Results colour-coded for hydrophobicity

The current colourscheme of the alignment is for **hydrophobicity**.

The hydrophobicity scale used is from Eisenberg *et al* (1984) <u>Abstract</u> The colour assignments **from hydrophobic to hydrophilic** are:

HYDROPHOBIC ILE PHE VAL LEU (I) (F) (V) (L)	TRP MET ALA (W) (M) (A)	GLY CYS TYR F	PRO THR SER HISPO (T) (S) (H)	GLU ASN GLN ASP (E) (N) (Q) (D)	LYS ARG (K) (R) HYDROPHILIC
10) 20	30) 40	50	
gi_13633932_sp					
gi_118573879_sp					
gi_13633915_sp gi_341942042_sp					
gi_82121811_sp					
gi_21264062_sp					
gi_13959533_sp					
gi_13959566_sp gi_13959559_sp					
gi_13633872_sp					
gi_13959539_sp					
gi_21264049_sp					
gi_66774168_sp					
gi_13959527_sp gi_51338669_sp					
gi_60414603_sp					
gi_117949830_sp					
gi_13633871_sp					
gi_13633914_sp					
gi_75041393_sp gi_110826300_sp					
gi_21264050_sp					
gi 341942043 sp					
gi_13959528_sp					
gi_13959561_sp					
gi_116256078_sp gi_13959531_sp					
gi_13959531_sp======== gi_13959540_sp_ <mark>MFRSKRSGLV</mark>					
gi_115502451_spMFRSKRSGLV					
gi_13959573_sp_ <mark>MFRSKRSGLV</mark>					
gi_13959541_sp_ <mark>MFRTKRSALV</mark>					
gi_13959538_sp_ <mark>MFRTKRSALV</mark> gi_13959529_sp_MFRTKRSALV					
gr_rsssssss_sp_ <mark>mr k r kks kt v</mark>	KKLWKSKAP G	GEDEEEGVGG	GGGGGGL	GE G	
				100	
gi_13633932_sp gi_118573879_sp					
gi_118573879_sp gi_13633915_sp					
gi_341942042_sp					
gi_82121811_sp					
gi_21264062_sp					
gi_13959533_sp					
gi_13959566_sp gi_13959559_sp					
gi_13633872_sp					
gi_13959539_sp					
gi_21264049_sp					
gi_66774168_sp					
gi_13959527_sp gi_51338669_sp					
gi_60414603_sp					
gi_117949830_sp					
gi 13633871 sp					
gi_13633914_sp					
gi_75041393_sp gi_110826300_sp					
gi_110826300_sp gi_21264050_sp					
gi_341942043_sp					
gi 13959528 sp					
gi 13959561 sp					
gi_116256078_sp					
gi_13959531_sp gi_13959540_sp_ <mark>EGGGCSRSEV</mark>	RSVAPRRPRD	AVGPRGAATA	GREEFTGGLE	RPVSESGAGA	
ar_rologo-or-or-	AL THE RE	SI MUNAIA	OHARA I GGHP	LIL VOLUGACA	

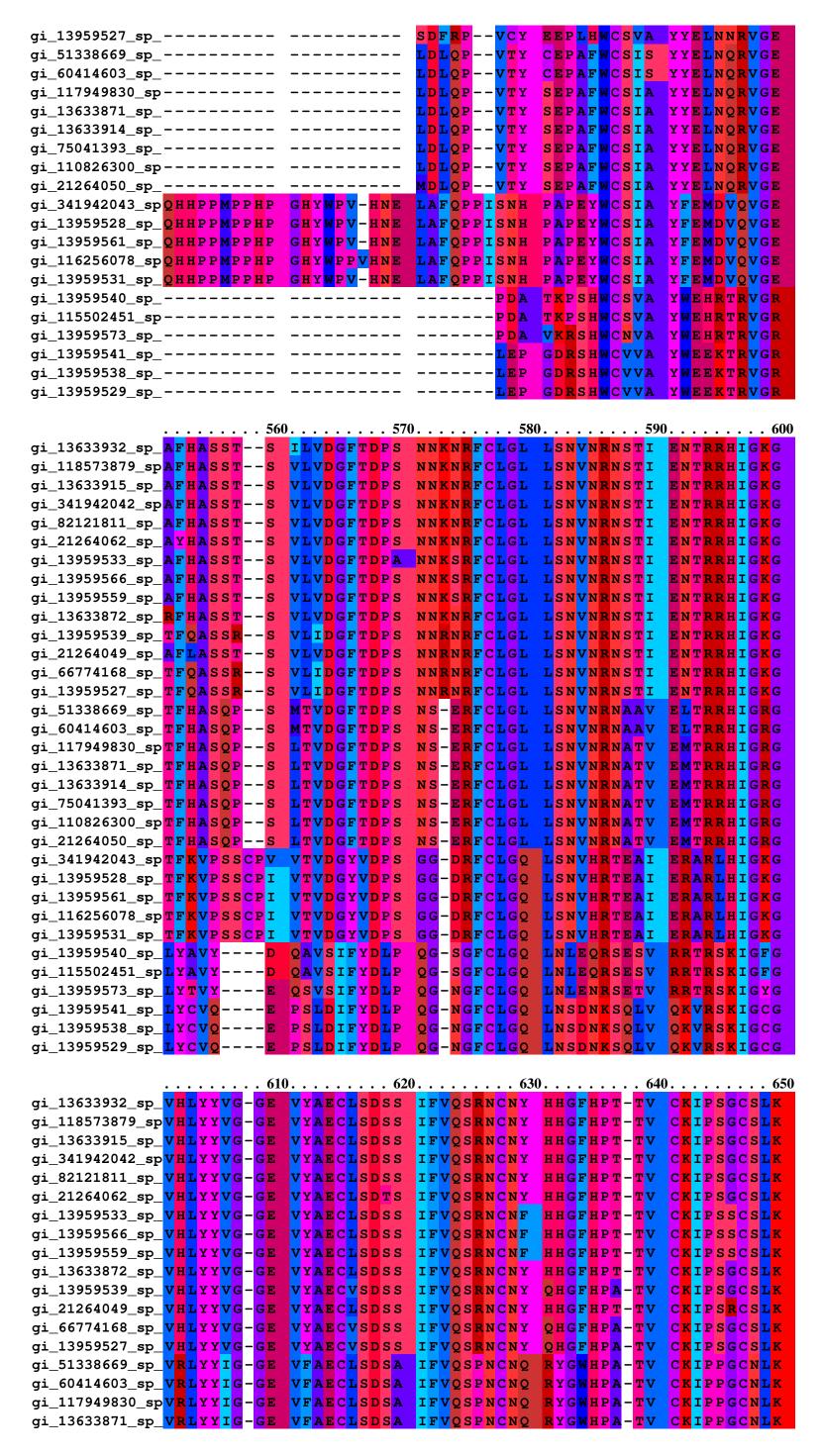
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gi_13959573_sp				
gi_13959541_sp				
gi_13959538_sp				
gi_13959529_sp				
				0 150
gi_13633932_sp				
gi_118573879_sp		<mark>M</mark> N	VTSLFS	
gi_13633915_sp		<mark>M</mark> N	VTSLFS	
gi_341942042_sp		<mark>M</mark> N	VTSLFS	
gi_82121811_sp		<mark>M</mark> T S	MASLFS	
gi_21264062_sp		MT S	MSSLFS	
gi_13959533_sp		MT S		
gi_13959566_sp		MT S		
-				
gi_13959559_sp		<mark>M</mark> <mark>T</mark> S	MASLFS	
gi_13633872_sp		<u>M</u> N	VTSLFS	
gi_13959539_sp		<mark>MHST</mark> T P	ISSLFS	
gi_21264049_sp		<mark>M</mark> N	VTSLFS	
gi_66774168_sp		<mark>MHPSTP</mark>	ISS <mark>LF</mark> S	
gi_13959527_sp		<mark>M</mark> HPSTP	ISS <mark>L</mark> FS	
gi_51338669_sp			MSS <mark>ILP</mark>	
gi_60414603_sp			MSS <mark>ILP</mark>	
gi_117949830_sp			MSS <mark>IL</mark> P	
gi_13633871_sp			MSSILP	
gi_13633914_sp			MSSILP	
gi_75041393_sp			MSSILP	
gi_110826300_sp			MSSILP	
gi_21264050_sp			MSSILP	
gi_341942043_sp		<mark>m</mark> dn <mark>m</mark> sitn		
gi_13959528_sp		<mark>M</mark> DN <mark>M</mark> SITN	TPTSND	
gi_13959561_sp		<mark>MDNM</mark> SITN		
gi_116256078_sp		<mark>M</mark> DN <mark>M</mark> SITN	TPTSND	
gi_13959531_sp		<mark>mdnm</mark> s <mark>itn</mark>	TPTSND	
