	NHS		
gi_75041393_sp_	MDTGSPA	ELSP TTLSPV	NHS		
gi_110826300_sp_	MDTGSPA	ELSP TTLSPV	NHS		
gi_21264050_sp_	MDTGSPA	ELSP STLSPV	NHG		
gi_341942043_sp_Q	IASGPQPGQ	QQNGFTAQPA	TYHHNSTTTW	TGSRTAPYTP	NLPHHQNGHL
gi_13959528_sp_Q	IASGPQPGQ	QQNGFTAQPA	TYHHNSTTTW	TGSRTAPYTP	NLPHHQNGHL
gi_13959561_sp_Q	IASGPQPGQ	QQNGFTGQPA	TYHHNSTTTW	TGSRTAPYTP	NLPHHQNGHL
gi_116256078_sp_Q	IASGPQPGQ	QQNGFTGQPA	TYHHNSTTTW	TGGRTAPYTP	NLPHHQNGHL
gi_13959531_sp_Q	IASGPQPGQ	QQNGFTGQPA	TYHHNSTTTW	TGSRTAPYPP	NLPHHQNGHL
gi_13959540_sp_	ITAPG	EFSDASMS			
gi_115502451_sp_	ITAPG	EFSDASMS			
gi_13959573_sp_	NVTPG	EFSDASTS			
gi_13959541_sp_	YLAPG	GLSDSQLL			
gi_13959538_sp_	YLAPG	GLSDSQLL			
gi_13959529_sp_	YLAPG	GLSDSQLL			

	510	520	530	540	550
gi_13633932_sp_D	IHR	GDVQA	VAY	EEP	PKHWCSIV
gi_118573879_spE	INR	GDVQA	VAY	EEP	PKHWCSIV
gi_13633915_sp_E	INR	GDVQA	VAY	EEP	PKHWCSIV
gi_341942042_spE	ISR	GDVQA	VAY	EEP	PKHWCSIV
gi_82121811_sp_N	IST	RDVQP	VAY	EEP	PKHWCSIV
gi_21264062_sp_N	MPR	GDVQP	VEY	QEP	SHWCSIV
gi_13959533_sp_S	ISS	RDVQP	VAY	EEP	PKHWCSIV
gi_13959566_sp_S	ISS	RDVQP	VAY	EEP	PKHWCSIV
gi_13959559_sp_S	ISS	RDVQP	VAY	EEP	PKHWCSIV
gi_13633872_sp_E	INR	GDVQA	VAY	EEP	PKHWCSIV
gi_13959539_sp_S	IPN	GDFRP	VCY	EEP	QHWCSVA
gi_21264049_sp_I	SNR	TDVHP	VAY	QEP	PKHWCSIV
gi_66774168_sp		SDFRP	VCY	EEP	QHWCSVA
gi_13959527_sp		SDFRP	VCY	EEPL	HWCSVA

gi_51338669_sp_-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	C	E	P	A	F	W	C	S	I	S	Y	Y	E	L	N	Q	R	V	G	E											
gi_60414603_sp_-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	C	E	P	A	F	W	C	S	I	S	Y	Y	E	L	N	Q	R	V	G	E											
gi_117949830_sp-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	S	E	P	A	F	W	C	S	I	A	Y	Y	E	L	N	Q	R	V	G	E											
gi_13633871_sp_-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	S	E	P	A	F	W	C	S	I	A	Y	Y	E	L	N	Q	R	V	G	E											
gi_13633914_sp_-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	S	E	P	A	F	W	C	S	I	A	Y	Y	E	L	N	Q	R	V	G	E											
gi_75041393_sp_-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	S	E	P	A	F	W	C	S	I	A	Y	Y	E	L	N	Q	R	V	G	E											
gi_110826300_sp-	-	-	-	-	-	-	-	-	-	-	L	D	L	Q	P	-	V	T	Y	S	E	P	A	F	W	C	S	I	A	Y	Y	E	L	N	Q	R	V	G	E											
gi_21264050_sp_-	-	-	-	-	-	-	-	-	-	-	M	D	L	Q	P	-	V	T	Y	S	E	P	A	F	W	C	S	I	A	Y	Y	E	L	N	Q	R	V	G	E											
gi_341942043_sp_Q	H	H	P	P	M	P	P	H	P	G	H	Y	W	P	V	-	H	N	E	L	A	F	Q	P	P	I	S	N	H	P	A	P	E	Y	W	C	S	I	A	Y	F	E	M	D	V	Q	V	G	E	
gi_13959528_sp_Q	H	H	P	P	M	P	P	H	P	G	H	Y	W	P	V	-	H	N	E	L	A	F	Q	P	P	I	S	N	H	P	A	P	E	Y	W	C	S	I	A	Y	F	E	M	D	V	Q	V	G	E	
gi_13959561_sp_Q	H	H	P	P	M	P	P	H	P	G	H	Y	W	P	V	-	H	N	E	L	A	F	Q	P	P	I	S	N	H	P	A	P	E	Y	W	C	S	I	A	Y	F	E	M	D	V	Q	V	G	E	
gi_116256078_sp_Q	H	H	P	P	M	P	P	H	P	G	H	Y	W	P	P	V	-	H	N	E	L	A	F	Q	P	P	I	S	N	H	P	A	P	E	Y	W	C	S	I	A	Y	F	E	M	D	V	Q	V	G	E
gi_13959531_sp_Q	H	H	P	P	M	P	P	H	P	G	H	Y	W	P	V	-	H	N	E	L	A	F	Q	P	P	I	S	N	H	P	A	P	E	Y	W	C	S	I	A	Y	F	E	M	D	V	Q	V	G	E	
gi_13959540_sp_-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	D	A	T	K	P	S	H	W	C	S	V	A	Y	W	E	H	R	T	R	V	G	R								
gi_115502451_sp-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	D	A	T	K	P	S	H	W	C	S	V	A	Y	W	E	H	R	T	R	V	G	R								
gi_13959573_sp_-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	D	A	V	K	R	S	H	W	C	N	V	A	Y	W	E	H	R	T	R	V	G	R								
gi_13959541_sp_-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	E	P	G	D	R	S	H	W	C	V	V	A	Y	W	E	E	K	T	R	V										

