

gi | 17567243 | ref | NP_509658.1 | **--MEPNLQAKLKGIDAFPCGE--** **--RYWDPVAVNASTVPIPLSQCQYHITLWVFPFAIVFLLAPILTAQIFVRRPNPFPWTRRIILKIGLACLILDIADSLSFVAIVE** 150
gi | 193209740 | ref | NP_510616.2 | **MEIDQLLN** **STGPPISILIP-SNQLVIVPSIFFWILIPVLIHDCKASRQTPPLPWSLMSLRKWFVASLLIIDLRLVFLAWVE** 150
gi | 90403595 | ref | NP_083876.3 | **MDRLCGSGELGSKF** **WDSNLSIYNTPTDLTPCFONSLLAWVPCYLWAAALPCYLFYLRHHLQGLYIVLSWLSRRLKTAIGVLLWCVSADLFFYSFHG** 150
gi | 18034783 | ref | NP_542148.1 | **MDRLCGSGELGSKF** **WDSNLSIYNTPTDLTPCFONSLLAWVPCYLWAAALPCYLFYLRHHLQGLYIVLSWLSRRLKTAIGVLLWCVSADLFFYSFHG** 150
gi | 9955970 | ref | NP_003777.2 | **MDALCGSGELGSKF** **WDSNLSVHTENPDLTPCFONSLLAWVPCYLWAAALPCYLLVLRHHCRGYIILSHLSKLMKVLGVLLWCVSWADLFFYSFHG** 150
gi | 114669484 | ref | XP_001158914.1 | **MDALCGSGELGSKFVVRRCAPGLRGCGRPASPGPRRLPSRGAGSTGEPGKVRKKSARLGRKGIVRWDNSNLSVHTENPDLTPCFONSLLAWVPCYLWAAALPCYLLVLRHHRHCRGYIILSHLSKLTIVLGVLLWCVSWADLFFYSFHG** 150
gi | 73966411 | ref | XP_548204.2 | **MDALCG---SKF** **WDSNLSVHTENPDLTPCFONSLLAWVPCYLWAAALPCYLFYLRHNRGYIVLSHLSRKLTAIGVLLWCVSWADLFFYSFHG** 150
gi | 194676033 | ref | XP_612461.4 | **MDALCGSGELGSKF** **WDSNLSLHTDNPDLTPCFONSLLAWVPCYLWAAALPCYLFYLRHNRGYIVLSHLSRKLTAIGVLLWCVSWADLFFYSFHG** 150
gi | 118099911 | ref | XP_420102.2 | **MEGCCRG---** **CDANLSIHTDSPDLTPCFONILAWIPSIYLVWALPFFVLLILKRSKRGYIVLMLRFRKILFGVLLWCVSWADLFFYSFHE** 150
gi | 145336268 | ref | NP_174331.2 | **MGFREALNWKYCKPIAEG** **FWEKIPDPGAFGAYTPCAIDSLVMVNSHVLGLCFYRIWITLINAQAQIYVLRKMYHCVLWIALACCVVPEVLRVLMGI** 150
gi | 186479062 | ref | NP_174330.2 | **MGFREALNWKYCKPVADG** **FWEKAVDGFAGAYTPCAIDSLVLMVNSHVLGLG** **LLACCVVPEVLRVLMGI** 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 17567243 | ref | NP_509658.1 | **--LFGQFPVAVD-FVYPLTTLCLAMVVLTALIVRCRNYGIIVTSGGLFISWLVFTLSAIPPELLYIQIVNPAEAWNWDYPRCIAFFIWFPCAFETVYLHCYADASPEGYKYL** 300
gi | 193209740 | ref | NP_510616.2 | **LFEHKNVITADLFIIFFHSFTLLALLIATNEVRRAHHSQGPLFCWMLFAVAAPVEFYQMTTGSQP-ELVARIDFFRYVAVLLYFPLVVAEVLHFDSDPFPMPRGYQ** 300
