

gi		17136968		ref		NP_477022.1	-----MAEYLQPGVIRKRLDEVVNR	IAAGEIIORPANALKELENSLDAQS	THIQVQVKGAGGLKLIQDNGT	GIRREDLIVCERFITSKLRFDLSQIA	IFGRFGEALASISH	111					
gi		158300415		ref		XP_320342.4	-----MDPQVIRKRLDEVVNR	IAAGEIIRPANALKELENSLDAKAS	ITITIVKAGGLRSLIQDNGT	GIRREDLIVCERFITSKLSQSFDDL	ISITYGFRGEALASISH	107					
gi		19387852		ref		NP_081086.1	-----MAFVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	NIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	109					
gi		13591989		ref		NP_112315.1	-----MSFVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	NIQVIVREGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLAM	ISITYGFRGEALASISH	109					
gi		4557757		ref		NP_000240.1	-----MSFVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	STIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	109					
gi		114585960		ref		XP_001170433.1	-----MSFVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	STIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	109					
gi		73989704		ref		XP_534219.2	-----MSLVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	STIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	109					
gi		194677180		ref		XP_001790604.1	-----MSLVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	STIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	109					
gi		50732924		ref		XP_418828.1	-----MALVAVGIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	STIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	109					
gi		41054934		ref		NP_956953.1	-----MAGVIRRLDETVVNR	IAAGEIIRPANAIKEMENCLDAKS	NIQVIVKVEGGLKLIQDNGT	GIRKEDLDIVCERFITSKLOTFEDLA	ISITYGFRGEALASISH	106					
gi		30680985		ref		NP_567345.2	-----MIDSSSLTAEEMEEESPATTIV	PREPKIQRLEESVNR	IAAGEIIRPVSAVKELVENS	LDAGSSISIVVVKGGKLIQVSD	DHGIRKEDLPILCERFITSKLT	FEDLSISMGRFGEALASMTY	130				
gi		115442355		ref		NP_001045457.1	-----MDEPSPRRGGGCAEPPRI	RRLLEESVNR	IAAGEIIRPVSAVKELVENS	LDAGSSISIVVVKGGKLIQVSD	DHGIRKEDLPILCERFITSKLT	FEDLSISMGRFGEALASMTY	119				
gi		50307053		ref		XP_453504.1	-----MSGRIKPLDVS	VVNKIAAGEIIVAPVNA	LKEMMENSIDAGASIMVD	ILVKDGGKLIQITDNGC	GIDKDDLPILCERFITSKLE	VEFDLSKIEITGFRGEALASIS	106				
gi		45198322		ref		NP_985351.1	MGISDAQRIPDFHHVRVTEKHS	AALLNATTSYLRCVQVPRMHL	SRIKALBASVVNKIAAGEI	IISFVNA	LKEMMENSIDAGASIMVD	ILVKDGGKLIQITDNGC	GIMKDDLPILCERFITSKLE	VEFDLSRIQITGFRGEALASIS	150		
gi		6323819		ref		NP_013890.1	-----MSLRIKALDAS	VVNKIAAGEIISFVNA	LKEMMENSIDANA	IMDILVKGGKLIQITDNG	SGINKADLPILCERFITSKLE	VEFDLSRIQITGFRGEALASIS	106				
gi		145612427		ref		XP_367196.2	-----MLQITDNGC	GIEKEDLPILCERFITSKLO	TFEDLSIATY	GFRGEALASISY		52					
