>AtSUS1

MANAERMITRVHSQRERLNETLVSERNEVLALLSRVEAKGKGILQQNQIIAEFEALPEQTRKKLEGGPFFDLLKSTQEAIVLPPWVALAVRPRPGVWEYLRVNLHALVVEELQPAEFLHFKEELVDGVKNGNFTLELDFEPFNASIPRPTLHKYIGNGVDFLNRHLSAKLFHDKESLLPLLKFLRLHSHQGKNLMLSEKIQNLNTLQHTLRKAEEYLAELKSETLYEEFEAKFEEIGLERGWGDNAERVLDMIRLLLDLLEAPDPCTLETFLGRVPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALEIEMLQRIKQQGLNIKPRILILTRLLPDAVGTTCGERLERVYDSEYCDILRVPFRTEKGIVRKWISRFEVWPYLETYTEDAAVELSKELNGKPDLIIGNYSDGNLVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLDDKYHFSCQFTADIFAMNHTDFIITSTFQEIAGSKETVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLTKFHSEIEELLYSDVENKEHLCVLKDKKKPILFTMARLDRVKNLSGLVEWYGKNTRLRELANLVVVGGDRRKESKDNEEKAEMKKMYDLIEEYKLNGQFRWISSQMDRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVHGKSGFHIDPYHGDQAADTLADFFTKCKEDPSHWDEISKGGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLEARRYLEMFYALKYRPLAQAVPLAQDD

>AtSUS2

MPTGRFETMREWVYDAISAQRNELLSLFSRYVAQGKGILQSHQLIDEFLKTVKVDGTLEDLNKSPFMKVLQSAEEAIVLPPFVALAIRPRPGVREYVRVNVYELSVDHLTVSEYLRFKEELVNGHANGDYLLELDFEPFNATLPRPTRSSSIGNGVQFLNRHLSSIMFRNKESMEPLLEFLRTHKHDGRPMMLNDRIQNIPILQGALARAEEFLSKLPLATPYSEFEFELQGMGFERGWGDTAQKVSEMVHLLLDILQAPDPSVLETFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIQKQGLEVIPKILIVTRLLPEAKGTTCNQRLERVSGTEHAHILRIPFRTEKGILRKWISRFDVWPYLETFAEDASNEISAELQGVPNLIIGNYSDGNLVASLLASKLGVIQCNIAHALEKTKYPESDIYWRNHEDKYHFSSQFTADLIAMNNADFIITSTYQEIAGSKNNVGQYESHTAFTMPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYSDKERRLTALHESIEELLFSAEQNDEHVGLLSDQSKPIIFSMARLDRVKNLTGLVECYAKNSKLRELANLVIVGGYIDENQSRDREEMAEIQKMHSLIEQYDLHGEFRWIAAQMNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVESMTCALPTFATCHGGPAEIIENGVSGFHIDPYHPDQVAATLVSFFETCNTNPNHWVKISEGGLKRIYERYTWKKYSERLLTLAGVYAFWKHVSKLERRETRRYLEMFYSLKFRDLANSIPLATDEN

>AtSUS3

MANPKLTRVLSTRDRVQDTLSAHRNELVALLSRYVDQGKGILQPHNLIDELESVIGDDETKKSLSDGPFGEILKSAMEAIVVPPFVALAVRPRPGVWEYVRVNVFELSVEQLTVSEYLRFKEELVDGPNSDPFCLELDFEPFNANVPRPSRSSSIGNGVQFLNRHLSSVMFRNKDCLEPLLDFLRVHKYKGHPLMLNDRIQSISRLQIQLSKAEDHISKLSQETPFSEFEYALQGMGFEKGWGDTAGRVLEMMHLLSDILQAPDPSSLEKFLGMVPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALETEMLLRIKRQGLDISPSILIVTRLIPDAKGTTCNQRLERVSGTEHTHILRVPFRSEKGILRKWISRFDVWPYLENYAQDAASEIVGELQGVPDFIIGNYSDGNLVASLMAHRMGVTQCTIAHALEKTKYPDSDIYWKDFDNKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHGAFTLPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYSEETRRLTALHGSIEEMLYSPDQTDEHVGTLSDRSKPILFSMARLDKVKNISGLVEMYSKNTKLRELVNLVVIAGNIDVNKSKDREEIVEIEKMHNLMKNYKLDGQFRWITAQTNRARNGELYRYIADTRGAFAQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGLSGFHIDPYHPEQAGNIMADFFERCKEDPNHWKKVSDAGLQRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKTVPSTADD

>AtSUS4

MANAERVITRVHSQRERLDATLVAQKNEVFALLSRVEAKGKGILQHHQIIAEFEAMPLETQKKLKGGAFFEFLRSAQEAIVLPPFVALAVRPRPGVWEYVRVNLHDLVVEELQASEYLQFKEELVDGIKNGNFTLELDFEPFNAAFPRPTLNKYIGDGVEFLNRHLSAKLFHDKESLHPLLKFLRLHSHEGKTLMLNNRIQNLNTLQHNLRKAEEYLMELKPETLYSEFEHKFQEIGLERGWGDTAERVLNMIRLLLDLLEAPDPCTLENFLGRIPMVFNVVILSPHGYFAQDNVLGYPDTGGQVVYILDQVRALETEMLQRIKQQGLNITPRILIITRLLPDAAGTTCGQRLEKVYGSQYCDILRVPFRTEKGIVRKWISRFEVWPYLETFTEDVAAEISKELQGKPDLIIGNYSDGNLVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLDEKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHRSFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFAYTEEKRRLTAFHLEIEELLYSDVENEEHLCVLKDKKKPIIFTMARLDRVKNLSGLVEWYGKNTRLRELVNLVVVGGDRRKESQDNEEKAEMKKMYELIEEYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYHGDKAAESLADFFTKCKHDPSHWDQISLGGLERIQEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRPLAQAVPLAHEE

>AtSUS5

MEMTSGSLGNGIPEAMGQNRGNIKRCLEKYIENGRRVMKLNELMDEMEIVINDVTQRRRVMEGDLGKILCFTQEAVVIPPNVAFAVRGTPGNWQYVKVNSSNLSVEALSSTQYLKLKEFLFDENWANDENALEVDFGALDFTLPWLSLSSSIGNGLSFVSSKLGGRLNDNPQSLVDYLLSLEHQGEKLMMNETLNTARKLEMSLILADVFLSELPKDTPFQAFELRFKECGFEKGWGESAGRVKETMRILSEILQAPDPQNIDRFFARVPRIFNVVIFSVHGYFGQTDVLGLPDTGGQVVYILDQVKALEDELLQRINSQGLNFKPQILVVTRLIPDAKKTKCNQELEPIFGTKYSNILRIPFVTENGILRRWVSRFDIYPYLERFTKDATTKILDILEGKPDLIIGNYTDGNLVASLMANKLGITQATIAHALEKTKYEDSDIKWKEFDPKYHFSSQFTADLISMNSADFIIASTYQEIAGSKERAGQYESHMSFTVPGLYRVVSGINVFDPRFNIAAPGADDSIYFPFTAQDRRFTKFYTSIDELLYSQSENDEHIGYLVDKKKPIIFSMARLDVVKNLTGLTEWYAKNKRLRDLVNLVIVGGFFDASKSKDREEISEIKKMHSLIEKYQLKGQFRWITAQTDRTRNGELYRSIADTRGAFVQPAHYEAFGLTVIEAMSCGLVTFATNQGGPAEIIVDGVSGFHIDPSNGEESSDKIADFFEKSGMDPDYWNMFSNEGLQRINECYTWKIYANKVINMGSTYSYWRHLNKDQKLAKQRYIHSFYNLQYRNLVKTIPILSDIPEPPPLPPKPLVKPSASKGSKRTQPRLSFRLFGA

>AtSUS6

MSSSSQAMLQKSDSIAEKMPDALKQSRYHMKRCFASFVGGGKKLMKREHLMNEIEKCIEDSRERSKILEGLFGYILTCTQEAAVVPPFVALAARPNPGFWEYVKVNSGDLTVDEITATDYLKLKESVFDESWSKDENALEIDFGAIDFTSPRLSLSSSIGKGADYISKFISSKLGGKSDKLEPLLNYLLRLNHHGENLMINDDLNTVAKLQKSLMLAVIVVSTYSKHTPYETFAQRLKEMGFEKGWGDTAERVKETMIILSEVLEAPDNGKLDLLFSRLPTVFNVVIFSVHGYFGQQDVLGLPDTGGQVVYILDQVRALEEELLIRINQQGLGFKPQILVVTRLIPEARGTKCDQELEAIEGTKHSHILRVPFVTNKGVLRQWVSRFDIYPYLERFTQDATSKILQRLDCKPDLIIGNYTDGNLVASLMATKLGVTQGTIAHALEKTKYEDSDAKWKELDPKYHFSCQFTADLIAMNVTDFIITSTYQEIAGSKDRPGQYESHTAFTMPGLCRVVSGIDVFDPKFNIAAPGADQSVYFPYTEKDKRFTKFHPSIQELLYNEKDNAEHMGYLADREKPIIFSMARLDTVKNITGLVEWYGKDKRLREMANLVVVAGFFDMSKSNDREEKAEIKKMHDLIEKYKLKGKFRWIAAQTDRYRNSELYRCIADTKGVFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPNNGDESVTKIGDFFSKCRSDGLYWDNISKGGLKRIYECYTWKIYAEKLLKMGSLYGFWRQVNEDQKKAKKRYIEMLYNLQFKQLTKKVTIPEDKPLPLRLASLRNLLPKKTTNLGAGSKQKEVTETEKTKQKSKDGQEQHDVKVGEREVREGLLAADASERVKKVLESSEEKQKLEKMKIAYGQQHSQGASPVRNLFWSVVVCLYICYILKQRFFGANSAQEY

>SlSUS1

MAERVLTRVHRLRERVDATLCAHRNEILLFLSRIESHGKGILKPHELLAEFDAIRQDDKDKLNEHAFEELLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALVVEELSVPEYLQFKEELVDGASNGNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMAPLLEFLRAHHYKGKTMMLNDRIHNSNTLQNVLRKAEEYLIMLPPETPFFEFEHKFQEIGLEKGWGDTAERVLEMVCMLLDLLEAPDSCTLEKFLGRIPMVFNVVILSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIIPRILIVTRLLPDAVGTTCGQRLEKVYGTEHSHILRVPFGTEKGIVRKWISRFEVWPYMETFIEDVAKEISAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKFDEKYHFSSQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGINVFDPKFNIVSPGADINLYFPYSESEKRLTAFHPEIDELLYSDVENDEHLCVLKDRTKPILFTMARLDRVKNLTGLVEWYAKNPRLRGLVNLVVVGGDRRKESKDLEEQAEMKKMYELIETHNLNGQFRWISSQMNRVRNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGGPAEIIVHGKSGFHIDPYHGEQAADLLADFFEKCKKEPSHWETISTGGLKRIQEKYTWQIYSERLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKYRKMAEAVPLAAE

