***Anst*ABCB2 gene**

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AnstABCB2   ------------------------NDFSRSTHVCT------------------------------------------------------CFANFPNLISD   100
AGAP005639  MTAKEYPQGNGTFQTMNLKNGNGADNMSVASHKSTKDILDVKAPTKEPVSQSVSYFKLFRFATWGEVCATLMGVLLASMASLGLPYGVILYGEFTTLLVD
                                    :::* ::* .*                                                       :.:*..*: *

AnstABCB2   YRR--------------------VNATEQENAAAIMEDAKAFGLGVVAVTILQFIFATLSVDIINRSAQKQISRIRQLFLKAVLRQDMTWYDLNSDDSFA   200
AGAP005639  RTIGIGKSTDTAILSIFGGGRVLVNATEQENAAAIMEDAKAFGLGVVAVTILQFIFATLSVDVINRSAQKQISRIRQLFLKAVLRQDMTWYDLNSDDSFA
                                   ***************************************:*************************************

AnstABCB2   VRITDDLDKLKEGIGEKLSIFTYLVMSFVISVIFSFFYGWKLTLVILSCAPIIILATAFVAKMQSTLTEKELKSYSSAGAVAEEVLGSIRTVVAFGGEKK   300
AGAP005639  VRITDDLDKLKEGIGEKLSIFTYLVMSFVISVIFSFFYGWKLTLVILSCAPIIILATAFVAKMQSTLTEKELKSYSSAGAVAEEVLGSIRTVVAFGGEKK
            ****************************************************************************************************

AnstABCB2   ELDRYRERLAGAELNGRRKGLFSGIGGGIMWFIIYCCYALAFWYGISLILEDRDKDLKDYTPAVLIIVLFGVLAGAQNLGLSSPHLEAFSTAKGSAATIF   400
AGAP005639  EADRYRERLAGAELNGRRKGLFSGIGGGIMWFIIYCCYALAFWYGISLILEDRDKDLKDYTPAVLIIVLFGVLAGAQNLGLSSPHLEAFSTAKGSAATIF
            * **************************************************************************************************

AnstABCB2   SVIDRKPEIDSLGDAGLRPKSMQGNIKFTNVCFRYPARNDVQVLQGLNLEIKTGQTVALVGPSGCGKSTCLQLIQRLYDPLSGTVTIDGTKVSELNIGWL   500
AGAP005639  SVIDRIPVIDSLGDAGLRPGSMQGNIKFSNVFFRYPARNDVQVLQGLNLEIKTGQTVALVGPSGCGKSTCLQLIQRLYDPLSGSVTIDGTKVSELNIGWL
            ***** * *********** ********:** ***************************************************:****************

AnstABCB2   RSFIGLVGQEPVLFATTIAENIRYGNPDATQSEIECAAKIANCHSFIMKLPNAYGTMIGERGAQLSGGQKQRIAIARALVRNPKILLLDEATSALDPNSE   600
AGAP005639  RSFIGLVGQEPVLFATTIAENIRYGNPDASQSEIERAAKIANCHSFITKLPNGYATMIGERGAQLSGGQKQRIAIARALVRNPKILLLDEATSALDPNSE
            *****************************:***** *********** ****.*.*********************************************

AnstABCB2   KRVQDALERASKGRTTLVVSHRLSTITNADKIVYIDKGVVMEQGTHEELMAARGLYYELVVASGSQKSADDDESVPLAPSAFSMRQESVEDGADGSDDES   700
AGAP005639  KRVQDALERASKGRTTLVVSHRLSTITNADKIVYIDKGLVMEQGTHEELMAARGLYYDLVVASGSQKTVDDDESVPMAPSALSMRQESVDDGAEASDDES
            **************************************:******************:*********:.*******:****:*******:***:.*****

AnstABCB2   DSGKSDEKNEEEQEEVYHVSVLRLLKLNSPEWHYILFGCAAAIVVGASFPAFAVLFGEMYGILSVADPAFVKQESNFYSLLFLALGLITGLGTFFQTYLF   800
AGAP005639  DSGKSDEKNEEEQEEVYHVSLMRLLKLNAPEWHYILFGCAAAIVVGASFPAFAVLFGEMYGILSVADPEYVKEESNFYSFLFLVLGLITGVGTFFQTYLF
            ********************::******:*************************************** :**:******:***.******:*********