gi		85108177		ref		XP_962522.1	-----MADAMAI	DGPRGEKRA	SVLGDSSCHAPRRIRPLD	PDVNNKIAAGEIIVAPV	HALKELMENA	VDAGSSTLEIVVKDGGKLI	QITDNGC	GIDKDDLPILCERFITSKLE	VEFDLSIATY	GFRGEALASISY	132
gi		19112991		ref		NP_596199.1	-----MDVNSRAKIR	PLDQLVINKIAAGEI	IERPENAIKELIENS	LDAGSSTIDVLLK	DGGKLIQITDNGSGIT	YDLPYLCQRFSTSKL	IDNFNDLQHLQITGFR	GEALASISH	110		



gi		17136968		ref		NP_477022.1	VAHLSIQTKAKEKCGYKATADGK	LQGGPKPCAGNOGTITICED	LFYNMPORRALRSPABE	QRISSEVLARYAVHNP	RVGFTLRKQGDAPALR	IPVASSRSENI	IRIIVGAATSKELLE	FSHRDEV	YKFEACLIT	249																
gi		158300415		ref		XP_320342.4	VAHLITVTKTKHEKCAKAC	YEDGKLGDDIKPIAGNOGTITIV	EDLFYNMRRKQALKT	PNBEQRISD	VVSKYAVHNP	HACFILKQFG	ETATIR	QAKITVAHNGAI	YAGIGKALVPIELR	DEV	MQLTVGEGYV	244														
gi		19387852		ref		NP_081086.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		13591989		ref		NP_112315.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		4557757		ref		NP_000240.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		114585960		ref		XP_001170433.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		73989704		ref		XP_534219.2	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		194677180		ref		XP_001790604.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		50732924		ref		XP_418828.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		41054934		ref		NP_956953.1	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	247												
gi		30680985		ref		NP_567345.2	VAHVITITTKTADGKCA	YRASYSDGKIQAPPKPCAGNOGT	LITVEDLFYNIITRR	KALKNPEEY	GKILEVVGRYS	IHNSGII	SIVKKGQEV	IVSDVRL	LPNATV	DNIR	SIFGNV	SRELIEVGCEDKT	LAFKMGYIS	244												
gi		115442355		ref		NP_001045457.1	VGHVITITTEGQLH	GVRSYRDMENE	PKCAAVKGTQ	IMVENLFY	NMIARRKTL	NSADDY	PKIVDL	SRMATHY	NNVNSG	IKRKHG	AVKADVH	SVSP	SRDL	SIR	SVY	SVAKN	LMK	VE	SDCCS	GCTPDM	MGFTS	271				
gi		50307053		ref		XP_453504.1	IARLVITITTEKDK	CAWKAS	FSGKILGQPKP	VAGKTGITIV	EDLFYNIITRR	KALKNPEEY	AKVIL	GRYS	INNNV	GVSC	CKKPG	KV	ALM	KADLS	KDR	VR	IV	F	GAN	S	RL	IE	IG	ED	KT	249
gi		45198322		ref		NP_985351.1	IARLVITITTEKDK	CAWKAS	FSGKILGQPKP	VAGKTGITIV	EDLFYNIITRR	KALKNPEEY	AKVIL	GRYS	INNNV	GVSC	CKKPG	KV	ALM	KADLS	KDR	VR	IV	F	GAN	S	RL	IE	IG	ED	KT	290
gi		6323819		ref		NP_013890.1	IARLVITITTEKDK	CAWKAS	FSGKILGQPKP	VAGKTGITIV	EDLFYNIITRR	KALKNPEEY	AKVIL	GRYS	INNNV	GVSC	CKKPG	KV	ALM	KADLS	KDR	VR	IV	F	GAN	S	RL	IE	IG	ED	KT	246
gi		145612427		ref		XP_367196.2	IARLVITITTEKDK	CAWKAS	FSGKILGQPKP	VAGKTGITIV	EDLFYNIITRR	KALKNPEEY	AKVIL	GRYS	INNNV	GVSC	CKKPG	KV	ALM	KADLS	KDR	VR	IV	F	GAN	S	RL	IE	IG	ED	KT	197
gi		85108177		ref		XP_962522.1	IARLVITITTEKDK	CAWKAS	FSGKILGQPKP	VAGKTGITIV	EDLFYNIITRR	KALKNPEEY	AKVIL	GRYS	INNNV	GVSC	CKKPG	KV	ALM	KADLS	KDR	VR	IV	F	GAN	S	RL	IE	IG	ED	KT	277
