

Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 -----MSALEKMVNKNKESATKTVLVPVPELSTPGMASQNIYTQILDTTEI-----TYSEDLKETAV  
Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 -----MDTDLNKSQKSNFENEIQMDIISNDTESK-----ECKETSVTNRPN  
Myessoensis.XP\_021350798.1\_uncharacterized\_protein -----MDIQHLRKGKTTNVLDLNPSSRHRCLDNGPIATIPLNKLDPDVRGMS-----SVDSQSDVVPQ  
Avaga.UJR10076.1\_hypothetical\_protein\_I4U23\_014298 -----MTKKFTDYDNSGFVTDLPQVYINRNLGVVTSKLKRN-----EEEEYDDDKDN  
Avaga.UJR35986.1\_hypothetical\_protein\_I4U23\_028726 -----MTKVAVDNDYELGELSSRRIQPVTEETQSQVQISQTYENSGFVKDQ-----IDAESGVITTK  
Egranulosus.XP\_024350707.1\_solute\_carrier\_family\_2 -----MTRFENSTRCFDETEPRETEIEEPLNSIEKQLYDDIAKILPT-----PTCEWTESDFPD  
Egranulosus.XP\_024352129.1\_solute\_carrier\_family\_2 -----MSPKKTDDEIEVGYEKEVSDSEGSFSDSSSDSYEESLEKPPDK-----PMTIEWGDDFFN  
Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp -----MSAESKGAINGYELDHKELDIRDSEEFTEH-----PLDDTSEVANKK  
Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp -----MAEP IEGEQEEKPPPSRAKRITYLVLHLLHIFISYFTAA-----TIIFIFDKDSKECWFN  
Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_m -----MELKEIRSERVDPDQTMNHVDCTEKAIVDVYVEDKRTQOS-----LLSKQCPNGTEK  
Aplanci.LOC110983407\_solute\_carrier\_family\_28\_memb -----MMNSDSTIYLEDGCGKEAGPAETLPLRWEGLSNKSQA-----RSTSDHAKIAID  
Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 -----MDTHKNSISRTVSRDITSDGSEELVSQLLTNGKASVVVDV-----DVLPEKKRSSER  
Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 -----MGVRGQDQLTEDTTEPLVNDHVNSTGPGDGRRT-----RRPPCAPP  
Hsapies.NP\_004203.2\_sodium/nucleoside\_cotransport -----MEKASGRQSIALSTVETGTVPNGLEIMEKEVEPEGSKRT-----DAQ  
Hsapies.NP\_004204.3\_sodium/nucleoside\_cotransport -----MENDPSSRRRESISLTPVAKGLNMGAD-----FLESLEEQQLP  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 -----MGEKEEPTELEECDELEKG-----EKVKLNEEVEPE  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran -----MSKNDASTMSFSTIPEKTPKPLNGESNQAFEDDDSVCKSDEK-----QOETIAIQELKE  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran -----MSRVRRVSGVPVPSCHNEAKYSVDFFAKNLPTSVEDLCAEEADLNESALPLPPNGNNGRDSFIVNIGDPNEDSSGFSFSSNRSDEADSNAGVDSQ-----QOENIADSTE  
Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 -----MNSTEVEVMTEEDLKAHREHLMICDEDKG-----QEHNTKQDEEQ  
Hsapies.NP\_001186562.1\_solute\_carrier\_family\_28\_m -----MELRSTAAPRAEAGYSNVGDNLENENTSGNRSIRSAVQS-----RHTMTKQDEEQ  
Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me -----MSKKFPQSDDLQVGFVDTLSNLTP-----DHDHLEETETVE  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor -----MEGKFORSSGGKDVSAHSYQNPALSTEDIAPEPTKRDEP-----RGVNDNVVDRLN  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 -----MPAYTYKEVEHEEKPDPEVFGQSADSIISQPPPYEDI-----AVNFGPEAKSSRRP  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 -----MPIELKSYQGGQDLTPDQDQEIQSPNNVT-----TQIKNGRPBGDID  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me -----MEYTTYTNPDSDGNFSTITDFPEDSKSWGNFSMTSKKPVSRALD-----TEYGPLINEVDN  
Aplanci.LOC110990438\_solute\_carrier\_family\_28\_memb -----MPSESPNSKKPLVDVPQASMQPMLKSDVSVNIEGYASEGYLSKATVSSLDGSN-----DELKVVINDGVP  
Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_m -----MGSMQRHDCASSAALGVVRMPKGSFELNDMK-TNGKERQVIVQDDVHDGATPGKQNT-----ALDSTYEEVIPPQGLMSEGNTGGNGLD  
Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_m -----MGSMQRHDCASSAALGVVRMPKGSFELNDMK-TNGKERQVIVQDDVHDGATPGKQNT-----ALDSTYEEVIPPQGLMSEGNTGGNGLD  
Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_m -----MPSKASFELSDMK-ANGKERQVIVQDDVHDGATPGKQNA-----AVDSTYEEVIPPQGLMSEGNTGGNGLD  
Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_m -----MDSNSPPIELSERPKDDEGPNIAATPDHVGAKTGQKEV-----PDEKISQVVPDH  
Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_m -----MSGDRHPLMYNKGQDDGLYGATSERDITDMSITESVELKGVKHSYEDENPAPAHSQESIAKSDVEAGNGHTIKNHAYEDVTEPKVGNPVVDAGMVSPTI-----RGVNDNVVDRLN  
Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_m -----MPHIEVTIVDGSKLPEIIELRGVPNQDSDSAYASLLETIDIAIESG-----DIDKKTAVTDTPT  
Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_m -----MPHIEVTIVDGSKLPEIIELRGVPNQDSDSAYASLLETIDIAIESG-----DIDKKTAVTDTPT  
Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 -----MGSVPGKGDVLNLI-GKQEVGDHSIGAPLYTGIRSKOHTY-----GGTDSWTH-----TGDTSSSGDIN  
Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 -----MSTAGVELTKVKPLGHKNGDADSLGSSVGVNDVALKLED-----EATTNDTKQKTT  
Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 -----MSTAGVELTKVKPLGHKNGDADSLGSSVGVNDVALKLED-----EATTNDTKQKTT  
0a 20a 40a 60a 80a  
Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 -----TVTINDGE-----MVPVSETKT-TERQKFSCEIATYATPVTKAT-KVIFPALFLAYVGYC-----M  
Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 -----IGIQSISS-----IVELETVITEDDTRGMEKFFFIID-KIFDGIQDITLHKKRLKQIT-YSILLLLYLAYVVYS-----L  
Myessoensis.XP\_021350798.1\_uncharacterized\_protein -----AYELEDPD-----QMPTEDEGLIAEKLVLFIID-KIYIGIRVVILKHQIKLKITI-YSILLLLYLAYVAYS-----L  
Avaga.UJR10076.1\_hypothetical\_protein\_I4U23\_014298 -----IGFDKLTD-----EVQPSGLWL-REFRKRIFKLIEQKRTTIVYGM-KLFFLLAFIIFYAFV-----M  
Avaga.UJR35986.1\_hypothetical\_protein\_I4U23\_028726 -----LQGNDEKE-----EEEDDDQDNDNAGFEKLSGEGMKVGLVVL-KLRDAIFQPIRGQKITFVVL-KVLGVGIIFYGFA-----M  
Egranulosus.XP\_024350707.1\_solute\_carrier\_family\_2 -----LPNHDPNV-----LTGLLQAYSRLFHRFDTSGRCEVED-ASTALSPP-----GSILELL-KIGILGVGIIFYVFA-----V  
Egranulosus.XP\_024352129.1\_solute\_carrier\_family\_2 -----LQGNDEKE-----LNILLQWYSNGRKFVCKKKP-IAEDVEPVCCDGIQGLCGLIF-LMLIDIAVAYCIVC-----N  
Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp -----GYFEKNPK-----SIDNSTEDDDDDYDTEE-TSEKPVPEVKPKLLCQNNWCHGYGFLVILFIFYI-----L  
Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp -----RGSEATTE-----ENVTDKTPNCVARGID-KVSQSVKAFYSRHRKRTISLT-RCVFVALWVAYLVIA-----A  
Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_m -----PTAEPENE-----VGSDDPEDVDVTDVAPRRQNGFNKRV-KVDKAIKGFIRSHRQPKWAV-YILLLLFLVAYVIAA-----V  
Aplanci.LOC110983407\_solute\_carrier\_family\_28\_memb -----LTEPLPPG-----FGQLLD-YCSDTLDSCRATQRWENDAI-FIALVYVYIIFYAIFI-----I  
Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 -----EPTLITDT-----FGQLLD-YCSDTLDSCRATQRWENDAI-FIALVYVYIIFYAIFI-----I  
Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 -----RVVEASDT-----FGTLFD-STSDLSNCKKWTWHRFIDLL-YLSTAGYVVVYVYA-----I  
Hsapies.NP\_004203.2\_sodium/nucleoside\_cotransport -----GHSGLDGL-----GPSTYQRRSR-WPFSKARSFCPTHASLFLKIF-LGLLLTGVMVYFIIA-----C  
