	1								
KAH8855123.1									
KAH9593836.1 VDP71164.1		<mark>MEN</mark>	KKLSNOLPGG	RVGNMLAF	CSRDLGFKPH				<mark>LG</mark>
TPP65121.1									
KAA0189413.1									
KAF7258038.1 KAG5442206.1									
XP_030837801.1									
XP_041482585.1 KRZ73557.1									
OUC42378.1									
CDW52968.1									
KHJ46144.1 VZI00627.1								MVTTLNIN	<mark>FKNLK</mark> N
XP_014681778.1									
VDM45293.1 KAF8385568.1									
PIO76965.1						<u>M</u>	VAFI	GKRATNA-L-	<mark>VETGSP</mark>
VDL66086.1									
CAD6194288.1 XP_045095542.1		- <mark>MCGSVLGLR</mark> 	AQL	G <mark>H</mark>	CD <mark>R</mark> YL <mark>RKTPH</mark>	KQFQEFQPQS	LLYF	KKRDFKYGK-	<mark>EQVQSM</mark>
EGT43056.1									
CAB3400100.1 KAF7639475.1									
CAD5226593.1									
XP_024510735.1									
VDN24694.1 KAH7730640.1									
TMS38138.1									
XP_013290959.1 RCN50005.1									
KJH42542.1									
VDM64099.1									
VD063723.1 VD044040.1									
CAD6198090.1									
KAF8373880.1									
XP_002632400.2 RDD39080.1									
XP_001632619.1									
XP_020895242.1 XP_027059688.1									
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XP_013069769.1 XP_013069770.1 KAH9514813.1 XP_033638319.1 XP_022095223.1 XP_038051194.1 AC015530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_03785798.1 GAU97340.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1	MPCSCRSADL MLCSAHELAC	LSN	SAAAQQEPHQ	CSSRAPST SVTSPRDPAG	DEDSLDSSPD	SGEK R	KTLE	RKESYNYCEC	VLE -REESVA
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XP_013069769.1 XP_013069770.1 KAH9514813.1 XP_033638319.1 XP_023095223.1 XP_038051194.1 AC015530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1301217.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_03308308.1 XP_03308308.1 XP_03308308.1 XP_03308308.1 XP_03308308.1 XP_03308308.1 XP_03308308.1 XP_03308308.1 XP_0330831.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_033785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_033785798.1 GAU97340.1 OQV34824.1 CAD5123165.1 XP_033785798.1 XP_033785798.1 XP_033785798.1 XP_0337859917.1 XP_0337859917.1 XP_0337859917.1 XP_0337859917.1 XP_041373453.1 XP_044373453.1 XP_044373453.1 XP_045848515.1 XP_04734441.1 CAB3245311.1 XP_011549456.2	MPCSCRSADL	LSN-VDCLATLKLA	SAAAQQEPHQ	GSSRAPST SVTSPRDPAG	DEDSLDSSPD	SGEK	KTLE	RKESYNYCEC	VLE -REESVA HEA -LVDGTA
XP_013069769.1 XP_013069770.1 KAH9514813.1 XP_033638319.1 XP_022095223.1 XP_038051194.1 AC015530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF13040180.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_03785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 XP_033086127.1 XP_009013880.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 XP_033096127.1 XP_009013880.1 XP_033759917.1 XP_04526548515.1 XP_047034441.1 CAB3245311.1 XP_047034441.1 CAB324531.1 XP_011549456.2 XP_0469688321.1	MPCSCRSADL	LSN-VDCLATLKLA	SAAAQQEPHQ	GSSRAPST SVTSPRDPAG	DEDSLDSSPD	SGEK	KTLE	RKESYNYCEC	VLE -REESVA HEA -LVDGTA

RVE42816.1	 		 				
KAF9415294.1	 		 				
XP 018897307.1	 		 				
XP 019763455.1	 		 				
XP_030749737.1	 		 				
KAF7270051.1	 		 				
XP 031343879.1	 		 				
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XP 018319432.1	 		 				
XP 026466152.1	 		 				
XP_022913687.1	 		 				
KAF5298473.1	 		 				
VEN57246.1	 		 				
XP_045472083.1	 		 				
XP 017768645.1	 		 				
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XP 028136465.1	 		 				
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KAF0770685.1 XP 015365968.1							
XP_015365966.1 XP_029341681.1							
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XP 024081347.1							
XP 014283188.1	 		 				
RZF32743.1							
CAB3380083.1							
XP_046989067.1	 		 				
GFG38476.1	 		 				
CAD7446618.1	 		 				
KAG8226740.1	 - <mark>MTPGP</mark> LGIE	DGVPKIA	EDD <mark>R</mark> TFHSPQ	DGELAADPLL	SSSL <mark>K</mark> LTLL	RSDSPLER	PGN-YPLLTF
XP_046392794.1							
XP_046459477.1							
XP_043227363.1							
XP_018006429.1							
AWH57222.1 XP_042865604.1							
XP_042865604.1 XP_045119740.1							
XP_045119740.1 XP 045613573.1							
XP_043013373.1 XP_021963432.1							
CAG7730563.1						C	<b>EVILFVIIGP</b>
						_	

RVE42816.1 KAF9415294.1 XP\_018897307.1

XP_019763455.1			MDKLLKGI	M KYRSTV	K-DTMVQ	QFVKVK	DNPTPKA	VFFTCIDSRM	LPTRFTQTNV
XP_030749737.1			MDKLLKGI	M KYRSTV	R-DTMVK	OFLKVK	DNPTPKA	VFFTCIDSRM	LPTRFTOTNV
KAF7270051.1				M OYRATV	R-DTMVO	~	DNPTPKA	VFFTCIDSRM	IPTRFTOTNV
XP 031343879.1			MDRILRGV	M KYRHID	K-AKMLO				LPTRFTDMNI
_								VFFTCMDSRM	
XP_044743527.1				M KYRHLD	L-KTMVQ	~ _ ~	DNPIPKA	VFF <mark>T</mark> CMDSRM	IPTRFTETNV
XP_018319432.1			MDRILRGI	M RYRQLD	R-KTMVE		NNPTP <b>K</b> A	VFFTCMDSRM	IPTRFTEMNV
XP_026466152.1			MDRILKGI	M KYREVT	K - KTM VK	QFECVK	DHPTPKA	VFFTCMDSRM	IPTRFTETNV
XP_022913687.1			MDRILRGV	M RYRNVG	K-EMMLK	OFOEVR	DNPTPKA	VFFTCMDSRM	<b>IPTRFTOTNV</b>
KAF5298473.1			MDRILRGI	M KYRNTD	K-VKMVO	OFLOVR	DNPTPKA	VFFTCIDSRM	IPTRFTEMNV
VEN57246.1			MDKILKGI	M RYRANK	R-EIMVK	~ ~	DNPKPKA	VFFSCIDSRM	IPTRFTQMNV
						~			
XP_045472083.1			MNRILRGI		K-ERMVQ		DNPMPKA	VFFTCIDSRM	IPTRFTQTNV
XP_017768645.1			MD <mark>R</mark> IL <mark>K</mark> GI	M KYRQLG	K-KTMVE		D <mark>NPIPK</mark> A	VFFTCMDSRM	IPTRFTETNV
CAH1369701.1			MDRILRGI	M RYRSVK	K-EQMVK	QFVQVK	DNPTPKA	VFFTCIDSRM	IPTRFTQTNV
XP_028136465.1			MDKLLKGI	I KYRGTA	R-DEMVK	QFLQVK	DHPTPKA	VFFTCIDSRM	IPTRFTQTEV
XP 023014099.1			MDKLLKGI	M KYRSNI	K-ENMVK	OFVOVK	DNPKPKA	VFFTCIDSRM	LPTRFTOTNV
XP 019875064.1			MDKLLKGI	M RYREVI	K-DKMVO	OFVOVK	DNPTPKA	VFFTCIDSRM	IPTRFTOTNV
CAH0557060.1			MDKLLKGI	M RYRSTK	K-NKMVE	~ ~	DNPVPKA	VFFTCIDSRM	IPTRFTOTNI
XP_037924690.1			MERILRGI	M RYRNSS	R-IQMVK		DNPEPKA	VFFTCMDSRM	IPTRFTETHV
XP_043863257.1				M CSRAHD	A-KIRRE		C <mark>KNK</mark> PKA	VFFTCMDSRM	IPTRYTDTHV
XP_039965629.1			MERILRGI	M RYRNTT	R - EQMVK		DHPEPKA	VFFTCMDSRM	IPTRYTDTHV
XP_001989827.1			MERILRGV	M RYRNTT	R-EQMVK	EFOKVR	DNPEPKA	VFFTCMDSRM	IPTRYTDTHV
XP 037896985.1			MERILRGI	M RYRNTT	R-EOMVK	EFORVR	DNPEPKA	VFFTCMDSRM	IPTRYTDTHV
XP_046805044.1			MERILRGI	M RYRNTT	R-EOMVR		DHPEPKA	VFFTCMDSRM	IPTRYTDTHV
KAG5681791.1			MERILRGI	M RYRNTT	R-AAMVK		DNPOPKA	FFFTCMDSRM	IPTRFTDTHV
				M BYBII					
XP_031629647.1			MDRIIRGI	M RYRHII	R-EQMVQ		NDPHPKA	VFFTCMDSRM	IPTRFTETHV
KAG4077403.1			MERILRGI	M RYRHTT	R-EQMVK	~	DNPQPKA	VFFTCMDSRM	IPTR FTETHV
XP_039430644.1			MDRILRGV	M RYRNTT	R-EQMVK	EFQKVR	D <mark>N</mark> PQP <b>K</b> A	VFFTCMDSRM	IPTRYTDTHV
XP_040221405.1			MERILRGV	M RYRHTT	R-EOMVO	EFRKVR	DNPQPKA	VFFTCMDSRM	IPTRFTETHV
CAA9998239.1			MSMCLSLI	м Ін		KLFNKV	FDKHPKA	VFFTCMDSRM	<b>IPSRFTOTNV</b>
KAF6203636.1			MDRLFRGI	M RYRNTE	R-RGMVA		NNPVPKA	VFFTCMDSRM	IPSRFTOTNV
KAG6800307.1			MDKIIKGI	M KYRKCH	R-EEMVK	~	DCPEPKA	AFFTCMDSRM	IPTRFTETNV
						~ ~			
XP_014230599.1			MDRIIKGV	M KYRKCH	R-EGMVK	~ ~~	DNPQPKA	VFFTCMDSRM	IPTRFTETNV
КАН0947068.1			MD <mark>K</mark> IL <mark>KG</mark> I	M KYRKCH	R-KG <mark>MV</mark> K	~ ~~	D <mark>HPEPK</mark> A	LFFTCMDSRM	IPTRFTETDI
XP_043590797.1			MDRIIKGI	M KYRNCH	K-KELVK	QFQKVR	D <mark>HPDPKA</mark>	VFFTCMDSRM	IPTRFTETNV
XP_034949379.1			MDRIIRGI	M KYRQCH	R-EGMVK	QFQQVR	D <mark>NPEPK</mark> A	VFFTCMDSRM	IPTRFTETNV
XP_012275169.1			MDRILKGV	M KYRKCH	K-EGMVK	OFEOVK	LHLEPKA	VFFTCMDSRM	IPTRFTETNV
XP_043464528.1			MDRILRGI	M KYROCH	R-EGMVK	OFEOVR	DNPEPKA	IFFTCMDSRM	IPTRFTETNV
XP 014220045.1			MDRILKGV	M RYRKCH	R-DVMVK		DHPEPOA	VFFTCMDSRM	IPTRFTETNV
_	<mark>M</mark>	TOTAL THE VOCA	AVMDRILKGI		R-EGMVK	~ ~~			IPTRFTETNV
XP_011160605.3		TVLLHSYCSN				~ ~~		VFFTCMDSRM	
XP_046741789.1			MD <mark>R</mark> IL <mark>KG</mark> V	M KYRKCH	R-EGMVK		DHPEPKA	VFFTCMDSRM	IPTRFTETNV
VVC24333.1			MD <mark>R</mark> IF <mark>R</mark> GI	M KYRQTN	R-KKMVE		NHPEPKA	LFFTCMDSRM	LPAR FTETNV
KAF0770685.1			MDRIFRGI	M KYRQTH	R-VEMVE	QFV <mark>K</mark> VK	NRPEPKA	LFFTCMDSRM	LPAKFTKSNV
XP_015365968.1			MDRIFRGI	M KYRRTN	R-VKMVE	QFIQVK	NRPEPKA	LFFTCMDSRM	LPARFTDSNV
XP 029341681.1			MDRIFRGI	M KYRRTN	R-GKMVE	OFVOVK	NHPEPKA	LFFTCMDSRM	LPARFTESNV
XP 026292519.1					RMVC		MPCOPKA	VFFTCMDSRM	IPTRFTETNV
XP_034238427.1			MDKILKGI	M KYRVTD	R-KTMVE		NNPAPKA	VFFTCMDSRM	IPTRFTETNV
_									
XP_024081347.1			MDRLFRGI	M NYRGTD	R-LYMLE		DHPVPKA	VFFTCMDSRM	IPTRFTKTNV
XP_014283188.1			MDRLLRGI	I KYRNTD	K-HIMLD	~- ' ~ '	NNPTPKA	VFFTCMDSRM	IPTRFTKTNV
RZF32743.1			MD <mark>R</mark> IL <mark>RGV</mark>	M RYRHTD	R-KTMVE	QFIQVK	NNPVP <mark>K</mark> A	VFFTCMDSRM	IPTRFTETNV
CAB3380083.1			MDRIIRGI	I KYHHHT	R-LGMVE	QFKRVR	D <mark>NPAPK</mark> A	VFFTCMDSRM	IPTRFTETNV
XP_046989067.1			MDRILRGI	M KYRATD	R-KTMVE	OFORVR	D <mark>NPEPK</mark> A	VFFTCMDSRM	IPTRFTETNI
GFG38476.1			MDRILRGI	M KYROTD	R-KKMVE	OFEVVR	NRPEPKA	VFFTCMDSRM	IPTRFTETNV
CAD7446618.1			MDKILRGV	M KYRHTD	R-KTMVA		DHPEPKA	VFFTCMDSRM	IPTRFTETNV
KAG8226740.1	LWATLFRCDN	GGAKLPPHST	SDMDRIIRGI	M KYROTG	R-KTMVO		DNPEPKA	VFFTCMDSRM	IPTRFTETNV
	TWAITERCON	GGANLPPROI			_	~ ~			
XP_046392794.1			MDRILRGI	M KYRVTD	R-KTMVE		DNPEPKA	VFFTCMDSRM	IPTRFTETNV
XP_046459477.1			MD <mark>K</mark> IL <mark>KG</mark> I	L KYRKTY	R-TEMVE		DRPEPKA	VFFTCMDSRM	LPTRFTQTDV
XP_043227363.1					R-PGMVE	QFQQVK	D <mark>NPVPK</mark> A	IFF <mark>T</mark> CMDSRM	LPTRFTYTNV
XP_018006429.1			MGID <mark>K</mark> ILQGV	M KYRQTC	R-DGMVQ	QF <mark>K</mark> VVR	NDPHPKA	VFFTCMDSRM	LPTRFTQTNV
AWH57222.1			MGMSRILLGV		R-AGMVK			VFF <mark>T</mark> CMDSRM	LPTRFTQTNV
XP_042865604.1					R-AGMVK			VFFSCMDSRM	LPTRFTQTNV
XP_042803004.1 XP_045119740.1					R-ERMVK		DDPHPKA	VFFTCIDSRM	LPTRFTQTNV
_									
XP_045613573.1			MGMH <mark>R</mark> ILQGV	M KYRRTK	R-EGMVK		DD <mark>PHPK</mark> A	VFFTCIDSRM	LPTRFTQTNV
XP_021963432.1			TIOTIDATEDATOR		R-SNLVQ			VFF <mark>T</mark> CMD <mark>SR</mark> M	L <mark>PTR</mark> FTQTHV
CAG7730563.1	FWP	VY <mark>G</mark> VA <mark>E</mark> VT	TEMFRIIHGV	M KYREAI	R-QGMVQ	EFSAVR	D <mark>HPDPK</mark> A	VFFTCMDSRM	IPTRFTQTHV

1	81											
KAH8855123.1	GE	LFI <mark>KR</mark> NP	<b>GNFVCCENTS</b>	L	<u>N</u>	HSN	ENYVTPGFLE	LTLIRCKITD	III	CGHSDC	<b>RAMNLLNNLG</b>	<b>K</b> CMHEQQYPY
KAH9593836.1	GE	LFIERNP	GNFICCENSS	L	<u>E</u>	HFN	KNCVTPGFLE	LTLIRCRIND	III	CGHSDC	RAMNLLNNLG	KCKYERSHPY
VDP71164.1	GE	LLIL <mark>R</mark> NA	GNFAPEHGEG	<del>-</del>			GSNTVLSTLE	LGCLHGKVKD	VVI	CGHSDC	KAMHLLCSIG	SKVTD
TPP65121.1	GE	LYVI <mark>RN</mark> A	GNFAPEDGAP				<b>AAGTVLSTLE</b>	LGCLRGSVKD	VII	CGHSDC	KAMHLLRSIG	PELDN
KAA0189413.1	GE	LYVV <mark>RN</mark> A	GNFVPENGAG				EAGTILSTLE	LGCLRGSVKD	III	CGHSDC	KAMHLLOSFG	SEAEN
KAF7258038.1	GO	LYIV <mark>RN</mark> A	GNFVPOANSS			D	KECNVLGTLE	LACIRNKVND	IVI	CGHSDC	KAMHLLÑSMG	PSIMN
KAG5442206.1	GR	MFTI <mark>R</mark> NA	GNFVPCGEPH	S		E	SSCTVLGTLD	LACIRGKANE	LIV	CGHSDC	KAMHLLNSIG	PSLVR
XP_030837801.1	GE	LLII <mark>R</mark> NP	GNFVPHSCKC	E	-P <mark>SEGS</mark> E	APA	FPSGELAGLQ	LAIOKMAIPD	VIV	CGHTDC	RAGEALRHLP	VSRPTGO
XP_041482585.1	GE	LLIIRNP	GNFVPHSCKC	E	-SSAEST		FPSGEMAGLQ	LAIQKMAIPD	VIV	CGHTDC	RAGEALRNLP	VSRPTGH
KRZ73557.1	GD	AYMVKNP	GNMIPCTYTC	7	C		ASLSALASIE	LACLMKNVKD	IVV	CGHSDC	SAMNLLRSME	QCEAE
				AKL		.~						
