

## Electronic Supplementary Information 2

### **Efficient Enzyme-catalyzed Production of Diosgenin: Inspired by the Revelation of Biotransformation Mechanisms of Steroid Saponins by *Talaromyces Stollii* CLY-6**

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A total of **867** genes in Talaromyces Stollii CLY-6 were classified as carbohydrate-active enzymes (CAZy), and the detailed amino acid sequences were shown as follows:

>2899\_t gene=2899\_g

MMVKSFLAALSALSALVQGHPSQERSLSERQSTDRLVFAHFMIGITSDRTSSADYDAD  
MQRAKSYGIDAFALNIGVDPYTDQQLGYAYASAANNGMKVFISFDFNWHTSQATAIG  
QKIAQYASLPAQLMVDNKVFVSSFAGDGVDAALRSAAGSELFAPNFHPSYGTDLNSV  
DGLLNWMAWPNNGNKAPDATGNVTVEQGDQQYISALAGKAYIAPASPWFSTHFGPE  
VSYSKNWVFPSDLWYNRWEELLTGPRFIEIWTWNDYGESHYVGPLESPHTDDGASK  
WVNDMPHDGWLDFAKPFIASFAGATAVDSYITSDELIYWYRPTPKDVDCATDCM  
DPNASNSSGNYFIGRPNGYQTMEDSVFVVLFTAAAETVTSNTQTFQASAGASAFQV  
PMGVTQTSVTRNGATVFQGTSLKIQINGCVCGLYNFNAYVGSPLAGFSDPLGPAGLA  
SLVQGLHVSTCAATPSLGTAPPVTTSPVTTSSSTTTSSTTRSTTSPTTSTSTT  
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>2921\_t gene=2921\_g

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GVFASAAAENGLNMDFALGPQNQGAGVPVQDQTAPGLSTGLEGYFYFNISGGQQYSGPLP  
DPDLSYSGRSPSYWVFPDTASPAVLAAVAGHITRYSNNEIFLNQSTMIDLTA  
MVVKDG NVNFTPGVVFYDQWTLFSWQRRTGQYESRQGLTSYPLTSNGSFIVDH  
FSAAGAQLSA QFMDQNAITAGDFETASMYAWEDSAELVAPLLWTDNFTQSFLSRR  
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TFLWAHSRGFQYSNQPYGFPIDF VAASSIADAPECESLEFNDNV  
DAYRQFAGGVNMAQARI  
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FIWEGYSGSHNVRQPSWPMYPS IIDQIARTNFV  
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GSLWSDQGLYDAGYTWN  
YISPA  
NLELPTG TLTDGV  
LAAQG  
PSYKAILV  
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NESSM  
PPAAR  
HISSY  
ANAG  
FPV  
IFIG  
TPS  
STPG  
NNITGD AYVN  
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ILSNT  
NVK  
TVPS  
QSDV  
VSA  
EELN  
VLPF  
VNTT  
FLTV  
HRW  
NATE  
LTHY  
VYF YNQGA  
ASTQ  
IVTL  
QTGEG  
VPFL  
LDLS  
LTGRI  
ERIAAY  
QTSL  
TTS  
VEV  
SLT  
QNE  
IALIA  
GPP DNFNG  
IGSRL  
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MRGDQVLAAPV  
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LDPT  
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ITTNC  
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TEYVISVN

>2939\_t gene=2939\_g

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LPAPYSASTGIATPSATTLSGETSSVTSAQSSTYSDSPVSQTLQDVQVPSIAPTASVISS  
STLVPPVSNSPAPSVSSTSSSQGSPSPSSPSAESPLGGIMHGQATSYDGGDVDGTCMFST  
AGYTLPGVYGAALSVDNWDT SAYCGACSVTQGDGKSVKLMIVNQCPGDCGLNHLD  
LLPNGFTQLADLKVG RIDVDWEFVECDISSPLYSTQSGSSKYWFSMQVVNSNPVKSL  
EVSTDGGNTWQATTRSEYNFFQNPSGFV D VDRITSATGGTIIVKNANSVGETRTDA  
TSNFS

>2972\_t gene=2972\_g

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RKPYLKVL CGFSRRFDASYRDAHTKMLAGTIGRPSVIRSQTC DKLDPGFFV TYAQFSGG  
IFVDCSIHDIDLALWFYTEDGKSEPMVKVS A VGITA VEPDLRKYDDRDNAVGLVEFND  
GRIAYFYASRMMAAGQEDSTEIIGTKGKLT VNTQPQINLVNIYEADGVRREL P QHYFDRF  
RDAFVTEAREFTDCCLDDKPVPLKLEGAVQAVRIGYALQEALISGKKISFDEEGQRFERA  
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>3068\_t gene=3068\_g

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ARIAIDLHGGSKAAASLKSSL YLAQALLELQR PQEAYDVAIDAYRASLSAMNAQTENLS  
KIVLRAKQQIWAAKETARLREM DGT LASVESLIEADLERELKELKQLDSGEIGEIGYNE  
DQKALRDEAEKKIQH VRDAFKAASGGQIAERVVPDYLIDNITFEVMHDPVLTISGH SYD  
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>3074\_t gene=3074\_g

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FNWDPKITT PPGYLWSYLDCTGRSLLKG SSEEVN VV DLRSTNSIAAFILPW RLQTL LD  
VLRKEQNTRAAGAWLSHTVLNICLFPPLFFFSGLYYT DILALIVVIQAYIW DTERSDANG  
QKKTAVEALRGHVSFKTLAFISIGCIALVFRQTNIFWV SVFMGLQAVRTIRQNTKSCGY  
TGPLEIMLKS FQAE LYDPLVEEASFADYFKTGLSLGCAALSELPLV VASIIPHLIVLGAFG  
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NLSNAHRLPSILTALA V I PLMLA AVHFNTV VHPFTLADNRHYV FYI F RLL TRVHPAVK YA  
VV PVYFLCAWA VL TAFG IFSPA APK P PPIQIATPQEA F PSS SKIQ NPSKKQ EKEAKKQQKK  
QTTKS NANKQSPSAAA AKSKQDQ QTQVLTPEI LAKI QAHVAIRQQQRENQQV RV SFV LI  
WLIATALSLITAPLVEPRYFIIPW VI WRIHLP RQPTPEIFKRERQSTFRAQVFTALPEIMETI  
WFLIINAVTGYVFLYKGFEWPQEPGKVQRFLW

>3105\_t gene=3105\_g

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LATM GDLIGFEGYLNTTPFKYEEHKVEYKSPRQYVDFHFGNDYNTTCDYPRF YNETGY  
PVDSYVYDDLKG C YNSDFDQYGDVEAFGVFPDYQRELAKFASVQDRLREWNPSVRERL  
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FGSIYLGRGRQPD MWP DNQ DAILMTNESSDKYFIRQDGQQAIDGAAFHYTVYRTLTRF  
LG LDGNLAAGYDLPPDWV TMWNLMLLSNDMVNANTGKF DPRHLYGTTNQDVFRWPA

IQNGTEKMLLGMFITLHMPGAPLVLWGEEQGFYILDATADNYVYGRQSMSPATAWWS  
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VTNSILLNSTETKQTATLNSSVSCQNINDGTTNFIGEIASAWWKATLDNVYNGIHRIT  
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ALRRRLKRARLDGIEVRNPFLRLANRSGFLQTTSAFAGATSGERRRMVMIAATMEYDIED  
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SRDPSPDGDERASNLFRQLSLGVRAFGHTAVIERRNRLRRKIHVAASEDITDSEREGD  
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GFSEGDDSLAPPTRPFATAPNRLSNSSVLSFDSVVGDKKNFKLQVDPFFTDATGEFYRIF  
EKKLEDLNGNSNDGQLCIEEFLVKSEKKWYDRFRAARLGRDWSPVPSIKKGILTSPNS  
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TLLTGQIGQTPEKLYAIATTYLITSIAWWCVFRSFKSVALSTPWFFYGLAFLIGIAHFEH  
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CSYAMSFYVFEAVRKAGLYEELRSTLLEPWRDMVRQNLSTWAESAAMPRSDCHAWSS  
VPIHDFVTNVAGLAPAAPGFKSIRLEPRRELWKEMSGTFAVGKGSIAMSWSPGEPELVP  
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>3128\_t gene=3128\_g