>SlSUS3

MAQRVLTRVHSLRERLDATLDAHRNEILLFLSRIESHGKGILKPHQLLAEFESIQKEDKDKLNDHAFEEVLKSTQEAIVLPPWVALAIRLRPGVWEYVRVNVNALSVEELTVPEFLQFKEELVNGTSSDNFVLELDFEPFTASFPKPTLTKSIGNGVEFLNRHLSAKMFHDKESMTPLLEFLRVHHYNGKSMMLNDRIQNLYTLQKVLRKAEEYLTTLSPETSYSSFEHKFQEIGLERGWGDTAERVLEMICMLLDLLEAPDSCTLEKFLSRIPMVFNVVIPSPHGYFAQENVLGYPDTGGQVVYILDQVPALEREMLKRIKEQGLDIKPRILIVTRLLPDAVGTTCGQRLEKVFGTEHSHILRVPFRTEKGIVRKWISRFEVWPYMETFIEDVGKEITAELQAKPDLIIGNYSEGNLAASLLAHKLGVTQCTIAHALEKTKYPDSDIYLNKFDEKYHFSAQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADVNLYFPYSEKEKRLTTFHPEIEDLLFSDVENEEHLCVLKDRNKPIIFTMARLDRVKNLTGLVEWYAKNPRLRELVNLVVVGGDRRKESKDLEEQAEMKKMYELIKTHNLNGQFRWISSQMNRVRNGELYRYIADTRGAFVQPAFYEAFGLTVVEAMSCGLPTFATNQGGPAEIIVHGKSGFQIDPYHGEQAADLLAEFFEKCKVDPSHWEAISKGGLKRIQEKYTWQIYSDRLLTLAAVYGFWKHVSKLDRLEIRRYLEMFYALKFRKLAELVPLAVE

>SlSUS4

MSNPKLSRIPSMRERVEDTLSAHRNQLVALLSRYVAQGKGILQPHHLIDELNNAVCDDTACEKLKEGPFC

EILKSTQEAIVLPPFVAIAVRPRPGVWEYVRVNVYDLSVEQLTVPEYLRFKEELVDGEDHNHLFVLELDF

EPFNASVPRPSRSSSIGNGVQFLNRHLSSNMFRSNESLDPLLDFLRGHNHKGNVLMLNERIQRISRLESS

LNKADDYLSKLPPDTPYTDFEYALQEMGFEKGWGDTANRVLETMHLLSDILQAPDPSTLETFLGRLPMVF

NVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALEAEMLLRIKQQGLNFKPRILVVTRLIPDAKGTTC

NQRLERISGTEYSHILRVPFRTENGILHKWISRFDVWPYLEKFTEDVAGEMSAELQGVPDLIIGNYSDGN

LVASLLAYKMGITQCTIAHALEKTKYPDSDIYWKKFEEKYHFSCQFTADLLSMNHSDFIITSTYQEIAGT

KNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYFDKEKRLTSLHPSIEKLLFDPEQ

NEVHIGSLNDQSKPIIFSMARLDRVKNITGLVECYAKNATLRELANLVVVAGYNDVKKSNDREEIAEIEK

MHALMKEHNLDGQFRWISAQMNRARNGELYRYIADKRGIFVQPAYYEAFGLTVVEAMTCGLPTFATCHGG

PMEIIQDGVSGYHIDPYHPNKAAELMVEFFQRCEQNPTHWENISASGLQRILDRYTWKIYSERLMTLAGV

YGFWKLVSKLERRETRRYLEMFYILKFRELVKSVPLAVDEKQ

>SlSUS5

MAASGLSIKERLEEAILARPDEISALKSRIESEGKGVMKPLDLLNHLISVNSKKNGVNVGNSALVEILSY

SQEAIVVPPQLALAVRPRPGVWEYLSLNLKQQKVAELTIPEYLQLKENVFDESGNILEMDFEPFTTVTPT

KTLSDSIGNGLEFLNRHIASTMFHDKEIAKCLLDFLRQHNYKGKSLMVKESIQSLESFQFVLKKAEEYLC

TLSSETPYSDFESKFEEIGLERGWGNTAERVQETIRHLLHLLEAPNASSLENFLGRIPLVFNVVILTPHG

YFAQENVLGYPDTGGQVVYILDQVPAMETEMLLRLKHQGLDDIVPRILVVTRLLPDAVGTTCGERMEKVY

GAEHSHIIRVPFRTEKGMLRKWISRFEVWPYMETFTEDVAEELVKELQAKPDLIIGNYSEGNLAASLLAK

KFGATQCTIAHALEKTKYPNSDLYWKKFDDKYHFSSQFTADLYAMNHTDFIITSTFQEIAGSKNTVGQYE

SHTAFTMPGLYRVVHGIDSFDPKFNIVSPGADMSIYFPYTEKEKRLTKFHPEIEELLYSPVENKEHLCVL

KDRSKPILFTMARLDRVKNLTGLVEWYAKNARLRELVNLVVVGGDRRKESKDLEEQAEMKKMYDLIETYN

LNGQFRWISSQMNRVRNGELYRYIADTRGAFVQPAFYEAFGLTVVESMTCGLPTFATCNGGPFEIIVHGK

SGFHIDPNQGDKATDLLVKFFEKSKEDPSYWENISKGGLQRIIEKYTWQIYSQKVMTLSGIYGFWKFATK

NDKVASAKKRYLEMFYELMFKKSAEKVPLAIDE

>SlSUS6

MATTPVADSMPDALKQSRYHMKRCFARFIATGSRLMKLKYLMEDIENTIEDKAERTKVLEGSLGQTLSST

QEAAVVPPYVAFAVRHNPGCWDYVKVNADNLSVEAISPKEYLKFKEMIFDEEWAKDDNALEVDFGAFDYS

NPRLALSSSVGNGLNFVSKVMSSKLGGKPEEAQPLLDYLLALNHQGENLMINENLNSVSKLQAALIVAEV

FVSSFSKDTPYKNFEHKLKEWGFEKGWGDSAGRVRETMRLASEILQAPDPINMESFFSRLPTTFNIVIFS

IHGYFGQADVLGLPDTGGQVVYILDQVRALEEEMLSRIKQQGLNMKPKILVVTRLIPDARGTTCNQELEP

ILNSSHSHILRIPFRTEKGVLRQWVSRFDIYPYLENYAKDATVKILELMEGKPDLIIGNYTDGNLVASLL

ANKLGVTQGTIAHALEKTKYEDSDVKLKEFDPKYHFSCQFTADLLAMNAADFIITSTYQEIAGSETRPGQ

YESHTAFTMPGLYRVVSGINVFDPKFNIASPGAEQSAYFPFTERKKRFVKFGPAIEELLYSKEENNEHIG

FLADRRRPIIFSMARFDSVKNLTGLTEWFGKNKKLQNLVNLVIVGGFFDPSKSKDREEAAEIKKMHELIE

KYNLKGQMRWIAAQTDKYRNSELYRTIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIV

DGVSGFHIDPYNGDESSNKIADFFEKCQVDSIYWNRISEGGLKRIEECYTWKIYANKVLNMGSIYGFWRR

FNVGQKQAKQRYFEMFYNPLFRKLANNVPIPYEEPLPVAPLDTIPSQEQKLPVPVPTAVAELPTLPTIAF

QRTEQKEEEKQVDTTTTSTTEIAKQATHWICLCVSASIIVYAMVKLYRIVE

>SlSUS7

MATTPALKRSESIADSMPEALRQSRYHMKRCFAKYIEQGKRMMKLHNLMDELEKVIDDPAERNHVLEGLL

GYILCTTMEAAVVPPYIAFATRQNPGFWEYVKVNANDLSVDGITATEYLKFKEMIVDESWAKDEYALEID

FGAVDFSTPRLTLSSSIGNGLSYVSKFLTSKLNASSMSAQCLVDYLLTLNHQGDKLMINETLSTVAKLQA

ALVVAEASISSLPTDTPYQSFELRFKEWGFEKGWGDTAERVRDTMRTLSEVLQAPDPSNIEKFFGRVPTV

FNIVLFSVHGYFGQADVLGLPDTGGQVVYVLDQVVAFEEELLQRIKQQGLNVKPQILVLTRLIPDAKGTK

CNQELEPINNTKHSHILRVPFRTEKGVLNQWVSRFDIYPYLERYTQDASDKIIELMEGKPDLIIGNYTDG

NLVASLMARKLGITLGTIAHALEKTKYEDSDIKLKELDPKYHFSCQFTADLIAMNSADFVITSTYQEIAG

SKDRPGQYESHSAFTLPGLYRVASGINVFDPKFNIAAPGADQSVYFPYTEKQKRLTDFRPAIEKLLFSKV

DNDEHIGYLEDRTKPILFTMARLDTVKNTTGLTEWFGKNKKLRSLVNLVVVGGSFDPTKSKDREEAAEIK

KMHVLIEKYQLKGQIRWIAAQTDRYRNSELYRTIADSKGAFVQPALYEAFGLTVIEAMNCGLPTFATSQG

GPAEIIVDGISGFHIDPNNGDESSNKIANFFQKCKEDPEHWNRISAQGLKRIYECYTWKIYANKVLNMGS

IYTFWRTLYKDQKQAKQRYIDTFYNLEFRNLIKDVPIKIDEKTEGPKERPERVKVKPQLSQRRSQSRLQK

LFGSSNSQS

>PsSUS1

MATDRLTRVHSLRERLDETLTANRNEILALLSRIEAKGKGILQHHQVIAEFEEIPEENRQKLTDGAFGEV

LRSTQEAIVLPPWVALAVRPRPGVWEYLRVNVHALVVENLQPAEFLKFKEELVDGSANGNFVLELDFEPF

TASFPRPTLNKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRLHSYKGKTLMLNDRIQNPDSLQHVLRK

AEEYLGTVAPDTPYSEFEHRFQEIGLERGWGDTAERVLESIQLLLDLLEAPDPCTLETFLDRIPMVFNVV

ILSPHGYFAQDDVLGYPDTGGQVVYILDQVRALESEMLNRIKKQGLDIVPRILIITRLLPDAVGTTCGQR

LEKVYGTEHCHILRVPFRDQKGIVRKWISRFEVWPYLETYTEDVAHELAKELQGKPDLIVGNYSDGNIVA

SLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDT

VGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADQTIYFPYTETSRRLTSFYPEIEELLYSTVENEE

HICVLKDRSKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDLEEKAEMKKMYEH

IETYKLNGQFRWISSQMNRVRNGELYRVICDTKGAFVQPAVYEAFGLTVVEAMATGLPTFATLNGGPAEI

IVHGKSGFHIDPYHGDRAADLLVEFFEKVKTDPSHWDKISQGGLQRIEEKYTWQIYSQRLLTLTGVYGFW

KHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVEE

>PsSUS2

MSTHPKFTRVPSIRDRVQDTLSAHRNELISLLSRYVAQGKGILQPHNLIDELDNILGEDHATLDLKNGPF

GQIINSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVFELSVEQLSVSEYLSFKEELVEGKSNDNIILELDL

EPFNASFPRPTRSSSIGNGVQFLNRHLSSNMFRNKDCLEPLLDFLRVHTYKGHALMLNDRIQSISKLQSA

LVKAEDHLSKLAPDTLYSEFEYELQGTGFERGWGDTAARVLEMMHLLLDILQAPDPSTLETFLGRVPMVF

NVVILSPHGFFGQANVLGLPDTGGQVVYILDQVRALESEMLVRIKKQGLDFTPRILIVTRLIPDAKGTTC

NQRLERVSGTEYTHILRVPFRSEKGILRKWISRFDVWPFLETFAEDVASEIAAELQCYPDFIIGNYSDGN

LVASLLAYKMGVTQCTIAHALEKTKYPDSDIYWKKFEDKYHFSCQFTADLIAMNNADFIITSTYQEIAGT

KNTIGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMTIYFPYSDKEKRLTALHSSIEKLLYGTEQ

TDEYIGSLTDRSKPIIFSMARLDRVKNITGLVESYAKNSKLRELVNLVVVAGYIDVKKSSDREEIEEIEK

MHDLMKQYNLNGEFRWITAQTNRARNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATNHGG

PAEIIEHGVSGFHIDPYHPDQASELLVDFFQRCKEDPNHWNKVSDGGLQRIYERYTWKIYSERLMTLAGV

YSFWKYVSKLERRETRRYLEMFYILKFRDLANSVPIAKG

>PsSUS3

MASLTHSTSLRQRFDETLTAHRNEILSLLSRIEAKGKGILQHHQIIAEFEEIPEENRQKLVNGVFGEVLR

STQEAIVLVPFVALAVRPRPGVWEYLRVDVHGLVVDELSAAEYLKFKEELVEGSSNENFVLELDFEPFNA

SIPKPTQNKSIGNGVEFLNRHLSAKLFHGKESLQPLLEFLRLHNHNGKTIMVNDRIQNLNSLQHVLRKAE

DYLIKIAPETPYSEFEHKFQEIGLERGWGDTAERVVETIQLLLDLLDGPDPGTLETFLGRIPMVFNVVIL

SPHGYFAQDNVLGYPDTGGQIVYILDQVRALEEEMLKRIKQQGLDITPRILIITRLLPDAVGTTCGQRLE

KVYNTEHCHILRVPFRTEKGIVRKWISRFEVWPYLETFSEDVANELAKELQGKPDLIVGNYSDGNIVASL

LAHKLGVTQCTIAHALEKTKYPESDIYWKKFDDKYHFSSQFTADLFAMNHTDFIITSTFQEIAGSKDTVG

QYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTETERRLTSFHPDIEELLYSTVENEEHI

CVLKDRSKPIIFTMARLDRVKNITGLVECYGKNARLRELVNLVVVAGDRRKESKDLEEIAEMKKMYGLIE

TYKLNGQFRWISAQMDRIRNGELYRVICDTKGAFVQPAIYEAFGLTVIEAMSCGLPTFATCNGGPAEIIV

HGKSGYHIDPYHGDRAAETLVEFFEKSKADPTYWDKISHGGLKRIHEKYTWQIYSDRLLTLTGVYGFWKH

VTNLERRESKRYLEMFYALKYSKLAESVPLAVEE

>PsSUS4

MATDRLTRVHSLRERLDETLTANRNEILALLSRIEAKGKGILQHHQVIAEFEEIPEENRQKLTDGAFGEVLRSTQEAIVLPPWVALAVRPRPGVWEYLRVNVHALVVENLQPAEFLKFKEELVDGSANGNFVLELDFEPFTASFPRPTLNKSIGNGVQFLNRHLSAKLFHDKESLHPLLEFLRLHSYKGKTLMLNDRIQNPDSLQHVLRKAEEYLGTVAPDTPYSEFEHRFQEIGLERGWGDTAERVLESIQLLLDLLEAPDPCTLETFLDRIPMVFNVVILSPHGYFAQDDVLGYPDTGGQVVYILDQVRALESEMLNRIKKQGLDIVPRILIITRLLPDAVGTTCGQRLEKVYGTEHCHILRVPFRDQKGIVRKWISRFEVWPYLETYTEDVAHELAKELQGKPDLIVGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPESDIYWKKFEEKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADQTIYFPYTETSRRLTSFYPEIEKLLYSTGGNEEHICVLKDRNKPIIFTMARLDRVKNITGLVEWYGKNAKLRELVNLVVVAGDRRKESKDLEEKAEMKKMYEHIETYKLNGQFRWISSQMNRVRNGELYRVICDTKGAFVQPAVYEAFGLTVVEAMATGLPTFATLNGGPAEIIVHGKSGFHIDPYHGDRAADLLVEFFEKVKTDPSHWDKISQGGLQRIEEKYTWQIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVEE

>GaSUS1

MAERALTRVHSLRERLDSTLTAHRNEILALLSRIEGKGKGILLHHQIILEFEAIPEENRKKLADGAFFEI

LKASQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELTVAEYLRFKEELVDGSSNANFVLELDFEPF

NASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLKVHCHKGKNMMLNDRIQNLNSLQHVLRK

AEEYLVALPAETPYAEFEHKFQEIGLERGWGDTAERVLEMIQLLLDLLEAPDPCTLEKFLGRIPMVFNVV

ILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLNRIKQQGLNITPRILIITRLLPDAVGTTCGQR

LEKVYGTEYSDILRIPFRTEKGIVRRWISRFEVWPYLETYTEDVAHEISKELQGKPDLIIGNYSDGNIVA

SLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLEDKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDT

VGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYYPYTEEKKRLKHFHSEIEELLYSKVENEE

HWCVLNDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEKAEMKKMFEL

IEKYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEI

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>GaSUS2

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>GaSUS3

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>GaSUS4

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>GaSUS5

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>GaSUS6

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GFWKYVSKLERRETRRYLEMFYILKFRELVKSVPLASDD

>GaSUS7

MTSTSTGKLSDSIADNIRNALKQSQSYMKRCFSKYMEKGKRILKAHELRDEFEKVMDDKNETLGTMFSSA

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SMPKLTLASSIGKGLNFVSKYITSKLSGSVDNAQPLVDYLLSLEYQGEKLMINEILNTAAKLQLALIVAE

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VDGVSGFHINPTNGDESSNKIADFFEKCKTNPAYWNQFSADGLKRINECYTWKIYANKVLNMGCMYRFWK

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>GhSUS-D

MAERALTRVHSLRERLDSTLTAHRNEILALLSRIEGKGKGILLHHQIILEFEAIPEENRKKLADGAFFEILKASQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELTVAEYLRFKEELVDGSSNANFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLKVHCHKGKNMMLNDRIQNLNSLQHVLRKAEEYLVALPAETSYADFEHKFQEIGLERGWGDTAERVLEMIQLLLDLLEAPDPCTLEKFLGRIPMVFNVVILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLNRIKQQGLNITPRILIITRLLPDAVGTTCGQRLEKVYGTEYSDILRIPFRTEKGIVRRWISRFEVWPYLETYTEDVAHEISKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLEDKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYYPYTEEKKRLKHFHSEIEQLLYSKVENEEHWCVLNDHNKPILFTMARLDRVKNLSGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEKAEMKKMFELIEKYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEALGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFNIDPYHGDQAAEILVDFFEKCKTDSSYWTKISEGGLKRIEEKYTWKIYSERLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVEE

>GhSUS-A

MAERALTRVHSLRERLDETLLAHRNEILALLSRIEGKGKGILQHHQIILEFEAIPEENRKKLANGAFFEVLKASQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELTVAEYLHFKEELVDGSSNGNFVLELDFEPFNSSFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCHKGKNMMLNDRIQNLNALQHVLRKAEEYLGTLPPETPCAEFEHRFQEIGLERGWGDTAERVLEMIQLLLDLLEATDPCTLEKFLGRIPMVFNVVILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLNITPRILIITRLLPDAVGTTCGQRLEKVYGTEHSDILRVPFRTEKGIVRKWISRFEKVWPYLETYTEDVAHEISKELHGTPDLIIGNXSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLEDKYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMEIYFPYTEEKRRLKHFHPEIEDLLYTKVENEEHLCVLNDRNKPILFTMPRLDRVKNLTGLVEWCGKNPKLRELANLVVVGGDRRKESKDLEEKAEMKKMFELIDKYNLNGQFRWISSQMNRIRNVELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFNIDPYHGDQAADILVDFFEKCKKDPSHWDKISQGGLKRIEEKYTWKIYSERLLTLTGVYGFWKHVSNLERRESRRYLEMFYALKYRKLAESVPLAEE

>GhSUS-B

MAERVITRVHSLRERLDDTLIAHRNEVLALLTRIEGKGKGILQHHQIILEFEAIPEETRKKLADGAFSEILRASQEAIVLPPWVALAVRPRPGVWEYIKVNVHALVVEELTVAEYLHFKEELVDGSANGNFVLELDFEPFNASFPRSTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLKVHCHKGKNMMLNDRIQNLNSLQYVLRKAEEYLGTLPAETPYTELEHKFQEIGLERGWGDTAGRVLEMIQLLLDLLEAPDPCTLEKFLGRVPMVFNVVILTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLNITPRILIITRLLPDAVGTTCGQRVEKVYGTEYSDILRVPFRTEKGIVRRWISRFVVWPYLETYTEDVAHEISKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKKLEDKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLKHFHPEIEDLLYSKVENEEHLCVLNDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESEDLEEKAEMKKMFELIETYKLNGQFRWISSQMNRVRNGELYRYICDTRVAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFNIDPYHGDQAAEILADFFDKCKKDPSHWNDISEGGLKRIQEKYTWQIYSERLLTLTGVYGFWKHVSNLDRRESRRYLEMFYALKYPKLAESVPLAEE