AnstABCB2   NIAGVRLTSRLRQKSFKAIVTQDMAWFDESRNAVGALCARLSGDCASVQGATGTRIGSLLQAASTICIGVGISFFYSWNLTLVSIVAIPVTLASITLESR   900
AGAP005639  NIAGVRLTSRLRQKSFKAIVSQDMAWFDESRNAVGALCARLSGDCASVQGATGTRIGSLLQAASTICIGVGISFFYSWNLTLVSIIAIPVTLASITLESR
            ********************:*****************************************************************:**************

AnstABCB2   YTQMSSLKEKQSLEGATKLAVEAISNIRTVASLGQEQHVLHRYSQETVKIDDACRRKTRLRGTVFALGQVMPFAGYGLALFYGGKLVSEKELEYKDVIKV  1000
AGAP005639  YSQTSSLKEKQSQEGATKLAVEAISNIRTVASLGQEKHVLQRYGEETVKIDDACRRKTRLRGTVFALGQVMPFAGYGLALFYGGKLVSEKELEYKDVIKV
            *:* ******** ***********************:***:**.:*******************************************************
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AnstABCB2    SEALIFGAWMLGQALAYAPNVNSAILSAGRLMKLLDRTPRMHNPSSSYHSLSQRTEGDIKFTDVEFRYPTRPSVPVLQGLNLDIGKGQTVALVGPSGCGK  1100
AGAP005639   SEALIFGAWMLG-ALAYAPNVNSAILSAGRLMKLLDRTPRMHNPSTSYHSLSQRTEGDIKFTDVEFRYPTRPTVPVLQGLNLDIGKGQTVALVGPSGCGK
             ************ ********************************:**************************:***************************

AnstABCB2    STCIQLLLRYYDPDSGKVDIDGTTTTEFSLNRIRAQMGLVSQEPILFDRTIAENIAYGDNTRDIAMPEIIEAAKMANIHEFIVNLPKGYDTSLGSKGAQL  1200
AGAP005639   STCIQLLLRYYDPDSGKVDIDGTTTTEFSLNRIRAQMGLVSQEPILFDRTIAENIAYGDNTREIAMPEIMEAAKMANIHEFIVNLPKGYDTSLGSKGAQL
             **************************************************************:******:******************************

AnstABCB2    SGGQKQRIAIARALVRNPRVLLLDEATSALDNQSEKIVQNALDHARTGRTCIIIAHRLTTIQNANLICVIQNGVVVEAGTHDELMAKNRIYAKLYQMQQVA 1301
AGAP005639   SGGQKQRIAIARALVRNPRVLLLDEATSALDNQSEKIVQNALDHARTGRTCIIIAHRLTTIQNANLICVIQNGVVVEAGTHDELMAKSRIYAKLYQMQQVA
             ***************************************************************************************.*************
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AnstABCB3 gene

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AnstABCB3   MLKLLLSPHRQCCWQGLLRSSPYSTDSKHVLVRKTLQSFGSGRTGFLQPFRNTTLR-AVRPSHTVTKTGSQGGRLIRVLLGGTAVTFTLGYQYRKLFVHC  100
AGAP006273  MLKLLLSPHRQCCWQGLTRSSPYSTEGKHVLLRKTVQSFGLGRNGFLQPIRNTIQRTVVRPSHTVTKTGSQGSRLIRVLLGGTVVSITLGYQYRKSFVHC
            ***************** *******:.****:***:**** **.*****:***  * .**************.**********.*::******** ****

AnstABCB3   EASVNRLAGQRNLLDDGTVRFDWWKFWRYLRHHLGKLIGAVLAALAVAYFNIQIPNLLGVIVNKLARYAGSSLKDINTASFFRDMRGPALQLFGMYLAQS  200
AGAP006273  EASVNRLAGQRQLVDDGAVRFDWWKFWHYLRRHLGKLIGAVMAALAVAYFNIQIPNLLGVIVNKLARYAGSSIKDINTASFFRDMRGPALQLFGMYLAQS
            ***********:*:***:*********:***:*********:******************************:***************************