gi_13959540_sp_ <mark>GGSPLDVAE</mark> P	GGPGWLPESD	CETVTCCLFS	ERDAAGAPRD	SGDPQARQSP
gi_115502451_spGSSLLDVAEP	GGPGWLPESD	CETVTCCLFS	ERDAAGAPRD	ASDPLAGAAL
gi_13959573_spQRM	AQPRRAQEGE	GRPVRCCLFA	ERPGPELPPP	PPPPPPGG
gi_13959541_spATD	GRAYGAGGGG	AGRAGCCLGK	AVRGAK	
gi_13959538_spATD	SRAHGAGGGG	PGRAGCCLGK		
gi_13959529_spATD	GRAYGAGGGG	AGRAGCCLGK	AVRGAK	
g1_13939329_sp <mark>k1D</mark>	GRAIGAGGG	AGRAGCCEGE	AVAGAR	
16	0 17	n 18	n 10	0
		KQ		EKWAEKAVDA
gi_13633932_spFT	SPAVKRLLGW			EKWAEKAVDA
gi_118573879_spFT		KQ	GDEE	
gi_13633915_spFT	SPAVKRLLGW			EKWAEKAVDA
gi_341942042_sp <mark>FT</mark>	SPAVKRLLGW		<mark>G</mark> DEE	E K W A E K A V D A
gi_82121811_sp <mark>FT</mark>	SPAVKRLLGW		<mark>GD</mark> EE	E <mark>KW</mark> AEK <mark>AVD</mark> A
gi_21264062_sp <mark>FT</mark>	SPAVKRLLGW		<mark>GD</mark> EE	E K W A E K A V D A
gi_13959533_sp <mark>FT</mark>	SPAV <mark>KR</mark> LLG <mark>W</mark>	KQ	<mark>G</mark> DEE	EK <mark>W</mark> AEK <mark>AV</mark> DA
gi_13959566_sp <mark>FT</mark>	SPAVKRLLGW	KQ	<mark>GD</mark> EE	EK <mark>W</mark> AEKAVDA
gi_13959559_sp <mark>FT</mark>	SPAVKRLLG <mark>W</mark>	KQ	<mark>G</mark> DEE	EK <mark>W</mark> AEK <mark>AVD</mark> A
gi_13633872_sp	SPAVKRLLGW		<mark>GD</mark> EE	EKWAEKAVDA
gi_13959539_sp	SPAVKRLLGW		<mark>GD</mark> EE	EKWAEKAVDS
gi_21264049_sp	SPAVKRLLGW		GDEE	EKWAEKAVDA
gi_66774168_spFT	SPAVKRLLGW		GDEE	EKWAEKAVDS
gi_13959527_sp	SPAVKRLLGW		GDEE	EKWAEKAVDS
gi_51338669_spFT	PPIVKRLLGW	KK	GEQNGQE	EKWCEKAVKS
gi_60414603_spFT	PPIVKRLLGW	KK	GEQNGQE	EKWCEKAVKS
gi_117949830_sp <mark>FT</mark>	PPVVKRLLGW	KKSAGGSG-G	AGGGE QNG QE	E K W C E K A V K S
gi_13633871_sp <mark>FT</mark>	PP <mark>VVKR</mark> LLGW	KKSAGGSG-G	AGGGE QNGQE	E K W C E K A V K S
gi_13633914_sp <mark>FT</mark>	PP <mark>VVKR</mark> LLG <mark>W</mark>	KKSAGGSG-G	AGGGEQNGQE	E K W C E K A V K S
gi_75041393_sp <mark>F</mark> T	PPVVKRLLGW	KKSAGGSG-G	AGGGEQNGQE	EK <mark>WCEKAVK</mark> S
gi_110826300_sp <mark>FT</mark>	PP <mark>VV</mark> KR <mark>LLGW</mark>	KKSAGGSG-G	AGGGEQNGQE	E <mark>KWCEKAVK</mark> S
gi_21264050_sp <mark>F</mark> T	PPVVKRLLGW	KKSASGSSGA	GGGGEQNGQE	E <mark>KW</mark> CEK <mark>AVK</mark> S
gi_341942043_sp <mark>AC</mark>			<mark>GG</mark> ES	ETFAKRAIES
gi_13959528_spAC	LSIVHSLMCH		<mark>GGE</mark> S	ETFAKRAIES
gi_13959561_spAC	LSIVHSLMCH	R0	<mark>GGE</mark> S	ETFAKRAIES
gi_116256078_spAC	LSIVHSLMCH		GGES	ETFAKRAIES
gi_13959531_spAC	LSIVHSLMCH		<mark>GGE</mark> S	ETFAKRAIES
gi_13959540_sp_EPEEGGGPRS	REARSRLLLL			
gi_115502451_spEPAGGGRS	REARSRLLLL			
gi_13959573_sp <mark>AS</mark>			<mark>LVLL</mark>	
gi_13959541_sp <mark>GH</mark>	HHPHPPTSGA		<mark>AGG</mark> A	EADLKALTHS
gi_13959538_sp <mark>GH</mark>	HHPHPPAAGA	GA	<mark>AGG</mark> A	EAD <mark>LKAL</mark> THS
gi_13959529_sp <mark>GH</mark>	HHPHPPSSGA		<mark>AGG</mark> A	EAD <mark>LKAL</mark> THS
				

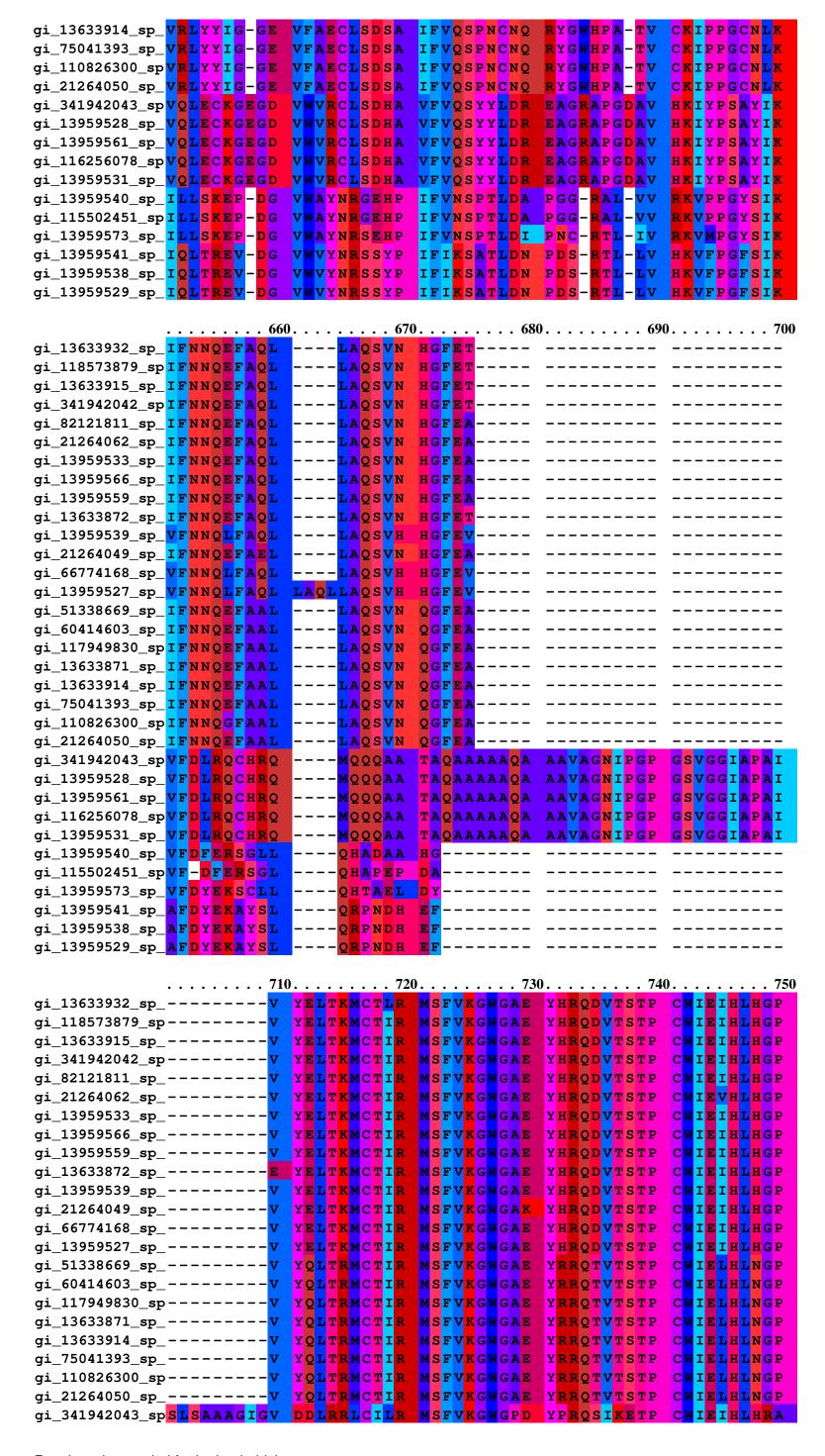
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gi_118573879_spLVKKLKKKKG AMEELEKALS CPG-QPSNCV TIP----- -----
gi_13633915_sp_LVKKLKKKG AMEELEKALS CPG-QPSNCV TIP----- -----
gi_341942042_spLVKKLKKKG AMEELEKALS CPG-QPSNCV TIP----- -----
gi_82121811_sp_LVKKLKKKG AMEELEKALS SPG-QPSKCV TIP----- -----
gi_21264062_sp_LVKKLKKKG AMEDLEKALS SPG-QPSKCV TIP----- -----
gi_13959533_sp_LVKKLKKG AMEELEKALS SPG-QPSKCV TIP----- ------
gi_13959566_sp_LVKKLKKKG AMEELEKALS SPG-QPSKCV TIP----- -----
