**S2. All terpene synthase sequences retrieved from different plants species used for phylogenetic analysis**

>OsaTPS01-scaffold8511.g82728.t1

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>OsaTPS02-scaffold943.g31068.t1

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>OsaTPS03-scaffold1616.g42691.t1

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>OsaTPS05-scaffold2018.g48302.t1

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>OsaTPS07-scaffold2421.g53050.t1

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>OsaTPS09-scaffold5167.g73736.t1

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>OsaTPS13-scaffold10009.g84172.t1

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>OsaTPS14-scaffold7925.g81842.t1

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>OsaTPS15-scaffold3188.g60854.t1

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>OsaTPS25-scaffold1263.g37014.t1

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>OsaTPS28-scaffold1797.g45336.t1

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>OsaTPS29-scaffold3344.g62122.t1

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>OsaTPS30-scaffold3344.g62123.t1

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>OsaTPS31-scaffold3957.g66769.t1

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>OsaTPS32-scaffold4479.g70152.t1

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>OsaTPS33-scaffold6266.g77960.t1

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>OsaTPS34-scaffold8396.g82581.t1

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>OsaTPS35-Scaffold3784.g65511.t1

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>OsaTPS36-Scaffold3016.g59254.t1

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>OsaTPS37-Scaffold2041.g48588.t1

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>OsaTPS38-scaffold7905.g81814.t1

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>OsaTPS39-Scaffold3756.g65332.t1

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>OsaTPS40-scaffold543.g21653.t1

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>OsaTPS41-Scaffold702.g25723.t1

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>OsaTPS42-scaffold930.g30815.t1

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>OsaTPS44-scaffold1569.g42016.t1

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>OsaTPS45-scaffold774.g27420.t1

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>OsaTPS47-scaffold774.g27424.t1

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>AB|O81086

MAGVSAVSKVSSLVCDLSSTSGLIRRTANPHPNVWGYDLVHSLKSPYIDSSYRERAEVLVSEIKAMLNPAITGDGESMITPSAYDTAWVARVPAIDGSARPQFPQTVDWILKNQLKDGSWGIQSHFLLSDRLLATLSCVLVLLKWNVGDLQVEQGIEFIKSNLELVKDETDQDSLVTDFEIIFPSLLREAQSLRLGLPYDLPYIHLLQTKRQERLAKLSREEIYAVPSPLLYSLEGIQDIVEWERIMEVQSQDGSFLSSPASTACVFMHTGDAKCLEFLNSVMIKFGNFVPCLYPVDLLERLLIVDNIVRLGIYRHFEKEIKEALDYVYRHWNERGIGWGRLNPIADLETTALGFRLLRLHRYNVSPAIFDNFKDANGKFICSTGQFNKDVASMLNLYRASQLAFPGENILDEAKSFATKYLREALEKSETSSAWNNKQNLSQEIKYALKTSWHASVPRVEAKRYCQVYRPDYARIAKCVYKLPYVNNEKFLELGKLDFNIIQSIHQEEMKNVTSWFRDSGLPLFTFARERPLEFYFLVAAGTYEPQYAKCRFLFTKVACLQTVLDDMYDTYGTLDELKLFTEAVRRWDLSFTENLPDYMKLCYQIYYDIVHEVAWEAEKEQGRELVSFFRKGWEDYLLGYYEEAEWLAAEYVPTLDEYIKNGITSIGQRILLLSGVLIMDGQLLSQEALEKVDYPGRRVLTELNSLISRLADDTKTYKAEKARGELASSIECYMKDHPECTEEEALDHIYSILEPAVKELTREFLKPDDVPFACKKMLFEETRVTMVIFKDGDGFGVSKLEVKDHIKECLIEPLPL

>AGO24474

MALVSISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDDGVQRRIGDYHSNIWDDDFIQSLSTPYGEPSYQERAERLIVEVKKIFNSMYLDDGRLMSSFNDLMQRLWIVDSVERLGIARHFKNEITSALDYVFRYWEENGIGCGRDSIVTDLNSTALGFRTLRLHGYTVSPEVLKAFQDQNGQFVCSPGQTEGEIRSVLNLYRASLIAFPGEKVMEEAEIFSTRYLKEALQKIPVSALSQEIKFVMEYGWHTNLPRLEARNYIDTLEKDTSAWLNKNAGKKLLELAKLEFNIFNSLQQKELQYLLRWWKESDLPKLTFARHRHVEFYTLASCIAIDPKHSAFRLGFAKMCHLVTVLDDIYDTFGTIDELELFTSAIKRWNSSEIEHLPEYMKCVYMVVFETVNELTREAEKTQGRNTLNYVRKAWEAYFDSYMEEAKWISNGYLPMFEEYHENGKVSSAYRVATLQPILTLNAWLPDYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRDRGEEASCISCYMKDNPGSTEEDALNHINAMVNDIIKELNWELLRSNDNIPMLAKKHAFDITRALHHLYIYRDGFSVANKETKKLVMETLLESMLF

>AGO24475

MALVSTAPLASKSCLHKSLISSTHELKALSRTIPALGMSRRGKSITPSISMSSTTVVTDDGVRRRMGDFHSNLWDDDVIQSLPTAYEEKSYLERAEKLIGEVKNMFNSMSLEDGELMSPLNDLIQRLWIVDSLERLGIHRHFKDEIKSALDYVYSYWGENGIGCGRESVVTDLNSTALGLRTLRLHGYPVSSDVFKAFKGQNGQFSCSENIQTDEEIRGVLNLFRASLIAFPGEKIMDEAEIFSTKYLKEALQKIPVSSLSREIGDVLEYGWHTYLPRLEARNYIQVFGQDTENTKSYVKSKKLLELAKLEFNIFQSLQKRELESLVRWWKESGFPEMTFCRHRHVEYYTLASCIAFEPQHSGFRLGFAKTCHLITVLDDMYDTFGTVDELELFTATMKRWDPSSIDCLPEYMKGVYIAVYDTVNEMAREAEEAQGRDTLTYAREAWEAYIDSYMQEARWIATGYLPSFDEYYENGKVSCGHRISALQPILTMDIPFPDHILKEVDFPSKLNDLACAILRLRGDTRCYKADRARGEEASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKKHAFDIARAFHYGYKYRDGYSVANVETKSLVTRTLLESVPL

>AGO64404

MAEISESSIPRRTGNHHGNVWDDDLIHSLNSPYGAPAYYELLQKLIQEIKHLLLTEMEMDDGDHDLIKRLQIVDTLECLGIDRHFEHEIQTAALDYVYRWWNEKGIGEGSRDSFSKDLNATALGFRALRLHRYNVSSGVLKNFKDENGKFFCNFTGEEGRGDKQVRSMLSLLRASEISFPGEKVMEEAKAFTREYLNQVLAGHGDVTDVDQSLLREVKYALEFPWHCSVPRWEARSFLEIYGHNHSWLKSNINQKMLKLAKLDFNILQCKHHKEIQFITRWWRDSGISQLNFYRKRHVEYYSWVVMCIFEPEFSESRIAFAKTAILCTVLDDLYDTHATLHEIKIMTEGVRRWDLSLTDDLPDYIKIAFQFFFNTVNELIVEIVKRQGRDMTTIVKDCWKRYIESYLQEAEWIATGHIPTFNEYIKNGMASSGMCILNLNPLLLLDKLLPDNILEQIHSPSKILDLLELTGRIADDLKDFEDEKERGEMASSLQCYMKENPESTVENALNHIKGILNRSLEEFNWEFMKQDSVPMCCKKFTFNIGRGLQFIYKYRDGLYISDKEVKDQIFKILVHQVPMEE

>AGO64405

MAQISESVSPSTDLKSTESSITSNRHGNMWEDDRIQSLNSPYGAPAYQERSEKLIEEIKLLFLSDMDDSCNDSDRDLIKRLEIVDTVECLGIDRHFQPEIKLALDYVYRCWNERGIGEGSRDSLKKDLNATALGFRALRLHRYNVSSGVLENFRDDNGQFFCGSTVEEEGAEAYNKHVRCMLSLSRASNILFPGEKVMEEAKAFTTNYLKKVLAGREATHVDESLLGEVKYALEFPWHCSVQRWEARSFIEIFGQIDSELKSNLSKKMLELAKLDFNILQCTHQKELQIISRWFADSSIASLNFYRKCYVEFYFWMAAAISEPEFSGSRVAFTKIAILMTMLDDLYDTHGTLDQLKIFTEGVRRWDVSLVEGLPDFMKIAFEFWLKTSNELIAEAVKAQGQDMAAYIRKNAWERYLEAYLQDAEWIATGHVPTFDEYLNNGTPNTGMCVLNLIPLLLMGEHLPIDILEQIFLPSRFHHLIELASRLVDDARDFQAEKDHGDLSCIECYLKDHPESTVEDALNHVNGLLGNCLLEMNWKFLKKQDSVPLSCKKYSFHVLARSIQFMYNQGDGFSISNKVIKDQVQKVLIVPVPI

>AGQ38710

MAMPSSSLSSQIPTAAHHLTANAQSIPHFSTTLNAGSSASKRRSLYLRWGKGSNKIIACVGEGGATSVPYQSAEKNDSLSSSTLVKREFPPGFWKDDLIDSLTSSHKVAASDEKRIETLISEIKNMFRCMGYGETNPSAYDTAWVARIPAVDGSDNPHFPETVEWILQNQLKDGSWGEGFYFLAYDRILATLACIITLTLWRTGETQVQKGIEFFRTQAGKMEDEADSHRPSGFEIVFPAMLKEAKILGLDLPYDLPFLKQIIEKREAKLKRIPTDVLYALPTTLLYSLEGLQEIVDWQKIMKLQSKDGSFLSSPASTAAVFMRTGNKKCLDFLNFVLKKFGNHVPCHYPLDLFERLWAVDTVERLGIDRHFKEEIKEALDYVYSHWDERGIGWARENPVPDIDDTAMGLRILRLHGYNVSSDVLKTFRDENGEFFCFLGQTQRGVTDMLNVNRCSHVSFPGETIMEEAKLCTERYLRNALENVDAFDKWAFKKNIRGEVEYALKYPWHKSMPRLEARSYIENYGPDDVWLGKTVYMMPYISNEKYLELAKLDFNKVQSIHQTELQDLRRWWKSSGFTDLNFTRERVTEIYFSPASFIFEPEFSKCREVYTKTSNFTVILDDLYDAHGSLDDLKLFTESVKRWDLSLVDQMPQQMKICFVGFYNTFNDIAKEGRERQGRDVLGYIQNVWKVQLEAYTKEAEWSEAKYVPSFNEYIENASVSIALGTVVLISALFTGEVLTDEVLSKIDRESRFLQLMGLTGRLVNDTKTYQAERGQGEVASAIQCYMKDHPKISEEEALQHVYSVMENALEELNREFVNNKIPDIYKRLVFETARIMQLFYMQGDGLTLSHDMEIKEHVKNCLFQPVA

>AGQ41594

MAQLSFNAALKMNALGNKAIHDPTNCRAKSERQMMWVCSRSGRTRVKMSRGSGGPGPVVMMSSSTGTSKVVSETSSTIVDDIPRLSANYHGDLWHHNVIQTLETPFRESSTYQERADELVVKIKDMFNALGDGDISPSAYDTAWVARLATISSDGSEKPRFPQALNWVFNNQLQDGSWGIESHFSLCDRLLNTTNSVIALSVWKTGHSQVQQGAEFIAENLRLLNEEDELSPDFQIIFPALLQKAKALGINLPYDLPFIKYLSTTREARLTDVSAAADNIPANMLNALEGLEEVIDWNKIMRFQSKDGSFLSSPASTACVLMNTGDEKCFTFLNNLLDKFGGCVPCMYSIDLLERLSLVDNIEHLGIGRHFKQEIKGALDYVYRHWSERGIGWGRDSLVPDLNTTALGLRTLRMHGYNVSSDVLNNFKDENGRFFSSAGQTHVELRSVVNLFRASDLAFPDERAMDDARKFAEPYLREALATKISTNTKLFKEIEYVVEYPWHMSIPRLEARSYIDSYDDNYVWQRKTLYRMPSLSNSKCLELAKLDFNIVQSLHQEELKLLTRWWKESGMADINFTRHRVAEVYFSSATFEPEYSATRIAFTKIGCLQVLFDDMADIFATLDELKSFTEGVKRWDTSLLHEIPECMQTCFKVWFKLMEEVNNDVVKVQGRDMLAHIRKPWELYFNCYVQEREWLEAGYIPTFEEYLKTYAISVGLGPCTLQPILLMGELVKDDVVEKVHYPSNMFELVSLSWRLTNDTKTYQAEKARGQQASGIACYMKDNPGATEEDAIKHICRVVDRALKEASFEYFKPSNDIPMGCKSFIFNLRLCVQIFYKFIDGYGIANEEIKDYIRKVYIDPIQV

>AGQ948Z0

MALLSITPLVSRSCLSSSHEIKALRRTIPTLGICRPGKSVAHSINMCLTSVASTDSVQRRVGNYHSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLEDGGNDLLQRLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNEKGIGCGRESVVTDLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVLNLFRASLVAFPGEKVMDEAETFSTKYLREALQKIPASSILSLEIRDVLEYGWHTNLPRLEARNYMDVFGQHTKNKNAAEKLLELAKLEFNIFHSLQERELKHVSRWWKDSGSPEMTFCRHRHVEYYALASCIAFEPQHSGFRLGFTKMSHLITVLDDMYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVYMMVYHTVNEMARVAEKAQGRDTLNYARQAWEACFDSYMQEAKWIATGYLPTFEEYLENGKVSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNDLICIILRLRGDTRCYKADRARGEEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVWHHGYRYRDGYSFANVETKSLVMRTVIEPVPL

>AGQ9M7D1

MALVSSAPKSCLHKSLIRSTHHELKPLRRTIPTLGMCRRGKSFTPSVSMSLTTAVSDDGLQRRIGDYHSNLWDDDFIQSLSTPYGEPSYRERAEKLIGEVKEMFNSMPSEDGESMSPLNDLIERLWMVDSVERLGIDRHFKKEIKSALDYVYSYWNEKGIGCGRDSVFPDVNSTASGFRTLRLHGYSVSSEVLKVFQDQNGQFAFSPSTKERDIRTVLNLYRASFIAFPGEKVMEEAEIFSSRYLKEAVQKIPVSSLSQEIDYTLEYGWHTNMPRLETRNYLDVFGHPTSPWLKKKRTQYLDSEKLLELAKLEFNIFHSLQQKELQYLSRWWIHSGLPELTFGRHRHVEYYTLSSCIATEPKHSAFRLGFAKTCHLITVLDDIYDTFGTMDEIELFNEAVRRWNPSEKERLPEYMKEIYMALYEALTDMAREAEKTQGRDTLNYARKAWEVYLDSYTQEAKWIASGYLPTFEEYLENAKVSSGHRAAALTPLLTLDVPLPDDVLKGIDFPSRFNDLASSFLRLRGDTRCYKADRDRGEEASSISCYMKDNPGLTEEDALNHINAMINDIIKELNWELLKPDSNIPMTARKHAYEITRAFHQLYKYRDGFSVATQETKSLVRRTVLEPVPL

>ObQ15GI4

MEENGMKSKILIFGGTGYIGNHMVKGSLKLGHPTYVFTRPNSSKTTLLDEFQSLGAIIVKGELDEHEKLVELMKKVDVVISALAFPQILDQFKILEAIKVAGNIKRFLPSDFGVEEDRINALPPFEALIERKRMIRRAIEEANIPYTYVSANCFASYFINYLLRPYDPKDEITVYGTGEAKFAMNYEQDIGLYTIKVATDPRALNRVVIYRPSTNIITQLELISRWEKKIGKKFKKIHVPEEEIVALTKELPEPENIPIAILHCLFIDGATMSYDFKENDVEASTLYPELKFTTIDELLDIFVHDPPPPASAAF

>ObQ2KNL6

MAKSPETEHPVKALGWAATDNSGTFSPFNFSRRATGERDVQFRVLYCGVCHSDLHMVKNEWGVTHYPIVPGHEIVGIVTEVGSKVEKVKIGDKVGVGVLVGSCRQCDQCSNDLENYCYKQILTYGAPYLDGTIARGGYSDIMVADEHFIIRWPENFPLDAGAPLLCAGITTYSPLKYFGLDKPGLRVGVNGLGGLGHVAVKFAKAFGTKVTVISTSLSKKEEAMQHLGVDEFVVSTDPQQMQAAVGTLDGIIDTVSAPHPIVPLLSLLKPHGKLIVVGLPDKPLQLPVFPLIQGRRTIAGSGIGGLKETQEMIDFAAKNNIVADVEVIPIDYINTAMDRLLKSDVKYRFVIDVEKSLKPQ

>ObQ5SBP0

MSTFVISNSMHVGISFSFLHKLPQTPPPQVVCCSGGLRLRPSCSLQLQPPPTTRRSGNYEPSAWDFNYLQSLNNYHHKEERYLRRQADLIEKVKMILKEEKMEALQQLELIDDLRNLGLSYCFDDQINHILTTIYNQHSCFHYHEAATSEEANLYFTALGFRLLREHGFKVSQEVFDRFKNEKGTDFRPDLVDDTQGLLQLYEASFLLREGEDTLEFARQFATKFLQKKVEEKMIEEENLLSWTLHSLELPLHWRIQRLEAKWFLDAYASRPDMNPIIFELAKLEFNIAQALQQEELKDLSRWWNDTGIAEKLPFARDRIVESHYWAIGTLEPYQYRYQRSLIAKIIALTTVVDDVYDVYGTLDELQLFTDAIRRWDIESINQLPSYMQLCYLAIYNFVSELAYDIFRDKGFNSLPYLHKSWLDLVEAYFQEAKWYHSGYTPSLEQYLNIAQISVASPAILSQIYFTMAGSIDKPVIESMYKYRHILNLSGILLRLPDDLGTASDELGRGDLAKAMQCYMKERNVSEEEARDHVRFLNREVSKQMNPARAADDCPFTDDFVVAAANLGRVADFMYVEGDGLGLQYPAIHQHMAELLFHPYA

>ObQ5SBP1

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>ObQ5SBP2

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>ObQ5SBP3

MSCARITVTLPYRSAKTSIQRGITHCPALLRPRFSACTPLASAVPLSSTPLINGDNSPLKNTHQHVEERSSKRREYLLEETARKLQRNDTESVEKLKLIDNIQRLGIGYYFEDAIDAVLRSPFSAEEEEDLFTAALRFRLLRHNGIQVTPEIFLKFKDERGEFDESDTLGLLSLYEASNLGVTGEEILEEAMEFAEPRLRRSLSELAAPLRSEVAQALDVPRHLRMARLEARRFIEQYGKQSDHDGDLLELAILDYNQVQAQHQSELTEITRWWKQLGLVEKLGFGRDRALECFMWTMGILPHPKYSSSRIESAKAAALLYVIDDIFDTYGKMDELILFTDAIRRWDLEAMEGLPEYMKICYMALYNTTNEICYRVLKDTGRIALPYLKSVWIETIEAYMVEVKWFSGGSAPKLEEYIENGASTVGAYMVLVHLFFLIGEGLTHQNVLFFKQKPYHKPFSAAGRIFRLWDDLGTSQEEEERGDMASSIRLFMKEYKLSTVEEARSCVLEEISRLWKDLNEGLISIKDALPLTIVKVALNIARTSQVVYKHEQHTYMLSVDNYVEALFFTPLLSS

>ObQ5SBP4

MESRRSANYQASIWDDNFIQSLASPYAGEKYAEKAEKLKTEVKTMIDQTRDELKQLELIDNLQRLGICHHFQDLTKKILQKIYGEERNGDHQHYKEKGLHFTALRFRILRQDGYHVPQDVFSSFMNKAGDFEESLSKDTKGLVSLYEASYLSMEGETILDMAKDFSSHHLHKMVEDATDKRVANQIIHSLEMPLHRRVQKLEAIWFIQFYECGSDANPTLVELAKLDFNMVQATYQEELKRLSRWYEETGLQEKLSFARHRLAEAFLWSMGIIPEGHFGYGRMHLMKIGAYITLLDDIYDVYGTLEELQVLTEIIERWDINLLDQLPEYMQIFFLYMFNSTNELAYEILRDQGINVISNLKGLWVELSQCYFKEATWFHNGYTPTTEEYLNVACISASGPVILFSGYFTTTNPINKHELQSLERHAHSLSMILRLADDLGTSSDEMKRGDVPKAIQCFMNDTGCCEEEARQHVKRLIDAEWKKMNKDILMEKPFKNFCPTAMNLGRISMSFYEHGDGYGGPHSDTKKKMVSLFVQPMNITI

>ObQ5SBP5

MDVSILRDVRPPVTSYAPNIWADTFSNISLDEEVQKKYAETIEALKQVVRGMLMAAATPIKQMIFIDTLERLGLAYHFETEIEHKLQKIYDDNVCGDDCDLFTTALRFRLLRQHRHHVSCDVFDKFLYEEGKFKGDAEGLLSLYEASHVRFHNEKILEEAERFTRQELSCWIKLQSPLKDKVKRALERPLHREVPILYARHFISIYEKDESMDEHLLKLAKFNFNFLQNLYKKELYDLSRWWNKFDLKTKLPYIRDRLAEAYLWGVGYHFEPQYSYVRKGVVLSIKIIGILDDTYDNYATVNEAQLFTEILDRWSMDEIDRLPDYMKIVLHFVMSAYEEYERDAKIVYGKKFASPYFKETIQQLARGYNQELKWVMEKQMPPFKDYLKNSEITSCIYIMFASIIPGLKSFTQEAIDWIKNEPNFAVKAGLIGRYWDDIGSHKRESKGGEMLTVMDCYMKQYSVSIQETISEFAKAVEDSWKEVNEGWVYTISMSKEITVQFLNYSRMCDASYNRNNGDGYTDPSFAKSNITALFVDPIII

>ObQ5SBP6

MTNMFASAAPISTNNTTVEDMRRSVTYHPSVWKDHFLDYASGITEVEMEQLQKQKERIKTLLAQTLDDFVLKIELIDAIQRLGVGYHFEKEINHSLRQIYDTFQISSKDNDIRVVALRFRLLRQHGYPVPSDVFKKFIDNQGRLDESVMNNVEGMLSLYEASNYGMEGEDILDKALEISTSHLEPLASRSRRINEALEMPISKTLVRLGARKFISIYEEDESRDEDLLKFAKLDFNILQKIHQEELTHIARWWKELDLGNKLPFARDRVVECYFWILGVYFEPQYNIARRFMTKVIAMTSIIDDIYDVHGTLEELQRFTDAIRSWDIRAIDELPPYMRLCYEALLGMYAEMENEMVKQNQSYRIEYARQEMIKLVTTYMEEAKWCYSKYIPNMDEYMKLALVSGAYMMLATTSLVGILGDPITKQDFDWITNEPPILRAASVICRLMDDVVGHGIEQKISSVDCYMKENGCSKMEAVGEFSKRVKKAWKNLNEEWVEPRAASMVILVRVVNLARVINLLYVGEDSYGNSSVKTKELIKGVLVHPIK

>ObQ5SBP7

MSANCVSAAPTSPKNSDVEEIRKSATYHSSVWGNHFLSYTSDVTEITAAEKEQLEKLKEKVKNLLAQTPDESTGKMELIDAIQRLGVGYHFTTEIQESLRQIHEGQIRNDDDDVRVVALRFRLLRQGGYRAPCDVFEKFMDDGGNFKESLKKDVEGMLSLYEASYYGIDGEEIMDKALEFSSSHLESMLHNISTKTNKSLLRRLQEALDTPISKAAIRLGATKFISTYREDESHNEDILNFAKLDFNILQKMHQEEANYLTRWWEDLDLASKLDFARDRMVESYFWSLGVYFQPQYRTSRIYLTKIISIVAVIDDIYDVYGSFDDLRSFTDVIQSWKISNADELPPYMRICFEALLGIYEDMGDRIGAPYAIDTMKELVDTYMQEAEWCYTEYVPTVDEYMKVALVTGGYLMVATTFLTGINNITKKDFDWIRNRPRLLQVAEVLTRLMDDIAGHGTEKKTTAVSCYMKEYECSEMEASRELSKQVKKAWKDLNDEWMEPRSSSAEIIGCIVNMSRVLHIMYSTGDDGFSDSSTRTTQAVKTLLVDHPMN

>ObQ6USK1

MSCARITVTLPYRSAKTSIQRGITHYPALIRPRFSACTPLASAMPLSSTPLINGDNSQRKNTRQHMEESSSKRREYLLEETTRKLQRNDTESVEKLKLIDNIQQLGIGYYFEDAINAVLRSPFSTGEEDLFTAALRFRLLRHNGIEISPEIFLKFKDERGKFDESDTLGLLSLYEASNLGVAGEEILEEAMEFAEARLRRSLSEPAAPLHGEVAQALDVPRHLRMARLEARRFIEQYGKQSDHDGDLLELAILDYNQVQAQHQSELTEIIRWWKELGLVDKLSFGRDRPLECFLWTVGLLPEPKYSSVRIELAKAISILLVIDDIFDTYGEMDDLILFTDAIRRWDLEAMEGLPEYMKICYMALYNTTNEVCYKVLRDTGRIVLLNLKSTWIDMIEGFMEEAKWFNGGSAPKLEEYIENGVSTAGAYMAFAHIFFLIGEGVTHQNSQLFTQKPYPKVFSAAGRILRLWDDLGTAKEEQERGDLASCVQLFMKEKSLTEEEARSRILEEIKGLWRDLNGELVYNKNLPLSIIKVALNMARASQVVYKHDQDTYFSSVDNYVDALFFTQ

