

gi|167860126|ref|NP_002630.2| MDALQLANSFAFVDFKQLCEKEPLGNVLFSPICLSTLSLAQVGAQGTANEIGOVLFH-- ENVKD-- VPFQFOTVTSVDNKLSSFYSLKLIKRLYVD 95
gi|114673424|ref|XP_523955.2| MLAVFPAPNPFLSTRNTAEGVKSLNHTRPMDALQLANSFAFVDFKQLCEKEPLGNVLFSPICLSTLSLAQVGAQGTANEIGOVLFH-- ENVKD-- VPFQFOTVTSVDNKLSSFYSLKLIKRLYVD 124
gi|6678103|ref|NP_033283.1| MDALRLANSFAFVDFKQLCEKRDPAAGNLFSPICLSTLSLAQVGAQGTANEIGOVLFH-- ENVKD-- VPFQFOTVTSVDNKLSSFYSLKLIKRLYVD 95
gi|16923954|ref|NP_476449.1| MDALRLANSFAFVDFKQLCEKEPAGNLFSPICLSTLSLAQVGAQGTANEIGOVLFH-- ENVKD-- VPFQFOTVTSVDNKLSSFYSLKLIKRLYVD 95
gi|118086487|ref|XP_418986.2| MDALQLANLAFVDFMFKLCEKDRJANIVFAPLCTSTLSLALYKATKGDADQMKKVLHL-- QVVDK-- VSFQFOTVTSVDNKLSSFYSLKLIKRLYVD 95
gi|73945849|ref|XP_533382.2| MECSGELLRPMDALRLANSFAFVDFKQLCEKEPAGNLFSPICLSTLSLAQVGAQGTANEIGOVLFH-- ENIKD-- VPFQFOTVTSVDNKLSSFYSLKLIKRLYVD 107
gi|194664929|ref|XP_001253249.2| MDSLIAANTKFCDFLQKRIISTDDCRKIFFCPLSLSAALGMVRLGARGSSARQIDQVLFHNFPSQNKGNPPDFCLKKAEQETSSKDESGLLSCYFGQLLKLARLKVVDYILSTANRLYGE 121
gi|194678197|ref|XP_001790210.1| MDSLIAANTKFCDFLQKRIISTDDCRKIFFCPLSLSAALGMVRLGARGSSARQIDQVLFHNFPSQNKGNPPDFCLKKAEQETSSKDESGLLSCYFGQLLKLARLKVVDYILSTANRLYGE 121



gi|167860126|ref|NP_002630.2| KSLNLSSTEFISSTKRPVAKLELVDFKDKLEETKGOINNSIKDLTDGHFENILADNSVNDQTKILVVNAAYFVGVKMMKFPSEETKECPFRVNRKDTKPVQMMNMEATFCMGNIDSINCKIIELPFONKHLSMFILLPKDVEDESTGLEK 245
gi|114673424|ref|XP_523955.2| KSLNLSSTEFISSTKRPVAKLELVDFKDKLEETKGOINNSIKDLTDGHFENILADNSVNDQTKILVVNAAYFVGVKMMKFPSEETKECPFRVNRKDTKPVQMMNMEATFCMGNIDSINCKIIELPFONKHLSMFILLPKDVEDESTGLEK 274
gi|6678103|ref|NP_033283.1| KSLNPSTEFISSTKRPVAKLELVDFKDKLEETKGOINNSIKELTDGHFEDILSENSISDQTKILVVNAAYFVGVKMMKFPSEETKECPFRVNRKDTKPVQMMNLEATFCLGNIDDISCKIIELPFONKHLSMFILLPKDVEDESTGLEK 245
gi|16923954|ref|NP_476449.1| KSLNLSSTEFISSTKRPVANELELVDFKDKLEETKGOINNSIKELTDGHFEDILPENSISDQTKILVVNAAYFVGVKMMKFPSEETKECPFRVNRKDTKPVQMMNLEATFCLGNIDDISCKIIELPFONKHLSMFILLPKDVEDESTGLEK 245
gi|118086487|ref|XP_418986.2| KSLSPSTDFVNSTKRPVSELELVDFKDKLEETKGOINNSIKELTDGHFEDILPENSISDQTKILVVNAAYFVGVKMMKFPSEETKECPFRVNRKDTKPVQMMNLEATFCLGNIDDISCKIIELPFONKHLSMFILLPKDVEDESTGLEK 245
gi|73945849|ref|XP_533382.2| KSLNPSTEFISSTKRPVAKLELVDFKDKLEETKGOINNSIKDLTDGHFENILADNSVNDQTKILVVNAAYFVGVKMMKFPSEETKECPFRVNRKDTKPVQMMNMEATFCMGNIDDISCKIIELPFONKHLSMFILLPKDVEDESTGLEK 257
gi|194664929|ref|XP_001253249.2| REFFICPEYLDGVIQFYHTTVEVDFRDKDEKSRQEIFWVESQSQGKIKELFSKDSINSEVVLVNVAVYFKAKWEKYFDCCENTVDVAVFSLSSEKKNVMMNQNGLEFRIGFVDELKAIILELPTTKGKLDVVLLPSSGADNLKALRE 271
gi|194678197|ref|XP_001790210.1| REFFICPEYLDGVIQFYHTTVEVDFRDKDEKSRQEIFWVESQSQGKIKELFSKDSINSEVVLVNVAVYFKAKWEKYFDCCENTVDVAVFSLSSEKKNVMMNQNGLEFRIGFVDELKAIILELPTTKGKLDVVLLPSSGADNLKALRE 271