>GhSUS-C

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>MdSUS1.1

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WKDVSNLDRLESRRYLEMFYALKFRKLAASVPLAVEE

>MdSUS1.2

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>MdSUS1.3

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>MdSUS1.4

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WKHVSNLDRLESRRYLEMFYALKYSKLAASVPLAVEE

>MdSUS2.1

MANRPKFTRALSLRERVEDTLSDHRNELVALLSRYLDQGKRILQPHDLIDQLDIVIGDDEAKRQLKTGPF

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NQRLERISGTEHTHILRVPFRSEKGILRKWISRFDVWPYLETFAEDAAGEIIAELQGYPDFIIGNYSDGN

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YGFWKYVSKLERRETRRYLEMFYILKFRDLAKSVPEAIDDAH

>MdSUS2.3

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SSSIGNGVQFLNRHLSSVMFRNKESLEPLLDFLRTHKHDGHAMMLNDRIQSIPRLQSALAKAEEYLSKFP

PTTSYSEFEFDLQGMGFERGWGDTAQRVSEMVHLLLEILQAPDPSTLENFLGRIPMVFNVVIVSPHGYFG

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KPIVFSMARLDRVKNLTGLVECYAKSAKLREMVNLVVVGGYMDVKNSRDREEXAEIEKMHDLIKKYNLXG

QFRWIAAQMNRARNGELYRYIADTKGVFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIXHGSSGF

HVDPYNPDQVAELLIDFFDXCQKXPGYWEKISQAGLKRIYERYTWKIYSERLLTLAGVYGFWKHVSKLER

RETRRYLEMFYILKYRNLVSNLIISFLVLXHAQNGTGXP

>MdSUS3.1

MASTSSALKRSDTIAETMPDALRESRFHMKKCFASFVGTGKRLIKPQHIMEELEKSIEDRHERSKVLEGL

LGYILSRTQEAAVVPPYVAFAVRPNPGFSEFVKVNADDLAVDGISATQYLKFKEMIFDESWANDENALEI

DFGAFDFSTPRMTLPSSIGNGLNFVLKLISSRLSTHASCSDYAKPLLDYLLPLNYHGENLMINESLDTVE

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>MdSUS3.2

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>PtrSUS2

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>PtrSUS3

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>PtrSUS4

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>PtrSUS5

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>PpSus2

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>PpSus4

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>PpSus5

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>PpSus6

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>CitSUS1

MAERALTRVHSLRERLDETLSAHRNEILALLSRIEGKGKGILQNHQLIAEFESISEENRKHLTEGAFGEVLRATQEAIVLPPWVALAVRPRPGVWEYIRVNVHALVVEELLVAEYLHFKEELVDGGSNGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHDKESMHPLLEFLRVHCHKGKNMMLNDRIQNLNSLQHVLRKAEEYLTTVVPETPFSELALRFQEIGLERGWGDTAERALEMIQLLLDLLEAPDPCTLETFLGRIPMVFNVVILTPHGYFAQDDVLGYPDTGGQVVYILDQVRALEDEMLLRIKQQGLDITPQILIITRLLPDAVGTTCGQRLEKVYGTKYSDILRVPFRTEKGVVRKWISRFEVWPYLETYTEDVAVEIAKELQGKPDLIIGNYSDGNIVASLLAHKLGVTQCTIAHALEKTKYPDSDIYWKNLDDKYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTEEKRRLKSFHPEIEELLYSDVENKEHLCVLKDRNKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYSLIDQYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVNGKSGYHIDPYHGEQAAEILVDFFEKCKADPSYWDKISLGGLKRIEEKYTWKIYSQRLLTLTGVYGFWKHVSNLDRLESRRYLEMFYALKYRKLAESVPLAVE

>CitSUS2

MFRFPPYFVFVCYSIERLGCGTYKRQQILSLLEAESNGAAIADVLNATQEAAVSSPWVAFAVRTSPGVWCYIRVNVQTVDVEEISVSKYLLFKEEIVDGRKSNGNFAFEVDFEPFRALPHPTLSNSIGHGMEFLNRHMSAKLFNDKESMQSLLEFLRVHSHMGKNMMLNEKIQDLGTLQSSLRMAEKYLSMLAPDTSYAEFEQKFQEIGLERGWGDNAEHVLGMIQLLLDLLQAPESSTLETFLGKIPRVFNVVIFTPHGYFAQDNVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPRILIITRLLPDAVGTTCGQRVEKVYGTKYSDILRVPFRTEEGIVRKWISRFEVWPYLETFTEDVATEIIQELQCKPDLIIGNYSDGNIVASLLAHKLDVTQCTIAHALELTKYPDSDINWKKLDDKYHFSCQFTADLFAMNRTDFIITSTFQEIAGSKDTVGQYESHTAFSLPGLYRVVNGIDAFDPKFNIVSPGADMTIYFPYMEEKRRLKHFHSEIEELLYSPVENKEHLCVLKDSSKPILFTMARLDRVKNLTGLVEWYGKNAKLRELVNLVVVGGDRRKESKDLEEQAEMKKMYGLVDTYKLNGQFRWISSQMNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVHGKSGFHIDPYKGDQAAGILVDFFEKCKVDPGHWDEISQGGLKRIQEKYTWKIYSERLLNLSGVYGFWKHLSKLDSREKNRYLEMFYSLMYRKQVQTVPLAVDE

>CitSUS3

MAAPKLSRIPSIRERVEDTLSVHRNELVSLLSRYVAQGKGILQPHVLIDELDNIFGDDEGRQNLRDGPFSEVIKSAQEAIVLPPFVAIAVRPRPGVWEYVRVNVYELSVEQLSVSEYLHFKEELVDAAFNERFVLELDFEPFNATFPRPNRSSSIGNGVQFLNRHLSSSMFRNKDCLEPLLDFLRAHKYKGHLLMLNDRIQSISRLQSSLSKAEDHLSKLPPDTPFSQFEYVLQGMGFEKGWGDTAEHVLEMMHLLLDILQAPDPSTLEKFLGRLPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIKRQGLDISPKILIVTRLIPDAKGTTCNQRLERVSGTEHTHILRVPFRSEKGILRQWISRFDVWPYLETFTEDVGSEITAELQGFPDFIIGNYSDGNLVASLLAYKMGITQCTIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADLIAMNNADFIITSTYQEIAGTKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMDIYFPYSEKQKRLTALHGSIEQLLFDPEQNDEHVGTLSDRSKPIVFSMARLDHVKNMTGLVECYGKNSQLRELVNLVVVAGYIDVNKSKDREEIAEIEKMHELMKTYKLDGQFRWIAAQTNRARNGELYRYIADTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIEHGASGFHIDPYHPDQAAELMADFFGKCKENPSHWKKISDGGLKRIYERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKSVPLASENQH

>CitSUS4

MSSSPSLKRSDTIADTMPDALRQSRYYMKKCFSRFVAKGKRLMKRHHLMDEVEKSIEDKIERGKVLEGLLGYILSSTQEAAVVPPNVAFAVRPNPGSWEYVKVNSEDLTVDGINVLEYLKFKETIFDQDWAKDENALELDFGAMDFSSPRLTLSSSIGNGVNYVSKFMSTRLSANSEKAKQFLDYLLALNHRGEQLMINDTLDTVDKLQAALIVAEVSISDLPKDTPYQEFQQRFKEWGFEKGWGNTAERVRETMRLFSEVLQAPDAAKLQVLFSRLPNMFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVRALEEELLLRIKQQGLSVKPQILVVTRLIPNSKGTKCNQELEPIYDTKHSHILRIPFKTEQAILPQWVSRFDIYPYLGRFAQDATAKILDLMEGKPDLIIGNYSDGNLVASLMASKLGITQATIAHALEKSKYEDSDAKWKELDPKYHFSCQFTADLIAMNQTDFIITSTYQEIAGSKDRPGQYESHTAFTMPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYTEKQKRLTSFHPDIEELLYSKEDNSEHIGYLADRKKPIIFSMARLDTVKNITGLTEWYGKNKRLRNMVNLVVVAGFFDPSKSHDREEIAEIKKMHTLIEKYQLQGQFRWIAAQTDRYRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIIDGVSGFHIDPNNGDESSNKIADFFEKCKTDAGYWNQMSAAGRQRIYECYTWKIYANKVLNMGSIYGFWRQINKEPKEAKQRYIQMFYSLLFRKLASNVPIKVPEPLQSAQTSPVESQQPAAATGIAKPQPPASAVIDKPNQQEKTAQQKKRHVRKTMTVI

>CitSUS5

MASATSLKRSDSIADNMPDALKQSRYHMKRCFVRYIEKGKRIMKLHDLMDELNEVIDDEDVRTQVLEGLLGYILCSTQEAVVMPPHVAFAIRPNPGFWEFVKVNSDDLSVEAITVTDFLKFKELVFDEDWAKDENALEVDFGAYEFSLPQLTLSSSIGNGISFVSKFVTAKLSGRQDCAQPLVDYLLSLDHQGEKLMINDNLNTAEKLQMALIVAEVSLSTLPKDTPYQKFELRFKEWGFEKGWGHTAERVRETMRSLSEVLQAPDPLHMEKFLSSLPILFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLLRIKQQGLYIKPQIVVVTRLIPDARGTKCNQELEPIEGTKHSNILRVPFKTDKGILHRWVSRFDVYPYLEGFAQDATTMILELLGGKPDLIIGNYSDGNLVASLMASKLGITQATIAHALEKTKYEDSDVKWKELDPKYHFSCQFIADTIAMNATDFIIASTFQEIAGSKDRPGQYESHTAFTLPGLCRVVKGIDVLDPKFNIAAPGADQSVYFPYTEKQRRLTKFHPEIEELLYNKEDNNEHIGYLADRKKPIIFSMARLDVVKNLTGLTEWYGKNKRLRNLVNLVIVGAFFDPSKSKDREETAEIKKMHALMEKYQLKGQMRWIAAQSDRLRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPYNGDESSDKIADFFEACKVDPTYWNKFSTEGLKRINECYTWKIYANKMLNMGCMYSFWKQLNKGQKLAKQRYIEMFYNLLFKNLVKNVPVPNEEAQQPMSEPAVKPQHSLRQARSSTNMLHF