>ObQ93WU2

MALQKVDISLSTEQLLQAQVHVWNHMYAFANSMSLKCAIQLGIPDILHKHGRPMTLSQLLQSIPINKEKTQCFQRLMRALVNSNFFIEENNSNNQEVCYWLTPASCLLLKEAPLTVTPLVQVVLDPTFTNPWHHMSEWFTHEKHATQFEAANGCTFWEKLANEPSKGRFFDEAMSCDSRLIAHVFTKDYKHVIEGIRTLVDVGGGNGTMAKAIVEAMPTIKCTVIDLPHVVAGLESTDNLNYIGGDMFQSIPSADAILLKSIIHDWDDVEGLKILKKCKDAVVMGGKVIIIDVVVGVNHDIDEVLEDQLHFDMAMMCYFNAKERTMSEWEKLIYDAGFKSYKLTPAFGVRSLIEAYP

>PFQ9AXM7

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>MLQ9SW76|

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>NTG3CCC0

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**Pseudogenes sequences:**

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>Sb04g001780

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>Sb04g001800

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>Sb04g001810

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>Sb05g006470

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>Sb05g019210

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>Sb05g022320

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>Sb06g002820

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>Sb06g028210

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>Sb06g028220

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>Sb06g031270

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>Sb07g003080

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>Sb07g004470

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>Sb07g004480

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>Sb07g004485

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>Sb07g005130

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>Sb07g020980

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>Sb07g025700

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>Sb09g000990

SDYDLGTVALWFCLLRKHRYRVSSDVFVRFKDEKGGFLVDSPQDLLNLYNAAHMRTHGEVILEKAILFSQRRLETMIPYMEGSLLAEIKSALEIPLPRRVRIYELKYYISTYEKDATVHEKVWQLAKLNSNIMQLHHQHELGIITSWDSKGAHDLPECMKFALEKIFDSYETIENMLHQEEKYRMAYLRYFVKDLVRSYSKEVKMLQEGYIPKSVEEHLKVSVITTTCPFLSCASFVGMHDIATKDFFDWVSSVPKMVQELSVILRLVDDLGSYEREQLIPHVASTINSYMKEHNVSIEVARGQIQVLKEKSWKDFNSEWLAYPKQLLERIFNFTRTMEFIY

>SollyTPS10

MASSSSTNKSRPLANFHPTVWGYHFLSYTPQFTEITNQEKVEVNEYKERIRKMLVKAPEGSLQKLVLIDAMQRLGVAYHFDNEIETSIQNIFDASSKQNDNDNNLYVVSLRFRLVRQQGHYMSSDVFKQFINQDGKFKETLTNDVQGLLSLYEASHLRVRDEEILEEALTFTTTHLESIIVSNLSNNNNSLKVEVSEALTQPIRKTLPRVGARKYISIYENNVAHNHVLLKFAKLDFNVLQKLHQRELNELTRWWKDLDFANKIPYARDRLVECYFWILGVYFEPKYSRARKMMTKVLKITSVIDDTFDAYATYDELVAFTDAIQRWDASAIDSISPYMRPLYQALLDIYSEMEQVLSNEGKLDRVYYGKHEIKKIVRAYFKEAQWLNDANYIPKYEEHMEISLVTAGYMMGATNCLVGVEEFISKDTFEWLKNEPLIVRAASLISRAMDDIVGHEDEQKRGHVASIIECYMKEYGASKQEAYAKFKKEVTNVWKDINKEFFRPTEVPMFVLERALNFARVIDTLYQEVDGYTNSKGLLKDLVNSLLIESVKISIS

>SollyTPS12

MASSSANKCRPLANFHPTVWGYHFLSYTHEITNQEKVEVDEYKETIRKMLVEAPEGSEQKLVLIDAMQRLGVAYHFDNEIETSIQNIFDASSKQNDNDNNLYVVSLRFRLVRQQGHYMSSDVFKQFINQDGKFKETLTNDVQGLLSLYEASHLRVRDEEILEEALTFTTTHLESTVSNLSNNNSLKAEVTEAFSQPIRMTLPRVGARKYISIYENNDAHNHLLLKFAKLDFNMLQKLHQRELSDLTRWWKDLDFANKYPYARDRLVECYFWILGVYFEPKYSRARKMMTKVIQMASFFDDTFDAYATFDELEPFNNAIQRWDINAIDSVPPYLRHAYQALLDIYSEMEQALAKEFKSDRVYYAKYEMKKLVRAYFKEAQWLNNDNHIPKYEEHMENAMVSAGYMMGATTCLVGVEEFISKETFEWMINEPLIVRASSLIARAMDDIVGHEVEQQREHGASLIECYMKDYGVSKQEAYVKFQKEVTNGWMDINREFFCPDVEVPKFVLERVLNFTRVINTLYKEKDEYTNSKGKFKNMIISLLVESVEI

>SollyTPS14

MATNLTLETDKEIKNMNQLSMIDTTITRPLANYHSSVWKNYFLSYTPQLTEISSQEKLELEELKEKVRQMLVETSDKSTQKLVLIDTIQRLGVAYHFDNEIKISIQNIFDEFEQNKNEDDNDLYIVALRFRLVRGQRHYMSSDVFKKFTNDDGKFKETLTKDVQGLLNLYEATHLRVHGEQILEEALSFTVTHLKSMSPKLDSSLKAQVSEALIQPIYTNVPRVVAPKYIRIYENIESHDDLLLKFVKLDFHILQKMHQRELSELTRWWKDLDHSNKYPYARDKLVECYFWATGVYFGPQYKRARRMITKLIVIITITDDLYDAYATYDELVPYTNAVERCEISAMDSISPYMRPLYQVFLDYFDEMEEELTKDGKAHYVYYAKVEMNKLIKSYLKEAEWLKNDIIPKCEEYKRNATITVANQMILITCLIVAGEFISKETFEWMINESLIAPASSLINRLKDDIIGHEHEQQREHGASFVECYVKEYRASKQEAYVEARRQIANAWKDINTDYLHATQVPTFVLQPALNLSRLVDILQEDDFTDSQNFLKDTIKLLFVDSVNSTSCG

>SollyTPS16

MELCTQTVPADHEVEITRRVGSHHPTVWGDHFLAYANLSGASEEEEKQHEDLKEEVRKMLVMAPSNALEKLELINTIQCLGVAYHFEHEIESYMCTHYEEYWIDDLHAIALCFRLLRQQGYRVSCDAYKKFTDDQGNFKIELINDVHGMLSLYEAAQFRVHGEEILDEALNFTTTQLKLILPKLSNSPLAQQVANALKFPIKDGIVRVEARKYISFYQQNQNHNQLLLNFAKLDFNILQMLHKKELCDITRWWKELEIVKTLPYVRDRLAEVYFWSLGVYFEPQYSTARKILTKNISMISLIDDTYDIYGTLDELTLFTEAIERWNIDASQQLQLPSYMKIIYCGLLDVYDEIKKDLANENKSFLINYSIIEMKKMVMAYFQEAKWYYGKTIPKMEEYMKSGISTSAYVQVATTSWLGMGNVATKDSFDWIVNEPPILVASSIIARLLNDLLSHEEEQKRGDAPSGVECYMKEYGVTKEEAHIKIRNTIENSWKDLYEEYFKVNGTIIPRVLLMCIINLARVIEFIYKDEDAYTFPKNNLKDVIYRILIDPII

>SollyTPS17

MELCTQTVAADHEVIITRRSGSHHPTLWGDHFLAYADLRGANEGEEKQNEDLKEEVRKMLVMAPSKSLEKLELINTIQCLGLGYHFQSEIDESLSYMYTHYEEYSIGDLHAIALCFRLLRQQGYYVSCDAFKKFTNDQGNFKEELVKDVEGMLSLYEAAQFRVHGEQILDEALNFTIAQLKQILPKLSNSQLAQQITNALKYPIKDGIVRVETRKYISFYQQNQNHNEVLLNFAKLDFNILQTLHKKELSDMTRWWKKMELVNTLPYARDRLVECYFWCLGTYFEPQYSVARKMLTKISFYISIIDDTYDIYGKLDELTLFTQAIERWNIDASEQLPLYMKIIYRDLLDVYDEIEKELANENKSFLVNYSINEMKKVVRGYFQEAKWYYGKKVPTMEQYMKNGISTSAYILLTTTSWLAMGNVATKDAFDWVATEPPIVVASCYIIRLLNDLVSHEEEQKRGNAASAVECYMNEYSVTKEEAHIKIRDIIENYWKDLNEEYFKVDMIIIPRVLLMCIINLTRVAEFIYKDEDAYTFSKNNLKDVISDILVDPII

>SollyTPS18

MIIGYRINFRPLSHDKLRSHVMWQRQCSYNTASSMDGFEEAKERIRESFSKVELSPSSYDTAWVAMVPSKYSLNEPCFPQCLDWIIENQREDGSWGLNPTHPLLLKDSLSSTLACLLALTKWRVGDEQIKRGLGFIETQSWAIDNKDQISPLGFEIIFPSMIKSAEKLNLNLAMNKIDSTIKRALQNEFTRNIEYMGEGVGELCDWKEIIKLHQRQNGSLFDSPATTAAALIYHQHDQKCYEYINSILQQHKNWVPTMYPTKIHSLLCLVDTLQNLGVHRHFKSEIKKALEEIYRLWQQKNEEIFSNVTHCAMAFRLLRMSYYNVSSDELAEFVDEEHFFSTSGKFISDVAIIELHKASQLTINEKDDILDKINNWTGIFMQQKLLNNDFLDIKSKKEVELALRMFYVTYDRAENRRYIESYQENNFKMLKTAYRCGSMNNIDLLTFSMQEFELGLSQYQEEVEQLKRWYEDYRLEQVGLAQEYIYRTHLISVAVFFEHELSNARIMYAKYAMFLTLSDDLFEHLASKDELLNIIELVQRWDEHTNVGFHSEKVKLFFTALYDTIEEVATNAQIKQGRNVKHHIIELFVEGLNSMLVDRVEWGTRIPSIEEYLRVSLSTFGGKCMVLTSQYVVGIHLCNYQSDDEIQDLCYCSGIVMRLLNDLQSFKRERSDSRLVNMVKLVMKQRSGTICEEEEEEAIKHIKETIECNRRKLLRMVLQSKGKGSKVPQALKDLFWRTTKAVYFFYSDHDEFRSPNKVKHHINQVIYKPLHNR

>SollyTPS19

MIVGYRSTIITLSHPKLGNGKTISSNAIFQRSCRVRCSHSTTSSMNGFEDARDRIRESFGKLELSPSSYDTAWVAMVPSRHSLNEPCFPQCLDWIIENQREDGSWGLNPTHPLLLKDSLSSTLACLLALTKWRVGDEQIKRGLGFIETYGWAVDNKDQISPLGFEVIFSSMIKSAEKLDLNLPLNLHLVNLVKCKRDSTIKRNVEYMGEGVGELCDWKEMIKLHQRQNGSLFDSPATTAAALIYHQHDQKCYQYLNSIFQQHKNWVPTMYPTKVHSLLCLVDTLQNLGVHRHFKSEIKKALDEIYRLWQQKNEQIFSNVTHCAMAFRLLRMSYYDVSSDELAEFVDEEHFFATNGKYTSHVEILELHKASQLAIDHEKDDILDKINNWTRAFMEQKLLNNGFIDRMSKKEVELALRKFYTTSHLAENRRYIKSYEENNFKILKAAYRSPDINNKDLLAFSIHDYELCQAQHREELQQLKRWFEDYRLDQLGLGERYIHASYLFGVTIIPEPELSDARLMNAKYAMLLTIVDDHFESFASKDECLNIIELVERWDDYASVGYKSEKVKIFFSTFYKSIEELATIAEIKQGRSVKNHLINLWLEMMKLMLMEQVEWCSGKTIPSIEEYLYVTSITFCAKLIPLTTQYFLGIKISKDLLESDEICGLWNCSGRVMRILNDLQDSKKEQKEGSITLVTLLMKSMSEEEAVMKTKEILEMNRRELLKMVLVQKKGSQLPQLCKDIFWRSSKWAHFTYSQTDGYRIPEEMKNHIDEVFYKPLNH

>SollyTPS20

MIVGYRSTIITLSHPKLGNGKTISSNAIFQRSCRVRCSHSTTSSMNGFEDARDRIRESFGKLELSPSSYDTAWVAMVPSRHSLNEPCFPQCLDWIIENQREDGSWGLNPTHPLLLKDSLSSTLACLLALTKWRVGDEQIKRGLGFIETYGWAVDNKDQISPLGFEVIFSSMIKSAEKLDLNLPLNLHLVNLVKCKRDSTIKRNVEYMGEGVGELCDWKEMIKLHQRQNGSLFDSPATTAAALIYHQHDQKCYQYLNSIFQQHKNWVPTMYPTKVHSLLCLVDTLQNLGVHRHFKSEIKKALDEIYRLWQQKNEQIFSNVTHCAMAFRLLRMSYYDVSSDELAEFVDEEHFFATNGKYKSHVEILELHKASQLAIDHEKDDILDKINNWTRAFMEQKLLNNGFIDRMSKKEVELALRKFYTTSHLAENRRYIKSYEENNFKILKAAYRSPNINNKDLLAFSIHDFELCQAQHREELQQLKRWFEDYRLDQLGLAERYIHASYLFGVTVIPEPELSDARLMYAKYVMLLTIVDDHFESFASKDECFNIIELVERWDDYASVGYKSEKVKVFFSVFYKSIEELATIAEIKQGRSVKNHLINLWLELMKLMLMERVEWCSGKTIPSIEEYLYVTSITFCAKLIPLSTQYFLGIKISKDLLESDEICGLWNCSGRVMRILNDLQDSKREQKEVSINLVTLLMKSMSEEEAIMKIKEILEMNRRELLKMVLVQKKGSQLPQLCKDIFWRTSKWAHFTYSQTDGYRIAEEMKNHIDEVFYKPLNH

>SollyTPS21

MLIGCRSKIIIISHHKLGNGKTISSNAIFQRSCRARCSHSTTSSMNGFEDARDRIRESFGKLELSPSSYDTAWVAMVPSRHSLNEPCFPQCLDWIIENQREDGSWGLNPTHPLLLKDSLSSTLACLLALTKWRVGDEQIKRGLGFIETYGCAVDNKDQISPLGFEVIFSSMIKFAEKLNLNLPLNLHLVNLVNCKKDSTIKRNDEYMGEGVGELCDWKEIIKLHQRQNGSLFDSPATTAAALIYHQRDQKCYEYLNSILQQHKNWVPTMYPTMIHSLLCLVDTLQNLGVHRHFKSEIKKALDEIYRLWQQKNEEIFSNITHCAMAFRLLRMSNYDVSSDELAEFMDEEHFFTTSGKYTSHVEILELHKASQLAIDQEKDDILDKINNWTRTFMEQKLLNNGFIDRMSKKEVELALRKFYTTYDRAENRRYIKSYEENNFKILKAAYRSPNINNKDLLIFSIHDFDLCQTQHREELQQLKRWFQDCRLDQLGLSEQFISTTYLIGIAVVSEPEFSNARLMYAKYVMLLTIVDDLFDGFASKDELLNIIQLVERWDDYASVGYNSERVKVFFSVFYKSIEELATIAEIKQGRSVKNHLINLWLEVMKMMLIERIEWWTSKTIPSIEEYLYVTSITFGSRLIPLTTQYFLGIKISKDLLESDEIYGLCNCTGIVMRLLNDLQTYKREQGESSMNLVTILMTQSPRRTNICEEEAIMKIKEILEMNRRELLKMVLVQKKGSQLPQLCKDIFWRTSKMVYFTYSHGDEYRFPEEMKNHIDEVIYKPLNH

>SollyTPS24

MSATIIFPAASSSSSYLSVVKHQMIRDITIPSRRLGGGLSFTQHSSSTAACVVDATRGPDFALQCNETTKERIRKLFHKVEFSVSSYDTAWVAMVPSPHSAKVPCFPECLHWVLHNQLEDGSWGLPHHQPLLLKDVLSSTLACVLALKRWGIGEQLISNGLRFIELNFASATDEDQYSPIGFDVIFPGMLEYAQHLSLKLHLESGVFNELLHKRAIQLTRPYDSSSLELNAYLAYVSEGIGELQDWKMVMKYQRKNGSLFNSPSTTAASLIHLHDSGCLDYLRGALKKFGNAVPTIYPINIHASLCMVDDLKKLGICRHFSEEIQNVLDETYRCWLQGEDEIFTSAGTCSMAFRILRGYGYNVSSDPVAQFLEQEQYSGHLNDIHTMLDLYQALEMIIATDKPVSMKLNSSSLQSLIQRLSDEFYPPNGLTKQIREQVDDVLKFPSHANIKRVANRRNIKHYDVDNTRVLKTSYSSSNFGNKDFLTLAVEDFNLCQSIHRNELKQLERWLTQNRLDKLKFVRERSAYCYFSAAATIFQPELSDARMSWAKNGVLTTVIDDFFDVGGSMEELNNLILLFKKWDVDVSTDCCSERVGIIFSALHSTISEIGDKASKWQARSVTRHITDIWLNLLNAMLREAEWAKDMSVPSLDKYMANGYVSFALGPIFLPALYFVGPKLPDDVVQHPEYHSLFELVSTCGRLLNDIRSFERESKDGKLNAVTLSVTHGNGRISEEAAIEGLSHRVEMQRKELLKLVLQREGSVVPNACKDLFWEMSKVLHQFYIKDDGFSSMGMADTVNAIIHEPITLNYLGDSKLITDYN

>SollyTPS25

MACINMVSIASTMQTQKLHSTTEKDSQPERISTYKPNIWKYDHLLSLTNQYSEAKYKIEAEKLKEEVGCMFSNTTSPVAQLQLIDGIDKLGLSAYFEVDTKETLENIILYMKTSSTSKDLYATALCFRLLREHGYHASQDMLKDLFDGKGKLPLDMKTSLELFEGSHLSIDGENLLNDIRLFSTKNLKNLSLDVDRLTSNPLAWRVRWYDVRKHIITAQNCNDTNPMLLKLAKLNFNIIQATHQKDLKDVIRWWRNVSIIENLEFTRERIVESFFFAVGIASEGEHGSMRKWLAKVIQLILIIDDVYDIYGTLADVQQFTVAIEKWDPEEVQRLPKSIQICFGALHDTMEDISVEIQRQKGGPSVLPHLKQVWVNFCKALLVEATWYHKGHIPTLEDYLHNGWTSSSGPLLSLHVILGLTNENLHLCKNCQEIIYYTSLIIRLCNDQGTSTVELERGDVASSIICYMHQENVSEDVAREHIESIILNSWEKTNYHFNRLSTSHRKIMKHVINEARMAHVMYLSGDGFGVQDGETQDQVLINLFRPLGRNPGHHFGRLYRPNFIVMGLGPVIFEVPI

>SollyTPS27

MTSEQQSVFCNQIHSTTSFRKSNIDETLIQRRNANYKPNIWKYDILQSLKSQYSECKYKKEAQKLKEEFLWVVAEIENPLAKLELIDSINKMALSHLFDKEIMVFLQNMEKLKDSDNEMDLYSTALYFRIFRQYGYNVTQDVFLSYMDEMGEKINVDTNMDPKTMMQLFEASHLALKDENMLDEARIFCTNNLKNIIPMEMPLHWKVEWYNTREHISKQANEKEEGVSKLKLLQLAKLNFNMVQAEHQKDLVHILRWWRNLGLIENVSFSRDRIVESFLWSVGVAFEPQHSNFRNWLTKAITFIIVIDDVYDIYGTLQNLQLFTDAVVRWDPKVVEQLPSCMQICFWKLYDTTNDVALEIQQQKGCKFPVLTYLQKVWAEFCKALLVEAKWDSKGYTPTFSEYLENGWKSSGGTVLSLHVLLGLAQDFSQVDYFLENERDLIYYSSLIIRLGNDLGTSTAELERGDVSSSILCYMRKENVKEDVARKHIEEMVIETWKKMNRHCFENSSPLIKYIMNIARVTHFIYQNGDGFGVQDRETRQQILSSLVQSLPLN

>SollyTPS28

MSLLEGNVNHENGIFRPEANFSPSMWGNIFRDSSKDNQISEEVVEEIEALKEVVKHMIISTTSNAIEQKIHLIDTLERLGIYYHFEKEIEDQLSKMFDQNLIHEEDDLYKVALYFRLFRQHGYPISSDCFNQFKDTKGKFKKTLLIDVKGMLSLYEAAHVREHGDDILEEALIFATFHLERITPNSLDSTLEKQVGHALMQSLHRGIPRAEAHFNISIYEECGSSNEKLLRLAKLDYNLVQVLHKEELSELTKWWKDLDFASKLSYVRDRMVECFFWTVGVYFEPQYSRARVMLAKCIAMISVIDDTYDSYGTLDELIIFTEVVDRWDISEVDRLPNYMKPIYISLLYLFNEYEREINEQDRFNGVNYVKEAMKEIVRSYYIEAEWFIEGKIPSFEEYLNNALVTGTYYLLAPASLLGMESTSKRTFDWMMKKPKILVASAIIGRVIDDIATYKIEKEKGQLVTGIECYMQENNLSVEKASAQLSEIAESAWKDLNKECIKTTTSNIPNEILMRVVNLTRLIDVVYKNNQDGYSNPKNNVKSVIEALLVNPINM

>SollyTPS3

MSIFSTRYLVTPFSSFSPPKAFVSKACSLSTGQPLNYSPNISTNIISSSNGIINPIRRSGNYEPTMWNYEYIQSTHNHHVGEKYMKRFNELKAEMKKHLMMMLHEESQELEKLELIDNLQRLGVSYHFKDEIIQILRSIHDQSSSEATSANSLYYTALKFRILRQHGFYISQDILNDFKDEQGHFKQSLCKDTKGLLQLYEASFLSTKSETSTLLESANTFAMSHLKNYLNGGDEENNWMVKLVRHALEVPLHCMMLRVETRWYIDIYENIPNANPLLIELAKLDFNFVQAMHQQELRNLSRWWKKSMLAEKLPFARDRIVEAFQWITGMIFESQENEFCRIMLTKVTAMATVIDDIYDVYGTLDELEIFTHAIQRMEIKAMDELPHYMKLCYLALFNTSSEIAYQVLKEQGINIMPYLTKSWADLSKSYLQEARWYYSGYTPSLDEYMENAWISVGSLVMVVNAFFLVTNPITKEVLEYLFSNKYPDIIRWPATIIRLTDDLATSSNEMKRGDVPKSIQCYMKENGASEEEARKHINLMIKETWKMINTAQHDNSLFCEKFMGCAVNIARTGQTIYQHGDGHGIQNYKIQNRISKLFFEPITISMP

>SollyTPS31

MAPAAALMSKCQEEEEIVRPVADFSPSLWGDRFHSFSLDNQVAEKYVEEIETLKEQTRSMLMSGKTLAEKLNLIDIVERLGIAYHFEKQIDDMLNHIFNIDPNFEAHEYNDLCTLSLQFRILRQHGYYISPKIFSRFQDANGKFKESLCDDIRGILNLYEASHVRTHGEDTLEEALAFSTAHLESAAPHLKSPLSKQVTHALEQSLHKSIPRVETRYFISIYEEEELKNDVFLRFAKLDFNLLQMLHKQELSEVSRWWKDLDFVTTLPYARDRAVECYFWTMGVYAEPQYSQARVMLAKTIAMISIVDDTFDAYGIVKELEVYTDAIQRWDVSQIDRLPEYMKISYKALLDLYNDYETELSNDGRSDVVQYAKERMKEIVRNYFVEAKWFIEGYMPPVSEYLSNALATSTYYLLTTTSYLGMKSATKKDFEWLAKNPKILEANVTLCRVIDDIATYEVEKGRGQIATGIECYMRDYGVSTQVAMDKFQEMAETAWKDVNEGILRPTPVSAKILTRILNLARIIDVTYKHNQDGYTHPEKVLKPHIIALLVDSIEI

>SollyTPS32

MALLNNQDEIVRPVANFSPSLWGDRFHSFSLDNQVADKYAQQIETLKEQTRSLLSDAACGTTLAEKLNLIDIVERLGLAYHFEKQIEDMLDQIYKADPNFEAHDLNTLSLQFRILRQHGYNISQKIFSRFQDANGKFKESLSNDIKGLLNLYEASHVRTHGEDILEEALAFSTAHLESAAPHLKSPLSKQVTHALEQSLHKSIPRVETRYFISIYEEEEFKNDVLLRFAKLDYNLLQMLHKQELSEVSRWWKDLDFVTTLPYARDRAVECYFWTMGVYAEPQYSQARVMLAKTIAMISIVDDTFDAYGIVKELEVYTDAIQRWDISQMDRLPEYMKVSFKALLDLYEDYEKELSKDGRSDVVQYAKERMKEIVRNYFVEAKWFIEGYMPPVSEYLSNALATSTYYLLTTTSYLGVKSATKEDFEWLAKNPKILEANVTLCRVVDDIATYEVEKGRGQIATGIECYMRDYGVSTQVAMDKFQEMAEIAWKDVNEGILRPTPVSTEILTRILNLARIIDVTYKHNQDGYTHPEKVLKPHIIALLVDSIEI