AnstABCB3   GFTFLYILLLSQIGEQMAASIRQDLFKQIIIQDLEFFDHNRTGELVNRLTADVQDFKSSFKQCISQGLRSFAQLVGGGISLFWISPQLASIALVSVPLAV  300
AGAP006273  GFTFLYILLLSQIGEQMAASIRQDLFKQIIIQDLEFFDHNRTGELVNRLTADVQDFKSSFKQCISQGLRSFAQLVGGGISLFWISPQLASIALVSVPVAV
            *************************************************************************************************:**


AnstABCB3   AMFSLLGRSLRHLSKKAQAQSERATSVSEEALSNIRTVRASASEYSEVELFRAETEKSAVISQQLGAGIAVFQALSNLCLNGMVLTTLLLGGHFMSANSI  400
AGAP006273  AMFSLLGRSLRHLSKKAQAQSERATSVSEEALSNIRTVRASASEYSEIELFRVETDKSAVLSQQLGAGIAVFQALSNLCLNGMVLTTLLLGGHFMSANSI
            ***********************************************:****.**:****:***************************************

AnstABCB3   SAGDLMAFLVAAQGVQRSLAQGSILLGSVIRGMTAGARVFEFLSLEPRVDLKHGLIIPHGNLKGEIRFEGVQFVYPTRPNQRVLKDFNLVLRPGQTVALV  500
AGAP006273  SAGDLMAFLVAAQGVQRSLAQGSILLGSVIRGMTAGARVFEFLSLEPRVDLKHGLIIPDSNLRGEIRFEGVQFIYPTRPNQRVLKDFNLVLRPGQTVALV
            **********************************************************..**:**********:**************************


AnstABCB3   GASGSGKSTVAALLERFYEPTAGRITIDGYELGHLSPSWLRGELIGFIEQQPVLFGTTIYENIRYGRPNATREEVMEAAKMSQSHEFVSRLPDGYDTMVG  600
AGAP006273  GASGSGKSTVAALLERFYEPTAGRITIDGYELGHLAPSWLRGELIGFIEQQPVLFGTTIYENIRYGRPNATREEVMEAAKMSQSHEFVSRLPDGYETMVG
            ***********************************:***********************************************************:****


AnstABCB3   ERGIQLSGGQRQRIAIARALLKQPLILILDEATSALDAASESIVQSALDAAVLDRTTLVIAHRLSTIRNADVIVVLDQGQIVEVGTHDSLIKAQGYYYEL  700
AGAP006273  ERGIQLSGGQRQRIAIARALLKQPTILILDEATSALDAASEAVVQRALDAAVLDRTTLVIAHRLSTIRNADVIVVLDQGQIVEVGTHDSLLKAQGYYYEL
            ************************ ****************::** ****************************************************** 


AnstABCB3   VKQQERQQRQEQDSRALG  718
AGAP006273  VKQQERQQRQEHDARSYG
            ***********:*:*: *
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AnstABCB4

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AnstABCB4     MAALLLQVVSKQAPQLNRNLLEGVRLSYKNHHPLCENYCRLHSRQLHVSGVVVANWYNDDARSRKGGRREPWAQRRNYSTE----TKNQQATENALLNIS  100
AGAP006364    MAA-LLHVVSKQAPQLNRNLLEGVRLSFKNHHPLSETHCRLQSRQLHVSAVAVANWYHD---NRKRKHSEPWGQRRSYATQGALPEKNQQATENALLNIF
              *** **:*****************:******.*.:***:*******.*.*****:*    .**  : ***.***.*:*:     ************* 

AnstABCB4     QKKKKAPLLLAGVSGCGSQPLQSPNPRPQQQHQEQERCNRRDDGRNTPNRLHPSSTTSSSFAGGPLATKRFIITSSGLSFLPCQLTTNSLQAAPLTKQTP  200
AGAP006364    QKKRKAPWEIRTTDSSHSATRQ----RPQAQ---QERYYRRSGDSSMTNRLHPSSFSSSMLRGPPLAKPTSAITSNGSSIL--LPATQPSLQAPFTKQPP
              ***:***  :  .... * . *    *** *   ***  **... . .******* :** : * ***.    ***.* *:*    :*:.   **:***.*