gi_13959559_sp_LVKKLKKKG AMEELEKALS SPG-QPSKCV TIP----- -----
gi_13633872_sp_LVKKLKKKG AMEELEKALS CPG-QPSNCV TIP----- -----
gi_13959539_sp_LVKKLKKKG AMDELERALS CPG-QPSKCV TIP----- -----
gi_21264049_sp_LVKKLKKKG AMEELERALS CPG-QPSNCV TIP----- -----
gi_66774168_sp_LVKKLKKKG AMDELERALS CPG-QPSKCV TIP----- -----
                   AMDELERALS CPG-QPSKCV TIP----- -----
qi_13959527_sp_LVKKLKKKG
gi_51338669_sp_LVKKLKK-TG
                   QLDELEKAIT TQN-VNTKCI TIP----- -----
                   QLDELEKAIT TQN-INTKCI TIP----- -----
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gi_117949830_sp_LVKKLKK-TG
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gi_13633871_sp_LVKKLKK-TG
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gi_13633914_sp_LVKKLKK-TG
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gi_75041393_sp_LVKKLKK-TG
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gi_110826300_spLVKKLKK-TG
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gi_21264050_sp_LVKKLKK-TG
                   QLDELEKAIT TQN-RNTKCV TIPSNCSEIW GLSTPNTIEQ
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qi_13959528_sp_LVKKLKEKKD_ELDSLITAIT_TNGAHPSKCV_TIQ----- -----
gi 13959561 sp LVKKLKEKKD ELDSLITAIT TNGAHPSKCV TIO----- -----
gi_116256078_spLVKKLKEKKD_ELDSLITAIT_TNGAHPSKCV_TIQ------ ------
gi_13959531_sp_LVKKLKEKKD_ELDSLITAIT_TNGAHPSKCV_TIQ------ ------
gi_13959540_sp_LLKRLKE--R SLDTLLEAVE SRGGVPGGCV LVP----- ----
gi_115502451_spLLKRLKE--R SLDTLLEAVE SRGGVPGGCV LVP----- ----
gi_13959573_sp_LLKRLKE--R SLHSLLQAVE SRGGTPGGCV LVA----- -----
gi_13959541_sp_VLKKLKE--R_QLELLLQAVE_SRGGTRTACL_LLP----- -------
gi_13959538_sp_VLKKLKE--R_QLELLLQAVE_SRGGTRTACL_LLP----- ------
gi_13959529_sp_VLKKLKE--R_QLELLLQAVE_SRGGTRTACL_LLP----- --------
          ------- -QVS-HRKGL PH-----
gi_13633915_sp_----- --- --- RSLDGRL
gi 341942042 sp----- --- --- RSLDGRL ----- -QVS-HRKGL PH------
gi_82121811_sp_----- --- --- RSLDGRL ----- -QVS-HRKGL PH------
gi_21264062_sp_----- --- --- RSLDGRL
                            ----- -QVS-HRKGL PH-----
gi_13959533_sp_----- --- --- RSLDGRL ----- -QVS-HRKGL PH------
----- -QVS-HRKGL PH-----
gi_13959559_sp_----- --- --- RSLDGRL
gi_13633872_sp_----- --- --- RSLDGRL ----- -QVS-HRKGL PH------
qi_13959539_sp_----- --- --- RSLDGRL
                            ----- - QVS-HRKGL PH-----
gi_21264049_sp_----- --- --- RSLDGRL ----- -QVS-HRKGL PH------
gi 13959527 sp ----- --- --- RSLDGRL
                            ----- -QVS-HRKGL PH-----
                            ----- -QVS-HRKGL PH-----
qi 51338669 sp ----- --- --- RSLDGRL
gi_60414603_sp_----- --- --- RSLDGRL ----- -- QVS-HRKGL PH------
                            ----- -QVS-HRKGL PH-----
gi_117949830_spWDTTGLYSFS EQTRSLDGRL
gi_13633871_sp_wdttglysfs EQTRSLDGRL ----- -QVS-HRKGL PH-----
gi_13633914_sp_wdttglysfs Eqtrsldgrl ----- -Qvs-Hrkgl PH-----
gi_75041393_sp_WDTTGLYSFS EQTRSLDGRL ----- -QVS-HRKGL PH-----
gi_110826300_spWDTTGLYSFS EQTRSLDGRL ----- -QVS-HRKGL PH-----
gi_21264050_sp_WDTSGLYSYP DQTRSLDGRL ------ -QVS-HRKGL PH------
gi_341942043_sp----- --- --- RTLDGRL
gi_13959528_sp_------ --- --- RTLDGRL ----- -QVA-GRKGF PH------
gi_13959561_sp_------ --- --- RTLDGRL ----- - QVA-GRKGF PH------
qi 116256078 sp----- --- --- RTLDGRL ----- - QVA-GRKGF PH------
gi_13959531_sp_----- --- --- RTLDGRL ----- -QVA-GRKGF PH------