>SollyTPS33

MASAAALMSNCQDIVRPVADFSPSLWGDRFHYFSLDNQVAEEYAQEIETLKEQTRSLLSDAACGTTLAEKLNLIDIVERLGLAYHFETQIEDMLDQIYKSDPNFEAHDLNTLSLQFRILRQHGYNISPKIFCRFQDANGKFKESLSNDIKGLLNLYEASHVRTHGEDILEEALAFSTAHLESAAPHLKSPLSKQVTHALEQSLHKSIPRVETRYFISIYEEEEQKNDVLLRFAKLDFNLLQMLHKQELSEVSRWWKDLDFVTTLPYARDRAVECYFWTMGVYAEPQYSQARVMLAKTIAMISIVDDTFDAYGIVEELEVYTDAIQRWDISQIDRLPDYMKISYKALLDLYDDYETELSKDGRSDVVHYAKERMKEIVRNYFVEAKWFIEGYMPPVSEYLSNALATSTYYLLTTTSYLGVKSATKEDFEWLAKNPKILEANVTLCRVIDDIATYEVEKGRGQIATGIECYMRDYGVSTQVAMEKFQEMAEIAWKDVNEGILRPTPVSTEILTRILNLARIIDVTYKHNQDGYTHPEKVLKPHIIALLVDSVEI

>SollyTPS35

MASAAALVSNYREEEIVRPVADFSPSLWGDRFHSFSLDNKIAGKYAQEIETLKEQSRVILSASSGTTLAQKLDLIDIVERLGLAYHFEKQIDDVLDQIYKADPNSEAQEYNDLQTSSIQFRLLRQHGYNISPKLFSRFQDAKGKFNESLSNDIKGLLNLYEASHVRTHGEDILEEALAFSTAHLESAAPHLKSPLSKQVTHALEQSLHKSIPRVETRYFISIYEEEEQKNDLLLRFAKLDFNLLQMLHKQELSEVSRWWKDLDFVTTLPYARDRAVECYFWTMGVYAEPQYSQARVMLAKTIAMISIVDDTFDAYGIVKELEVYTDAIQRWDISHIDRLPDYMKISYKALLDLYDDYETELSKDGRSDVVHYAKERMKEIVRNYFVEAKWFIEGYMPPVSEYLCNALATSTYYLLTTTSYLGVKSANKEDFEWLAKNPKILEANVTLCRVIDDIATYDVEKGRGQIATGIECYMRDYGVSTEEAMEKFEEMAEIAWKDVNEGILRPTPVSTEILTRILNLARIIDVTYKHNQDGYTHPEKVLKPHIIALLVDSIEI

>SollyTPS36

MSGAMATFSVFPHSLINFNIWRYTCEPKVHSLKRKLMSPLLAMDVNSSRHLANFHSNIWGYHFLSYTSQLTEITTQEKLEVDELKEKVMNMLMEIRDDNSTQKLVLIDAIQRLGVAYHFHNEIETSIQNIFDASKQNDNDNNLYVVSLRFRLVRQQGHYISSDVFKQFMERDGKFKKTLNNDVQALLSLYEAAQIRVRGEDILEEALTFTTTHLESMIPLLSDNPLKAQIIEALTHPIHKVIPRLGARKYIDIYENMESHNHLLLKFSKLDFNMLQKQHQRELSELTSWWKDLDLASKVPYARDKLVEGYTWTLGVYFEPQYSRARRMLVKVFKMLSICDDTYDAYATFDELVLFTNAIQRWDINAMDSLPPYMRPFYQAILDIFDELEEELTKEGKSDRVYYGKFEMKKLARAYFKEAQWLNAGYIPNCDEYIKNAIVSTTFMALGTTSLIGMEEFITKDIFEWITNEPSILRASSTICRLMDDISDHESDQQRGHVASVIECYTKEYGASKQEAYVKFRKEVKDAWKGINKALLRPIEVPIFVLQRILNLARTMDTFFQDEEDGYTNSNSKCKDIVTLLLVDSVTIGRS

>SollyTPS37

MANITKAFSPLPLYLCQIGSKRSSIKVSCRSSNRWNFQEDLLKKTSYLQTSYNRDGFNSTKFGLLVKDVKYALRTQINNNNNLVLVDTLQRMGIEHHFQQEIQSILQKEYEQNTCFLKYQNHHDISLCFRLLRQEGYHVSADVFKKLKNNDDGTFGLNLNQDVNGLIGLYEASQLGVEGEYILDEIAKFSGDHLNACLANSDEARIIKETLKYPYHKSLSRWKNKSFINNFKGINGWGKNTLKELANMDYFITKEIHQHELAQVFRWWKSLGLAEELKLLRDQPLKWYTWPMAMLTDPKMSQERIELAKCISFVYVIDDIFDVYGTIEELTLFTQAVHRWELSAMMDLPEYMRSLYKALYNTINSIGYNIYKIYGQNPTQNLQNTWAHLCSAFLIEAKWFACGMVPTTDEYLKNGLVSSGVYVALIHLFYILGLGVSSMHLQDISLMSTSIAKILRLWDDLGSAKDENQEGKDGSYVEYYMKENKDSSMELAREHVIKLIEDEWKQLNKEHFCLMSQSTRSFSKASLNSARMVSLMYSYDDKQSLPILQEYIKSMLDGNL

>SollyTPS38

MLQSCISTMDIRRSGNYKPSIWEDGYVQSRPNLYAEEKYCERAEKLKEEVRKMLQKRMTNSLEQLELVDILQRLGIYYHFEEEIDTVLKQIYVNYNKRDHHNEELYDTALEFRLLRQHGYHLPQEIFCSFMNEEGKFKTALVEDTKGLLSLYEASYLCMEDENIMENARDFATHYLMENVKKKMDEQVSHALEMPVHWRMERLEARWFIEIYHKKENMNPLLLELAKLDYNMVQATYLEELKQMSRWDKNMKLVKKMSFVRDRLVEGFFWAVGFTPNPQFGYCRKLSTKLSVLLTTIDDIYDVYGTLDELELFTDIVDRWDINAIEQLPEYMKISFLALFNSMNELAYDILKEQGFSIISHIRKQWANLCKAYLLEVKWYQRGYTPSLDEFLRNAWITNTGPVLIMHAYFCITNPIKEDELQRLNHYPAIIYSPSLILRLANDLATSPDEIKKGDYLKSIQCYMHDSKSCEENARNYIKKLIDETWKKMNRDILRDESLSKDFRRTSMNLARIAQCMYQHGDGFGIPDRETKDRILSLFFQPIPLT

>SollyTPS39

MEMTKVLISPSQYLSMHIISGNIIQNERSIQVSCKSSNKWAVQEDLLRATSTYNQDGFDSTKFGLLMKDVKYALRTQINNNNNLVLVDTLQRMGIEHHFQQEIQSILQKEYEQNTCFLKYQNHHDISLCFRLLRQEGYHVSADVFKKLKNNDDGTFGLNLNQDVNGLIGLYEASQLGVEGEYILDEIAKFSGDHLNACLVNSDEARIIKETLKYPYHKSLSRWKAKSFINNFKGINGWGKSTLQELANMDYSITKEIHQHELIQVSRWWSSLGLAEDLKLLRDQPLKWYTWPMTMLTDPKMSQQRIELAKCISFVYVVDDIFDVYGTIEELTLFTQAVNRWELCVMKDLPEYMRATYKALYDTINSIGYNIYKIYGQNPTQNLRNAWANLCNAFLKEAKWFASGELPTTDEYLKNGLVSSGVHVVLVHMFYLLGFGLNNQNSIYLEDSSAMASSVATILRLWDDLGSAKDENQEGNDGSYIECYMKGQKNASIELAREYVVKLIEDEWKQLNKKHFNLMNGSLGSYSKASLNLARMVPLMYNYDDKQSLHVLQEYINTMLYDV

>SollyTPS4

MKAILLNNIGVLSSRPPRATCLFSINGGKPSSLIVVSKASSPNPTTIRRSGNYKPTMWDFQFIQSVNNLYAGDKYMERFDEVKKEMKKNLMMMVEGLIEELDVKLELIDNLERLGVSYHFKNEIMQILKSVHQQITCRDNSLYSTALKFRLLRQHGFHISQDIFNDFKDMNGNVKQSICNDTKGLLELYEASFLSTECETTLKNFTEAHLKNYVYINHSCGDQYNNIMMELVVHALELPRHWMMPRLETRWYISIYERMPNANPLLLELAKLDFNIVQATHQQDLKSLSRWWKNMCLAEKLSFSRNRLVENLFWAVGTNFEPQHSYFRRLITKIIVFVGIIDDIYDVYGKLDELELFTLAVQRWDTKAMEDLPYYMQVCYLALINTTNDVAYEVLRKHNINVLPYLTKSWTDLCKSYLQEARWYYNGYKPSLEEYMDNGWISIAVPMVLAHALFLVTDPITKEALESLTNYPDIIRCSATIFRLNDDLGTSSDELKRGDVPKSIQCYMNEKGVSEEEAREHIRFLIKETWKFMNTAHHKEKSLFCETFVEIAKNIATTAHCMYLKGDSHGIQNTDVKNSISNILFHPIII

>SollyTPS40

MSISASFLRFSLTAHYQPSPSSSPPNQPFKFLKSNREHVEFNRILQCHAVSRRRTKDYKEVQSGSLPVIKWDDIAEEVDVETHTLEVYDPSSNEDHIDAIRSMLGSMGDGEISVSAYDTAWVAMVKDVKGTETPQFPSSLEWIANNQLADGSWGDNSIFLVYDRVINTLACVIALKSWNLHPDKILLGMSFMRENLSRIGDENAEHMPIGFEVAFPSLIEIAKKLGLDFPYDSPVLQDIYASRQLKLTRIPKDIMHKVPTTLLHSLEGMTDLDWQKLLQFQCTDGSFLFSPSSTAYALMQTQDHNCLNYLKNAVHKFNGGVPNVYPVDLFEHIWTVDRLQRLGISRYFELEIKECIDYVSRYWTNKGICWARNSPVQDIDDTAMAFRLLRLHGYAVSADVFKHFESKGEFFCFVGQSNQAVTGMYNLYRASHVMFSGEKILENAKIFTSNYLREKRAQNQLLDKWIITKDLPGEVGYALDVPWYASLPRLETRFFLEHYGGEDDVWIGKTLYRMPLVNNSLYLELAKSDYNNCQALHQFEWRRIRKWYYECGLGEFGLSEKRLLVTYYLGSASIFEAQRSTERMAWVKTAALMDCVRSCFGSPQVSAAAFLCEFAHYSSTALNSRYNTEDRLVGVILGTLNHLSLSALLTHGRDIHHYLRHAWENWLLTVGEGEGEGEGGAELIIRTLNLCSVHWISEEILLSHPTYQKLLEITNRVSHRLRLYKGHSEKQVGMLTFSEEIEGDMQQLAELVLSHSDASELDANIKDTFLTVAKSFYYSAYCDDRTINFHIAKVLFERVV

>SollyTPS41

MRNLREEIKNMLSSMGDGRSSVSPYDTAWVSFIEDTNTNINGTSKRPLFPSCLQWIIDNQLDDGSWGEELVFCIYDRLLNTLACVVALTLWNTCLHKRNKGVMFIKENLRKLEGGEVVNMTSGFEFVFPSLLDKAQQLHIDNIPYDAPVFRDIYARREVKFTRFPKDLIHTIPTIVLFSLEGLRDLDWQRLLKLQMEDGSFLTSPSSTAIVFMNTNDDKCFTFLQNAVQKFNGGVPCSYPADIQARLWAIDRLQRLGISYYFEEEIKDLLEYVFRYWDKENGFFSARNSNICEVDTTCMAIRLLRLHGFDVSPDVLHKFKDGDEFFCLRGESNKSATVMFNLYRCSQALFPGEIICEEAKNFTYNFLHQYLANNQSKDKWVIAKDIPGEIRYALEFQWYASLPRVESRLYIDQYGGADEIWISKTLYRMPDVSNNVYLEAAKLDYNRCQSQHRFEWLIMQEWFEKGNFQKFGISKKEVLVSFFLAASSIFEVEKSRQRLAWAKSCILCKMITSYINQEATTWNSFLMEFKNYRDMSIKKSNETKEIIVLNNLCQFLHQLTKETYQDLGKDIHHQLHNVWEEWLEENNTTCQEAAVLLVQTINLSSGHMTHDEILSKYTNKVCHMLNEFQNDQICNSSKARDIELHMQALVKLVFSNTSSNNINQGIEDTYFKVVKTFYYTAHVSEETINNHISKVLFQKA

>SollyTPS5

MVSILSNIGMMVVTFKRPSLFTSLRRRSANNIIITKHSHPISTTRRSGNYKPTMWDFQFIQSLHNPYEGDKYMKRLNKLKKEVKKMMMTVEGSHDEELEKLELIDNLERLGVSYHFKDEIMQIMRSINININIAPPDSLYTTALKFRLLRQHGFHISQDILNDFKDENGNLKQSICKDTKDILNSSKDEHDNLKQSTCNNTKGLLKLYEASFLSIENESFLRNTTKSTLAHLMRYVDQNRCGEEDNMIVELVVHALELPRHWMVPRLETRWYISIYERMSNANPLLLELAKLDFNIVQATHQQDLRILSRWWKNTGLAEKLPFSRDILVENMFWAVGALFEPQHSYFRRLITKVIVFISIIDDIYDVYGTLDELELFTLAIQRWDTKAMEQLPDYMKVCYLALINIINEVAYEVLKNHDINVLPYLTKSWADLCKSYLQEAKWYHNGYKPNLEEYMDNARISIGVPMVLVHSLFLVTNQITKEALDSLTNYPDIIRWSATIFRLNDDLGTSSDELKRGDVSKSIQCYMNEKGASEEEAIEHIEFLIQETWEAMNTAQSKNSPLSETFIEVAKNITKASHFMYLHSDVKSSISKILFEPIIISNVAFALK

>SollyTPS7

MVSIFSNAGMMMVTFNRPSFTCFSSLHHYSISARGAINNISTPISATRRSGNYKPTMWDFQFIQSLHNPYEGDKYMKRLNELKKEVKKMMMTVEGSHDEELEKLELIDNLERLGVSYHFKDEIMQILRSINININIAPPDSLYTTSLKFRLLRQHGFHISQDVLKDFKDENGNLKQSICKDTKGMLELYEASFLSTETENTLKSATRFTMSHLKNYVDNHSCGNQDDDIIVELVVHALELPRHWMMPKLETEWYIRIYGRMPNANPLLLELAKLDFNIVQAAHQQDLKILSRWWKSMSLAEKLSFSRDRLVEDFFWSVGLAFEPQHSLCRRMLAKNVAFIIVIDDIYDVYGSLDELEIFTHAVERWDIKAMEQLPDYMKICYLSLFNTTNEMAYHILKQQGINVLPYLTKQWTDLCKSYLQEAKWYHNGHKPRLEEYMDNAWISIATPLVLLHAFIFLTNPITQEALESLNNYPDIIRRCAIINRFVDDLGTSSDELKRGDVPKSIQCYMNDTGASEEEAREHINLLIKEMWEVMNKDQISKQVLFSEEFIKIVFNFSRTSHCVYQHGDGHGIQNSHITNRISKLLFEPLII

>SollyTPS8

MYKLEMTMSISKSNLISKLEVPKSCISNVPIRRSGNYQPSIWDYNHIQSLKNHYSDEKFMRRRNELKMEVKIMLSDRNMKQLEQLEIIDNLQRLGLSYHFEDEIYSILNNLSDKGSKRDHLYAKALEFRLLRQHGFNIVSQETFGGFYDNTTGFGEIHHNEDTKGMLYLYEASFLAIEGEKELELARNLTEEHLREYLADQNKNDVDQNLVELVHHALELPLHWRMLRLETKWFINYYKKRQDKMIPFLLELATLDFNIVQAAHIEDLKYVARWWKETCLAENLPFARDRLVENFFWTIGVNFLPQYGYFRRIATKVNALVTTIDDVYDVFGTLDELQIFTHAIERWSIDELDRLPDNMKMCYYALDNFINQLADDAFEEQGIFISPYLRNSWRDLCKSYLREAKWYHSQYIPSMEEYMDNAWISISAPVILVHAYFLVANPVNKEALHYLENNYHDIIRCSALILRLANDLGTSSDELKRGDVPKSIQCYMNETQASEEEARQYIRLLISQTWKKLNEAHWLAADPFPKIFVTCAMNLARMAQCMYQHGDGHGGNNSTTKNHIMALLFESVPLGHKHSSAEKEDHSMVNYREKFMI

>SollyTPS9

MAASSADKCRPLANFHPSVWGYHFLSYTHEITNQEKVEVDEYKETIRKMLVETCDNSTQKLVLIDAMQRLGVAYHFDNEIETSIQNIFDASSKQNDNDNNLYVVSLRFRLVRQQGHYMSSDVFKQFTNQDGKFKETLTNDVQGLLSLYEASHLRVRNEEILEEALTFTTTHLESIVSNLSNNNNSLKVEVGEALTQPIRMTLPRMGARKYISIYENNDAHHHLLLKFAKLDFNMLQKFHQRELSDLTRWWKDLDFANKYPYARDRLVECYFWILGVYFEPKYSRARKMMTKVLNLTSIIDDTFDAYATFDELVTFNDAIQRWDANAIDSIQPYMRPAYQALLDIYSEMEQVLSKEGKLDRVYYAKNEMKKLVRAYFKETQWLNDCDHIPKYEEQVENAIVSAGYMMISTTCLVGIEEFISHETFEWLMNESVIVRASALIARAMNDIVGHEDEQERGHVASLIECYMKDYGASKQETYIKFLKEVTNAWKDINKQFFRPTEVPMFVLERVLNLTRVADTLYKEKDTYTNAKGKLKNMINSILIESVKI

>Vv01000402001

MAYHTLKEQGHNILPYLTKAWADLCKVFLVEAKWAHKEYIPTFEEYLENGWRSASGVAILIHAYFLMSKNITKEALECLENDHELLRWPSTILRLCNDLATSKAELERGESANSISCYMHQTGVSEESAREHMKILTGESWKKMNKVPDPFSKPFMEIFNLARISECTY

>Vv01000410001

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>Vv01000414001

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>Vv01001153001

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>Vv1007468001

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>Vv01001155001

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>Vv01005217001

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>Vv01005218001

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>Vv01005221001

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>Vv01005268001

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>Vv01005271001

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>Vv01005272001

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>Vv01006399001

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>Vv01006465001

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>Vv01006466001

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>Vv01006467001

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>Vv01006642001

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>Vv01013515001

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>Vv01013517001

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>Vv01013518001

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>Vv01014174001

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>Vv01014175001

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>Vv01014323001

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>Vv01014324001

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>Vv01014557001

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>Vv01014558001

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>Vv01014566001

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>Vv01014569001

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>Vv01030646001

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>Vv01030647001

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>Vv01033458001

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>Vv01036308001

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>Vv01036315001

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>Vv01036317001

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>Vv01036320001

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>Vv01036322001

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>Vv01036330001

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>Vv01036343001

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>Vv01036344001

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>Vv01036348001

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>Vv01036351001

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>Vv01036360001

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>Vv01036361001

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>Vv01036366001

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>Vv01036367001

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>Vv01036370001

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>Vv01036372001

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>Vv01036374001

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>Vv01036376001

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>Vv01036724001

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>Vv1002718001

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>Vv1007468001

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>AT1G31950

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>AT1G33750

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>AT1G48800

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>AT1G48820

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>AT1G61120

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>AT1G61680

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>AT1G66020

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>AT1G70080

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>AT1G79460

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>AT2G23230

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>AT2G24210

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>AT3G14490

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>AT3G14520

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>AT3G14540

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>AT3G25810

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>AT3G25820

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>AT3G25830

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>AT3G29110

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>AT3G29190

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>AT3G29410

CLISDEDDLETIAIMFEVFRLYGHKMPCDVFERFKSEDGKFKESLVGDVRGLLQLYEAAHLGAPSEDIMDEALSFARYHLEPLAGTETSSNLFKHVENVLYRARYHSIEILVARQYISFYDQEEDQDETLLRFSKLNFNFCQMHYVKELKIVTRWWKELGIASKLPYSIRERNVETYLGGLGVLFEPRYSLARIFLAKLTLIMTVVDDTCDAYATLPEVQSLHDAFHRWDLRAMEELPRYMRIIYQSVFETVEDIDREMIARGKHGRLQLTIDEIKSLMIWYLGIAKWARSDQVPSFEDYMEIGTPSSALDDFASYGFIAMDDCDQKQLKEWFYSKPKIFHALNALFRIRNDIVTFEQEMSRGEVANGVNCYMKQHGVTKEAAVEELRKMERESYKIMIEEFMAMPRQILVRPVNIARVMDLFY

>AT3G32030

MIIAEEDDLETISIMFEVFRLYQHKMSCDSFVRFKGEDGRLKESLVGDVRGMLQLYQAAHLGTPSDQYIMEEAKSFTRNHLESLVESTTIPPHFSSHIRDALYIDRYHNMEILVARKYISFYEQEEGHDLTLLKFGKLSFNYCRLHYIQELKTLTKWWKDQDIPSNLPCVRDRIVETYFPTLGLYFEPRFSLGRIIIAKMTIIVVALNDVCDSYATYPEAKSLIDSLQRWDIEAIDELPNYSRIVLRLILETIGEIEREMKPRGRSASVQHTIDETKSLGRAYLALSKWASEGYMPTFDEYMEVGEVTGGMDDFALYSFIAMEDCDEKPLYEWFDSKPKILQALSVLYRINNDIVTYEREMSKGEVVNGVNSYMNQHGVTKEEAVEELRKMARDNYKIVMEELLDVPRPVLVRCLNLARLFDVFC

>AT4G02780

ARCSHVQDIDDTAMAFRLLRQHGYQVSADVFKNFEKEGEFFCFVGQSNQAVTGMFNLYRASQLAFPREEILKNAKEFSYNYLLEKRERELIDKWIIMKDLPGEIGFALEIPWYASLPRVETRFYIDQYGGENDVWIGKTLYRMPYVNNNGYLELAKQDYNNCQAQHQLEWDIFQKWYEENRLSEWGVRRSELLECYYLAAATIFESERSHERMVWAKSSVLVKAISSSFSSDSSFDQFHEYIANARRSDHNDRNDRPVQASRLAGVLIGTLNQMSFDLFMSHGRDVNNLLYLSWGDWMEKWKLYGDEGEGELMVKMIILMKNNDLTNFFTHTHFVRLAEIINRICLPRQYKARRNDEKEKTIKSMEKEMGKMVELALSESDTFRDVFLDVAKAFYYF

>AT4G13280

DITGDEKDLSTISIMFRVFRTYGHNLPSSVFKRFTGDDGKFQQSLTEDAKGILSLYEAAHLGTTTDYILDEALKFTSSHLKSLLAGGTCRPHILRLIRNTLYLPQRWNMEAVIAREYISFYEQEEDHDKMLLRLAKLNFKLLQLHYIKELKSFIKWWMELGLTSKWPSQFRERIVEAWLAGLMMYFEPQFSGGRVIAAKFNYLLTILDDACDHYFSIHELTRLVACVERWSPDGIDTLEDISRSVFKLMLDVFDDIGKGVRSEGSSYHLKEMLEELNTLVRANLDLVKWARGIQTAGKEAYEWVRSRPRLIKSLAAKGRLMDDITDFDSDMSNGFAANAINYYMKQFVTKEEAILECQRMIVDINKTINEELLSVPGRVLKQALNFGRLLELLY

>AT4G13300

DITGDENDLSTISIMFRVFRTYGHNLPSSVFKRFTGDDGKFERSLTEDAKGILSLYEAAHLGTTTDYILDEALEFTSSHLKSLLVGGMCRPHILRLIRNTLYLPQRWNMEAVIAREYISFYEQEEDHDKMLLRLAKLNFKLLQLHYIKELKTFIKWWMELGLTSKWPSQFRERIVEAWLAGLMMYFEPQFSGGRVIAAKFNYLLTILDDACDHYFSIPELTRLVDCVERWNHDGIHTLEDISRIIFKLALDVFDDIGRGVRSKGCSYYLKEMLEELKILVRANLDLVKWARGNQLPSFEEHVEVGGIALTTYATLMYSFVGMGEAVGKEAYEWVRSRPRLIKSLAAKGRLMDDITDFESDMSNGFAANAINYYMKQFVTKEEAILECQKMVVDINKIVNEELLTVPRRVLKQALNFGRLLEVLY

>AT4G15870

EMIAGEDDLYTISIMFWVFRTYGYNMSTDVFKRFKGENEKFMESITSDVKGMVSLYEAAHLRTTREDILEEALSFTTRNLESLARAGASSPHILMRIRNALCMPQHYNAEMIFAREYISFYEQEEDHNKMLLRFAKINFKFLQLNWIQELKTLTKWWKQQDLASKLPPYFRDRLIECYLFAIMIYFEPQFSLGRVSLAKINTVFTLVDDTCDRYGNVSEVAALVQCVERWDPDCMDSLPDYMKTVFKFAWNTFEECENAGIMEEGLSYDVQGALEEWEQGDVVPTFDEYLEIGGVEVTMYVSIACSFLGLGSSREQAYKWLKSRPKFVEAQAKRARLMNDIAGFEGDMSRGFDVNAIMYYMKQYKVTEEETFTRLQKMARDLDTTVNEEILSVPRQILKRAIDFGKMIEFTY