OUC42378.1	GD	AYMVKNP	GNMIPCTYTC	AKL		QNA	AGLSALASIE	LACLMKNVKD	IVV	CGHSDC	SAMNLLHSMK	QCEAE
CDW52968.1	GD	AYTV <mark>R</mark> NP	GNIIPFCFPG	GSVANLL	IFLYGTK		AITEATASLQ	LACCESKVPE	VIV	CGHSDC	KAMKLLWSLR	NEKHE
KHJ46144.1	GD	AYTV <mark>R</mark> NP	GNIIPFCDSD	G	<b>T</b> K		AIAEATASLK	LACCESKVPE	VIV	CGHSDC	KAMKLLWLLR	TEKHQ
VZI00627.1	GD	LY <mark>TV</mark> RNA	GNFIPHAQEF	A		_	PISNEPGALE	LACCRSGVKD	III	CGHSDC	KAMNLLMKVG	EDSAIN
XP_014681778.1	GD	MYVI <mark>R</mark> NS	GNLVPHSDHC	G	<u>-</u> ED		HPSCETAALD	LCCVRSNVGN	VIV	TGHSDC	<mark>K</mark> AMNALY <mark>D</mark> VV	STVAA
VDM45293.1	GD	MYIV <mark>R</mark> NG	GNMIPSATHF		<mark>A</mark> CG		LVA <mark>TEP</mark> AALD	LTLKQGGLKH	AIV	CGHSNC	<mark>K</mark> AMNALY <mark>Q</mark> MH	LHPKK
KAF8385568.1	GD	IFVV <mark>R</mark> NA	GNLIPDACNY	G			SCTTEPAALE	LAV <mark>KR</mark> GGVKH	VIV	CGHSDC	<mark>K</mark> AM <mark>N</mark> MLFGLH	ACPSN
PI076965.1	GD	MFVV <mark>R</mark> NA	GNMIPDAPHY		<mark>TS</mark>		SITTEPAALE	LAVTRGGIRH	IIV	CGHSDC	<mark>K</mark> AMNLLH <mark>S</mark> LH	QCPKN
VDL66086.1	GD	MFVV <mark>R</mark> NA	GNMIPDAPRY	G	<mark>VS</mark>	SEI	SVTTEPAALE	LAVKRGGIRH	IVV	CGHSDC	KAMNLLHSLH	QCCTN
CAD6194288.1	GD	MFVV <mark>R</mark> NA	<b>GNMIPEAPNY</b>	G	<b>F</b> S	SEV	SVTTEPAALE	LAVKRGGINH	IVV	CGHSDC	KAINTLYGLH	QCPKN
XP_045095542.1	GD	MFVV <mark>R</mark> NA	<b>GNMIPAAPNY</b>	G	<mark>S</mark> Y	SEV	SINTEPAALE	LAVKRGKIRH	VVV	CGHSDC	KAMNTLYQLH	OCPTK
EGT43056.1	GD	MFVV <mark>R</mark> NA	GNMIPDAPNY	G	AF	SEV	SVNTEPAALE	LAVKRGGIRH	IVV	CGHSDC	KAINTLYGLH	OCPKN
CAB3400100.1	GD	MFVV <mark>RN</mark> A	GNMVPDAPNY	G			SVNT <mark>EP</mark> AALE	LAVKRGGIRH	VVV	CGHSDC	KAINTLYGLH	OCPKN
KAF7639475.1	GD	LFVV <mark>R</mark> NS	ANMVPLARNF		<b>GT</b> A		SVTTEPAALE	LAIKRGNVCO	VLV	CGHSDC	KAINTLYQLY	NGR-A
CAD5226593.1	GQ	MFVVRNS	<b>GNMIPHAQNY</b>		G <mark>SS</mark>		SITTEPAALE	LAVKRGNIHH	VLV	MGHSDC	KAINMLHNLC	OCPOH
XP_024510735.1	GD	MFVVRNS	GNMIPGSRSF	G			SVNTEPAALE	LAVTRGKINH	VIV	CGHSDC	KAINTLYNLH	TGVNK
VDN24694.1	GD	MYVVRNP	GSMIPRAENY	G			SLSTEAAGLE	LTVKRGGIKH	VII	CGHSNC	KAMNTLYNLH	KNPKK
KAH7730640.1	GD	MFVVRNS	GNMVPHAQNY	G	<b>IS</b> G		SVTTEPAALE	LAVKRGKIKH	VIV	CGHSDC	KAINTLYNLH	TCTSA
TMS38138.1	GD	MFVVRNS	GNMVPHAONY	G			SVTTEPAALE	LAVKRGGIKH	VIV	CGHADC	KAINTLYNLH	OCPKH
XP_013290959.1	GD	MFVVRNS	GNMIPHANNY	EGMYRD	-VSGPAG		SVTTEPAALE	LAVKRGHINH	VIV	CGHSDC	KAINTLYNIH	TCPQN
RCN50005.1	GD	MFVVRNS	GNMIPHANNY	G	PAG		SVTTEPAALE	LAVKRGHINH	VIV	CGHSDC	KAINTLYNIH	ECPHT
KJH42542.1	GD	MFVVRNS	GNMIPHANNY	G	P <b>T</b> G		SVITEPAALE	LAVKRGHINH	VIV	CGHSDC	KAINTLYNIH	KCPKS
VDM64099.1	GD	MFVVRNS	GNMIPHANNY	GKMLNTSTSV	AYVGSSG		SVTTEPAALE	LAVKRGHINN	VIV	CGHSDC	KAINTLYNIH	RSPKS
VDM64099.1 VD063723.1	GD	MFVVRNS	GNMVPHAEHY	GLIHGIWLAC	VFLGPAG		SVITEPAALE SVTTEPAALE	LAVKRGHINN	VIV	CGHSDC	KAINTLYNLH	KCPKT
VD044040.1	GD	MFVVRNS	GNMVPHAAHY		PSG		SVTTEPAALE	LAVKRGHINH	VIV	CGHADC	KAINTLYNLH	KNPKC
CAD6198090.1	GD	MFIV <mark>R</mark> NS	GNMIPHAKNY	G			SVTTEPAALE	LAVKRGKIKH	VIV	CGHSDC	KAINTLYNLH	TCPGA
KAF8373880.1	GD	MFVV <mark>R</mark> NS	GNMIPHANNY		<b>PV</b> G		SVTTEPAALE	LAVKRGKINH	VIV	CGHSDC	<mark>K</mark> AINTLYNLH	CCPKS
XP_002632400.2	GD	MFVV <mark>R</mark> NS	GNMIPHANNY	G			SVTTEPAALE	LAVKRGKINH	VIV	CGHSDC	KAINTLYNLH	KCPKS
RDD39080.1	GE	SFIV <mark>R</mark> NA	GNIVPHS <mark>K</mark> LI	Y	E		WTPAEAAALE	LACVRNQVSS	VVV	CGHSDC	KAMDGLHSLG	GTAPS
XP_001632619.1	GD	MFVV <mark>R</mark> TA	GNLLPHAKLY	G	<u>D</u>	V	GSCSELAALQ	MAIQEGKVEN	$\nabla\nabla\nabla$	CGHSNC	KGMTFLLSHD	SR
XP_020895242.1	GQ	MFVV <mark>R</mark> NV	GNLFPHARLF	G			ASSAEPAALE	LAVINYGI <mark>K</mark> H	VAV	CGHSDC	KAMHALYD <mark>T</mark> A	SSSST
XP_027059688.1	GD	MFIM <mark>R</mark> NA	<b>GNVVPHNQLF</b>	G	E	NQQ	SPLSE <mark>R</mark> AALE	LAIS-TGVKD	ITV	CGHSDC	KAMDCLYHMH	NTTDKKK
XP_029213515.2	GD	MFIV <mark>R</mark> NA	<b>GNTMPHSQLF</b>	G	E	SCS	SALSERAALE	LAVA-TGVEH	IAV	CGHSDC	KAMACLHQSS	STA
GF016554.1	GE	VFCI <mark>R</mark> NP	GNMVPHYCEA	E	A	E	GISAEGAGLE	LGCIMNDIGN	VVV	CGHSDC	KAVNSLYAQR	NCWH <mark>R</mark> IQ
RUS89945.1	GE	IFII <mark>R</mark> NP	GNMVPFFDPA	G	<u>Q</u>	H	TLSAEGGGLE	LGCIMNGIGD	$\nabla\nabla\nabla$	CGHSDC	KAVNSLYTQR	YDHAM
GFR80859.1	GE	VFVV <mark>R</mark> NP	<b>GNMVPLFDPS</b>	K	<u>P</u>	D	NASAEGGGLE	LGCIMNGIGD	VVV	CGHSNC	KAVNSLYSQR	HVCHEAQ
XP_005106142.1	GE	TFFVQNA	<b>GNMVPHFQSI</b>	V	<mark>S</mark>	G	<b>QMSTEGAALE</b>	LGCLSKGIRS	VVV	CGHSDC	KAVHALYDM <mark>R</mark>	SVCDHT
CAG5118574.1	GE	TFYV <mark>R</mark> NA	GNMIPHHEDY	L	A	G	YISSEGGGLE	LGCIVNEIRN	VVI	CGHSDC	RALYALYDM <mark>R</mark>	KECD <mark>HK</mark>
XP_013069769.1	GQ	IYFL <mark>RN</mark> A	<b>GNIVPHFDDF</b>	K	E	G	RISSEGAGLE	LGCVTNQVKN	VVV	LGHSDC	<b>R</b> AAQALFEIR	HSCNHE
XP_013069770.1	GE	IYFL <mark>RN</mark> A	<b>GNMVPHFDAY</b>	K	<mark>S</mark>	– – G	KISSEGGGLE	LGCITNKIRN	VVV	CGHSDC	<mark>K</mark> AAQALFEIR	HNCDHQ
KAH9514813.1	GE	IYFL <mark>R</mark> NA	<b>GNMVPHFDDY</b>	K	S	– – G	KISSEGGGLE	LGCIRNKIRN	$\nabla\nabla\nabla$	CGHSDC	KAAKALFEIR	DTCDHH
XP_033638319.1	GD	MFIL <mark>R</mark> NA	<b>GNVLPRANYS</b>	E	G	EPT	QLSCEVVALE	ITCNRSKVEH	VVI	CGHSDC	QALYAAY <mark>K</mark> HY	TEEEETS
XP_022095223.1	GD	MFLL <mark>R</mark> NA	GNVIPQANYT	Q	G	EYT	QSSS <mark>E</mark> VVAL <mark>E</mark>	ITCNRSKVEH	VVV	CGHSDC	<b>QALYAAYS</b> HY	RERE-GK
XP_038051194.1	GD	MFIL <mark>R</mark> NA	GNVIPRANYS	E	G	EPT	HVSCEVVALE	ITCNRSKVEH	VVV	CGHSDC	<b>QALYAAYS</b> HY	TEKE-TK
ACO15530.1	GD	AF <mark>TV</mark> RNA	GNIVPKSGLV	H	G	$\mathbf{L} - \mathbf{V}$	NPAPEPAGLE	LGCVLNSIKN	VIV	CGHSDC	KAMIAVHSL <mark>K</mark>	DSNGWSE
XP_040566914.1	GD	VFTV <mark>R</mark> NP	<b>GNIVPNASYV</b>	A	N	IS-R	TPAPEPAGLE	LGCVVNSIKN	V-V	CGHSDC	KAMIALOSFG	DSKGCSE
VDP33652.1	GD	LYLVKNP	SNMVPAMRGN	D	V	N-O	AAVAAVAAL <mark>Q</mark>	MTTVLGGIRD	IIV	<b>FGHGNC</b>	SAISAMYOLF	KENKP
PAA53847.1	GD	MYVM <mark>RN</mark> A	GNMAPPDELG	R			GATAAGVE	LGCIHNDIKD	VII	CGHSDC	KAMALLWKLR	DTIDT
RNA13068.1		ILITRNP	GNLVPNYNVL	P	A	K	TSRPEEAALE	LACLHDHVDT	IVV	AGHADC	KAMNLVHDNR	DQLF <mark>K</mark> PA
CAF0715750.1		ILI <mark>TR</mark> NP	<b>GSLVPNYNVL</b>	P	<u>P</u>	N	TSRPEEAALE	LACLHONIDT	VAI	<b>AGHADC</b>	KAMNLVHDNR	HQIF <mark>K</mark> SP
CAF0950609.1		FFLI <mark>R</mark> SP	GNFIPKYESL	D	<mark>T</mark>	s	VASGTPAALE	LACVNNNANT	IVV		KPLNMLFDMK	DNLEEH
CAF1119542.1		LFIV <mark>R</mark> NP	GNLVPHHNCF	R	N	N-V	TVGGECGALE	LACSINKVOV	IVV	IGHSDC	KAMNLLYSIR	NELKS
CAF1301217.1		LFIV <mark>R</mark> NP	<b>GNLVPNHNCF</b>	R	N	N-V	TVGGECAALE	LACSINKAOV	IVV	IGHSDC	KAMNLLYSIR	DDLKS
CAF3941029.1		LFIV <mark>R</mark> NP	<b>GNLVPHHNCF</b>	R	N	H-V	TVGGECGALE	LACSINKVOV	IVV	<b>IGHSDC</b>	KAMNLLYSIR	NDLOS
CAF0867361.1	GÕ	LFFV <mark>R</mark> NP	GNLVPPYDYF	E	K	N-N	IVGGECAALE	LACSENNVPV	ITV	FGHSDC	KAMNLLYRIR	NEISI
UJR16523.1		LFIVENP	GNLVPSYDYF	E	K	N-C	IVSGECAALE	LACSENNUDV	IAV	FGHSDC	KAMNLLYRIR	NEISI
CAF1340180.1		LFFVRNP	GNLVPPYEYY	0	N	M – A	LVGGECAALE	LACSRNNVDV	IAV	FGHSDC	KAMNLLYRIR	NEIAI
CAF1025683.1	GQ	LFIVEND	GNLVPPYEYY	ĸ		N-S	LVGSECAALE	LACSENNUPM	IAV	FGHSDC	KAMNLLYKIR	NEIST
ALS04255.1		MFIVRNA	GNMVPHSSKV	S		T	NVATEPAVLE	LACVMNTVKH	VVV	CGHSDC	KAINLLYNLY	SNPDTQD
XP 023329171.1		MFIVRNA	GNMVPHSSKV	S			AVATEDAVIE	LACVINTVE	$\nabla\nabla\nabla$	CGHSDC	KAINLLYSLH	TDPKTQN
KAH3870454.1		MYIVKNA	GNFVPYPDDL	E		) T _ 7	NTTTAACALE	LTCVEORTDU	$\nabla\nabla\nabla$	AGHSDC	KAMRLLYDLR	KQMDA
XP_045201158.1		NYMV <mark>KN</mark> A	GNFVPYPDDL	K		T – A	NTTSAACALD	LTCVENINGE	$\nabla\nabla\nabla$	AGHSDC	KAMSLLYDLR	TEMDI
XP_045201156.1 XP_009053308.1		HFMVRNV	GNMIPDADTL	N			TVSTEACALD	ECCNORMAN	VIV	CGHSDC	KTVSMLYEKC	VAEEF
XP_009053308.1 XP_033096127.1		IFFVRNP	GNVVVPSNLC				DOMECDAALE	MACMANAMA	$\Lambda\Lambda\Lambda$	LGHSDC	KTVSMLYEKC KAMNALYSLC	
	GD	MFVVRNA	GNLVPSSNHQ	S		5	DO VEGPAALD	T A CALL TO VIOLE	V V V	CGHSDC	KAMNRLYKMH	EEETL
XP_013785798.1			GNLVPSSNIQ	5		T - D	T T SINE PAAME	LACVLIGVEN	VVI			
GAU97340.1		MFIV <mark>R</mark> NA	GVLIPHYKYY	G	<u>k</u>	E-A	TITTEPGALE	LACVINTVQD	IIV	CGHSDC	KAMNLLQSLK	AENTPED
OQV24824.1	GE	MFIV <mark>R</mark> NA	GVLIPHHKYY	G	N	D-A	TITTEPGALE	LACVINAVQD	IIV	CGHSDC	KAMNLLQSLK	ED <mark>KS</mark> CEV
CAD5123161.1		MFII <mark>RN</mark> A	GNFIPKGEGA	E	S		STEGGALE	LGCVINKIRH	VIV	CGHSDC	KAMHALYGMR	DIINE
ELT97609.1		MYLV <mark>R</mark> NA	GNLVPHCETL	S	<u>Y</u>		AVSTEPGALE	LGCVMNEIPN	$V\Gamma V$	CGHSDC	KAMNALYGMR	DQTQI
XP_009013880.1		MFLV <mark>RN</mark> A	GNLIPNNDSL	D	<b>F</b>	D	BVITEPAALE	LGCVINKIRH	VLV	CGHSDC	KAMNALYEMM	DSVQK
KAI0233246.1		MLLV <mark>RN</mark> A	GNLVPHSDTL	<u>K</u>	N	D	EVSTEVAALE	LGCVTTNIRH	VVV	CGHSDC	KAMTALFEIR	DKAEE
XP_029642194.1		AYIV <mark>R</mark> NA	GNLFPPRDAI	T	<b>F</b>	N	SVTAEAGAIE	VACVLNNVRH	IFV	CGHSDC	KAMSLLFSLK	NQCHT
NP_001171747.1		MFMV <mark>R</mark> NA	GNLIPHSELF	<u></u>	G	D	SLNTEPAALE	LACTINDINH	VIV	CGHSDC	KAMNCLYGIR	NVTSH
CAH1781438.1		MFVV <mark>R</mark> NA	GNMVPHSDFC	5	<u>Y</u>	D	HITTEPGALE	LACTHNPIRH	VIV	CGHSDC	KAINLLLNMR	DKKAL
XP_013382323.1	GD	VYLV <mark>R</mark> NA	GNLVPHSKGL	G	<u>W</u>	H	NATTEPGALV	LGCQMGDIRH	VVV	CGHSDC	KAMNLLYSMR	NELDH
XP_033759917.1		NFVV <mark>R</mark> SA	GNLIPHACNF	S	<u>Y</u>	E	SATTEAGALE	LGCIVNGVKH	VVV	CGHSDC	KAMNLLYSMR	KEVDN
XP_041373453.1	GE	TFFV <mark>R</mark> NA	GNIV <mark>PHVK</mark> IS	S	K	D-I	GGSTEPGALE	LGCVVNNIRH	VVV	CGHSDC	KAMNMLYG <mark>IK</mark>	HDMCN-H
XP_046548515.1	GD	NFFI <mark>R</mark> NA	GNLIPNAKHF	S	<u>Y</u>	E	SVTTEPGALE	LGCIINNIKH	VVV	CGHSDC	KAMNALY <mark>G</mark> LR	HDCHH
XP_047034441.1		MFVV <mark>R</mark> NA	GNLVPHSRHF	K	<u>D</u>	) – – E	MTSCEPAALE	LGCITYDIRH	IIV	CGHSDC	KAMNLLY <mark>K</mark> LK	DD <mark>K</mark> E <mark>T</mark>
CAB3245311.1		MFVV <mark>R</mark> NA	GNVIPHSQYF	<u>V</u>	<u>D</u>	)——E	MTSCEPAALE	LGCIVNNIRH	IIV	CGHSDC	<mark>K</mark> AMNLLH <mark>S</mark> LR	CKKES
XP_011549456.2	GD	MFVV <mark>R</mark> NA	GNVV <mark>P</mark> HSQYF	<u>s</u>	D	)E	MTSCEPAAME	LGCVINDVRH	IIV	CGHSDC	<mark>K</mark> AMNLLY <mark>K</mark> LK	SPQES
XP_045761472.1	GD	MFVV <mark>R</mark> NA	GNLIPHSQHF	V	<u>D</u>	) – – E	MTSCEPAGLE	LSCIINDIRH	IIV	CGHSDC	<mark>K</mark> AMNLLY <mark>KL</mark> K	SKEES
XP_046968321.1	GD	MFVV <mark>R</mark> NA	GNLVPHSQAF	V	<u>D</u>	) – – E	MTSCEPAGLE	LSCVLNDVKH	IIV	CGHSDC	<mark>K</mark> AMNLLY <mark>KL</mark> K	SDKES
XP_026323335.1	GD	MFVI <mark>R</mark> NA	GNVIPHSEYF	L	<u>D</u>	) – – E	MTSCEPAGLE	LACIINNIRH	IIV	CGHSDC	<mark>KAMN</mark> LLY <mark>KL</mark> K	SKEES
XP_045529909.1	GD	MFVV <mark>R</mark> NA	GNLI <mark>PHSE</mark> AF	<b>I</b>	D	) – – E	MTSCEPAGLE	LSCIINNVRH	IIV	CGHSDC	KAMNLLYHL <mark>R</mark>	SKEES
RVE42816.1		MFVV <mark>R</mark> NA	GNLLPHSQHF	M	<u>D</u>	) – – E	MTSCEPAGLE	LACVINDIRH	IIV	CGHSDC	<mark>K</mark> AMNLLY <mark>KL</mark> K	SKEES
KAF9415294.1	GD	MFVV <mark>R</mark> NA	GNVVPHSQYF	V	<u>D</u>	) – – E	MTSCEPAALE	LGCILNDIRH	IIV	CGHSDC	KAMNLLY <mark>KL</mark> K	SKEES
XP_018897307.1	GD	MFVV <mark>R</mark> NA	GNLIPHSQHF	L	<u>D</u>	) – – E	QSSSEVALE NPAPEPAGLE TPAPEPAGLE AAVAAVAALQGATAAGVE TSRPEEAALE TSRPEEAALE TVGGECGALE TVGGECGALE TVGGECAALE TVGGECAALE TVGGECAALE LVGGECAALE LVGGECAALE LVGGECAALE TVGGECAALE TVTEPAALE TTTEPGALE TTSCEPAGLE	LGCVVNDIRH	IIV	CGHSDC	<mark>K</mark> AMNLLHALQ	DVDFA
					_	_						_

XP_019763455.1	GD	MFII <mark>R</mark> NA	<b>GNLVPHSQRF</b>	R			LGCVMNDIRH	IIV	CGHSDC	KAINLLY <mark>KL</mark> R	DPEFA