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FPDYNCPDGLRAQVFFPSCWDGVNLDSDAHKSHMSYPISGAYNDGVCPTHVHLVSIF  
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GLISDCLAADGSEHFDLFTNEESQFCFLPAFVDETIGPVVEALPGCNPVTYGPEEATPSKC  
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AAGYSYAGLEYSTQCYCGNSIAANAPIAGVVGGLFPCGGNSTQMCGSAALSVYHK  
CAGSSCANANIGVIEGAASVAASAAAGSSATAATSAASAVSSGSTGATATAVATT  
AATSATATAVANVSSKTTSVGATSPVAPATVVVTGGEVVQVTSTITKGVTHWKTV  
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>3135\_t gene=3135\_g

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RQAKFRVATGFAGTPIITHALTSGYPQIAYRMLQEKNRPSWMYPITMGATTWWERWD  
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KYDTPYGRLECRWSIENEADIFNMALLIPPNTSALVMLPNTEKMMKHTVSQEDEGQWV  
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>3147\_t gene=3147\_g

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NSVEMVLANGEVVKTSRDEKKDLFRGAAGAVGSLGITLIELNLVEAKKFVKVTYERKP  
TIKAAIEALEKDSANPDTAPFEYIDGIQFSPDHGVVIKGELTDELPANVKPQTFSNPWDPW  
FYLHVQEITKQQELVTEYVPLAEYLFRYDRGGFWVGASAFKYFRFVPFNKTRWFLLDF  
LHTRMLYKALHASGESNRYIVQDLALPYETAEEFVDYTTKTFDIWPLWYCPLKQSPTPT  
MHPHNTETKHAGRLLNIGLWGFGPAESTEFVAKNRDLEHKLNDLGGMKWLYAHTYYP  
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>3188\_t gene=3188\_g

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WTSGIVTAAQYAKSLKAFNDYLAHTSSGKPGAFDEAASPILSFIFIQKLGQITSLSIL  
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DLETMKNAYAIFCETATDLRRVKGLIFPFVFQAILPGWMNKGDPNILGLENCTEPLIINY  
SASWINAEDDDFVRSTIRRSLERIEAATEGRKTGHRYRFINYCMEWQRRYEGCGEENLK  
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>3229\_t gene=3229\_g

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LQADSKFC  
LTLRDRSLVIVDVNYRHC  
PETIMGK  
NVEDAWAALSWVRDES  
VKLN  
VNKS  
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ISAGGYL  
SCILQH  
LARDNN  
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VTDC  
CSYK  
KLED  
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ESFR  
QYSRAP  
LLN  
WARISYF  
QQYVFP  
DDRVDY  
IRSLW  
PEWWL  
SPIK  
APNF  
ANLC  
DTFL  
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GKKL  
VAA  
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>3251\_t gene=3251\_g

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PSDDQ  
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VEG  
NSDLT  
WYYDY  
TDP  
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NKYASSSTNGIGKDDIITEGVFTSPVLDYAESLSPSTRPAFLKALKAAIVNVGFFYLKNT  
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>3255\_t gene=3255\_g

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FLPIYDSYRHPVQRVDALKYFIMRHGGIYVDMDNGCLESLEPLRYYPAFTTDGGEGPL  
FINILGAAPHHPFYEYMTNNIWAYNLFYYPLPYLTISYNSGRWFFTSMWEKYHDSVNRR  
NWNLVHSAGEGADQIHASGINNKDQLYRVMMENRRGAEPWFVNNEGAGLTWENWD  
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>3270\_t gene=3270\_g

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PLVEYYILESYGTYNPASGLTSLGQVTSDDGTYDIYSTQRVDQPSIEGTSTFNQYWSVRT  
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>3295\_t gene=3295\_g

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VGKYPAGTILATGNAIPADFSSTNIEIYASKDHGLNWEFVSVVATGGAPNTDNGATPVW  
EFIGIYNNQILVYYSQDRPLHGQKLSLQTSQWSTVINAVAYGNYTQRPGMATV  
AQINGNGKWMISHEVGLAPQGDLAPYAVHYSIADSPLFGSAPSHLLQARNTGTTISSAGPY  
TVWTPAGGPSGTIVVSDSTYSQVFINKNDGDPNMWEEIETGLGSYTRGLRVMPDESVI  
LFLNGGGYGLPAASVTAGEWKVPGPSSSRDTISNCKNPHGP

>3315\_t gene=3315\_g

MADVQSIQRRFQEHLNVRFAHNSPEFQDIRAAYIKNIPVPLGIARPQTAEDVANVIRYI  
KKEGLKFSIRAGGHDLYGRSFIQDGIVIDMRDISYVQVNESNSVAQIGGGALASSVAKAL  
SDEGMATALGSFPSVGYAGWATHGGYGPAPNYGLGVDQIVGARLVNWEQIVDANE  
GMLKALRGGGGAIGVIVELTVKIYPLKQILAGIVLFESKDIESTIRKIINAFSHLRANGLPV  
ELGLQQSVVNTLHGKLFAIGFMWSSEDMELGKIYLQQVLFGEVVDNSVIPTNLSDWLE  
ESGRLPPPNAVGAICSAVRVQTDQIADILAKFAKSMPEDRGTLYSVHEIRGPSAKPCSNS  
IFRTRERHFLIECIGTAATAEAAPQSWEWALQLRHAIMQTEPANIIPGSYLPNPPDEFSSD  
EVYGEYWWEFKELKKNYDPQNVFKNALPRFGPSDHV

>50\_t gene=50\_g

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PINDGWDAFQYIVTNLSSLLANLAPGMTNLVSGTSSGGQIAIVSRRAQTWMKGNVSC  
VNITMSGVLLRAPVTVRATEARFVPPAFRDLHKSWRAELETVRLTRQEMEEMHDTLG  
PPDIRDSPEAYPLWGPFHGLPKTYIQICEVDILRDDAVCYAQGLQDAGVEVQKSLYTV

>52\_t gene=52\_g

MACYSVVRLSILLHWLCIFACSAVAAITAATDLANLRAQLSPNTSISWSTSDAPRWSDYD  
APQPIAVINVAAEKDVQITIQFCNSESIPYLVQNGAHGSSTTLGQLYYNGIINLAALNRVT  
FNSEKTLVSLEGGTLMSEMIQSAYSNSALVLSGTNCIGYLGALLGGGIGYLMGQYGLM  
LDNVVSLNVVLASGQAITITPSADAELYDESLWWALRGAGPNFGAVTSAVVKSYPVDST  
ALKAWLGPLIFEESQLGTLVQAMNDITLQPQMAMSLTFASSGNTSVSPLIILTUVFYHGTE  
AQGKAFAPIYEIGPVADNTSIIAYPDWNAAQDTSCIKGGNKPSFGAGLAEPESWEAV  
YDAYKEFLNPEAQDSVILLDAYSTAQISSIPDSSAAYPFRSTVRFNAQASLAWNDSGFD  
ASALAFGSFCRDKWRLSSGLKNNSTYINNAFGDESLTTVYVGQLHRLQALKKIYDPYGR  
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>58\_t gene=58\_g