>AT4G16730

EIERETQDLHATSLEFILLRQHGFDVSQDAFDVFISETGEFRKTLHSDIKGLLSLYEASYFSMDSEFKLKETRIYANKRLSEFVAESKTICREDETYILEMVKRALETPYHWSIRRLEARWYINVYEKKHEMNPLLLEFAAIDFNMLQANHQEELKLISSWWNSTGLMKQLDFVRDRITESYFWTIGIFYEPEFKYCRKILTKIFMLIVIMDDIYDIYGTLEELELFTNVVEKWDVNHVERLPNYMRMCFLFLYNEINQIGYDVLRDKGLNVIPYLKQVWTDLFKTFLTESKWYKTGHKPSFEEYMQNGVISSSVPTILLHLFSVLSDHISDQTLTDDSKNHSVVRSCATILRLANDLATSTEEMARGDSPKSVQCYMYETRASEEEARRHMQSMISDSWDIINSDLKSLPRGFLAAAANLNRVVQCIY

>AT4G16740

IDRNRWGDLYATALEFRLLRQHGFSIAQDVFDGNIGVDLDDKDIKGILSLYEASYLSTRIDTKLKESIYYTTKRLRKFVEVNKNETKSYTLRRMVIHALEMPYHRRVGRLEARWYIEVYGERHDMNPILLELAKLDFNFVQAIHQDELKSLSSWWSKTGLTKHLDFVRDRITEGYFSSVGVMYEPEFAYHRQMLTKVFMLITTIDDIYDIYGTLEELQLFTTIVEKWDVNRLEELPNYMKLCFLCLVNEINQIGYFVLRDKGFNVIPYLKESWADMCTTFLKEAKWYKSGYKPNFEEYMQNGWISSSVPTILLHLFCLLSDQTLDILGSYNHSVVRSSATILRLANDLATSSEELARGDTMKSVQCHMHETGASEAESRAYIQGIIGVAWDDLNMESCRLHQGFLEAAANLGRVAQCVY

>AT4G20200

KMMDGEDDLYTVSIIFWVFRRHGYHISYGVFQRFKGSNGNFKESLTRDAKGMLSLYEAANLGTTKDFILEEALSFTSSHLESLAASGTCPPHLSVRIRNALGLSQHWNMEMLVPVEFIPFYEQEIEHDEMLLKFAKLSFKLGQLQYLQELKTLTKWYKELDFATNLPPYFRDRIVEHHFLVQAVFFSPQLSRERIMMIQYFTGLALLDDTFDRYASLHEAESLANSLERWAPDQAMDQPDYLRFVLNFILDTFEEFKRELGPEERSYSVNATIEEFKAAAKANIDLEKWAQADHIPSFEEYMEVGEVEVTVYASLAGIFMSMGMATKEAFEWLKSRPKLVQYLSIKGRLMNDLMGYEDDMSRGYVTNAVNCYMKQYGVTKEEAFRELYKIVVAANKTLNEEFLGVPHFLLKATIDLARMMTVAY

>AT4G20210

EMMAGEDNLYTISIIFLVLRTYGHHMSSDIFQKFKGNDGNFKGCISGDAKGLLALYEAAQLRTTTEYIMEEALSFTSSNLELLAADGRCPPHLSKHIRNALGLSQHKQMEVLVAVEYISFYEQEKDHDKILLKFAKLNFKLMQLHYLEELKVVTKWYKEHDFASNLPPYFKYVIVENHFFAITMYFEPKFSQKRIMLAKYFTVLVLLDDTCDRYASLSEAESLTNSLERWAPDDAMDQPHYLKFVFKFIMGCFEEFERELASEGRSYSVKATLEEFKTIVKANFDFAKLAHTGHVPSFKEYMEVGEVEVGVCATLAGNLMCIGHIGDEGVYEWLKSRPKFLKAASTYGRLMNDIAGFEDDMKREYVITGVNTYMKQYGLTKMEAIRELQNLVEYNHTIMNEEFLDLPRQIRKQVINVARSLNVSY

>AT4G20230

KIMAGEEDLYTVSIIFWVFRRYGHYISSDVFQRFKGSNGSFKESLIGDAKGMLSLYEAAHLATTKDYILDEALIFTSSHLETLVATGTCPPHLLARIRNALSICQHWNFEVLVPLDFIPFYEQEKDHDEMLLKFAKLSFKYLKLIYLQDLKILTKWYKKLDFPSKFPPYFKDRCVENYFFVLPVFFEPQLSSARMLLTKGFILLGIQDDTFDRYASISEAESLGNSLKRWAPDHSMDQPEYLKSVLKVILDTFQEFEKELSPEGRSYSVKYTIEEFQASSKANVELAKWAQVSHVPSFEKYMEVGQMEITACVTVAYILMSMGKTGTKEAFEWLKSRPKLVQSLCTKGRLMNDIAGFEDDMSRGYVVNAVNCYMKQYGVTEKEAFKELRKMVVNTHKTLNEEFLCVSHYVLRETMDFARMIIVTY

>AT5G23960

MVRQEGCDLYTVGIIFQVFRQFGFKLSADVFEKFKDENGKFKGHLVTDAYGMLSLYEAAQWGTHGEDIIDEALAFSRSHLEEISSRSSPHLAIRIKNALKHPYHKGISRIETRQYISYYEEEESCDPTLLEFAKIDFNLLQILHREELACVTRWHHEMEFKSKVTYTRHRITEAYLWSLGTYFEPQYSQARVITTMALILFTALDDMYDAYGTMEELELFTDAMDEWLPVVPDEIPDSMKFIYNVTVEFYDKLDEELEKEGRSGCGFHLKKSLQKTANGYMQEAKWLKKDYIATFDEYKENAILSSGYYALIAMTFVRMTDVAKLDAFEWLSSHPKIRVASEIISRFTDDISSYEFEHKREHVATGIDCYMQQFGVSKERAVEVMGNIVSDAWKDLNQELMVFPFPLLMRVLNLSRVIDVFY

>AT5G44630

DLIADENKLHTISTIFRVFRTYGYYMSSDVFKIFKGDDGKFKESLIEDVKGMLSFYEAVHFGTTTDHILDEALSFTLNHLESLATGRRASPPHISKLIQNALHIPQHRNIQALVAREYISFYEHEEDHDETLLKLAKLNFKFLQLHYFQELKTITMWWTKLDHTSNLPPNFRERTVETWFAALMMYFEPQFSLGRIMSAKLYLVITFLDDACDTYGSISEVESLADCLERWDPDYMENLQGHMKTAFKFVMYLFKEYEEILRSQGRSFVLEKMIEEFKIIARKNLELVKWARGGHVPSFDEYIESGGAEIGTYATIACSIMGLGEIGKKEAFEWLISRPKLVRILGAKTRLMDDIADFEEDMEKGYTANALNYYMNEHGVTKEEASRELEKMNGDMNKIVNEECLTMPRRILMQSVNYARSLDVLY

>AT5G48110

DMNLGEEDMYSISVIFRVFRLYRHKLSSDVFNRFKEENGDFKKCLLDDKKSLTKQWASRGNTWNYFVGGSNEEHLSGHIKNVLYLSQQENAEVVMSREYIQFYEQETHHDETLLKFAKINFKFMQLHYVQELQTIVKWWKELDLESKIPNYYRVRAVECLYWAMAVYMEPQYSVARIILSKSLVLWTIIDDLYDAYCTLPEAIAFTENMERWETDAIDMPDHMKVLLRSLIDLMEDFKGEVRSEGRLYSVEYGIDEWKRLFRADLTISKWARTGYIPNYDEYMEVGIVTGGVDVTVAFAFIGMGEAGKEAFDWIRSRPKFIQTIDLKSRLRDDVATYKDEMARGEIATGINCYMKQYKVTEEEAFLEFHRRIKHTSKLVNEEYFTVPLKLVRIAFNVGRVIDTNY

>EglobTPS002

MSARFSVIPSSSLPQETGCVEGRRSANFHPSIWGDYFLKYASDSACGKLGIAYHFELEIDKELEQIHRGYFEFHCDDNDNDLDTVALLFQLLRQRGYHVSCEIFNKFKDGDGNFGKSLIADVQGLLSLFEACHMRYHGDDNLEDALDLSVCCRWWKGLDVQKKFPFARDRLWWLGEYYEPEHEAAREILTKLISVTSIIDDIYDVYGTWEELELFTRWDVNAKDGLPEYMQECYKIVLDLYDEIGYEFSQKGRSYRLFYAKEVVSHLMILAWSFLGMGDIVTKDVFDWLLFNDPKKASSIIGRLLNDIAGHQFEQERGHVASAVECFMKQYRVTEEEAKEELRKQVTDAWKDINEELRGPTVVPMPILVRILNLTQALHMMYK

>EglobTPS003

EERIERLKGEVGKMLTSAMYKPAEKLNLIDQIQRLGISYHFELEIDKELEQIRKGYFEYHYDDNDNDLDTVALLFRLLRQRGYRVSCEIFNKFKDGDGNFGKSLIADVQGLLSLFEACHLRYHGDDNLEDALAFTTTHLESIDKRKASLHLEKKVSHALNQPIHKGMSRLEARHYIPLYQEEPSHNEVLLSLAKLDFNLVQEQHRKELGNLTRRWWKGLDVQRKFPFARDRLVEMYVWWLGEYYEPEHEAAREILTKLSSVGSIIDDIYDVYGTWEELELFTEAIERYRWDVDAKDGLPEYMQECYKIVLDLYDEIGYEFSQKGRSYRLFYAKEVVSHMKNQARAYLVEAKCFHQNHVPTMEEYMSIALPSSGIVSILAWSFLGMGDIVTKDVFDWLLFNDPKMVKASSIIGRLLNDIAGHQFEKERAHVASAVECFMKQYRVTEEEAKEELRKQVTNAWKDINEELRRPTVVPMPILVRILNLTQALHMMYTGETDHYTNAGTKMKEVVTSLLVDPLPM

>EglobTPS004

VEEQIEELKGEVRKMLTDVVDKPSQMLHLIDQIQRLGIDYHFEHDIDEHLEEIHKHYSRLDHGDFKGDDFHMVALIFRLLRQQGYDVSHDRTEVFNKFKDSEGNFRASLTSDVCGLLSLYEACHLRCHGDTILEEALPFAITHLESINESKVSTSFAKQVSHALKQPLRKGLPRLEARHYISLYQEDPSHDEVLLTLAKLDFNLLQEQHQKELGKITRFINWWKDIDVPRNFPFARDRIVELFFWVSGVYFEPEFVEARDILTKVIALTSILDDIYDVYGTLEELVLITEAIQKYVIRWDVDAIDVLPEYLQAYYKELLHLYEEIGNEVAAKGRSYRLVYAKETVMKRQARAFFQEAKWFQTNYTPTMEEYMPLQLKTTGYGMLATTSLVGMGDVVTKHAFEWSLSDCKIVKAAETICRLMDDISSHEQKRGHLVSSVELLMKEHGFSEQEAEKELRKRVNDAWKDTNEEFLRPTAVPMPILTRVLNLSRAMDVLYSDGDNYTHSGTKLKGYVTSLFVSPLPM

>EglobTPS005

VEEQIEELKGEVRKMLTNAVDKSSQMLHLIDQIQRLGIDYHFDRDIDEHLEQIHKHYSRLDHGDFRGDDLHMVALIFRLLRQQGYDVSSGVFNEFKDSEGNFRASLINDVPGLLNLYEACHLRCHGDAILEEALPFATTYLESINESKVSTSFAKQVSHALKQPLRKGLPRLEARHYIPLYQEEPSHDEVLLTLAKLYFNLLQEQHQKELDKITWWKDIDVPRNFTLAREKKVIALTSILDDIYDVYGTLEELVLITEAIQRWDVDAMDVLPEYMQVYYKELLHLYEEIGNEVAAKGRSYRLVYAKETVSIIAFFQEAKWFQTNYTPMMEEYMPLQLTTTGYGMLATTSLVGMGDVVTKHAFEWSLSDCKIVKAAETICRLMDDIFEQKRGHLISSVELLMKEHGISEQEAEKELRKRVNDAWKDTNEEFLRPTA

>EglobTPS006

LKGELRKMLVGAMDKPSQKLNLIDQIQRLGIAYHFEIEIYQQLEQIHKSYFELHDGDKDNDLHTIALLFRLLRQQGYAIEELELFTEAIERWDVEVKDGLPEYMQVCYKIVLDLYDEIDYEVTRKGRSNYLFYAKEAVSHMKNQVRAYFTEAKWFHQNHIPMMEEYMPIALSTIAIELLLVMLLLLGMGDTVTKDVFDWLLYSNPKIVNAMKIVYRLMDDIAGHKFEQERGHGPSSMECFMKQYGVTEEEAKEELHKQVANAWKDINEGLCCSTNVPRQLLVRILNFTRVVHVVYKDEIDLYTHAGTKLKEHVTNLYVNPLPM

>EglobTPS007

SPARETSRVVERRLANFHPSIWGDYFLKYASDIEGLKGELRKMLAGAMDKPSQKLNLIDQIQRLGIAYHFEIEIYQQIHKSYFELHDGDNDNDLHTNALLFRLLRQQGYAISCGMEIFNKFKDINGNFSESLIVDVQGLLSLFEACHMRFHGDDVLNDALAFAMTHLESIDKGKASPNLKKQVRHALKQPIHKGIPRLEARRYISLYQEEPLHNEVLLSLTKLDFNLLQEQHQKELGNLTWKDLDVERKFPFARDRLVEMYLWMSGGYFEPEHKATREILTKVFSIVTIIDDIYDVYGTLEELELFTEAIERWDVEVKDGLPDYMQACYKIVLDFYDEIGYEVTRKGRSDYLFYAKEAVSHMKNQVRAYFTEAKWFHQNHIPTMEESIALPTTAIELLLVMLLLGMGGNVTKDVFDWLLYSDPKMVNAVRMTFEQERGHVGFSKVCSNNIVLQRKRLRRNSINKWPMHGRTLMKGCAATNVPRQLLVRILNFTRVVHVVYKDEIDLYTHAGTKLKEHVTNLYVNPLPM

>EglobTPS008

LKGELRKMLIGAMDKPSQKLNLIDQIQRLGIAYHFEIEIYQQLEQIHKSYFELHDGDNDNDLHTNALLFRLLRQQGYAISCHNTFGTSSVASPNLKKQVRHALKQPIHKGIPRLEARRYISLYQEEPLHNEVLLSLTKLDFNLLQEQHQKELGNLTRRWWKDLDVERKFPFARDRLVEMYLWMSGGYFEPEHKATREILTKVFSIVTIIDDIYDVYGTLEELELFTEAIERRWDVEVKDGLPEYMQACYKIVLDLYDEIGYEVTRKGRSMKNQVRAYFTEAKWFHQNHIPTMEEYMPIALPTTAIELLLVMLLLGMGDTVTKDVFDWLLYSNPKMVNAVKVVCRLMDDIAGHKVFEQERGHGPSSVECFMKQYGVTEEEAKEELHNQVANAWKDINEGLCCSTNV

>EglobTPS009

IEKLKGEVRKMLTDATDKPSQKLNLIDQIQRLGIADHFEIEFHNSNKDGHLHTTALLFRLLQQQGYTISCLVDLYVEHEFFIVSHDNIFSHVLFGHSEIFNKFKDSNGNFNESLIADVQGLLSLFEACHTRFHGDDVLNDALAFTMTHLKSIDEGKASPNLKKQVSHALNQPIHKGIPRLEARQYIPLYQEKPSHNEVLLALAKLDFNLLQEQHQKELGNLTRRWWKNLDIERKFPFARDRLVEMYLWMSIVYFESDYEAAREILTKVASMVSIIDDIYDVNGTLEELGLFTEAIERYNWDINAKEGLPEYMQACYKTVLDLYDEIGYEVTSKGQSYRLFYAKEAVSHLIMKNLVRAYFAEAKWFHLNHVPTMEEYMPIALTSAAVELLLVTSLLGMEDFVTKDAFDWLLYGNSKMVKAVKLVGRLMDDIAGHKFEQERGHGPSSVECFMKQYKVTEEEAKVELRKQVADAWKDINEGLCCPAIVPRPLLVRILNFVRAMHVMYKDEIDIYTHAGTKLKEYVTSLYVNPLPM

>EglobTPS010

SSPTKSDDRIEKLKGEVRKMLTDATDKPSQKLNLIDQIQRVGIAYHFEIEINQQLEQIHDSYFNFHNSNKDGHLHTTALLFRLLRQQGYTISCEIFNKFKDSNGNFSESLIADVQGLLSLFEACHTRFHGDDVLNDALAFTMTHLKSIDEGKASSNLKKQVSHALNQPIHKGIPRLEARHYIPLYQEEPSHNEVLLALAKLDFNLLQEQHQKELGNLWKNLDVERKFPFARDRLVEMYLWMSMVYFEPDYEAAREILTKVASMVTIMDDIYDVHGTLEELGLFTEAIERYWDINAKEGLPEYMQAFYKAVLDLYDEIGCEVTRKGRSYQLFYAKEAVSHLMKNQVRAYFAEAKWFHQNYVPTMEEYMPIALATAAIELLLVTSLLGMEDFVTKDAFDWLLYGNSKMVKAVKLVGRLMDDIAGHKFEQERGHGPSSVECFMKQYEVTEEEAKEELRKQVADAWKDINEGLRCPTIVPRPLLVRILNFARAMHVVYKDEIDIYTHAKTKLEEHVTSLYVNPLPM

>EglobTPS011

IEKLKGEVRKMLTDAMDKPSQKLNLIDQIQRVGIAYHFKIEINQQLEQIHESCFNFHNGDKDSHLHTTALLFRLLRQEGYTISCEIFNKFKDSNGNFNESLIADVQGLLSLFEACHTRFHGDDVLNDALAFTMTHLKSIDEGKASPNLKKQVSHALNQPIHKGIPRLEARQYIPLYQEKPSHNEVLLALAKLDFNLLQEQHQKELGNLTRRWWKNLDIERKFPFARDRLVEMYLWMSIVYFESDYEAAREILTKVASMVSIIDDIYDVNGTLEELGLFTEAIERYNSHSWDINAKEGLPEYMQACYKTVLDFYDEIGYEVTSKGQSYRLFYAKEAVSHLMKNLVRAYFAEAKWFHLNHVPTMEEYMPIALTSAAVELLLVTSLLGMEDFVTKDAFDWLLYGDSKMVKAVKLVGRLMDDIAGHKFEQERSHGPSSVECFMKQYKVTEKEAKVELRKQVANAWKDINEGLCCTAIVPRPLLVRILNFVRAMHVMYKDEIDIYTHAGTKFKEYVTSLYVNPLPM

>EglobTPS012

VEEQVEELKGEVRKMVTNAVDKPSRMLHLIDQIQRLGIDYHFEQEIDAQLERIHKSYSQLDHGDFKGDDLHMVALMFRLLRQQGFNISEVFNNFKDNEGNFKKSLITDVRGLLSLYEACHLRCHGDAILEEALPFAITHLESIDERKVGTSLAKQVSHALKQSKGLPRLEARHYIIFYQEEPSHDKVLLTMAKLDFNLLQEQHQKELGAITWWKNIDVARKFPFARVYFQPEFAVARNILTRVTGLISILDDIYDAYGTLEELVPYTEAIEKYVIRWDVDAMDGLPEYMQAYYKEILNLRSYRLTYAKEAMKKQAKWYFHEAKWFHTGYTPTLEEYIPLALLTTGYEALSITSLVGMGDVVTRDAFEWLLGDCKILSASQIICRFMDDISSHKFEQKRGHVASSSEQEAEEELQKRVVDAWKDINTALMLVLTAILNLSRVMDLLYSNGGDHYTHSKTELKEHITSLFVSP

>EglobTPS013

LKGEVRKMVTNAVDKPSQMLHLIDQIQRLGIDYHFEQEIDAQLERIHKSYSQLDHGDDDLHMVALMFRLLRQQTEVFNNFEDNEGNFKKSLIIDVQGLLSLYEACHLRCHGDAILEEALPFAITHLESIDERKVGTSLAKQVSHALKQPLRKGLPRLEARHYIIFYQEEPSHVAKLDFNLLQEQHQKELGKITWWKNIDVARKFPFARDRIAEMFFWMVGVYFQRNILTRVTGLISILDDIYDAYGTLEELVPYTEAIEKYVIRILLDYQSTCKLIIRRFSISDEIGNDLATKGRSYRLTYAKEKAKWFHTGYTPTLGEYIPLALLTAFEWLLGDCKILSASQIICRFMDDISSHKFEQKRGHVASSVELFMKENHVSEQEAEWRSLHPLQDDHYTHSKTELKEHITSLFVSPLPI

>EglobTPS014

VEEQVEELKGEVRKMVTNAMDKPSRMLHLIDQIQRLGIDYHFEREIDEQLEVFNNFKDNEGNFKKSLITDVRGLLSLYEACHLRCHGDAILEEALPFAVTIDEMKVSTSLAKQVSHALKQPLRKGLPRLEARHYLYQEKPSHDEVLLTLAKLDFNLLQEQHQKELGKITWWKNIDVARKFPFARDRIAELFFWMVGTYFQPEFAMARNILTRVTGLISILDDIYDAYGTLEELVPYTEAIEKYVIRWDVDAMDGLPEYMQAHYKELLNLYDEIGNDLATKGRSYRLAYAKEAMKKQAKGYFHEAKWLHSDYTPTLEEYMPLALLTTGYEALSITALVGMGDVVTRDAFEWLLGDCKILSASQIICRFMDDISSHKFEQKRGHVASSVELLMKENRISEQEAEEELQKRVVDAWKDINEEFLRPTVGPRSVLTLILNLSRVIDVLYTNGDHYTHSKTKLKEHITSLFVSPLPI

>EglobTPS015

VEEQVEELKGEVRKMVTNAVDKPSRMLHLIDQIQRLGIDYHFEREIDEQLEQLDHGDFRGDDLHMGALMRQQGFEVFNNFKDNEGNFKKSLITDVHGLLSLYEACHLRCHGDAILEEALPFAVTHLESIDEMKVSTSLAKQVSHALKQPLRKGLPRLEKVLLTLAKLDFNLLQEQHQKELGGITWWKNIDVARKFPFARDRIAELFFWMVGTYFQPEFAMARNILTRVTGLISILDDIYDAYGTLEELVPYTEAIEKYVIRWDVDAMDGLPKYMQAHYKELLNLYDEIGNDLATKGRSYRLAYAKEAMKKQAKGYFHEAKWLHSDYTPTLEEYMPLALLTTGYEALSITALVGMGDVVTRDAFEWLKILSASQIICRFMDDISSHKFEQKRGHVASSVELLMKENRISDRPTVGPRSVLTLILNLSRVIDVLYTNGDHYTHSKTKLKEHITSLFVSPLLI

>EglobTPS017

EEQVEELKGEVRKMVTNAMDKPSRMLHLIDQIQRLGIDYHFEREIDEQLERIHKSYSQLDHGDFKGDDLHMVALMFPTLFGRTEVFNNFKDNEGNFKKSLIIDVQGLLSLYEACHLRCHGDAILEEALLAKQVSHALKQPLRKGLPRLEARHYIKLYQEKPSHDEVLLTLAKLDFNLLQEQHQKELGKITRSTNRWWKNIDVARKFPFARDRIAELFFWMVGTYFQPEFAMARNILTKVAGLISILDDIYDAYGILEELLVHEQVKGYFHEAKWLHSDYTPTLEEYMPLALLTTGYEALSITALVGMGDVVTRDAFEWLLGDCKILSASFEQKRGHVASSVELLMKEKQEAEEELQKRVVDAWKDINEEFLRPTVGPRSVLTLILNLSRVIDVLYTNGDHYTHSKTKLKEHITSL

>EglobTPS018

ADYHPSIWGDYFLVYEEQIEGLKGEVRKISNPTLGNIQRLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQQGYNVSSGMFVFNKFKNSERNFNVRGLLSLYEACHLRCHGDSILEEALPFAITHLESINESKVSTSLAKQVKRALRQPLRKGLPRLEARYYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFAVARDILTKVTALISILDDMYDVYGTLEELVILTEAIERWDVDAMDGLPDYMQAWYKVLLDVYDAVGNEVATKERSYRLTYVKEAVFEQKRGHVASSVELFMKEHNVSEQETEKELRKRVVDAWKDINEAFLRPTAVPMPILMRILNLSQVIHVLYSDGDNYTHSGTLLKDHVTSLFISPLPV

>EglobTPS019

NKGSSRVVERRWADYHPSIWGDYFLAYASVEEQIEGLQGEVRKMLTDVVNKPSQVLHLIDQIQRLGIFYHFKREIDEQLEQIHKSYSRLVYRDFKGDHLHMIALIFRLLRQQGYNVSSGMFEVFNKFKDGEGNFRELLITDVQGLLSLYEACHLRCHGDSILEEALLFAITHLESLNESKVSTSLAKQVKHALRQPLHKGLPRLEARHYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRWWKDIDVARKFPFARDRIVELFFWISGAYFEPEFAVARDILTKVIALTSILDDMYDVYGTLEELVILTEAIERWDVDAMDGLPEYMQAWYKVLLDVYDAVGNEVATKERSYRLTYAKEAMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLAITSLVGMGDVVTNMLLNFEQKRGHVASSVELFMKEHDVSEQETEKELRKRVVDAWKDINEAFLRPTAVPMPILMRILNLSRVIHVLYSDGDNYTHSGALLKDHVTSLFISPLPV