Hsapies.NP\_004204.3\_sodium/nucleoside\_cotransport -----SDLSPAEI-----RSSWSEAAKPFPSWRNLQPALRARSFCREHMQLFRWIG-TGLLCTGLSALFLVA-----C  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 -----VASQRNKR-----SCIGILL-IPVLFLKSFYSERKTVFKYIF-LGLLLTGVMVYFIIA-----I  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran -----QITDDHDE-----DLYFDESKVNPVKVILI-SPVKMLEELFNRYKRFPIIV-VVIFLGVTAVMVA-----L  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran -----KMLMSDPH-----ASKIEMNKDDSDDEMDFVQNTNPLRCLV-LPIEMFSKFVTLNKRLILLIF-GACLAGVLAVYVMAA-----L  
Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 -----VGVIQDGD-----SRDRSVFSLSLGII-IVRRSCDRYFKKNNHVRVQAT-KVILLGLYLAIFYVYA-----M  
Hsapies.NP\_001186562.1\_solute\_carrier\_family\_28\_m -----VTVQDQSP-----RNREHEDDDDEEMQKQGLE-RRYDTVCGFCRKHKTTLRHII-WGLLLAGYLVYVISA-----C  
Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me -----KNERTNPP-----HAYGNALTQVFS-NCIARCKTFLSTHNRTIKRLE-WGLLLSYLAFLIISG-----L  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor -----SLSLSDPS-----PSYHEDDIDGEEEEEEEDQSRCKMGVS-MISEGINFVKKHNVVIRVV-YAVLGLYLAFLIIA-----C  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 -----QRNSGDL-----ACAIDYGHEDKPTSEDFNLFSSCI-RTHSTLTDFYRSRKAKICRGF-YAFLAMAYVAYFVAS-----M  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 -----VTVQDQSP-----PTGRCALCVF-NIRQNVVSGLMSSQIQRCV-IIIILCLYFAYFGYC-----M  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me -----VTVQDQSP-----MSTRVLRVCKEHKPKLATI-GVLLLLGLIYFLVAYA-----I  
Aplanci.LOC110990438\_solute\_carrier\_family\_28\_memb -----PAFDASKP-----VNAERSNGSSYDPERAVDETGDGDDQDQSGKLMWLD-SNFGAVKDMYTHEHNIWNFI-FVLLLLAGYLYIIA-----C  
Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_m -----KGGDFDSD-----SGSAESDVISNCARLE-AVQGAVDTFLEEHKRTIEIIA-VLULLIGYAIYFVMA-----L  
Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_m -----KAFVHDEQCEHHTKDKVISIYEDDGEDVEEAMPELIEDGETSCLOQLE-KQLAFSSFLNSHNKKLWAL-YALLTAAYAYFGYA-----M  
Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_m -----KAFVHDEQCEHHTKDKVISIYEDDGEDVEEAMPELIEDGETSCLOQLE-KQLAFSSFLNSHNKKLWAL-YALLTAAYAYFGYA-----M  
Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_m -----VLRIRQSQ-----QOETIEVEEELFEDLEDEPCFHRNAA-KIQKTLSAFYQDQHNKPNLWSP-YAVLLIGYIIFYVYA-----M  
Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_m -----AGDGDTPQ-----TGSDNEFDLEEEPPNGFYRGIA-AIQESFOAAYQSGHIFVWVI-YAFLLGLVIFYVYA-----M  
Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_m -----VANDISEQ-----DKQSHPDGDESDVMEELVEEPPNGFVRGVA-IQTTVSQGYATYNIYGLVYVGLA-----M  
Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_m -----VANDISEQ-----DKQSHPDGDESDVMEELVEEPPNGFVRGVA-IQTTVSQGYATYNIYGLVYVGLA-----M  
Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 -----PSFYKNVV-----TGQEKVEDTTFQVSKSEDDKGGDDNDSDSVTCGPCRCVG-AIQNHGLDLYTSHKTVIRNIF-YVLLTLLIYAFYSYA-----M  
Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 -----NGVPAPAV-----EFEQTTGFVY-HLQTSVRTTYTNNYNGWTCV-NVILLVLVIFYYFGA-----M  
Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 -----NGVPAPAV-----MDRKKSRQMLDAL-RMPVVIQITGLFIV-----M  
100a 120a 140a 160a 180a  
Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 -----TV-EFGSENSLR-----LLIGTILWYLLSWNLI-----KWKWFANIYA-----DLRQVKCQGRMQL-----KIRK-----YIRWG-----  
Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 -----SF-RFGDEGSRW-----LLICTILLMYSGR-GI-----IKKLSLYQLFEKTFGSKNPNENIVMKK-----ILRWT-----  
Myessoensis.XP\_021350798.1\_uncharacterized\_protein -----SF-RFGDEGSLR-----LLVCTILLMYLGM-GI-----IKMVSLYRAFKKSLGSKNPNENITAKK-----IVRWT-----  
Avaga.UJR10076.1\_hypothetical\_protein\_I4U23\_014298 -----SS-KFGTPPPPIRGNIIFYGNSGFALFLVLVLSL-----FVFAWEKFLGRLLLEHWYDQLPIASKEH-----EIIY-----TFSWI-----  
Avaga.UJR35986.1\_hypothetical\_protein\_I4U23\_028726 -----SS-RYGTAPFPIVGNVFSGNAGFAFLFLVAFAI-----FVIAWEKILGRLLLENFINYLTTSTNNITGGKRIITALISRFPSWI-----  
Egranulosus.XP\_024350707.1\_solute\_carrier\_family\_2 -----KVR-ROEAEDIT-----LWMSTIFWILLILW-----LIFKHLKVLGKERGGCFHFFVCLADRF-----  
Egranulosus.XP\_024352129.1\_solute\_carrier\_family\_2 -----KLATEDDIR-----LWLWSAIVLWLVILV-----KICHLRSLRGLRVGGCFTPFVGLGDKISEGWNFNKDSIHNRWQSMWIDPNEKTQKKKK  
Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp -----YWKDNPCLCGINFCTGYGMLLLLLGFIYGLVYVVY-----FKPMVGHSLHR-----NYKFPFSKWHNF-----SRTI-----VVSIA-----  
Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp -----WL-NL-----YVWV-----FKPFVGIKLYN-----NYLEPVIDKWIAF-----SRQWI-----  
Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_m -----YL-NGQRALV-----LIITIAIVFFVFSY-EY-----LQRRYGDVIYD-----VICRLLAGVKCGKR-----MWK-----YTHWT-----  
Aplanci.LOC110983407\_solute\_carrier\_family\_28\_memb -----VL-DPHRALA-----LFVLMSMLAYATC-RV-----IQHFCGARIVSGAVSCRQRKCGVISE-----RKLLITCLVYI-----  
Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 -----VFDTSTA-----FWTCVDVLVFLVAV-----VHRFWG-----IATLLSHVTTPLLEIRRRHCFPSQKRR-----LAGKL-----  
Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 -----IY-DPSSAFL-----SVDATLVVLVFLVH-RFRLQDIKFIKPIR-----RILARKCRIRKTL-----IWR-----IFRC-----  
Hsapies.NP\_004203.2\_sodium/nucleoside\_cotransport -----IL-NFORALA-----LFVITCLVIFVLVH-SF-----LKKLLGKKLTR-----CLKPFENSRLL-----WTKWV-----  
Hsapies.NP\_004204.3\_sodium/nucleoside\_cotransport -----LD-DFORALA-----LFVITCLVVLFLGH-RL-----LKKLLGPKLRR-----FLKPGQHPRLLL-----WFKRG-----  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 -----ARD-PLAAKP-----LIITLVLFVLVLY-EL-----RFFKLFLFFFK-----QIKSKVHIKKETK-----NK-----ITRFL-----  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran -----IW-NFNRALT-----LMVLWLVVYVYNIY-AF-----IRDYFGNDLMP-----YLPKPVYKTVNKN-----MFWLQWV-----  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran -----IT-NFORALT-----LMLWLVVYVYNYM-AL-----LRDNFGDSITH-----HMRPVFKSGCN-----MEFIQWV-----  
Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 -----IY-RFGDEGSRV-----LMVGTIVVLIGVYV-RH-----VFKVIGPVSS-----SLQSTKCVIKITR-----HIQRYRYVLOQM-----  
Hsapies.NP\_001186562.1\_solute\_carrier\_family\_28\_m -----VL-NFHRALP-----LFVITVAIAFFVWV-DI-----LMAKYEHRIDE-----MLSPGRRLINSR-----WQ-----LKWV-----  
Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me -----VL-NFCRSPA-----LLIMTLVLVAYVY-AL-----VDRWNGPKIRQ-----NYLKPCCVTKVPS-----WR-----YKLW-----  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor -----VL-NFCRAFA-----LIITLVVLVYVYVY-GH-----IRDKWGKTIYK-----SCLPASCVRGKVV-----WK-----YAKWV-----  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 -----MYESSOENSIS-----VLCTQGERPDPPLVLIVTCVVVVVITL-GF-----IEGHFGERIQT-----TVIQPMENFFNKV-----KGMVNIYKGL-----  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 -----BBLCHERI-----YF-RFGDEGSIR-----LLVCTVFGVLLAFS-LI-----VAGTRINQRRLWERSLKPCTVSRAGR-----RCHAIFSL-----  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me -----PYFLNNGHPLGGCRNLIGLLIGLVGV IGLY-IC-----ISRFGGDIIYE-----HCLKHGVFTVTGNI-----WVKRV-----