XP_030749737.1	GD	MFII <mark>R</mark> NA	<b>GNLVPHSHCF</b>	P	 DE	QNSNEPAALE	LGCVVNDIRH	IIV	CGHSDC	<mark>K</mark> AINLLY <mark>KL</mark> R	DPEFA
KAF7270051.1	GD	MFIV <mark>R</mark> NA	<b>GNMVPHSQFF</b>	P		QHSNEPAALE	LGCVVNDIRH	IIV	CGHSDC	<mark>K</mark> AINLLY <mark>KL</mark> R	DPEFA
XP_031343879.1	GD	MLIV <mark>R</mark> NP	GNVIPNSQHF	Q			LGC IVNNIRH	VIV	CGHSDC	<mark>KAVNE</mark> LY <mark>K</mark> LQ	DREFG
XP_044743527.1	GD	MFVV <mark>R</mark> NA	GNLIPHSQHF	M	DE		LGCIINDIRH	IIV	CGHSDC	KAMNLLY <mark>K</mark> LR	DQEFA
XP_018319432.1	GD	MFIV <mark>RN</mark> A	GNVIPHSHHF	L	DE		LGCVINDIRH	IIV	CGHSDC	KAINLLYQLQ	DTNFS
XP_026466152.1	GD	MFVV <mark>RN</mark> A	GNLVPHSQHF	L			LGCVVNDIRH	IIV	CGHSDC	KAMNLLYKLQ	DNAFA
XP_022913687.1	GD	MFVV <mark>RN</mark> A	GNLIPHSQHF	M	DE		LGCIVNDIRH	IIV	CGHSDC	KAMNLLHKLQ	DAEFA
KAF5298473.1 VEN57246.1	GD GD	MFVV <mark>R</mark> NA MFIVRNA	GNVIPHSQHF GNIIPHSOHF	L	DE DE		LGCIVNDIRH LGCVVNDIRH	VIV	CGHSDC	KAINLLYKLQ KAINLLHKLO	DSEFS
XP_045472083.1	GD	MFVVRNA	GNIIPHSQHF	E	DE		LGCVVNDIRH	IIV	CGHSDC	KAINLLYKMO	DSKFA
XP_017768645.1	GD	MFVVRNA	GNIIPHSQHF	M	DE		LGCVVNDIKH	IIV	CGHSDC	KAMNLLFKLO	DSEFA
CAH1369701.1	GD	MFVVRNA	GNIVPHSQHF	F			LGCVVNDIRH	IIV	CGHSDC	KAINLLHKLO	DGEFA
XP_028136465.1	GD	MFVVRNA	GNVIPHSQHF	V	DE		LGCVVNDIRH	IIV	CGHSDC	KAINLLYKLO	DSEFA
XP_023014099.1	GD	MFIV <mark>R</mark> NA	GNLIPHSOHF	L	DE		LGCVVNDIRH	IIV	CGHSDC	KAMNLLH <mark>K</mark> LÕ	NVDFA
XP_019875064.1	GD	MFIV <mark>R</mark> NA	GNIIPHSOHF	M	DE		LGCVVNDIRH	IIV	CGHSDC	KAINLLY <mark>K</mark> LÕ	DSEFA
CAH0557060.1	GD	MFII <mark>R</mark> NA	GNIIPHSQHF	M	 DE	LTTNEPAALE	LGCVVNDVRH	IIV	CGHSDC	KAINLLY <mark>K</mark> LQ	DSDFA
XP_037924690.1	GD	MFVV <mark>R</mark> NA	<b>GNVIPHSHHF</b>	V	 DE	FF <mark>S</mark> CEPAALE	LGCIVNDIRH	IIV	CGHSDC	KAMNLLY <mark>KL</mark> K	DPEFA
XP_043863257.1	GD	MFVV <mark>R</mark> NA	<b>GNLIPHAQHF</b>	Q			LGCVVNDIRH	IIV	CGHSDC	<mark>K</mark> AMNLLY <mark>QL</mark> R	DPDFA
XP_039965629.1	GD	MFVV <mark>R</mark> NA	GNVIPHAQHF	Q	DE		LGCVINDIRH	IIV	CGHSDC	KAMNLLY <mark>K</mark> LQ	DEEYS
XP_001989827.1	GD	MFVV <mark>R</mark> NA	GNLIPHAHHF	H			LGCVVNDIRH	IIV	CGHSDC	KAMNLLYQL <mark>R</mark>	DPEFA
XP_037896985.1	GD	MFVV <mark>RN</mark> A	GNLIPHAHHF	Q			LGCVVNDIRH	IIV	CGHSDC	KAMNLLYMLR	DPDFA
XP_046805044.1	GD	MFVV <mark>RN</mark> A	GNLIPHAQHF	Q	DE		LGCVVNDIRH	IIV	CGHSDC	KAMNLLYQLR	DPEFA
KAG5681791.1	GD	MFVVRNA	GNLVPHSHFF	Q			LGCVVNNIRH	VIV	CGHSDC	KAINLLHQLQ	CTQFA
XP_031629647.1	GD GD	MFVV <mark>R</mark> NA MFVVRNA	GNLVPHAQHF	Q	DE DE		LGCVVNNIRH LGCVVNNIRH	III	CGHSDC	KAMNLLYSLR KAMNLLYSLR	DKEKA DPELA
KAG4077403.1 XP_039430644.1	GD	MF V VRNA MFVVRNA	GNLIPHAQHF GNLVPHAEHF	0			LGCVVNNIKH	IIV	CGHSDC	KAMNLLYOLR	DPOFA
XP_040221405.1	GD	MFVVRNA	GNLVPHAEHF	0			LGCVVNNIKH	IIV	CGHSDC	KAMNLLYKLK	DPEFA
CAA9998239.1	GD	MFIVRNA	GNIIPHSHHF	M	GE		LGCVVNDIRH	III	CGHSDC	KAMNLLYKLK	DSTFS
KAF6203636.1	GD	MFIVRNA	GNVIPHSHHF	N		VTMNEPAALE	LGCVVNDIRH	III	CGHSDC	KAMNLLYKLK	DQSFS
KAG6800307.1	GD	MFVV <mark>RN</mark> A	GNIIPHSQHF	E	DE		LVCLMNEIKH	IIV	CGHSDC	KAMNMLYSLR	EEELA
XP_014230599.1	GD	MFVV <mark>R</mark> NA	GNIVPHSSHF	M	 DE		LGCVVNDIRH	III	CGHSDC	KAMNLLYAL <mark>R</mark>	DOEFA
KAH0947068.1	GD	MFVV <mark>R</mark> NP	<b>GNLIPHPHHF</b>	V	 DE	YTTCESAALE	LSCVVNAIRH	VIV	CGHSDC	KAMNLLY <mark>TL</mark> R	DEE <mark>LA</mark>
XP_043590797.1	GD	MFVV <mark>R</mark> NA	GNLIPHSQHF	V	 DE	L <mark>TM</mark> CEPAALE	LGCVINNMKH	IIV	CGHSDC	<mark>K</mark> AMNLLYAL <mark>R</mark>	DEE <mark>FA</mark>
XP_034949379.1	GD	MFVV <mark>R</mark> NA	GNVIPHSQHF	I	DE		LGCVINNIRH	IIV	CGHSDC	<mark>K</mark> AMNLLYAL <mark>Q</mark>	DEEFA
XP_012275169.1	GD	MFVV <mark>R</mark> NA	GNIVPHSQHF	A			LGCVVNNIKH	IIV	CGHSDC	KAMNLLYAL <mark>R</mark>	DQEFS
XP_043464528.1	GD	MFVV <mark>R</mark> NA	GNIVPHSQHF	L	DE		LGCVVNDIRH	VIV	CGHSDC	KAMNLLYALR	DEEFS
XP_014220045.1	GD	MFVV <mark>R</mark> NA	GNIVPHSHHF	D	DE		LGCIVNDIRH	VIV	CGHSDC	KAMNLLYALR	DENFA
XP_011160605.3	GD GD	MFVV <mark>RNP</mark> MFVVRNA	GNVVPHSRHF	V			LGCVVNDIKH LGCVVNDIRH	VIV	CGHSDC	KAMNLLYALR	DEEFA
XP_046741789.1 VVC24333.1	GD	MF V VRNA MFIVRNA	GNVVPHSQHF GNLIPHSQHF	T	DE		LGCVHNDIRH	IIV VIV	CGHSDC	KAMNLLYAL <mark>R</mark> KAMNLLHLLR	DTEFA
KAF0770685.1	GD	MFIVRNA	GNLIPHSQHF	0		YTTCEPAALE	LGCIHNDVRH	VIV	CGHSDC	KAMNLLYLLK	DTEYG
XP_015365968.1	GD	MFIVRNA	GNLVPHSRHF	0			LGCVHNDVRH	VIV	CGHSDC	KAMNLLHLLR	ETEYS
XP_029341681.1	GD	MFIVRNA	GNLIPHSQHF	P	DE		LGCVHNDIRH	VIV	CGHSDC	KAMNLLHLLR	DTEYG
XP_026292519.1	GD	MFVVRNA	GNIIPHCGHF	L		YHTNEPAALE	LGCIVNDIRH	IIV	CGHSDC	KAMNLLYALR	DAEMS
XP_034238427.1	GD	MFVV <mark>R</mark> NA	GNVIPHCGHF	L	 DE		LGCIINDIRH	IIV	CGHSDC	<mark>K</mark> AMNLLYAL <mark>R</mark>	DAEMS
XP_024081347.1	GD	MFVV <mark>R</mark> NA	<b>GNIIPHAHHF</b>	R	 DE	ITTNEPAALE	LGC IVNDIRH	IIV	CGHSDC	KAMNLLY <mark>KL</mark> R	DEE <mark>FS</mark>
XP_014283188.1	GD	MFVV <mark>R</mark> NA	GNIIPHSQHF	L	DE	YTTNEPAALE	LGCVVNDIRH	IIV	CGHSDC	<mark>K</mark> AMNLLY <mark>KL</mark> R	DE <mark>NFA</mark>
RZF32743.1	GD	MFVV <mark>R</mark> NA	GNLIPHSQHF	L	 DE		LGCVVNDIRH	IIV	CGHSDC	KAMNLLH <mark>K</mark> LR	DE <mark>K</mark> FA
CAB3380083.1	GD	MFVV <mark>R</mark> NA	GNLIPHSQHF	<u>V</u>	 NE		LGCIVNDIKH	VIV	CGHSDC	KAMNLLHSLQ	DEEYA
XP_046989067.1	GD	MFVV <mark>RN</mark> A	GNVIPNSQNF	P	 EE	VTTTEPAALE	LGCVINDIRH	VIV	CGHSDC	KAMNLLH <mark>R</mark> LK	CEEFS
GFG38476.1	GD	MFVV <mark>RN</mark> A	GNVIPHSQHF	L	 DE		LGCIVNDIRH	VIV	CGHSDC	KAMNLLYSLQ	CQEFS
CAD7446618.1	GD	MFVV <mark>R</mark> NA MFIVRNA	GNLIPHSQHF	<u>V</u>	 DE NE		LGCIINDIKH LGCIVNDIKH	IIV	CGHSDC	KAMNLLHALR	DEEFS
KAG8226740.1	GD GD	MFTVRNA MFFVRNA	GNVIPHSQHF GNLIPHSOHF	T	 NE	MTTTEPAALE MTTTEPAALE		IIV	CGHSDC	KAMNLLHAL <mark>R</mark> KAMNLLHDLR	DEEFS
XP_046392794.1 XP 046459477.1	GD	MFIVRNA		G			LGCIVNDIKH		CGHSDC	KAMNLLYSFK	KGIET
XP_040439477.1 XP_043227363.1	GD	MFIVRNA		D	 TE		LGCIVNGIKN	VII	CGHSDC	KAMNLLYDLR	
XP 018006429.1	GD	MFIVRNA				EITTEPAALE			CGHSDC	KAMNMLHLLR	NSDMS
AWH57222.1		MFIVRNA		G	 HE	EITTEPAALE			CGHSDC	KAMNMLHLMR	NSDRT
XP_042865604.1	GD	MFIV <mark>RN</mark> A		G	 HE	EITTEPAALE	LGCVINGIRH		CGHSDC	KAMNMLHLLR	NTDRL
XP_045119740.1	GD	MFIV <mark>R</mark> NA	<b>GNLVPHANLS</b>			E <mark>ITTEP</mark> AALE			CGHSDC	<mark>K</mark> AMNMLHMMR	NSD <mark>R</mark> T
XP_045613573.1	GD	MFIV <mark>RN</mark> A		G	 HE	EITTEPAALE	LGCVINGIKH	VIV	CGHSDC	<mark>K</mark> AMNMLHMM <mark>R</mark>	NSD <mark>R</mark> T
XP_021963432.1	GD	MFIV <mark>RN</mark> A		A			LGCIINEIKH		CGHSDC	<mark>K</mark> AMNLLY <mark>D</mark> LG	
CAG7730563.1	GD	MFIV <mark>R</mark> NA	GNLVPHSKFF	V	 AE	NTTT <mark>EP</mark> AAL <mark>E</mark>	LGCVINKIQH	VVV	CGHSDC	<mark>K</mark> AMNLLY <mark>TL</mark> K	DEALT

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KAH8855123.1	<b>LSHHYHQSNS</b>	IDKEVNKLKS	SPLEKWIWEN	GC-K	TLQNF	HL <mark>K</mark> SN	IL <mark>S</mark> FT	-SSLHS-NCP	KLELDL <mark>N</mark> LV <mark>K</mark>	HLTEIDLLSQ
KAH9593836.1	LAHHEHQPID	VQTENNKITS	SPLEKWIWEN	GC-K	TLQNF	NTKSG	ILSFK	SSSIHS-KCP	TLELDLNSAK	HLTEVDLLSQ
VDP71164.1			SPLOKWVAGQ	G <mark>I</mark> -K	CWKKW	QS <mark>K</mark> TN	AV <mark>R</mark> FP	AFKEEQL	ILNMRSDLIK	NLEPVDIISQ
TPP65121.1		KKLDEQKI	SPLQKWISQN	GV-K	C <mark>WKK</mark> W	HA <mark>K</mark> TN	TVQFS	TLE-DHL	TLNMRSDAMR	N <mark>LEPVDVL</mark> SQ
KAA0189413.1		H <mark>K</mark> SD <mark>K</mark> NSA	SPLQKWVSQN	G <mark>I-</mark> K	G <mark>WNK</mark> W	RAKSD	<mark>SIEFP</mark>	AMK-DHL	TLNMHADQVK	K <mark>LEPVDVL</mark> SQ
KAF7258038.1		D <mark>K</mark> LQTTQM	TPLQQWAA <mark>K</mark> N	GM-E	G <mark>FRK</mark> Y	ERKPN	<mark>LLE</mark> FP	VNDMLT-LKT	PLRLKLTSLK	DLSDVDRLSQ
KAG5442206.1		GELPVSQM	SPIEKWVALN	GL-A				VVDPQV-RKS	NFNL <mark>K</mark> LSSL <mark>K</mark>	DFEECDRLSQ
XP_030837801.1			DLMNNWL <mark>R</mark> AY	GS-P			<mark>NP</mark> AEEV	TYEGGGRKGA	K <mark>LSAVIEDNG</mark>	KLSKTDRLAQ
XP_041482585.1		-AGSGSQHSL	DLTNNWLHSY	GS-P		EQHME	<mark>K</mark> PGEEV	EFEGGGRKGA	KFSALIDDEN	K <mark>LSKTDK</mark> LAQ
KRZ73557.1		<mark>WK</mark> PD	<mark>K</mark> PL <mark>K</mark> SWLQIH	G <mark>S</mark> -P		NCLMK	GQQVF	QFIPEY-PLL	QFSA <mark>K</mark> IDPSG	<mark>K</mark> LANAD <mark>K</mark> LSQ
OUC42378.1		WKPD	EPL <mark>K</mark> SWLQIH	GS-P			GQQVL	QFIPEY-PFL	QFSA <mark>K</mark> IDPSG	KLTNADKLSQ
CDW52968.1		WDSR	MPLNAWLMLQ	GR-A		EQMEE	TDGSI	SFLNKW-QSL	SFEASIDR-K	KWNELDQLSQ
KHJ46144.1		<mark>WD</mark> LH	KPLSSWLMLQ	GK-A	TLEKY	EEMEE	<mark>THG</mark> SI	SFLNKW-QNL	SFEASIDR-K	KLNELDQLSQ
VZI00627.1		LTRYS	SPLERWVVQM	GK-S		LRSDA		TFDLGSD-FR	PMNATVDAER	RFSPVDRLSQ
XP_014681778.1			GPLHTYL <mark>R</mark> SY	AV-P		QQLLRS		EFSVTPR-HR	SFRAFIDPEH	ELSEMDKLSQ
VDM45293.1		FDES	SPLHHWVRKH	GY-V			EGASCRL	VFAENDR-HQ	SFKALIDPEN	ELDVEDKLSQ
KAF8385568.1		FDHA	SPMDHWLRKN	GH-R			KGPQPL	QFDSEVAPSQ	SFEALIDPFD	RLKAEDKLSQ
PIO76965.1		FDMD	SPMDHWVRRN SPMDHWVRON	GF-R			<mark>KGAK</mark> IM KGGTPL	KFETDIAPSQ	NFEALIDPFD	KLPVEDKLSQ
VDL66086.1		FDVS	SPMDOWVRON SPMDOWVRNN	GY-R GY-Q			KGAAKM	KFESSVAPSQ TFNCEMSPNO	NFEAIVDPFD SFEAIIDPMD	LLPVEDKLSQ RLPVEDKLSQ
CAD6194288.1 XP_045095542.1			SPMDQWLRRN SPMDQWLRRN	GF-E		NERLH		KFESEVAPSQ	SFEATIDPME SFEATIDPME	KWSAEDKLSO
EGT43056.1		FDVT	SPMDHWVRRN	GF-A			LGPSNM	SFESEVSPSQ	SFEALIDPMD	RLPVEDKLSQ
CAB3400100.1		FDVE	SPMDHWVRRN	GF-K		NERLH		KFESEVSPSQ	SFEALIDPFE	KLTVEDKLSO
KAF7639475.1		FDPE	SPMDHWLRHN	GH-L		EKLIKN		EFASENG-LM	KFKAKIDPEN	KYGVEDKLSO
CAD5226593.1		FDOT	SPVDHWLRKN	GF-R		TOMLKAE	ENCDPDARRI	HFAAEEPELL	NFHAQIDPDR	KFGVEDWLSO
XP_024510735.1			SPMDRWLRLN	GY-H			DGPNVPL	KFENDDQ-KF	CFYAYIDKEN	KLNIEDKLSO
VDN24694.1		FDAN	SPLDLWIREH	GF-L			SKTAKPL	KYSTPDG-AF	SFEALIDEEN	KFDVEDKLSQ
KAH7730640.1		FDPE	SPMDHWLRKH	GY-S			STGAKPI	<b>EFVAENPSLL</b>	RFHAVIDEER	RFNVEDRLSO
TMS38138.1		FDPA	SPMDHWLRRH	G <mark>F-T</mark>		E <mark>NR</mark> LK	SEPEKPL	VFL <mark>SDFP</mark> -YF	KFEAVIDPQN	EFNTEDKLSQ
			<mark>SPMDHWLRR</mark> H	G <mark>F-</mark> T			D <mark>KNL</mark> KPL	<mark>K</mark> FVSD <mark>NP</mark> -AH	SFEAMIDEED	<mark>K</mark> WSVED <mark>KL</mark> SQ
RCN50005.1		<mark>FDPQ</mark>	<mark>SPMDHWLRR</mark> H				D <mark>KTAKPI</mark>	KFVSDNP-SF	SFEAVIDPED	<mark>K</mark> WGVED <mark>KL</mark> SQ
KJH42542.1		<mark>FDPQ</mark>	SPMDHWL <mark>RR</mark> H	GF-T			DESAKAL	KFSSTGS-NF	SFEAIIDQEN	K <mark>WG</mark> VED <mark>KL</mark> SQ
VDM64099.1		<mark>FDPQ</mark>	SPMDHWL <mark>RR</mark> H	G <mark>F</mark> -T			D <mark>KSDKPL</mark>	QFISDNP-VF	<mark>NFEALID</mark> YED	K <mark>WG</mark> VED <mark>KL</mark> SQ
VD063723.1		<mark>FD</mark> PQ	SPMDHWLRRH	GF-T			<mark>DKTAAP</mark> L	KFVSDNP-VF	NFEAIID <mark>K</mark> ED	K <mark>LNVED</mark> KLSQ
VDO44040.1		<mark>FDPQ</mark>	SPMDHWLRRH	G <mark>Y</mark> -E			NTAKPL	TFVSEVP-GY	TFEALIDPEN	KWGVEDKLSQ
CAD6198090.1		FDPQ	SPMDHWLRRH	GF-H			AEKKTPL	EFVVDNP-LF	SFSAIIDEED	KLNVEDKLSQ
KAF8373880.1		<b>F</b> DPE	SPMDHWLRRH				DDKAGPL	EFVSSNP-LF	SFSAIIDAEG	KWNVEDRLSQ
XP_002632400.2			SPMDHWLRRH	GF-N			DKKAGPI		SFQAIIDPED	KLNVEDKLSQ
RDD39080.1		ES	SFVLDWIY <mark>R</mark> F	AS-Q	TYTKW	EKTTLVD			KFEAKINQ	NLLPKDQLSQ
XP_001632619.1		TD	NHYIPWLKKT	GA-S	SLTRF		EGGVKL	LFEDAT-GGE	PMEVTIDEGN	KLDSVDKLSQ