gi | 90403595 | ref | NP_083876.3 | **LIHGSSPAPVFFVTPLVVGITMLLATLTIQYERLQGVSSGVLIIWFLLCVCAIIPFR** **SKILLSALAEKGLDPPFRFTTFYIYFALVFCALILSCFKEKPP-LFSPE** 300
gi | 18034783 | ref | NP_542148.1 | **LIVHGSSPAPVFFVTPLVVGITMLLATLTIQYERLQGVSSGVLIIWFLLCVCAIIPFR** **SKILLSALAEKGLDPPFRFTTFYIYFALVFCALILSCFKEKPP-LFSPE** 300
gi | 9955970 | ref | NP_003777.2 | **LIVHGRAPAPVFFVTPLVVGITMLLATLTIQYERLQGVSSGVLIIWFLLCVCAIIPFR** **SKILLAKAEGEISDPFRFTTFYIHFALVLSALILACFREKPP-FFSAK** 300
gi | 114669484 | ref | XP_001158914.1 | **LIVHGRAPAPVFFVTPLVVGITMLLATLTIQYERLQGVSSGVLIIWFLLCVCAIIPFR** **SKILLAKAEGEISDPFRFTTFYIHFALVLSALILACFREKPP-FFSAK** 300
gi | 73966411 | ref | XP_548204.2 | **LIVHGWAPAPVFSVFTPLVVGITMLLATLTIQYERLQGVSSGVLIIWFLLCVCAIIPFR** **SKILAAAKGEVSDPFHFTTFYIYFALVFCALILSCFREKPP-FFSPA** 300
gi | 194676033 | ref | XP_612461.4 | **LIVHGWAPVFFVTPLVVGITMLLATLTIQYERLQGVSSGVLIIWFLLCVVCGIIPFR** **SKILLSALTKGISDPFRFTTFYIYFALVLSALILSCFREKPP-FFSPA** 300
gi | 118099911 | ref | XP_420102.2 | **LLQSRTPPPVYFVTPLVIGITVLLATLTIQYERLQGVSSGVLIIWFLLCVCAVAPFR** **SKIMTITLQNHVNERFRSAIFYIYFVLLIVELILSCFREKPP-FFSPA** 300
gi | 145336268 | ref | NP_174331.2 | **SLFDMDEETDLPPEVASLMEFAFAMFLMVLIGLETQYVKFRWYVRGVVYVLVADAVLDDVLLPKNSINRTALYLCCISRCCQALFILLVYIPELDLPPYHILNNSLDNVEYDALPGGYNICEPYASIFSGIYFSWMTPL** 300
gi | 186479062 | ref | NP_174330.2 | **SLFDMDEETDLPPEVASLMEFAFAMFLMVLIGLETQYVKFRWYVRGVVYVLVADAVLDDVLLPKNSINRTALYLCCISRCCQALFILLVYIPELDLPPYHILVNNPLDNVEYDALRGGEHICEPRAHSIFSRIFYGWIITPL** 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 17567243 | ref | NP_509658.1 | **CSLGVKPLFVSDLYSNEADTNLNVLPKWYLWDMKQSKKFEETAARRIGSNASRTNRRIRSNDTTPLLNDQSTDDYGVSPAG--QSTQKMPILWFLMFKWQVIAMFVKLLSDVLLFCNPLLLKSLIRFEELERPMWQGVVLA** 450
gi | 193209740 | ref | NP_510616.2 | **ISLGYERTLVADDVFEKMSMDQDYIKARWKTEMLKQTEKAREKQVK---LDDKRERARIGS-EKAPLLG--HFNNYGAVNLDDKDRVIVQPSVTIYVLMQMKWELGGSFILKFLSDLLQFANFTPLNLIIFETPNAPLNGIGLA** 450
gi | 90403595 | ref | NP_083876.3 | **AILGYRRPLEDRDLWSLSBEDCSHKVVQRLLEAWKQKQASRSTATA---TAEPKIP--GEDAVLLK--RPKSKQPSFLRALVRTPTSILLMSACFNLIQDNLGFSVNPOLLSILIRFIDPTAPFWGFLLA** 450