Aplanci.LOC1010990438\_solute\_carrier\_family\_28\_memb -LY--DFQEAMI-----LVIITGIALGLYMY-SV-----IRDFYKGQIYD---VTCKPGGRFVVDKY-----WR---YIRWP-----

Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_memb -VL--DFERATA-----LFVITLLLVISVAY-AL-----IKKQIGGWMNT---RIFKPVQKFGNSN---RR---VLKWW-----

Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_memb -WY--QFGDEGSIR---LLWISCLVTAGVLL-SV-----ILDRWGDGLYR---TCVHPVSVLIERR---GR---YIRWI-----

Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_memb -WY--QFGDEGSIR---LLWVSCLVTAGVLL-SV-----ILDRWGDGLYR---TCVHPVSVLIERR---GR---YIRWI-----

Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_memb -WY--SFGDEGSIR---LVVLTVFLVLMALA-AI-----LKPRLK-----NCVLPVSVKRFDKS---CLK---YVRWA-----

Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_memb -YY--RFGDEGSVR---LLVITITIVTVLVAL-TI-----VMSVLGNVVDQ---VGEALAKFGETR---AWN---VKIV-----

Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_memb -RH--RFGDEGSVR---LVVATVVAALVGLA-TV-----IWHYCEASLTS---YIGEPVMNLKTA-----YWRWF-----

Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_memb -RH--RFGDEGSVR---LVVATVVAALVGLA-TV-----IWRYCEASLTS---YIGEPVMNLKTA-----YWRWL-----

Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 -YF--RFGDEGSVR---LLVVTALVAVGLSV-TL-----LMELYGTKLGI---CWRHVSSEKTKRK---ASK---SINIF-----

Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 AHE--KFGDEGSIR---LLVCTILFVIGLCL-HF-----LFKHYGNTMRMPKINMDPRKEKILKI-----GYAIV-----

Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 -----

200a 220a 240a 260a 280a

Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 -----LYITMLVVVG---SLVGTSIAGKNFRNLVSLGGILVFLLLYVTVSDRSNLSNHSVFWGFIQGITLAILVLYTSGGKDAVVCSSRRLLTELLAHSK

Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 -----LYFVVLTLLIA---VYIGLTVIQTTPRNVLVSLGGIFVFIFILFIMSNKKANINNHTVFWGLSLQFGFALIVLRTWEGINAVRMTDRFLEFVFDN

Myessoensis.XP\_021350798.1\_uncharacterized\_protein -----LYFVVLTLLIA---VYIGLAVIQTTPRNVLVSLGGIFVFIFILFIMSNKKANINNHTVFWGLSLQFGFALILRTWEGINAVNMTDRFLEFIAFSD

Avaga.UJR10076.1\_hypothetical\_protein\_14U23\_014298 -----WHLSVATAIA---LYVGTTV---TPRPNVYSLIGIVILILLGTGSKYPHRIKWTYVYFVPIQPLLATVIRSESGFRFFELGKEVSKFMHNA

Avaga.UJR35986.1\_hypothetical\_protein\_14U23\_028726 -----GHILVLCGVA---LYGLTV---KQASNVYSLSGIVLITLGTGSKYPHRIKWTYVYFPIIQFLAAIVIRLEVGQFFDFLGKEVSKFINDA

Egranulosus.XP\_024350707.1\_Solute\_carrier\_family\_2 -----LMVVLGLITALLYLFFVLMRPNRNFVSLIGIVAMVILCMLISVHPAKIKQWPVLMGFFLQPTFAVILITQKFGYVTFEFIAQOTALMDNSGV

Egranulosus.XP\_024352129.1\_Solute\_carrier\_family\_2 KLATKIVVLMALMGIPTTICLIFFIYILKSVQNLISLSGIVVLLIIAIAISKHPGKINWQPVGFIQVQLVAVLTLTQTRPGYVVFQFLGDRMSEFLSHSTA

Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp -----SIALLLALLA---IFVYFECR---DETQKIVSLVACPFFILCGYVFTSNRRAINRWIRITGITGQFLGFIICRMEVGKRIKIFCELGKNVATFLLGYAD

Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp -VSGVMLATVLAUVV---AYLGFECR---NDAKYAIGLLGPGVCFVLIGFAVSKHHQVPRWIRITHGLLGQLLGLLCLRLPFGRSIFQCLGDKVITFILNAYQH

Lanatina.XP\_013392414.1\_solute\_carrier\_family\_28\_memb -----FYALLLAGLT---VFLVLDTG---RVPKQNFASAGLLTLLLLTLFTVTSKYPAKIRWRPVLWGLAQFQFLMGMLVLRWSAGAFALQFLGQAQVQTFAGVDA

Aplanci.LOC1010983407\_solute\_carrier\_family\_28\_memb -----LFTALLIAMCALITGVQISIV---REPERKLSLFGVLVCFLLSFLVSKQPGLINNRWTVFWGLWLMQFIALILILRTQPGFDSFNWLGRQVSEFLNFTNA

Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 -----FTALLFVAIG---VYVLIDTG---RHPNLIPLGGLLFLVIMFVTSKAPSKQVRAVLWGLLLQFLMGVILIRWMPGGVFCMKMGDAVAKFLSTDY

Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 -----VTILVFLAII---IFLAIIDL---ADTERLPLISVGGCLLCLVIVFITSKAPSKVCMTVPLWGLLIQFVLMGILIRWMPGVEICKFVGDGMAGFLSTDE

Hsapies.NP\_004203.2\_sodium/nucleoside\_cotransport -----FAGSVLVGLI---LWLALDGL---RPEQLVIFPAGIGMELILILFACSKHHSAYSWRTVFSGLGQVFGVGLILVITRDLGYTVFNGLEQVQITFLNITYA

Hsapies.NP\_004204.3\_sodium/nucleoside\_cotransport -----LALAAPFLGLV---LWLSDLS---ORPEQLVFSFAGICFVALLFACSKHHCAYSWRAVSWGLGLOFVLGLLILVITRTEPGFIAFELWELGQIRIFLSYTKA

Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 -----PYVQILICVAFICLWLDVMIIRNPSTLISVSGVIFILVVICASTQPKCINWRPVWIGLQFQFLGVLVIRTPGFIKQIATFIMTKYDTS

Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran -----FVACVVGGLA---TWIADTS---KRPEQLISGAGYLVEFLIFLTSKHPERVRWRPFWGLLLIQVCLGMFLIRTAQAGDAFNLGNIFQTFINYADE

Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran -----FVALVVGGLA---TWIADTS---KRPEQLISGAGYLVEFLIFLTSKYPKRVIRWPRVFWGLFIQVCLGMILIRTAQAGDAFNLWGLSLAQTFINVDA

Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 -----VSMIAVLAI---IYILVEVFIEPPSNVISAAGLVVIFIMIFFSKDPKAKVWVRPVLWGLLLQFIFALVVLRTSWGAGDAFNLQIRIFTEYKHSID

Hsapies.NP\_001186562.1\_solute\_carrier\_family\_28\_memb -----IWSSLVLAIV---FWLAFDTAKLQQQLVSFSGGLIMYIVLLFLFSKYPTRVYWRPVLWGLIGLOFLGLLILRLDTPGFIADFNLGRQVQTFLEYTDA

Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_memb -----VFLGALLCIG---LFLGLETA---KOPQDLISIGGVYIILLICFVCSKHPGQVWRPVLWGLALQFCLGLFLVLRTSVGVQVFNLLGGTFEGFIKFADE

Bbelcheri.LOC109476916\_sodiumnucleoside\_cotransp -----IYGLVILGIG---LFLGLETG---KOPQDLISIGGVYIILLICFIFSPGKVKWRPVLWGLSLQFLLGLLFLVLRTSVGVQVFNLLGGTFEGFIKFADE

Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 -----FLLCVLVAIV---VIIGTSV---VRPHNATSMAGIIVLLLMMLLSFSAHPTKVNWRPVAGGLLQFQFFSALLLKLVSQVYAFKFLGDKQIFILSTFNT

Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 -----LKIAPFCVIA---AYIIFVDHDPHONLAVSQAIYIIFVFSISPAPKVRWHTIFWGFALQYILALIILRQEWGFIKFLYGLDRVGEFLQHSDA

Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_memb -----FYVLCILGLI---LWLIALDA---RNTQNLISGAGLILIMVILYIFSKHPDHVKWRPVLWGLALQFIFGLLILRTQVGFDFKFMGEKQFSFTEYADV

Bbelcheri.LOC1010990438\_solute\_carrier\_family\_28\_memb -----LYLLILAGVA---VALVFLTK---DNPQLISAGGLVAFILFCYVFSKHPRHVKWRPVLWGLALQFILGLFLIRTSIQVGFIFNFIPLGVDVQTFLEFIDA

Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_memb -----SAAVLACFI---TFVIVDIK---PAPKQIFSLGGLALFVLLMFVFSKHPSKVDLRPVWGFALQFLFGLLILRTWGDVAFFLGKEINQFLKYTDO

Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_memb -----IGVAAVCGVG---AVLILEVALKOPRNLYSGGIGIIVVSVLLWIFSKNPARVKWRPVLWGLLQFPTALLILRTWGFHFIWNLGRVAEFLAHTEA

Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_memb -----IGVAAVCGVG---AVLILEVALKOPRNLYSGGIGIIVVSVLLWIFSKNPARVKWRPVLWGLLQFPTALLILRTWGFHFIWNLGRVAEFLAHTEA

Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_memb -----FYIATVLIWA---SIIIAEVAVKPPANLMSGCVIIVVAVVFIIFSHNPAKVKWRPVLWGLLQFIPALIILRTESGHSFIMNLGRDVRSEFLDHTNF

Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_memb -----LCVLLLVALL---VYIVVEVAIPNPNVLSVITGMVLVIILFVFSNPARVKVQPVWGMALQFIPALLILRTSWGGEAFKWLGRDVRTEFLAHSDA

Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_memb -----TICLVYALLIAL---VYLVVEVAIPNPNVLSAAGILVYVLLMFVFSHNPARKVWRPVLWGLSLQFIALLILRTSWGGEAFKWLGRDVRTEFLAHSDA

Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_memb -----TICLVYALLIAL---VYLVVEVAIPNPNVLSAAGILVYVLLMFVFSHNPARKVWRPVLWGLSLQFIALLILRTSWGGEAFKWLGRDVRTEFLAHSDA

Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 -----LSVGTSAFV---VVIVIEALKTPRNLSVAGGALTLLVLFYIFSVNPAKVKWRPVLWGLLQFIPALIILRSKGGDFNMEFWELGRVAEFLKYSID

Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 -----AAIVFIFI---VYIIAIVANSPDNLSLGLVFFVFVAFICSRNPAQIKWRPVLWGLLQFIPALIILRSKGGDFNMEFWELGRVAEFLKYSID

Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 -----IYIMDIAMETPRNLTSLTGLVFFVFVFSHPDPSGVKWRPVLWGLALQFLFALLILRCRFGQAFKWLGRVYEFLLSYTDE

300a 320a 340a 360a 380a

Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 GSEFVFG-----KRYGQFYFAGLLPKVIFVAVRVLTHLGLVFSINRNLGTFLSFCGTGTSNPESICAAANVFGVGGQAI

Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 GSASFIS-----KRYKEKFVIFKVPVSVIVFCFVAVLSYLGLVAFIFLSNLGCVLIGYQTHPLRESINAVTIFMSGIESL

Myessoensis.XP\_021350798.1\_uncharacterized\_protein GSASFIS-----KRYKEFNLIIFKVPVSVIVFCFVAVLSYLGLVAFIFLSNLGCVLIGYQTHPLRESINAVTIFMSGIESL

Avaga.UJR10076.1\_hypothetical\_protein\_14U23\_014298 GAVFVFG-----KTYEEHFVFKLTSIIIFPLGSIINVLVLYLVMQYIIGKIAWMSQKCLINTTAESMTAAANIFVGMSEAP

Avaga.UJR35986.1\_hypothetical\_protein\_14U23\_028726 GAIFVFG-----ESEDHGFYFVKTSIIIFPLGSIINVLVLYLVMQYIIGKIAWMSQKCLINTTAESMTAAANIFVGMSEAP

Egranulosus.XP\_024350707.1\_Solute\_carrier\_family\_2 GASFVFG-----DLQVECFALKVLPVLFVSSSIFIMFHLGVMQYIIPQSNFIRHIMGTGTGPEAINATINIFLMSNEAP

Egranulosus.XP\_024352129.1\_Solute\_carrier\_family\_2 GSSFVFG-----DLTFFAENVLPVIFVSSSISVAFHGLGISILIDKPSVAVTKVLGTGTGPELNAVANIIVFSMTESP

Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp GAEFVFGD-----FLVNNMGFAAILPVIFVFFSFIILYMGTMQVWVILKWLIIQQILGTTCVCSVTAAGNIFLGMSESP

Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp GARFVYGD-----RICDEYFAEAILAVVFFSVITSIMYLVGMQVILNGGFLQLQAMVGTTCVCSVTAAGNIFLGMSESP

Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_memb GSKMVFGD-----PGYKMHFAFVKQLPIIFYSAVINVLVYGAIQWVMKRWMLMVKMTKITPILIAHTAASIFLQVTEAP

Aplanci.LOC1010983407\_solute\_carrier\_family\_28\_memb GAEFVFGD-----APYLSNHEILLTVLPVITSSVFALMYVYGMQVITLIRGLAVIMQFTMDVSGAESFATASNIFVGMGTAP

Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 GSKFVFGD-----KNYTHMVFVKILPVVYVFSVAVSIIYVGMQVIVIKGLAKLFQYTMKTATTESFATAHNIIFGVQSTAP

Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 GSKFIFGE-----KNYTHMVFVKILPVVYVFSVAVSIIYVGMQVIVIKGLAKLFQYTMKTATTESFATAHNIIFGVQSTAP

Hsapies.NP\_004203.2\_sodium/nucleoside\_cotransport GSSFVFGD-----DTLVKDFVFAEQALPIIFFGCVSVIILYVLGVQVWQVAMVFLQITMGTTATETLAVAGNIFVGMTEAP

Hsapies.NP\_004204.3\_sodium/nucleoside\_cotransport GSSFVFGD-----EALVLDKDFVFAEQALPIIFFGCVSVIILYVLGVQVWQVAMVFLQITMGTTATETLAVAGNIFVGMTEAP

Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 GSTFVFGD-----VLSHDHFAFKVLPMLVIFSMVNTMLFVYVGLMQWIKLQWIAKLAYITQITLGTSAESAVAIANIFVGMTEAP

Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran GARFLYG-----DDPADHFAFMKVLISIVYGFAPISVYMIYIGAMQWILFKIAFLMOITLGTSTAESVMAAGNIFVSMTESP

Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran GASFVFGD-----KNYLDHFAFMKVLISIVYGFAPISVYMIYIGAMQWILFKIAFLMOITLGTSTAESVMAAGNIFVSMTESP

Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 GANFVFGD-----PALDQHLFAFVLPVIVFFSATISVLYLVGLIQLVIRGLIRVMEHSLISAMESLHAAPNIFVGMWETP

Hsapies.NP\_001186562.1\_solute\_carrier\_family\_28\_memb GASFVFGD-----KNYLDHFAFMKVLISIVYGFAPISVYMIYIGAMQWILFKIAFLMOITLGTSTAESVMAAGNIFVSMTESP

Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_memb GSQFVFGDLPVVTSPSGNLT-----DLTLTRAYLVHNVAFQVMPVTFEATVLSLXHLGWMQVFIHKLALMQLTLTGITGPEAVSAAGSIFLGLTDCA

Bbelcheri.LOC109476916\_sodiumnucleoside\_cotransp GTSFVFGDNLVMSNTANLSEVTSFADLTVPAYLVHNVFVQVLEPTIIFSTVMSLLYVFGMGIIVINKLAINMQFTLGTSGPESISAGNIFVQGTAP

Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 GTEFVFGD-----EKYTDHFFAMKVLPIVVFSCAISVLYSGVMQVIGKIAWMLMRVLTGTTAESVCAAGNIFVGLTEAP

Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_memb GAIFMFS-----PLISAHIFAFVLPVIVFFYTIMSIIYLVGLVQVIVRVLGRALAFSMDTTPAESLNAAGNIFVGMTEAP

Bbelcheri.LOC1010990438\_solute\_carrier\_family\_28\_memb GSKFVFGD-----EKYTDHFFAFKVLPIVVFSSVMVLYIYGLMQVIVKMAWLLQRTMETSSPESINAAGNIFVQGTAP

Aplanci.LOC1010990438\_solute\_carrier\_family\_28\_memb GSEFVFGD-----AGQEHEFFAFKVLPIVVISACISIFYYLVGMQVIAKLAWLMQKTMHTSASESLNAAGNIFVQGTAP

Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_memb GSEFVFGD-----KLYENHFAFVKVLPIVVFSCAISALYHVGMQVIGKIAWVMQVMTAATAESLSACAGNIFVQGTAP

Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_memb GAKFVVF-----NLEPHYFAFALPVIIVFFSSCVSVLFYLGAMQWILIGKVAVMVRVAMGTAAESMTAAANIFIGQSEAP

Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_memb GAKFVVF-----NLEPHYFAFALPVIIVFFSSCVSVLFYLGAMQWILIGKVAVMVRVAMGTAAESMTAAANIFIGQSEAP

Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_memb GAEFVLG-----DATHHFFAFKILPIVFFSTCISIIYLVGMQVIFRVAVMQVAMGTAAESVMAAGNIFIGQSEAP

Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_memb GAGFVFGD-----DATYHFFAFKVLPIVVFSTAIISVLYLVGMQVIRKVAVMQVMSMGTTAESLNAAGNIFIGQTEAP

Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_memb GAAFVFGV-----DTYMDHFFAFKVLPIVVFSTAIISVLYLVGMQVIRKVAVMQVMSMGTTAGESLNAAGNIFIGQTEAP

Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_memb GAAFVFGS-----DTYMDHFFAFKVLPIVVFSTAIISVLYLVGMQVIRKVAVMQVMSMGTTAGESLNAAGNIFIGQTEAP

Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 GAEFVFGD-----ENYTDHFFAFVSLPVIIVFFSTSVIYLVYLVGMQVIRNARVAFLANALGTSPAESLNAAGNIFLQGTAP

Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 GAIFVFGD-----KDYTDHFFAFKVLPIVVFSTAVSVLYIYGMQVIFIRLARFMSVMSMGTTSPESLNAAGNIFIGQSEAP

Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 GSMFVFGD-----EKYTDHFFAFKALTVVFFSTSVIYLVYLVGMQVIFIRLARFMASTLGTSPESLNAAGNIFIGHSEAP

400a 420a 440a 460a 480a

Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 LFIREYMDYLTESEIFCVFVGLDASIGGAVVLYSGYGPVQVYLSASVLSAPALAAAKLNYPSPPSLPK-----TDENVK-KDN

Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 VVINEYIDSLTSQVFCVYINGLSSAGFAVFNAGFIPVEYLLTASIMSAPALVASKVIVFVSETLKK-----KDDKKFYIA

Myessoensis.XP\_021350798.1\_uncharacterized\_protein MVISEYIDSLTSHIFCIYINGLSSAGSALVIFSNFGVPEYLLTASVMSAPALVASKVIVFVSETLKK-----TKICVQD

Avaga.UJR10076.1\_hypothetical\_protein\_14U23\_014298 LIMPLVPMKMTSELHSLVGGFATMAGSVLAFITFPGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Avaga.UJR35986.1\_hypothetical\_protein\_14U23\_028726 LIMPLVPMKMTSELHSLVGGFATMAGSVLAFITFPGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Egranulosus.XP\_024350707.1\_Solute\_carrier\_family\_2 LM1KPVMSQMTSELHSLVGGFATMAGSVLAFITFPGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Egranulosus.XP\_024352129.1\_Solute\_carrier\_family\_2 LITRPMHMMNSELNLAIVNGFASVAGTVLAAVYISFGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp LLIRPIYNKLTKSELHSLVGGFATMAGSVLAFITFPGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp LIRPIYNKLTKSELHSLVGGFATMAGSVLAFITFPGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_memb LLIRPIYNKLTKSELHSLVGGFATMAGSVLAFITFPGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Aplanci.LOC1010983407\_solute\_carrier\_family\_28\_memb LITRPMHMMNSELNLAIVNGFASVAGTVLAAVYISFGVPANHLIAASVMAAPGALGAKLLP-LTHQSK-----TTWEAV-KNT

Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 VALKPFLRDLTSELNAVMTSGFATVAGTVIAAYIEFGVPAEHVITASFMSAPALVASKVLMW-EDEVFP-----DKEDIYVKL

Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 VALKPFLRDLTSELNAVMTSGFATVAGTVIAAYIEFGVPAEHVITASFMSAPALVASKVLMW-EDEVFP-----DKEDIYVKL