MLQLPWIWYITLCVACTSSFAAALSGSPFSPPDPSFGIPGDDASYDYVVVGGTAGLTIA  
ARLAESGTYSVAVVEAGGFYEEADGNLSVIPSDDIWYAGSSPTDFNPSVDWGFVTPQA  
GMNERQLHYARGKCLGGSSARNYFTYHHGTYDAYHMATTVDNSSEYYSLPYFKK  
SVYFTPPDNEQRPRNASVGYNPAAFSPTGGPLQVSVPWANSFSSFAKKGYERLGLQQV  
VDFVSGTLIGVQYNMTIDPSRQTRSSSETSYLRMVESNNALRVYNQTMAQRILFNGTT  
ASAVAVRSGNLDYTLFAKREVIVSAGAFQSPQILMVSGVGPQTLRQFNIPVIADLSGVG  
QNMWDHVLFGTSYRVSTLTHSATSNATFLAEVLEEVYMRNGSGMLGNPGGLIAFEKL  
PSSDRESLSPETLASLAEFPADWPEIEYLALDAYSGNNSDYITGAPKTPYMYVPSAALV  
APLSRGNVITSASMNDPPLINPNWLTHPADQELAVAALKVRQLMDTEIVSEVVVGEE  
LLPGGRNVKSDSDILYAIRENGIQVFHAAATCKMGNSSDPSAVVDSKARVFGTRGLRVVD  
ISAFPFLPPGHPQATVYALAEKIADEILCADV

>92\_t gene=92\_g

MADKSHARSEEQHATTDAKLVNRLNESRSPYVRGHMNNPVAWQLWDSKIELAKKH  
NRLIFVSIGYSACHWCHVMEKESFMSTEVATILNESFIPKVDREERPDIDDVYMNYVQA  
TTGSGGWPLNVFLTPDLEPVFGTYWPGPQASSHSHAAESPIGVEILEKL RDVWQTQ  
QARCLDSAKEITKQLREFAAEGTHAQGAKGDGEDLEIELIEEAQHFASRYDPVYGGFG  
GAPKFPTPANLSFLIRLGMYPSAVSDIVGLDECVRATAMATNTLLNIARGGIRDHIGHGL  
ARYSVTSDWLLPHFEKMLYDQAQLLDVYVDAFRATHEPELLGAVYDLVSYLTSEPIQAP  
TGGYFSSEDADSLPTPNDEKREGAFYVWTMKELKQVLGQRDAGVCARHWGALADGN  
IAPENDPHDEFMDQNILSIKVTPSKLAKEFGLSEEEVIKIITGKQKLREYREKTRVRPDLD  
DKIIVAWNGLAIGALAKASILLEIDKVKAQQCRDSAHKAVEFIRKTLFEPSSGQLWRIYR  
AGSRGNTPGFADDYAYLTGLVAMYEATFDDSYLQFAEQLQKHLNQYFIAQGESGTTA  
GYYTTSKPIPGEPGPLLRLKGTDSATPSINGIARNLVRLGAILEDDETYRQLARQTCGTF  
SVELMQHPFLYVNLLDALVGLELGVRNITGVLATDTVATTIQKDAAETQPHKNATDVV  
RERVRAEAGSAASTSVTTVSMVDIRGSNVSTTWLQSRNPLFKDLKPGTPLKNYLLVCET  
GSCRIVDI

>116\_t gene=116\_g

MTSTEASQDITDAIAAGFDGFALNTHTISSKDTWNTDAINYLLDAASGTSFKMFLSFDM  
WGLDVSSLGSFLTQFSNHSQYYTTSDFGRPWVSTYSGGSSVSNDQWNSEFIQPLVAQGVT  
PYFVPDFDDWPGYPTGFFDAFPVLDGAFSWESA WPGAGTVANVSDSVDES LIEQAHG  
AGKIYMMPLSTFQFKYLGSGSDWYRIGETNLPERIAQILSLQPDFVEVITWNDAGESHYV  
GNFWPEQIAGTSEGDYANGYDHTGWQQVITPFITAYKNGATSVGQITTQSGSPEGAIWY  
RTLLKSASCANTINYQQAEDAINFAVVL PASDAAYTIEVYNSDALIGTFSGV EGLNYES  
VPGLQAGSGQSIRVLDGSGNVVKTANGTKDVLNESSDSSMCNWNYEVVGLS

>134\_t gene=134\_g

MPTSTLLKGTLIHGEHDLVQSTISDLLIQDSIIVRINPDIDADGEKIDRVIDCTGKIISPGF  
IDTHHHVWQTCLKGTHADETLLDYFWSGNFINSLLSPEEIFWSELAGTMECIDS GTTVV  
DHATVNYTPEHSIEALRATIGSGIRSIFGYCPTPRVRSWKPEFKLDDDLLPPWVMETFDQL  
AALNPLGPSGLVRLAFADGVWLPKEQLQPLFSKVRQAGSQLITSHSVYAAFGAPHAPS  
VVQTMHEKGLLGPDVLLSHNNNPRPQDTDVLLRLNTKVSCPSTELQMGGNPVCFMD  
KLKTSSLGIDCHSLCSAFIPGQMNLAQWARGRRNEEYESQGKWAKTLTSLVQEAYNL  
GTIQGARSIGMEAEIGSIAVGKKADLVIFECQTPGMIVAADRDPAAIVLHSSVRDVETVII  
DGVIRKQRGVLLADVPDKINPSTTDKWRRVVSWKDICGKVLALSKEVDKRKKSIDPKV  
AVDGIMRGFYMNLEARC

>142\_t gene=142\_g

MYINTKHLGIALLAPSLVAANSMKTL SKRDATTYEQNAVCTADQLRSYGTVN TGLFG  
QDLWWQSGNFISALATFFQLDPDYGSIHNNIFATTLEAPGYGNYANFLNGWYDDEGW  
WGNAFLDVYDYS TSDSTYLNQAITIYNDIVGLGTPCGGIWWWDKDHTY VAAISNGLYTEL  
AAGLANRAGGGSYLA NAEANWNWFFSSGIVGSDHIVRDGLNSDDSCSLNGNVFTYNQG  
VILGAAAELYKATGNQTYLTAA ALADASTASGSDVTSSGILTEGCDKSASC DTTAEM  
FKGAYIRGLRKLQLVDPESNWNLNYLTANAQSLWNHDLSVQNVNGDSECIVGSAWAGPF  
NSNQANVVTQGAAL DALNAALAATHDEEEEDDEEEENEP RRLYGGEESEQSENAESERSF  
NRSDADYY YELKEQGEDQKREVREGKS KAYVFDKSKEVEVQSAYDAVKLDKKSPVDL  
RLFDPKISNNFRIYSTDWVKHCFSSLHASPYVKFYEMDENHFQPSSERGTRQIEGHLYIH  
GTLD CGFNPFRPPKLSSFEEIELQKQVRNNNYSILQS

>147\_t gene=147\_g

MFPTTWRLGFFALLVWLTTAQAAKTDQAATTNVDTCACGFYDDTADLYFTDSTIVYFN  
ESGSIPSDFVVEEFEHRYDRGWNM YM RMGAAVDNVQVTKDVTAKNLTSLELSCLPSDQ  
DHLVVGSSVRTARQDIFFGSFRSTLRPARN YSLGSAISMNLVHNQTESWQVDVMNADNS  
SQA WVDMLMQGFANTWLGTNFTNLTGEGLKPWYYLEYRVDWTRDSSLNYYIGDVL R  
TSYNTSVNSSIPSTPAPLK FQHWSTGNKYTSQGPPIFTNL ANVGYARLFFNSSTWNDTTR  
AA YDQRC SIQKACDMNDLSLRGSSNFDPQSLDPWQHQPPYKIRWVPLIIDIIFAAIFVVL  
TGKTLWRRFTWHKLMVFLGVHERDPPKPRSF DAPACSTPSLDRDHSNRDSADAASSSP  
ASHNDTQRDLSRNESFATLPPYRGSQTLPQYQSPAASRPSLTNMAGNSFAYPTSLNNT  
VQGESSRVTSRAASRAPSLHAVPM LDYLSTPSQE VYSSGAMQVDGSSEKNKEATKTEE A  
LPAKDGQTKPGEASKDGKPTAGAAAASAKPPRVDYL AFGFISI SALLVTVNHFGLTYFGA  
VIMP GNSPHYHSEVIARKSFATYFLDPLWIGPFLMISTRFLTSNYIRTGKLDNMAQKIVAR  
PF RLLTPV ASIAFLEYFLMDAGALN WLEYLPSVTWSDWPFTAIASNPGTFISEILQLAFLIP  
NAAPMITNNYCTGVLWTIPVQLQAWQTLLGLIMIRQIKTPWKRFSFYVFCTVMHWYA  
LSWG SYYYVGILLADLDLT KYKQKWLWPHPWIYWPVLILMACTAIGGFSIDLVTQHT  
GVNYAQIEYGWHPDVKTGLTLAQ AQSASYPDYFIPRLNAFLTTITMQGVVEISPTLQKIL  
SIKMLQWLFPHIFIYLIHG FVMWSVG SWAMISMFSHGYPYWLCLITAIVCYGTLFAVL  
PILT PPIE ALGKGFTQRLWQFASMEPVERKPTTYPFGE EFLTRDQLQDPSKPGSLNGVPP  
SSASSSSGRVTGVNEKDVGKGKEAEVTTELKNGPGPTMDQKNEF