XP_020895242.1			SMIASWITTH SWVSGWLRRY	GK-S		EKLGF	<mark>NK</mark> <mark>V</mark>	VFNDEI-ESE IDGSSK-EKD	KFEAVIDE	K <mark>LPIQDK</mark> LSQ DLSDVDKLSQ
XP_027059688.1		<mark>QDSET</mark> NAA	SWVSLWLKRY	AQ-S		EQLEVQG		VGSGSK-END VGSGSK-DLE	NLEIMFD <mark>KEK</mark> TLELMFDOEK	MLPAVDKLSO
XP_029213515.2 GF016554.1		ERTMD	SPLKSWLSLH	AQ-A GL-Q	TVOKE	TKLFSEEDOO	RSARGETILG		EFVCNVDPNN	KFNLEDKLSO
RUS89945.1		LOEPN	SPLKSWLSAH	GL-R		NELFSEEEQQ	RSVKGETILG	GFKLNF-GLD	SFVCHVDPEN	KFPIEDKLSQ
GFR80859.1		DOEHTVD	SPLKTWLSAH	GL-R		TKLFSEEEOL		GFKLNF-GKE	EFLCAVDPON	DFSIEDKLSO
XP_005106142.1			SPLMSWVAFH	GK-N			TGPN	TFTFSI-GGK	EVKALIDSEN	OFDVODKLSO
CAG5118574.1		LYHQK	SPLKTWVALN	GR-R	TANKF	SQLFPDEVKR		IFDVNL-GQG	HVKALIDPEN	DFCIQDKLSQ
XP_013069769.1		OYIHT	SPMKTWVALH	G <mark>A</mark> -K		CNIYNDKDIP	<b>EDTYFMKQPM</b>	NFTVNL-NGK	DIOTILDPCN	KFNIKDKFSM
XP_013069770.1		HFLLD	SPLRTWVALH	G <mark>S</mark> -R		SKIYSEENQL		HFTVNL-TGQ	DVDAIIDPDN	QFSIQDKFSQ
кан9514813.1		<mark>K</mark> YLLE	SPLKTWVALH	G <mark>S</mark> -K	TVVNF	SKIYHEDDSL	PNSYHLKQPL	HFTVNL-NGQ	<b>DIDAIIDPEN</b>	<b>QFCIEDKFSQ</b>
XP_033638319.1		APLKRVS	EIIHGWCRTH	GVEA	S <mark>LNK</mark> V	QDTSN-R	TSKGAAF	KFNIGSTPQ-	E <mark>VFIDPK</mark> N	EMALLDKLSQ
XP_022095223.1		<mark>K</mark> PITQVS	QLIHQW <mark>SR</mark> TH	GVEA		QDLSA-K	<mark>TPEGGTM</mark>	TFDVGAKPLE	AYFQDFDIAE	E <mark>KSLLDK</mark> LSK
XP_038051194.1		<mark>KPLKR</mark> VS	QVIHQWCRTH	GVEA		QDLSA-R	<mark>TPSEGVM</mark>	TFDVGATP IE	AYF <mark>K</mark> DFD <mark>ST</mark> D	E <mark>KSLL</mark> DKLSK
ACO15530.1		<mark>EE</mark> LLQ	SPL <mark>K</mark> AWLY <mark>K</mark> H	GM-D		ND <mark>K</mark> LT	<mark>S-PESPL</mark>	TFMKDTQH	EFEANMDN	KLLESDQLSQ
XP_040566914.1		FDVMQ	SPLKAWLQRN	GM-V			MGKEDSL	IFM <mark>KNTK</mark> H	EFEARIDS	QLDEADQLSQ
VDP33652.1		<b>LDHS</b>	SPVDLWLRGN	AA-S	SWERF		<mark>NR</mark> QPL		SIEVHIDVER	MLDEKDTLSQ
PAA53847.1		QRP	DALSEWVRKY	GR-S	SLKHY	LAERD	<mark>-AQP</mark> M NSFKKTS		SISAHIDPDK	RYQPHDQLSQ
KNA13008.1		KSEKE	SLLKSWLMAN	SA-P SV-P			GDFKKPA	SFSIVDGQ KFSITNGR	<mark>K</mark> FEAYIDPEN TFEAYIDPEN	EYGNNDKFSM
CAF0/15/50.1		IIERE	SATMAMENTAL	GK-D			SGFNKCL		QFDAYIDPDN	AYPNNDKFSM QFSPQDKFTM
CAF1119542 1			CDI.EDWI.EEH	GR-G			SGFDRKL	VFAGAOHSED		EFKPSDKFSQ
CAF1301217.1		PSK	GPLEDWLRVH	GR-G			TCFERKL			QFKPSDKFSQ
CAF3941029.1		PSK	GPLEDWLRVH	GR-G		KKLEM-S	TGFDRKL	KFAGAQHYED		QFKPSDKFSQ
CAF0867361.1		PSK	NPLDOWLKVH	AK-G		OKLES-S	SDFKRKL	VFA <mark>SAO</mark> HHED		EYKPSDKLSQ
UJR16523.1		P <mark>SK</mark>	NPLEQWL <mark>K</mark> TH	AK-G		QKLEL-S	GDYROKL	VFASAQHHED		<b>EFKSSDKLSQ</b>
CAF1340180.1		<mark>PSS</mark>	NPLEKWLKVH	AR-G	TVEOF	KKLES-S	GDYTKKL	IFSSAOHHED	<b>DFEAYIDPNN</b>	EFKHSDKLSQ
CAF1025683.1		<mark></mark> PSN	TPLEQWL <mark>K</mark> VH	AQ-G GA-S	TVEQF	KKLES-S	GD <mark>YKCK</mark> L	IFA <mark>S</mark> AQHH <mark>ED</mark>	DFEAYID <mark>PNN</mark>	E <mark>FK</mark> HSD <mark>K</mark> LSQ
ALS04255.1		<mark>S</mark> AAA <mark>R</mark>	GPLSAWITQH	GA-S	TMHEF	E <mark>KIER</mark>			<mark>K</mark> FPAYVDVDE	KYNINDKISM
XP_023329171.1		<mark>S</mark> AVAH	GHLSSWI <mark>K</mark> QH	GD-S	TMVEF		AQF <mark>RR</mark> PI		KFPAYVDVDE	KYNINDKISM
KAH3870454.1		<mark>K</mark> TG	SPLELWIKKN	GW-R			NSFTGPV	PFMQES-ENT	KFKITIDPGQ	QFNIVD <mark>K</mark> LSQ
XP_045201158.1		PSG	SPLELWIKKH	GK-R			NGFIGPV		KFEIYIDPDH	NFNMVD <mark>K</mark> LSQ
XP_UU9U533U8.1		SKSPT	TE LEMMTKTH	G <mark>R</mark> -N GM-A	TLKAF		<mark>NNFMGP</mark> L CEPGAL		SFEAYIDPEN	KFSIVDKFSQ
XP_033096127.1		DDEVPPD	COLUCIA COL	GM-A	TIEKF				SFRAFIDPEK	QLSLTDKLSQ
AF_U13/03/98.1			SDID SWIT MEN	G <mark>I-A</mark> GG-D			<mark>NNF</mark> KNPL SKKNRL		<mark>K</mark> F <mark>R</mark> AFIDPEN AYEAVIDAKN	<mark>K</mark> FSHVD <mark>K</mark> LSQ EFNMAD <b>K</b> FSQ
00724824 1		KNEHD	SPILESWIMEY	GG-D		ETMI.R	AEKNRL	VFKEGNH	AHEAVIDPRN	QFSIADKFSQ
CAD5123161 1		DKKE	SPLTSWIOKO	GK-P		GELEK-S	DGRGPI	SFSEELK	PFTAKIDT	SFSTVDRLSM
ELT97609.1		KEG	TPLTLWLKKH	GH-S	SVKRY	NELLN-S	PDGIGPL	EFKIPGK	TLRAYIDPDK	KLSEVDKLSQ
XP_009013880.1		<mark>HE</mark> G	TPLQIWLKRH	G <mark>H-S</mark> GA-R	TIVKY		GGVGPI		VFDAYIDVDN	KFKPVDKLSQ
KAI0233246.1		<mark>V</mark> GG	PPLASWIKKH	GL-A	SVKKY	ROLEA-A	GG <mark>V</mark> GPI		RFTAFIDRON	QFAPVDKFSQ
XP_029642194.1		H <mark>S</mark> G	TPLQMWL <mark>KK</mark> Y	GV-A	SVRKF	DQLDS	<mark>KFV</mark> GPL	TFQGRF-SQL	NFQVNID <mark>PE</mark> N	KFPVEDKLSQ
NP_001171747.1		D <mark>K</mark> DK	<mark>NP</mark> FAAWLA <mark>K</mark> F	G <mark>K-A</mark>	SLNAF		G <mark>SK</mark> SPL	KFTGET-PKH	NFEAFIDPDD	<mark>KFG</mark> IED <mark>KL</mark> SQ
CAH1781438.1		<mark>ENK</mark> DG	TPLENWVKKH	G <mark>L</mark> -S	SVMKF	EQLENLG		IFQGAS-PKH	TF <mark>E</mark> AFID <mark>PQ</mark> N	EYSILD <mark>K</mark> LSQ
XP_013382323.1		<mark>H</mark> DG	DALQLWL <mark>RR</mark> H	GS-S GT-A	SVQ <mark>K</mark> F		KGREPI	TFQAET-PRH	NIEALID <mark>PE</mark> N	N <mark>FGIVD</mark> KFSQ
XP_033759917.1		<mark>K</mark> EG	GPLQLWL <mark>KR</mark> H	GT-A	SLEKF		<mark>neyk</mark> gpv		KFNAFIDPEN	RFNLADKLSQ
XP_041373453.1		AACSH	SPLRAWLQKH	GA-P	TV <mark>KK</mark> F		NNFSGPL		SFAAYIDPEN	NFSLPDKLSQ
XP_046548515.1		<mark>QV</mark> G	TPLQMWLKKH	GQ-P	TVSKF		NNYSGPL		NFDAYID <mark>PE</mark> N	KFSMADKFSQ
XP_047034441.1		TTEKRRL	SPLTSFMCSY	A <mark>K</mark> -S AT-T	SLDKF		GDFTKPV		KFVAYIDPEN	KFCIEDKLSQ
CAB3245311.1		SIEQRRL	SPLKSWLATH	AT-T	SLEKF		GDFSKPM		KFVAYIDPDN	KFCIEDKLSQ
AP_U11549456.2		NIEQRRI	SPLESWLCNH	AK-T GK-S	SLDKF SLDKF		GDFKKPM		K FVAYIDPED	KECIEDKLSO
AF_U45/014/2.1		SLEQKKI	CDI POUT CETT	GK-S		T DYTE	GDFEKPI G <mark>NF</mark> DKPI	LFTAET-PQR	K FVAYIDPDN	KFCIEDKLSQ
XD U3633371.1		SIEQRRI	SPLIKSWLCTH	GK-S		T.AMN	GNEDKPI	VFSAET-PQR LFSAET-PHR	<mark>K</mark> FVAYIDPEN KFVAYIDPDN	NFCIEDKLSQ TFCIEDKLSQ
AC015530.1  XP_040566914.1  VDP33652.1  PAA53847.1  RNA13068.1  CAF0715750.1  CAF0950609.1  CAF1119542.1  CAF3941029.1  CAF3941029.1  CAF3941029.1  CAF1301217.1  CAF3941029.1  CAF1340180.1  CAF1025683.1  ALS04255.1  XP_023329171.1  KAH3870454.1  XP_045201158.1  XP_009053308.1  XP_033096127.1  XP_033096127.1  XP_033096127.1  XP_013785798.1  GAU97340.1  OQV24824.1  CAD5123161.1  ELT97609.1  XP_009013880.1  KA10233246.1  XP_029642194.1  NP_01171747.1  CAH1781438.1  XP_033759917.1  XP_013382323.1  XP_033759917.1  XP_041373453.1  XP_046548515.1  XP_047034441.1  CAB3245311.1  XP_011549456.2  XP_045761472.1  XP_046968321.1  XP_046529909.1  RVE42816.1  KAF9415294.1  XP_045897307.1			SPLKSWICTU	AQ-S		I.E.W.K	GDFSKPM GDFNKPM GDFTKPM	LFSAET-POR	KFVAYIDPEN KFVAYIDPEN	KFCIEDKLSQ
RVE42816.1		NKEORRI	SPLKSWLCTH	GQ-S		IEMN	GDETKPM	LFTAET-POR	KFVAYIDPEN	OFCIEDKLSO
KAF9415294.1		SIEORRI	SPLKSWLCSH	AH-T		IEMN	NDFTKPM	LFTGET-POR	KFVAYIDPDN	KFCIEDKLSO
XP_018897307.1		SKENRRI	SPLRAWLCTH	AM-S			AGFHTPL		KFVAYIDPEN	KFSVEDKLSQ
										×

XP_019763455.1	 SKENRRL	SPLRSWLCTH	AQ-S	SIDTF	NELEK	·HNYDKPL	LFQGET-PLR	<b>K</b> FAAYIDPEK	KFSIEDRLSQ
XP 030749737.1	 SKENRRL	SPLRSWMCTH	AQ-S	SIDKF	EESIP	NDFNKPL	LFOGET-PLR	KFVAYIDPDK	KFSIEDRLSO
KAF7270051.1	 SKDNRRL	SPLRSWMCAH	$\widetilde{AQ}-T$	SIEKF	EDILIA	DDFNKPL	LFOGET-PLR	KFAAYIDPEK	KFNIEDRLSO
									~
XP_031343879.1	 SPENRKL	FPVRSYLCTH	AL-P	SLEKF	QQFQL	·TDYQ <mark>K</mark> PL	LFQAET-PMK	HFVAHIDPDN	KFAFEDKLSQ
XP_044743527.1	 SLTNRRI	SPLKAWLCTH	AQ-S	SLDKF	MQL <mark>K</mark> L	·SDY <mark>K</mark> MPL	IFQAET-PMR	KFVAYIDPDD	K <mark>FSIEDK</mark> LSQ
XP_018319432.1	 SQVNRRK	SPIRAWLCAH	AW-S	SLEKF	QQLEL	·TDYSMPL	IFQAET-PQR	<b>K</b> FVAYIDPEN	K <mark>LALEDKL</mark> SQ
XP 026466152.1	 SODNRRI	SPLRAWLCSH	AQ-S	SLDKF	OOLAL	SDYKTPL	IFTAET-PLR	KFVAYIDPED	KFSVEDKLSO
XP 022913687.1	 SLRNRRI	SPLRAWLCTH	AL-S	SLEKF	OOLOL	TDFAKPL	LFOAET-PMR	KFVAYIDHDN	KFAIEDKLSÕ
KAF5298473.1	SLKNRRL	SPLRSWLCTH	AL-P	SLEKF	OOLEV	TDYOKPL	IFOAET-PMR	KFVAYIDPDN	EFALEDKLSO
VEN57246.1	 <mark>SQDNRRK</mark>	SPLRAWLCAH	AL- <mark>S</mark>	SLEKF	QQL <mark>S</mark> M	· <mark>TDYSMP</mark> L	LFQAET-PMR	KFVAYIDPDN	<mark>K</mark> FNIED <mark>K</mark> LSQ
XP_045472083.1	 SQEN <mark>RR</mark> L	SPLRAWLSSH	AC-T	SLEKF	QQLEI	GDFTNPL	IFQAET-PMR	<b>K</b> FVAYIDPDN	QFTLEDKLSQ
XP_017768645.1	 SQENRRI	SPLRSWLCTH	AL-S	SLEKF	QQLEI	TDYSKPL	LFQGET-PLR	KFVAYIDPEN	KFALEDKLSQ
CAH1369701.1	 SODNRRI	SPLRAWLCTH	AL- <mark>T</mark>	SLEKF	OOLEV	TDFGKPL	IFOAET-PLR	KFVAYIDPEN	RFALEDKLSO
XP_028136465.1	 SOENRRI	SPLRAWLCTH	AL-S	SLEKF	OOLEV	SDYSKPL	IFOAET-PMR	KFVAYIDPEN	KFAIEDKLSO
	SKDNRRI		AL-S		~~				
XP_023014099.1		SPLRAWLCTH		SLEKF	QQLEV	·TDYSKPL	IFQAET-PLR	KFVAYIDPEN	KFNIEDKLSQ
XP_019875064.1	 SQDNRRI	SPLRAWLCSH	AL- <mark>S</mark>	SLEKF	QQLQV	·TDYSKPL	IFQAET-PLR	KFVAYIDPDN	QFSIED <mark>K</mark> LSQ
CAH0557060.1	 SQVNRRI	SPLRAWLCTH	AL-S	SLEKF	QQLEL	·TDYNKPL	IFQAET-PLR	<b>K</b> FVAYIDPEN	KFNIEDKLSQ
XP 037924690.1	 SLDNRRL	SPLRSWLCTH	AQ-S	SLDRF	OKWVA	GGMKDPL	IFSSET-PLR	KFVAYIDPEN	KFAIEDKLSO
XP_043863257.1	 SKLNRRL	SPLRSWMCTH	$\widetilde{AN} - S$	SLEKF	ÕEWRD	·AGMKDPL	IFSSET-PLR	RFVAYIDEEO	KFAVEDKLSÕ
XP 039965629.1	SOLNERL	SPLRSWMWTH	AS-S	SLDHF	KAWKK	EGMOGPL	IFSSET-PLR	RFVAYIDPEN	KFALEDKLSO
_				_					
XP_001989827.1	 S <mark>KLNRR</mark> L	SPLRSWLCTH	AN-T	SLDRF	QEWRD	· <mark>AGMK</mark> DAL	VFSSET-PLR	RFVAYIDQDD	<mark>K</mark> FAIED <mark>K</mark> LSQ
XP_037896985.1	 SKNNRRL	SSLRSWLCTH	AT-T	SLEKF	LEWGE	·KGMRDPL	IFYSES-GLR	RFVAYIDPDN	QFAIEDKLSQ
XP_046805044.1	 SKRNRRL	SPLRAWLCTH	AS-T	SLEKF	EEWVE	KGMSDPL	LFSSET-PLR	RFVAYIDPEN	KFAIEDKLSO
KAG5681791.1	 SRKNRRL	SPLRSWLATH	AS-T	SLEKF	OYLSE	HGFDKPL	MFTAET-PLR	KFVAYIDPDN	KFAIEDKLSO
XP_031629647.1	 SADORRI	SPLKAWLCAH	ATDS	SLDRF	LKWQE	AGMKDPL	IFSSET-PLR	KFIAYIDTEN	KFGIEDKLSQ
_									
KAG4077403.1	 SLDNRRI	SPLKAWLCEH	AN-S	SLDRF	LEW <mark>K</mark> N	·NGMKDPL	LFSSET-PLR	KFVAYIDPDN	<mark>K</mark> FAVED <mark>K</mark> LSQ
XP_039430644.1	 SRKNRRI	SPLRAWLCEH	AD-T	SLEKF	QNLQE	· <mark>TGLDKPI</mark>	IFSSET-PLR	<b>K</b> FVAYIDPEN	QFAIEDKLSQ
XP_040221405.1	 SLDNRRI	SPLRAWLCEH	AN-T	SLAKF	ONLKE	IGLDKPL	IFSSET-PLR	KFVAYIDPEN	NFAIEDKLSO
CAA9998239.1	 SKTNRQL	SPLRAWLCNH	AH-T	SLEKY	HOLEL	CGTNRPL	MFSSEL-PLK	KFAAYIDPEK	KWSVEDRLSO
KAF6203636.1	 SKTNRQL	SPLRAWLCNH	AH-S	SLDKF	NOLEL	CGTTRPL	MFQSEM-PLK	KFVAYIDPEK	RWSVEDRLSO
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KAG6800307.1	 SKVNRRI	SPLKAWLCAH	AS-N	SLTRF	QQLEI	·SDFRDPI	LFQGET-SLR	KFVAYIDPED	KFGVEDKLSQ
XP_014230599.1	 SQ <mark>K</mark> NRRI	SPLRAWLCAH	AS-N	SLEKF	EQL <mark>R</mark> V	<mark>S</mark> GYEEPL	IFRAET-PMR	<b>K</b> IVAYIDPEN	RFAVEDKLSQ
KAH0947068.1	 SQTNRRM	SPLRAWLYAH	GS-S	SLAKF	QHLEI	CGFHQPI	VFQAET-SVR	KFVAYIDPEN	KLAVEDKLSQ
XP_043590797.1	 SKVNRRI	SPLRAWLCAH	AR-N	SLAKF	QQLEI	AGFHEPI	LFQAET-PLR	KFVAYIDSDN	KFAIEDKLSO
XP 034949379.1	 SKINRRI	SPLRAWLCAH	AD-S	SLRKF	LOLKK	TSFREPI	IFOAET-PMR	KFVAYIDPDD	KFAIEDKLSO
_		SPLRAWLCAH	AS-S	SLAKF		KGFOEPT	LFOAET-PLR	KFVAYIDPED	KYPVEDKLSQ
XP_012275169.1	 SQANRRI				QQLQE				
XP_043464528.1	 SQNNRRI	SPLRAWLCAH	GS-S	SLAKY	QQLEV	<mark>TGFREP</mark> I	VFQAET-PLR	<b>K</b> FIAYIDPEN	<mark>K</mark> FVIQD <mark>K</mark> LSQ
XP_014220045.1	 SQAN <mark>RR</mark> L	SPLRAWLCAH	GT-S	SLAKF	QQLEI	TNFKEPL	MFQAET-PMR	RFVAYIDPEN	KFAVEDKLSQ
XP_011160605.3	 SOTNRRM	SPLRAWLCAH	AS-N	SLAKF	OHLEI	TGFREPI	LFOAET-PMR	KFVAYIDPED	KFAIEDKLSO