>CitSUS6

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>GmSUS1

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>GmSUS2

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>GmSUS3

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>GmSUS4

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>GmSUS5

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>GmSUS6

MASAPALKRTDSVVDNMPDALRQSRYHMKRCFAKYLGKGRRIMKLHHLMEEMELVIDDKSERSQVLEGILGFILSSTQEAVVDPPYVAFAIRPYPGVWEFVKVSSEDLSVEAITPTDYLKFKERVHDEKWATDENSFEADFGAFDFQIPQLTLSSSIGNGLQFTSKFLTSKLTGKLEKTQAIVDYLLTLNHQGESLMINESLNSSAKLQMALVVADAFLSGLPKDTAYQNFELRFKEWGFERGWGDTAGRVKETMRTLSEVLQAPDPVNLEKFLSSLPIIFNVVIFSVHGYFGQADVLGLPDTGGQVVYILDQVKSLEAELLLRIKQQGLNVKPQILVVTRLIPDARGTKCHQELEPISDTKHSHILRVPFQTDKGILHQWISRFDIYPYLERFTQDATAKILEFMEGKPDLVIGNYTDGNLVASLMARKLGITQGTIAHALEKTKYEDSDVKWKELDPKYHFSCQFMADTVAMNASDFIITSTYQEIAGSKDRPGQYESHAAFTLPGLCRVVSGINVFDPKFNIAAPGADQSVYFPYTEKEKRLSQFHPAIEDLLFSKVDNIEHIGYLADRRKPIIFSMARLDVVKNLTGLVEWYGKNKRLRNLVNLVIVGGFFDPSKSKDREEMAEIKNMHDLIDKYQLKGQFRWIAAQTNRYRNGELYRCIADTRGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPLNGDESSNKIADFFEKCKMNQSQWNVISAAGLQRINECYTWKIYANKMVNMGNIYTFWRQVNKEQKEAKQRYIQMFYNLIFKNLVKTVPVPSDEPQQPVGKQPSLKSRSTGRSHSRLQRLFGN

>GmSUS7

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>GmSUS8

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>GmSUS9

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>GmSUS10

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>GmSUS11

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>VvSUS1

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TN

>VvSUS2

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>VvSUS3

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>VvSUS4

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>VvSUS5

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YLLMKL

>ZmSH1

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>ZmSUS1

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>ZmSUS3

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>OsSUS1

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>OsSUS2

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>OsSUS3

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VENTEHKFVLKDKKKPIIFSMARLDHVKNLTGLVELYGRNPRLQELVNLVVVCGDHGKESKDKEEQAEFK

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>OsSUS4

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>OsSUS5

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>OsSUS6

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>BD1G20890

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>BD1G29570

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>BD1G46670

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>BD1G60320

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>BD1G62957

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>BD3G60687

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>BeSUS1

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>BeSUS3

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>BeSUS4

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>BeSUS5

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>HV1558277G00010

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>HV1561797G00010

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>HV2547343G00020

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>HV355646G00010

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>HV43511G00010

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>HV49320G00010

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>HV66958G00020

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>MA02G22450

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>MA03G01920

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>MA03G14280

MAAVSLSFKRSDSIAEGMPEALKESRYQMKKCFARYVSKGKRVMKNPQLMEELEKSIDDEAEKAKVMEGFLGYIICSTQEAVVLPPFVAFAVRPHPGIWEYVKVHSVDLSVDGITPCEYLKNKETIYDEKWATDEHALEVDFGALEPSTPLLTLPSSIGKGAQFISRFISAKLNASSESMKPLLDYLLALNHGGQKLMINNTFDTVNKLQTALLLAEVFVSGLPKNTPFQKFEPRFEEWGLEKGWGDTAATVKETLNCLSEVLQAPDPVNLEKFFGRVPSIFNIVILSPHGYFGQADVLGLPDTGGQIVYILDQVKAFEEELLLRIKQQGLTIKPQILVVTRLIPEAKGTKCNQELEPILNTKHSHILRVPFKTETGVVQQWVSRFDVYPYLERYAQACLDILQGKPDLIIGNYTDGNLVASLMATKLGVTQGTIAHALEKTKYEDSDVKWKELEPKYHFSCQFTADMIAMNTTDFIITSTYQEIAGSKDRPGQYESHHAFTLPGLCRFVSGIDVFHPKFNIASPGADQSVYFPYTQKQKRLTSLHPAIEELLYSKTDNEEHTGYLEDRKKPIIFSMARLDTVKNITGLVEWYGKNKKLRGLVNLVVVAGFLDPSKSKDREEISEIKKMRSLIEKYQLKGQMRWIAAQTDRVRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDGVSGFHIDPTDGEEASGKMADFFERCKDASYWNKISTAGLQRIYECYTWKIYATKVLNMGSIYGLWRQLNKEEQLAKEKYLQLFYNLQFRNLAKTVPIATDQAQQEAKPKPVAIPASQPSQNPIRKLLAICTRKHKGGQ\*

>MA06G11150

MPQRTLTRAHSVRERIGDSLSSHPNELVALFSRFINQGKGMLQPHQLLAEYAAAFSEADREKLKDGAFEDVIKAAQEAIVIPPWVALAIRPRPGVWEHVRVNISELAVEELTVPEYLHFKEELVDGSSQNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRQHNYKGMSMMLNDRIQSLSALQAALRKAEQHLLSIPSATPYSEFNHRFQELGLEKGWGDTAQRVYENIHLLLDLLEAPDPCTLENFLGTIPMMFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRALENEMLLRIKRQGLDITPRILIVTRLLPDAVGTTCGQKLEKVIGTEHTHILRVPFRTENGIVRKWISRFEVWPYLETYTEDVANELAGELQTTPDLIIGNYSDGNLVSTLLAHKLGVTQCTIAHALEKTKYPNSDIYWKKFENQYHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTEKQKRLTSLHPEIEELLFNPEDNTEHKGVLNDTKKPIIFSMARLDRVKNLTGLVEFYGRNERLKELVNLVVVCGDHGKESKDLEEQAEFKKMYDLIEKYNLNGHIRWISAQMNRVRNGELYRYIADTKGAFIQPAFYEAFGLTVVESMTCGLPTFATVHGGPGEIIVDGVSGFHIDPYQGDKAAEIIVNFFEKCKEDPTHWDKISLGGLKRIEEKYTWKLYSERLMTLSGVYGFWKYVSNLDRRETRRYLEMFYALKYRNLAKSVPLAVDGEAINGSK\*

>MA07G20260

MAGRTLTRVLSVKERLSGTLSASPNELLAVFSRYVNQGKGMLQRHQLLAEFEAAFSEDEKEKLKGGVFEDVLRAAQEAIVVPPLVALAIRPRPGVWEYVQVNVNELVVGELSASEYLQFKEKLVNGESESNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFVDKESMYPLLEFLRTHSYKGTVMMLNDKLQSPRALQSALRKAEQYLLSIPADTPYSEFNNRFQELGFEKGWGDTVQRVLETMHLLLDLLEAPDPCTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPRILIVTRLLPDAVGTTCGERLEQVDETQHTSILRVPFRNEKGILRKWISRFDVWPYLETYTEDVAKELAEELQATPDLIIGNYSDGNLVASLLAHKLGVTQCTIAHALEKTKYPNSDIYWKKFDDQYHFSCQFTADLFAMNHTDFIITSTFQEIAGSKDTVGQYESHTAFTLPGLYRVVHGINVFDPKFNIVSPGADMSVYFPHVEVDKRLTHFHPEIEELLFSSVENDEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRNARLRELANLVVVAGDHGKESKDIEELAERKKMFGLIEEYNLNGQIRWISAQMDRVRNGELYRYIADTKGAFVQPALYEAFGLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGFHIDPYQKDKAAEILVGFFEKCKEDPTHWDKISQGGLQRIYEKYTWKLYSERLMTLAGVYGFWKHVSNLERRETRRYLEMFYALKYRKLAASVPLAVDAESTVDGQNV\*

>MA08G23060

MTTKKLERIPSMRERVEDTLSAYRNDLVSLLSRFVSQGKGMLQPHHLVDALATLGDDGRTKLSEGPFSEVLRSAQEAIVLPPFVAIAIRPRPGVWEYVRVNVYELSVEQLSVSEYLQFKEELVDGRSDDRYTLELDFEPFNASFPRPNRSSSIGNGVLFLNRHLSSIMFRNKDCLEPLLDFLRAHKYKGHVMMLNDRVQSVSRLQSVLAKAEEYLSKLIPETPFSEFAYKLQEMGLEKGWGDTAQHVLEMIHLLLDILQAPDPSTLEMFLGRIPMVFNVVILSPHGYFGQANVLGLPDTGGQVVYILDQVRALENEMLLRIKKQGLDIDPKILIVTRLIPDAKGTTCNQRLERVSGTQHSHILRVPFRTEKGILKKWISRFDVWPYLETFTEDVASEIAAELHGTPDLVIGNYSDGNLVASLLAYKLGITQCNIAHALEKTKYPDSDIYWRKFEDKYHFSCQFTADLIAMNNADFIITSTYQEIAGSKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFTYSEKGKRLTSLHGSIEKLLYDPEQCDLHIGCLDDRSKPIIFSMARLDKVKNITGLVEWFGKSTKLRELVNLVVVAGYIDVKKSSDREEIQEIEKMHQLISSYNLSGQFRWISAQTNRARNGELYRYIADTGGAFVQPAFYEAFGLTVVEAMTCGLPTFATCHGGPAEIIENGLSGFHIDPYHPDQSAVVMVEFFERCKEDSGYWKKISDGGLRRIQERYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRDLVKSVPRAVDDDH\*

>MA09G21760

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>MA10G19100

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>SB01G033060

MGEAAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQIIAEYNSAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSTLQADTPYSEFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGTTCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLHPEIEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRNKRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGFHIDPYQGDKASALLVDFFEKCQTDSSHWNKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPLAVEGEPSSK\*