gi | 18034783 | ref | NP_542148.1 | **AILGYRRPLEDRDLWSLSBEDCSHKVVQRLLEAWKQKQASRSTATA---TAEPKIP--GEDAVLLK--RPKSKQPSFLRALVRTPTSILLMSACFNLIQDNLGFSVNPOLLSILIRFIDPTAPFWGFLLA** 450
gi | 9955970 | ref | NP_003777.2 | **AIVGYRRPLEEKDLWSLKEEDRDOMVVOQLLEAWRKQEKOTARHKAS---AAPGKNA--GEDEVLLGA** **RPRPRKPSFLKALLAIFGSFLLSACFKLIODLLSFVNPOLLSILIRFISNPMAFSWGWFLVA** 450
gi | 114669484 | ref | XP_001158914.1 | **AIVGYRRPLEEKDLWSLKEEDRDOMVVOQLLEAWRKQEKOTARHKAS---AAPGKNA--GEDEVLLGA** **RPRPRKPSFLKALLAIFGSFLLSACFKLIODLLSFVNPOLLSILIRFISNPMAFSWGWFLVA** 450
gi | 73966411 | ref | XP_548204.2 | **AIVGYRRPLEEKDLWSLKEEDRDOMVVOQLLEAWRKQEKOTARHKAS---AAPGKNA--GEDEVLLGA** **RPRPRKPSFLKALLAIFGSFLLSACFKLIODLLSFVNPOLLSILIRFISNPMAFSWGWFLVA** 450
gi | 194676033 | ref | XP_612461.4 | **AIVGYRRPLEEKDLWSLKEEDRDOMVVOQLLEAWRKQEKOTARHKAS---AAPGKNA--GEDEVLLGA** **RPRPRKPSFLKALLAIFGSFLLSACFKLIODLLSFVNPOLLSILIRFISNPMAFSWGWFLVA** 450
gi | 118099911 | ref | XP_420102.2 | **AIVGYRRPLEEKDLWSLKEEDRDOMVVOQLLEAWRKQEKOTARHKAS---AAPGKNA--GEDEVLLGA** **RPRPRKPSFLKALLAIFGSFLLSACFKLIODLLSFVNPOLLSILIRFISNPMAFSWGWFLVA** 450
gi | 145336268 | ref | NP_174331.2 | **MQLGYRKPITEKDVWLQDQDQWQETLIKRFQRCWTEESSRRP---HALNHVGDGPEEAELVIRD** **KRHNKPSFLKALMRIFGYPFLIGSFVFLIODLLSFVNPOLLSVILSIFVQKDDAPYWGFLIA** 450
gi | 186479062 | ref | NP_174330.2 | **MQLGYRKPITEKDVWLQDQDQWQETLIKRFQRCWTEESSRRP---HALNHVGDGPEEAELVIRD** **KRHNKPSFLKALMRIFGYPFLIGSFVFLIODLLSFVNPOLLSVILSIFVQKDDAPYWGFLIA** 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 17567243 | ref | NP_509658.1 | **FVLLFSAELSILLSHFVFLMYRQVITLCLTAAYVKRKTLLNNAARRKTVGEIVNLMALDVDRFQMITPQIQWYNSNFFIIGLALFLFQLGVVFGGVAWVLLFPINPFIIMIRKWOIAGMYYKDERIKMVEVNLGKIKVKIL** 600
gi | 193209740 | ref | NP_510616.2 | **VGLFLAQKILSFLMNTFIAMTRVGAKVITMLSCAVYKESLNSARRRTEVDGMRNILSDVDRFRMITPQIQWYNSNFFIIGLALFLFQLGVVFGGVAWVLLFPINPFIIMIRKWOIAGMYYKDERIKMVEVNLGKIKVKIL** 600
gi | 90403595 | ref | NP_083876.3 | **GLMFLSSMOILLILHGHYHICIFVMAALRLRTAIIGVYRKKALVTINSVKRESTVGEIVNLMVSDAQRFMDSVFFINLLWSAPLQVILAIYFLWQILGFSBALAGAVIVLLIPLNGAVSMRKKYTVQVKMKFDSRIKMLSEILNGIKVKIL** 600