gi		19112991		ref		NP_596199.1	IARLVITITTEKDK	CAWKAS	FSGKILGQPKP	VAGKTGITIV	EDLFYNIITRR	KALKNPEEY	AKVIL	GRYS	INNNV	GVSC	CKKPG	KV	ALM	KADLS	KDR	VR	IV	F	GAN	S	RL	IE	IG	ED	KT	258



gi		17136968		ref		NP_477022.1	QVNSYAKKCO	MLLFINQR	LVESTALRT	EVDSIYATY	PRGHPFV	YMSLTL	PQNL	VDVNV	HPTK	HEVH	FLH	YEEI	VEK	VKLL	VER	ALL	G	SN	AT	RF	V	K	L	R	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	371																																															
gi		158300415		ref		XP_320342.4	VNVSFL	KKGI	SLMFIN	HRAVE	CS	ALKKA	IDA	IY	AV	YL	PKGS	AP	FV	YLS	LEL	NP	Q	ND	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	372																
gi		19387852		ref		NP_081086.1	NANYSV	KKCI	FLLFIN	HRLVE	S	A	L	K	A	E	I	V	Y	A	A	L	P	K	N	H	P	F	L	L	S	L	E	I	S	P	Q	N	V	D	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	380
gi		13591989		ref		NP_112315.1	NANYSV	KKCI	FLLFIN	HRLVE	S	A	L	K	A	E	I	V	Y	A	A	L	P	K	N	H	P	F	L	L	S	L	E	I	S	P	Q	N	V	D	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	380
gi		4557757		ref		NP_000240.1	NANYSV	KKCI	FLLFIN	HRLVE	S	A	L	K	A	E	I	V	Y	A	A	L	P	K	N	H	P	F	L	L	S	L	E	I	S	P	Q	N	V	D	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	380
gi		114585960		ref		XP_001170433.1	NANYSV	KKCI	FLLFIN	HRLVE	S	A	L	K	A	E	I	V	Y	A	A	L	P	K	N	H	P	F	L	L	S	L	E	I	S	P	Q	N	V	D	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	380
gi		73989704		ref		XP_534219.2	NANYSV	KKCI	FLLFIN	HRLVE	S	A	L	K	A	E	I	V	Y	A	A	L	P	K	N	H	P	F	L	L	S	L	E	I	S	P	Q	N	V	D	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	380
gi		194677180		ref		XP_001790604.1	NANYSV	KKCI	FLLFIN	HRLVE	S	A	L	K	A	E	I	V	Y	A	A	L	P	K	N	H	P	F	L	L	S	L	E	I	S	P	Q	N	V	D	V	N	V	H	P	T	K	H	E	V	H	F	L	H	E	S	I	L	R	V	Q	H	E	S	K	L	L	G	S	N	S	R	M	Y	F	Q	L	L	P	G	APDL	-----E	QLAD	-----K	T	Q	R	I	Y	P	380

gi|17136968|ref|NP_477022.1| KEMVRLDSTEG--KLDKFLAPLVKSD--SGVSSS-----SQQEASRLPEE--SFRVTAAKSR-----EVRLSSVLDMRKRVERQCSVQ 444
gi|158300415|ref|XP_320342.4| YKFRVRIHSHSE--KLEKFFN-IGSGG--AGISAG-----GDDPKMKEPQDEVVPEKLLQPSPRKKKV-----VKREIRLHSHITLROVESDGDEN 454
gi|19387852|ref|NP_081086.1| YQMVRLDTRD--KLDAPLQPVSLV--PSQPQDPAVVRGARTEGSPERATREDEEMLALPAPAEAAASLENLRESLMETSDTAQKAAPTSSP--GSSRKRHRSDVEMVENA--GKEMTAACYPRRRIINLTSVLSLOEETSERCHET 524
gi|13591989|ref|NP_112315.1| YQMVRLDTRD--KLDAPMOPVSRRL--PSQPQD--PVPGNRTEGSPKAMQKQDEISELPAPMAAASLERSVIGASEVVPQRHPSSE--GSSRKRHRSDVEMMENDSRKEMTAACYPRRRIINLTSVLSLOEINDRGHET 522
gi|4557757|ref|NP_000240.1| HQMVRLDTRD--KLDAPLQPLSKPL--SSQPQA--IVTDEKDIISGRARQDDEEMLELPAPAEVAANKSLEGGDTTKGTSEMSEKRGPTSS--NPKRHRSDVEMVEDDSRKEMTAACYPRRRIINLTSVLSLOEINERGHEV 520
gi|114585960|ref|XP_001170433.1| HQMVRLDTRD--KLDAPLQPLSKPL--SSQPQA--IVTDEKDIISGRARQDDEEMLELPAPAEVTAKNQSLGGDTTKGTSEMSEKRGPTSS--NPKRHRSDVEMVEDDSRKEMTAACYPRRRIINLTSVLSLOEINERGHEV 520