>148\_t gene=148\_g

MEKQVDVEVNA LHTPVEPLRSSERRCNVRSGLKKVYQDV SWVFTTASDG VQDWTPF V  
LV SYFVFSTTIY MNATSGITEIFWFIYLM TNTYIATATVIESISALGNFQDAKRA LEKVA K  
KNW VFPTAENDLPKLDIIIVAYLPNEQDIVMDRVKYLLEEIVYPRDRYRVNLLYNTPYAI

QPLESELFALADEYAKNLRVIKVPGSKSKADNINYYCNVIQTDAEISAIFDCDHYPHYAP  
KWAMEQFAKDKELEIVQGRCVVLNANDNFLTAMIGIEFDKIYAVSHPGRSAMFHGLFC  
GSNGYWRTPLLKELKMDDSLMLTEDIDSALRAFGHGAKAIHDINVTSFELAPITSAFWK  
QRLRWSQGWIQASMRHVHLVWSRSREGKHRTMRQRFGISLLFVREISYYLITQYLCLV  
LSVVITEFPKNGHDLYKLVFFQYPVAWWLFIFSLLAFVGLWVTFHFRSEFCRWYMIPIF  
AATYLPQLVLTAIIGLFGHARQVSKYVKWNPTPRN

>175\_t gene=175\_g

MDPSYPIPAGLHKVPDHLLRPDEEVQDQLNPKAUTDEKNVWFFWHTGYKTMHPYT  
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QHTSDLVRWPPLLKYGGVYADVGLIQIGDLNRLWDETIGNPDSPFEVVSYNAGGVSDRS  
LTNYFLASNRNNPLFERCHRLLELWAADGGKTSTEGMHSSPLLKEVPLMHIDSTIVDG  
DKVLSDDSVSRLTDYIIQGQVLTVMGLIDEEDGWNGPQYADHVYGIEMEGSQLI  
NEFTNWDGQKAFDLMSPLPKPGEPESAQQKEAREIVEGCLQRSFGKLAHGLILRVFKS  
TLGSLWRANPGSDDVPGTYAHWLRHATIYWNQDHIPTLKFVIPAKNGPLRAS

>193\_t gene=193\_g

MCDFSRYGIPSKEWLEVETLPSRQDKSIEELKTSNNNTREARAKEEMKELQDKVSLTD  
YSIPTRDGSHLEARIYRPKSRTGEALPIYMHFHHGGFLFGTLNSEDSICSRIATNVETIVC  
NINYRHTPEHKYPTAWNDAEDALIWLCCNNYSVFNGDCQRLVIGGISAGAWLTASLVQT  
VLRGDITLAHKSTILGQVLMIPCVCVSTPCYAPIEKLLDSVSSYQQAKDAPILNEKTKSL  
FNSLLQVQRDPNDRRLNPGLTAQEAGRPLPPTLGIAGNDPLRDEGLLYGKFLAENGVP  
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>222\_t gene=222\_g

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PVMVWIYGGGFQFGASNQPNYNGANLAQQGVVLVSFNYRLGVLGFLGLSELDVPGVE  
NSGNFGLQDQLAALRWVKENIAFGGDPDNVTVFGESAGAHSVGLLLSSPLSGSLFNKA  
IMESGAYWDSEHGSIQNFTETRTKGSAFMQKLGVSTVSDLRALSATVNNAALWNSSTD  
PAITAFAPNIDNYVVPAPAETFNRGNAQKVSVLAGFNAEEYLFLPRAIPHNTTDQFRQ  
SAQVLFGPQTAEFLSFYDGATDAQATQSALLDGDLIREQTFEALDRQASVNHQTVYA  
YYFTYTSPYSPVAAHTAEINFVFGNLGPNIPEGTPGPSATDVSLSRMMEYWTNFAKFG  
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>225\_t gene=225\_g

MFSRTNFLPFLGVGLSISQQTAKALVIQTTSGLVQGKVASGRTNQVEEYLGIPYAQPPV  
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GVQYSEDCLTNWTKRSVNNTLKPVLWIYGGGFNTGTTNTAYNGKYIVDLEDVIIIV  
SANYRLNIFGPGDPNIRNNLGLLDQRLAIEWVRDNIAFGGDPNRITIFGQSAGGESVDY  
YTYAWTSDPIAGFISESGTVYSPGAQTDVATSASRWYYVTATLGCGDASSDPDALLTC  
MRSKDWDQDIQDVIPASTGIAVTGLFGPTIDNIVFSDYAARSAAGNFIKRPLFLGSNNYE  
VGLFRPIFGAENVTFTEAQWDYLNFIYTCPTAFRAEASFNGVPTWRYRFFDEFPNRL  
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>232\_t gene=232\_g

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WDSTSWSDPVYFDEVGFDQDLFWDDDGTVYLSTTRKLHRTPGVNLKDFAIHICTVDL  
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KKRDYSLIKSPSCLRHLGGPYRLPDACPACPTFLRKQSERFCTWETRLSFTPSSLYTEAGTA  
VWMDYFTYSTIGIRLKDYNSSGTNESLKENALRIIRFTPPAGSGVDLTEHELKSLSDIIL  
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>234\_t gene=234\_g

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VIVGGTVGGIQKAAVPTVAVVTVTYTPTKTTSAASETFAAAVTTAVCVGGYQQGN  
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>240\_t gene=240\_g

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AYTILNPGSPMASCfedtMDTLLTFELDYAAYTGSYTPNNWVPKDPRLWVHIVNVPES  
AITEVVNLSKERGAGFLQLTDDLLPNPYDTLPSDSYIQTLLGAVAGGSLLNADASAWSA  
GGAAGTVSDLSSILFSYDSSAKLSSWTTTGALGYHIYQGETIVASVPSSMTTITIGGLQPGT  
SNAFSVRAVGGGGVTGSASNTVNTNSLPNGKTIADYNVTAGATSTTYHADILVPYAF  
VRLYIWDSVECDFNDPGWSVNFVVDYVCTHYMVEGTTLYKYSGTVPSGSTAPPWS  
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>246\_t gene=246\_g

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VIEYDFGKQYPNGFQRKRGVLDLGRPSPEIRARLVALSGDRTSIEFQRKMAMHAQKVQ  
PVGSKWRRPASDDILFNSTYAHKHYKNSKADSCCLCLSDHISDAICEGAMRVDCALGCD  
ESEVRRRTQTDMGNAVIHIGPIASADTVMKSGIHRDQLAHEGIIALEMEGAGVWDNF  
PCIIKGVCDYADSHKDSKWQLYAAANAAATVKAFLEYLNNDTKIESMAKTDKQVQW  
TVPFRNPKFVGRRVQLEQLRALMSDPNGPRELAITGLGGVGKTAVAIELAYQLRDADP  
DCSIFWIPCTSQASVEQAYSDIARRLRLPDQTDVKTMDYLSQTISEKWILIFDNADSEH  
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LQQDLLNDHKTVLLLSSLTFLPLAITQAVAFINRNQISLSTYIEILDKQEMEMIELLSENF  
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QFIQISSTQEGFDYGTLYILECLITILAIGQRQRKMKKVLDPFIKRLKVILDQFSATIGSWIP  
SPTTSDEKVGFTSAILETREPDIFAILNYQRIIAMFFRVIDRLTVSEALFQFTIRISQLILGP  
DHPNTLLCQRCLATQYHELQQNTRAEKIYLQLINTTSAIRPDQKELLEYEASLAEVYCD  
ESRYAEAECYQLQAIISLSEVIHGPNLKTLFNFQFCLA VMYQNQSRYHEAEDIMLRVIQM  
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>264\_t gene=264\_g