gi | 18034783 | ref | NP_542148.1 | **GLMFLSSMOILLILHGHYHICIFVMAALRLRTAIIGVYRKKALVTINSVKREYTVGEMVNLMVSDAQRFMDSVFFINLLWSAPLQVILAIYFLWQILGFSBALAGAVIVLLIPLNGAVSMRKKYTVQVKMKFDSRIKMLSEILNGIKVKIL** 600
gi | 9955970 | ref | NP_003777.2 | **GLMFLCSMMSLILIQHYHYIFVTGMLKFRGTGMGVYRKKALVTINSVKRASTVGEIVNLMVSDAQRFMDLAPFNNLWSAPLQVILAIYFLWQILGFSVLAGVAFVLLIPLNGAVAVKMFRAFOVKMMLKDSRIKMLSEILNGIKVKIL** 600
gi | 114669484 | ref | XP_001158914.1 | **GLMFLCSMMSLILIQHYHYIFVTGMLKFRGTGMGVYRKKALVTINSVKRASTVGEIVNLMVSDAQRFMDLAPFNNLWSAPLQVILAIYFLWQILGFSVLAGVAFVLLIPLNGAVAVKMFRAFOVKMMLKDSRIKMLSEILNGIKVKIL** 600
gi | 73966411 | ref | XP_548204.2 | **GLMFLCSMMSLILIQHYHYIFVTGMLKFRGTGMGVYRKKALVTINSVKRESTVGEIVNLMVSDAQRFMDLAPFNNLWSAPLQVILAIYFLWQILGFSVLAGVAFVLLIPLNGAVAVKMFRAFOVKMMLKDSRIKMLSEILNGIKVKIL** 600
gi | 194676033 | ref | XP_612461.4 | **GLMFLCSMMSLILIQHYHYIFVTGMLKFRGTGMGVYRKKALVTINSVKRESTVGEIVNLMVSDAQRFMDLAPFNNLWSAPLQVILAIYFLWQILGFSVLAGVAFVLLIPLNGAVAVKMFRAFOVKMMLKDSRIKMLSEILNGIKVKIL** 600
gi | 118099911 | ref | XP_420102.2 | **GLMFLCSMMSLILIQHYHYIFVTGMLKFRGTGMGVYRKKALVTINSVKRESTVGEIVNLMVSDAQRFMDLAPFNNLWSAPLQVILAIYFLWQILGFSVLAGVAFVLLIPLNGAVAVKMFRAFOVKMMLKDSRIKMLSEILNGIKVKIL** 600
gi | 145336268 | ref | NP_174331.2 | **ALMFACAVLQTLILHGHYHICIFVMAALRLRTAIIGVYRKKALVTINSVKRASTVGEIVNLMVSDAQRFMDLVFTNLLWSAPLQVILAIYFLWQILGFSVLAGVAFVLLIPLNGAVAVKMFRAFOVKMMLKDSRIKMLSEILNGIKVKIL** 600
gi | 186479062 | ref | NP_174330.2 | **FLIFFGVTFGVLCQSQVQFQVGRVGRFLRSLVAAIFHKSLRLLNKARKNFAGKVTNMTITDANALQLIAEQHLGLWSAPFRIVSMVLLVYQQLGVAIFGSLLIFLIPQTLIVRKRKLTKEGLDQWTKRVGIIYELASMDIVKC** 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 17567243 | ref | NP_509658.1 | 750
gi | 193209740 | ref | NP_510616.2 | 750
gi | 90403595 | ref | NP_083876.3 | 750
gi | 18034783 | ref | NP_542148.1 | 750
gi | 9955970 | ref | NP_003777.2 | 750
gi | 114669484 | ref | XP_001158914.1 | 750
gi | 73966411 | ref | XP_548204.2 | 750
gi | 194676033 | ref | XP_612461.4 | 750
gi | 118099911 | ref | XP_420102.2 | 750
gi | 145336268 | ref | NP_174331.2 | 750
gi | 186479062 | ref | NP_174330.2 | 750



gi | 17567243 | ref | NP_509658.1 | 900