gi_13959541_sp_----- --- GRLDCRL GPGAPASAQP AQP-PSSYSL P------
gi_13959538_sp_----- --- GRLDCRL ----- -GP-GAPAGA QPAQPPSSYS
gi_13959529_sp_----- --- GRLDCRL GPGAPASAQP AQP-PSSYSL P------
qi_118573879_sp--VIYCRVWR WPDLQSHHEL KPLECCE-FP FGSKQKEVCI NPYHYKRVES
gi_13633915_sp_--VIYCRVWR WPDLQSHHEL KPLECCE-FP FGSKQKEVCI NPYHYKRVES
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gi_341942042_sp <mark>VIYCR</mark> VWR	WPDLQSHHEL	KPLECCE-FP	FGSKQKEVCI	NPYHYKRVES
gi_82121811_spVIYCRVWR		KPLDICE-FP	FGSKQKEVCI	NPYHYKRVES
gi_21264062_spVIYCRVWR		KPLEVCE-YP	FGSKQKEVCI	NPYHYKRVES
gi_13959533_sp VIYCRVWR		KPLDICE-FP	FGSKQKEVCI	NPYHYKRVES
gi_13959566_spVIYCRVWR		KPLDICE-FP	FGSKQKEVCI	NPYHYKRVES
_		KPLDICE-FP		NPYHYKRVES
gi_13959559_spVIYCRVWR			FGSKQKEVCI	
gi_13633872_spVIYCRVWR		KPLECCE-FP	FGSKQKEVCI	NPYHYKR <mark>V</mark> ES
gi_13959539_sp <mark>VIYCR</mark> VWR		KPLECCE-FP	FGSKQKEVCI	NPYHYRR <mark>VE</mark> T
gi_21264049_sp <mark>VIYCRVWF</mark>		KALECCE-FP	F G S K Q K D V C I	NPYHY <mark>KR</mark> VDS
gi_66774168_sp <mark>VIYCRVWR</mark>	WPDLQSHHEL	KPLECCE-FP	F G S K Q K E V C I	NPYHY <mark>RR</mark> VET
gi_13959527_sp <mark>VIYCRVWR</mark>	WPD <mark>L</mark> QSHHEL	KPLECCE-FP	F G S K Q K E V C I	NPYHYRR <mark>V</mark> ET
gi_51338669_sp <mark>VIYCRLWE</mark>	WPDLHSHHEL	RAMELCE-FA	F N M K K D E V C V	N P Y H Y Q R V E T
gi_60414603_sp <mark>VIYCRLWE</mark>	WPDLHSHHEL	RAMEMCE-YA	FNMKKDEVCV	NPYHYQRVET
gi_117949830_sp <mark>VIYCRLWE</mark>		KAIENCE-YA	FNLKKDEVCV	NPYHYQRVET
gi_13633871_sp <mark>VIYCRLWE</mark>		KAIENCE-YA	FSLKKDEVCV	NPYHYQRVET
gi_13633914_spVIYCRLWB		KAIENCE-YA	FNLKKDEVCV	NPYHYQRVET
gi_75041393_sp VIYCRLWR		KAIENCE-YA	FNLKEDEVCV	NPYHYQR <mark>VE</mark> T
gi_110826300_spVIYCRLWR		KAIENCE-YA	FNLKKDEVCV	NPYHYQRVET
gi_21264050_spVIYCRLWE		RAIETCE-YA	FNLKKDEVCV	NPYHYQRVET
gi_341942043_sp <mark>VIYARLWE</mark>		KHVKYCQ-YA	FDLKCDSVCV	NPYHYER <mark>VV</mark> S
gi_13959528_sp <mark>VIYARLW</mark>		KH <mark>V</mark> KYCQ-YA	FDLKCDSVCV	NPYHYER <mark>VV</mark> S
gi_13959561_sp <mark>VIYARLWF</mark>	WPDLH-KNEL	KH <mark>VK</mark> YCQ-YA	FDLKCDSVCV	NPYHYER <mark>VV</mark> S
gi_116256078_sp <mark>VIYARLWF</mark>	. WPDLH-KNEL	KH <mark>VK</mark> YCQ-YA	FDLKCDSVCV	NPYHYER <mark>VV</mark> S
gi_13959531_sp <mark>VIYARLW</mark> F	. WPDLH-KNEL	KHVKYCQ-YA	FDLKCDSVCV	NPYHYER <mark>VV</mark> S
gi_13959540_sp <mark>LLLGRLFF</mark>	WPDLQHAVEL	KPLCGCHSFT	AAADGPTVCC	NPYH <mark>FSRL</mark> CG
gi_115502451_sp <mark>LLLGRLF</mark>	WPDLQHAVEL	KPLCGCHSFA	AAADGPTVCC	NPYH <mark>FSRL</mark> CG
gi_13959573_spLLLGKLFF		KALCECQ-SF	GAADGPTVCC	NPYHFSRLCG
gi_13959541_spLLLCKVFF		KRLCCCE-SY	GKINPELVCC	NPHHLSRLCE
gi_13959538_sp_LPLLLCKVFF		KRLCCCE-SY	GKINPELVCC	NPHHLSRLCE
gi_13959529_sp LLLCKVF		KRLCCCE-SY	GKINPELVCC	NPHHLSRLCE
g1_13939329_sp	MPDTKU22F	KKLCCCE-51	GRINPELVCC	NPHHLSKICE
2	60 27	20	0 20	0 400
	60370	LAQFRNL		-QNEPHMPHN
gi_13633932_sp_PVLPPVLVPF			G	
gi_118573879_spPVLPPVLVPF				
gi_13633915_sp_PVLPPVLVPF		LAQFRNL	<mark>G</mark>	-QNEPHMPLN
gi_341942042_sp <mark>PVLPPVLVP</mark>		LAQFRNL	<mark>G</mark>	-QNEPHMPLN
gi_82121811_sp_ <mark>PVLPPVLVPF</mark>	. HSE <mark>F</mark> NPQHS <mark>L</mark>	LVQFRNL	s	-HNEPHMPHN
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF	HSEFNPQHSL HSEFNPQHSL	LVQFRNL LVQFRNL	s s	-HNEPHMPHN -HNEPHMP <mark>L</mark> N