[illegible]

	610			620			630			640			650																																					
gi_13633932_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_118573879_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_13633915_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_341942042_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_82121811_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_21264062_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	T	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_13959533_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	F	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	S	C	S	L	K
gi_13959566_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	F	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	S	C	S	L	K
gi_13959559_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	F	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	S	C	S	L	K
gi_13633872_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_13959539_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	V	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	Q	H	G	F	H	P	A	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_21264049_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	L	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	H	H	G	F	H	P	T	-	T	V	C	K	I	P	S	R	C	S	L	K
gi_66774168_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	V	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	Q	H	G	F	H	P	A	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_13959527_sp	V	H	L	Y	Y	V	G	-	G	E	V	Y	A	E	C	V	S	D	S	S	I	F	V	Q	S	R	N	C	N	Y	Q	H	G	F	H	P	A	-	T	V	C	K	I	P	S	G	C	S	L	K
gi_51338669_sp	V	R	L	Y	Y	I	G	-	G	E	V	F	A	E	C	L	S	D	S	A	I	F	V																											

gi_75041393_sp	VRLYYIG-GE	VFAECLSDSA	IFVQSPNCNQ	RYGWHPA-TV	CKIPPGCNLK
gi_110826300_sp	VRLYYIG-GE	VFAECLSDSA	IFVQSPNCNQ	RYGWHPA-TV	CKIPPGCNLK
gi_21264050_sp	VRLYYIG-GE	VFAECLSDSA	IFVQSPNCNQ	RYGWHPA-TV	CKIPPGCNLK
gi_341942043_sp	VQLECKGEGD	VWVRCLSDHA	VFVQSYYLDR	EAGRAPGDAV	HKIYPSAYIK
gi_13959528_sp	VQLECKGEGD	VWVRCLSDHA	VFVQSYYLDR	EAGRAPGDAV	HKIYPSAYIK
gi_13959561_sp	VQLECKGEGD	VWVRCLSDHA	VFVQSYYLDR	EAGRAPGDAV	HKIYPSAYIK
gi_116256078_sp	VQLECKGEGD	VWVRCLSDHA	VFVQSYYLDR	EAGRAPGDAV	HKIYPSAYIK
gi_13959531_sp	VQLECKGEGD	VWVRCLSDHA	VFVQSYYLDR	EAGRAPGDAV	HKIYPSAYIK
gi_13959540_sp	ILLSKEP-DG	VWAYNRGEHP	IFVNSPTLDA	PGG-RAL-VV	RKVPPGYSIK
gi_115502451_sp	ILLSKEP-DG	VWAYNRGEHP	IFVNSPTLDA	PGG-RAL-VV	RKVPPGYSIK
gi_13959573_sp	ILLSKEP-DG	VWAYNRSEHP	IFVNSPTLDI	PNC-RTL-IV	RKVMPGYSIK
gi_13959541_sp	IQLTREV-DG	VWVYNRSSYP	IFIKSATLDN	PDS-RTL-LV	HKVFPGFSSIK
gi_13959538_sp	IQLTREV-DG	VWVYNRSSYP	IFIKSATLDN	PDS-RTL-LV	HKVFPGFSSIK
gi_13959529_sp	IQLTREV-DG	VWVYNRSSYP	IFIKSATLDN	PDS-RTL-LV	HKVFPGFSSIK