gi|73989704|ref|XP_534219.2| HQMVRLDTRD--KLDAPLQPMKAL--SSQLQA--VVPEDRIVDSGRTGQDDEEMLELPAPQVAATNGMEEETTBGTSETSEKKGPPSP--GNPKRHRSDVEMVEDDSRKEMTAACYPRRRIINLTSVLSLOEINERGHEV 521
gi|194677180|ref|XP_001790604.1| HQMVRLDTRD--KLDAPLQPMKAL--SSQPQA--VVPEDRIVDSGRTGQDDEEMLELPAPQVAATNGMEEETTBGTSETSEKKGPPSP--GNPKRHRSDVEMVEDDSRKEMTAACYPRRRIINLTSVLSLOEINERGHEV 522
gi|50732924|ref|XP_418828.1| HQMVRLDTRD--KLDAPLQPMNPL--SAGPTE--ETTGDVGPPECTVVRQDAEMEDVSELLETADLIEMADVQDQAVMPPGPKSGHLSPEKALPKRKRPREDDIOMEED--NRKEMTAACYPRRRIINLTSVLSLOEINERGHEV 521
gi|41054934|ref|NP_956953.1| HQMVRLDTRD--KLDAPLQPSASS--SSAAQR--KTEK--SSTSTAVQSVLELDDAELLTAADVPECGGDDPQTDAPPDGE--APPKRPR--HVEVEKEDLTAASLPRRRIIVKLTSLIKGLRDLQELQTHKG 494
gi|30680985|ref|NP_567345.2| NKMVRLDTRD--KLDAPLQPSASS--SSAAQR--KTEK--SSTSTAVQSVLELDDAELLTAADVPECGGDDPQTDAPPDGE--APPKRPR--HVEVEKEDLTAASLPRRRIIVKLTSLIKGLRDLQELQTHKG 494
gi|115442355|ref|NP_001045457.1| SKQMVRLDTRD--KLDAPLQPSASS--SSAAQR--KTEK--SSTSTAVQSVLELDDAELLTAADVPECGGDDPQTDAPPDGE--APPKRPR--HVEVEKEDLTAASLPRRRIIVKLTSLIKGLRDLQELQTHKG 494
gi|50307053|ref|NP_453504.1| NKLVRIDSSV--KITYLRLSK--FEFGAS--KNKTKMMNIEKIADNDNLQNDGM--ETIENDIEASYQDETSTQH--TTLNNTYIVLQKQVNLTSIKKLLKQAVDQSHSE 488
gi|45198322|ref|NP_985351.1| NMLVRLDTRD--KITYNVRASQ--SSTSSS--FTSLRKKSHAAASDELGSDGSDQ--D--ATSMTTSTQEPNHTKSR--ILLTLLNNEYEVQORETEVNLTSIKKLLKQAVDQSHSE 532
gi|6323819|ref|NP_013890.1| NKLVRIDSSV--KITYLRLSK--FEFGAS--KNKTKMMNIEKIADNDNLQNDGM--ETIENDIEASYQDETSTQH--TTLNNTYIVLQKQVNLTSIKKLLKQAVDQSHSE 488
gi|145612427|ref|XP_367196.2| NMLVRLDTRD--KITSMFAPVA--GSSRS--AAAATVTT--PAST--QAAASLAAPEA--I--EYELERGVVFKLAVKELRSVAVREMDH 422
gi|85108177|ref|XP_962522.1| SSLVRLDTRD--KITSMLPPA--MAAG--SRGDEIFSTSGVKTATINGNMDVM--IKYE--VEREATA--CRLL--VRELRA--VREEMH 497
gi|19112991|ref|NP_596199.1| NMLVRLDTRD--KITSMLPPA--MAAG--SRGDEIFSTSGVKTATINGNMDVM--IKYE--VEREATA--CRLL--VRELRA--VREEMH 497
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|17136968|ref|NP_477022.1| LRSLLKLLVVGCVDE--RRALFOHETRLMYCNRFSFEEELFYQRMIIYEFQNCSETTISPLPLKELLILSLSE--AAGWTPEDGDKAELADGAADILLKAPIMREYFGLRIS--MLESPLLLHQHRPCV 574
gi|158300415|ref|XP_320342.4| LRKIFRELLTVGIDR--EQVLIQYDTRKMYLSEKQVSIABEELFYQLLNFNGFERLTLSEPLDLKRLVHAGLDDP--ASGWTEDDGPADLADVIVQKLVSKAPVRLREYVNLISREDE--CLESEPKLLDNVTPSL 584
gi|19387852|ref|NP_081086.1| LREMLRNHSFVGCVP--QWALAQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 654
gi|13591989|ref|NP_112315.1| LREMLRNHSFVGCVP--QWALAQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 652
gi|4557757|ref|NP_000240.1| LREMLRNHSFVGCVP--QWALAQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 650