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>281\_t gene=281\_g

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>285\_t gene=285\_g

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>309\_t gene=309\_g

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>9\_t gene=9\_g

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>3887\_t gene=3887\_g

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D G S W Y A F G T N G N G K R I Q V A Y S T N F E S W T L L D V E A L P T L S G W E T P D H W A P D V F Q R S D G  
K Y V M Y Y S A I V S S N P N R H C I G V A I A D S D N P A G P Y I P A S T N P L A C P L E Q G G A I D A S G F Q D S D  
G T R Y I V Y K I D G N S V G H G G D C N S V E P L A A T P I M L Q R V A E D G I T P L G D A V Q L I D R D A S D G  
P L V E A P S L V R A D D G T Y L L F Y S T H C F T D V K Y D V R V A T A S S I A G P Y S K N G V S V L A A N D E L Y  
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>3901\_t gene=3901\_g

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D P N Y D W G F R T V S E Q G L N G R V I L Q P R G K L W G G S S A I N S H A L V Y P S R G Y H D A W G T L V G A  
G N S W D W N G I S K Y Y R R F Q N L Q A P S E E V K R E L G L G D F A V D G G N S A C E L D E Y E E R V Q A S Y P  
V T V H P M Q Q A W E A I Q D L G Y G S S K N P V D G D V L G G S T T N V I D S S K G E R S H A G V A F L E P S T  
E R S N L V V R G N V L V N K I I F E E E K R D G N L V A K G V L Y S Q E D G K T M I A Y A K R E I V L C A G T F G S  
P K V L E L S G I G Q R E K L A A A G V K C L R E L E G V G G N L Q D H L N F G P S V E V L E S I G T S D V A A R D P I  
V A E A D K K L Y E A K H E G R L S Q G A A Y S F S Y M P L K V F N S E D E E R E L T S L V N M T L E K T S L T I S K  
G L K A Q Y D I I Q R L I L N P E Q A S A T W V M I R K Q R Y T P S I T P A P G N Y M T V L A M L S Y P F S R G S S H I T  
S A D P S A Y P E I K F N Y L K H P L D A E I L S R H V I K I G Q M L E Q P K V S A L L K P D G N T L P R G F P R R A N S  
V E E V T R F I R Q F G A T N Y H P V G T C A M L R E D L D G V V N E D L V V Y G T A N L R I C D A S V I P I V P H G  
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>3902\_t gene=3902\_g

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W T S D G K V L V E G N S L S A L S S G L Y H Y L S D V A H V G I Y W F I G S R L E T V S T L P P L I E P L M G S S V V  
P W R Y H F N T V T F S Y T A A F W S W D D W E L Q L D W M A L H G I N L P L A W V G A E K I L V D I F R E L G L T  
N S E I Q S F L S G P A F Q P W N R L G N I Q G S W G G E I P F D W I D R Q F E M Q L Q I V S R M A E L G M T P V L P  
A F S G Y V P Q A I T R V L P N A T V V N G S Q W D G F P I K Y T N D T F L E P S D P N F A A I Q K S Y I G R Q Q A A Y  
G S N V T H I Y T L D Q Y N E N A P Y S G D L N Y L Q N V T R N T W R S L K A A D P E A V W M M Q G W L F Y A N  
S A F W T D D R I E A F L S G V E T D S D M I I L D L V S D A A P L W Q D T K S Y Y G K P W I W C Q M H D F G G N M  
G F M G R I L N V T Q N A T L A L A E S G S L V G F G N T M E G Q E G N E V I Y D L L S Q A W S D S P I E T E N Y F  
H R W V T A R Y G P S T P P A D T Y A A W E I L R T S V Y D V T D P N S V V V P W P V V V Y T P G I G I A N V T G V  
T S L P Y D P S F V V E A W S L L Y N S A I D E P S L W N N P S Y Q H D I V D L T R Q V L E N A F I P R Y E T L D L Y  
T G T N A S T E A L S A A G K V L I D L L E T L D T V L A T N K N F L L S T W L T D A R S W A G D N S S V E D F F E Y  
D A R N I I T L W G P N G E I K D Y A S K S W A G L V S S Y Y A P R W E I F V E Y L I S T P A S A Y N S T V I N A E L L D  
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>3915\_t gene=3915\_g

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S R L Y K I F V Y D G L C P E K E R A M H K K Y G P V V R T G P H H V S F S D P A A I S S I Y G I S A N L M K V F L L  
L I V L L D P A L T F L T Q S D F Y T P F G A R H E G K A F D T I F S T R D T V F H K H L K V H V S Q I F S L G S I R T L E  
P M V D E C S D I F L R T M H E L A G E K V D L G E W L H W Y A F D V I G S I T F N K R F G F M E Q R K D I G H M I A  
V I D K V L M Y G T V I G Q V P Y L H R Y L L G N D Y L P A L I A K L A P D V P N P I V S I I E F A K T E L I R Y D R S K  
N V S D R G D F L A W I R R E M Q K G K D I S E D D M V N H L A N N L L A G G D T T I S L R A I I Y F L I K N P P A Y

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>3941\_t gene=3941\_g

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YLSGVI

>3986\_t gene=3986\_g

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>3995\_t gene=3995\_g

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SLV

>3996\_t gene=3996\_g

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>4007\_t gene=4007\_g

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>4014\_t gene=4014\_g

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>4018\_t gene=4018\_g

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>4039\_t gene=4039\_g

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>4048\_t gene=4048\_g

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>4051\_t gene=4051\_g

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>4094\_t gene=4094\_g

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>4131\_t gene=4131\_g

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>4144\_t gene=4144\_g

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DEIIWFAITGPGNYTVDFAHNRGGFRYLNLHNSTGTVSLSSLTTYFNAAPSLQNYTGYF  
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LVDGAKRDKLIWPGDFGISVPAVFLSTNEVDTIKVSIQQLFAEQNATTGAMPYAASPIIED  
PPNPAVSGITSVFSFTYHLHSLLGLYYYYKYTGADFAEQWNRFKFAINYSLSYVDESG  
LAYIPVNNPDWLRNDMGYHNEANSILVYTLKAGLSLADVMADTSITANWTSTITGIETA  
ANQLLNSTQGLYKDNEENATIYPQDGNAWSIISGVANSTTAVTISNSLSRWGTYGAPA  
PEAGDTISPFISSGYELQAHFLAGQPQNAIDLIRYMWADFMLDDPRMTNSTFIEGYDVSGA  
LHYPAYSDRARVSHAHGWSTGPLLALSSYVAGLQVLNSTDWIAYPRPGNLSAFEAGFEL  
SYGSYASSIKVDSDCCTYSLYTPPGTSGSIIIDVPAFDANITVTGANNDFFWTKEVDAWT  
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>7882\_t gene=7882\_g

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TITLLTDDTIVVSNPGEFEPSVEVCPTDTLPGSFSASVQNYTEIWGLGARAVQLACFDKNSQ  
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ATGTAGIDVYINDTLSVTPLVSTGTWGFDFMDQIAYVKDVQVTASNGTVIYQNNMK  
SDQTLAEYGVQSNTVAVCDGGKDRRVIWVGDFVHTARVLPATTYRVEFIRGVIESSFS  
WQLPAGAEGSGLVATRASLGDDNTYKDHFYVTNYGITDYQIFFLLVVGDDYYTLNDLA  
FLTPYWSQVQALVSRMEEYLDPNNSGLGDSYDNYYTAGPVPNATAAALFAYVLKKL  
VPLAEAIGDTASASAYSSTAQSIANAINNLLWNPTTGTGVLYRTLIESLTALPKLFY  
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STSRYYTGASWEYVLPDGSPGLELFTSLAHPWGSAPTYLLTEYVLGVGPKTAGYEQWSF  
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>7883\_t gene=7883\_g