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF gi_13959533_sp_PVLPPVLVPF	HSEFNPQHS <mark>L HSEFNPQHSL HNEFNPQHSL</mark>	LVQFRNL	s s	- HNEPHMPHN - HNEPHMP <mark>L</mark> N - HNEPHMPQN
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF	HSEFNPQHS <mark>L HSEFNPQHSL HNEFNPQHSL</mark>	LVQFRNL LVQFRNL	s s	-HNEPHMPHN -HNEPHMP <mark>L</mark> N
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF gi_13959533_sp_PVLPPVLVPF	HSEFNPQHSL HSEFNPQHSL HNEFNPQHSL	LVQFRNL LVQFRNL LVQFRNL		- HNEPHMPHN - HNEPHMP <mark>L</mark> N - HNEPHMPQN
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF gi_13959533_sp_PVLPPVLVPF gi_13959566_sp_PVLPPVLVPF	HSEFNPQHSL HSEFNPQHSL HNEFNPQHSL HNEFNPQHSL	LVQFRNL LVQFRNL LVQFRNL LVQFRNL		- HNE PHMP QN - HNE PHMP LN - HNE PHMP HN
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF gi_13959533_sp_PVLPPVLVPF gi_13959566_sp_PVLPPVLVPF gi_13959559_sp_PVLPPVLVPF	HSEFNPQHSL HSEFNPQHSL HNEFNPQHSL HNEFNPQHSL HNEFNPQHSL HNEFNPQHSL	LVQFRNL LVQFRNL LVQFRNL LVQFRNL		- HNEPHMPHN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN
gi_82121811_sp_PVLPPVLVPF gi_21264062_sp_PVLPPVLVPF gi_13959533_sp_PVLPPVLVPF gi_13959566_sp_PVLPPVLVPF gi_13959559_sp_PVLPPVLVPF gi_13633872_sp_PVLPPVLVPF gi_13959539_sp_PVLPPVLVPF	HSEFNPQHSL HSEFNPQHSL HNEFNPQHSL HNEFNPQHSL HNEFNPQHSL HNEFNPQHSL HSEYNPQHSL	LVQFRNL LVQFRNL LVQFRNL LVQFRNL LVQFRNL LVQFRNL		- ONE BHWB TN - HNE BHWB ON - HNE BHWB ON - HNE BHWB ON
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gi_82121811_sp_ gi_21264062_sp_ PVLPPVLVPF gi_13959533_sp_ PVLPPVLVPF gi_13959566_sp_ gi_13959559_sp_ PVLPPVLVPF gi_13633872_sp_ PVLPPVLVPF gi_1364049_sp_ gi_66774168_sp_ PVLPPVLVPF gi_60414603_sp_ PVLPPVLVPF gi_60414603_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_110826300_sp_ PVLPPVLVPF gi_1264050_sp_ PVLPPVLVPF gi_13959528_sp_ PG_ID_LS_GLTI gi_13959528_sp_ PG_ID_LS_GLTI gi_13959540_sp_ PG_ID_LS_GLTI gi_13959540_sp_ PG_ID_LS_GLTI gi_13959540_sp_ PE_SPPPF gi_13959538_sp_ PG_ID_LS_GLTI gi_13959541_sp_ PE_SPPPF gi_13959538_sp_ PE_SPPPF gi_13959538_sp_ LE_SPPPF gi_13959538_sp_ LE_SPPPF gi_13959538_sp_ LE_SPPPF gi_13959529_sp_ LE_SPP	H S E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H S E Y N P Q H S L H S E Y N P Q L S L H S E Y N P Q L S L H S E Y N P Q L S L H T E I P A E F P P H T E I L T E L P P H T E	L V Q F R N L	QPSLPTEGHS QPSLPTEGHS QPSLSTEGHS QPSLSTEGHS QPSLSTEGHS QPSLATEGHS QPSLATEGHS	- HNEPHMPLN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN LHSEPLMPHN LHSEPLMPHN SHSIPEN THSIPEN THSI
gi_82121811_sp_ gi_21264062_sp_ PVLPPVLVPF gi_13959533_sp_ PVLPPVLVPF gi_13959566_sp_ gi_13959559_sp_ PVLPPVLVPF gi_13633872_sp_ PVLPPVLVPF gi_1366774168_sp_ PVLPPVLVPF gi_66774168_sp_ PVLPPVLVPF gi_66774168_sp_ PVLPPVLVPF gi_51338669_sp_ PVLPPVLVPF gi_60414603_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_1264050_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_13959528_sp_ PG ID LS GLTI gi_13959528_sp_ PG ID LS GLTI gi_13959540_sp_ PG ID LS GLTI gi_13959540_sp_ PE SPP PF gi_13959538_sp_ PG ID LS GLTI gi_13959540_sp_ PE SPP PF gi_13959538_sp_ PE SPP PF gi_13959538_sp_ PE SPP PF gi_13959538_sp_ LE SPP PF gi_13959538_sp_ LE SPP PF gi_13959529_sp_ LE	H S E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H S E Y N P Q L S L H T E I P A E F P P H T E I L T E L P P H T E	L V Q F R N L		- HNEPHMPHN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPQN - HNEPHMPLN LHSEPLMPHN LHSEPLMPHN SHSIPEN THSIPEN