gi | 193209740 | ref | NP_510616.2 | 900
gi | 90403595 | ref | NP_083876.3 | 900
gi | 18034783 | ref | NP_542148.1 | 900
gi | 9955970 | ref | NP_003777.2 | 900
gi | 114669484 | ref | XP_001158914.1 | 900
gi | 73966411 | ref | XP_548204.2 | 900
gi | 194676033 | ref | XP_612461.4 | 900
gi | 118099911 | ref | XP_420102.2 | 900
gi | 145336268 | ref | NP_174331.2 | 900
gi | 186479062 | ref | NP_174330.2 | 900



gi | 17567243 | ref | NP_509658.1 | 1050
gi | 193209740 | ref | NP_510616.2 | 1050
gi | 90403595 | ref | NP_083876.3 | 1050
gi | 18034783 | ref | NP_542148.1 | 1050
gi | 9955970 | ref | NP_003777.2 | 1050
gi | 114669484 | ref | XP_001158914.1 | 1050
gi | 73966411 | ref | XP_548204.2 | 1050
gi | 194676033 | ref | XP_612461.4 | 1050
gi | 118099911 | ref | XP_420102.2 | 1050
gi | 145336268 | ref | NP_174331.2 | 1050
gi | 186479062 | ref | NP_174330.2 | 1050



gi | 17567243 | ref | NP_509658.1 | 1200
gi | 193209740 | ref | NP_510616.2 | 1200
gi | 90403595 | ref | NP_083876.3 | 1200
gi | 18034783 | ref | NP_542148.1 | 1200
gi | 9955970 | ref | NP_003777.2 | 1200
gi | 114669484 | ref | XP_001158914.1 | 1200
gi | 73966411 | ref | XP_548204.2 | 1200
gi | 194676033 | ref | XP_612461.4 | 1200
gi | 118099911 | ref | XP_420102.2 | 1200
gi | 145336268 | ref | NP_174331.2 | 1200
gi | 186479062 | ref | NP_174330.2 | 1200



```

gi |17567243|ref|NP_509658.1|
gi |193209740|ref|NP_510616.2|
gi |90403595|ref|NP_083876.3|
gi |18034783|ref|NP_542148.1|
gi |9955970|ref|NP_003777.2|
gi |114669484|ref|XP_001158914.1|
gi |73966411|ref|XP_548204.2|
gi |194676033|ref|XP_612461.4|
gi |118099911|ref|XP_420102.2|
gi |145336268|ref|NP_174331.2|
gi |186479062|ref|NP_174330.2|

```

NVQFFAQCLLQVVTLLIIMISITPVFGVIVIIPLSVMLVMRYIATSRQLKRLSEITRSPISYHLSSEIQQSARIRAYHLVDRFCKLEBTKVDVSHVCRVNLNIVANRWLSVRLFEFIGNCIVLFSALFAALTR----TTTTSGVIGLGV 1350
SFRFLVMAIIN--MVLIVSYTIPFLFAIITIPVFIYFVFLKYSIKSTRQLQRIASLTRSPIFNFSSETLQGITVIRAFQWSDFVRRNDEHLNTHVKCSYYSQMANRWLSIRLELLGNIVFSAAILAITGKE----SGITAGMLGLSV 1350