>SB01G035890

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>SB04G038410

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>SI001G39400

MDGLMRRSDSIADMMPEALRQSRYHMKRCFQRYVAGGSRLMKKTQLLEELHRSAEDGRIHKDRLAEGFLGYVISSTHEAVVLPPLVNFAVRTNPGIWEYIKVHSADLTVDQITPSQYLKCKEMLYDHQWAQDDNSLEVDFGALDDLSTPRLTLPSSIGNGMHFVSRFMSSKLAGTTMSMKPLLDYLLALTHRGHDLMVNATLDTVSKLQTALLHADVFLAGLHGDTPYQKFEHKFQEWGLERGWGHTAEACRETISCLSEVLQAPDPTNMDSFFSRVPSLFSIVIFSIHGYFGQEKVLGLPDTGGQVVYILDQVRALEDELLQRINQQGLHFTPRILVLTRLIPEAKGTKCNVELEPIHNTRHSTILRVPFKTEDGQDLPHWVSRFDIYPYLERYAEDSCAKILETLQGKPDLVIGNYTDGNLVASLVSRKLGVTQGTIAHALEKTKYEDSDVKWREMDRKYHFSCQFTADMIAMNTSDFIIASTYQEIAGSKEKPGQYESHYAFTMPGRCRFATGINVFDPKFNIAAPGADQSVYFPFTLKQKRLTDLHPQIEELVYSKEDNDEHIGYLEDRSKPVIFSMARLDKVKNITGLVEWYGQNKRLRDLVNLVVVGGLLDPSQSKDREEIEEINKMHSLINKYQLKGQIRWIRAQTDRVRNGELYRCIADTKGAFVQPAFYEAFGLTVIEAMNCGLPTFATNQGGPAEIIVDEVSGFHINPLDGKKASNKIADFFQKCKEDPMYWNKISTAGLQRIYECYTWQIYATKVLNMGSMYGFWRTMDKEERQAKQRYLQMFYNLQFRKLAKAVPKVGERPEQPTAATVPDRLVSRPKERQVCPLLRNLLKKEQGSC\*

>SI004G04220

MASKLTRLHSLRERLGATFSSHPNELIALFSRYVNQGKGMLQRHQLLAEFDALFDSDKEKYAPFEDILRAAQEAIVLPPWVALAIRPRPGVWDYIRVNVSELAVEELSVSEYLAFKEQLVDGQNTSNFVLELDFEPFNASFPRPSMSKSIGNGVQFLNRHLSSKLFQDKESLYPLLNFLKAHNYKGTTMMLNDRIQSLRGLQSSLRKAEEYLLSIPQDTPYSEFNHRFQELGLEKGWGDTAKRVLDTLHLLLDLLEAPDPANLEKFLGTIPMMFNVVILSPHGYFAQSNVLGYPDTGGQVVYILDQVRALEDEMLLRIKQQGLDITPKILIVTRLLPDAVGTTCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFDVWPYLETYTEVYRLIFLLDVVHNLDFSVNTEVMHSVLQDVASEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPNSDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYESHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFHPEIEELIYSDVENSEHKFVLKDKNKPIIFSMARLDRVKNMTGLVEMYGKNARLRELANLVIVAGDHGKESKDREEQAEFKRMYSLIDQYNLKGHIRWISAQMNRVRNAELYRYICDTKGAFVQPAFYEAFGLTVIESMTCGLPTIATCHGGPAEIIVDGVSGLHIDPYHSDKAADILVNFFDKCKADPSYWDKISQGGLQRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYRSLASAVPLSFD\*

>SI004G29780

MASNLSFKRTDSIADSMPDALRQSRYQMKRCFQRYVSKGKRLLKNQQLLEELEKSLDDKVEKEKLVEGFLGYIICSTPEAVVLPPYVAFAVRMNPGIWEYVKVHSDDLSVEGITPSEYLKFKETLYDENWAKDDNSLEVDFGALDLSTPHLTLPSSIGNGLQFVSKFMSSKLGDKPETSMKPLLDYLLSLNYRGEKLMINDIIDTVNKLQTALLLAEVFVSGLPRYTPFAKFEQRFQEWGLEKGWGDTAERCKETLNCLSEVLQAPDPINMEKFFSRVPTIFNIVVFSIHGYFGQEKVLGLPDTGGQVVYILDQVRALEEELLQRIKQQGLKVTPKILVLTRLIPDAKGTKCNVELEPVENTKHCSILRVPFKTEDGKDLRQWVSRFDIYPYLERYAQDSCAKILDILEGKPDLIIGNYTDGNLVASLMSSKLGVTQGTIAHALEKTKYEDSDVKWRDLDQKYHFSCQFTADMIAMNTSDFIITSTYQEIAGSKEKPGQYEHHYAFTMPGLCRYATGINVFDPKFNIAAPGADQSIYFPFTQKQKRLTDLHPQIEELLYSKQDTDEHIGYLADRNKPIIFSMARLDKVKNITGLVEWYGQNRKLRDLVNLVVVAGLLEASQSKDREEIEEINKMHNLIDKYQLKGQIRWIKAQTDRVRNGELYRCIADTKGAFVQPALYEAFGLTVIEAMNCGLTTFATNQGGPAEIIVDGVSGFHINPMNGREASNKIADFFQKCKEDPSYWNKVSTAGLQRIYECYTWKIYATKVLNMGSTYTFWKTLNKEERAAKQRYLQMFYNLQFRNLAKTVPRVFEHPPQTPAGAGPSTVTVVRPKERKPQTRIQRIMTSLMGNKSSTSD\*

>SI009G38390

MGEAAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQIIAEYNSAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVWEYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNFVLELDFEPFNASFPRPSLSKSIGNGVQFLNRHLSSKLFHDKESMYPLLNFLRAHNYKGMTMMLNDRIRSLSALQGALRKAEEHLSSLPADTPYSDFHHRFQELGLEKGWGDCAKRAQETIHLLLDLLEAPDPSTLEKFLGTIPMVFNVVILSPHGYFAQANVLGYPDTGGQVVYILDQVRAMENEMLLRIKQCGLDITPKILIVTRLLPDATGTTCGQRLEKVLGTEHCHILRVPFRTENGIVRKWISRFEVWPYLETYTDDVAHEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPNSDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYESHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTESHKRLTSLHPEIEELLYSQTENNEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRNKRLQELVNLVVVCGDHGNPSKDKEEQAEFKKMFDLIEQYNLNGHIRWISAQMNRVRNGELYRYICDTQGAFVQPAFYEAFGLTVVEAMTCGLPTFATAYGGPAEIIVHGVSGYHIDPYQGDKASALLVDFFEKCKEDSSHWSKISQGGLQRIEEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMLYALKYRTMASTVPLAVEGEPSSK\*

>SI009G42350

MSAPKLDRTPSIRDRVEDTLHAHRNELVALLSKYVNKGTCILQPHHILDALDEVQGSEGRALAEGSFLDVLRSAQEAIVVPPFVAIAVRPRPGVWEYVRVNVHELSVEQLTIPEYLCFKEALVDGQHNDPYLLELDFEPFNVSVPRPNRSSSIGNGVQFLNRHLSSIMFRNRDCLEPLLDFLRGHRHKGHVMMLNDRIQSLGRLQSVLTKAEEHLSKLPADTPYSQFAYQFQEWGLEKGWGDTAEHILEMIHLLLDILQAPDPSTLETFLGRIPMIFNVVVVSPHGYFGQANVLGLPDTGGQIVYILDQVRALENEMVLRLKKQGLDVTPKILIVTRLIPDAKGTSCNQRLERISGTQHTYILRVPFRNENGILKKWISRFDVWPYLERFAEDAAGEIAAELQGTPDFIIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPDSDIYWKKFDEKYHFSCQFTADIISMNNADFIITSTYQEIAGSKNTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTEKAKRLTSFHGSIESLIYDPEQNDEHIGYLDDRSKPILFSMARLDRVKNITGLVEAFAKCSKLRELVNLVVVAGYNDVKKSKDREEIAEIEKMHELIKTYNLFGQFRWISAQTNRARNGELYRYIADTHGAFVQPAFYEAFGLTVVEAMTCGLPTFATLHGGPAEIIEHGISGFHIDPYHPDQAANLMADFFERSKQEPNHWVKISEAGLQRIYEKYTWKIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYILKFRELVKTVPLAIDQPQ\*

>PAB00010305

MAAPVQRADSVADKLPEALRQNRYQIRKCFSRFVSQGKRILQTQELLNELATIIEDPVERNKIQEGMFGRMLQSTQEVVIVPPFIGLAIRTKPGIWEYASVNDNDLSIEQITVSEYLKLKECLVDEEWPKNDYALELDFEPFNASFPRMARPSSIGNGVHFLSQHLSCRLFHDAQSMQPLLHFLQTCNYCGEKRMVGDSINTVSQLQTALGKAEKILSDLRKDAPYEEFEHRFQDIGLEKGWGNNANNVLHTIHLLLEVLQEPDPIALEKFLGKIPNVFNVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEELLSRIEQQGLDITPQILVVTRLIPEAQGTRCNQRIEKVLNTQYSQILRVPFKTEKGVLRRWVSRFDVWPYLEKFAEDAANEIVTALQGKPDLIIGNYSDGNLVASLVANKLGIIQCNIAHALEKTKYANSDLNWKKFDEKYHFSCQFTADILAMNNADFIITSTYQEIAGSEDTVGQYESHGAFTLPGQYRVVSGIDVFDPKFNIVSPGADMSIYFPYKEKQSRLTQFHEAIEELLFNPEDTLEHKGFLNDKKKPIIFSMARLDRVKNMTGLVEWFGKNRRLRKLVNLVVVAGFIDSSKSKDREEIAEIEKMHGLIRKYNLNGDFRWICAQKDRIRNGELYRYIADTKGAFIQPALYEAFGLTVIEAMTCGLPTFATCKGGPAEIIIDGVSGFHIDPHNGDEASEKIANFFGKCKRNTNYWNVVSDAGLQRIYDSYTWKIYAEKLINLTNIYGFWKYVSKNNRREIQEYMKLFYNLKFQNLVKNSPKQELYGSHARIKR\*