gi|167860126|ref|NP_002630.2| IEKQLNSELSQWTPNPMANAKVKLSIPKFKVEKMIIDPKASLENLGLKHIFSEDTSDFSGMSETKGVALSNVHVRVCLLEITDGGDSIEVPGARILQHK--- DELNADHPFIYIIRHNKTRNIIFFGKFCSP 375
gi|114673424|ref|XP_523955.2| IEKQLNSELSQWTPNPMANAKVKLSIPKFKVEKMIIDPKASLENLGLKHIFSEDTSDFSGMSETKGVALSNVHVRVCLLEITDGGDSIEVPGARILQHK--- DELNADHPFIYIIRHNKTRNIIFFGKFCSP 404
gi|6678103|ref|NP_033283.1| IEQQLNPETLLOWTNPSTMANAKVKLSIPKFKVEKMIIDPKASLESGLKSLFNESDSDSGMSETKGVSLSNVHVRVCLLEITDGGESIEVPGSRILQHK--- DEFNADHPFIYIIRHNKTRNIIFFGKFCSP 375
gi|16923954|ref|NP_476449.1| IEKQLNPETLLOWTNPSTMANAKVKLSIPKFKVEKMIIDPKASLESGLKSLFNESDSDSGMSETKGVSNVHVRVCLLEITDGGDSIEVPGSRILQHK--- DEFKADHPFIFVIRHNKTRNIVFLGKFSPP 375
gi|118086487|ref|XP_418986.2| LEKALTPETLLOWTNPSTMANAKVKLSIPKFKVEKMIIDPKASLENLGLKNIFNENTSDSGMSETKGVSLSNVHVRVCLLEITDGGESIEVPGSRILQHK--- DEFKADHPFIFVIRHNKTRNIVFLGKFSPP 375
gi|73945849|ref|XP_533382.2| VEQQLNSETLLOWTNPSTMANAKVKLSIPKFKVEKMIIDPKASLENLGLKNIFNENTSDSGMSETKGVALSNVHVRVCLLEITDGGDSIEVPGSRILQHK--- DEFNADHPFIYIIRHNKTRNIIFFGKFSPP 403
gi|194664929|ref|XP_001253249.2| LERNITYEKLVSWSSENNMSEKRVAVSFRPFLTLEDSYDLNPIIDDMGITDIFDETADLSGISEPPPSLYLKVYVHKTFLEVDENGTQAVAAAGVVGMEKSSPSWETFANRPPFLFIRHNKTRNITLFGYRVCSP 405
gi|194678197|ref|XP_001790210.1| LERNITYEKLVSWSSENNMSEKRVAVSFRPFLTLEDSYDLNPIIDDMGITDIFDETADLSGISEPPPSLYLKVYVHKTFLEVDENGTQAVAAAGVVGMEKSSPSWETFANRPPFLFIRHNKTRNITLFGYRVCSP 405



gi|167860126|ref|NP_002630.2| ----- 375
gi|114673424|ref|XP_523955.2| ----- 404
gi|6678103|ref|NP_033283.1| ----- 375
gi|16923954|ref|NP_476449.1| ----- 375
gi|118086487|ref|XP_418986.2| LVAANTKFCDFLQKRIISTDDCRKIFFCPLSLSAALGMVRLGARGSSAEQIDQVLFHNFPSQNKGNPPDFCLKKAEQETSSKDESGLLSCYFGHLLSKIDRIRVDYILSTANRLYGEQGFPCPEYLDGVI 375
gi|73945849|ref|XP_533382.2| ----- 553
gi|194664929|ref|XP_001253249.2| ----- 405
gi|194678197|ref|XP_001790210.1| ----- 405



gi|167860126|ref|NP_002630.2| ----- 375
gi|114673424|ref|XP_523955.2| ----- 404
gi|6678103|ref|NP_033283.1| ----- 375
gi|16923954|ref|NP_476449.1| ----- 375
gi|118086487|ref|XP_418986.2| ----- 375
gi|73945849|ref|XP_533382.2| QFYHTTIESIDFRKETEKSRQEIFWVESQSQGKIKELFDFKDAIDSTIVLVNVAVYFKAKWEKYFDCKNTVDAPFSLNENKKTVMKMHQRGLFRIGFTBELKAIILEMRYIKGALSMFVLLPPYSADNVKGLESELEKNITHEKIVAWS 703
gi|194664929|ref|XP_001253249.2| ----- 405
gi|194678197|ref|XP_001790210.1| ----- 405



gi		167860126		ref		NP_002630.2		-----	375
gi		114673424		ref		XP_523955.2		-----	404
gi		6678103		ref		NP_033283.1		-----	375
gi		16923954		ref		NP_476449.1		-----	375
gi		118086487		ref		XP_418986.2		-----	375
gi		73945849		ref		XP_533382.2		-----	823
gi		194664929		ref		XP_001253249.2		-----	405
gi		194678197		ref		XP_001790210.1		-----	405
						SSENMSEETVEVSFPQFTLEDSYDLNSLILODMGIIDVFEFGKADLIGISPPNLYLSKVVHKTFVEVDEDEGTOAVAASGAVGMERSLSSGVIFTVDPFLFFIRHNKTKILLFYGRVCSF		-----	
					760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870			