XP_046741789.1	 SQANRRI	SPLRAWLCAH	AS-S	SLAKF	QOLEI	<mark>TGFHEPI</mark>	IFQAET-PLR	RFVAYIDPED	KFAIEDKLSÕ
VVC24333.1	 SIDNRRL	SPLRSWLCTH	GI-S	SLDKY	MOLEA	AGFDTPL	VFOAET-PLR	KIIAYIDPEN	KFSVTDKLSO
KAF0770685.1	 SIIN <mark>RR</mark> M	SPLRSWLCTH	AM-S	SLEKY	EQLEE	·SGFNTPL	IFQAET-PLR	RISAYIDLGN	KFSVTDKLSQ
XP_015365968.1	 NIAN <mark>RR</mark> M	SPLRSWLCSH	AM- <mark>S</mark>	SLEKY	QQLEV	A <mark>G</mark> FHAPL	IFQAET-PLR	RISAYIDPDD	KLSVTDKLSQ
XP_029341681.1	 STVNRRK	SPLRAWLCSH	AM-S	SLEKY	QQLEA	AGFGTPL	VFQAET-PLR	RISAYIDPED	KLSVTDKLSQ
XP_026292519.1	 SOTNRRL	SPLRSWLCTH	AH-S	SLEKF	OOLAL	TGYHSPL	IFOAET-PMR	KFVAYIDPDD	KFAIPDKLSÕ
XP_034238427.1	 SOKNRRL	SPLRSWLCTH	AH-S	SLEKF	QQLAL	·TGYQHPL	IFQAET-PMR	KFVAYIDPDD	KFAIPDKLSO
XP_024081347.1	 SKDNRRI	SPLRSWLCNH	AY-S	SLEKF	OELEI	SGYKDPL	IFQSET-PLR	KFVAYIDHEN	RESTEDELSO
XP_014283188.1	 SKDNRRI	SPLRSWLCTH	AS-S	SLEKF	HQLEA	GGYHNPL	IFQSET-VLR	KIVAYIDPED	DFCIEDKLSQ
RZF32743.1	 SKDNRRI	SPLRAWLCTH	AQ-S	SLDKF	QQLEL	·AGYHTPL	IFQSET-PMR	KFIAYIDPDD	RFSIEDKLSQ
CAB3380083.1	 <mark>SVDNRRK</mark>	SPLRAWLCRH	AD-T	SLEKF	QQL <mark>K</mark> S	·TNFTEPL	TFQAET-PMR	KFVAYIDPDN	K <mark>FSIEDK</mark> LSQ
XP_046989067.1	 SRDNRLI	SPLRAWLIAH	AN-A	SLKKF	EKLET	GGFHOPL	LFOAET-PMR	KFVAYIDPDN	KFSIEDKLSO
GFG38476.1	 SQTNRRI	SPLRAWLSAH	AS-S	SLAKF	QQLEV	SGYOKPL	IFOAET-PMR	KFVAYIDPED	KFSVADKLSO
CAD7446618.1			AS-S	SLEKF			~		
	 SQENRRK	SPLRAWLCAH			TQLEA	SGYHTPL	~	KFAAYIDPDD	KFAITDKLSQ
KAG8226740.1	 SVENRRR	SPLRAWLCTH	AH-S	SLTKY	QQLET	SGFGTPM	LFQAET-PMR	KFVAYIDPEN	RFSVTDKLSQ
XP_046392794.1	 SVENRRR	SPLRAWLCTH	AQ-S	SLTKF	QQLQ <mark>K</mark>	· <mark>TGYSSPM</mark>	LFQAET-PMR	KFVAYIDPEN	RFSVTDKLSQ
XP_046459477.1	 NMRTLER	SPLKAWLHRH	GS-I	SLTKF	ERLEV	HGFQQPL	TFPMEG-PFR	<b>QFVAYIDPDN</b>	KFSLTDKLSQ
XP 043227363.1	 <mark>TPEK</mark> LHM	SPLSAWVCRH	GS-G	SLTKL	MOLKV	·SDF <mark>K</mark> APL		<b>R</b> FVAYID <mark>PE</mark> N	
XP_018006429.1	 TREIVKQ	SDI.KAWI.WBU	CH_D	SLIKY			VFQGET-PLR		
_		SPL <mark>K</mark> AWLVRH SPL <mark>K</mark> AWLVRH	GII C	OTATI					
AWH57222.1	 SQEII <mark>K</mark> H	SPLKAWLVRH	GH-S	SIAKY	AQLEV	·ADFQAPL			KFNEEDKLSQ
XP_042865604.1	 HHEIIRM	SPLKAWLVRH	GS-S	SLAKF	AQLEV	·A <mark>N</mark> FQA <mark>P</mark> L	IFQGET-PMR		HFNDED <mark>K</mark> LSQ
XP_045119740.1	 LQEML <mark>K</mark> L	SPLKAWLVRH	GH-S	SIVKF	AQLEV	· <mark>SDFQAP</mark> L	VFQAET-PMR	<mark>R</mark> FVAYIDPDN	<b>R</b> FSVEDKLSQ
XP 045613573.1	 L <mark>OEVLK</mark> V	SPLKAWLMRH	GH-S	SAGKF	AQLEL	SNFQAPL		RFIAYIDPEN	KFSEEDKLSO
XP 021963432.1	 TIENQVK		GS-D	SYDKF	KQLET	·RGFKMPL	LFTAET-PMK		
CAG7730563.1	 CPVSQKR	SALTGWLCNH	GS-D GL-S	SLEKL	VTLQE		LFEGET-PLR		
C110 / / 50505.1	CI VOQICIC	OTTE TOWN CIVIT			4 T T Z T	HOLDALD	TI TOUT I LIK	T ANT TOE RIN	T TIDELDO

3	61										
KAH8855123.1	ANVLQ	QMIN	VYSYEML <mark>TK</mark> Q	LQQNFIRVHG	MWFELHSGDT	LVYN <mark>R</mark> QNK	SFIPINEATI	SSLIDE	V		
KAH9593836.1 VDP71164.1	ANVLQ INVLO	QMIH OMSN	VYSYEMLTNQ VYAYPLLAEK	LAQNLL <mark>R</mark> IHG LAAKALRVHG	IWFELYSGRV FWFSVHAGOM	LIY <mark>SR</mark> LN <mark>K</mark> YVYNPORE	AFLPITEETI GFVPITEETL				
TPP65121.1	INVIO	QMSN	VYSYPLLACK	LMNKELRVHG	FWFNVHTGQM	YLYSPHKQ	GFLPIIEENL	SEIMRE	TAA		
KAA0189413.1	INVLO	<b>OMSN</b>	IYSYPLLSOK	LMENEVRVHG	LWFDIHTGOM	YQFSRNKQ	AFLPINEETL	SELVRE	SSS		
KAF7258038.1	INVVQ	<b>QMSH</b>	VY <mark>SHP</mark> LLTER	FKSGTLNVHG	IWFHVHEAQL	HMYS <mark>R</mark> PRQ	SFVLITEVTI		LNC	DSRHS	
KAG5442206.1	VNVVQ	QMTN	FYCQPLLAER	LRNGSLNVHG	LWFHIHSGQL	HMFSREAQ	SFVPVTGDTL		LDS	P	
XP_030837801.1 XP_041482585.1	INVLO	QLEH QLEH	LQSYDFIGKR LQSYDFISKR	METDQI <mark>R</mark> LHA TETDQIRLHA	TFYDTFSGNV TFYDTFTGNM	YVFNQ <mark>K</mark> QG FVFNKVOS	RFNFLPTADI RFNILPTNDI		IFQ IFO	LRSS	
KRZ73557.1	IHCLQ	QLEN	IASHHFLOOR	LLEGLAKLHA	VWFDVTEGKM	YYFSRKHE	EFVDINKDTI				
OUC42378.1	IHCLO	QLEN	IASHHFLOKR	LLEGLAKLHA	VWFDVTEGKI	LICEKNKV	QYGKLLITNE		LNT		TLHVY <mark>G</mark> LTES
CDW52968.1	INCLQ	QLEN	IA <mark>SHN</mark> FMA <mark>S</mark> F	L <mark>K</mark> SD <mark>K</mark> AFLHA	LWL <mark>N</mark> FEDCVV	HYF <mark>S</mark> KKKK	KFVPITSESA	<b>AELQSE</b>			
KHJ46144.1	INCLQ	QLEN	IA <mark>SHD</mark> FMASI	L <mark>K</mark> SD <mark>KAR</mark> LHA	LWL <mark>N</mark> FEDCMV	HYFS <mark>KKKK</mark>	QFVAITSDSV				
VZI00627.1	VNVLQ	QMAN	VYSHPILKDA	IALGNV <mark>R</mark> VLG LGDELVNLHA	MWYNISTADV	YLYSWLRR	KFVLVDESSS RFIKLTEESA		YGS VGK		
XP_014681778.1 VDM45293.1	VNVLQ INTLO	QMEN QMAN	ISSLSFLQTH ITTHGFLAEI	LKTKOADLHA	WWFNL <mark>TTGE</mark> Y FWF <mark>QVENAE</mark> M	HMF <mark>SPRDE</mark> HIF <mark>SKK</mark> QH	RFVIINEKTV		VEH	HKD	
KAF8385568.1	INVLO	QLVN	IASHDALKEA	FDOGKLHIHG	MWFDVYKGED	YLFSKEKR	OFVIIKEDTF		LHR	RCNVPLGECP	
PI076965.1	INVLQ	QLEN	IASHEFLKQY	FESGNLFLHG	MWFDIY <mark>S</mark> GDD	YLF <mark>SK</mark> DKK	RFILID				
VDL66086.1	INVLQ	QLVN	VSSHEFLQSY	FE <mark>SGLVFVH</mark> G	MWFDIY <mark>NG</mark> DD	YLFS <mark>K</mark> DKK	QFVLIDESTV		LES	RCGPGLSSSE	TA <mark>K</mark> A
CAD6194288.1	VNVLQ	QLVN	IASHSFLSEH	FEKKKLFVHG	MWFDIYKGEV	YIFSREKK	RFIVIDDNSI		LSQ LER	YAPAEPNPPK RCPLPEDKAG	DE DVVIQNLH
XP_045095542.1 EGT43056.1	INVLO	QIMN QLIN	ISTHEFLKDY ICSHEFLKEY	LEAGNLHLHG LESGRLHIHG	AWFNIYDGEV MWFDIY <mark>K</mark> GED	FLFSKDRK YLFSKDKK	RFVVIDEKTV RFVVIDEKTV		LNT	RYPLPEDQDG	PVAFAQSN
CAB3400100.1	INVLQ	OMIN	ISSHEFLKEY	LENGKLHVHG	MWFDVYKGED	YLFSKDKK	RFIVVNEETV		LNA	RCPVPTGENE	KVAITHSN
KAF7639475.1	INTLQ	QLTN	IASHEFLREH	<b>IEKRLVGLQA</b>	FWLDIFTGEL	YFF <mark>SRR</mark> QE	SFVPIDEENS		ALC	SVDD	
CAD5226593.1	INTLQ	<b>QLVH</b>	VA <mark>S</mark> HGFLRDY	LL <mark>EEK</mark> VHLHA	LWFDVY <mark>KGD</mark> M	HMF <mark>SRRK</mark> E	RFVEIDEDSA		VQT	NY <mark>QEP</mark> I <mark>K</mark> AAA	<u>Q</u> V
XP_024510735.1	INTLQ	QVLN	IASHEFMFDY	IANNEVFIHA	MWFDIYTGNM	YMFSKPEQ	SFKMIDEMNT		VED	EM <mark>KGMK</mark> NNHQ	KSNNCC
VDN24694.1 KAH7730640.1	INTLO	QMEN QLVH	CASHGFLADI VASHGFLREF	LA <mark>NK</mark> AA <mark>D</mark> LHA LEOGDVHLHA	MWFDIFA <mark>GET</mark> MWFDIY <mark>TGE</mark> M	YLF <mark>SRPRR</mark> YLFSRERO	KFILIDEKTV RFVVVNEQTS		V <mark>K</mark> Q IHR	HVA	VOAANGAS
TMS38138.1	INTLO	QLEN	IASHGFLREF	LESGSVNLHA	MWFDIYTGNM	FMFSKPRK	MFVLVDEESV		VDP		VQAANGAS
XP_013290959.1	INTLQ	QLEN	CASHGFLTEF	LEKKTVDLHA	MWFDIY <mark>TGE</mark> M	YLF <mark>SKPRR</mark>	KFILVNEDTV		VNQ	HKA	
RCN50005.1	INTLQ	QLEN	CASHGFLTEF	LE <mark>KK</mark> TVDLHA	MWF <mark>DIFAGE</mark> M	YLF <mark>S</mark> KPRR	KFILIDEGTV		<mark>V</mark> NQ	HKA	
KJH42542.1	INTLQ	QLEN	VASHGFIVER	LEQKTVNLHA	MWFDIF <mark>TGE</mark> M	YLFS <mark>KPRR</mark>	MFILIDENSL		VEQ	C	
VDM64099.1	VNTLQ	QLEN	IASHGFIAEH IASHGFITEF	LEKRTVDLHA LEKKTVDLHA	MWFDVY <mark>TGE</mark> M MWFDIFAGEM	YLFSKPRR YLFSKPOK	MFVVIDEDSV EFVLIDEGSV	DLLKKE DELEKO	IEE IMK	HKA HVA	
VD063723.1 VD044040.1	INTLO	QLEN QLEN	MASHGFITEM	LEKKTVDLHA	MWFDIFAGEM MWFDIFAGEM	YMFSKPRK	QFILIDEKSV		IEO	HKA	
CAD6198090.1	INTLO	<b>OLEN</b>	VASHGFLKEF	LETHAVNLHA	MWFDIYTGEM	HMFSKGKK	RFILIDESTV		IEK	TTR	
KAF8373880.1	INTLQ	QLEN	IASHGFLNEF	LESRQVDLHA	MWFDVYAGEM	YMF <mark>SKPRK</mark>	<b>QFVLIDEESV</b>		VIQ	HRS	
XP_002632400.2	INTLQ	QLEN	VASHGFLKEF	LESQTVDLHA	MWFDIY <mark>TGE</mark> M	HMF <mark>SK</mark> PNN	RFVLIEESNV		VEK	HQT	
RDD39080.1	INTLQ	QLLH	VNSYSFMKEK	IAAGTVKLYS	LWFDIKDATC	YVFNKRDK	LFQPIVSEEM		FQI	NQK	
XP_001632619.1 XP 020895242.1	VNVLQ VNVLQ	QLHN QLHN	LKSFPFISNP IGSYSFVREQ	L <mark>SKGALNLYG</mark> L <mark>RNR</mark> QLNLHA	LWFDI <mark>KEGEM</mark> LWFDIANGEM	YMF <mark>SRK</mark> QK YMFSKEKT	KFVLINKDTV SFQLVNEDTI	NNLCSE KTIFKS	VD-		
XP_027059688.1	VNVLQ	OMON	IRSYGFVRNK	LDEGSVQLYG	LWFNIGEGEM	LLYSKTRK	RFVVINKETG				
XP_029213515.2	VHVLE	QMKN	<b>VKSYGFVREK</b>	LDTKALQVHG	LWFDIGGGEM	FMY <mark>SK</mark> MHN	RFIVVNEQTL	_	LTN	EVIDKSLFS-	
GFO16554.1	FHCLQ	QASN	VASYPLLQPY	L <mark>KKGEVK</mark> IHA	MWFDV <mark>SKGQ</mark> M	HLF <mark>SPTNG</mark>	YFI <mark>PIEE</mark> TSA		ITS		
RUS89945.1	FHTLQ	QASH	IASYPILRPY	IATGDIR VHA	MWFDI <mark>PR</mark> GEM	HLF <mark>NASR</mark> G	HFAPVTESEL		EQS		
GFR80859.1	FHCLQ	QTSN	VASYPILQPY	IASGDVRVHA	MWFDIFRAQM	FMFSRTRG	HFVAIEESSV RFVIVTEENL		AKS		
XP_005106142.1 CAG5118574.1	INCLE	QASH QASH	VSSYPFLHSL VTTYPLLOPF	IQSGELTVNA IKTGELQIHA	LWF <mark>DVQSG</mark> YV MWYDVYTGNV	YMF <mark>SPK</mark> DE YLFSPSER	KFVIVSDSNV		ITK CGC	NSCTGVIKEK	OP
XP_013069769.1	LHCLO	QASH	VOTYPMLKPF	LDAGDFOIHA	LWYDVYTGDV	YMFSTSON	KFIEVNEKNI		IAP	LRI	<b>QP</b>
XP_013069770.1	LHCLE	<b>QASH</b>	VKTYPMLHSY	L <mark>SS</mark> GELHIHA	LWF <mark>D</mark> VY <mark>TGN</mark> V	YMF <mark>SVSQ</mark> K	KFILVDDNSF	DILMQD	<b>V</b> GE	SPPSSF	
КАН9514813.1	FHCLV	QASH	V <mark>KTYP</mark> MLHPY	VSSGELQIHV	LWY <mark>DVFTGN</mark> V	YMFS <mark>K</mark> SQR	KYILVND <mark>K</mark> NL		V <sub>ED</sub>	NVGLTC	
XP_033638319.1	VNVLQ	QLEH	LSSYRSISKR	VDSGQLSVHG	MWYDVSEDKI	YWFSRQRK	GFIEICADTI		CKR	TVRPEEEQGD	
XP_022095223.1 XP_038051194.1	VSVLQ VNVLQ	QLEH QLEH	LSSYHSIRRR LSSYRSIRRR	VIDGSLSLHG VIAGTLSLHG	MWYDIAID <mark>K</mark> I MWYDVA <b>T</b> DTV	YWF <mark>SR</mark> QRK YWFSRARR	VFLEINEENI MFLEINEDNI	EETVOD	CQP CQP	SVAD <mark>K</mark> ASQND TVTDTTTPND	I-GHKIPS
ACO15530.1	INTLV	OIEN	IYSYGFMKER	MDOHOSVAHG	LWLSLSSGEA	HFFSKKDK	AFVNVTEDNV	EELVCR			
XP_040566914.1	INTLV	<b>QMEN</b>	IYSYDFMKNR	IDDKTAFVHG	LWFSLTTGDV	HYFL <mark>KNEK</mark>	VFI <mark>NVSED</mark> NI	DNLVQR	SEE		
VDP33652.1	IHCLQ	QLEN	IASYPIIRDP	LE <mark>SGK</mark> VKIHA	MWF <mark>N</mark> IY <mark>TGE</mark> V	SLF <mark>SRKNK</mark>	KFVVVTEDTI	NSVD	==-		
PAA53847.1	VHCLQ	QMIN	LTTYPFLSER	LLQ <mark>RR</mark> V <mark>R</mark> LSA	MWFDVDSADV	YMFSRATE	RFLVICEDNI	EKLLPE	PL-		
RNA13068.1 CAF0715750.1	INTLV INTLI	QLEN QLEN	LKHYSFLKEP LKHYSFLKEP	LE <mark>TNK</mark> V <mark>R</mark> AYA LEKKEIHPYA	LWLDIY <mark>NG</mark> DI LWLDIYNGDI	LIF <mark>SF</mark> KEK LVFCFKEK	RFVKLNDESY	OKLVSD	LNA	A	
CAF0713730.1 CAF0950609.1	INTLK	QLKN	VNNYNFLRDR	ITKKLLRGYA	LWTDITTNDV	YMFSYKAK	RFVKIDESTY	NDLYKE	CDT	TNO	
CAF1119542.1	INTLE		FLTYPFLKER	LNRNELEVHA	LWTDIYKGEV	YMFSFQEK	TFVKIDESTY	KTLALQ	CV-		
CAF1301217.1	V <mark>N</mark> ALE	QLKN	FL <mark>SYP</mark> FLKDR	L <mark>NR</mark> NELEVHA	LWTDI <mark>SK</mark> GEV	YMF <mark>S</mark> FQEK	TFVKIDETSY	KTLALE	CI-		
CAF3941029.1	INTLE	QLKN	FLSYPFLKER	L <mark>NR</mark> NELEVHA	LWTDISEGEV	YMF <mark>SFKEK</mark>	TFVKIDE ISY	KTLSLE	CI-		
CAF0867361.1	VNTLE		FLSYPFLRER	LNRKELQVHA	LWTDIYKGEV	YMFSFKEK	TFIKIDENTY	NKLSLE	CNP	YK	
UJR16523.1 CAF1340180.1	VNTLE VNTLE	QLRH QLQH	FLSYPFLKDR FLSYPFLRER	LNRKELQVHA LNRKQLQVHA	LWTDIY <mark>KGE</mark> V LWTDIYKGEV	YMF <mark>SFKEK</mark> YMF <mark>SFNDK</mark>	CFIKIDENTY CFVKIDDETY	KCLAHE	CN	NK	
CAF1025683.1	VNTLE	QLRH	FLSYPFLRER	LNRKELQVHA	LWTDIYRGEV	YMFSFKEK	CFVKIDENTY	EKLSHE	CI-		
ALS04255.1	<b>VNT</b> LI	QMQN	VTTYPFMHSC	L <mark>RDGRTHIHA</mark>	LWFDVY <mark>TGE</mark> I	HCFSRKEK	TFIPVNENTV	EELIN-	==-	<mark>ELTES</mark>	AAR FKVNSNF TK NWYIRK ET
XP_023329171.1	VNTLV	QMQN	VTSYPFMHNC	LRDGRTHIHA	LWFDVYTGEV	HC <mark>FS</mark> RKEKVK	EKKEFDKNMI	KQSKKT	HSK	PIKRISIE	TKNWYIRKET
KAH3870454.1 XP_045201158.1	VNCIQ	QLEN QLEN	IAAYPFLKER IAAYPFLKDR	L <mark>SQND</mark> LLLHA L <mark>SKK</mark> DLFLHA	FWYDIHSGNV LWYDVHSGNV	FLL <mark>SRER</mark> Q FLLSKKRQ	RFVEVNERSY KFVEVNERSF		V <mark>K</mark> N VQS	KASAKILSES VECC	