>PAB00011567

MVAATLTRVLSSRERVQDTLFEHRNEIVSLLSRYVAKGKKILQPHDLLDGLAEVTGENDEGQKLRDGPFGDVLRSTQEAIILPPWVVLAVRPRPGVWDYVRVNVDELAVEQLSVAEYLEFKEHLVNGSDKDNYVLELXXXFNASFPRPTRPSSIGSGVQFLNRHLSSRLFRDKESMQPLLDFLRAHNYRGQKLMLNERIQSLPRLRSALVKAEEHLHKFPKDTPYTEFEHKLQEMGLEKGWGDNAEHVLGTIHLLLEILQAPDPSNLETFLGRIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALESEMLLRIKQQGLDITPEIIVVTRLIPEAHGTTCNQRIEKVSGTQHSRILRVPFRTEKGVLRDWVSRFDVWPYLERFSEDVSNEVTAELKGQPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDIYFPYTEKQHRLTALHGSIEELLFNPEQTAEHMCVLNDHKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRGLVNLVVVAGDIDPSKSRDREEVAEIEKMHRLIKEYNLDGQFRWICAQKNRVRNGELYRYICDTKGAFVQPAIYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGVSASERIADFFEKCKTDPSYWIKISNGGLQRIYERYTWKIYAEKLMTLSGVYGFWKYVSKLERLETRRYLEMFYTLKYRDLVKTVPLAVEESANGIEEKTLSGTRSDQKRLFYYPTFRIYERGLAYFVLGCYVFLMYERGRHSIILMEHYAAAHPDELLMTPIVMY\*

>PAB00021357

MCYVCYRYIADGKRILHPQQLFDELAAVIEGQDERKKIQQGAFGNILQCTQEAVIVPPFIGLAIRTKPGIWEYVRVNVENLSIDQLTVPEYLQLKECLVDEQWAKDEYALELDFECFNASLPHMGRSSSVGNGIHFLSKHLASRLFRDGESMQPLLDFMQGHNYQGQKFMVNESINSLSKLQSALSKAEEMLSSLPKDTLYEEFDHRFQDIGLEKGWGENAGHALDMIQSVLEILEAPDPALLEKLLGKIPTVFSVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEEMLLRIKQQGLDITPQIIVVTRLIPEAQGTKCNQSIEKILNTQHSHILRVPFRTEKGVLRHWVSRFDVWPYLEKFAEDSSKEIIAKLQDKPDLIIGNYSDGNLVASLVAKKLEVTQCNIAHALEKTKYADSDINWKKFDEKYHFSCQFTADILAMNHADFIITSTYQEIAGSKDTVGQYESHAAFTLPGEYRVVSGIDVFNAKFNIVSPGADMTIYFPYTEKQSRLTAFHESIEELLFNPAETTEHMKLVNLAVVGGFIDSSKSKDREEIAEIEKMHGLIKKYSLKGDFRWICAQKDRVRNGELYRYIADTKGAFIQPALYEAFGLTVIEAMTCGLPTFATSKGGPAEIIIDGLSGFHIDPNNGDEASDKIAKFFERCKQEPSYWNKISDAGLQRIYESYTWKIYAEKLINLASVYGFWKYISKSGVHQTQRYMEMFYILKYRNLVKNMPIAKEEPETQIIEKGTRPAMEDNKANGRVASQSGIKRILSTWISTCGMPTCGEDSLVKEKNHT\*

>PME00009680

MVAATLNNALSSRERVEDMLSEHRNEIVSLLSRYVAEGKKILQPHQLLDGLEEVIGQNVELQSLRHGLFGEVLRSTQEAIVLPPWIVLAVRPRPGVWEYVRVNVDELAAEQLSVAEYLEFKEHLVNGSIKDDYILELDLEPFNASFPRPTRPSSIGSGVQFLNRHLSSRLFRDKESMQPLLNFLRVHKYRGQKLMLNERVQNLPKLRSALVKAEEHLKKFPKNTPYTEFEHKLQEMGLEKGWGDNVEHVLDTIHLLLEILQAPDPSMLETFLGRIPMVFHVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMLRRIKQQGLDITPEIIVVTRLIPEAHGTTCNQRIERISGTQHSRILRVPFRTEKGVLRQWVSRFDVWPYLERFSEDVSNEITVELKGQPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYFPYTEKQHRLTALHGSIEELLFSPEQTTEHMCVLNDRKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDIDPSKSRDREEVAEIEKMHELVKEYNLNGQFRWICAQKNRVRNGELYRYICDTRGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVDGVSGFHIDPYHGVSASERIADFFEKCKTDPGHWDKISNGGLQRIYERYTWQIYADRLMTLSGVYGFWKYVSKLERRETRRYLEMFYSLKYRNLVKTVPLAVEESVNGVEEKSAELPVGDALPNGASALVHNH\*

>PME00012638

MVAAMLTRALSSRERVQDTLSEHRNEIVSLLSRYVAKGKKILQPHHVLDGLAEVTGGTDEGQKLRDGPFGDVLRSTQEAIILPPWVVLAVRPRPGVWEYVRVNVDELAVEQLSVAEYLEFKEHLVNGSVKDSYVLELDLEPFNASFPRPTRPSSIGSGVQFLNRHLSSRLFHDKENMQPLLDFLRVHNYRGQMLMLNERIQSLPKLRSALVKAEEHLNKFPKDTPYTEFEHKLQEMGLEKGWGDNAEHVLGMIHLLLDLLQAPDPSTLETFLGRIPMVFNVVILSPHGYFGQEKVLGMPDTGGQVVYILDQVRALEHEMLLRIKQQGLDITPEIIVVTRLIPEAHGTTCNQRIEKISGTQHSRILRVPFRTEKGVLRDWVSRFDVWPYLERFSEDVTNEVTAELKGQPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYFPYTEKQHRLTALHGSIEELLFNPQQTDEHMCVLNDPKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDIDPSKSKDREEVSEIEKMHQLIKEYNLNGQFRWICAQKNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVDGVSGFHIDPYHGDSVSDRIADFFERCKTDPSYWINISNAGLQRIYEKYTWKIYAEKLMTLSGVYGFWKYVSKLERRETRRYLEMFYTLKYRDLVKTVPLAEEETVDGIEGKSTE\*

>PME00027252

MNTEISKTGYLEMSLRSTQEAIVFPPWVVLAVRPRPGVWEYVRVNVDERAVEQLSVAEYLEFKEQLVNESVKDNYVLELDLEPFNASFPRPTQPSSIGSGVQFLNRHLSSRLFHDKDKMQPLLDFLRAHKYQGQRLMLNERIQSLPKLRASLVKAEEHLNKFPEDTPYVEFEHKLQEMGLEKGWGDNAEHVLEMIHLLLEILQAPDPATLETFLGRIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALESEMLLKIKQQGLDITPEIIVVTRLIPEAHGTTCNQRIEKISGTQHSRILRVPFRTEKGVLRHWVSRFDVWPYLEKFAEDVASEIAAELKGQPDLIIGNYSDGNLVASLISHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADIIAMNTADFIITSTYQEIAGSKDTVGQYESHSAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYFPYTEKQRRLTALHGSIEELLFSPEQTAEQMCVLNDHKKPIIFSMARLDRVKNITGLVEWFAKNKRLRELVNLVVVAGDFDPLKSNDREEVAEIEKMHGLIKEYNLNGQFRWICSQKNRVRNGELYRYICDTRGAFVQPALYEAFGLTVVEAMTCGLPTFATRHGGPAEIIVDGVSGFHIDPYHGDSTSELIADFFERCKTDPGHWDAISNAGLQRIYERYTWKIYAERLMTLAGVYGFWKYVSKLGRRETRRYLEMFYILKYRNLVKTVPFAVEENADGIEEKTV\*

>PME00028776

MVAATLTRALSSRERVQDTLSEHRNEIVSLLSRYVAKGKKILQPHHLLDGLEEVMGENDELQKLRDGPFGDVIRSTQEAIIFPPWIALAVRPRPGVWDYVRVNVHELAVEQLSVAEYLEFKEHLVNGSIKDNYVLELDLEPFNASFPRPTRPSSIGSGVQFLNRHLSSRLFHGKESMQPLLDFLRAHNYRGQKLMLNERIQSLPRLRSALVKAEEHLKKFPDNTPYTEFEHKLQEIGLEKGWGDNAEHVLDMIHLLLEILQAPDPSTLETFLGKIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPEIIVVTRLIPEAYGTTCNQRIERISGTQHSRILRVPFRTEKGILHNWVSRFDVWPYLEQFSEDVTNEVTAELKGQPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYFPYTEKQHRLTALHGSIEELLFNPEQTADHMCVLNDRKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDIDPSKSRDREEVAEIEKMHTLIKEYNLNGQFRWICAQKNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGDSATERIADFFEKCKIDSSYWDKISNAGLQRIYERYTWKIYAERLMTLAGVYGFWKYVSKLDRRETRRYLEMFYTLKYRDLVKTVPLAIEESDGIEEKSTE\*

>PPI00011864

MVLARLTRVQSSRELVQDTLFEHRNEIVSLLSSYVAQGRKILHPHHLLDGLAEILGEDDELQNLRDGSFGDVLRSTQEAIILPPWVVLAVRPRPGVWEYVRVNVDELAVEQLSVAEYLEFKENLVTGSVKDNYVLELDLEPFNASFPRPTQPSSIGSGVQFLNRHLSSRLFHDKDSMQPFLDFLRAHSYRGQKLMLNERIQSLPKLRSALVKAEEHLNKFPLNTPYMEFEHKLQEMGLEKGWGDNVEHVLDMIRLLLEILQAPDPSTLETFLGRIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALEKEMLLRIKRQGLDITPQIVVVTRLIPEAYGTTCNQRIERISGTQHSRILRVPFKTDKGVLRKWVSRFDVWPYLERFSEDVSNEINAELQGQADLIIGNYSDGNLVASLIANKQGITQCNIAHALEKTKYPDSDLYWKNFEEKYHFSCQFTADIMAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGHYRVVNGIDVFDAKFNIVSPGADMQIYFPYTEKQRRLTALHDSIEELLFNPEQTAEHMCALNDHKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDFDPSKSKDREEVAEIEKMHTLIEEYNLNGQFRWICAQKNRVRNGELYRYICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGDNASECIADFFERCKTDPGYWDRISNAGLQRIYERYTWQIYSERLMTLAGVYGFWKYVSKLERRETRRYLEMFYALKYRDLVKTVPLAAEEITDGIEEKSTK\*