gi|114585960|ref|XP_001170433.1| LREMLRNHSFVGCVP--QWALAQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 650
gi|73989704|ref|XP_534219.2| LREMLRNHSFVGCVP--QWALAQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 651
gi|194677180|ref|XP_001790604.1| LREMLRNHSFVGCVP--QWALAQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 652
gi|50732924|ref|XP_418828.1| LQEMLRDHSFVGCVP--QWALVQHRTKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 651
gi|41054934|ref|NP_956953.1| LQELQLQHSFVGVSP--QVTLVQHQKLYLLNNTKLSSEELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 624
gi|30680985|ref|NP_567345.2| MLETVRNCIVVMADD--VFALVQVNTHLVLANVNLKELMYQQLLRRFAHFNAQLSDPAPLSELLILLALKEED--LDPGNDTKDDLKERIAEMNTELLKKAEMLEEFVSLDIDSA--NLISRLPVLLDQVTPDM 603
gi|115442355|ref|NP_001045457.1| LLDIVKNCIVVGLADE--AFALIQHNTRLVYLVNVIKELMYQALCRFGFNALQLEPAPLQELVLMALKDDE--LMS--DEKDEKLEIAEVNTEILKENAEMLEEFVSLDID--KLRRLPVLLDQVTPDM 620
gi|50307053|ref|NP_453504.1| LTNIFANLTVGVIVDE--RRLLASIQCDLKLFLVDYGSICNELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 591
gi|45198322|ref|NP_985351.1| LTVSFADMTYVGVVDA--RRLLASIQCDLKLFLVDYGSICNELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 591
gi|6323819|ref|NP_013890.1| LTDIFANLTVGVVDE--RRLLAAIQHDLKFLFLVDYGSVCELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 663
gi|145612427|ref|XP_367196.2| LTDIFANLTVGVVDE--RRLLAAIQHDLKFLFLVDYGSVCELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 663
gi|85108177|ref|XP_962522.1| LTDIFANLTVGVVDE--RRLLAAIQHDLKFLFLVDYGSVCELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 663
gi|19112991|ref|NP_596199.1| LTNIFANLTVGVVDE--RRLLAAIQHDLKFLFLVDYGSVCELFYQILYDFANFVGLRLEPAPLFDLAMLALD--ESGWTEDDGPKEGLAEYIVFELKKAEMLADYFSLDIDEG--NLIGLPLLLIDNVVPL 639
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



gi|17136968|ref|NP_477022.1| AHLVYLLRLATE--VDWEQETRCFEFCRETARFYAQL--DWREGATAGF-----SRWTEHVLPAPFKKYLPPPRIKD--QIVELTNL 654
gi|158300415|ref|XP_320342.4| VFLPMYVIRLAD--VEWEEQECFRIFRSRETAHFFSRI--ALPKPEKE-----YRWELEHVLPAPVNRVLIIPPKEMARKNSLLQLASL 664
gi|19387852|ref|NP_081086.1| EGLPIFILLRLATE--VNWDEKKECFEFLSKKECAMFYSIR--KQYILEESTL-----SGQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 750
gi|13591989|ref|NP_112315.1| EGLPIFILLRLATE--VNWDEE--ECFESLKECAVFSYR--KQYILEESAL-----SGQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 747
gi|4557757|ref|NP_000240.1| EGLPIFILLRLATE--VNWDEKKECFEFLSKKECAMFYSIR--KQYIIEESTL-----SGQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 746
gi|114585960|ref|XP_001170433.1| EGLPIFILLRLATE--VNWDEKKECFEFLSKKECAMFYSIR--KQYIIEESTL-----SGQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 746