ITLMLLNSFFTSISITMIVIVASIPLEFCVVVLPVAVLYGFVORFYVATSRQLKRLSEISRSPIFSHFSEITVGTSVIRAYGRIDQFKVLSDTKVDNNQKSSYPYIASNRLGVHVEFVGNCCVFLFAALFAVIGR----NSLNPGLVGLSV 1350
ITLMLLNSFYTSITMIVIVASIPLEFCVVVLPVAVLYGFVORFYVATSRQLKRLSEISRSPIFSHFSEITVGTSVIRAYGRVQDFKVLSDAKVDSNQRTTTPYIASNRLGVHVEFVGNCCVFLFAALFAVIGR----NSLNPGLVGLSV 1350
VILMLLNSFFNAISTLVVIMASITPLFTVVILPLAVLYTLVORFYAATSRQLKRLSEISRSPIYSHFSEITVGTGAVIRAYNRSRDFEIIISDTKVDAQRSCVPIIISNRWLSIGVEFVGNCCVFLFAALFAVIGR----SSLNPGLVGLSV 1350
VILMLLNSFFNAISTLVVIVASTPLFTVVILPLAVLYTLVORFYAATSRQLKRLSEISRSPIYSHFSEITVGTGAVIRAYNRSRDFEIIISDTKVDAQRSCVPIIISNRWLSIGVEFVGNCCVFLFAALFAVIGR----SSLNPGLVGLSV 1350
ITLMLLNSFFNSVATLVVIVASTPLFTVVILPLAVLYTLVORFYVATSRQLKRLSEISRSPIYSHFSEITVGTGAVIRAYGRSDQDFKAIISDAKVDVAQRSCVPIIASNRLGIRVEFVGNCCVFLFAALFAVIGR----NSLNPGLVGLSV 1350
ITLMLLNSFYNSITLVVIVASTPLFAVVVPLAVLYYVORFYVATSRQLKRLSEISRSPIYSHFSEITVGTGAVIRAYGRSDQDFEITINDAKVDTNOKSCVPIIASNRLGIRVEFVGNCCVFLFAALFAVIGR----SSLNPGLVGLSV 1350
ITLMLFLGTFFAASLTMIVIVASTPLFAVVVPLAVLYYVORFYVATSRQLKRLSEISRSPIYSHFSEITVGTGAVIRAYQRERSFIDIDDKVDENOKSYPGIISNRWLGIRVEFVGNCCVFLFAALFAVIGK----SSLNAGLVGLSV 1350
LNMFMNQLWQLLSTFALIGIVTITSLWAIMPLLILFYAYLYYQSRSRVRRLDVTSPRYIALFGALNGLSIRAYKAYDRMAKINGKSMDDNIRFTLASSTSNRRLTIRSESLGGVMWLITATFAVLRGNAENQAVFASITMGLL 1350
LNMFMNQLWQLLSTFALIGIVTITSLWAIMPLLILFYAYLYYQSRSRVRRLDVTSPRYIALFGALNGLSIRAYKAYDRMAKINGKSMDDNIRFTLANSTSNRRLTIRLETLGGVMWLITATFAVLRQNGTNNQAGFASITMGLL 1350
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



```

gi |17567243|ref|NP_509658.1|
gi |193209740|ref|NP_510616.2|
gi |90403595|ref|NP_083876.3|
gi |18034783|ref|NP_542148.1|
gi |9955970|ref|NP_003777.2|
gi |114669484|ref|XP_001158914.1|
gi |73966411|ref|XP_548204.2|
gi |194676033|ref|XP_612461.4|
gi |118099911|ref|XP_420102.2|
gi |145336268|ref|NP_174331.2|
gi |186479062|ref|NP_174330.2|

```

SYALNITITVLNFAVRQITIKLETINIVSVERVKYEAETEAEWKESEPGKEPPQNWPSEGRIVMNNYSARYRPGLNLVVVKQLNVEIKPHEKVGIVGRGAGKSSVITLSFRITIEAAGEQIVVDGILNLAETIGLHDLRSLNLTITIPDPVLFSGT 1500
SYSLNITFMLNMFVRQINEVETINIVSVERIDYSKTKSEAEWRILD--NNNLPNSNWPGGAVNIEDYSCRYRDELVLKQISLNLILPGQKVGVCGRGAGKSSALALALFRIVEAADGNISIDQITTSHTGLHDLRSLNLTITIPDPVLFSGT 1500