>PSI00012809

MVAATLTRVLSSRERVQDTLFEHRNEIVSLLSRYVAKGKKILQPHDLLDGLAEVTGENDEGQKLRDGPFGDVLRSTQEAIILPPWVVLAVRPRPGVWDYVRVNVDELAVEQLSVAEYLEFKEHLVNGSDKDNYVLELDLEPFNASFPRPTRPSSIGSGVQFLNRHLSSRLFRDKESMQPLLDFLRAHNYRGQKLMLNERIQSLPRLRSALVKAEEHLHKFPKDTPYTEFEHKLQEMGLEKGWGDNAEHVLGTIHLLLEILQAPDPSNLETFLGRIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALESEMLLRIKQQGLDITPEIIVVTRLIPEAYGTTCNQRIERVSGTQHSRILRVPFRTEKGVLRDWVSRFDVWPYLERFSEDVSNEVTAELKGQPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVLNPKFNIVSPGADMQIYFPYTEKQHRLTALHGSLEELLFNPEQTAEHMCVLNDHKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRGLVNLVVVAGDIDPSKSRDREEVAEIEKMHRLIKEYNLDGQFRWICAQKNRVRNGELYRYICDTKGAFVQPAIYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGDSASERIADFFEKCKTDPSYWIKISNGGLQRIYERYTWKIYAEKLMTLSGVYGFWKYVSKLERLETRRYLEMFYTLKYRDLVKTVPLAVEESANGIEEKSIE\*

>PSY00009688

MVAATLTRALSSRERVQDTLSEHRNEIVSLLSRYVAKGKKVLQPHHLLDGLAEITGENDEGQKLRDGPFGDVLRSTQEAIILPPWVVLAVRPRPGVWDYVRVNVDELAVEQLSVAEYLEFKEHLVNGSDKDNYVLELDLEPFNASFPRPTRPSSIGSGVQFLNRHLSSRLFRDKESMQPLLDFLRAHNYRGQKLMLNERIQSLPKLRSALVKAEEHLHKFPKDAPYAEFEHKLQEMGLEKGWGDNAEHVLSTIHLLLEILQAPDPSNLETFLGRVPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMILRIKQQGLDITPQIIVVTRLIPEAHGTTCNQRIEKVSGTQHSLILRVPFRTEKGVLRNWVSRFDVWPYLEKFSEDVTNEVTAELKGQPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYFPYTEKQHRLTALHSTIEELLFNPEQTAEHMCVLNDPKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDIDPSKSMDREEVAEIEKMHELIKKYNLNGQFRWICAQKNRVRNGELYRYICDTKGAFIQPAIYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGDSASDRIADFFERCKTDPSYWVKISNGGLQRIYERYTWKIYAEKLMTLSGVYGFWKYVSKLERRETRRYLEMFYTLKYRNLVKTVPLAVEESADGESAE\*

>PSY00015731

MVAATLTRVLSSRERVEDTLSEHRNEIVSLLSRYVAKGKKILQPHHLLDGLTEVLGENDELQTLKYGLFGDVLRSTQEAIILPPWIVLAVRPRPGVWDYVRVNVDELAVEQLSVAEYLEFKEHLVDESVKDKYALELDLEPFNESFPRPTRPSSIGSGVQFLNRHLSSRLFHDRESMQPLLDFLRAHSYRGQKLMLNERIQSLSKLRSVLVKAEEHLKKFPKNTPYTEFEYKLQEMGLEKGWGDNAEHVLDMIHLLLETLQAPDPSTLETFLGRIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMLLRIKHQGLDIKPEIIVVTRLIPEAYGTTCNQRIERIGGTQHSRILRVPFRTEKGVLQKWVSRFDVWPYLERFSEDVLNEVTAELKGQPDLIIGNYSDGNLVASLISERQGITQCNIAHALEKTKYPDSDIYWKKYEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYFPYTEKQHRLTALHGSIEELLFNPEQTAEHMCILNDRKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDIDPSKSRDREEVVEIEKMHTLIKEYNLNGQFRWICAQKNRVRNGELYRYICDTRGAFIQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGASASEYIVEFFERCKSDPSCWDKISNAGLQRIYERYTWQIYAEKLMTLSGVYGFWKYVSKLERRETRRYLEMFYTLKYRDLVKTVPLAVEESADGLEEKSAE\*

>PTA00028412

MASSMQRSESITDALPEIVRQNRFLLRKLFPRYAVEGKRILHPQQLIEELAAVIESQDERKKILQGAFGHILECAQEAVVVPPFIGFAIRTKPGIWEYVRVNVENLSTYQLTVAEYLQLKECLVDERWYLVSSVSANAEFEVRMPPWSNDEYALELDFECFNASFPRMRRPSSIGNGIHFLSKHLSSRLFRDGDSMQPLLDYMQEHKYQGQKFMVNESINSLPKLQSALSKAEDILSNLPKDTRYEEFDYGFQNIGLARGWGDNAGRALDMIQSVLKNLEAPDPAILEKFLGKIPTVFSVVIFSPHGYFGQADVLGLPDTGGQVVYILDQVKALEEEMLLRIKQQGLEITPQIIVVTRLIPEAQGTKCNQKIEKILNTQHSQILRVPFRTEKGVLRHWVSRFDVWPYLETFAEDSSKEIIAKLQDKPDLIIGNYSDGNLVASLVSKKLEVTQCNIAHALEKTKYADSDINWKKFDEKYHFSCQFTADILAMNHADFIITSTYQEIAGSKDTVGQYESHAAFTLPGEYRVVSGIDVFNAKFNIVSPGADMSIYFPYTEKQRRLTAFHESIQELLFNPTESTEHIGFFSDRKKPIIFSMARLDRVKNLSGLVEWFGKNERLRKLVNLAVVGGFIDSSKSKDREEIAEIEKMHGLIKKYSLRGNFRWICAQKDRVRNGELYRYIADTKGAFIQPALYEAFGLTVIEAMTCGLPTFATSKGGPAEIIVDGLSGFHIDPNNEDETSDKIANFFERCKREPSYWNKVSDGGLQRIYESYTWKIYAENLINLASVYRFWKYISNREMHQSQRYMEMFYILKYRNLVKNFPTAKEESEAQIIEKGTRPAAEDNKADRRAAGKSGIKRILSACVSTCGMPNCGEDSLLKEKEPT\*

>PTA00049304

MVAATLTRALSSRERVQDTLSEHRNEIVSLLSRYVAQGKKILHPHHLLDGLAEIIGENNEPHKLRDGPFGDVLRSTQEAIILPPWVVLAVRPRPGVWDYVRVNVDELAVEQLSVAEYLEFKEHLVNGSVKDNYVLELDLEPFSASFPRPTRPSSIGSGVQFLNRHLSSRLFRDKESMQPLLDFLRAHNYRGQKLMLNERIQSMPKLRSALVKAEEHLNKFPLNTPYTKFEHKLQEMGLEKGWGDNAEHVLDMIHLLLEILQAPDPSTLETFLGKIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPEIIVVTRLIPEAYDTTCNQRIEKISGTQHSRILRVPFRTEKGVLRNWVSRFDVWPYLERFSEDVSNEITAELKGQADLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDLYWKNFEEKYHFSCQFTADLIAMNTADFIITSTYQEIAGSKGTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMQIYYPYTEKQHRLTTLHRTIEELLFSPEQTAEHMCVLNDRKKPIIFSMARLDRVKNMTGLVEWFAKNKRLRELVNLVVVAGDIDPSNSKDREEVAEIEKMHRLIKEYNLNGQFRWICAQKNRVRNGELYRYICDTRGAFVQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGDYASECIAEFFERCKTDPGYWDKISNAGLQRIYEKYTWKIYSEKLMTLAGVYGFWKYVSKLERRETHRYLEMFYTLKYRDLVKTVPLAVEEIADGTEEKTTA\*

>PTA00057970

MVTAMLNRALSSLERVEDTLSERRNETVSLLSRYISRGKKILQPHQLLDGLAELIGQNDERQNLHFFGLFGDVLKSTQEAIILPPWVVLAVRPRPGVWEYVRVHVDELAVEQLSATKYLEFKEHLVDESFKNNYVLELDLEPFNASFPRPTRPSSIGSGVQFLNRHLSSRLFHGKESMQPLLNFLLAHKYRGQGVGRLQEMGFEKGWGDNVEHVLDMIHLLSEILQAPDPSTLEMFLEKIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPQIIVVTRLIPEAHGTICNQRIERVIGTQHSRILRVPFRTEKGILRNWVSRFDIWPYLERFAEDVSSEVTAELNGQPDLIIGNYSDGNLVASLIANKQGITQCNIAHALEKTKYPNSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVIHGIDVFDPKFNIVSPGADMQIYFPYTEKQRRLTALHDSIEELLFSFEQTTEHMCALNDVKKPIIFSMARLDRVKNITGLVEWFAKNKRLRELVNLVVVAGDIDPLKSRDREEVAEIEKMHRLIKEYNLNGQFRWICAQKNRVQNGELYRYICDTRGAFIQPALYEAFGLTVVEAMTCGLPTFATCNGGPAEIIVDGVSGFHIDPYHGDSASEHIVKFFERCQTDPTHWDKISSAGLQRIYERYTWQIYAKRLMTLSGVYGFWKYVSKLERQETRRYLEMFYILKYRNLVSVVAILDWLKLCHYLLKKVSMGLKIKV\*

>TBA00005121

MVTATLSRVVSMRERVEDTLSEHRNEIVALLSRYVAQGKSILQPHHLLDGLAEVKGESDEHEKLKDGLFGDVLRSTQEAIILPPMVALAVRPRPGVWEYVRVNVDELSVDQLSVSEYLEFKEHLVNGSVKDNYVLELDLEPFNSSFPRPTRPSSIGSGVQFLNRHLSSRLFRDKESMQPLLDFLRQHNFRGQRLMLNERIQNLPKLRAALVKAEEYLHKLPKDAPYAEFEHKFQEMGLEKGWGDNSERVLDMIHLLLENLQAPDPSTLEKFLGRIPMVFNVVILSPHGYFGQANVLGMPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPEILVVTRLIPEAHGTTCDQRIERISGTQHSRILRVPFKTEKGILRQWVSRFDVWPYLETFAEDAYNEITAELQAPPDLIIGNYSDGNLVASLIAHKQGITQCNIAHALEKTKYPDSDIYWKNFEEKYHFSCQFTADLIAMNHADFIITSTYQEIAGSKDTVGQYESHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMRIYFPYTDKQHRLTALHSSIEKLLFSPEQTAEHIGFLKDPKKPIIFSMARLDRVKNMTGLVEWFAKNSRLRDLVNLVVVAGDIDPSKSRDREEIDEIEKMHRLMKEYNLSGQFRWIVAQKNRVRNGELYRYICDTRGAFIQPALYEAFGLTVVEAMTCGLPTFATCKGGPAEIIVDGVSGFHIDPYHGESASEKIADFFERCKTEPSYWDAISNAGLQRIYERYTWQIYADTLVNLAGVYGFWKYVSKLERRETRRYLEMFYILKYRNLVKTVPLAIHEEHVDGVEEKTASAVANNH\*