gi|73989704|ref|XP_534219.2| EGLPIFILLRLATE--VNWDEKKECFEFLSKKECAMFYSIR--KQYIIEESTL-----SGQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 747
gi|194677180|ref|XP_001790604.1| EGLPIFILLRLATE--VNWDEKKECFEFLSKKECAMFYSIR--KQYIIEESTL-----SGQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 747
gi|50732924|ref|XP_418828.1| EGLPMFILLRLATE--VNWDEKKECFEFLSKKELSMFYSIR--KQYIIDEENL-----SRQSDMPGTSKPKWVVEHIIKAFRSHLLPPKHFTEDGNVLQANL 748
gi|41054934|ref|NP_956953.1| EGLPMFILLRLATE--VNWDEKKECFEFLSKKELSMFYSIR--KSYTLLEADN-----EPDQDAMS--WQWVVEHVLPKALRSLSFPAKHLSEBDGVLQASL 714
gi|30680985|ref|NP_567345.2| DRVPEFLCLGND--VEWDEKSCFCQVSAAGNFYAMHPPLLPNPSGDGIFQYKRGESSQEKSELDGNVMDENL--DQDLSDAENAMAQREWIQHVLFFSMRLFLKPPASMASNGTFVQVSL 727
gi|115442355|ref|NP_001045457.1| DRLEPEFLVLAGND--VTWDEKKECFRIVASAVGNFYALHPPILPNPSGNGIHLKKNRDMADHAEADNLSDENV--DQELLAEEAAMAQREWIQHVLFFSMRLFLKPPASMASNGTFVQVSL 714
gi|50307053|ref|NP_453504.1| SKLPPFLVRLGTE--VNWDEEKECLDGILRQLALFVIPP--IEKHIDENP-----EHLSTYAAEMNEIDTMDHVVVFPVVKRRLAPKILLK--VVEVANL 714
gi|45198322|ref|NP_985351.1| SKLPPFLVRLGTE--VNWDEEKECLDGILRQLALFVIPP--IEKHIDENP-----EHLSTYAAEMNEIDTMDHVVVFPVVKRRLAPKILLK--VVEVANL 714
gi|6323819|ref|NP_013890.1| VKLPPFFVIRLGE--VDWEDEKECLDGILREIALLIPDM--VPKVDTSDAS-----LSEDEKAQFINRKEHISLLEHVLFPCKIKRFLAPRHLK--VVEVANL 759
gi|145612427|ref|XP_367196.2| VKLPPFFVIRLGE--VDWEDEKECLDGILREIALLIPDM--VPKVDTSDAS-----LSEDEKAQFINRKEHISLLEHVLFPCKIKRFLAPRHLK--VVEVANL 759
gi|85108177|ref|XP_962522.1| AKLPRFLELQPR--VDWSEKAKCFEGLKALAIKVFVPER--LPAITGTDLSSVQF-----GDKVDVVEVARRHVFALHVLFPAPKRLVATKSLMTG--ILVEVANL 741
gi|19112991|ref|NP_596199.1| QLPPLLSLTPKFFDNLKSKLNGIMKAIKAIKVFVPL--LSVEE--SDVKSIRLESLEKIDVFPFRFRVCPKRVFEKQVITSL 674
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



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gi|17136968|ref|NP_477022.1| PTLYKVFERC 664
gi|158300415|ref|XP_320342.4| PELYRVFERC 674
gi|19387852|ref|NP_081086.1| PDLYKVFERC 760
gi|13591989|ref|NP_112315.1| PDLCKVFERC 757
gi|4557757|ref|NP_000240.1| PDLYKVFERC 756
gi|114585960|ref|XP_001170433.1| PDLYKVFERC 756
gi|73989704|ref|XP_534219.2| PDLYKVFERC 757
gi|194677180|ref|XP_001790604.1| PDLYKVFERC 758
gi|50732924|ref|XP_418828.1| PDLYKVFERC 757
gi|41054934|ref|NP_956953.1| PDLYKVFERC 724
gi|30680985|ref|NP_567345.2| EKLYKIFERC 737
gi|115442355|ref|NP_001045457.1| EKLYKIFERC 724
gi|50307053|ref|XP_453504.1| PGLYKVFERC 724
gi|45198322|ref|NP_985351.1| PGLYKVFERC 771
gi|6323819|ref|NP_013890.1| PDLYKVFERC 769
gi|145612427|ref|XP_367196.2| KGLYRVFERC 690
gi|85108177|ref|XP_962522.1| KGLYRVFERC 751
gi|19112991|ref|NP_596199.1| PRLYNVFERC 684
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