XP_045201158.1 XP_009053308.1	INCVQ VNCLQ	OLHH	ISTYPFLKLK	LSKADLF LHA LMTGQLFLHA	FWFDVHSGNV	YMFSRSRK	QFIPVSDDTY		CHK	OK	
XP_033096127.1	VNTLQ	QLVN	LSTHTMIKPQ	LHDGRVRLHA	MWFDIFTGNM		RFIEIREDTI		VKH	NESKOHTETT.	TNSVKMSK
XP_013785798.1	INCLQ	QLEN	ATSHAFLKPL	LEQD <mark>K</mark> LRFHA	LWFDINTGDV	HCF <mark>SNKK</mark> E	QFVEVNDHSV	EELLVE	SDQ	NIFSGPNK	LRNLVI
GAU97340.1	VSTLH	QLEN	ITSYPFMQRL	VD <mark>S</mark> GLV <mark>R</mark> LHA	MWF <mark>D</mark> IY <mark>TGS</mark> I	FYFN <mark>K</mark> PH <mark>K</mark>	TFIEITEKNW		KDR.	EAL <mark>KK</mark> QQIFG	L <mark>RN</mark> LVI
OQV24824.1	VSTLH	QLEN	ITSYPFMORL	VDGGLV <mark>R</mark> LHA	MWFDIYTGNI	FYFS <mark>K</mark> PHK	SFIEITEENW		KER	EALNKQVKFG	MRQNLMT
CAD5123161.1 ELT97609.1	VNTLQ VNVLQ	QISH QVEN	ISAFPIIKKS ACSYDMLKDK	LEEGHI <mark>K</mark> IHA LOSGOVNVTA	LWFNTFTGDV LWFNIQTADF		EFINITEDTY RFLEVNESTI		GES AGG	Y	
XP_009013880.1	VNTLQ	QLQN	IASYPFLEDK	LESGLVRMHA	LWIDIYTGDF		RFVLVDEESY		GES	VTDY	
KAI0233246.1	VNTLQ	QLEN	IVSHGFMKEH	LGSD <mark>K</mark> VRLNA	MWFDIY <mark>TGD</mark> V	YMFSRERQ	SFIQVTKATY		GES	W	
XP_029642194.1	VNCLQ	QLQN	IATFPILHEK	LSKNQIRLHA	IWIDVRTGNV	FIF <mark>SR</mark> DEK	QFVEITERNY	LQLVRE	CFP	VD	LRNLVI MRONLMT
NP_001171747.1	VNCLQ	QLQN	ISSYGFLKDR	LESGRVRLHA	MWFDIYAGDV		RFVEINEETC		CEH	QKCHPIED	
CAH1781438.1	VHCLQ	QLQN	IASQDFLKEK IASYPFLKEK	L <mark>SKNE</mark> VHLHA LQTGKVRLHA	MWYDM <mark>K</mark> LADM LWFDIH <mark>SGN</mark> V	LIF <mark>SR</mark> QRK YIF <mark>SK</mark> MEK	QFVTVNEDNY KFVEINEENY		SMT SVK	MPDHKEMEKP	SPVWRG
XP_013382323.1 XP_033759917.1	VNCLQ	QLQN QLQN	VASYPFLKEK VASYPFLKDL	LOTGKVRLHA ISREEVKLHA	MWFDIY <mark>TGEV</mark>		RFIEINDQNI	MHLLHD	AYR	KAEKIDILEO	RRK
XP_041373453.1	VNCLQ	QLQN	IASYPFLREK	LMRDEVRLHA	MFFDIYTGNV	YMFSRKEK	QFIEICKENY		ADS	LEVNEE	
XP_046548515.1	VNCLQ	QLQN	IASYDFLREK	LH <mark>RNDVR</mark> LHA	MWFDIY <mark>TGN</mark> C	FMF <mark>SRERK</mark>	MFVEITEDNY	AHLI <mark>K</mark> D	AHS	DLH	
XP_047034441.1	<b>VNT</b> LQ	QLSN	IASYGMLKKR	L <mark>EK</mark> YDLHIHA	LWFDIY <mark>TG</mark> DI	FYFS <mark>RRAK</mark>	RFVIIDESSY		VRR.	YY <mark>S</mark>	
CAB3245311.1	VNTLQ	QLQN	IASYGMLKKR	LEKHDLHIHA	LWFDIYTVCR	YKIVTMSNRP	TFDYNDESQS		SKD	SPFMIIGIIG	RRK LIGVCGFGAY
XP_011549456.2 XP_045761472.1	VNTLQ VNTLQ	QLQN QLQN	VASYGMLKKR IASYGMLKKR	L <mark>OK</mark> HDLHIHA LORHDLHIHA	LWFDIY <mark>TG</mark> DI LWFDIY <mark>TG</mark> DI	YYFSRRAK YYFSRRAK	TFVIIDESTY KFLIIDESSY		VRR IRR	YYS	
XP_045761472.1 XP_046968321.1	VNTLQ	QLQN	IASYGMLKKR	LERHDLHIHA	LWFDIYTGDI	YYFSRRAK	RFLIIDESSY	EIILAE		YYS	
XP_026323335.1	VNTLQ	QLQN	VASYGILKKR	L <mark>EK</mark> HDLHIHA	LWFDIY <mark>TG</mark> DI	YYFS <mark>RRAK</mark>	RFILIDESTY	EEILAE		YY <mark>S</mark>	
XP_045529909.1	VNTLQ	QVQN	VA <mark>S</mark> YGMLKKR	L <mark>EK</mark> HDLHIHA	LWF <mark>D</mark> IY <mark>TGD</mark> I	YYF <mark>SRR</mark> AK	SFVIIDESTY	ESILAE	<mark>V</mark> RR	YY <mark>S</mark>	
RVE42816.1	VNTLQ	QLQN	VASYGMLKKR	T <mark>OK</mark> HDTHIHA	LWFDIYTGDI	YFFSRRAK	RFILLDESSY	ESILSE		YYS	LIGVCGFGAY
KAF9415294.1 XP_018897307.1	VNTLQ INCLQ	QLQN QLQN	VASYGMLKKR IASYGFLKKR	L <mark>EK</mark> HDLHIHA LESHDLHIHA	LWFDIY <mark>TG</mark> DI LWFDIY <mark>TG</mark> DI		RFIIIDESSY KFVEINEMTV		V <mark>RR</mark> VLR	FYS	
111 _01009/30/.1	THELL	Z T VIV	LIBIOTORIKK		THE DETTODE	TIT ON QUINT	TT A TO TIME IN T A		V III		

XP_017763451.1												
RAPTONSIL   ILLIA QUI   RAYOFLEKE LENGININA LENGIN   SEPTIMEN   PILOSE   CLUB   N. Y. Y.	XP_019763455.1	INTLQ	QLQN	IASYGFLKKR	LERNQLHIHA	LWFDIYTGEI	YYF <mark>SR</mark> GAK	RFVIIDESNF	EKLTEE	VVL	YY <mark>S</mark>	
RAPY270051.1   INTLO QUO   LAYGPLEAS LEPOINTIN   MPD1YTOE!   MPSEAL   MPS	XP_030749737.1	INTLO	OLON	IASYGFLRKK	LEKHOLHIHA	LWFDIYTGEI	YYFSRRHK	RFIVIDEENF	<b>AKLFEE</b>	VIV	YY <mark>S</mark>	
XP_031343879.1 INTLO_QOD   DAYGPLAND LEVELINIA MERLYTCEL   TYPESCAL   SVOUDENH VILLOW   VILLO		INTLO	OLON	IASYGFLKKK	LENHOLHIHA	LWFDIY <mark>TGE</mark> I	YYF <mark>SRR</mark> HK	RFVIIDEEHF	DKLFKE	VIV	YY <mark>S</mark>	
XP_04474557.1	XP 031343879.1	IHTLO		IASYGFLKKR	LETDOIHIHA	MWFDIY <mark>TGE</mark> I	YYF <mark>SROAK</mark>	RFVVIDENNF	DRLVGE	VER	YHM	
XP_01819482.1   MAID   GUD   LAYGHUES   STOCKHOOL   MATCHING   M	XP_044743527.1	INTLO	OLON	ISSYGFLKKR	LEOYDLHIHA	LWFDIYTGEI	YYF <mark>SRRAK</mark>	<b>OFVOINEHNY</b>	NVLLQE	IQT	YY <mark>S</mark>	
XP_024466152.1   MTD   QC   LAYGRED   LETTER   MFD17105   YF5504   TTUTOTT	XP 018319432.1	INALO		IASYGFLKSR	LEKHOLHIHA	LWFDIY <mark>TGE</mark> I	YYF <mark>SROAK</mark>	OFVIINEDNI	ETLMDE	VEN	YYM	
XF_022913667.1	XP 026466152.1					LWFDIY <mark>TGE</mark> I			NYLMKE		YY <mark>S</mark>	
RAFS294473.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPITIORING CELLE VE YN- XP_04472083.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_04872083.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048136465.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048136465.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_049875064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_049875064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_049875064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_049862064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_049862064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_049862064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGEN CELLE VE YN- XP_048605064.1 INTLO QUON RAYOFLESS LITTORHER MYDITYCE: YFSCAR SPIVINGE		VNTLÕ		IASYGFLKKR	LETNELHIHA			TFVCINEESI	DKILEE	VEE	YY <mark>T</mark>	
NEWLY   1976	KAF5298473.1	INTLO		IASYGFLKKR	LETHOLHLHA	LWFDIY <mark>TGE</mark> I	YYF <mark>SR</mark> OAK	RFILIDEKNF	DKLLME	VEK	YYM	
XP_045472083.1   NNTL0   LIDN   TASYOFLESS   LETIQLHIMA INPOLYTOS   YPERGAL   TYVLIDENIS   ELLID VID   YES	VEN57246.1			IASYGFLKRR				RFVPVDESNI			YY <mark>S</mark>	
XP_017766645.1	XP_045472083.1	INTLO		IASYGFLKKR	LETHOLHIHA	LWFDIYTGEI	YYF <mark>SR</mark> GAK	KFVVIDEGNI	EKLLDE	VDN	YY <mark>S</mark>	
CART 168701.1 INTIC CLOR IASYGLIKE EMPLEMENT MYDTYTOE YTYSKAA RYVUDDDHI DELLEW VIS		INTLO		IASYGFLKKR	LEKHELHIHA	LWFDIY <mark>TGE</mark> I	YYFSRGSK	TFVLIDEHNI	DALVGE	VKK	YY <mark>S</mark>	
XP_028136465.1 INTLO GLOS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDEDIN DELLE VER YYS.  XP_019875064.1 INTLO GLOS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDENIN DELLE VER YYS.  XP_019875064.1 INTLO GLOS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDENIN DELLE VER YYS.  XP_019875064.1 INTLO GLOS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDENIN DELLE VER YYS.  XP_019875064.1 INTLO GLOS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDENIN DELLE VER YYS.  XP_01987506529.1 INTLO GLOS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDENIN GLOSE VER YYS.  XP_01987506529.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVVILDENIN GLOSE VER YYS.  XP_0198750858.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GLOSE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GUS ELLIE VUR YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GUS ELLIE VUR YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GUS ELLIE VUR YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GUS ELLIE VUR YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GUS ELLIE VUR YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILDENIN GUS EVILLE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILLE VER YYS.  XP_0188750851.1 INTLO GUS IANGGLEGE GENERALINA MYDITYGDI YYPSGA. EVILLE VER YYS.  XP_0188750851.1 INTLO GUS I				IASYGFLKKR	LEKHOLHIHA			RFVVVDEDNI	DKLMGE	<mark>V</mark> GK	YY <mark>S</mark>	
XP_012014099.1   INTIO   OLD IANGPLICES   ERRECHIEM   NFDITIOE    YYSEAA   RFVIIDNMF   DRILLE   VE   YYS   YE   YE   YYS   YE   YYS   YY	XP_028136465.1	INTLO		IASYGFLKKR	LEKHELHIHA	LWFDIYTGDI	YYF <mark>SR</mark> GAK	RFVLIDEDNV	DKLLQE	VKK	YY <mark>S</mark>	
XP_019875064.1	XP 023014099.1	INTLO		IASYGFLKKR	LEKHELHIHA	LWFDIY <mark>TGE</mark> I	YYF <mark>SR</mark> AAK	KFVIIDENNF	DKLLSE	VER	YY <mark>S</mark>	
CAHOSTOROLD INTIL OLD IASYGPLEME LEHGLHIHA MWDLYTGD MYSGAA GYVIDESTU GELLGE VIR YYSGAA GYVIDESTU GYVIDESTU GELLGE VIR YYSGAA GYVIDESTU GYVIDESTU GYVIDESTU GELLGE VIR YYSGAA GYVIDESTU GYVIDES				IASYGFLKRR	LEKHOLHIHA	LWFDIY <mark>T</mark> GDI	YYF <mark>SR</mark> AA <mark>K</mark>	KFVIIDENNF			YY <mark>S</mark>	
XP_037924690.1   XTILG   ORN:   ARYPFLETE   ECHICIHINA   AMPLITYOD    YFFSGA				IASYGFLKRR	LEKHÖLHIHA		YYF <mark>SR</mark> AAK	KFVVIDEENV	EKLLNE	VNT	YY <mark>S</mark>	
XP_043863257.1   NNTLO QUEST LASYGELERS   LESENLETTE   MPDITTOD   YFFSGAL   REVIVOEST OLLSE VER FYS   YES	XP 037924690.1	INTLO		VASYGFLKHR	LEOHDLHIHA	LWFDIY <mark>T</mark> GDI	YFF <mark>SRGAK</mark>		GKLLOE	VNR	YY <mark>S</mark>	
XP_039965629.1   NNTLO QUEST VARSGELEGE LESEDLETTE AMPLYTYDD   YFFSRAAL - RETVOUESTS CALTEE VER YEAR					LESHNLHIHA	LWFDIY <mark>T</mark> GDI				VRR	FYS	
XP_037896985.1   INT.					LESHDLHIHA		YYF <mark>SR</mark> GAK	RFIPVDESTV		<b>V</b> RR	YY <mark>S</mark>	
XP_037896985.1   INT.	_				LESHNLHIHA					<b>V</b> RR	FYS	
MPD197101   MYTE   MAN				IASYGFLKPR	LESHDLHIHA			RFVPVDEOSV		<b>V</b> KR	YY <mark>S</mark>	
RAG5681791.1  TYPLO QLON IASYGPICHE RAG4077403.1  INTLE QLSN VASYGPICHE RAG4077403.1  INTLE QLSN VASYGPICHE RAG4077403.1  INTLE QLSN VASYGPICHE RAG707403.1  VYPLO QUEEN RASYGPICHE RAG707403.1  VYPLO QUEEN RASYGPICHE RAFYCOULD QUEEN RASYGPICHE RAFYGOUND QUEEN RASYGPICHE RAFYCOULD QUEEN RASYGPICHE RAFYGOUND QUEEN RASYGPICHE RAFYCOULD QUEEN RASYGPICHE RAFYGOUND QUEEN RASYGPICHE RAFYGOUND QUEEN RASYGPICH RAFYGO				IASYGFLKAR	LESHDLHIHA			RFIPVDEDTV	DKLTSE	<b>V</b> RR	FYS	
XP_031629647.1 INTLE QLSW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERGER - REVENUENS QILEE VN FYS-  KAG4077403.1 VNILG QLEW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERGER - REVENUENS QILEE VN FYS-  PX_040221405.1 VNILG QLEW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERGER - REFINDETT BELLEE VN FYS-  CAA998239.1 VNILG QLAW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERGER - REFINDETT DELBE VN FYS-  KAG68030307.1 INTLG QLOW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERGER - REVENUENT DELSE VS FYS-  KAG68030307.1 INTLG QLOW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERGER - REVENUENT DELSE VS FYS-  KAH0947068.1 INTLG QLOW VASYGPIKER EMPHDHHHA LWFDIYTGDI YYFERAM - REVENUENT TILLER IKK YYS-  PX_043599797.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_043597971.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_043597971.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_043649379.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_01237169.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_0124364528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE TILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 INTLG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 VNILG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE SILLEE IM YYS-  PX_014564528.1 VNILG QLOW VASYGPIKER EMPHDHHA LWFDIYTGDI YYFERAM - REVENUENTE S	_				LEOFDLHIHA					vkk	YY <mark>S</mark>	
