

gi		17136430		ref		NP_476699.1		-----		
gi		158284907		ref		XP_307965.3		-----	TTTITTN	7
gi		15718761		ref		NP_004976.2		-----		
gi		114645662		ref		XP_528758.2		-----		
gi		158508555		ref		NP_001103471.1		-----	MRASIGRPRGWRGALRSFSVETGQRGGGAARGVVAARGVSLVSAQLFFFLVFCRELSYAGRRRNAGIASIGVPIAAARPRTHRCARSSIFLGGRRGGGSSGGGEGGGDGGGGASIPGPRHFGGLGASAAQALKAAAGPEAQRLLPG--	148
gi		50729116		ref		XP_416436.1		-----		
gi		84370270		ref		NP_067259.3		-----		
gi		13928698		ref		NP_113703.1		-----		
gi		51230609		ref		NP_001003744.1		-----		
gi		73982108		ref		XP_540523.2		-----	MHSGPPLLSCEARAAAGLGLPPGQEGGPLAPGA	33
gi		71999796		ref		NP_502213.3		-----		
								1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150		

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gi		17136430		ref		NP_476699.1		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLAWNVNNEQAREVAKQVGIPIYIETSA	146
gi		158284907		ref		XP_307965.3		-----	PVQTMTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLQAWAVDMNQARDVAKQVGVPPVETSA	157
gi		15718761		ref		NP_004976.2		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
gi		114645662		ref		XP_528758.2		-----	LLKMTTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	297
gi		158508555		ref		NP_001103471.1		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
gi		50729116		ref		XP_416436.1		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
gi		84370270		ref		NP_067259.3		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
gi		13928698		ref		NP_113703.1		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
gi		51230609		ref		NP_001003744.1		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
gi		73982108		ref		XP_540523.2		-----	AAGAMTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	183
gi		71999796		ref		NP_502213.3		-----	MTEYKLVVVGGAGVGKSAITLIQHNFVDEYDPTIEDSYRKQVVIDGETCLLDILDITAGQEEYSAMRDOYMRTEGEGFLLVFAVNSAKSFEDIGTYREQIKRVKDAEEVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSA	146
								.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300		



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gi		17136430		ref		NP_476699.1		-----	KTRMGVDDAFYTLVREIRKDKDNKGRGRKMNK--PNRRFKCKML	189
gi		158284907		ref		XP_307965.3		-----	KTRMGVDDAFYTLVREIRKDKKE-RGKKNRKHHLVSSRRFKCQLL	201
gi		15718761		ref		NP_004976.2		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	188
gi		114645662		ref		XP_528758.2		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	339
gi		158508555		ref		NP_001103471.1		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	188
gi		50729116		ref		XP_416436.1		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	188
gi		84370270		ref		NP_067259.3		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	188
gi		13928698		ref		NP_113703.1		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	188
gi		51230609		ref		NP_001003744.1		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	188
gi		73982108		ref		XP_540523.2		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	226
gi		71999796		ref		NP_502213.3		-----	KTRMGVDDAFYTLVREIRKHK-EKMSKDGGKKKK--KSKTKCIVM	184
								.....310.....320.....330.....340.....		