>EglobTPS020

ADYHPSIWGDYFLVVEEQIEGLKGEVRKMLTDAVNKPSQVLHLIDQIERLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQQGYNVSSGMFIADHRCTWTSKPISINESKVSTSLAKQVKRALRQPLRKGLPRLEARDYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITWWKDIGIARKFPFARDRIVELFFWISGVYFEPEFAEARNILTKVIALTSILDDSTGEELVSLTKAIEKRWDVDAMDGLPKYMQAWYKLLLNVYDAIGNEVAMKERSYRMKKQARVSFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLAITSLVGMGDVVTKHAFEWLLGDCKILKASQIICRLMDDIASHFEQKRGHVASSVELFMKEHNVSEQETEKELRKRVVDAWKDINEVPVPILMRTLNLSRVIHVLYSDGDNYTHSGTSLKDHVTSLFISPLPVS

>EglobTPS022

KGTSRAVEPRWADFHPSGWGDYFLVYASPTNSMVSGMVEEQIEGLKGEVRKMVTAVVTAVVDKPSQMLLLIDQIQHLGIFYHFEREIDEQIEQIHKSYSRLVHRVLKGDNLHMIALTFQLLQGYHVSSGMFSTEAFNKFNDGEGNFESLITDAHGLLSLYEAWHLRCHGDAIPEEALPFAITHLQWWKDIGIARKFSFARERIVELFFPEFAVARDILIKVTALLSILDNIYNVWYGTLEELVIFTEAIERWNVDAIDGLPGYMQAWSKVLLDVFDAIGNEMIIKERSYRLIYAKESVRSIVMKKQAKVYLYKTKWFYSNTPTLEEYKPLALSTSSYELLLITSLMGMGNVVTKHVFEWLLVNYKILKEGARGICSGVVHTQRFGAGNRKGVVDAWKDINEAFLHPTVVRLSTLMQVVDISQVIHVVYSYG

>EglobTPS024

VERRSADYHPSIWGDYFLVYASPTNSMVSSFSYGHLKGEVRKMLTDAVNKPSQVLPLIDQIERLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQRGYNVSSGMFVFNKFKNSEGNFRESLITDVRGLLSLYEACHLRCHGDSILEEALPFAITHLESINESKVSTSLAKQVKRALRQPLHKGLPRLEARYYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFAVARDIFTKVIALTSILDDMYDIYGTLEELVILTEAIERWDVDAMDGLPEYMQAWYKLLLNVYDAIGNEVATKGRSYRLTYAKEAVMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLAITSLVGMGDVVTKHAFEWLLGDCKILKASQIICRLMDDIASHQFEQKRGHVASSVELFMKEHNVSEQEAEKELRKRVVDAWKDINEAFLRPTVVPLPILMRTLNLSRVIHVLYSDGDNYTHSGTSLKDHVTSLFISPLPV

>EglobTPS025

PLQKLHLIDQIQRLGIEFHFEREVDEQLEQIHKSYSRLDHEDFKVDDLHTVALIFRLLRQHGYNISEVFDKFKDSKGNFRESLISDVHGLLSLYEACHLTTTHLESINESKVSTSLAKQVSHALKXPLRKGLPRLEASHYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITKFPFARDRIVELFFWTTGIYFEPEFAAREILTKVISLTSIMDDIYDVYGTPEELALLNEAIQRWDFDAMDGLPEYMQAYFKEFLQLYEYIGNQLAAKGKSYRLIYAKEVVSIIDKLYMMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLVGMGDVVTEHVLQWSVSDCKFEQKRGHVVSAVEVLMKYRGISEQEAAEELHKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDVLYSDGDNYTHSKTKLKDYVTSLFINP

>EglobTPS027

DQHAEQEIQKLDDEVKRMLCADADKPSLKLDMIDQIQRLGIAHRFASDIDHVLKQLSETCFACNNGDRDIDDLYTAALLFRLLRQQGYRVSDIFNKFKDPSGKFSEKHASDVRGLLSLYEASHLSVHGEDVLDQALSFSLTHLESVKEQLSPPLATQVRHALKQTIRKGVPRLEARQYISMYEAEPLHNEVLLSLAKLDFNRLQKQHQKELFDITRWWMGLDFKRKLPFARDRLVEGYFWIVGVHFEPELAVARRMMTKVIAVTSVLDDIYDVYGTYEELELFTQAIQRRWDIDCIHELPEYMQVFYKALINIYVEIEEILACTGKSYCLCYAVEAVRSMKRQARSYFAEAKWLHQQHKPTMDEYMSIALVSSGYPLLAVTSFVGMPDIVTKDDLDWLFNDPKILKASTIICRLMDDLATHKFEQSRGHVDSAVQCYMKQYGVTEQEAENNLRKQVNDSWKDINEECLRPTAVAMPLLVGILNLSRVMDVLYKDGGDHYTNPHIALKDYIHSVLIDPV

>EglobTPS028

PDLQVSAIPRSSPNIGTDHVIERRSAGYHPSIWGDYFLKYAEEQIEELKGKVRKMLASVVDKPSQMLHLIDQIQRLGFDYHFEHEVDEQLEQIHKSYSQLHLEDFKVDDLHIVALIFRLLRQQGYNVSVGCTEIFNKFKDSEGNFRESLVTDARGLLSLYEACHLRCHGDSILDEALPFATTHLESIDESKVSTSLAKQVSHALEQPLRKGLPRLEARRYIPLYQEEPSHDEVLLALAKLDFDLLQEQHQKELGEITRFRWWKEIDVPRKFPFARDRIVELFFWISGIYFEPEFAMARNILTRVISLTSILDDIYDVYGTLEELALLTEAIQKYGIRTLSQTSEFDQFCIESRWDVDAMDGLPVYMQAYYKELLHLYEYIGNELATKERSYRLVYAKEVVSIIGTLYMKKLARAYFQEAKWFHTNYIPTLEEYMSLQLITTGYGMLATTSLVGMGDVVTKHALEWSVGDCKIVKAAQTISRLMDDIASHQFEQKRGHVVSAVELLMKYHGVSEQEAGEELQKGVIDSWKDINEEFLRPTAVPMPILTRMLNFSRVMDVLYSDGDNYTHSETKLKDYVMLLFVSPL

>EglobTPS029

EHIERLKGEVRKMLTGAMDKPSQKLNLIDEIQRLGFAYHFEHEIDEQLEQIHRSYFEFHYGDNDDNLHTVAVLFRLLRQQGYNVSCEIFNRFKDSEGNFNKSIIADVQGMLSLFEACHLSYHGDDILNDALAFTISHLESIEKKKVSPNLVKQVSHALHQPIQKGLPRLEARRYIQFYQEEPLHNEVLLSLAKLDFNSLQEQHQKELGNLTRRWWKDINIEREFPFARDRLGELYVWMLGIYFEPKYEIARGIVTKMMVILSILDDIYDVYGTLEELELFTEAIERYRWDVDAKEGLPKCMQVFYKTLLDFYDEISNELARKGRSYRLFYAKEVVSMKIQVRAYLAEAKWFHHSHVPTMEEYMPIALISIGTQLTFVTAFLGMGDIVTKDAFDWLLSSDPRIVKASQVIGRLMNDIAGHKFEQERGHVASSVECFMKQYSVTEEEAKKELCKQVANAWKDINEELRRPTAVPMVLLMRIINLARATHAVYEDETDH

>EglobTPS031

FHACFLKHCVIYLQKFKFLGRVEGQIEELKGEVKKMLIDAVDKPLPKLHLIDQIQRLGIEYHFEREVDEQLEQIHKSYSRLDHEDFKVDDLHTVALIFRLLRQHGYNISRCLISDVPGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSTSLAKQVSHALKQPLRKGLPRLEASCYIPLYQEEHSHDEVLLTLAKLDFNLLQEQHQKELGKITWWKNIDVPRKFPFARDRIVGVFFWTTGIYFEPEFAMAREILTKVISLTSIMDDIYDVYGTPEELALLNEAIQKYRWDFDAMDGLPVYQYMQAYFKEFLQLYEYIGNQLAAKGKSYRLIYAKEVVMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLIGMGDVVTEHVLKWSVGDCKSVKATQTICRLMDDVSSHEFEQKRGHVVSAVELLMKYRGISEQEAAEELHKGVIDAWKDTNEEFLRPTAAPMSVLTRMLNFSRVIDVLYSDGDNYTHSNTKLKDYVTSLFINPLPM

>EglobTPS032

IEELKGEVKKMLTDIMDKPLQKLHLIDQIQRLGIEYHFEREIDEQLEQIHKSYSRLDHEDFKVDDLHIVALIFRLMRQHGYNVSSEVFDKFKDSGGNFRESLISNVLGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSTNLAKQVSHALKQPLRKGLPRLEARHYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITWWKNIDVPRKFLFARDRLVELFFWTTGVYFEPEFAMARDILTKVISLTSIIDDVYDVYGTLEELALFNEAVQRWDVDAMDGLPEYMQALFKEFLQLYEYIGNELATKGRSYYLVYAKEVVSIRGKIYMKKLVSAYFQEAKWFHTNYIPTLEEYMSLQLITSGYEMLATTSLMGMGNVVTEHALKWSISDCKIGKAAQTIGRLMDDIVSHEFEQKRGHVVSAVELLIKYRGVSEQEAVEELQKRVIDAWKDTNEEFLRPTAVPMPILTRVLNLSRVVDVLYSDGDNYTHSETKLKDYVTSLFVNPLPM

>EglobTPS033

SQVSATPCAPPNKGTGHVIERRSAGYHPSVWGDYFLKYDSPSDKLRKKLHLIDQIQRLGMEYHFEREIDEQLEQIHKSYSRLDHEDFKVDDLHIVALIFRLLRQHGYNISVFDKFKDSKGNFRESLISDVRGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSASLAKQVSHALKQPLRKGLPRLEASCYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRFFARDRIVELFFWTTGIYFEPEFAMAREILTKVISLTSIMDDIYDVYGTLEELALLNDAIQTYRWDFDAMDGLPEYMQAYFKEFLQLYEYIGNQLAAKGRSYRLIYAKEVVSIIDKLYMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLIGMGDVVTEHVLKWSVGDCKSVKATQTICRLMDDVSSHEFEQKRGHVVSAVELLMKYRGISEQEAAEELHKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDGLYSDGDNYTHSKTKLKDYVTSLFLNPL

>EglobTPS036

VEEQIEKLKGNVRKVLAGVMDKPSQMLHLIDQIQRLGIDYHFEHEVDEQLEQINKSYSQLHLEDFKVDDLHMAALIFQLLRQQGYNVSVGCTEIFTKFEDSEGNFRESLVTDARGLLSLYEACHLRCHGDSILDEALLFATTHLESIDERKMSTSLLKQVSHALEQPLHKGLPRLEARHYISLYQVEPSHDEVLLTLAKLDFNLLQEQHLKELGKITWWKEIDVPRKFPFAREMIVELFFWISRIYFEPEFVMAKNILTKVISLTSILNDIYDVYSTLEELALLTEAIQKYGIRWDVDAMDGLPVYMQAYYKEFLQLYEYIGNELATKERSYYLVYAKEVVMKKLARAYFQEAKWFHTNYVPTLEEYMSLQLITIGYGMLATTSLVRMGDVVTEHALEWSIGDCKIVKVAQTIYRLMDDIASHQFEQKRGHVVSAVELLMKYHGVLEQEAREELQKGVIDAWKDINEEFLCLTAVPMPILTRMLNFSRVMDVYSNGDNYTHSETKLKYYVTLLFVSPLPM

>EglobTPS038

EHIERLKEVRKMLMGAMDKPSQKLNLIDQIQRLGFAYHFEHEINERLEQIYKSYFEFHYGDNDDNLHTVAVLFLLQQQGYNVIFNRFKDSEGNFNKSSIAEVQGMLSLFEACHLSYHGDDILNDALAFIISHLESIEKKKVSPNLVKQVSHALHQPIQKGLPRLEARRYIQFYQEEPSHNEVLLSLAKLDFNSLQEQHQKELGNLTRRWWKDIDIEREFPFARDRLGELYVWMLGIYFEPVYKIARGIVTKMMVILSILDDIYHVYGTLEELELFTEAIERYDRWDVDAKEGLPKCMHVFYKTLLDFYDEIGNELARKGRSYMKIQVRAYLVEAKWFHHSQPMMEEYMPIALISICSQLTFVTAFLGMGDIVTKDAFDWLLSSDPRIVKEVVGQLMNDIAGHKFEQERGHVASSVECFMKQYSVTNGRSVGEIFLKYFEAVKTFPSV

>EglobTPS039

SGVPFPSPAEETSPVAERRSAIFHPTIWTDYFLKYASDSTSTVEEQIKRLKGEVRKMLTGAMDKPSQKLNLIDRIQRLGLAYHFEHEIDEQLEQIHRSYFEFHCEDNNNNLHTIALLFRLLRQQGYNVSCGMCSNFLDEIFNRFKDNEGNFSKSIIADVQGLLSLYEACHLSYHGEDILNDVLTFTITHLESIDKRKSEPNLEKQVSHALHQPIQKGLPRLEARRYIQFYQEEPSHNEVLLSLAKLDFNSLQEQHRKELGNLAWWKDIDIEREFPFARDRLGELYIWNLGVHFEPEYEISRGILTKMMAILTILDDIYDVYGTIEELELFTEAIERYNRWDVDAKEGLPECMQVIYKILLNFYDEIGYELTRKGRSYRLFYAKEAVSHMKIQVRAYLAEAKWFHHSHVPTMEEYMPIALTTIGIQMALVASFLGMGDTVTKDVFDWLLFSDPKIVKALRVIGRLMNDIAGHKFEQERGHVASSVECFMKQYKVTEEEAKKELRKQVADAWKDINEELCRPTAIPRVLLMRIINLAGAIHAVYEDETDNFVNAGTNFKEFVTCLLVNP

>EglobTPS040

EIFEKFKDSDGNFRESLTADILGILSLYEACHLRVHGEDVLDEALSFTVTHLESIDKNQVSPTLAKQLSHALKQPIYKGLPRLEARQYIPIYQEEPSHNEVLLSLAKLDFNLMQEQHQKELGHIARSLNLANNLQVVEGIRCCKNFPFARDRLVECYFWILGVYFEPEFILARKFMTKVIAMTSIIDDIYDVYGTLEELKLFTEAMERWSIDAIDGLPKYMQVCYKALLDVYDDTEKAIAENGTSYGLYHAKEAVRWSIDAIDGLPKYMQVCYKALLDVYDDTEKAIAENGTSYGLYHAKEAVMVKASTTICRLMDDIVSHQMVKASTTICRLMDDIVSHQGHVASAVECFVHQHGVTEQEAKDELWRRVVEAWKDVNEECLAPTAIPSRLLTLILNLTRVIDVLYTDEDNYTNAGTKLKNYVASLLIYPLPM

>EglobTPS041

PQISAMPSPSPALETSHVAERRSGNFHPSIWGDYFLKYASDSERIERLKGEVKKMLTSAMDKLSQKLNLIDQIQRLGLAYHFEIEIEKELEQIHRSYFEHHCGDNDEDLHTTALLFRLLRQQGYDVSCGMEIFNKFKDNEGHFSKSLIADVRGLLSLFEACHVGFHSDDILNDALAFTVTHLESIDKEKVSRNLEKEVSHALSQPIHKGLSRLEARHYIQLYQEEPLHNEVLLSLARLDFNLLQKQHQKELGNITRLTRWWKDLDGERKFPFARDRLVELYFWMSGVYFEPKYEATREILTKMIVIVSIFDDMYDMYATLEEVEVFTEAIERYRWDVNAKDGLPKYMQVCYETLLDLYDEFGDKFTRKGQSYSLFYAKPIASTSIGCELLLGTSFLGMGDIVTKNDFDWLLYSDSKMVKASKVVARLMDDIAGHKEQERGHSPSSVECFMKQYRVTEEEAKEELRKQVVNAWKDMNEELRRSSAVPKLLRTRILNFAQVFDVVYNDEKDHYSHAGTKFKEHVTSLYVDPLPM

>EglobTPS042

VEEQIEELKGVVRKMLAGVVDKPSQMLHLIDQIQRLGIDYHFEHEVDEQLEQIHKSYSQLHLEDFKVDDLHMVALIFRLLRQQGYNVSEIFNKFKDNEGNFWESLVTDARGLLSLYEACHLRCHGDSILDEALPFATTHLESIDESKVSTSLAKQVNHALEQPLPKGLPRLEARRYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGEITRFWKEIDVPRKFPFARDRIVELFFWTSGIYFEPEFAMARNILTKVISLTSILDDIYDVYGTLEELALLTEAIQKYRWDVDAINGLPVYMQAYYKELLQLYEYIGNELATKERSYRLVYAMKKLARAYFQEAKWFHTNYVPALEEYMSLQLITTGYGMLATTSLVGMGDVVTEHALEWSIGDCKIVKAAQTICRLMDDIVSHQFEQKRGHVVSAVELLMKYHGVSEQEAGEELQKGVIDAWKDINEEFLRPTTVPMPILTRMLNFSRVMDVLYSDGDNYTHSETKLKDYVTLLFISPL

>EglobTPS043

MSLPVSTIPSPSPAHETGQVAERRSGNFHPSIWGDYFLKYERIEKLKGEVRKMLTSAMDKPSQKLNLIDQIQRLGLAYHFEIEIDEQLEQIHRSYFEFHCGDNDSNLHTTALLFRLLRQHGYNIPCGMSFQFEIFNKFKDNEGNFSKSLIADVQGLLSLFEACHLGFHGDVILNDALAFTITLLESIDKGKVTGNLEKQVTHALNQPIHKGLPRVEARHYIQLYQEEPSHNEVLLSLAKLDFNLLQEQHQKELGNITRFMERESFRLPEIGLCFEPEYEATREILTKVMVIVSIFDDVYDIYATLEELELFTKAIERWAVDAKDGLPEYMQVCYKTLLDLYDEIGYEVTRKGQSYCLFYAKEVVMKNHMRTYLAQAKWFQQNYVPTMEEPIASLSIGCELLLGTSFLGMGDVVTKSYFDWLLLSDNKMVKASGVISRLMNDIAGHKVYKSYTIEQHSNGIYELRSKRLRTLSVNKKPLLVRILNFARVFHVVYNDEVDHYSHAGAKFKEFVTSLLVDPLPM

>EglobTPS044

KERIEKLKGEVRKMLTSAMDKPSQKLNLIDQIQRSGLAYHFEIEIDELEQIHRSYFEFHCGDNDNNLHTTALLFRLLQHGYNIPCGMSFQFEIFNKFKDNEGNFSKSLITDVQGLLSLFEACHLGFHGDVILNDALAFTITLLESIDKGKVSGNLEKQVTHALNQPIHKGLPRVEARHYIQLYQEEPSHNEVLLSLAKLDFNLLQEQHQKELGNITRFNFMIARWWKDLDGERKFPFARNRLVELYFWMSGVYFEPEYEATREILTKVMVIVSIFDDVYDIYATLEELELFTKAIERWAVDAKDGLPEYMQVCMKNHMRTYLAQAKWFQQNYVPTMEEYLPIASLSIGCELLLGTSFLGMGDVVTKSYFDWLLLSDNKMVKASGVISRLMNDIAGHKFEQERGHTASSVECFMKQYRVTEQEAKDALRKQCPQATPCANSQVPKPLLVRILNFARVFHVVYNDEVDHYSHAGAKFKEFVTSLLVDPLPM

>EglobTPS045

DQQAEQEIQKLKDEVKRMLCAHADKPSLKLDMIDQIQRLGIAYHFASEIDNVLKKLSQTYFVSNNGNYDNDDLYTVSLLFRLLRQQGCRISCDIFNKFKDTSGKFTEKHASDVRGLLSLYEASHLSVHGEDVLDQALSFSLKHLESIDKEQLSPPLAAQVQHALKQTIRRGVPRLEARRYISMYEAEPLHNKVLLSLAKLDFNHLQKQHQEELFDLAWWMGLDFKSKLPFARDRLVEGYFWILGVHFEPELAPVRRMMTKVIAMTSVLDDIYDVYGTYEELELFTRAVQRSDRWDIDCINELPEYMQVFYKALIDVYVEIGEKLACTGRSYGLDYAKEAVRMKRQARSYFAEAKWLHQQHKPTMDEYMSVALVSSGYPLLAITSFVGMQDIVTKDDLDWLFNDPKILKASTVICRLMDDLATHKFEQGREHADSAVQCYMKQYNVTEQEAENDLRKQVDDAWKDLNEESLCPTAVAKPLLMGILNLTRVMDVLYKDGGDHYTNPHIMLKDYIRSVLMDPV

>EglobTPS046

IFNKFKDTSGKFGEKHASDIRGLLSLYEASHLSVHGEDVLDQALSFSLKHLESIDKEQLSPPLAAQVQHALKQTIHRGVPRLEARQYISMYEAEPLHNKVLLSLAKLDFNHLQKQHQKELFDLAWWMSLDFKNKLPFARDRLVEGYFWILGVHFEPELALVRRMMTKVIAMTSVLDDIYDVYGTYEELELFTRAVQRSDWYRTVLSIYIRMRWDIDCINELPEYMQVFYKALIDVYVEIGEKLASAGRSYGLDYAKEAVRMKRQDRSYFAEAKWLHRQHKPTMDEYMSVALVSSGYHLLAITSFVGMQDIVTKDDLDWLFNDPKILKASTVICRLMDDLATHKFEQGREHADSAVQCYMKQYNVTEREAENDLRKQVDDAWKDLNEECLCPTAVAKPLLMGILNLTRVMDVLYKDGGDHYTNPHIMLKDYIRSVLMDPV

>EglobTPS047

DQQAEQEIQKLKDEVKWMLCAHADKPSLKPDMIDQIQRLGIAYHFASEIDNVLKKLSETYFVSNNGDHDNDDLYTVALLFRLLRQQGYRISCDIFNKFKDTSGKFGEKHASDIRGLLSLYEASHLSVHGEDVLDQALSFSLKHLESIDKEQLSPPLAAQVQHALKQTIHRGVPRLEARQYISMLHEAEPLHNKVLLSLAKLDFNHLQKQHQKELFDLAWWMGLDFKNKLPFARDRLVEGYFWILGVHFEPELALVRRMMTKVIAMTSVLDDIYDVYGTYEELELFTRAVQRSDRWDIDCINELPEYMQVFYKALIDVYVEIGEKLASAGRSYGLDYAKEAVRMKRQDRSYFAEAKWLHRQHKPTMDEYMSVALVSSGYHLLAITSFVGMQDIVTKDDLDWLFNDPKILKASTVICRLMDDLATHKFEQGREHADSAVQCYMKQYNVTEREAENDLRKQVDDAWKDLNEECLCPTAVAKPLLMGILNLTRVMDVLYKDGGDHYTNPHIMLKDYIRSVLMDPV

>EglobTPS048

VSATPCAPPNKGTGHVIERRSAGYHPSVWGDYFLKYQIEELKGEVKKMLIDVVEKPLQKLHLIDQIQRLGIEYHFEREVDEQLEQIHKSYSRLDHEDFKVDDLHTVALIFRLLRQHGYNISEVFDKFKDSKGNFRESLTSDVHGLLSLYEACHLRCHGDSILDKALPFATTHLESSNKSKVSTSLAKQVSHALKQPLRKGLPRLEASRYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRFSNRWWKNIDVPRKFPFARDRIVELFFWTTGIYFEPEFAMARELLTKVISLTSIMDDIYDVYGTVEELALLNAAIQKYGIRWDVDAMDGLPEYMQTYFKEFLQLYEYIGNQLAAKGRLYRLIYAKEVVSIIDKLYMKKLVRAYFQEAKWFHTNYIPTLEEYMPLQLITTDYGMLATTSLVGMGDVVTEHVLKWSVSDCKSVKATQTICRLMDDVSSHEFEQKRGHVVSAVELLMKYHGVSEQEAGEELLKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDVLYSDGDNYTHSKTKLKDYVTLLFVNPLP

>EglobTPS049

SHGIAEERIERLKGEVGKMLTSAMYKPAEKLNLIDQIQRLGIAYHFELEIDKELEQIHRGYFEFHCDDNDNDLDTVALLFQLLRQRGYHVFHAPFGHTEIFNKFKDGDGNFGKSLIADVQGLLSLFEACHLRYHGDNLEDALAFTTTHLESIDKRKASLHLVKKVSHALNQPIHKGMSRLEARRYIPLYQEEPSHNEVLLSLAKLDFNLVQEQHRKELGNLTRRWWKGLDVQKKFPFARDRLVEMYVWWLGEYYEPEHEAAREILTKLISVTSIIDDIYDVYGTWEELELFTEAIERYNRWDVNAKDGLPEYMQECYKIVLDLYDEIGYEFDFCGTFPKYQVSRMKNQARAYLVEAKCFHQNHVPTMEEYMSIALPSAGIVSILAWSFLGMGDIVTKDVFDWLLFNDPKMVKAFTEEEAKEELRKQVTNAWKDINEELRGPT