Hsapiens.NP\_004203.2\_sodium/nucleoside\_cotransport LLIRPYLGDMTSEIHAVMTGGFATISGTVLGAFIAFGVDASSLISASVMAAPCALASSKLAYP-EVEESK-----FKSEEG-VKL  
Hsapiens.NP\_004204.3\_sodium/nucleoside\_cotransport LLIRPYLADMTLSEHVVMVTGGYATAGSLLGAYISFGIDATSLIAASVMAAPCALASSKLAVP-EVEESK-----FRREEG-VKL  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 LIVRPLYPELTKAIEHSVLTGLASISFSVFGVYIGFVGVDGHLLTACVMSAPAGLVVSRLLYP-EVEKSK-----FMNTGS-LAL  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran LLIRPYINDLTSELHAVMTAGFTIAGSVLGAYLFGFQKAVYVITACVMAAPCALAVSKLVYP-ETKKS-----FLSYEG-LVV  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran LLIRPYLDDLTSELHAVMTAGFTIAGSVLGAYLFGFQKAVYVITACVMAAPCALAVSKLVYP-ETKKS-----FRSHAG-LLL  
Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 TFLRPFDDMTLPHELTVMTNGFATVSGSTLVVYHMYGAPANHLLSASVMSAPAALALSCLFYP-DDKVR-----SKV-TLD  
Hsapiens.NP\_001186562.1\_solute\_carrier\_family\_28\_m LLVRPLYPYITKSELHAIMTAGFTIAGSVLGAYISFGVPSHLLTASVMSAPASLAALKLEW-ETEKPK-----ITLKNA-MKM  
Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me MLVRPFLPAMTNSLFTVTMAGFTSIAGSVLAFTSLGISASFLLTANVMAAPTSLALSCLVYP-ETDTR-----HGNKKDDR-LDV  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor LLVRPFLPMTKSELHAVMTGGFTVAGVGLGAFISFGINPASHLLACTVMAAPTALAMSKLVYP-EIERKR-----TKKDDR-LQV  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 ILIRPLYGVMTKSELHAVITCGFATAGVGLAAYIEFGVPAEHLILCASVMMNAPALAVSKLLYP-ETEEKSLKVLPSGRQELTPEQIEEGLDPEDVFIKP  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 LMIGPFLKDMTSELHAVMTGGFATIAGSVLGAYISFGVPAANHLLSASVMSAPAALAIKSLAY-EVEVSK-----TTTKDF-DRM  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me LLIRPLIKDMTKSELHAVMTGGFATIAGSVLGAYIAFGVPPTHLLTASVMSAPAALAVSKLFYP-ETEET-----MRLODN-VKL  
Aplanci.LOC1010990438\_solute\_carrier\_family\_28\_memb LLIRPLYPKMTSELHAVMTGGYATIAGSVLGAFIAGVGPANHLLSASVMSAPAALAMAKLFYP-ETESQ-----TRTAQ-VOL  
Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_m LLIRPFLSMTKSELHAVMTGGFATIAGVGLAAYILFVGPAEHLILCASVMMNAPALAVSKLFYP-ETEEK-----TKKFDQ-KVM  
Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_m LVIRPFLTKMTSELHAVMTGGYATIAGSVLGAFIAGVGPANHLLSASVMSAPAALAMAKLFYP-ETRVS-----TMADI-INI  
Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_m LVIRPFLAKMTSELHAVMTGGYATIAGSVLGAFIAGVGPANHLLSASVMSAPAALAMAKLFYP-ETRVS-----TMADI-KNI  
Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_m LMIRPLLPKMTSELHAVMTGGFATIAGTVLGAFIAGVGPANHLLSASVMSAPAALAMAKLFYP-ETKKS-----TVQDI-ENN  
Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_m LMIRPLLPNMTKSEHMAVMTGGFATIAGSVLAAYILFVGPAANHLLSASVMSAPAALAMAKLFYP-ETKKS-----TTAAV-SAM  
Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_m LMIRPLLPNMTNSEIHAVMTGGFATIAGSVLAAYILFVGPAANHLLSASVMSAPAALAMAKLFYP-ETKKS-----TTSKOI-QVM  
Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_m LMIRPLLPNMTNSEIHAVMTGGFATIAGSVLAAYILFVGPAANHLLSASVMSAPAALAMAKLFYP-ETKKS-----TTSKOI-QVM  
Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 LMIRPFLSKLTKSELHAVCTGGFATIAGSVMAAYILYGVPAANHLLSASVMSAPAALAMSKLIP-ETEKSE-----TESSDV-YKM  
Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 LLIQPFLKDMTSELHAVLTGGFATIAGTVMAAYILINVPANHLLSASVMSAPAALAMSKLIP-ETEGSK-----SDPEKV-YNM  
Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 LLIKPFLPMTNSEIHAVLTGGFATIAGTVMAAYILINVPANHLLSASVMSAPAALAMSKLIP-ETDRP-----VHNKV-YQM  
500a 520a 540a 560a 580a  
Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 IIRTESN1LHLSAGSRQGLAFVASILVNMVMLAVLGLVDTALEWFGARAGIE-----NLNF-----ETISSYLYFPFAFLMGVDVSDCSR  
TKSDRKSVMFAAMKAGGLQGLQVKGVLINILTYISLLAFANATITWGERAGVK-----ELTI-----GKIFSYCLWPLAFVGMGIDAIDCKL  
TKSGTKLMQALSLGGMQGLQMVNVLNLLYISLFAFVNASITWFGDRAIVE-----ELTL-----QKIFSYCLWPLAFIMGIDAIDCKL  
PIPEQHNVIDALSLGAGHTMKICGYLIANLFIATSVLRFHADMTISWLFNLHHP-----EINF-----QFLGLFIYFPFALIIGIPPHOCDL  
PLPDQHNVIDALMTGAGNALIKICGYLIANLFIATSVLRFADMTISWLFALVHYV-----EVNF-----QSILGFLFIYFPFALIIGIPSKOCDL  
HSSPFTNLIEAATVGALEAIPLCAGIIVNLMFAISFISVFNRLTLWGHRIGMA-----QDLTFEGGVCFVLRLYTAEILFIAYLLMLLAFMGVPAEDCFK  
VKSPYNNVLEAMVGMDSIP1VAGIAANLFIATSVLRFADMTISWLFALVHYV-----QDLTF-----EVVFSYLLWPLAFIMGVDVSDCKL  
EKSQDSSLLDAASSGASNAVPIVLGIIANVAFVAFIAPLNLVSWFGYLVGLE-----QIDF-----EWIFSCLFIPLVWAMGVPEKDCDI  
ESSTDTSILDAASAGAAALLVLGIVSNIIAFLAIVFFLDVATEWIFELIGLH-----NITL-----LYLSQIFIP1VFMGVPAWGHDCQA  
APPPERSLVEAVCNGLMAALIKLTAUVAGLITFISLVEAMDTITGLYGLDLDVDP-----DVMF-----QLICSYVFPPLAVVGLTQWQDALI  
AKALESNALEAMVGAIDGLKICAYI1GNLVAISVLAFINSALAWGLGLVDIE-----NLFS-----QLICRYVLP1LAWLGLVDGADCLV  
NVGNEHNVMEEAASGATIAKILISYVTVNLIATSVLRFADMTISWLFALVHYV-----EVTF-----QFLCSYTFMPLALVWAMGVPEKDCGK  
EVGKELNMLEAASGAVASIKLVSNVYVNNLFIATSVLRFADMTISWLFALVHYV-----EFTF-----EFLCSYTFMPLALVWAMGVPEKDCGK  
PRGKERNVLEAASNGAVDAIGLATNVNLIATSVLRFADMTISWLFALVHYV-----GLTF-----QVICSYLLRPMFVWAMGVPEKDCM  
TYGDAQNLTEAASTGAISVKKVYVANNLFIATSVLRFADMTISWLFALVHYV-----GLSF-----QLICSYLLRPMFVWAMGVPEKDCM  
SAGTNRNIVLEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----QLSF-----EVICSYLLRPMFVWAMGVPEKDCM  
ESDGYRNVLEAASGASQAI1PVLVNLGNLFIATSVLRFADMTISWLFALVHYV-----ELSF-----QMICSYVFPMT1LPMGISTWDCFK  
EKTEHRNIIEAAPVGAQAI1PVLVNLGNLFIATSVLRFADMTISWLFALVHYV-----QLSF-----EFLCSYTFMPLALVWAMGVPEKDCM  
KKGHQQNIIDAASIGAGISVYAVI1VNSVLAFFSLLGFCNATLEWLGDRVGLTPPDVPLSF-----QLSF-----QLICSYLLRPMFVWAMGVPEKDCM  
EISQDGNLLEAATQAGASNSIVANVGNLISFISLAFINTVLTLWGRMVNIQ-----QLSF-----ELICSYVFPMT1LPMGISTWDCFK  
EPFKDRNLLEAASGASMGVSIVANVGNLISFISLAFINTVLTLWGRMVNIQ-----DLTF-----QTICSYVFPMT1LPMGISTWDCFK  
ETSQERNIIEAASGACVAVTANVGNLFIATSVLRFADMTISWLFALVHYV-----NLTF-----ETICSYVFPMT1LPMGISTWDCFK  
EQPKKKNVIEAAGGASASIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----NFSF-----MICSYLLRPMFVWAMGVPEKDCM  
EKAKERNIIEAATGATAGTALVAA1VNNLFIATSVLRFADMTISWLFALVHYV-----GFTL-----EFLCSYVFPMT1LPMGISTWDCFK  
KGGEERNVIEAQAQAQAI1TILVANVNIATSVLRFADMTISWLFALVHYV-----ILSF-----ETICSYVFPMT1LPMGISTWDCFK  
PKGEERNIIEAASTGASTA1MLANLFIATSVLRFADMTISWLFALVHYV-----GLSF-----ELICSYVFPMT1LPMGISTWDCFK  
EKGTERNLIEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----EFSF-----QMICSYVFPMT1LPMGISTWDCFK  
EKSPERNALQAASNGASNSIKLVANVNIATSVLRFADMTISWLFALVHYV-----KLTV-----QICSYVFPMT1LPMGISTWDCFK  
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EKG-----EKG-----ELICSYVFPMT1LPMGISTWDCFK  
ERPERNIIEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----HLSF-----QLICSYVFPMT1LPMGISTWDCFK  
ETPKERNIIEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----HLSF-----QLICSYVFPMT1LPMGISTWDCFK  
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SKGPERNIEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----DELTF-----EFLCSYVFPMT1LPMGISTWDCFK  
EASPERNIEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----DELTF-----EFLCSYVFPMT1LPMGISTWDCFK  
DKGPERNIEAASGASMSIKLVANIGANLFIATSVLRFADMTISWLFALVHYV-----DELTF-----EFLCSYVFPMT1LPMGISTWDCFK  
600a 620a 640a 660a 680a  
Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 VSNLLGLRSMIDLTVAYIRMEYVQNKVAFNA-----SSLFNDTVFYQDSYDIDL-----LS-DRSEVISAYALCGFASLS  
VAEMLGVRMFATLILSYIRMGKLNKKEYNIE-----TAIYNNVTLTASDDIFL-----PNMNTTLENGI-----LT-DRSEVIATYALCGFANLGS  
VAEMLGVRMFATLILSYIRMGKLNKKEYNIE-----NEIYNNVTLTSSGDFL-----PNMNTTLENGI-----LT-DRSEVIATYALCGFANLGS  
ASKLIGIKVSNLNEFIAYQELIKRILNRDLNLI-----NTFPLYNLGTQLPDMNEMLW-----D-SSSVVILTYALCGFANLGS  
ASKLIGIKVSNLNEFIAYQELIKRILNRDLNLI-----NTLALYNGITSLPANTQMLW-----D-SSSVVILTYALCGFANLGS  
VAGLVGKIKTFINEFVAYERLQGLIEDSSVDSF-----HNKSLPVTYLANGSIITDGLSNRTLQYGF-----LHATVSSYALTYALCGFANLGS  
IABLGVKTKTFINEFVAYERLQGLIEDSSVDSF-----SGNSTQTQVNLGNSWIFVDTKGERYIFDYG-----LHTRDAEVIATYALCGFANLGS  
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IGLVVAQKSFINEFVAYERNLIGLISVSKK-----VD-PRSAVIATYALCGFANLGS  
VGKLGKIKTFINEFVAYERLQGLIEDSSVDSF-----GL-----IT-ERTRVCTYALCGFANLGS  
VAELIGIKVTFINEFVAYERNLIGLISVSKK-----IS-TRQVIATYALCGFANLGS  
VAELIGKIKTFINEFVAYERLQGLIEDSSVDSF-----IN-ERSVIATYALCGFANLGS  
VAKLIGKIKTFINEFVAYERLQGLIEDSSVDSF-----VD-NRSVIATYALCGFANLGS  
VAEMVGKIKTFINEFVAYERLQGLIEDSSVDSF-----MEEWIEGKQW-----IS-VRAEITITFSLCGFANLGS  
VAELLGKIKTFINEFVAYERLQGLIEDSSVDSF-----AEEWVGDRKQW-----IS-VRAEITITFSLCGFANLGS  
VGQLFQMKTFINEFVAYERLQGLIEDSSVDSF-----PKFINGITQY-----MS-ERSEVIATYALCGFANLGS  