gi_82121811_sp_ pVLPPVLVPF gi_21264062_sp_ PVLPPVLVPF gi_13959533_sp_ PVLPPVLVPF gi_13959566_sp_ PVLPPVLVPF gi_13959559_sp_ PVLPPVLVPF gi_13633872_sp_ PVLPPVLVPF gi_13959539_sp_ PVLPPVLVPF gi_21264049_sp_ PVLPPVLVPF gi_666774168_sp_ PVLPPVLVPF gi_13959527_sp_ PVLPPVLVPF gi_13959527_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_341942043_sp_ PVLPPVLVPF gi_341942043_sp_ PG ID LS GLTI gi_13959528_sp_ PG ID LS GLTI gi_13959531_sp_ PG ID LS GLTI gi_13959531_sp_ PG ID LS GLTI gi_13959531_sp_ PG ID LS GLTI gi_13959540_sp_ PE SPPPF gi_13959573_sp_ PE SPPPF gi_13959573_sp_ PE SPPPF gi_13959538_sp_ LE SPPPF gi_13959538_sp_ LE SPPPF gi_13959538_sp_ LE SPPPF gi_13959529_sp_ LE SPPPF gi_13633932_sp_ ATFPDSFQQF gi_341942042_sp ATFPDSFQQF gi_341942042_sp ATFPDSFQQF	H S E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H S E Y N P Q L S L H S E Y N P Q L S L H T E I P A E F P P H T E I L T E L P P H T E	L V Q F R N L	QPSLPTEGHS QPSLPTEGHS QPSLSTEGHS QPSLSTEGHS QPSLSTEGHS QPSLSTEGHS QPSLSTEGHS QPSLSTEGHS QPSLSTEGHS	- HNEPHMPLN - HNEPHMPQN - LHSEPLMPHN LHSEPLMPHN SHSIPEN THSIPEN
gi_82121811_sp_ gi_21264062_sp_ PVLPPVLVPF gi_13959533_sp_ PVLPPVLVPF gi_13959566_sp_ gi_13959559_sp_ PVLPPVLVPF gi_13633872_sp_ PVLPPVLVPF gi_1366774168_sp_ PVLPPVLVPF gi_66774168_sp_ PVLPPVLVPF gi_66774168_sp_ PVLPPVLVPF gi_51338669_sp_ PVLPPVLVPF gi_60414603_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633871_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_1264050_sp_ PVLPPVLVPF gi_13633914_sp_ PVLPPVLVPF gi_13959528_sp_ PG ID LS GLTI gi_13959528_sp_ PG ID LS GLTI gi_13959540_sp_ PG ID LS GLTI gi_13959540_sp_ PE SPP PF gi_13959538_sp_ PG ID LS GLTI gi_13959540_sp_ PE SPP PF gi_13959538_sp_ PE SPP PF gi_13959538_sp_ PE SPP PF gi_13959538_sp_ LE SPP PF gi_13959538_sp_ LE SPP PF gi_13959529_sp_ LE	H S E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H N E F N P Q H S L H S E Y N P Q L S L H S E Y N P Q L S L H S E Y N P Q L S L H T E I P A E F P P H T E I L T E L P P H T E	L V Q F R N L		- HNEPHMPLN - HNEPHMPQN LHSEPLMPHN LHSEPLMPHN SHSIPEN THSIPEN THSI

gi_13959533_sp_ATFPDSFHQP NSTPFPLSPN -----SPYP PSPA--SSTY PNSPAS---gi_13959566_sp_ATFPDSFHQP NNTPFPLSPN -----SPYP PSPA--SSTY PNSPAS----

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NNAPFPLSPN -----SPYP PSPA--SSTY PNSPAS----
qi_13959559_sp_ATFPDSFHQP
gi_13633872_sp_ATFPDSFQQP
                     HSHPFAQYPN ----SSYP NSPGSSSSTY PHSPTS----
gi_13959539_sp_ATYPDSFQQP
                    PCSALPPSPS -----HAFS QSPC--TASY
                                                   PHSPGS----
                    PANALPETPN SPINSYPSSP NSGIGSTATE PHSPSS----
gi_21264049_sp_ATFPDSFPQQ
gi 66774168 sp ATYPDSFOOS
                     LCPAP----
gi_13959527_sp_ATYPDSFQQS
                     LGPAP----
                     QSN<mark>I-PETPP</mark>
                               ----PGYL SEDG--ETSD HOMNHS----
gi_51338669_sp_TNFPAGI-EP
gi_60414603_sp_TNFPAGI-EP
                     QSNYIPETPP
                                   --<mark>PGYL SEDG--ETSD HQM</mark>NPS----
gi_117949830_sp TNFPAGI-EP
                     QSNYIPETPP
                               ----PGYI SEDG--ETSD QQLNQS----
                     QSNYIPETPP
gi_13633871_sp_TNFPAGI-EP
                               ----PGYI SEDG--ETSD QQLNQS----