AnstABCB4     PIRHCFHLGHHPASGESIGTYDGPEITATDMIKAMATYIWPKDDAMVRKRVLISLSLLGGAKVLNVCVPFLFKMGVDNLNLLSMDTVPQAASALTISVLL  300
AGAP006364    PIRHCFHLGHHPASGESIGTYDGPEITATDMIKAMATYIWPKDDAMVRKRVLISLGLLGGAKVLNVCVPFLFKMGVDNLNVLSMDTVPQAASALTISVLL
              *******************************************************.************************:*******************

AnstABCB4     GYGIARAGAAGFNELRNAVFARVAQHSIRKIATNVFLHLHNLDLQFHLSKQTGALSKTIDRGSRGINFVLTAMVFNVVPTMFELALVSSILGVKCGMAYA  400
AGAP006364    GYGIARAGAAGFNELRNAVFARVAQHSIRKIATNVFLHLHNLDLQFHLSKQTGALSKTIDRGSRGINFVLTAMVFNVVPTMFELALVSSILGMKCGMAYA
              ********************************************************************************************:*******

AnstABCB4     ALSMGCVGVYSAYTLAVTQWRTKFRIYMNQAENEAGNKAVDSLINYETVKYFNNEQYEANRYDQVLKKYEDASLKTSTSLALLNFGQNAIFSVALSTIMV  500
AGAP006364    ALSMGCVGVYSAYTLAVTQWRTKFRIYMNQAENEAGNKAVDSLINYETVKYFNNEQYEANRYDQVLKKYEDASLKTSTSLALLNFGQNAIFSVALSTIMV
              ****************************************************************************************************

AnstABCB4     MAANEIAQGRMTVGDLVMVNGLLFQLSIPLGFLGSVYREVRQALLDMRTMFTLMGVQSAIQSRVNAPPLDVSRETASIEFRNVGFRYAQSNDIFKDLSFT  600
AGAP006364    MAANEIAQGRMTVGDLVMVNGLLFQLSIPLGFLGSVYREVRQALLDMRTMFTLMGVQSAIQSRANAPPLDVRRETASIEFRNVGFRYAQSNEIFKDLSFT
              ***************************************************************.******* *******************:********

AnstABCB4     IPAGKKIAIVGGSGSGKSSMVRLLYRFFEPTTGEILINGQNIREVDLQSLRRAIAVVPQDSVLFHDTIRHNIHYGDLSKSQEELENAARMADLHESIQQW  700
AGAP006364    IPAGKKIAIVGGSGSGKSSMVRLLFRFFEPSTGQILINGQNIREVDLQSLRKAIAVVPQDSVLFHDTIRHNIHYGDLSKSQTELENAARMADLHDSILQW
              ************************:*****:**:*****************:***************************** ************:** **

AnstABCB4     PKQYDTQVGERGLKLSGGEKQRVAIARAILKNSPILIFDEATSSLDSITEHNILQALARATDNRTSICIAHRLSTVMDADEILVLENGRVAQRGTHDQLL  800
AGAP006364    PKQYETQVGERGLKLSGGEKQRVAIARAILKNSPILIFDEATSSLDSITEQNILQALARATDNRTSICIAHRLSTVMDADEILVLENGRVGQRGTHDQLL
              ****:*********************************************:***************************************.*********

AnstABCB4     RSGGLYTKLWDTQNRLYNIGGKKLNAEEKK--  831
AGAP006364    RSGGLYTKLWDTQNRLYNIGSKKPTKPEGEEK
              ********************.** .  * :
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AnstABCBmember6

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AnstABCBmember6     MIHYCPTNTSMNVVWFNHGVSQCFMDTVAMGTIGGFMLIFGTLQLLMYLRHATEIDTQRIRKSRLYNFQLFLLLLMPLLTVARFVLEGFI   90
AGAP002278          MIRYCPTNTSMDVVWFNHGVSQCFMDTVAMGTIGGFMLIFGTLQLIMYLRHATEIDTQRIRKSRLYNFQLFLLVLMPLLTTARFVLEAFV
                    **:********:*********************************:***************************:******.******.*:

AnstABCBmember6     FDGAQVYGFMVLSIAVALFAYPFAIVLLVKERYYQLPSVPTRGHGLVLLLFWTLVFIVQNIAFINLNYHDAWFRLETLRDKVEFGMFVAR  180
AGAP002278          FEGAQVYGFMVLSIAVALFAYPYSIVLLVKERYYQLPSVPTRGHGLVLLVFWTLLFIVQNIAFVNLNYRDAWFRLETVRDRVEFGMFVAR
                    *:********************::*************************:****:********:****:********:**:*********


AnstABCBmember6     YTITMLLFVIGLKAPGITSTQFTEEYQNLHQAQ-ENQSTFSNAWTKMRTLLPFLWPKKDAFLQFRVVFCFLLLIAGRLINVYVQIYNKKI  270
AGAP002278          YTVTMLLFVIGLKAPGITSTQFTEEYQHLHQAQ-ENRSTFANAWTKMRTLLPFLWPKKDALLQFRVVFCFLLLIAGRLINVYVQIYNKKI
                    **:************************:***** **:***:*******************:*****************************

AnstABCBmember6     VDSLTEKPATFRWDWILLYVGFKFLQGGGTGSMGLLNNLRSFLWIRIQQYTTREIELELFRHLHSLSLRWHLNRKTGEVLRVMDRGTDSI  360
AGAP002278          VDSLTEKPTVFRWDWILLYVGFKFLQGGGTGSMGLLNNLRSFLWIRIQQYTTREIELELFRHLHSLSLRWHLNRKTGEVLRVMDRGTDSI
                    ********:.********************************************************************************


AnstABCBmember6     NNLLNYILFSITPTIVDILIAVVFFITAFNWWFGFIVFLTMTLYIVATIMVTEWRTKFQRRMNLADNQQKARSVDSLLNFETVKYYGAEQ  450
AGAP002278          NNLLNYILFSITPTIVDILIAVVFFITAFNWWFGFIVFLTMTLYIVATIMVTEWRTKFQRRMNLADNQQKARSVDSLLNFETVKYYGAEQ
                    ******************************************************************************************

AnstABCBmember6     YEVSCYRDAILKFQDEEWRSIITLNILNTMQNVIVCGGLLAGSMLCAYLVVYEEGLTVGDYVLFASYIIQLYVPLNWFGTFYRAIQKNFV  540
AGAP002278          YEVSCYRDAILKFQDEEWRSIITLNILNTMQNIIVCGGLLAGSLLCAYLVVYEEGLTVGDYVLFASYIIQLYVPLNWFGTFYRAIQKNFV
                    ********************************:**********:**********************************************


AnstABCBmember6     DMENMFDLMREEQEVLDAPSAPGLAVARGRIDFNDVTFGYNAERLVLRNVSFTVPGGKTVAIVGPSGAGKSTIMRLLFRFYDVNSGSISV  630
AGAP002278          DMENMFELMREDQEVVDAPSAPGLAVARGRIDFNDVTFGYNAERLVLRNVSFSVPGGKTVAIVGPSGAGKSTIMRLLFRFYDVNNGSILV
                    ******:****:***:************************************:*******************************.*** *

AnstABCBmember6     DGQNIKIVRQASLRQAIGVVPQDTVLFNNTIKYNIQYGRVGAPEADVIMAARSADIHERILTFPEQYETQVGERGLRLSGGEKQRVAIAR  720
AGAP002278          DGQNIKTVRQASLRQAIGVVPQDTVLFNNTIKYNIQYGRVGAPEADVIMAARSADIHERILTFPEQYETQVGERGLRLSGGEKQRVAIAR
                    ****** ***********************************************************************************