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DMVMPSWALYPDFDEYPSGLSKKWLQELRGRLFRGVTISDAIEAGALTAFGSDSD  
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>7894\_t gene=7894\_g

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>7907\_t gene=7907\_g

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>7911\_t gene=7911\_g

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GPVQVILNTEDSGAGYINDFREILADGYRVYLQVLSDWTRNLYGLAFSSQVSYNLPMDT  
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>7922\_t gene=7922\_g

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>7929\_t gene=7929\_g

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>7931\_t gene=7931\_g

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>7948\_t gene=7948\_g

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>7981\_t gene=7981\_g

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>7987\_t gene=7987\_g

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>7994\_t gene=7994\_g

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RPGLSTKRAHSYIPSFFNATESGLPGNDDSGAMASFSIFSQLGMFPVAGQNVYLISSPFFES  
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SIYDGQSWKAAADMQIPRGYQASTTTDGRVFTIGGSFSGGIGGKNGEYDPEVDKWMT  
LPGCSAEPILTNDAGGLYRSDNHAWLFAWSNGSVLQAGPSPKMHWFDTRGDGSTTFAG  
FRANDSDAMTGTAIMYDAGKGKILTLGGAPSNDLATSNAHLITVRKPGEPVKVETLD  
NMHSARAFANSVILPDGKVFVVGQSHPIVFTDGNSSMIPEMWDPKTKFTELPALPTPR  
NYHSTALLPNATVFVGGGLCPWKCDINHLDACHIYTOPYFFESDGVTPATRVITHIPNP  
ILKVGQTLNVTLSKPVESYQKLTFSIRMASATHTVNTDQRRVNVPQAATSTLFTLGLP  
RDPGVLLPGYWHLFAMLNGVPSVAETILVEPPLA

>8432\_t gene=8432\_g

MSCPDCFRGSERTDATPTGEVITLHGLPTYAA YPSAGKDPKGIVVIIPDAFGWEFVNRL  
LVDEYARKGDFTVLMPDMNGNACPLWVIEPLDTAMRTESFMGFLRNWYD VIRVYVG  
FVPHLIKNRMSVTM P RVIDFLT KLRQAEAA NLPVG VAGFCW GGLHTIHLAAEAPGNSKD  
LVDVFFTAHPSSVSFPKDI EGIKKPISIAVGDKDPLTPKQAEETEAILRKNKVEQEIVIFE  
GAGHGFSVRIDRTNPQTEQAIQAEVQAIRWFTKH FEMVRSGGGTV

>8433\_t gene=8433\_g

MSVTSDNL SVTHPSSSGGRVLQAKFIRPAQMSLFARLT CYPPLGEVTCVKRS LQPGSVAD  
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YLYSAELKL PSCAGG SFTVRYRTGP DT DWQ WANQ RRYVK DGEV VFGEK NLAILSNTN  
TAPESGAGHSPR DEIGEYI QGLPTQ LEVHAK KSETPV NLLWSITGT APPAEG ETS GRAEIS  
LGTPKSFL RYFTL VRV WSPWL APRH GEKT FR LTED AMLCSFL RSDGLNLVFL AVSGVND  
ILTLFGSGTEGDIVIKARNENTEAARFQILA SVAETFE ECICSLIYEARKV VRD STT VELP  
VVSDLPPQPSSPISDDIVVGDDARTQWLADWYEGLSYCTWNALGQNLTEDKILEALDA  
LKSHGIQVVNLII DDNWQSLDNEGKEQWHRAWKSFEANKKGPSGLRHTTSVIRQRHPN  
IGHIAVW H ALMGYWG GISPEGELAQ KYKL KEVDRKDTVAGGKMLAIDPDDINQFYND  
YSFLTSAGIDAVKTDAQFYIDL VSAEDRKRFISSYQDAWTIASLRHFSTRAISCMSMTPQ  
LIFHSHLPTNKPSILVRNSDDFFPDIA DSHPWHVFCNAHVS LFSAHLN IIPD WDMF QTSHP  
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EGNILRIGTYSGWARTGSGILGLFNISPADVSTIVPLNIFPGVSTTGANSSSSFPSNEHSDGS  
SSYIIRSHSTGVISDIMPTGAHSLVS VSL TARGWEILTAYPLRTFTLEGSRGCSSTSSSMS  
LLTHVAVLGLIGKMTGVA AVV TSGIAV VDSGRLKFDVNLKALGV LGIFHSSLESKDIDK  
HIMVMISGLAVPRETVWKDRDNVIAVDVLRAWKALKDAGWSNEVRVQ

>8447\_t gene=8447\_g

MGN TTS A VARQCLL DAVG NDASL VAFPT ALLYESVDVNPY NLDY PVTPA AVTF PETAD  
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IGAGTLLGDIDTKLHDAGN RAMTHGTSPQVGIGGHATIGGLGPTARQYGMALDHIESAQ  
VV LAN SSIVN ASTTEY PDIFYAIRGAGASFGV TEFTV RTEAEPGIAVQYQITFNIEDTSSR  
ANTFKAWQNFISDPTL PREFSCQLV LAEGLLLIEGEFFGPLADFEALQLES KFPANQGYN  
VTVFNDWLALVA AWG IQLGEDLSGGIPA HFYSKSLPFTNTT LIPDNLVDDFFEYIDTADK  
DTLLWFIIFDLEGGAISDVPVHATSYGHRDALFWLQSYAINLLGPVSATT KTFLNQANNV  
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>8453\_t gene=8453\_g

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EFYNDRFTLRQSLFAKPRHTELFIVITMYNEDEF L FARTLIGVFKNIEYMC SRTNSKT WGK  
DAWKKIVVCV ISDGRAK INP RTRA VLA ALGVYQD GIAKQQVNGKDVT AHIYEYTT QLA  
LGLKGTQVSIKGRSATPVQMIFCLKEKNQKKINSHRWFFQAFGRVLDPNICVLLDAGTKP  
GKDSIYHLWRAFDLEPMCGGACGEIKVMLDKGKNL INPLVAAQNF EYKMSNILDKP LES  
AFGFISVLPAGAFSAYRYVALQNDKTGQGP LEKYFAGEKMHGANAGIFTANMYLAEDRIL  
CFEIVTKRNCRWVLSYVKSSTGETDVPDRMAEFILQRRWLNGSFFAAVY AIAHFYQIG  
RSSHSFMRQFMLGF EFIFQTINMLFAIGNFFLVFHILTQYLGSS DLLGTPGAILGVVF

EWIYLSTLVACFILSLGNRPQGSNKFYMTMVYFWVVVMIYLTFAAIFVTVKSIQEQTKEN  
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AFCNTHDVTWGTGDDKAEKLPSATVKPGGVLDVSIPQDGGLDNAQYDIELSAFATKP  
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TAINS  
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VSSIIDYYFTQLIGNPN  
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WTYSGLT  
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VALNN  
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DTLQSKYLLGLTLYHQQRYEEAEKLFSQIVQGRERTLGEDHRDTLQSKNWLA  
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>8505\_t gene=8505\_g

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RSRSSKN NHKRДWYIWRPA  
K YDADGTRQPPNNW  
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DЛN WENPATRAAIYESAMEFWLRKG  
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>8507\_t gene=8507\_g

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V рука V RND  
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FLTYET  
QRLTDS QLDVMFAARKHS  
ITMIHAENG  
DMIGWL  
TDKLEAK  
GMVAP  
YYHAL  
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LIQNP  
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ANVR  
RAQIM  
GLPV  
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MICS  
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LQNG  
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SSDHCP  
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DPHG  
KPSGV  
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ASAVILISGAGGGVSGPAGIYPSLADKLAMLLSIPCIRLDYREPAQTKYCSADVIAAIDYL  
AGEFSSKHFVLVGWSFGGSPCFTVAAKDPNRVAGVATVASQTAQTDGVEMLSPRPLL  
LHGTGDTCLSSRCSQLFEAYQSGKKELKLFDGDDHGLSRNAMQVEKMIFQFVARTL  
GFNEMLGDPYIDIQAGQDLAGSRQERIREMREGHDFEGERL