>EglobTPS050

EQERGHSPSSVECFMKQYRVTEEEAKEELRKQVVNAWKDMNEELRRSSAVPKLLRTRILNFAQVFDVVYNDEKDHYSHAGTKFKEHVTSLYVERIERLKGEVKKMLTSAMDKLLQKLNLIDQIQRLGLAYHFEIEIDKELEQIHRSYFEFHSGDNDDDLHMTALLFRLLRQQGYDVSCGMIFNKFKDNEGHFSKSLIADVRGLLSLFEACHVGFHGDDILNDALAFTVTHLESIDKGKVSRNLEKEVSHALSQPIHKGLSRLEARHYIQLYQEEPLHNEVLLSLARLDFNLLQKQHQKELGNITRRWWRDLDGERKFPFARDRLVELYFWMSGVYFEPKYEATREILTKMIVIVSIFDDMYDVYATLEEIEVFTEAIERYSWHSRWDVDAKDGLPKYMQVCYETLLDLYDEFGNKFTRKGQSYCLFYAKEVVSMKNHLKAYFAEAKWFHQNHMPTMEEYMPIASTSIGCELLLGTSFLGMGDIVTKNDFDWLLYSDSKMVKASKVVARLMDDIAGHKFEQERGHSPSSVECFMKQYRVTEEEAKEELRKQVVNAWKDMNEELRRSSAVPKLLRTRILNFAQVFDVVYNDEKDHYSHAGTKFKEHVTSLYVD

>EglobTPS051

EEQIEGLKGEVRKMLTDAVNKPSQVLHLIDQIERLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQHNVSSGMFVFNKFKNSEGNFRESLITDVRGLLSLYEACHLRCSVFESLLQEKKKEFKLYESVKQKYFRFHSYLFNHRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFVEARDILTKVIALTSILDDMYDVYGTLEELVILTEAIERWDVDAMDGLPEYMQAWYKVLLDVYDVGNEVATKERSYHLTYAKEAVMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLGMGDVVTKHAFEWLLGDKILKASQIICRLMDDIFSHQFEQKRGHVASSVELFMKEHDVSEQETEKELRKRVVDAWKDINEAFLRPTAVPVPILFSIILNLSQVIHVLYSDGDNYTHSGTLLKDPVSHL

>EglobTPS058

DQHAEQEIQKLDDEVKRMLCADADKPSLKLDMIDQIQRLGIAHRFASDIDHVLKQLSETCFVCNNGDRDIDDLYTAALLFRLLRQQGCRVSNIFNKFKDPSGKFSEKHASDVRGLLSLYEASHLSVHGEDVLDQALSFSLTHLRLEARRYISMYEAEPLHNEVLLSLAKLDFNRLQKQHQKELDITRRWWMGLDFKRKLPFARDRLVEGYFWILGVHFEPELAVARRMMTKVIAVTSVLDDIYDVYGTYEELELFTQAIQRRWDIDCIHELPEYMQVFYKALINIYVEIEEILACTGKSYCLCYAVEAVRSMKRQARYYFAEAKWLHQQHKPTMDEYMSIALVSSGYPLLAVTSFVGMPDIVTKEDLDWLFNDPKILKASTIICRLMDDLATHKFEQSRGHVDSAVQCYMKLYGVTEQEAENNLRKQVNDSWKDINEECLRPTAVAMPARVMDVLYKDGGDHYTNPHIALKDYIHSVLIDPV

>EglobTPS059

DALTFTITHLESIDKRKVSPNLEKQVSHALNHPIRKGLPRLEARHYIQFYQEEPSHNEVLLSLAKLDFNSLQGQHQKELGNLTRFRWWKDLDIKREFPFTRDRLAELYVWMLGVHFEPDYEIARGIVTKMMVIISILDDIYDVYGTLEELEIFTEAIERYRWDVDAIEGLPECMQVIYKIIFELYDEIGYELTRKGRSYRLFYAKEAVSHMKIQVRAYLVEAKWFHKSHIPTMEEYMPIASTTIGNQMAFVASFLGMRDIVTKDTFDLLLSSNHKIVKASKVIGRLMNDIAGHKFEQERGHVASSVECFMKQYKVTEEEAKKEIRKLVADAWKDINEELRHPTAVPMVVLMRIVNLAGAIHAVYEDETDHYVNAGTNFKEFVTCLLVNP

>EglobTPS060

ERIERLEGEVKKMWIGAMDKPSQNLIDHIQRLEFAYHFEHEIDEQLEQNHRSYFEFHYDDNNGNLHTIANRFKDSKGNFSKCITDVQGMLSLFEACHLSYHGNDILNGALAFTITHLESIKKKKVTPNLKKQVSHALHQPIQKGLPRLEARLYIQFYQVEPLHNEVLLSLAKLDFNSLQEQRQKELGNLTRRWWKDIDMEMEFPFARDRLGEVHVWMLGIDFEPVYEITRGMVTKMMVILYILDDIYDVYGILEELELFTKAIERRWDVDAKEVLPKCMQVFYKTLLDFYDELGNELTRKERSYRIMKIQVSMYLAEAKWCHQNHIPTMEEYIPVGLISNGSQLVFVTAFLVMGDIVTKDTFDWLLSGDPKIVKASQVIGWLMNDIAGHKFEDRGHVASLMEGFTEYRVMEEVAKKELCKKSGQCWTDIKEELPRLIAVPMVLLMRIINLARAMHVVYEDETNHYVNAGT

>EglobTPS062

MALPVLCPTFLPSTICHNQPSLLSFRHLRFAQFVTCASKIEDQEIVRRSANWQPSVWDYDFVQSLSVDYTEDKHMEQVQRLKEEVRGLFDREINQVAKLEFIDVVQRLGLGYHFEMEIKNALSSIYNNTEDAQISDNLYATSLRFRLLRQHGYNVPQGACQDVFQRFMSKMGTFNELLHEDVKGLLGLYEASFHGLEGETILDEGWNFASKHLNDLNLDKVPTNIASHVSHALDMPIHWRPNRLEARWFMDMYGKQQDMIPSLLRLAKIDFNLVQSIHRKEVSNLARYRWWVELGANKMTFSRDRLVENYFWSCIFVFEPQYTAFRELSTRIGCMVSLIDDIYDIYGTPEELELLTDFDYFSRWDITNIDKLPPTIRDGFMVLYNTTNELGYWTMRERGINPIPYLRKLVISTCWADECKAYMKEVYWYNKGIKPTLKEYMDVGVDSIGGLILLLDSYFLTTDKLTEEGLDYVSKIPGVMHSSAKILRFNDDLSTSSHELARGDNSKALECYMNETGASEEAAREHIKHLVRETWKKMNKEVFEDYPFSGFGPFLSACLNLARASHCFYDYGDGHGLPGHQTKDHVVSTIFESVPLD

>EglobTPS063

MALPALFTSFVPSSISHNQPSLLSFRHPRVTCAVTIENPEIVRRSANWKPTVWDYEFLQSLRVDYTEDKYAEQVQRLKEEIRGLFNREMNQVAKLEFIDTVQRLGLGYHFEMETKNALSSIYDNTGYAQLLNDLHAVSLGFRLLRQHGYKIPQGIDVFQQFMNKTGTFNESLNKDVRGLLSLYEASFHGLEGETILDEARNFASKHLKDLNLDKVPTMLASYVRHALDMPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARYRWWVELGANKMTFFRDRLVEHYFWCCAMVFEPQYTAYREMTTKLTCMVTLIDDVYDVYGTQEELELLTDFLVRWDITEIDKLPPIIRDSYMALYNTTNEIGYWTMRELGINTIPYMQKVWADECKAYIKEVHWYNKGIKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDQSLITCRKFRVSCIALPRSFDSTMISVPHRYELARGDNFKALECYMNETGASEEATREHVKKMVHETWKRMNKDVFEDYPYSGFGPFLGACLNLARASQCFYQYGDGHSLPDNETKDHLVRALFDPVPLD

>EglobTPS064

MVLPALFTSFVPSPISHNQPSLLSFRHPRCSSSSFSSGAKSVTCAMTIENPEIARRSANWKPNVWDYEFLSLIVDYTEDKYAEQVQRLKEEIRGLFNREMNQVAKLEFIDAVQRLGLGYHFETETKKNALSSIYDNAGYAQLLNDLHAVSLGFRLLRQHGYKISQGIDVFQQFMNKTGTFNESLNKDVRGLLSLYEASFHGLESETILDEVRNFASKHLKDLNLDKVPAMLASYVRHALDMPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARWWVELAANKMTFFRDRLVEHYFWTCAMVFEPQYTAYREMTTKLTCMVTLIDGVYDVYGTQEELELLTDFLVDILSRWGIIEINKLPPTIRDSMALYNTINEIGYWTMRELGINTIPYMQKVDECKEYIKEVHWYNKGIKPTLKEYMDNAVDSIEGLIMLLGSYFLTTDKLTEEGLGYVSKIPSVMHCSAKILRLNNDLSTSSSHELARGDNFKALECYMKETGASEEATHEYVRQMVHETWKRMYPYSGFGPFLGACLNLARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPLD

>EglobTPS065

MALPVLCPSILPSTIFHNQPSLLSFRHLHSSFSCSANWEPSVWDYGVVQSLSVDYEDKYMEQVQRLKEEVRGLFDREINQVAKLEFIDVVQRLGLGYHFETEIKNALSSIYNNTEDAQVSDNLYVASLRFLLRQHGYNIPQGTCQDVFQRFMSKMGTFNESLHEDVKGLLGLYEASFHGLEGETILDEGWKFASKHLKDLNLNEVPTNIASNVSHALDMPIHWRPNRLEARWFMDMYGKQQDTIHSLLQLAKIDFNLVQSIHRKEVSNLARYRWWVELGANKMTFFRDRLVENYFWSCIFVFEPQYTAFRELNTRIGCLDTTLIDDVYDIYGTPEELELLTDFILRWADECKAYMKEVYWYNKGIKPTLKEYMDVAVDSIGGLILMLDSYFLTTDEVTEEGLDYEIPGVMHSSARILRFNDDLSTSSHELARGDNSKALECYMNETGASEEAAREHIKHLVRETWKKMNKEVFEDYPFSGFKPFLGSCMNLARASHCFYDYGDGHGLPGHQTKDHLVSTIFESVPLD

>EglobTPS066

MALPALFTSFVPYSISHNQPSLLSFRHPRCSSSSFSSGAKSVTCAVTIENPEIVRRSANWKPNVWDYEFLQSLRVDYTEDKYAEQVPRLKEEIGGLFNREMNQVAKLEFIDAVQRLGLGYHFETEIKNALSSIYDNAGYAQLLNDLHAVSLGFRLLRQHGYKISQGIDVFQQFMNKTGTFNKSLNKDTRGFLGLYEASFHGLEGETILDEARNFASKHLKDLNLDKVPAMLASYVSHALDMPIHWRPNRLEARWFMDMYEKQQDMILSLLRLAKLDFNLVQSVHKKEVSNMARYRWWVELGANKMTFFRDRLVEHYFWTCAMVFEPQYTAYREMTTKLTCMVTLIDDVYDVYGTQEELELLTDFLVRDILSRWDITEIDKLPPTIRDSYMALYNTTNEIGYWTMRELGINTIPYMQKVWADECKAYIKEVHWYNKGIKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDKLTEDGLDYVSKIPSVMHCSAKILRLNNDLSTSSYELARGDNFKALECYMNETGASEEAAREHVRQMVHETWKRMNKDVFEDYPYSGFGPFLGACLNLARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPLD

>EglobTPS068

MALPALFTSLVPSSISHNQPSLLSFRHPRCSSSSFSSGAKLVTCAVTIENPKIVRRLANWKPNVWDYEFLQSFGVDYEDKYAEQVQRLKEEIRGLFNREMNQVAKLEFIDAVQRLGLGYCFETEIKNALSSIYDNTGYAQLLNDLHVVSLGFRLLRQHGYKISQGIDVFQQFMNKTGTFNESLNKDVRGLLGLYEASFHGLEGETILDEARNFASKHLKDLNLDKVDVFQQFMNKTGTFNESLNKDVRGLLGLYEASFHGLEGETILDEARNFASKHLKDLNLDKVVSNMARYRWWVELGTNKMTFFRDRLVEHYFWCCAMVVEPQYTAYREMTTKLTCMVTLIDDVYDVYGTQEELELLTNFLVRDITEIDKLPPIIRDSYMALYNMTNEIGYWTMRELGINTIPYLQKVNKGIKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSAKILRLNNDLSTSYELAGDNFKALECYMNETGASKEAMREHVRQMVHKTWKRMNKDVFEDYPPSGFGPFLGACLNLAQASQCFYQYEDGHSLPDNETKDHLVRALFDPVPLD

>EglobTPS069

ASSGAQFVTCASKIEDQEIARRSANWEPSVWDYGVVQSLSVDYTEDKYMEQVQRLKEEVRGLFDKLEFIDVVQRLGLGYHFETEIKNALSSIYNNTEDAQVSSNLYAASLRFRLLRQHGYNIPQDVFQRFMSKMGTFNESLHEDVKGLLGLYEASFHGLEGETILDEGWKFASKHLKDLNLNEVPTNIASNVSHALDMPIHWRPNRLEARWFMDMYGKQQDMIPSLLRLAKIDFNLVQSIHRKEVSNLARYRWWVELGANKMTFFRDRLVENYFWSCIFVFEPQYTAFRELNTRIGCLVTLIDDVYDIYGTPEELELLTDFILRWDITNIDKLPPTIRDSFMVLYNTTNEVGYWTMRERGINPIPYLRKVWADECKAYMKEVYWYNKGIKPTLKEYMDVAVDSIGGLILMLDSYFLTTDEVTEEGLDYVSKIPGVMHSSARILRFNDDLSTSSHELARGDNSKALECYMNETGASEEAAREHIKHLVRETWKKMNKEVFEDYPFSGFKPFLGSCMNMARASHCFYDYGDGHGLPGHQTKDHLVSTIFESVPLD

>EglobTPS071

MALPALSTSFLPSSIHHNQPSLLFFRHLCSSSSASTSSTSFGAQFVTCTLKIEAQEIGRRSANWQPNVFDYDFLQSLNVDYTEDKYSEEAQRLKKEVKGLFNKDMNLVAKLEFIDLVQRLGLGYQFEMEIKNALSSIYNNAEDAQLLDDLYAISLRFRLLRQHGFNILQDVFQRFMSKSGTFNESLNEDVKGLLGLYEASFHVLEGETILDEAWTFASKHLKDLNLNKIPTNLATHVDHALEMPIHWRPNRLEARWFIDMCEKQQDMIPSLLRLAKLDFNSVQSIYRKEVSTLARYRWWVELGANKMTFCRDRLMENYFWSMIMVFEPQHTAFREMNGKIASMVTLIDDVYDVYGTPEELELLTDFIVRFWDITDIDRLPPIIRDSFMALYNTTNEIGYWTMRERGINAIPHLQKWAEECKAYLKEVHWCSKGIKPTLKEYMDVATYSTGGLVMLLASYFLTTDKLTEEGLNYVSEIPSIMHSSCEMLRLINDFSTSSYELARGDNLKALECYMNETGASEEAAREHIMHKVREGWKLMNRAMFEDYPIPGLRPFLGACLNQARVSHTFYRYGDGFGRPDNDTKDYLASAIYKPVPLD

>EglobTPS073

MALPALFTSFVPSSISHNQPSLLSFRHPRCXSSSFSSGAKSCAVTIENPEIVRRSANWKPNVWDYEFLQSLRVDYTEDKYAEQVQRLKEEIKGLFNREMNQVAKLEFIDVVQRLGLGYHFEKEIKNALSSIYDNTGYAQLLNDLYAISLGFRLLRQHGYNIRQGIDVFQQFMNKTGTFNESLNKDVKGLLGLYEASFHGLEGETMLDEARNFASKHLKDLNLDKVPTMLASYVSHTLDIPIHWRPNKLEARWFMDMYEKHQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARYRWWVELGANKMTFFRDRLVEHYFWNCTMVFEPQYTAYREIVYDVYGTLEELELLTDFLVRWDITEIDKLPPTIRDSYMALYNTTNEIGYWTMRELGINTIPYMRKVWADECKAYIKEAHWYNKGMKPTLKEYMDNAVDSIGGSIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSAKILRLNNDLSTSSYELARGDNFKALECYMNETGASEEAAREHVKQMVHETWKRMNKDVFEDYPARAF

>EglobTPS075

FTSFVPSSIRHNQPSLLSFRHPRCSFSNPEIVRRSANWKPNVWDYEFLQSLRVDYTEDKYAGQVQRLKEEIRGLFNREMNQVAKLEFIDAVQRLGLGYHFETEIKNALSSIYDNTRYAQLLNDLHAVSLGFRLLRQHGYKIPQDVFQQFMNKTGTFNKSLNKDVRGLLGLYEASFHGLEGETILDEARSFASKHLKDLNLDKVPAMLASYVSHALDIPLHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARYRWWVELGANKMTFFRDRLVEHYFWNCTMVFEPQYTAYREMTTKLACMVTLMHSMKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDQLTGEGKALECYLTEIGASEEAAREHVKQMVHKTWKRMNKDVFEDYPYSGLGPFLDACLNFARASQCFYQYGDGHGLPDKETKDHLVRALFDPVPLD

>EglobTPS076

SIHHNQPSLLFFRHLCSSSSSGAQFLTCTLKIEAQEIGRRSANWQPSVWDYDFVQSLGVDYDKYSEEAQRLKKEVKGLFDKDMNLVAKLEFIDVVQRLGLGYQFETEIKNALSSIYNNTEVAQLSDDLDAVSLRFRLLRQHGFNVSQDVFQRFMSKSGTFNESLNEHVKGLLGLYEASFHVLEGETILDEAWTFASKHLKDLNLDEIPTNLVSHVDHALEMPIHWRPNRLEARWFIDMCEKQQDMIPSLLQLAKLDFNLVQSIYRKEVSSLARYTINLAARWWVDLGANKMTFCRDRLVENYFWSSIMVFEPQHTAFREMNGKIASMVTLIDDVYDVYGTLEELELLTDFIVRFWDITDIDRLPPTIRDSFMALYNTTNEIGYWTMRERGINPIPHLQKVVISTCWANECKAYLKEVQWCSKGIKPTLEEYMDVATYSAGGLVMLLASYFLTTDELTEEGLNYVSKIPSIMHCSSKMLRLINDFSTSSYELARGDNLKALECYMNETGTSEEAAREHIMHMVREAWKWMNRAVFEDYPIPGLRPFLGACLNLARVSHTFYRYGDGFGLPNNDTKDYLVSAIYKHVPLD

>EglobTPS077

EERYMERVENMKEEVKDFICSEMPQVEKLEHIDAVQRLGLGYHFEVEIKKALQTIINGKTNRSGAFDDDLPATALLFRLLRQNGFNVEQGIFERFMTEDVSNFKESLREDVQGLLSLYEASFCGFKGEAIIDEAKIFSSTCLENLKGDHIWAKKIDRALDMPVHWRPNRLEARWFMDMYEEDQCDRSNPILLDLAKLDFNIVQSVYRDEVSKLARRWWVNLGLNKMDFCRDRLMEHYLWNALMVYEPQFGAFREMSTKITCMITLMDDVYDVFGSWEELQLLTKFIWDISQIDKLPLTIRTCFLAMYNTTNEVGYWTMKEQGFNIIPYLHKLWVNQGKTWLEEAKWYHEGHKPTLKEYLNASVTSIGGHLVLLCSYFTTSDKLSKEILEYLCNIPNVMYCSSLILRLTNDLSTSSDELVRGDNFKSLHCYMNETGASEEATRQHIKSLVQDAWKQMNEDAFCYNPCPGPFRGACLNLARASQLFYQYGDGHGIPDRETKDN

>EglobTPS078

RPSVLLFKFPRPTPSYSIADVATTAGIWCISCIDPNTNEQSPVARRSANYMPSVWDYDILKSPSADFAEERCTEPVQRMKEEVKDTLERENHLLAKLELIDAIQRLGLQYHFENDIKRALQVIRDDSNDACFSNDLHSTALRFRLLRQHGYDLSQGIDAFQRFINKTGTFEESLKKDVKGLLGLYEASFHGLEGENILDEAQDFASKHLKNLNLNEIPTCLAKQVLHALDMPIRWRPNRLEARWFMDMYGKQQDMIPSLLRLGKLDFNLVQTIHRKEVSNLARYRWWVELGANKMTFSRDRLVENYFWSCLMVFEPQYTAYREMTTKIGCMVTLIDDVYDVYGTLEELVLLTDFIVRFWDITDIDNLPPTIRDSFMALYNTTNEIGHWTMREQGINPIPYMRKWADECRAYIKEVHWYNEGIKPTLKEYMSNAVDSIGGLIMLLHSYFLTTDNLTKEGLDYVSKIPRIMHCSAKILRLNDDLGTSSYELARGDNFKALECYMNETGASTEAAQQHIKHLVRETWKTMNKDACEDYPFPGFKPFLGACLNLARASQCFYQYGDGHGLPGHETRDHIVSTLFKPVPLD

>EglobTPS081

MALPALLTNFLPSSIRPNQHSFLLVSRPCSSFSSPSAISSGARFAKCSLTIEDQDTARRSANWKPSVWDYGSVQSLNTDFEDKYTEQVQRLKEEVKGLFHREINQVAKLEFIDVVQRLGLGYHFETDIKNALSSIYNNTEDAQLSDDLYAVSLRFRLLRQHGYNLQQDVFQRFMNKMGTFNESLKEDVRGLLSLYEASFHGLEGETIVDEAWNFASKHLKDLNLDDVPANLASNVSHALDMPIHWRPNRLEARWFMDTYEKQQDKIPCLLRFAKVDFNIVQSIHKKEVSNMARYRWWVELGANKMTFFRDRLVEHYFWCCAMVFEPQYTEFREMTTKLTCMVTLIDDVYDVYGTLEELEVLTDFIVRFWDITDVDKLPLKIRACFLALYNTTNEIGYWMMRERGINPIPHMRKVVISTCWADECKAYIKEARWYNKGIKPTLDEYVDNGVTSIGGLIMLLGSYFLTTDKPTEEGLDYVSNIPSVMHCSAKILRLNNDYELARGDNFKALECHMNETGASEEATREHIKHLVRKTWKRMNRDVFEDYPYSGFGPFLGACLNLARASQCFYQYGDGHGLPDHETKAHIVSSLFDPVPLD

>EglobTPS082

MALPAVSTSFPPSSIHHNQPSLLFFRNLRSSSSVATSSNSSGAQFVTCASKIEVQEIGRRPANWQPSVWDYDFVQSLSVDYTEDKYSEEVQRLKKEVKGLFDKEMNQVAKLEFIDMVQRLGLGYQFKMEIKNALSSIYTEDAQFSDDLEAVSLRFRLLKQHGYNIPQDVFQRFMSKTDTFNESLNEDVKGLLGLYEASFHGLEGETILDEAWTFASKHLKDLNLDEIPTNLVSHVSHALDMPIHWRPNRWFINMYEKQQDMIPSLLRLAKLDFNLVQSIYRMEVSHLARYRWWVELGANKMTFCRDRLVESYFWSNTMVFEPQHTAVREMNGKIASMVVLIDDVYDIYGTPEELELLTDFIVRFWDITNIDSLPPTIRDSFMALYNTTNEIGYWIMRERGINPIPYLQKVWANECKAFLKEVHWCSNGIKPTLKEYMDVATYSAGGLVLLLASYFLTTDKLTKEGLDYVSKIPSIMHCSSKMLRLINDFSTSSYEVARGDNLNALECYMNETGASEEAAREHITHMVREAWKWMNRAVFEDYPIPGIGPFLGACLNLARVCHTFYRYGDGFGHPSNDTKDYLVSAIYEPVPLD

>EglobTPS083

SNKYDSILQKEGIKERMEGLVEEVKPMLSEAVDSLAKLELIDCMTKLGLSNLFENEMKEALETVASIHNGVFTMEEHLYASALRFRLLRQHGHIVSQSEFNRSNGEDVKTMIELLEASHLALEGENILHEAKAFSTGILRERVSSLDGRLFKRTVHALELPLHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRRWWRDLGLMEHVDFTRDRLVESFLCALGLSQETRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAIWDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHRVLPHLAKAWADFCKALLTEAKWDNMGYTPSTIEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDVADLLERNKDLIYNVSMIIRLCNDLGTSAERDRGDAPSSVVCYMQEANVPEDVARKHIKELINQAWKSINAHCFGNVETPFVRTFIDVTVNASRVAHMLYQFGDGFGVQDGDIRRQILSAVIHPIALN

>EglobTPS084

MEYGTQQAQFKPCQANLPEVVGTMNQRRTANYKPNIWNYDFLQSLSSKHDSNKYDSILQKEGIKERIEGLVEEVKRILSEVVDSLAKLELIDSMTKLGLSNLFENEMKEALETVASINNDIFNMEDHLYANALWFRLLRQHGHIISQSEVELLEASHLALEGENILHEAKTFSTGILRKRVSSLDGRLFKRAVHALELPMHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRRWWRDLGLMEHVDFTRDRLVESFLCALGLSQEPRLSSHGSARKSLTKVVILILVIDDVYDLYGSLEELECFTSAISRRDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHRVLPHLAKAWEDFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNWEDVADLLERNKDLIYNVSMIIRLCNDLGTSAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAYCFSNADTPFVRTFIDVTANAARVAHMLYQFGDGFGVQDGDIRRQILSAVIHPLALN