CAELIGKIKTFINEFVAYERLQGLIEDSSVDSF-----HVPDVTGVVYV-----VD-ERSEVIATYALCGFANLGS  
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AARMVGKIKTFINEFVAYERLQGLIEDSSVDSF-----NGTWHLDTTGNIVMDTPGNATILIGGV-----MS-ARSEVIATYALCGFANLGS  
VARLIGKIKTFINEFVAYERLQGLIEDSSVDSF-----GPKFVGVQVY-----IS-IRSEVIATYALCGFANLGS  
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VAGLIGKIKTFINEFVAYERLQGLIEDSSVDSF-----LVGTS-----IS-ARSEVIATYALCGFANLGS  
IABLIGKIKTFINEFVAYERLQGLIEDSSVDSF-----TSFNNNTAHWYNNNGVNL-----NNTQELVGGV-----IS-SKEVIATYALCGFANLGS  
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700a 720a 740a 760a 780a  
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Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 VVISIGSFVALAPSRIGELPRMAIRALIAAGTITASYLTACVAG-----  
Myessoensis.XP\_021350798.1\_uncharacterized\_protein VGITLGSFAVLAPGRVGELSKLAMRGLIAGTITASYLTACVAG-----  
Avaga.UJR10076.1\_hypothetical\_protein\_I4U23\_014298 MGVALATLGVFAPTRKRRLVNIAPRALIAANMVSIMTASIAG-----  
Avaga.UJR35986.1\_hypothetical\_protein\_I4U23\_028726 MGIALATLGVFAPGRRRALIKMAPRALNWR-----  
Egranulosus.XP\_024350707.1\_Solute\_carrier\_family\_2 VGILLGTFTIKLLPHRRKDLSGMVVHGMIGGTIAAFVTACFAEAEASATWHHESSRKLSSTILRPVPSIHIKEVVREIAINFQDKMVRGGTVQPASSMNP  
Egranulosus.XP\_024352129.1\_Solute\_carrier\_family\_2 IGIMLGAMVSMPLPHRRQDLSRMVLGAMVGGTIACFLTGCFFAG-----  
Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp LGILIGSLSAMAPHRRSTITAVAFRAFVVGSI VCFVSASFAG-----  
Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp LGIVIASLSAMAPSRRSIDITRVAFRSYFAGSFVSFTSASLAG-----  
Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_m IGIYMSLLITIEPRKKENIVDVAVRAMVYGNIAACMNTASMAG-----  
Aplanci.LOC110983407\_solute\_carrier\_family\_28\_memb IGVMMGGLIPLVPHRRKSEVSRLCVRALLASCVALFMTASIAG-----  
Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 MGINLGAFATAADPSRQKDYAKGMLRAMIGGNVACFMTACVAG-----  
Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 MGINLGSLLTAADPSRQDYAKGMLRAMIGGNVACFMTACVAG-----  
Hsapient.NP\_004203.2\_sodium/nucleoside\_cotransport IGITLGGTSTVPHRRKSDLSKVVRALFTGACVSLISACMAG-----  
Hsapient.NP\_004204.3\_sodium/nucleoside\_cotransport IGIMLGGTSMVPQRKSDFSQIVLRALFTGACVSLVSNACMAG-----  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 LGIITGGLSVLMPNKKKDLAEMSVRLMGMGIACCMTASISG-----  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran VGITLGGGLIMAPHRRGEMAKIVIRALITAGIFVSLNLACVAG-----  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran LGIMLGGLSMAPQRQGEAKIVIRALITAGIFVSLNLACVAG-----  
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Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me VGITLGGMGIMAPARRGDLADLALRSMLTGAVVGLLNACMAG-----  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor IGITLGGGLGPMAPNRKGDLAELALRAMITGVLSVNLNACMAG-----  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 IGIMLGALGPMAPNRKGDITATVVRALLGGIVVCLLTASIAG-----  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 IGITLLGAMGAIPTTRKRDLTRMVVRAMISGTVACFLTACIAG-----  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me IGVQITGGIGALAPERRGDIADMAVRGLVAGSVACFMTASLAG-----  
Aplanci.LOC110990438\_solute\_carrier\_family\_28\_memb VGVVLGGTTPMAPTRKRDLSSVLRALMAGTACFMTACIAG-----  
Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_m IGITLGGIGPMAPNRKGDIAKIVVRALITAGTVATLMTACIAG-----  
Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_m IGIMLGAFAMAPNRKSDCAKVVVRAMITAGNVASFTTACIAG-----  
Lanatina.XP\_013390240.1\_solute\_carrier\_family\_28\_m IGIMLGAFAMAPNRKSDCAKVVVRAMITAGNVASFTTACIAG-----  
Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_m IGIQLGGGLGAMAPSRKSDMAKIVVRAMITAGNVACFLTACIAG-----  
Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_m IGVQLGGGLGAMAPSRKRDLAKVVVRAMITAGNVACFLTACIAG-----  
Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_m IGVQLGGGLGAMAPSRKRDLAKVVVRAMITAGNVACFLTACIAG-----  
Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_m IGIMLGALGAMAPSRKSDLSQVVRAMITAGNVACFMTACIAG-----  
Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 LGIMLGALGALVPSRKSDVSSLVISAMITGNVACFMTASIAG-----  
800a 820a 840a 860a 880a  
Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021350798.1\_uncharacterized\_protein -----  
Avaga.UJR10076.1\_hypothetical\_protein\_I4U23\_014298 -----  
Avaga.UJR35986.1\_hypothetical\_protein\_I4U23\_028726 -----  
Egranulosus.XP\_024350707.1\_Solute\_carrier\_family\_2 RADAEEAAVEAFKGMGYKKDVLDDIFTNRSFTQRSLILNAYKAGFGESLQKRVRSSEINGDFKICLLSSFFDDQSHADARALFKAMSGISTHDKTLMVEICTS  
Egranulosus.XP\_024352129.1\_Solute\_carrier\_family\_2 -----  
Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp -----  
Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp -----  
Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_m -----  
Aplanci.LOC110983407\_solute\_carrier\_family\_28\_memb -----  
Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 -----  
Hsapient.NP\_004203.2\_sodium/nucleoside\_cotransport -----  
Hsapient.NP\_004204.3\_sodium/nucleoside\_cotransport -----  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 -----  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran -----  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran -----  
Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 -----  
Hsapient.NP\_001186562.1\_solute\_carrier\_family\_28\_m -----  
Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me -----  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor -----  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 -----  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me -----  
Aplanci.LOC110990438\_solute\_carrier\_family\_28\_memb -----  
Lanatina.XP\_013410730.1\_solute\_carrier\_family\_28\_m -----  
Lanatina.XP\_013418918.1\_solute\_carrier\_family\_28\_m -----  
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Lanatina.XP\_013389091.1\_solute\_carrier\_family\_28\_m -----  
Lanatina.XP\_013392255.1\_solute\_carrier\_family\_28\_m -----  
Lanatina.XP\_023930717.1\_solute\_carrier\_family\_28\_m -----  
Lanatina.XP\_013421719.1\_solute\_carrier\_family\_28\_m -----  
Myessoensis.XP\_021374214.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021376259.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021376258.1\_solute\_carrier\_family\_2 -----  
900a 920a 940a 960a 980a  
Myessoensis.XP\_021375138.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021350782.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021350798.1\_uncharacterized\_protein -----  
Avaga.UJR10076.1\_hypothetical\_protein\_I4U23\_014298 -----  
Avaga.UJR35986.1\_hypothetical\_protein\_I4U23\_028726 -----  
Egranulosus.XP\_024350707.1\_Solute\_carrier\_family\_2 TNQEIRDIKLAYQDILQEENKDNKTRNLNLEGLKSCSTGNFQRLLVAVSOGRRSETVDPQIASIDAKILYDAGEGRMGTDSTFIRIFASRSWESLRKTD  
Egranulosus.XP\_024352129.1\_Solute\_carrier\_family\_2 -----  
Dmelanogaster.CNT2\_concentrative\_nucleoside\_transp -----  
Dmelanogaster.CNT1\_concentrative\_nucleoside\_transp -----  
Lanatina.XP\_013392196.1\_solute\_carrier\_family\_28\_m -----  
Aplanci.LOC110983407\_solute\_carrier\_family\_28\_memb -----  
Myessoensis.XP\_021346669.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021346672.1\_solute\_carrier\_family\_2 -----  
Hsapient.NP\_004203.2\_sodium/nucleoside\_cotransport -----  
Hsapient.NP\_004204.3\_sodium/nucleoside\_cotransport -----  
Cintestinalis.LOC100175376\_solute\_carrier\_family\_2 -----  
Cintestinalis.LOC100184618\_sodiumnucleoside\_cotran -----  
Cintestinalis.LOC100187062\_sodiumnucleoside\_cotran -----  
Myessoensis.XP\_021365661.1\_solute\_carrier\_family\_2 -----  
Hsapient.NP\_001186562.1\_solute\_carrier\_family\_28\_m -----  
Bbelcheri.LOC109471258\_solute\_carrier\_family\_28\_me -----  
Bbelcheri.LOC109476916\_sodiumnucleoside\_cotranspor -----  
Myessoensis.XP\_021376437.1\_solute\_carrier\_family\_2 -----  
Myessoensis.XP\_021369774.1\_solute\_carrier\_family\_2 -----  
Bbelcheri.LOC109468925\_solute\_carrier\_family\_28\_me -----  
Aplanci.LOC110990438\_solute\_carrier\_family\_28\_memb -----