                               ----PGYI SEDG--ETSD QQLNQS----
gi_13633914_sp_TNFPAGI-EP
                     QSNYIPETPP
gi_75041393_sp_TNFPAGI-EP
                               ----PGYI SEDG--ETSD QQLNQS----
                     QSNYIPETPP
                     QSNYIPETPP -----PGYI SEDG--ETSD QQLNQS----
gi_110826300_spTNFPAGI-EP
gi_21264050_sp_TNFPTGI-EP
                               ----PGYI SEDG--EASD QQMNQS----
                    PNNYIPETPP
                     ALLAPAESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
gi_341942043_spRASTETYSAP
                     ALLAPSESNA TSTTNFPNIP VASTSOPASI LAGSHSEGLL
gi_13959528_sp_RASTETYSAP
                                         VASTSQPASI LGGSHSEGLL
gi_13959561_sp_RASTETYSTP
                    ALLAPSESNA TSTANFPNIP
gi_116256078_spRASTETYSTP
                     ALLAPSESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
gi_13959531_sp_RASTETYSTP
                    ALLAPSESNA TSTTNFPNIP VASTSQPASI LAGSHSEGLL
                     TETEATNSL - ----- ----- -----
gi_13959540_sp_LDLSDSTLSY
gi_115502451_spLDLSDSTLSY
                     TETEATNSL - ----- ---- -----
gi_13959573_sp_LDLSDSTLSY
                     TETEATNSP- ----- ---- -----
qi_13959541_sp_AGCPDAVPSS AETGGTN--- ------ ----- ------
gi_13959538_sp_ADCPDAVPSS AETGGTN--- ------ ------ -----
gi_13633932_sp_---SDPGSPF QMPADTPPPA YLPPEDQMTH DTSQPMDT-- -NMMAPGIHP
gi_118573879_sp---SDPGSPF QMPADTPPPA YLPPEDPMTQ DGSQPMDT-- -NMMAPSLPS
qi 13633915 sp --- SDPGSPF QMPADTPPPA YLPPEDPMTQ DGSQPMDT-- -NMMAPPLPS
gi_341942042_sp---SDPGSPF QMPADTPPPA YLPPEDPMAQ DGSQPMDT-- -NMMAPPLPA
gi_82121811_sp_---SGPSSPF QLPADTPPPA YMPPDDQMGQ DNSQSMDTS- -NTMIPQIMP
gi_21264062_sp_---SGPSSPF QLPADTPPPA YMPPDEQMGQ DGSQSMETG- -SSLAPQ---
gi_13959533_sp_---SGPGSPF QLPADTPPPA YMPPDDQMGQ DNSQPMDTS- -NNMIPQIMP
gi_13959566_sp_---SGPGSPF QLPADTPPPA YMPPDDQMGQ DNSQPMDTS- -NNMIPQIMP
gi_13959559_sp_---SGPGSPF QLPADTPPPA YMPPDDQMAP DNSQPMDTS- -SNMIPQTMP
gi_13633872_sp_---SDPGSPF QMPADTPPPA YLPPEDPMAQ DGSQPMDTNM TNMTAPTLPA
qi_13959539_sp_--PSEPESPY QHSVDTPPLP YHATEASETQ SG-QPVDA-- --TADRHVVL
gi_21264049_sp_---SDPGSPF QMP-ETPPPA YMPPEEPMTQ DCPQPMDTN- -LLAPNLPLE
gi_66774168_sp_----PSSPG HVFPQSPCPT SYPHSPGSPS ESDSPYQH-- ------
gi_13959527_sp_----PSSPG HVFPQSPCPT SYPQSPGSPS ESDSPYQH-- -------
gi_51338669_sp_---<mark>MDAGSPN -LSPNPMSPA HNN</mark>----- ----- ----- -----
gi_60414603_sp_---<mark>MDAGSPN -LSPNPMSPA HNN</mark>----- ---- ---- ----
gi_117949830_sp---MDTGSPA ELSPTTLSPV NHS----- ----- -----
gi_13633871_sp_---MDTGSPA ELSPTTLSPV NHS----- ----- -----
gi_13633914_sp_---MDTGSPA ELSPTTLSPV NHS----- ---- ---- ----
gi_75041393_sp_---MDTGSPA ELSPTTLSPV NHS----- ----- -----
gi_110826300_sp---MDTGSPA ELSPTTLSPV NHS----- ---- ----- -----
qi_21264050_sp_---MDTGSPA ELSPSTLSPV NHG----- ---- ---- -----
gi_341942043_spQIASGPQPGQ QQNGFTAQPA TYHHNSTTTW TGSRTAPYTP NLPHHQNGHL
gi_13959528_sp_QIASGPQPGQ QQNGFTAQPA TYHHNSTTTW TGSRTAPYTP NLPHHQNGHL
gi_13959561_sp_QIASGPQPGQ QQNGFTGQPA TYHHNSTTTW TGSRTAPYTP NLPHHQNGHL
qi 116256078 spQIASGPQPGQ QQNGFTGQPA TYHHNSTTTW TGGRTAPYTP NLPHHQNGHL
qi 13959531 sp QIASGPOPGO QONGFTGOPA TYHHNSTTTW TGSRTAPYPP NLPHHONGHL
gi 13959540 sp ---- ITAPG
                    EFSDASMS-- ------ ----- -----
gi_115502451_sp----<mark>ITAPG</mark>
                     EFSDASMS-- ------