>EglobTPS086

EVVGTMHQRRSANYKPNIWNYDFLQSLSSKHEGIKERMEGLVEEVKPMLSKSVDSLAKLELIDSMTKLGLSNLFENEMKEALERVASNNNGVFTMEEHLYASALRFRLLRQHGHIVSQSEFLFNRSNCEDVEAMIELLEASHLASEGENILHEAKAFSTGILRERVPSLDGRLFKCTVHALEIPLHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRRWWRDLGLMEHVEFTRDRLVESFLCALGLSQETRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAIWDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHLVLPHLAKAWADFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDVADLLERNKDLIYNVSMIIRLCNDLGTAERDRGDAPSSVVCYMREANVPEDVARKHIKELINQAWKSINAHCFGNVETPFVRTFIDVTVNASRVAHMLYQFGDGFGVQDGDIRRQILSAVIHPVALN

>EglobTPS087

SNKYDSILQKEGIKERMEGLMEEVKRMLSEVVDSLAKLELIDRMTKLGLSNLFENEMKEALETVASINNGAFTMEEHLYANALRFRLLRQHGHIISQSEFNRSYCEDVEAMIELLEASHLALEGENILHEAKTFSTGILHDRVSSLDGRLFKRAVHALELPSDWRVQFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDRWWRDLGLMEHVEFTRDRLVESFLCALGLSQEPRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAITRLSTRDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHRVLPHLAKWADFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDVADLLERNKDLIYNVSMIIRLCNDLGTSTAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAYCFSNAETPFVRTFIDVTVNAARVAHMLYQFGDGFGVQDGDIRRQILSAVIHPLALN

>EglobTPS088

MEYATEQAQFQPCQANLPEVVGTMHQRRSANYKPNIWNYDFLQSLSSKHDSNKYDSILQKQGIKERMEGLVEEVKPMLSEEVNSLAKLELIDRMRKLGLYNLFNDEMKEALEPVAFNRSYCEDVEAMIELLEASHLALEGENILHEAKAFSTGILRERVCPRFGASVALEGSVVRHQMANKLGEDKQSNLLELAKLNFNARESVHALELPLHWRVQWFDIKWQISLGRTSKAICLSLPNISTTHQRDLREISRRWWRDLGLMEHVDFTRDRLVESFEPRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAITRLSTWADFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDVADLLERNKDLIYNVSMIIRLCNDLGTSTAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAYCFSNAETPFVRTFIDVTANAARVAHMLYQFGDGFGVQDGDIRRQILSSVIHPLALN

>EglobTPS089

CLAHSPQVGSKTHQRRSANYKPSIWKYEFLQSLNDKYDELRSFKEGSNGLNGSNCQDVEAIVELLEASHLALEDENILNEAKTFSTGILHERVPGLDGLPFKRAAHYLELPMHRRVQWFDIKWQIDLYEQQEDKQSNLLELAKLNFNTVQATHQRDLIEISRWWRDLGLLEHVDFTRDRLVESFLCALGLSQEPRFSSLRKSLTKVIILILVIDDVYDLYGSLKELECFTSAITWDSEQIQQLPDCMKICFQVLHDVTYENAYDIGKDEDWHRVLPNLTKAWADFCKALLTEAKWDNIGHIPSLEEYLSNAWTSSSGPLILSHAYYFVGHMKLEDVEELLERNKYLIYNVSMIIRLCNDLGTAEKDRGDAPSSVVCYMREANVSEDVARKHIKELINQAWKSINAHCFGNAELPFLQPFIDVAMNAARVAHMLYQFGDGLGIQDGDIRRQILSTVIQPLALD

>EglobTPS090

MHQRRSANYRPNLWKYDFLQSLNNSYDLVRFEQVERLVEEVKPTLSEAVNSLLKLELIDKMKKLGLSNLFGNEIKEVLQTVASTNNGVFNMEDHLYASALQFRLLRQHGHVVSQGKFDVEAMIELLEASYLAMEGENILEEAKAFSTGILQERVSGLDGQLLKRAVHALELPMHWRVQWFDIKWQIDLYEQQEDKQSSLLQLAKLNFNIVQATHQRDLRDISRRWWRDLGLIEHVDFARDRLVESFFCALGLSQEPQFSSFRKSLTKVIILILVIDDLYDLYGSLEELECFTDAIWDLEQIQQLPECIKVCFQALRDVTYEIAHEIGKDEDWHQVVPHLMKAVSWADFCKALLNEAKWDKMGYTPSLEEYLSNAWTSSSGPLILSHAYYFMGQMKLEDAADMLKRNKDLIYNVSIIIRLCNDLGTSTAERERGDAPSSVVCYMREANVS

>EglobTPS091

QRRSANYKPNIWKYDFLRSLNNNFVHALELPMHWRVQWFDIKWQIDLYEQQEDKQSNLLELAKLNFNTVQATHQRDLIEISRRWWRDLGLIEPVQLTVYDLYGSLEKLECFTSAVTRLALSPPELFLEISKEEDWHRVLPCLTKAYLSNAWTSSSGPXLLSHAYFFVGAEIERGDAPSSMVCYMREANVSEDVARKHIKGLIDQAWKNINAHCFVNAETPFLRPYIDVTVNAARAAHMIYQSGDGFGVQDGTIGQQMLSAVIEPLSLD

>EglobTPS092

MALPALSTSFLPSSIHHNQPSLLFFRHLRSSSPAATSSTAFGAQFVTRASRIEVQEIGRHSANWQPSVWDYDYLQSLSVNYTEDKCSEEVQRLKKEVKVLLDGEMNQVAKLKLIDAVQRLGLGYQFEMEIRNALSSIYNNTEDAQLSENLDVVSLRFRLLRQHGYNIPQDVFQRFMSKTGTFNESLNEDVKGLLGLYEASFHGLKGETIIDEAWTFASKHLKDLNLNEIPTNLASHVSHALDMPIHWRLNRLEARWFIDMYKKQQDMIPSLLRLAKLDFNLVQSVYRKEVSNLARYTINLRWWVELGANKMTFCRDRMVESYFWSNSMVFEPQHTAFREMNGKIASMVVLIDDVYDIYGTLEELELLTDFIVRFRWDITDIDRLPPIIRDSFMAMYNMTNEIGYWTMRERGINPIPYLRKVWADQCKAYLKEVHWRSKGIKPTLKEYIDVATNSSGGLVLLLPSYFLTTDKLTEEGLDYVSKIPSIIRCSCKMTRLINDFSTSSHELARGDNLKALECYMNETGASEEAAREHIMHMVREAWKWMNRAVFEDYQIPGLRPFLGACLNMARICHTFYGCGDGFGQPSNDTKDSLASAIYEPVPLD

>EglobTPS093

MALQALSTSFLPSSFHHNQSPLLFFRHLRSSSSAATSSTTSSAQFVTCASKIEVQEIGRHSANWQPSVWDYDFLQSLTVNYTEDKCSEEVQRLKKEVKGLFDGEMNQVAKLKFIDVVQRLGLGYRFEMEIKNALSSIYNNTEDAQLSDNLDVVSLRFRLLRQHGYNTPQDVFQRFMSKTGTFNESLNEDVKGLLGLYEASFHGLEGETILDEAWTFASKHLKDLNLNEIPTNLASHVSHALDMPIHWRLNRLEARWFIDMYKKQQDMIPSLLRLAKLDFNLVQSVYTKEVSNLARYTINLAARWWVELGANKMTFCRDRIVESYFWSNSMVFEPQHTAYREMNGKLASMVVLIDDVYDIYGTPEELELLTDFIVRFRWDITDIDRLPPIVRDSFMAMYNTTNEIGYWTMRERGINPIPYLRKVWAEECKAYLKEVHWRSKGIKPTLKEYIDVATNSSGGVVLMLPSYFLTTDKLTEEGLDYVSKIPSIMRCSSKMLRLINDLSTSSHEVARGDNLKALECYMNETGASEEAAREHIMHMVREAWKWMNRAMFEDYRIPGLGPFLGACVNTARICHTFYGCGDGFGQPSNITKDSLASAIYDPVPLD

>EglobTPS095

MALPALSTSFFPSSIHHNQPSLLFFRHLRSSSSAATSSTASGAQFVTCASKIEVQEIGRHSANWQPSVWDYDFLQSLGVNYTEDKCSEEVQRLKKEVKGLFDREMNQVAKLKFIDVVQRLGLGYQFETEIKNALSSIYNNTEDAQLSDNLDVVSLQFRLLRQHGYNIPQDVFQRFMSKTGTFNESLNEDVMGLLGLYEASFHGLEGETIIDEAWTFASKHLKDLNLNEIPTNLASHVSHALDMPIHWRLNRLEARWFIDMYKKQEDMIPSLLRLAKLDFNLVQSVYRKEISNLARYRWWVELGANKMTFCRDRIVESYFWSNSMVFEPQHTAYREMNGKLASMVVLIDDVYDIYGTPEELELLTDFIVRFRWDITDIDRLPPIIRDSFMAMYNTTNEIGYWTMRERGINPIPYLRKVWAEECKAYLKEVHWRSKGIKPTLKEYVDVATNSSGGVVLMLPSYFLTTDKLTEEGLDYVSKIPSVMRCSSKMLRLINDLSTSSHEVARGDNLKALECYMNETDASEEAAREHIMHMVREAWKWMNRAVFEDYRIPGLGPFLGACVNTARICHTFYGCGDGFGQPSNITKDSLASAIYEPVPLD

>EglobTPS097

PVPCSASTRAALSQGGWRSPRYQPTLWSYDYLRSLPTSFLEQEVRSAMKDESAELSTILALVDDIQRLGLVFLFEEDVKRALRRYHSPDGGYKNRDQKTLHGTALFFRILRQNGFEVSDVFRIFMDERGTFMESLGRDVEGLLSLYEASHLAFEEEGILLEAKEFAVKHLKRLNDIDNGKDLEYFRVNRGSVPALHQRMPLLEARQSIEAYSPQRDVERRLLELAVYNFNMVQSILQRDLQEMSRSVWERGRWWNDVSLANELSFARDRLMECFFWTVGMAYEPQFSNLRKGLTKVTALVTTIDDVYDVYRSMDELELFTDAVWDVNALSNLPSCMKLCFLALYNAVHEMAYDVLKQNGENIIPCLTKAVSWSDMFKAFLQEAKWKHDKVTPTFEEYMNNGWISVSGLVILIHAFFLSTPDVRKEEIELIETHGHDLLKSPAIIFRLCNDLGTSSVRIAELERGETANSILCYMQDTGVSENVAREHIKELIDVEWKNMNRYQVDDSMFGKSFVRLAFNLARIAHYTYQDGDAHGDPDDRAKYRIHSLLIDPISL

>EglobTPS098

RVQMLEQEVRSAMKDENAELSTILALVDDIQRLGLIFLFEEDVKRALRRYHSLDGGHKNRDQKTLHGTALYFRILRQNGFEVQTDVFWIFMDEQGTFMESLGRDVEGLLSLYEASHLAFEDEDILHEAKAFAIEHLKRLNNIDVSKDLEYFQVNWGLALPLHQRMPLLEARRSIEAYRTRRDADRRLLELAVYNFNMVQSILQRDLQEMSRANETALVTTIDDVYDVYGSLDELELFTDAVHRFRWDVDAVSSLPGCMKLCFLALYNAVHEMAYDVLKQNGENIIPCLTKAWSDMLKAFLQEAKWKHNKVTPTFEEYMNNGWISVSGLVILIHAFFLSTPHIRKEELELIETYGHDLLKSPSIIFRLCNDELERGETANSILCYMQDTGVCENVAREHIKELIDSTFTLPRIAHHTYQDGDAHGAPNDRSKYRIHSLLIDPISL

>EglobTPS099

MALHLFSLPSVFSEKISRQVPRSTSTKAAFPQGGRRSANYQPSVWTHNDLPSLVTDEDRQSCRVVKVELQREKAQMVEEVRGALHDENAELITIFALVDDIQRLGLGRHFEEDISRALHRCLSPDVVYEGLQKSLHGTALSFRILRQHGFEVSQDVFKIFMDESGSFLKNLGQGMLSLYEASRLAFEDEDILREAETFTIEHLKNHNRDINKDLQGEVNHELEWPLHRRMSLLEARRFIEAYSRRRYTSHRILKFSATNFNTLQSTLQGDLQEVLWWDNVGLANELNFARDRLVECFFAAVAVADEHPLSNCRKGLTKANILNVIIDDVYDIYGTLDELGCSQVHRSSTNAVEDLPGYMKLCFLALYNCVNELAYDTLKETRENVIPYLTKAVHDWYDACEAFLQEAKWSHNKITPRVEEYLNNGWISVSGHVMLIHAYFLSSPSMRKEELESLEHYHDLLRLPSMIFRLTNDLATSSAELERGETTNSIWCYMQEMGVSELEARKYVIKMIDTTWKKLNKYLVNDSTFNQSFVRMAFNLARMAHCMYHDGDAVGAPDDLSMNRVHSLIIDPVSLEP

>EglobTPS100

RVQMLEQEVRSAMKDENAELSTILALVDDIQRLGLIFLFEEDVKRALRRYHSLDGGHKNRDQKTLHGTALYFRILRQNGFEVSKEQTDVFWIFMDEQGTFMESLGRDVEGLLSLYEASHLAFEDEDILHEAKAFAIEHLKRLNNIDVSKDLEYFQVNWGLALPLHQLIRWWNDVSLANKLSFARDRLMECFFWTVGMAYEPQFSNLRRGLTKVTALVTTIDDVYDVYGSLDELELFTDAVHRFRWDVDAVSSLPGCMKLCFLALYNAVHEMAYDVLKQNGENIIPCLTKAWSDMLKAFLQEAKWKHNKVTPTFEEYMNNGWISVSGLVILIHAFFPPHIRKEELELIETYGHDLLKSPSIIFRLCNDAELERGETANSILCYMQDTGVCENVAREHIKELIDTAWKKMNRYQVNNSLFGKSFVRLAFNLARIAHHTYQDGDAHGAPNDRSKYRIHSLLIDPISL

>EglobTPS101

LATPLLKLSSLTANGRVHCSVSTQVSDTQGGRRWANYQPTVWTYNYLSLVADGGRQSHCAVKVELQREKAQMLEEEVRGALNDEKAEPMTIFALVDDFQRLGLGQHFEEDISRALRRCLSNDAVNKSRQKSLHGTALSFRILRQHGFEVSQDVLKIFMDESGSFMKTLGGDVQGMLSLHEASHLAFEEEDILHGARSFAIEHLRNLNRNVNKDLQDQVKHELELPLHRRMPLLEARQSIEAYSRHGYTNHRILEFAVLNFNTSQSILQRDLQEMWWNNVGLANELNFARDRLVECFFAAVAVADEHPLSNCRKGLTKVNILNVIIDDVYDIYGTLDELELFTDAVRRRWDINAVEDLPGYMKLCFLALYNSVNELAYDTLKETRENVIPYLTKAVHDWYDSCEAFLQEAKWSHNKITPRVEEYFGWISVSGHVMLIHAYFLSSPSMRKEELESLEHYHDLLRLPSMIFRLTNDLATSSAELERGETTNSIWCCMQEMGVSELEARKYVIKLIDTTWKKLNKYLVNDSTFNQSFVRMAFNLARMAHCVYHDGDAVGAPDDLSRNHVHSLITDPVSLEPC

>EglobTPS102

MALRLLSAPYLPKLPSPTANGRVHCLASTQVSDTQGRRRSANYQPTVWTHNYLQSLDSDESRQSRHAVKQREKAQMLEEVRGALNDEKAEPMTIFALVDDFQRLGLGQHFEEDISRALRRCLSNDAVNKSRQKSLQGTALSFRIFRQHGFEVSQFKIFMDKSGSFMKTLGGDVQGMLSLHEASHLAFEEEDSLQEARSFAIEHLRNLNCNVDKDLKDQVKHELELPLHCRMPMLEAQSIEAYRRCGYTNHRIPEFAVTNFNTSQSILQRDLQEMEKVNFVRDRLMECFFWAVGVADEPTLANCRKRLTKVTSLITIIDDVYDVYGTLDELELFTDAVRRWDINAVDDLPGYMKLCFLALFNSVNEIAYDTLKETGKIVIPYLAKWYDLCKSFLQEAKWSYNKTNPRFEEYLNNGWISSSGHVILIHAYFLSSPSMRREEPESLEHYHDILRLPSMILRLTNDLGTSSELERGETTNSIMCYMQEMGVSESEARDYVMKLIDTSWKQMNKYLVNGSTFDQSFVRMAYNLARTTHFMYQDGDAHGAPDNRSRNRMHSLIIEPISL

>EglobTPS103

LLKLSSLTANGRVHCSVSTQVSDTQGGRRWANYQPTVWTYNYLQSLVADGGRQSRCTVKVELQREKAQMVEEVRGALHDENAELITIFALVDDIQRLGLGRHFEEDISRAVCLSPDVVYEGLQKSLHGTALSFRILRQHGFEVSDVFKIFMDESGSFMKTLGNDVQGMLSLYEASRLAFEDEDILREAETFTIEHLKNHNRDINKDLQGEVNHELEWPLHRRMSLLEARRFIEAYSRRRYTSHRILKFSATNFNTLQSTLQGDLQEVLWWDNVGLANELNFARDRLVECFFAAVAVADEHPLSNCRKGLTKANILNVIIDDVYDIYGTLDELYSQTLFAGPRWDINAVEDLPGYMKLCFLALYNCVNELAYDTLKETRENVIPYLTKAVHDWYDACEAFLQEAKWSHNKITPRVEEYLNNGWISVSGHVMLIHAYFLSSPSMRKEELESLEHYHDLLRLPSMIFRLTNDLATSSAELERGETTNSIWCYMQEMGVSELEARKYVIKMIDTTWKKLNKYLVNDSTFNQSFVRMAFNLARMAHCMYHDGDAVGAPDDLSMNRVHSLIIDPVSLEP

>EglobTPS104

VELQREKAQMLEEVRGALNDEKAEPMTIFALVDDFQRLGLGQHFKEDISRALRRCLSNDAVNKSRQKSLHGTALSFRILRQHGFEVSQDDFKIFMDKSGNFMKTLGGDVQGLLSLHEASHLAFEEEDILQEARSFAIEHLRNLNCKVDKDLQDQVKHELELPLHCRMPMLEAQRSIEAYRGCGYTNHRIPKFAATNFNTLQSILQRDLQEMWWNDVSLARNLNFVRDRLTECFFWAAGVADEPTLTNCRKRLTKVTSLITIMDDVYDVYGTLDELELFTDAVRRWDINAVDDLPGYMKLCFLALFNSVNEIAYDTLKETGKIVIPYLAKSYVNLVAPRFEEYLNNGWISSSGHVILIHAYFLSGPSMGREELESLEHYHDILRLPSMIFRLTNDLVTLSELERGETTNSITCYMQEMGVSESEARDYVMKLIDTSWKQMNKYLVNGSTFDQSFVRMAYNLARTTHFMYQDGDAHGSPDNLSRNRMHSLIIEPISLEPC

>EglobTPS105

YQPTVWTHNYLQSLEADESHQSRRAVKVELQREKAQMLEEVRGALNDEKAEPMTIFALVDDIQRLGLGQHFEEDISRALRRCLSNDAVNKSRQKSLHGTALSFRILRQHGFEVSQGIDVFKIFTDESGSFMKTLGGDVQGMLSLHEASHLAFEEEDILQEARSFAIEHLRNLNCNVDKDLQDQVKHELELPLHCRMPLLEARWSIEAYRRCRYPDHRIPEFAAMNFNTLQSILQRDLQEMWWNDVSLARNLNFVRDRLMECFFWAAGVADEPTLANCRKRLTKVTSLITIIDDVYDVYGTLDELELFTDAVRRWDINAVDDLPGYMKLCFLVLFNSVNEIAYDTLKETGKIVIPYLAKWYDLCKSFLQEAKWSYNKTNPRFEEYLNNGWISSSGHVILIHAYFLSSPSMRREELESLEHYHDILRLPSMILRLTNDLVTSSELERGETTNSIMCYMQEMGVSESEARDYVMKLIDTSWKQMNKYLVNGSTFDQSFVRMANNLARTTHFMYQDGDAHGAPDNRSRNRMHSLIIEPISL

>EglobTPS106

MALRLLFTPHLPVLSSRRANGRVRCSASTQISDPQEGRRSANYQPSVWTYNYLQSIVAGEGRQSRREVKVEQQKEKVQILEEEVRGALNDEKAETFTIFATVDDIQRLGLGDHFEEDISNALRRCVSKGAVFMSLQKSLHGTALGFRLLRQHGYEVSQGIDVFKIFLDESGSFVKTLGGDVQGVLSLYEASHLAFEEEHILHKARSFAIKHLENLNSDVDKDLQDQVKHELELPLHRRMPLLEARRSIEAYSRREYTNPQILELALTDFNVSQSTLQRDLQEMLGWWNNTGLAKRLSFARDRLIECFFWAVGIAHEPSLSICRKAVTKAFALILVLDDVYDVFGTLEELELFTEAVRRRWDLNAVEDLPVYMKLCYLALYNSVNEMAYETLKEKGENVIPYLAKAWYDLCKAFLQEAKWSNSRIIPGVEEYLNNGWVSSSGSVMLIHAYFLASPSIRKEELESLEHYHDLLRLPSLIFRLTNDAELERGETTNSIRCFMQEKGISELEARECVKEEIDTAWKKMNKYMVDRSTFNQSFVRMTYNLARMAHCVYQDGDAIGSPDDLSWNRVHSLIIKPISPAA

>EglobTPS107

MALPALFTTFLPSLTGYNQPSLFFSRLPRSSSSSSSSSTASGPQFMTRALKIEGQEIVRRSAEDQYTKQVQRLKKEVKGLFEREMNQVDKLEFFDVVQRLGLGYHFETEIKSALSLIYNNTEPSVWDYGLVQSLGVDYSDAQLSNDLYAASLRFRLLRQHGYNVPQDVFQRFMNMTGTFNESLSKDAKGLLGLYEASFHGLDGETILDEAWNFASKHLKDLNLDKVPSNLASNVSHALDMPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKIDFNLVQSIHRKEVGNLARYRWWVELGANKMTFFRDRLVESYFWTCIMAFEPQYTAFREMCTKIGCMVTLIDDVYDIYGTPEELELLTDFIIRFRWDITDIDKLPPTIRNSFMVLYNTTNEVGYQTMRDQGINPIPYLRKVWADECKAYMKEVHWYNSGIKPALKEYMDVAVDSIGGLILLLHSYFLTTDKLTKEGLDHVSKIPHELARGDNSKALECYMNESGASEEVAREHIRHLVRNIWKKMNKDVFEDYPFSGFGPFLGACLNLARASHCFYEYGDGHSLPGHQNKDHLVSTIFESVPLD

>EglobTPS108

MALPVLFPSFLPSSISHNQPSLLSFRHPRCSSSSFSSGAKSVTCAATIENPEIVRRSANWKPNVWDYEFLQSLRVDYTEDKYAEQVQRLKEEIKGLFNREMNQVAKLEFIDVVQRLGLGYHFEKEIKNALSSIYDNTGYAQLLNDLYAISLGFRLLRQHGYNIRQGIDVFQQFMNKTGTFNESLNKDVKGLLGLYEASFHGLEGETMLDEARNFASKHLKDLNLDKVPTMLASYVSHTLDIPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARYRWWVELGANKMTFFRDRLVEHYFWNCTMVFEPQYTAYREMTTKLACMVTLIDDVYDVYGTLEELELLTDFLVRLVLYDRWDITEIDKLPPTIRDSYMALYNTTNEIGYWTMRELGINTIPYMRKVWADECKAYIKEAHWYNKGIKPTLKEYMDNAVDSIGGSIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSTKILRLNNDLSTSSYELARGDNFKALECYMNETGASEEAAREHVKQMVHETWKRMNKDVFEDYPYSGLGPFLDACMNFARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPLD

>EglobTPS113

PHDLSFAKVAHPSSGITKRVEATKSMLGSMTDGEISISAYDTAWVALVEDVSGSGSPQFPEALRWIVDNQLPDGSWGDDLIFSPHDRIINTLACAQQVRNKKKRIPKDIMHQVPTTLLHSLEGMEGLNWEKLLKLQSADGSFLFSPSSTAFALMQTKDANCLDYLSRAVQRFNGGVPNVYPVDLFEHLWAVDRLQRLGVSRYFKDEIKECMSYVHRYCIRYWSEKGICWARNSRISDIDDTAMGFRLLRLHGHEVSAVSSDVFEQFKRGDVFSTFMGQSTEAVTGMFNLYRASELIFPGEKILEDAKSHAVKFLRRKREANELLDKWIRTKDLPGEVRVETRFYIEQYGGENDVWIGKTLYRFYLELAKLDYNNCQALHLSEWDNFQRRWYYESKLVDFGTSGKTLLYSYFTAAASIYEPERARERLAWAKTSVLVDAIASYCSRSSIPSKGGQGLIAALLGTLDQLSLEVLVARGKDIGHALRIAEKWLVGYEEEGDKYKGVVELLVQMIALGSGNSSFSDGRSSHPQYRHLCNLTNTICRHLAHRQTQKACENEDLPIQMAMQELVQLVLQDSAHRLDRDVKDAFFSVTRSFYYTAHCDPATIKSHIAKVLYERV