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Lanatina.XP_013418918.1_solute_carrier_family_28_m -----
Lanatina.XP_013390240.1_solute_carrier_family_28_m -----
Lanatina.XP_013389091.1_solute_carrier_family_28_m -----
Lanatina.XP_013392255.1_solute_carrier_family_28_m -----
Lanatina.XP_023930717.1_solute_carrier_family_28_m -----
Lanatina.XP_013421719.1_solute_carrier_family_28_m -----
Myssoensis.XP_021374214.1_solute_carrier_family_2 -----
Myssoensis.XP_021376259.1_solute_carrier_family_2 -----
Myssoensis.XP_021376258.1_solute_carrier_family_2 -----
1000a 1020a 1040a 1060a 1080a
Myssoensis.XP_021375138.1_solute_carrier_family_2 -----
Myssoensis.XP_021350782.1_solute_carrier_family_2 -----
Myssoensis.XP_021350798.1_uncharacterized_protein -----
Avaga.UJR10076.1_hypothetical_protein_I4U23_014298 -----
Avaga.UJR35986.1_hypothetical_protein_I4U23_028726 -----
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Egranulosus.XP_024352129.1_solute_carrier_family_2 -----
Dmelanogaster.CNT2_concentrative_nucleoside_transp -----
Dmelanogaster.CNT1_concentrative_nucleoside_transp -----
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Aplanci.LOC110983407_solute_carrier_family_28_memb -----
Myssoensis.XP_021346669.1_solute_carrier_family_2 -----
Myssoensis.XP_021346672.1_solute_carrier_family_2 -----
Hsapies.NP_004203.2_sodium/nucleoside_cotransport -----
Hsapies.NP_004204.3_sodium/nucleoside_cotransport -----
Cintestinalis.LOC100175376_solute_carrier_family_2 -----
Cintestinalis.LOC100184618_sodiumnucleoside_cotran -----
Cintestinalis.LOC100187062_sodiumnucleoside_cotran -----
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Bbelcheri.LOC109476916_sodiumnucleoside_cotranspor -----
Myssoensis.XP_021376437.1_solute_carrier_family_2 -----
Myssoensis.XP_021369774.1_solute_carrier_family_2 -----
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Aplanci.LOC110990438_solute_carrier_family_28_memb -----
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Lanatina.XP_013418918.1_solute_carrier_family_28_m -----
Lanatina.XP_013390240.1_solute_carrier_family_28_m -----
Lanatina.XP_013389091.1_solute_carrier_family_28_m -----
Lanatina.XP_013392255.1_solute_carrier_family_28_m -----
Lanatina.XP_023930717.1_solute_carrier_family_28_m -----
Lanatina.XP_013421719.1_solute_carrier_family_28_m -----
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Myssoensis.XP_021376258.1_solute_carrier_family_2 -----
1100a 1120a 1140a 1160a 1180a
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Myssoensis.XP_021350782.1_solute_carrier_family_2 -----
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Avaga.UJR10076.1_hypothetical_protein_I4U23_014298 -----
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Egranulosus.XP_024350707.1_solute_carrier_family_2 LLAILRESDS
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Dmelanogaster.CNT2_concentrative_nucleoside_transp -----
Dmelanogaster.CNT1_concentrative_nucleoside_transp -----
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Bbelcheri.LOC109476916_sodiumnucleoside_cotranspor -----
Myssoensis.XP_021376437.1_solute_carrier_family_2 -----
Myssoensis.XP_021369774.1_solute_carrier_family_2 -----
Bbelcheri.LOC109468925_solute_carrier_family_28_me -----
Aplanci.LOC110990438_solute_carrier_family_28_memb -----
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Number of sequences: 36
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