KAG4077403.1  KNILG OLSN VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- CFVAVDESN DELLDE VAC DEL CAP998039.1  KNILG OLEN VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFIADDESI DELLDE VAC CAP998039.1  KAF6203636.1  KNILG OLAN VASYDERER LEHDLHHA LWFDIYTGDI YYFERSK- FFIADDESI DELLDE VAT CAP998039.1  VNILG OLAN VASYDERER LEHDLHHA LWFDIYTGDI YYFERSK- FFIADDESI DELLDE VAT CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE YILFE KYS- CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE KYLFE KYS- CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE KYLFE KYS- CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE SALLÆE IM YYS- CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE SALLÆE IM YYS- CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE SALLÆE IM YYS- CAP998039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE SALLÆE IM YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE SALLÆE IM YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE SALLÆE IM YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE BALLÆE IM YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFERSK- FFUENETE FLLÆE IK YYS- CAP909039.1  VNILG OLON VASYGERER LEHDLHHA LWFDIYTGDI YYFER						LWFDIY <mark>T</mark> GDI					FYS	
XP_034230644.1	_	INTLE		VASYGFLKKR	LETHDLHIHA				DRLLDE		LDETK	
RP_040221405.1												
CAA998239.1  WITE CLAN VASYMFLERE LETHCHUMA LMPDIYTODI YYFSCON - RVVEINETV DELSEE VREDGEGGSSES APPIN- RAG680307.1  NITE CLAN VASYMFLERE LETHCHUMA LMPDIYTODI YYFSCAN - RVVEINESTE RVLITE KIT WEYS	_				LESHDLHIHA							
KAG68036.1 UNTLE CLAN VASYMFLERE LETHELHHA LMPDLYTODI YYFSANK - REVELNETTE DELISE IK YS	_			VASYNFLKRR	LESHOLHVHA			REVEINEFTV		VSR	YY <mark>S</mark>	
RAG6800307.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSAHR- RFVEINELTE RILE LTY YSSAMBARDAYONGS.1  KAH0947068.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSAHR- RFVEINELTE SHLLKE LHY YSSAMBARDAYONGS.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINELTE SHLLKE LHY YSSAMBARDAYONGS.1  KP_043590797.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINELTE SHLLKE LHY YSSAMBARDAYONGS.1  KP_043464528.1  INTLO QLON WASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINELTE SALLEE LIK YYSSAMBARDAYONGS.1  KP_043464528.1  INTLO QLON WASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINELTE SALLEE LIK YYSSAMBARDAYONGS.1  KP_0446741789.1  INTLO QLON WASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINELTE SALLEE LIK YYSSAMBARDAYONGS.1  KP_046741789.1  INTLO QLON WASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTE TPLLKE KYYSSAMBARDAYONGS.1  KP_046741789.1  INTLO QLON WASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTE TPLLKE KYYSSAMBARDAYONGS.1  KRF0770685.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTE TPLLKE KYYSSAMBARDAYONGS.1  KRF0770685.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTE TPLLKE LK YYSSAMBARDAYONGS.1  KRF0770685.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTE TPLLKE KYYSSAMBARDAYONGS.1  KRF0770685.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTE TPLLKE LK YYSSAMBARDAYONGS.1  KRF0784668968.1  INTLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTY DELLE VY YYSSAMBARDAYONGS.1  KRF0784689687.1  KRF078487.1  VNCLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTY DELLE VY YYSSAMBARDAYONGS.1  KRF078487.1  VNCLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTY DELLE VY YYSSAMBARDAYONGS.1  KRF078487.1  VNCLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTY DELLE VY YYSSAMBARDAYONGS.1  KRF078487.1  VNCLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTY DELLE VY YYSSAMBARDAYONGS.1  KRF078487.1  VNCLO QLON MASYGLKER LEREDLHIHA LWFDLYTGDI YYFSANR- RFVEINENTY DELLE VY YYSSAMBARDAYONGS.1  KRF078487.1												AFPLV
RP_014230599.1   NNTLO   CLON   ASYGFLEKE   LEPHDLHIHA   IMPDIYTODI   YYFSRANE   RFVEINSTE   SILLEE   IMT   YYS												
RAH0947068.1 INTLO   CLON   TASYGFLKKR   LEHDLHVHA   LWFD1YTGD1   YFSRANK   FFVEINSTE   SILLEE   LWT YYS										IKT	YY <mark>S</mark>	
NPI_043590797.1   INTLO   QLON   IASYGFLKER   LERHDLHHIA   LWFDIYTODI   YFFRANK -   RFVEINETE   ASLLEE   IK   YYS -										_		
NP-012975169.1									<b>ASLLAE</b>			
NP_01275169.1   NTLO   OLON   VASYGFLKKR   LERHCLHIHA   LWFDIYTGDI   YYFSRANK - RFIEVNENTE   RELLER   IKK   YYF		INTLO		IASYGFLKKR	LEOHDLHIHA		YYFSRGNK		SOLLEE	ILK	YY <mark>S</mark>	
XP_043464528.1 INTLO OLON VASYGFLKKR LERHOLHUHA LWFDIYTGDI YYFSRAKK- RFTEVNENTE KLLLKE IKK YYS	_										YY <mark>S</mark>	
XP_014220045.1	XP 043464528.1			VASYGFLKKR	LERHDLHIHA	LWFDIY <mark>T</mark> GDI	YYF <mark>SR</mark> ANK	RFIEVNENTE	KLLLKE		YY <mark>T</mark>	
XP_046741789.1	_			VASYGFLKOR	LEKHDLHVHA		YYF <mark>SR</mark> AGK			IKK	YY <mark>S</mark>	
XP_046741789.1											YY <mark>S</mark>	
VACC24333.1				VASYGFLKRR	LERHDLHIHA		YYF <mark>SR</mark> ANK	RFIEINELTE		IKK	YY <mark>S</mark>	
NATIO	_	VNTLO		IASYGFLRKR	LESHDLHIHA		YYFS <mark>ROKK</mark>		EKLVEE	VSK	YYC	
XP_015365968.1				IASYDFLKKR	LETYDLHIHA		HYFSROSK				YYC	
XP_029341681.1	XP_015365968.1	VNTLO	OION	IASYDFLKKR	LEAYDLHIHA	LWFDIYTGEI	HYFS <mark>R</mark> QNK	<b>OFVEINEKNV</b>	NR LVEE	<b>VSK</b>	YYC	
XP_026292519.1	XP_029341681.1	VNTLO		IASYDFLKKR	LETYDLHIHA	LWFDIY <mark>T</mark> GDV		<b>OFVEINEKNV</b>	DGLVEE	VSK	YYC	
XP_024081347.1	XP_026292519.1	VHCLQ		IASYSFLKPR	LEKHELHIHA		YYF <mark>SR</mark> GEK	RFVEINDSTI	DPLLKE	<mark>V</mark> KR	YY <mark>S</mark>	
XP_014283188.1 VNCLQ QMAN IASYGFLKRR LETHQLHIHA LWFDIYTGNI YYFSRQNK RFIDINEETV POLICY VNCLQ QLQN VASYGFLKRR LETHQLHIHA LWFDIYTGDI YYFSRQNK RFVEINETTU POLICY VNCLQ QLQN IASYGFLKRR LETHQLHIHA LWFDIYTGDI YYFSRQNK RFVEINETTU POLICY	XP_034238427.1	VHCLQ	QMQN	IASYSFLKSR	LEKHELHIHA	LWFDIY <mark>S</mark> GDI	YYF <mark>SR</mark> GEK	RFIEINENTI	DPLLKE	<mark>V</mark> KR	YY <mark>S</mark>	
XP_014283188.1 VNCLQ QMAN IASYGFLKRR LETHQLHIHA LWFDIYTGNI YYFSRQNK RFIDINEETV POLICY VNCLQ QLQN VASYGFLKRR LETHQLHIHA LWFDIYTGDI YYFSRQNK RFVEINETTU POLICY VNCLQ QLQN IASYGFLKRR LETHQLHIHA LWFDIYTGDI YYFSRQNK RFVEINETTU POLICY	XP_024081347.1	INCLO		IASYGFLKRR	LEKYELHIHA		FYFS <mark>R</mark> QNK	RFVEINEDTV	DKLSLE	Q		
CAB3380083.1 INCLQ QLQN VASYGFLKRR VPLOUD LASYGFLKRR VPLOUD VPSRQRK	XP_014283188.1	VNCLO	<b>OMAN</b>	IASYGFLKRR	LERHOLHIHA		YYFS <mark>R</mark> QNK	RFIDINEETV	DMLSHE	VKK	YY <mark>S</mark>	
XP_046989067.1 VNCLQ QLQN IASYGFLKKR LETHQLHIHA LWFDIYTGDI YYFSRQNK RFVEINETTI KQLLE VKT YYS CAD7446618.1 INCLQ QLQN IASYGFLKKR LETHLHIHA LWFDIYTGDI YFFSRQNK RFVEINETTI KQLLE VKT YYS CAD7446618.1 INCLQ QLQN IASYGFLKKR LETHLHIHA LWFDIYTGDI FYFSRQNK RFVEINETTI KQLLE VKT YYS CAD7446392794.1 VNCLQ QLQN IASYGFLKRR LETHLHIHA LWFDIYTGDI FYFSRQNK RFVEINETTI KQLLE VKT YYS CAD746459477.1 INCLQ QLQN IASYGFLKRR LETHLHIHA LWFDIYTGDI FYFSRQNK RFVEINETTI KQLLE VKT YYS CAD746459477.1 INTLQ QLQN IASYSFLQSA INSGRVHLHA LWFDIYTGDI FYFSRQNK RFVEINEETTY NLLLKE ILR YYS CAD746459477.1 VNTLQ QLQN VSSYGMLKRG LTRGEIHIHA LWFDIYTGDI HYFSRQNK RFVEINEETT DYLLDE IRE YFV	RZF32743.1	VNCLQ	QVQN	IASYGFLKKR	LETHQLHIHA	LWFDIYSGDI	FFFS <mark>R</mark> QNK	RFIEINENTV	EKLTDE	VNR	YY <mark>S</mark>	
GFG38476.1  VNCLQ QLQN IASYGFLKRR LETHELHIHA LWFDIYTGDI YFFRQNK RFVEINETTI KQLLLE VKT YYS CAD7446618.1  KAG8226740.1  VNCLQ QLQN IASYGFLKRR LETHSLHIHA LWFDIYTGDI YFFRQQK QFVEINEETS KTLLKE IKR YYS TYP-046459477.1  XP_046459477.1  XP_046459477.1  XP_043227363.1  VNTLQ QLQN VSSYGMLKRG LTRGEIHHA LWFDIYTGDI YVFFRQCK RFVEINEETS DYLLDE IRE YFV TYP-048026429.1  XP_018006429.1  XP_0486504.1  VNTLQ QLQN IASYNFMRDG LAKGRVYLHA LWFDIYTGDI YYFFRQQK TFVPMNEDTI DTLMDE VRT YYSSGR	CAB3380083.1	INCLQ	QIQN	VASYGFLKRR	LETHDLHLHA	LWFDIYTGDV	YYFS <mark>R</mark> QRK	RFVEINDLTA	RPILKE	IRR	YY <mark>S</mark>	
CAD7446618.1 INCLO OLON IASYGFLKRR LERHOLHIHA LWFDIYTGDI YFFROSK QFVEINETTI KOLLE VKT YYS CYP-046322794.1 VNCLO OLON IASYGFLKOR LETHOLHIHA LWFDIYTGDI FYFSROOK RFVEINETTI KOLLE IKR YYS CYP-046459477.1 LNTLO OLON IASYGFLKOR LETHOLHIHA LWFDIYTGDI YVFSROOK RFVEINETTI KOLLE IKR YYS CYP-046459477.1 LNTLO OLON VSYGMLKOR LETHOLHIHA LWFDIYTGDI YVFSROOK RFVEINETTI KOLLE IKR YYS CYP-046459477.1 LNTLO OLON VSYGMLKOR LETHOLHIHA LWFDIYTGDI YVFSROOK RFVEINETTI KOLLE IKR YYS CYP-046459477.1 LNTLO OLON IASYNFMROG LAKGRVYLHA LWFDIYTGDI HYFSROOK RFVEINETTI KOLLE IKR YYS CYP-0450459477.1 LNTLO OLON IASYNFMROG LAKGRVYLHA LWFDIYTGDI HYFSROOK RFVEINETTI KOLLE IKR YYS CYP-0450459477.1 LNTLO OLON IASYNFMROG LAKGRVYLHA LWFDIYTGDI YVFSROOK RFVEINETTI KOLLE IKR YYS CYP-0450459477.1 LNTLO OLON IASYNFMROG LAKGRVYLHA LWFDIYTGDI YVFSROOK RFVEINETTI KOLLE IKR YYS CYP	XP_046989067.1	VNCLQ	QLQN	IASYGFLKKR	LETHQLHIHA	LWFDIYTGDI	YYFS <mark>R</mark> QNK	RFVEINEHTV	MGLIKE	VNR	YY <mark>S</mark>	
KAG8226740.1  VNCLQ QLQN IASYGFLKRR LETHSLHIHA LWFDIYTGDI XP_046392794.1  VNCLQ QLQN IASYGFLKQR LETHQLHIHA LWFDIYTGDI XP_046392794.1  VNTLQ QLQN IASYGFLQR LETHQLHIHA LWFDIYTGDI XP_043227363.1  VNTLQ QLQN VSYGMLKRG XP_043227363.1  VNCLQ QLQN IASYNFMRDG LAKGRVYLHA LWFDIYTGDI XP_018006429.1  VNCLQ QLQN IASYNFMRDG LAKGRVYLHA LWFDIYTGDI XP_042865604.1  VNTLQ QLQN IASYNFMRDG LYRGRVYIHA LWFDIYTGDI XP_045613573.1  VNTLQ QLQN IASYNFMREG LYRGRVYIHA LWFDIYTGDI XP_045613573.1  VNTLQ QLQN IASYNFMREG LAKGRVYIHA LWFDIYTGDI XP_045613573.1  VNCLQ QLQN IASYNFMREG LAKGRVYIHA LWFDIYTGDI XP_021963432.1  VNCLQ QLQN IASYNFMREG LAKGRVYIHA LWFDIYTGDI XP_045613573.1  VNCLQ QLQN IASYNFMREG LAKGRVYIHA LWFDIYTGDI XP_021963432.1  VNCLQ QLQN IASYNFMREG LAKGRVYIHA LWFDIYTGDI XP_VCLQ QLQN IASYNFMREG LAKGRVYIHA LWFDIYTGDI XP_V	GFG38476.1	VNCLQ	QLQN	IASYGFLKRR	LETHELHIHA	LWFDIY <mark>T</mark> GDI	YYF <mark>SR</mark> QN <mark>K</mark>	RFIDINEGTF	SMLEKE	VLK	YY <mark>S</mark>	
XP_046392794.1 VNCLQ QLQN IASYGFLKQR LETHOLHIHA IWFDIYTGDI YYFSRQK- RFVEINEETY NLLLKE IIR YYS TYP_046459477.1 LNTLQ QLQN IASYNFMRDG LAKGRVYHA LWFDIYTGDI YYFSRQK- RFVEINEETY DYLLDE IR YYS TYP_045613573.1 VNTLQ QLQN IASYNFMRDG LAKGRVYHA LWFDIYTGDI YYFSRQK- KFVDLNEDTI DYLNDE VLY YYSGR	CAD7446618.1	INCLQ	QLQN	<b>IASYGFLKKR</b>	LERHDLHIHA	LWFDIY <mark>T</mark> GDI	YFF <mark>SR</mark> QS <mark>K</mark>	RFVEINETTI	KQLLLE	VKT	YY <mark>S</mark>	
XP_046459477.1 LNTLQ QLQH IASYSFIQSA INSGRVHLHA LWFDIYTGDI YVFSRQK RFVDLNEDTL PQISEE VRT YYSGR					L <mark>ET</mark> HSLHIHA		FYFS <mark>R</mark> QQK	<b>QFVEINEETS</b>		IKR	YY <mark>S</mark>	
XP_046459477.1 LNTLQ QLQH IASYSFIQSA INSGRVHLHA LWFDIYTGDI YVFSRQK RFVDLNEDTL PQISEE VRT YYSGR	XP_046392794.1	VNCLQ	QLQN	IASYGFLKQR	L <mark>ETHQ</mark> LHIHA	IWFDIY <mark>TG</mark> DI	FYF <mark>SR</mark> QQK	RFVEINEETY	NLLL <mark>K</mark> E	ILR		
XP_043227363.1 VNTLQ QLQN VSSYGMLKEG LTRGEIHIHA LWFDIYTGNI HYFSRQQK TFVPMNEDTI DTLMDE VHK YYS		LNTLQ			INSGRVHLHA		YVF <mark>SRKQK</mark>	RFVEISEETS	DYLLDE	IRE		