SYALQVITMALNMMIRMSDLESNIIVAVERVKEYSKTTEAPWVVE--SNRAPEGWPPRGVMEFRNYSVRYRPGLELVLKNNVIVVQGGKGVVIGRGTGAGKSSMLLCLFRILEAAEGEIVIDGLNVAHTIGLHDLRSQTLTIIPDPILFSGT 1500
SYALQVITLALNMMIRMSDLESNIIVAVERVKEYSKTTEAPWVVE--SNRAPEGWPPRGVMEFRNYSVRYRPGLELVLKNNVIVVQGGKGVVIGRGTGAGKSSMLLCLFRILEAAEGEIVIDGLNVAHTIGLHDLRSQTLTIIPDPILFSGT 1500
SYSLQVITFALNMMIRMSDLESNIIVAVERVKEYSKTTEAPWVVE--GSRPPGWPPEGRVEFRNYSVRYRPGLDLVLKDLNLSLHVHGGKGVVIGRGTGAGKSSMLLCLFRILEAAEGEIRIDGLNVAHTIGLHDLRSQTLTIIPDPILFSGT 1500
SYSLQVITLALNMMIRMSDLESNIIVAVERVKEYSKTTEAPWVVE--GSRPPGWPPEGRVEFRNYSVRYRPGLELVLKDLNLSLHVHGGKGVVIGRGTGAGKSSMLLCLFRILEAAEGEIRIDGLNVAHTIGLHDLRSQTLTIIPDPILFSGT 1500
SYALQVITLALNMMIRMSDLESNIIVAVERVKEYSKTTEAPWVVE--GSRPPAAMPKGEVEFRNYSVRYRPGLELVLKDLNLSLHVHGGKGVVIGRGTGAGKSSMLLCLFRILEAAEGEIRIDGLNVAHTIGLHDLRSQTLTIIPDPILFSGT 1500
SYALQVITLALNMMIRMSDLESNIIVAVERVKEYSKTTEAPWVVE--GSRPPAAMPKGEVEFRNYSVRYRPGLELVLKDLNLSLHVHGGKGVVIGRGTGAGKSSMLLCLFRILEAAEGEIRIDGLNVAHTIGLHDLRSQTLTIIPDPILFSGT 1500
SYTLNITITLLSGVLRQASKAENSLSNVSVERVGNVYIDLPEAATIE--NRRPVCGWPPRGSIQFEDVFRYRPGLELVLKDLNLSLHVHGGKGVVIGRGTGAGKSSMLNLYRIVELEKGRILIDYVAKPGLDRLRRLSITIPDPVLFSGT 1500
SYTLNITITLLSGVLRQASKAENSLSNVSVERVGNVYIDLPEAATIE--NRRPVCGWPPRGSIQFEDVFRYRPGLELVLKDLNLSLHVHGGKGVVIGRGTGAGKSSMLNLYRIVELEKGRIMIDDCDVAKPGFLDVRRLSITIPDPVLFSGT 1500
.....1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



```

gi |17567243|ref|NP_509658.1|
gi |193209740|ref|NP_510616.2|
gi |90403595|ref|NP_083876.3|
gi |18034783|ref|NP_542148.1|
gi |9955970|ref|NP_003777.2|
gi |114669484|ref|XP_001158914.1|
gi |73966411|ref|XP_548204.2|
gi |194676033|ref|XP_612461.4|
gi |118099911|ref|XP_420102.2|
gi |145336268|ref|NP_174331.2|
gi |186479062|ref|NP_174330.2|

```

LRFNLDPPFNHYSDGDIWKLLEMANLKEFATAHNEQLNIIPEGGDNIS-----VGRQLVCLARALLRKRIVLILDEATAAVDVSTDALIQKTIREFEFANAHLITIAHRLNITIMDYD----- 1650
LRFNIDPKQFIDQLWLALLENLKAHVLELPHLKESEPAVEGGENFS-----VGRQLLCLTRALLRKRKSVLVLDEATAGIDNRTDTMVAQTIREFKADSRILITIAHRLNITIDYD----- 1650
LRNMLDPPFCRYSBEDIWRLELHSLNTHVSSQPAGLDFQCAEGEDNLS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDN----- 1650