 660..... 670..... 680..... 690..... 700				
gi_13633932_sp	IFNNQEF AQL	LAQSVN	HGFET		
gi_118573879_sp	IFNNQEF AQL	LAQSVN	HGFET		
gi_13633915_sp	IFNNQEF AQL	LAQSVN	HGFET		
gi_341942042_sp	IFNNQEF AQL	LAQSVN	HGFET		
gi_82121811_sp	IFNNQEF AQL	LAQSVN	HGF EA		
gi_21264062_sp	IFNNQEF AQL	LAQSVN	HGF EA		
gi_13959533_sp	IFNNQEF AQL	LAQSVN	HGF EA		
gi_13959566_sp	IFNNQEF AQL	LAQSVN	HGF EA		
gi_13959559_sp	IFNNQEF AQL	LAQSVN	HGF EA		
gi_13633872_sp	IFNNQEF AQL	LAQSVN	HGFET		
gi_13959539_sp	VFNNQLFAQL	LAQSVH	HGF EV		
gi_21264049_sp	IFNNQEF AEL	LAQSVN	HGF EA		
gi_66774168_sp	VFNNQLFAQL	LAQSVH	HGF EV		
gi_13959527_sp	VFNNQLFAQL	LAQLLAQSVH	HGF EV		
gi_51338669_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_60414603_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_117949830_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_13633871_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_13633914_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_75041393_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_110826300_sp	IFNNQGF AAL	LAQSVN	QGFEA		
gi_21264050_sp	IFNNQEF AAL	LAQSVN	QGFEA		
gi_341942043_sp	VFDLRQCHRQ	MQQQAA	TAQAAAAAQA	AAVAGNIPGP	GSVGGIAPAI
gi_13959528_sp	VFDLRQCHRQ	MQQQAA	TAQAAAAAQA	AAVAGNIPGP	GSVGGIAPAI
gi_13959561_sp	VFDLRQCHRQ	MQQQAA	TAQAAAAAQA	AAVAGNIPGP	GSVGGIAPAI
gi_116256078_sp	VFDLRQCHRQ	MQQQAA	TAQAAAAAQA	AAVAGNIPGP	GSVGGIAPAI
gi_13959531_sp	VFDLRQCHRQ	MQQQAA	TAQAAAAAQA	AAVAGNIPGP	GSVGGIAPAI
gi_13959540_sp	VFDERSGLL	QHADAA	HG		
gi_115502451_sp	VFDFERSGL	QHAPEP	DA		
gi_13959573_sp	VFDYEKSCLL	QHTAEL	DY		
gi_13959541_sp	AFDYEKAYSL	QRPNDH	EF		
gi_13959538_sp	AFDYEKAYSL	QRPNDH	EF		
gi_13959529_sp	AFDYEKAYSL	QRPNDH	EF		

	710	720	730	740	750																																								
gi_13633932_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	L	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_118573879_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_13633915_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_341942042_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_82121811_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_21264062_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	V	H	L	H	G	P				
gi_13959533_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_13959566_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_13959559_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_13633872_sp	-	-	-	-	-	E	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_13959539_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_21264049_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	K	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_66774168_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_13959527_sp	-	-	-	-	-	V	Y	E	L	T	K	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	H	R	Q	D	V	T	S	T	P	C	W	I	E	I	H	L	H	G	P				
gi_51338669_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_60414603_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_117949830_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_13633871_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_13633914_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_75041393_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_110826300_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_21264050_sp	-	-	-	-	-	V	Y	Q	L	T	R	M	C	T	I	R	M	S	F	V	K	G	W	G	A	E	Y	R	R	Q	T	V	T	S	T	P	C	W	I	E	L	H	L	N	G	P				
gi_341942043_sp	S	L	S	A	A	A	G	I	G	V	D	D	L	R	R	L	C	I	L	R	M	S	F	V	K	G	W	G	P	D	Y	P	R	Q	S	I	K	E	T	P	C	W	I	E	I	H	L	H	R	A
gi_13959528_sp	S	L	S	A	A	A	G	I	G	V	D	D	L	R	R	L	C	I	L	R	M	S	F	V	K	G	W	G	P	D	Y	P	R	Q	S	I	K	E	T	P	C	W	I	E	I	H	L	H	R	A

gi_13959561_sp	SLSAAAGIGV	DDLRRLCILR	MSFVKGWGPD	YPRQSIKETP	CWIEIHLHRA
gi_116256078_sp	SLSAAAGIGV	DDLRRLCILR	MSFVKGWGPD	YPRQSIKETP	CWIEIHLHRA
gi_13959531_sp	SLSAAAGIGV	DDLRRLCILR	MSFVKGWGPD	YPRQSIKETP	CWIEIHLHRA
gi_13959540_sp	- - - - - P	- - - YDPHSVR	ISFAKGWGPC	YSRQFITS CP	CWLEILLNNH
gi_115502451_sp	- - - - - A	DGPYDPNSVR	ISFAKGWGPC	YSRQFITS CP	CWLEILLNNP
gi_13959573_sp	- - - - - A	DGPYDPNSVR	ISFAKGWGPC	YSRQFITS CP	CWLEILL SNN
gi_13959541_sp	- - - - - M	QQPWTGFTVQ	ISFVKGWGQC	YTRQFISSCP	CWLEVIFNSR
gi_13959538_sp	- - - - - M	QQPWTGFTVQ	ISFVKGWGQC	YTRQFISSCP	CWLEVIFNSR
gi_13959529_sp	- - - - - M	QQPWTGFTVQ	ISFVKGWGQC	YTRQFISSCP	CWLEVIFNSR

[illegible]