XP_018006429.1 VNCLQ QLQN IASYNFMRDG LAKGRVYLHA FWFDIYSGDI HYFSRQQK TFVPMNEDTI DTLMDE VHK YYS VNTLQ QLQN IASYNFMRDG LVRGRVYIHA LWFDIYTGDI YYFSRQQK KFVDVVSENNI ERLLDE AKQ YYT VNTLQ QLQN IASYNFMREG LSRGKVYIHA LWFDIYTGDI YYFSRQQK MFVDVNEGNI EKLLEE VVK YYT VNTLQ QLQN IASYNFMREG LSRGKVYIHA LWFDIYTGDI YYFSRQQK MFVDVNEGNI EKLLEE VVK YYT VNTLQ QLQN IASYNFMREG LSRGKVYIHA LWFDIYTGDI YYFSRQQK MFVDVNESNM EKLEE VVK YYT VNTLQ QLQN IASYNFMREG LSRGKVYIHA LWFDIYTGDI YYFSRQQK MFVDVNESNM EKLEE VVK YYT VNTLQ QLQN IASYGFLREG LSRGKVYIHA LWFDIYTGDI YYFSRQKK EFVDINETTF PKLLEE VSE FYYH VNTLQ QLQN IASYGFLREG LASGKIFIHA LWFDIYTGDI YYFSRQKK EFVDINETTF PKLLEE VSE FYYH VNTLQ QLQN IASYGFLREG LASGKIFIHA LWFDIYTGDI YYFSRQKK EFVDINETTF PKLLEE VSE FYYH VNTLQ QLQN IASYGFLREG LASGKIFIHA LWFDIYTGDI YYFSRQKK EFVDINETTF PKLLEE VSE FYYH VNTLQ QLQN IASYGFLREG LASGKIFIHA LWFDIYTGDI YYFSRQKK EFVDINETTF PKLLEE VSE FYYH VNTLQ VSE FYYH	XP_043227363.1	VNTLQ			LTRGE IHIHA	LWFDIY <mark>TGN</mark> I	HYFS <mark>R</mark> QQK				YYSSGR	
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XP_045613573.1 VNTLO OLON IASYNFMREG LSRGRVYIHA LWFDIYTGDI YYFSROOK MFVDVNESNM EKLEEE VFK YYT		VNTLQ	QLQN	IASYNFMREG	LSRGKVYIHA		YYF <mark>SR</mark> QQ <mark>K</mark>	MFVDVNEGNI	E <mark>KLL</mark> EE	VVK		
XP_045613573.1 VNTLO OLON IASYNFMREG LSRGRVYIHA LWFDIYTGDI YYFSROOK MFVDVNESNM EKLEEE VFK YYT	_	VNTLQ	QLQN				YYFS <mark>R</mark> QQ <mark>K</mark>				YY <mark>T</mark>	
							YYFS <mark>R</mark> QQK				<b>Y</b> Y <mark>T</mark>	
CAG7730563.1 VNCLQ QLQN IASYGFMRDI LMQGKTFIHA MWFDIYTGDI YYFSRQKK QFVEINEENY YGLLEE VMT YYSQYD											FYYH	
	CAG7730563.1	VNCLQ	QLQN	IASYGFMRDI	LMQG <mark>K</mark> TFIHA	MWFDIYTGDI	YYFS <mark>R</mark> QKK	QFVEINEENY	YGLLEE	VMT	YY <mark>SQYD</mark>	

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ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1					  		
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ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1					    		 
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1					   		  
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1					    		   
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1					     		   
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF0867361.1					     		   
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF0867361.1 UJR16523.1 CAF1340180.1 CAF1025683.1					      		
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF0867361.1 UJR16523.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1	GDAMP	TGYRKDVS	DEETLOKTA	QRMMHTA	       RQ	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF0867361.1 UJR16523.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1	GDAMP	TGYRKDVS	DEETLOKTA -	ORMMHTA	      RQ RK	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF0867361.1 UJR16523.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1	GDAMP	TGYRKDVS	DEETLOKTA -	QRMMHTA	     RQ RK	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF6867361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1 XP_045201158.1	GDAMP	TGYRKD - VS	DEETLOKTA -	ORMMHTA	     RQ RK	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XAP_023329171.1 XP_045201158.1 XP_045201158.1 XP_009053308.1	GDAMP	TGYRKD VS	DEETLQKTA-TRKRLIKK	ORMMHTA	    RQ RK 	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1	GDAMP	TGYRKD - VS KVLRKG - NY	DEETLOKTA-TRKRLIKK	ORMMHTA	    RQ RK 	TPHVCDQNCK PI	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1	GDAMP	TGYRKD VS KVLRKG NY	DEETLOKTA -	QRMMHTA	    RQ RK 	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_013785798.1 GAU97340.1	GDAMP	TGYRKD - VS	DEETLOKTA-TRKRLIKK	QRMMHTA	    RQ RK  	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF13667361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1	GDAMP	TGYRKD VS KVLRKG NY	DEETLOKTA -	ORMMHTA	         	TPHVCDQNCK PI	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_013785798.1 GAU97340.1	GDAMP	TGYRKDVS KVLRKGNY	DEETLOKTA-TRKRLIKK	ORMMHTA		TPHVCDQNCK PI	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 XP_023329171.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1	GDAMP	TGYRKDVS KVLRKGNY	DEETLOKTA-TRKRLIKK	ORMMHTA		TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1	GDAMP	TGYRKD - VS KVLRKG - NY	DEETLOKTA	QRMMHTA		TPHVCDQNCK PI	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF13667361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XAP_023329171.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI02233246.1 XP_029642194.1	GDAMP	TGYRKD VS KVLRKG NY	DEETLOKTA-TRKRLIKK-	ORMMHTA		TPHVCDQNCK	#DD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_001171747.1	GDAMP	TGYRKD - VS KVLRKG - NY	DEETLOKTA-TRKRLIKK-	ORMMHTA		TPHVCDQNCK PI	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 KAH3870454.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_0201771747.1 CAH1781438.1	GDAMP	TGYRKDVS KVLRKGNY	DEETLOKTA-TRKRLIKK	ORMMHTA		TPHVCDQNCK PI	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF13667361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_01378579.1 GAU97340.1 CAV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 XP_009013880.1 XP_009013880.1 XP_009013880.1 XP_029642194.1 NP_001171747.1 CAH1781438.1 XP_013382323.1	GDAMP	TGYRKD VS KVLRKG NY	DEETLOKTA - TRKRLIKK	QRMMHTA		TPHVCDQNCK	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF13667361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 CAF1025683.1 ALS04255.1 XP_009053308.1 XP_033096127.1 XP_013785798.1 GAU97340.1 CAP1023246.1 XP_009013880.1 KAI0233246.1 XP_009017717747.1 CAH1781438.1 XP_013382323.1 XP_033759917.1	GDAMP	TGYRKD VS KVLRKG NY	DEETLOKTA-TRKRLIKK	QRMMHTA		TPHVCDONCK	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF13667361.1 UJR16523.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_01171747.1 CAH1781438.1 XP_013382323.1 XP_033759917.1 XP_041373453.1	GDAMP	TGYRKD - VS KVLRKG - NY	DEETLOKTATRKRLIKK	ORMMHTA	RQ RK	TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF3941029.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 CAF1340180.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KA10233246.1 XP_029642194.1 NP_01171747.1 CAH1781438.1 XP_0133759917.1 XP_0141373453.1 XP_046548515.1	GDAMP	TGYRKDVS KVLRKGNY	DEETLOKTA - TRKRLIKK	ORMMHTA	RQ RK	TPHVCDONCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1367361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 CQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_001171747.1 CAH1781438.1 XP_033759917.1 XP_041373453.1 XP_033759917.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_041373453.1	GDAMP	TGYRKD - VS KVLRKG - NY	DEETLOKTA - TRKRLIKK	QRMMHTA		TPHVCDQNCK	
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF13667361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_001171747.1 CAH1781438.1 XP_013382323.1 XP_033759917.1 XP_041373453.1 XP_046548515.1 XP_047034441.1 CAB3245311.1	GDAMPNKATE	TGYRKD - VS KVLRKG - NY	DEETLOKTA-TRKRLIKK	QRMMHTA L		TPHVCDQNCK	HD
ACO15530.1  XP_040566914.1  VDP33652.1  PAA53847.1  RNA13068.1  CAF0715750.1  CAF0950609.1  CAF1119542.1  CAF1301217.1  CAF3941029.1  CAF138067361.1  UJR16523.1  CAF1340180.1  CAF1025683.1  ALS04255.1  XP_023329171.1  XP_045201158.1  XP_045201158.1  XP_033096127.1  XP_033096127.1  XP_013785798.1  GAU97340.1  CQV24824.1  CAD5123161.1  ELT97609.1  XP_009013880.1  XP_009013880.1  XP_029642194.1  NP_0171747.1  CAH1781438.1  XP_033759917.1  XP_013382323.1  XP_033759917.1  XP_045485451.1  XP_046548515.1  XP_047034441.1  XP_0470344441.1  XP_041549456.2	KYKNRGKMST	TGYRKD - VS KVLRKG - NY	DEETLOKTATRKRLIKK	QRMMHTA 	RQ RK 	TPHVCDQNCK	HD
ACO15530.1  XP_040566914.1  VDP33652.1  PAA53847.1  RNA13068.1  CAF0715750.1  CAF0950609.1  CAF1119542.1  CAF1301217.1  CAF3941029.1  CAF3941029.1  CAF1340180.1  CAF1340180.1  CAF1340180.1  CAF1340180.1  XP_023329171.1  XP_023329171.1  XP_023329171.1  XP_045201158.1  XP_033096127.1  XP_033096127.1  XP_013785798.1  GAU97340.1  OQV24824.1  CAD5123161.1  ELT97609.1  XP_009013880.1  XP_009013880.1  XP_029642194.1  NP_01171747.1  CAH1781438.1  XP_013382323.1  XP_033759917.1  XP_041373453.1  XP_045548515.1  XP_047034441.1  CAB3245311.1  LCAB3245311.1  LCAB3245311.1	GDAMPNKATE	TGYRKD - VS KVLRKG - NY	DEETLOKTA-TRKRLIKK-	ORMMHTA	RQ RK 	TPHVCDQNCK PI	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1367361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_01171747.1 CAH1781438.1 XP_033759917.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_047034441.1 CAB3245311.1 XP_015766.2 XP_046761472.1 XP_046968321.1	GDAMPNKATE	TGYRKDVS KVLRKGNY	DEETLOKTATRKRLIKK	ORMMHTA L		TPHVCDQNCK	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1301217.1 CAF3941029.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_045201158.1 XP_033096127.1 XP_013785798.1 GAU97340.1 CQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 XP_009013880.1 XP_009013880.1 XP_001171747.1 CAH1781438.1 XP_013382323.1 XP_033759917.1 XP_046548515.1 XP_046548515.1 XP_047034441.1 CAB3245311.1 XP_011549456.2 XP_045761472.1 XP_046968321.1 XP_046968321.1 XP_0264233335.1	KYKNRGKMST	TGYRKD - VS KVLRKG - NY	DEETLOKTATTKKLIKK	QRMMHTA	RQ RK 	TPHVCDQNCK PI	HD
ACO15530.1 XP_040566914.1 VDP33652.1 PAA53847.1 RNA13068.1 CAF0715750.1 CAF0950609.1 CAF1119542.1 CAF1301217.1 CAF3941029.1 CAF1367361.1 UJR16523.1 CAF1340180.1 CAF1025683.1 ALS04255.1 XP_023329171.1 XP_023329171.1 XP_045201158.1 XP_033096127.1 XP_033096127.1 XP_033096127.1 XP_013785798.1 GAU97340.1 OQV24824.1 CAD5123161.1 ELT97609.1 XP_009013880.1 KAI0233246.1 XP_029642194.1 NP_01171747.1 CAH1781438.1 XP_033759917.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_041373453.1 XP_047034441.1 CAB3245311.1 XP_015766.2 XP_046761472.1 XP_046968321.1	KYKNRGKMST	TGYRKD - VS KVLRKG - NY	DEETLOKTATTRKRLIKK	QRMMHTA	RQ RK 	TPHVCDONCK PI	HD
ACO15530.1  XP_040566914.1  VDP33652.1  PAA53847.1  RNA13068.1  CAF0715750.1  CAF0950609.1  CAF1119542.1  CAF1301217.1  CAF3941029.1  CAF1301217.1  CAF3941029.1  CAF1340180.1  CAF1025683.1  ALS04255.1  XP_023329171.1  XAH3870454.1  XP_045201158.1  XP_033096127.1  XP_033096127.1  XP_013785798.1  GAU97340.1  CQV24824.1  CAD5123161.1  ELT97609.1  XP_009013880.1  XP_009013880.1  XP_033759917.1  XP_013785798.1  CAH1781438.1  XP_033759917.1  XP_04521316.1  LET97609.1  XP_07034441.1  CAH1781438.1  XP_013382323.1  XP_045548515.1  XP_047034441.1  CAB3245311.1  XP_045529909.1	GDAMPNKATE	TGYRKD - VS KVLRKG - NY	DEETLOKTATRKRLIKK	ORMMHTA	RQ RK 	TPHVCDQNCK PI	HD
ACO15530.1  XP_040566914.1  VDP33652.1  PAA53847.1  RNA13068.1  CAF0715750.1  CAF0950609.1  CAF1119542.1  CAF1301217.1  CAF3941029.1  CAF1340180.1  CAF1340180.1  CAF1340180.1  CAF1340180.1  XP_023329171.1  XP_023329171.1  XP_045201158.1  XP_033096127.1  XP_033096127.1  XP_013785798.1  GAU97340.1  OQV24824.1  CAD5123161.1  ELT97609.1  XP_009013880.1  XP_009013880.1  XP_009013880.1  XP_0137340.1  CAP102346.1  XP_029642194.1  NP_01171747.1  CAH1781438.1  XP_013382323.1  XP_033759917.1  XP_045761472.1  XP_045761472.1  XP_046968321.1  XP_046529909.1  RVE42816.1	GDAMPNKATE	TGYRKD - VS KVLRKG - NY	DEETLOKTATRKRLIKK	ORMMHTA	RQ RK 	TPHVCDQNCK PI	HD

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