LRNMLDPPFCRYSBEDIWRLELHSLHSAFVSSQPTGLDFQCEGGENLS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDN----- 1650
LRNMLDPPFGYSSEDIWALELHSLHTFVSSQPAGLDFQCEGGENLS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDY----- 1650
LRNMLDPPFGYSSEDIWRLELHSLHTFVSSQPAGLDFQCEGGENLNEPFPFEMISSQVFCVGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDYTSWRPTEQOQOQOQOQPPDLOP 1650
LRNMLDPPFGYSSEDLWRLELHSLHTFVSSQPAGLDFQCEGGENLS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDY----- 1650
LRNMLDPPFCYSEEDMWALELHSLHTFVSSQPAGLDFQCEGGENLS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDY----- 1650
LRNMLDPPFNKYSDEEVWKALELHSLKRFVSSQPSMLPEFCEGGENLS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIMDY----- 1650
VRFNIDPFSEHNDADLNEALERAHIKDVIDRNPFGLDAEVSEGGENFS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIDCD----- 1650
VRFNIDPFSEHNDADLNEALERAHIKDVIRNPFGLDAEVSEGGENFS-----VGRQLVCLARALLRKRIVLVLDEATAAIDLETDDLIOQTIRTOFEDCTVLTIAHRLNITIDCD----- 1650
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



```

gi |17567243|ref|NP_509658.1|
gi |193209740|ref|NP_510616.2|
gi |90403595|ref|NP_083876.3|
gi |18034783|ref|NP_542148.1|
gi |9955970|ref|NP_003777.2|
gi |114669484|ref|XP_001158914.1|
gi |73966411|ref|XP_548204.2|
gi |194676033|ref|XP_612461.4|
gi |118099911|ref|XP_420102.2|
gi |145336268|ref|NP_174331.2|
gi |186479062|ref|NP_174330.2|

```

RIIVLNDGKVGDFSPANLLSNRNSFYVSMARAGLI-----1726
RIIVMDAGRIVEDGIPGELLKNRNSQFYGLAKSAKIV-----1726
RVVLVDKGVVAEFDSPVNLIAAGG--IFYGMARDAGLA-----1726
RVVLVDKGVVAEFDSPVNLIAAGG--IFYGMARDAGLA-----1726
RVVLVDKGVVAEFDSPANLIAARG--IFYGMARDAGLA-----1726
KPGIIPVSAISLQLVSCRVLLVVLVDKGVVAEFDSPANLIAARG--IFYGMARDAGLA-----1726
RVVLVDKGMIAEAFDSPANLIAARG--IFYGMARDAGLA-----1726
RVVLVDKGTIAEAFDSPANLIAARG--IFYGMARDAGLA-----1726
RILVLDNGTIAEAFDSPANLIAASKG--IFYGMARDAGLV-----1726
KILVLSSQVLEYDSDPQELLSRDTSAFFRMVHSTGPEVGOVLSNLFERRNGMSVGG-----1726
KILVLSSQVLEYDSDPQELLSRDTSAFFRMVHSTGPAVQVLSNLFERRNGMSVGG-----1726
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....