>9212\_t gene=9212\_g

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ASLVVGISVGSEDLYRNSPTGIAAKAGIGKNPEDIVNDIKTVRSTISGTGLADVPIGHVDT  
WTAWYNSSNNAVIEAVDWLGLDAYPYFQNTQSNDITSGKSLFQDAINKVNSASGNKAL  
WVTETGPVSGDTENLAVASTDNAKYWDDVGCGLLFDKVNTYWYILQDAKSTPSP  
SFGLVGSELTTPLYNLTCPAVVSSSTSATSSATSTGSSTGSATGSATSSPTSPASNATGT  
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>9231\_t gene=9231\_g

MRTRCQCPNIPGLSSSCLRWGLLLALWLQVQAMKDYEIRDLRLQTEQMFYHGYDNY  
IKYAFPEDELRLTCGPLTRDRDHPEKIELNDVLGNYSLTLIDSSTLAILASSNDTGSRA  
WSHFENGVQEIVRLYGDGSQGSEGQGERARGFDLDSKVQVFETVIRGLGGLLSAHLFAV  
GDLPIRGYKPSAEASEYAKAWDKSALSRSYSGKIVWSNGFIYNGQLLRLARDLADRL  
PAFYPTGTYPRVNLRGYTFYENSPLSKDYPGQKTDDQRKYTRYQSRPEVTETCSA  
GAGSLVLEFTTLSRLTGDGRYEDLAKRAFWAVWLRRSEIDLIGAGIDAETGNWVAPFTG  
IGAGIDSFFEYAFKAYVLLSTGEPPDFDTSSPWSVMDNYFLPLEEAHSPEFYFQVWQDA  
QDAIKHHLYRGHGYQHPHYVQADLQTGATRAFWIDSLSAFYPGVLTLAGRIEATEIHL  
LATALWTRFSALPERWNVATGEIDNGLGWWGGRPEFIESTYYLHRATKDPWYLHVGE  
MVLRIKRCWCWRCGWAGLQDVRTGELQDRMESFFLGETAKYMFLLFDTDHPLNNMD  
APFVFTTEGHPLIIPKSVPKPSFSTPKSNSEEVVAEVCEIAPVSPPFSATAARPDIFHASSL

ARLHLLPGRNEAGGALFDAHDHSVTSDLFSPSNYTFYPWTLPELVPYNAMSSPMI  
RPTLDISFPKLPGMIGSGSMERVRDGVLKSIIGMRLGMQDMPLGVDHGSAFYTDLF  
RIQVINNPLGRDEKVYLSREIVFDVLSPNDPHFSRVRDSIMLDIVDVEPESTRVKNKNH  
TKSSRHQSYYKQDAAIIRQESATISDAGTPLKRISPASSVRTALSALMDHISTMLSDENSG  
GLDDDNESGGYVGQSSLFKKTSSNVPTTRLILPAINSIGASAPLPDVDAIFSHNGK  
PSTTRLTWSKIYLTDELCDHRLPANVPREYQVLVVKRGGSFAEKLKNIPGYPNSGSSNN  
NNRLQLVVVSYPEHDADSVSSLYQDVEGLQASAEQNFYEEERYYQRPFTSTPNQMQA  
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>9258\_t gene=9258\_g

MAFPFMRSFILLFLYRYVRLVVNLWSFYTFKPIPIPENPKLTAEDVTIVPSLECGCDELV  
ETIRTILDTPHELLLVTIEANRKDAEKMLKAMPAYLHDRIRLFITHPNKRRQMTRAYPE  
VRTSITFADDVSWPITALPWILAPFDTDERYGGVVTQRLLRAVNATFSEKIWNFLGA  
LYLERRNFDCAATTHIDGGVPCLSGRTVAYRTKILQDEVFTNDFTNEEWFGKYQLNA  
DDDNFIRWMVSHGWETYIQQYHPEVEVKTLENNPKFLQCARWSRSNWSNLTSMFA  
ERHIWYRQPWSTYAVHLTTLSPPALLGDCLLIYLCHKATELDGDVHWWAMRALGIW  
MFISKFIKLLGHYRRYPADFLLPVSILFGYFHGAIKIYAAVTLNVTAWGSREGADANDA  
ERMRKRSDIEREKHARRLASIYPLNKVVWPSSGYAPIA

>9270\_t gene=9270\_g

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PVKHNTTPANLQAAWADFVNILGKENVSTDDFDLESHSGSEFSTYSQKSNEKPFIVVYPE  
TTEEVSRIMKVCYERVIPVTPYSGTSLEGHYAPTRGGVCVDERRMNKILSFHKEDLDV  
VVQPAVGWEDLNEEIAKEGLFFPDGPAGAMIGGMVGTGCSGTNARYGTMREWVVS  
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DVAVPISRLPDIVERTKKDLTQSGLLAGICGHVGDGNFHAIILFSDKQKALAEVVHRMV  
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>9279\_t gene=9279\_g

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KQVLP SLAPTGKRN PEDGAESLGAHVEGPFINPSRNGIHKPEVLLASTQGFQDIENCYGLE  
NIPDIAKNTEDEIADEDAVTPTPATPIAKSLQKGIRANGLVNGHRHHNVSTATSRPAIKMI  
TAAPEVGTMIQHIPDLVSRGIY SIGHSDATYEQAMSAVGQGAMMITHLFNAMRPFYHR  
NPGVFGLLQSDLPKPYFGVIADGIHLHPTSIKIA YNAHSEGLIL VTDAMRLCGLPDGVY  
DWTNGDRIKKGVRLTLEGSDKIAGSSATLIECVNNFRRWTNATTAEALNAVFTPAKM  
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>9280\_t gene=9280\_g

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GCTGWSFDMFTRVL DNL RNTVQPVHARHRNQLCKDWVQSCSTALNIPVIEDFNKEIRSK  
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TGVDVTLESGKKYSIHPKETVICAGAVDTPRLLLLSGLGPKDQLSSLGIPVVKDIPGVGE  
NLLDPETIIIWELNPVPPNQTTMDSDAGIFLRREAPNAAGSDGTAADLMMHCYQIPFC  
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AGFKAAREVAKQAPFKDWIKREVAPPGPIDIITLEALSEYGRRVAHTVYHPAGTTKMGN  
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>9283\_t gene=9283\_g

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EAGLVTCGKHFPSYGNIEFGSQTDVPVITESLEQLSLSALVPRNAIANGDAVMVGGV  
AMSSAGVNVMHACLSEQVVDGLLRKDLKFDDGVVSECLEMEALTHNIGVGGGTVM  
MKAGCDLILLCRSYFPQLEALNGLKLGVENGMSRSRIRQLRVLAMKARCTTWEQAL  
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AVSRSMDDMMTTSPDPSASSEKGSSITSGESVFREFGRSLARQRSGRVLHTSYTSTGVRPI  
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FAIDPSISTYICTYDFTETALQALVKVLYGELSPTGSLPGTISRSQKIHQSRQHWLVETWN  
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EYIPALHKKDKEKEKVNGSNSSANGSSNGTAGGGVSSPVISPSVGEYATLMQGLILLG  
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>9303\_t gene=9303\_g

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LYPPRPVRTGIPDTSERVESLRQALKCFFEEASKASGGRNVMAHSLARAQYSLGNYADA  
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LARKAIEQTDVVSIASEGWYLLGRKAHYEGDTAKASEYFNRSQARGGGDGGFLPAKF  
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TTKAISLLENVRSLWKDPTKNIPADESVLIYLSRLYESTSPDKSMQCLTQLEIQMDQIPD  
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DRARDAQILA CLGRVWWLRGKHEKNLTAMKTALDYANRALEVAPEQAHLEFNVAFVQ  
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>9333\_t gene=9333\_g