                    EFSDASTS-- ----- ----- -----
gi_13959573_sp_----NVTPG
gi_13959541_sp_---- YLAPG GLSDSQLL-- ----- ---- ----- -----
gi_13959538_sp_-----YLAPG GLSDSQLL-- ------ ----- ------
gi_13959529_sp_----<mark>YLAPG</mark>
           \ldots \ldots \ldots 510 \ldots \ldots 520 \ldots \ldots 530 \ldots \ldots 540 \ldots \ldots 540 \ldots \ldots 550
EEPKHWCSIV YYELNNRVGE
EEPKHWCSIV YYELNNRVGE
                                         EEPKHWCSIV YYELNNRVGE
gi_13633915_sp_E------ -----INR GDVQA--VAY
qi 341942042 spE------ ----- ISR GDVQA--VAY
                                         EEPKHWCSIV YYELNNRVGE
                                         EEPKHWCSIV YYELNNRVGE
gi_82121811_sp_N------ -----IST RDVQP--VAY
OEPSHWCSIV YYELNNRVGE
EEPKHWCSIV YYELNNRVGE
RDVQP--VAY
                                         EEPKHWCSIV YYELNNRVGE
EEPKHWCSIV YYELNNRVGE
EEPKHWCSIV YYELNNRVGE
EEPQHWCSVA YYELNNRVGE
qi 21264049 sp I------ ------ SNR TDVHP--VAY
                                         QEPKHWCSIV YYELNNRVGE
qi 66774168 sp ----- ---- SDFRP--VCY
                                         EEPOHWCSVA YYELNNRVGE
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qi_13959528_sp_SLSAAAGIGV DDLRRLCILR
                                 MSFVKGWGPD YPRQSIKETP CWIEIHLHRA
gi_13959561_sp_SLSAAAGIGV DDLRRLCILR
                                 MSFVKGWGPD YPRQSIKETP CWIEIHLHRA
gi_116256078_spSLSAAAGIGV DDLRRLCILR
                                 MSFVKGWGPD YPRQSIKETP CWIEIHLHRA
gi_13959531_sp_SLSAAAGIGV DDLRRLCILR
                                 MSFVKGWGPD YPRQSIKETP CWIEIHLHRA
qi_13959540_sp_-----P_---YDPHSVR
                                 ISFAKGWGPC YSRQFITSCP CWLEILLNNH
qi 115502451 sp-----A DGPYDPNSVR
                                 ISFAKGWGPC YSRQFITSCP CWLEILLNNP
                                 ISFAKGWGPC YSRQFITSCP CWLEILLSNN
gi_13959573_sp_-----A DGPYDPNSVR
ISFVKGWGQC YTRQFISSCP CWLEVIFNSR
gi_13959538_sp_-----M QQPWTGFTVQ
                                 ISFVKGWGQC YTRQFISSCP CWLEVIFNSR
gi_13959529_sp_-----M QQPWTGFTVQ ISFVKGWGQC YTRQFISSCP CWLEVIFNSR
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. 760 770 . . gi_13633932_sp_LQWLDKVLTQ MGSPHNPISS gi_118573879_spLQWLDKVLTQ MGSPHNPISS gi_13633915_sp_LQWLDKVLTQ MGSPHNPISS gi 341942042 spLOWLDKVLTO MGSPHNPISS qi_82121811_sp_LQWLDKVLTQ MGSPLNPISS gi_21264062_sp_LQWLDKVLTQ MGSPLNPISS VS gi_13959533_sp_LQWLDKVLTQ MGSPLNPISS gi_13959566_sp_LQWLDKVLTQ MGSPLNPISS gi_13959559_sp_LQWLDKVLTQ MGSPLNPISS gi_13633872_sp_LQWLDKVLTQ MGSPHNPISS gi_13959539_sp_LQWLDKVLTQ MGSPHNPISS gi_21264049_sp_LQWLDKVLTQ MGSPHNPISS qi_66774168_sp_LQWLDKVLTQ MGSPHNPISS V S qi_13959527_sp_LQWLDKVLTQ MGSPHNPISS VS gi_51338669_sp_LQWLDKVLTQ MGSPSIRCSS gi_60414603_sp_LQWLDKVLTQ MGSPSIRCSS gi_117949830_spLQWLDKVLTQ MGSPSVRCSS gi_13633871_sp_LQWLDKVLTQ MGSPSVRCSS gi_13633914_sp_LQWLDKVLTQ MGSPSVRCSS qi 75041393 sp LQWLDKVLTQ MGSPSVRCSS gi_110826300_spLQWLDKVLTQ MGSPS<mark>VR</mark>CSS gi_21264050_sp_LQWLDKVLTQ MGSPSVRCSS gi_341942043_spLQLLDEVLHT MPIA-DP-QP gi_13959528_sp_LQLLDEVLHT LD MP I A - DP - QP gi_13959561_sp_LQLLDEVLHT MPIA-DP-QP gi_116256078_spLQLLDEVLHT MPIA-DP-QP gi_13959531_sp_LQLLDEVLHT MPIA-DP-QP gi_13959540_sp_R-----gi_115502451_spR----- --- --- -gi_13959573_sp_R----- ---- --gi_13959541_sp_----- --- --gi_13959538_sp_----- --- --qi_13959529_sp_----- --- --- --