

gi	10092671	ref	NP_064434.1	-----MASLWCGNLLRLGSGLEMSCLALSVLLLAQLTGAAKNFEDVRCRCICPPYKENPGHIYNKNISQKDCDCLHVVEPMP-----VRGPDVEAYC	150
gi	27679422	ref	XP_215038.1	-----MASLWCGSLLRLGSGLSMSCLALYVLLLAPLTGAAKNFEDVRCRCICPPYKENPGHIYNKNISQKDCDCLHVVEPMP-----VRGPDVEAYC	150
gi	11034855	ref	NP_065695.1	-----MATLWGG-LLRLGSLLSLSCALSVLLLAQLSDAAKNFEDVRCRCICPPYKENSGHIYNKNISQKDCDCLHVVEPMP-----VRGPDVEAYC	150
gi	114636058	ref	XP_001168900.1	-----MATLWGG-LLRLGSLLSLSCALSVLLLAQLSDAAKNFEDVRCRCICPPYKENSGHIYNKNISQKDCDCLHVVEPMP-----VRGPDVEAYC	150
gi	73988420	ref	XP_534047.2	-----MATVWGG-FLRLGSLLSLSCALSVLLLVQLSDAAKNFEDVRCRCICPPYKDNVSGHIYNKNISQKDCDCLHVVDPMP-----VRGPDVEAYC	150
gi	77735961	ref	NP_001029679.1	-----MATLWAG-LLRLASMLLSLSCALSVLLLVQLSDAAKNSEDVRCRCICPPYKDNVSGHIYNKNISQKDCDCLHVVDPMP-----VRGPDVEAYC	150
gi	50747768	ref	XP_420984.1	-----MATLGG-----WLCCLGLLAVLAGLGAQAKNSEDVRCRCICPPYKDHSGHIYNKNVSKDCDCLHVVEPMP-----VPGPDVEAYC	150
gi	56118787	ref	NP_956026.2	-----MYRLIHR--AAVNLLIFSSLLCFLLLLAQNSEAKNSEDIRRCRCICPPYKKEVDGKIYNQVSLKDCNCLHVVEPMP-----VEGKDEAYC	150
gi	62472401	ref	NP_001014606.1	-----MAHKRFLVAVLLVICYLGVVWAEATAAQTFPAIGNSNNSNAQAPAPVPAPAAPAAAAAFLAKQVSAPTAAPPAKVIQPPVLAAPGKNSNSNSTTECVACAGALLPRLD--ANGKEL-PIC	150
gi	158285965	ref	XP_308543.4	-----MNHK--LLYSITLVVIFHV--ATIQSQSY-----EDKRRCICPSFKTADN-----FTIQEGTDRMLIIDN-----VPPNK-----CNCDGVLIPRLVGIKKGGO-EIC	150
gi	115532562	ref	NP_001040796.1	MRQPSRKAPVSCITGALLVLLVVFYS EHFLLFSCKNKKKYSPTFSVIFSDLMIVLFIALFLPALSQAGTEANFEDTRCRCICPSLLKFLDLAENITTEKTEGLRRRFYTKTN--IEPSH-----CKPSNIVKDVSNFVDETHMDAPL	150



gi	10092671	ref	NP_064434.1	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHSOLLOSDDDDVG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	27679422	ref	XP_215038.1	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHSOLLOSDDDDIG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	11034855	ref	NP_065695.1	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHAQLIOSDDDDIG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	114636058	ref	XP_001168900.1	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHAQLIOSDDDDIG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	73988420	ref	XP_534047.2	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHSOLIOSDDDDVG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	77735961	ref	NP_001029679.1	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHSOLIOSDDDDVG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	50747768	ref	XP_420984.1	LRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHSOLIOSDDDDIG-----DHOPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	56118787	ref	NP_956026.2	LRCECKYEERSSGTIKVTIIIIYLSILGLLLLYMVVLTLPVEPILKRRFLFGHSOLIOSDDDDVG-----DQPFANAH-----DVLARSRSRANVLNKVEYAQRWKLQVQEQRKS VFDRHVLS	297
gi	62472401	ref	NP_001014606.1	AECKSHVARNTLIIKVVVIVVWIIISILVIYMLFLMCLDPLLN-KRVKANYQEHINEDVHNLKSRVKGIOYSLLVTAQGEDDDDDVDAEAAQLDEPTPPLPAVNNQEL SARAN-VLNRVGHQDDKWKROVREORRHIVDRHTMLN	297
gi	158285965	ref	XP_308543.4	PRCDCKYENRNTIIKVVVIVVWIIISLVIYMLFLMCLDPLLN-KRVKANYQEHINE-----DDDTAVTVG-----NGQDMHVREN-VLNRVGHQDDKWKROVREORRHIVDRHTMLN	297
gi	115532562	ref	NP_001040796.1	ANCDCRYESRNTVLLKVVVIVVWIIISLVIYMLFLMCLDPLLRKKRLSISYQQHNMEDEN-----IFAAAPSTIDDESSAEN-----EMDIQGTIRASNVLGRVEAENRWMKVEEORRNIFEDHTMLN	297