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>9359\_t gene=9359\_g

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>12013\_t gene=12013\_g

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QASITADGRVDIDISEPTSRLRSMFKLPTFGPRSATTTSATIPSSLDRRRDQKPPPLNIVIQ

VVGSRGDVQPFIALGRVLKFHGHHRVRLATHASFQGFVEENGLEFFCIGGDPMELMAFM  
VKNPGLMPGFDALKNGDIHRRRVEIAAIISGCWRSCFEAGDTGPVSDRTVDNNFKA  
GNVPFADAIIANPPSFAHVHCAEKGIPHLHMMFTMPWSPTQAFPHPLATIHKSKADVGI  
TNYVSYAIVEMMTWQGLGDIINRFRERSLGLAPISIMWAPSMVSRLKIPQTYCWSPALIP  
KPNDWGS HIDISGFYFLSLASNYTPPDLAAFLAAGPPP YIGFGSIVVDDPNHMTQLIFD  
AVRLTGRRALVSKGWGLGAEQLSVPEGVFMLGNCPHDWLFFFHSCVVHGGAGTTA  
AGIAAGRSTVIVPFFGDQPFWGAMVAKAGAGPQPPIYKELTAEKLADAIFALEPATSEK  
AASLA AVIEAEHGADDGAISFENHLKVDKMRCSDLPDRVAVFRIKRTHIRLSALAFAML  
NAEGKLGVDDVKLYRSQEYMTEPDPTPVIGGGAAMLD SIEEFLMGFADLSMDVKRSL  
NSRISRSSRSSTNRSGSQRTVSPNAAARAKLLSDDSSLKPFTDTSSISTKDSFSMPLA  
GDTVTSSPATDGATEDSTPLKAHTVDSTVKEARIRKHARTINDRDLIDGILSAGKSAAK  
VVNVGLRAPASFTMAVAKGFHNMPLLYGDDTVREQPKVGTGKSGLKAAGKEFGYGFY  
D GISGLATQPVQGAKKEGAVGAIKGFSKGIGGLIFKPA AA VWSLTGYTMSGIYQEIQKRF  
GESVENYIMASRCAQGLIDL SACTTEEKENILT KWSIFEAEVEAKNARRNRYKLDGDG  
KRIKTRTMSEKSKDAGKTQEEQEAESLKAERANRRESLRQLFRGRASSSSPPRKTTSES  
VLPDEYEHAIRHSV LATSQGDDTEDEM IERALRASMTELENA KVAGEEEDRAYDLAVQ  
ASVREAERVIEEKKREHNERSAVGKDEKS NYI HQPQAQPPPYSVDETDQNKP RR PPTLP  
PRSPVPI TDHEIELQNAINESQR SYDDNLREQREKEEMDIIMEYVKR QSLAEAEQQRRQ  
EQREEA

>12026\_t gene=12026\_g

M RGFAQLAA ALAAF MVGQ TLASP VARSLPGPVQVTPKKGDVVITPQNFLNGTWKGNET  
TKSDALNAAAISGTLPIEIVNNLAGSASGSINAYIQQQDTTGAI FVLA DGSFYYP PG TSS  
GVPVQISEN LAIPLGAQGTTTITIPNYLISGRVYLA VGD LAFY MVSG GLVQPSATNPSDA  
SANINWGFIELTNSPTAGLFTNISYVDFIGLILGMSVTSSD GTVQTALGLTSGAVQDICTK  
LASQTASDGYPWASLCQTDTS GAYL RVLSPNDYISTDGS AFSDY WNSY VSQV STYASS  
PLTINTQNT PGDV TCTGGSAILTCQGSDVTF A EPTARDIFGCNSGPFA VTGNAV DTAIVP  
RLCAAFNRGTL LSGGNVQPSL SADSYYT TSPCN YYSKF VHQN EVDGKGYAFSYDDVN  
PDGENASGEL TSTDASLLSITVGGPST

>12031\_t gene=12031\_g

MAPIETK TYDFIVIGGSGGSGSARRASGWYGAKTLIVERGRSGGTCVNVCVPKKMT  
WNFASINENLHAARHYGYDVDDNIKF DYAHFKSIRD SRIQRLNGAYENN WGKEGIDL V  
HGRARFVEPKVIEV TSNDGSE SKTRYTAKHILIAVGGHPV VPGI QGA EH GITS DGFFEIEE  
LPKKWAVVGAGYIAVELAGV LAAVG VETHMFIRGDTFLRKFDPMIQETMTARYEAGI  
KIHKQHKG FQEIQ LLKEGKGAEKVLKLIGVEGDEIEV NELLWA VGRAPEVEDLHLDIPG  
VKQAHSGHII VDEFQNTSAEGIYALGDVTGQAE LTPVAIAAGRKLGSRLFGPPEFKTAKL  
SYENIPTVVF SHPEV GTIGL TEPQARQRF GDDKIKVYKTRFTNMFYDFFPDEEKKQNP TQ  
MKIICAGPEEKVVGLHILGLGVG EMLQGF GVAIKMGATKQDFDSCV AIHPTASEEL VTM  
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>11558\_t gene=11558\_g

MVVQTAIGQTDNSQWQSLNASL SGALRSIYPLALPCFGNYNGTAVD TDPTDCATIQANY  
TSAAFRANLPNAWMSNQDEM CSSDPQNQCLLDNTNPTDPLAYGNGAVCNQGIVPPVYL  
EVREPDDVIAAFKHSRRTGTKLAIKN SGHDYLTRSSGQGRLLWTRNLQSKS YNSFVPC  
GCPTTDIYNAITAGAGVNMDQAFSFAE QNNVTFIGAYASTVGVSGGWVQAGGHSV LSP  
VYGLGVDRVLEFKVVT PDGIYRTANACQNQDLFWALRGGGGGTGFV VLETTHRVEPLL

SIVADIAIPASAATFTPWEIMVNNSLQWSQQGWGGHITPSSLIHVNPLTLQEAKDAMA  
PAVAFAEANNGSVTFEFSSYYPFYLKYVGSNQLNVGNVHIAGSRLIPQALFSYETGRAQ  
LMQYLQQVQAQGLSPYIPVVGPTLYNTANSTSATPAWREAVWELGAGASAWNSTL  
AQREAVVTKLNNLTNLVEQITPSGGAYQNEANPFTGDWQEAWWGQENYDSLLAIKHK  
YDPHGLLSCWKCVGWTENANEGLSCLSGFADST

>11602\_t gene=11602\_g

MKFRQNAALFLIAVFSLFTSTVCQNDESAAVYISTLRSSRNLTALSVADPTVSQDMYF  
HISGPSSYSYMGIGTGTVMQDSLIFVIYPNATGDGITLSPRIATGNKEPVLA  
PSLDVEVLPG  
SNTSNGLMTVNAHCKNCNSWISGALDLSDTAYPWNYALGPN  
TAQYVRIKSNSPSADLE  
MHVEYGLFTLDMTRATGGAGALPTSLNPIGSNATRPRVLT  
SNYPTIIHAVLATLPLVFL  
LPTGVIFLRFPGSVRWHWVSQLSSVISV  
LGI  
AVGIYLSTWFNKS  
KSFGSGH  
QIIGY  
LICA  
GILA  
AQWFLGF  
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>11648\_t gene=11648\_g

MVYNARWGILATGGIAKTFVKDLLKDASARNASDISHTVTAVASSSSASRAQDFITELSI  
PGSPKAYGSYEELVNDPNVDIVYVATPHSHHYQNARLA  
EAGKHVLCEKAFTVNA  
AQT  
KILVDIAKAKGLFLMEAVWTRYFPLSVQVRDIIQKG  
EEIGEV  
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QADLS  
IGNPDGF  
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SRMVNL  
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>11655\_t gene=11655\_g

MVAIYLICRPYIMPFIFYLLLHFVGASQPIEYHGSRH  
MTRFLEPRTANVTQAGVGSINFAG  
VSIFPNGSLSNLNLTNCENL  
LYQKIN  
CDDSI  
SKLWTRGYV  
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