AnstABCBmember6     TILKSPAIVLLDEATSALDTQTERNIQTALAKVCANRTTIIIAHRLSTIIHADEILVLKEGSIVERGRHEMLLDQNGVYAEMWNQQLKNL  810
AGAP002278          TILKSPAIVLLDEATSALDTQTERNIQSALAKVCANRTTIIIAHRLSTIIHADEILVLKDGSIVERGRHDNLLEQSGVYAEMWNQQLKNL
                    ***************************:*******************************:*********: **:*.**************
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AnstABCBmember6  ELGASATEEAALVDGNGQVANGTPNKLPAIAPPNHQHHPHH  851
AGAP002278       ELGGSGAAEEGVDAANGQVANGTPNKVAAIAAPPAHHHHH-
                 ***.*.: * .:  .***********:.***.*  :** *
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AnstABCG4

```
AnstABCG4    DKDQENLSVASSGFGYSKTYEVVVLLHFQQANKTSKEGSAGPRDGQKMVGLKNKQLINFLSSCDFCFRFRLASAFFAYRPLVPYLHFEGFFLWLFSIELI  100
AGAP001333   ----------------------------------------------------------------------------------------------------


AnstABCG4    LCFVQFYLLPALPKRTAGVFRYGKGAHLLNDLFYGILGNKRLVVFETILRVFVELDHFGVREARASASVMSTWETIANESWAVVDNLDGMPPVAGRSSTD  200
AGAP001333   ---------------------------------------------------------MSAREAVVSTAVCCTVDNLDGMPGVTVAQHE---VAAAAADDD
                                                                      :..*** .*::* .* :.: . . ..* : :    .*. :. *


AnstABCG4    VTLMWQNLTITPVRSTPSSGGGGQLPVLNDISGTLQPGTLVALMGPSGAGKTTLMSALAYRMSDKMTITGDIRVNGCPIGPFMYNISGYIYQDELLPDSI  300
AGAP001333   VTLIWQNLTITPIRSKP--GAGEQHPVLNDISGTLQPGTLVALMGPSGAGKTTLMSALAYRMSDKMTIAGDIRVNGCPIGPYMYNISGYIYQDELLPDSI
             ***:********:**.*  *.* * *******************************************:************:******************


AnstABCG4    TVQEHLQLMAHLKLGKRVSADRKRTMIADILSKTGLERCANTKIANASGIGKTLSGGEKKRLAFAVELLSKPKFLFCDEPTTGLDSYSARQLVEMMKSLT  400
AGAP001333   TVQEHLQLMANLKLGKSVTAERKRAMIAHILSRTGLERCANTKIADATGIGKTLSGGEKKRLAFAVELLSKPKFLFCDEPTTGLDSYSARQLVEMMKSLT
             **********:***** *:*:***:***.***:************:*:****************************************************

AnstABCG4    RAGTTVLCSIHQPAEKLLYEFDSLILLTGGQTGFIGSPHEAVQFFRLQGLECEHGYNTADFLIKVLSSTTTAKTTKGNQFTTGAICPKTICNNYIASEAA  500
AGAP001333   RTGTTVLCSIHQPAEKLLYEFDSLILLTGGRTGFIGAPSEAVQFLRLQGLECEAGYNTADFLLKVLSSTTTT-TRKGNQFTTGAIGPKTICNNYSASEAA
             *:****************************:*****:* *****:******** ********:********: * ********** ******** *****


AnstABCG4    RRQEALISAELYSTAVD-GRDEAFRKQLTKARDRCWFYTLYWLMYRHVLQAHRNPNLQYFKIAQRIAIAVLVGLCFSDAIELSQRGVQAMQGVIFLIVSE  600
AGAP001333   RRQEALISVELYRTTVDSGGDEAFRRRLTESRDRCWFYTLYWLMYRHVLQSHRNPNLQYFKIVQRIAIAVLVGLCFSDAIELSQRGVQAMQGVIFLIVSE
             ********.*** *:** * *****::**::*******************:***********.*************************************


AnstABCG4    NTFLPMYAALSMFPDSFPLFQREKKANLYSTAQFYISSILSMSPFVLLETCAFILIVYFLANLRPTLLGLIVTVAVSVLVMNVSIACGCFFSTLFPTVAS  700
AGAP001333   NTFLPMYAALSLFPERFPLFQREKKANLYSTAQFYISTIMSMTPFVLLETCAFILIVYFLANLRPTLLGLLVTVVVSVLVMNVSIACGCFFSVLFPTVAS
             ***********:**: *********************:*:**:***************************:***.*****************.*******

AnstABCG4    AMSYLVPFDYILMITSGIF-  720
AGAP001333   AMSYLVPFDYILMITSGIFI
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