>EglobTPS114

SSEIGERVKAIKLMFWSMSDGKISTSAYDTAWVALVEDVGGSGNPQFPEALQWIANNQHPDGSWGDDLLFCPHDRILNTLACVVALKYWKIHPDKCDKGVGMSFFKDNISKLAEEKPEHMPIGFEVAFPSLIETAWKLEIEICDDSPVLQEIYANRNTKLNKRIPSDLLHQVPTSLLHSLEGMKELKWEKLLKLKNADGSFLFSPSATAFAFLQTRDLNCLNYLSRTVQRFHGGVPNVYPVDLFEHLWAVDRLQRLGVSRYFKEEIKECMSYVYRYCIRYWSDKGISWARNSNVADIDDTSMGFKLLRLHGYEVSAGTCQLLLRFFSFSCHSVSLEVFENFKNGNEFFSFMGQLIEPVTGMLNLYKASELIFPGEKILEDANRHAAKFLRRKQEANELFDKWIITKDLPGEVVGYALDVPWYANLPRVESRFYIDQCGGQNDVWIGKTLYRRMEYVDNDVYLELAKLDYNNCQALHLSEWDNFQRWYCESKLVDFGISGKTLLYSYFTAAASIYEPERAGERLAWAKTRVLVDAIASYLEGEGATREQRGAFVRAFIPDERGEGLIAALLGTVDQLSLEVLEARGKDISHPLRWEKWLVGYGEEGDKYKGVVELLVQMIALGACNSLLSDDLSSHPECHRLCNLTSTICRQLAHHQTQKVRKNENDQIEMAMQELAQLVLQNSTRGLNRDVKDAFFAVTRSFYYTAHCDTGTINSHIAKVLFER

>EglobTPS115

MSNKVELSISWYDTAWVAMVPFPGSPKSHRFPRSLSWLLNNKATPIRFNILLSGMIEQAGCLNLNLPLRSANLDSVSYERNFAVLRGLSEGSRIYLSHVSEGMGSLSDWEMIKKHQRKNGSLFNLPSTSAAALTHLQNVGCLRYLKLVVEKFGDASAPTIYPLGIYARLCMTENLERMGINCHFRKEIIDTLDDTYATSAMAFRILRSHGYDVSSRGEEEIFQHIATSAIAFRILCSHGYNVSSDNLFSCAIDQCGEIILDKINSWTGDFLKEGLLAGEMHADRLKDDMHEVDFPLDIQVDDALRFPLEESLTRAANRINIQLHNTNSMGILKCELQNFRNKDFLNLAMQDFNMCQAIILFSYARSYNFCNKDFLNLAVIDFNNCAIREEFKYLKRWVKEKKLDLKLARQKLAYCYFSAAETFLARQLLDTHISWAKNSVVVTVADDLFDVSGSAEGNEVLIRLLRKTISETGDKAVTWHGRNLTVHVAQIWLETLESMLTEAERARKKTVPTMDEDIANAHVSFGLGPTVLPALYLVGPKLSEKQVESPEYHNLFRLMSTSRRLLNDIQSYERESKQGKLHAVTLQMLDGSGTSEREAIERISSIIISMRRELLKLVLQEKDSIIPRACKDLFWKMSAVMHLFYMNADGFASDEKTSAVKALLDQPITLNEL

>EglobTPS116

EGSKERISDMFNKVELSLSSYDTAWVAMVPSPCSPQSPLFPRSVSWLMNNQLCDGSWGLPDHHPLLIKDALLSTLACVLALKQWGVGERQINKGLEYIASNSASVIDDRQHTPIGFNILLSGMIEQADCLNLNLPLRPADVDSVSYKRNLEVKRGRYLSYVAEGMGSSADWEMIMKYQRKNGSLFNSPSTTAAALTHLQNASCLHYLESVLEKFGDASVPTIYPLEIYARLCMIENLERLGIDRYFRKEVIHVLDDTYRTNRCWLQGEEEIFLDIATTAMAFRMLRSHGYDVSSEDQFCNTLEGYVKDAGSVLELYRASQLIINDDEIILDKINSWTYDFLRKGLHTGKMHANRLESYICGEVQVDDALKFPLHANLERVANRRNIELYNIDSTRVLKCGLRYSSCNFCNKDFLNLAVNDFNNCQAIYQEELKYLERRWVKEKRLDKLKFARQKLAYCYFSAAASFSPPQLSEARISWAKNGVLTTVVDDFFDVGGSAEELENFIWLVKRRWNVNMSADCCSEQVQIIFSALHSTISEIGDKAVTWQGRNVTGHVAQIWLELLESMLTEAKWTRKKVVPTMDEYMANAYVSFALGPIVLPALYLVGPKLSEEQVESLEYRKLFKLMSTCGRLLNDMQGFKQRESREGKLNAVTLQMLDRSSTSEREATERISSIIISKRRELLKLVLQERDSIVPRACKDLFWKMSTVLHFFYMDDDGFTSDEKTSAVKALLDQPITLNEL

>EglobTPS117

SQKSSIQSLINMIKRDLLSVIGSHSFLSPSPYDTAWLAMIPDPGLKFIHKNAELLLSRYTHGKFSRWIAIVLPGMVELARASSLEVVFPESVDRALADLFINRRQILREELVDKNQYCPLLSYLEALPSTYKISHETILKHLDSDGSLFQSPSATSRAYLSTGNEACLAYLQSLASNCASSGVPSLYPVDEDLTKLSMVHQLVRLGLTEYFDRENDEILAKIYRHINISFFRNYKHEKQITKSIHSIAAELYKDCLEFWLLRMHGYRVSPCMSCELYKFLNWFLFCWFLDHEEVRDHIWNTCNLMLPDEYELEKARIFSKKFLEKIASRETRDSSIISSSHCRMIEHELGLPWMARLDHLEHRTWMEEKDACVLWMGKFPYNRYLCLKRDSLLFFGFIRPSFVHNQDIVQLALQNYVLRQSVYRMELDVVKRYRWSETTGLRKMGFGREKTLYSYFAVAASISLPCNSDVRVLVAKSAIMITVADDFFDMEGSLEDLEKLTNAVQRYRWDGEGLTAHAKTIFEALDDLVTDFRMKCFKQSGKDIKKNLQEIWGETFHSWLMEAKWSKSGGAPPTQEYLDVGMTSIAAHILVLPSSCLASPTTPLHQLWSNAYQPITKLLMVITRLLNDIQSYLILSPCFYDFLTIQKEEKQGKLNFVLLYLKENPEASIEDSINFVQLLLEQLKKEFLLHVLEELCNLPEPSRRLHLGCLKVFHMFFNSSNRYDSETGMLHDIQKA

>EglobTPS119

IQIFMEFQKPSIQSLVQMIKREILPNMSSHSFLSSSPYNTAWLAMIPNPYQHDLPMFKGCLNWVLQNQNEEGFWGDYDHDEDEVSNKVECLASTLICMIMLKKWHVGLPSIEKGIREKLVDKKQYFPLLSYLEALPPTYKVSHETILKHLDSDGSLFQSPSATASAYLATGNACLAYLQSLALNCASNGGHINISFCRNYKHEKPIVKSIHSIAAELYKDCLGFWLLRMHGYKVSPCTSCKLYESLNWFLCWFLDREEVRDHIEKHYEYFSSVLLNIYRASNLMLPNEHELEKARTFSKKFLEKIASRGTRDSSIISSSHCRMVSGNIQIKHELGLPWMARLDHLEHRMWMEEKDACVLWMGKFSCHRFIRSSLVHNQDILQLALQNFEQRQSIYRMELDVLKRWSETTGLSKMGFGREKTVYSYFAVAASVSVPCNSDVRVLVAKGAVILTVADDFFDMEGSLEDLEKLTEAVQRYRWDGEGLSAHAKTIFEALDDLKCFKQLGKDIKKNLQNILVRKWGETFHSWLIEAKWSRSGDVRPTQEYLDVAMTSVGAHVLVLPPSCLASPTTSLHQLWSNPYQPITKLLMVISRLLNDIQTYDFLTFQKEEKQGKLNFVLLYLKENPGASIEDSINFVQLLLDQLKKEFLQHVLEEPCSVPELSRLLHLACLKVFNMFFNSSNRYDSDTDMLHDIQKANCALLFLKENPEASIEDPIKFVQLLLNQMKKEFLQHVLGDVCNLPEPGRRLHLGSLKVFHMFFNS

>EglobTPS120

NIVSSSFLSPSPYNTAWLAMIPNPHRHDCPMLCLNWVLHNQNEEGFWGDYDYEEHEMSDGGECLASTLVCMTVLKKWHVGSTLIEKGLVALATRPRHYFLPNHPKDLIIPVSTLAFCREKLVDRNQYYPLLSYLEALPPTYKIDGDGSLFQSPSATASAYLSTGHKTCLAYLQSLASNCSFCWFLDREEVRDHIEKHYEYFSSVLLNVYRASNLMLSDEQQLERVRTFSRKLLEKILSGETRDECIISSSHIEHELGLPWMARLDHLEHRMWLEEKDACVLWMGKLSVHNQDILQLALQDFVLRQSTYRMELDDEFRWSETTGLSKMEFCREKTTYSYFAVAASISLPCNSDIREVVAKSAIIVTVADNFFDMEGSLEDLEKLTDAVQRYRWDGEGLSGHAETIFKALVDLVTDFRVKCFKQSGKDIKKNLQDIWGETFHSWLMEAKWSRSGGAPPMQEYLDVGMTSIATHILVLPSSLHASPTTPLHQLWSSPYQPITKLLMVITRLLNDIQSYQQKEEKQGKLNFVLLYLKENPEASIEDSINFVQHLLDQLKKELLQHLKVFHMFFNSSNRYDSDMDMFHDIQKALVVPPRVPK

>EglobTPS121

MESQKSSFQSLVSTIKRDILSVMGSHSFLSPSPYDTAWLAMIPDPHRHERPMFEGCLNWVLQNQNEEGFWGHHDRPMFEGCLNWVLQNQNEEGFWGHHDYDRHEMPGGVECLASTLVCMTVLKKWHAGSPLIEKGGLKFIHKNAELLLSRYTHGKFSRWIAIVLPGMVELARASSLEVVFPESVDRALADLFINRRQSPFCREELVDKNQYCPLLSYLEALPSTYKISHETILKHLDSMVLYFNHPGSLFQSPSATSRAYLSTGNEACLAYLQSLASNCEAVPSLYPVDEDLTKLSLVHQLVRLGLTEYFDRENDEILAKIYRFCWFLDHEEVRDHIEKHYEYFSSVLLYIYRASNLMLPDEYELEKARIFSKKFLEKIASIEHELGLPWMARLDHLEQRRWSETTGLRKMGFGREKTLYSYFAVAASISLPCNSDVRVLVAKSAIMITVADDFFDMEGSLEDLEKLTNAVQRYRWDGEGLTAHAKTIFEALDDLVTDFRMKCFKQSGKDIKKNLQEIWGETFHSWLMEAKWSKSGGAPPTQEYLDVGMTSIAAHILVLPSSCLASPTTPLHQLWSNAYQPITKLLMVITRLLNDIQSYELILSPCFYDFLTIQKEEKQGKLNFVLLYLKENPEASIEDSINFVQLLLEQLKKEFLLHVLVELCNLPEPSRRLHLGCLKVFHMFFNSSNRYDSETGMLHDIQKA

>EglobTPS123

SSSPYNTAWLAMIPDPHQHDLPMFKGCLNWVLQNQNEEGFWGDYDHDEDEVSNKVECLASTLICMTMLKKWHVGSPLIEKGGLKFIHENMELLLPRNKHGKFPRWIAIVFPGMVDLARASGLEVVFPESVERIIADLFSNRQRILKRREKLVDMKQYFPLLSYLEVSHETILKHLDSDGSLFQSPSATASAYLATGNEACLAYLQTLALNCASNGGHINISFCRNYKHEKPIVKSIHSIAAELYKDCLGFWLLRMHGYKVSPCTISIVFCCWFLDREEVRDHIEKHYEYFSSVLLNIIEPAILCFRTNMNSRKQELSQRNFLRKSYQDILQLALQNFEQRQSIYRMELDVLKRRWSETTGLSKMGFGREKTVYSYFAVAASVSVPCNSDVRVLVAKGAVILTVADDFFDMEGSLEDLEKLTEAVQRYRKWGETFHSWLIEAKWSRSGDVRPTQEYLDVAMTSVGAHVLVLPPSCNDIKTYEVKFLWPSSYNWPLLPKWRSFIVALSPCFYDFLTFQKEEKQGKLNFVLLYLKENPGASIEDSINFVQLLLDQLKKEFLQHILEEPCSVPE

>EglobTPS125

REKLVDRNQYYPLLSYLEALPPTYKISHETILKHQDNDGSLFQSPSATASAYLSTGNETFLACLQSLVSFCWFLYREEVRDHIKKHYEYFSNVLLNVYRASNLMLPDEHKLEKARTFSKKFLEKIASGGTRGESILSLPWMARLDHLEHKMRLEEKDAFILWMGKLSCHRRSSLVHNQDILQLALHNFVLRQSIYRMELDVVKGYLCIWSSLINESRWSETTGLSKMGFGREKTTYSYFAVATSVSLPCNSDIREVVAKSAIIITVADDFFDMEGSLEDLEKLTNAVQRYPITKLLMVITRLLNDIQSYQQKEEKQGKLNFVLLYLKENPKASIEDSINFVQYLLEQLKKEFLKHVLEEPCSLPKPSKRLHLGCLKVFHMFFNSSNRYDSDMDMFHDIQKALVVPPLIPKLKSPMPLPEQLGPKPRVSVTKSLSGQFSLERFPRKSFVGCQMPP

>EglobTPS126

MEAQISLIQSLVNTIKREILLPNMVSSSFLTPSPYNTAWLAMIPNPHRHDCPMFKGCLNWVLHNHNEEGFWGDYDYEEHEMSDGGECLASTLVCMTVLKKWREKLVDRNQYYPLLSYLEALPPTYKISNETISVDGDGSLFQPPSATASAYLSTGHKTCLAYLQSLFCWFLDREEVRDHIEKHYEYFSSVLLNVYRASNLMLSDEQQLERARTFSRKLLEKILLRETRDECIISSSHRRMVIEHELGLPWMARLDHLEHRMWLEEKDACVLWMGKLSWHRNQDILQLALQDFVLRQSTYRMELDVVKRWSETTGLSKMEFCREKTTYSYFAVATSISLPCNSDIREVVAKSAIIVTVADDFFDMEGSLEDLEKLTNAVQRYWGETFHSWLMEAKWSRSGGAPPMQEYLDVGMTSIATHILVLPSSCLASPTTPLHQLWSSPYQPITKLLMVITRLLNDIQSYQQKEEKQGKLNFVLLYLKENPEASIEDSINFVQHLLDQLKKELLQHVLEEPCSLPKPSRRLHLGCLKVFHMFFNSSNRYDSDMDMFHDIQKALVVP

>EglobTPS128

MEFQKSSIQSLVNMIKRDILSIMGSHSFLSPSPYDTARLAMIPDPRRHDHPMFEGCLNWVLHNQNEEGFWGYHDYDTHEIPDGVECLASTLVCRIVLKKWHAGSPLIEKGTACFTSNGLKFIHKNGELLLSRYKHRKFSRWIAIVLPGMVELARASSLEVVFPESIERALANLFINRRQILERQEELVDKNQYCPLLSYLEALPPTYKISHETILKHLDSDGSLFQSPSATSSAYLSTGNEACLAYLQSLASNCVPSLYPVDEDLTKLSMVHQLVRLGLTEYFDRENDEILGQIYRFRNYKHEKQITKSIHSIAAELYKDCLEFWLLRMHGYFCWFLDHEEVRDHIKKHYEYFSSVLFYIYRASNLMLPDEHKLEKARIFSKKFIEKIASRETRDSSIISSSHCRMVIEHELGLPWMARLDHLEHRTWMEEKDACLLWMGKFPYNRYCLKRNSLILSNQDIVQLALQNYVLRQSVYRMELDVVKRYRWSETTGLRKMGFGREKTLYSYFAVAASISLPCNSDVRVLVAKSAIIITVADDFFDMEGSLEDLEKLTNAVQRYRWDGEGLTAHAKTIFEALDDLVTDFRMKCFKQSGKDIEKNLQEIVSWGETFHSWLMEAKWSKSGAAPLMQEYLDVGMASIAAHILVLPSSCLASPTAPLHQLWPNAYLPITKLLMVITRLLNDIQSYKTLQKEEKQGKLNFVLLYLKENPLLEQLKKEFLQHVLEELCNLPEPSRRLHLGCLKVFHMFFNSSNRYDSETGMLHDIH

>EglobTPS129

HINISFFRNYKHEKQITKSIHSIAAELYKDCLEFWLLRMHGYRVSPCMSCELYKFLNWFLCWFLDHEEVRDHIGIHYEYFSSVLLYIYRASNLMLPDEYELEKARIFSKKFLEKIVSIEHELGLPWMARLDHLEHRTWMEEKDACVLWMGKFPYLFFGFIRPSFVHNQDIVQLALNYLLRQSVYRMELDVVKRYRWSETTGLRKMGFGREKTLYSYFAVAASISLPCNSDVRVLVAKSAIMITVADDFFDMEGSIEDLEKLTNAVQRYRWDGEGLTAHAKTIFEALEDLVTDFRMKCFKQSGKDIKKNLWGETFHSWLMEAKWSKSGGAPPTQEYLDVGMTSIAAHILVLPSSCLTSPTSPLHQLWSNAYQPITKLLMIITQLLNDIQSYENPEASIEDSINFVQLLLEQLKKEFLQHVLEEHCNLPEPSRRLHLGCLKVFHMFFNSSNCYDSKTGMLHDI

>EglobTPS131

RLAIDYHFEDEIEAILQRHLLISTSRSHSRSIDADNLHEAALRFRLLRQGGYPVPSGSFNDGTQNEKPQDNDILGLTSLFEASQLGIEGEDALDQVGESTRLRLHSSLADLDHVQARFVRNSLGNPFHKSLARFTANDFLRNFVGHSCSWTKNLGELAHLDMNIVRSVHQREILQVSKYTKPISFIYIIDDIFDVYGTMDELSSFMDVVNRYIIRWECTEKDNIPDYMRMCFHALDDITNEFSLAVYKNHGWNPLHSLRKESVDHLENIPEIVSSTASILRLWDDLGSAEQDEFQDGRDGSYVECYKREFQGSSEEAARDHVKKMISEAWKSLNKACLYPQPFTNSFSKASLNTARMVPLMYNYDDSHSLPLLEHHMKSLLFK

>EglobTPS132

KHDQKIKSLIDFLNKVVNEPVESLIIVDMIQRLGVKSLFREQIKARQYTHFSSLNHGKDDVYEIALRFRLLRQEGYRVPAGLFDVFEYFNEKGKGFVMKLEGNIKGMMELYEASQMSTEGEDILDEAECFSSKCLNALLTCDLDNEQARMIESTLQYPYRKSFARLLAPQSFVNDIANLWMEDLLEVANRKRRIDQYVHQKEIHQINKRWWKELGLGEKMEFARDQPLKWYMWSMAILTDPSLSELRVELSKPISLVYIIDDIFDVHGTVDELILFTELIKRYRWDNACAEQLPEYMKICFKVLNDIANDFGRIIFENHGWNPTRFLKQWANLCNAFLVEFQWNASGKLPKADDYLKNAIITSGVPLVLTHLMGQNIANQSMDSKKEEVQLPNIIYLIAEILRLWDDLGCAQSMKDENQNGYDGSYVDCYLGENEGSSYQSAREHVMKLISKLWKLLNKECLSPCPSSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQDHMKSL

>EglobTPS133

DALQRLAIDYHFEDEIEAILQRHLLISTSRSHSRPIDADNLHEAALRFRLLRQGGYPVPSGVFQRFLHDGTQNEKPQDNDILGLTSLFEASQLGIEGEDALDQVGESTCLRLHSSLADLDHVQARFALGNPFHKSLARFTANDFLRNFVGHSCSWTKNLGELAHLDMNIVRSVHQREILHVSKWWKELGMAKELKCARDQLTETGLSQERVLVTKPISFIYIIDDIFDVYGTIEDLTAFTDRWECTEKDNIPDYMRMCFHALDDITNEFSLAVYKNHGWNPLCSLRKWASLLNAFLVEARWLASGHSPTTQDYLDNAIVSSGVHVLLVHLFFILGERIAPESVDHLENIPEIVSSTASILRLWDDLGSAEQDEFQDGRDGSYVECYKREFQGSSEEAARDHVKKMISEAWKSLNKACLYPQPFTKSFSKASLNTARMVPLMYNYDDSHSLPLLEHHMKSLLFK

>EglobTPS134

DNSGTKHEEKIKSIIGFLNNVGGEPVESLIIVDMIQRLGIKPLFQEQIKAILRWQYTHFTSLNHGKDNVYEIALRFRLHRRYAFYADVFEYFKDKGKGFIMKVEGNVKGMMELYEASQMSIEGEDILDEAKCFSSKCLNELLTCDLDPEQVRMIESTLRYPYRKSFARSLAPLSFVNNMPGVNSWIEDLLEVANRERRIVQSMHQKENHQINWWKESGLGEEMKFARDQPLKWYLWSIAILTDPLSELRVELVKPISLVYIIDDIFDVYGKVDELILFTGVIKRYTYRWDDACAEQLPEYMKKCFKVLSDITNDFGNIIFEKHGWNPTRFLKQWANLCNAFLVEFQWNASGTLPKADDYLKNGIITSGVPLVLAHLFFQMGQNIANQSMDSKKEEVPLPNTIFLVAEILRLWDDLGCAQSSKNKNQNGYDGSYVECYLRENQGSSYQSAREHVMELISKSWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKNGLGLLQDHMKSL

>EglobTPS136

DDSRIKHDEKTKSLIDFLNKVVNEPVESLIIVDMIQRLGVKSLFREQLKIKAILRWQYTHFSSLNHGKDDVYEIALRFRLLRQEGYHVPAGLFADVFEYFNDKGKGFVMKLEGNIKGMMELYEASQMSTEGEDILDEAGCFSSKCLNALLTCDLDHEQARMIESTLQYPYRKSFARLLAPQSFVNDMPGANSWMEDLLEVANRKRRIDQYVHQEEIHQINKYWKELGLGEKMEFARDQPLKWYMWSMAILTDPSLSELRVELIKPISLVYIIDDIFDVHGTVDELILFTRWDNACAEQLPEYMKICFKVLNDIANDFGKIIFEKHGWNPWANLCNAFLVEFQWNASGKLPKADDYLKNAIITSGVPLVLTHLFFLMGQNIANQSMDSKKEEVQLPNIIFLVAEILRLWDDLGCAQSLKDENQNGYDGSYVECYLRENEGSSYQSAREHVLNKECLSPCPFSAPFLEACVNAAKMVSLMYYEDKHGLGLLQDHMKSL

>EglobTPS137

ISTVQDDSRIKHEEKVKSITGFLNNVVSEPVESLIIVDMIMRLGIKSLFQEQIKAILQWQYTHFTSLNHGKDDVYEIALRFRLLRQEGYYVPAGLYAFYADVFEYFKDKGKGFIMKLEGNAKGMMELYEASQMSIEGVDILDEAECFSSKCLNELLTCDLDPEQVRMIESTLRYPYRKSFARSLAPLSFVNDMPVANSWMEDLLEVANRERRIIQSLHRKEIHQIRWWKELGLGEEMEFVRDQPLKWYMWSMAILTDPSLSELRVELIKPISLVYIIDDIFDVYGKADELILFTEVIERYTVRWDNACAEQLPQYMKKCFKVLSDITNDLGNIIFEKHGRNPMGFLKQWANLCNAFLVEFQWNASGKMPKADDYLKNGIITSGVPLVLAHLFFLMGQNIANQSMDSKKEEVPLPNTIFLVAEILRLWDDLGCAQSLKDENQNGYDGSYVECYLRENQGSSYQSARKHVMELISKSWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQDHMKSL

>EglobTPS138

IKHEEKIKSIIGFLNNVGGEPVESLIIVRLGIKPLFQEQIKAILRWQYTHFTSLNHGKDNVYEIALRFRLLRQEGYYAFYADVFEYFKDKGKGFIMKVEGNVKGMMELYEASQMSIEGEDILDEAECFSSKCLNELLTCDLDPEQVRMIESTLRYPYRKSFARSLAPLSFVNDMPGLNSWIEDLLEVANRERRIVQSVHQKENHQINWWKESGLGEEMKFARDQPLKWYLWSIAILTDPSLSELRVELVKPISLVYIIDDIFDVYGKVDELILFTGVIKRRWDDACAEQLPEYMKKCFKVLSDITNDFGNIIFEKHGWNPTRFLKQWANLCNAFLVEFQWNASGTLPKADDYLKNGIITSGVPLVLAHLFFLMGQNIANQSMDSKKEEVPLPNTIFLVAEILRLWDDLGCAQSSKDENQNGYDGSYVECYLRENQGSSYQSAREHVMELISKSWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKHGL

>EglobTPS139

DDSRIKHDEKTKIDFLNKVVNEPVESLIIVDMIQRLGVKSLFREQIKAILRWQYTHFSSLNHGKDDVYEIALRFRLLRQEGYHVPAGLFADVFEYFNDKGKGFVMKLEGNIKGMMELYEASQMSMEGEDILDEAGCFSSNCLNALLTCDLDHEQARMIESTLQYPYRKSFARLLAPQSFVNDMPGANSWMEDSLEVANRKRRIDQYVHQEEIHQINKRWWKELGLGEKMEFARDQPLKWYMWQFSMVHVAILTDPSLSELRVELIKPISLVYIIDDIFDVHGTVDELILFTEVIKRYTIMKICFKVLNDIANDFGKIIFEKHGWNPTRFLKQWANLCNAFLVEFQWNASGKLPKADDYLKNAIITSGVPLVLTHLFFLMGQNIANQSMDSKKEEVQLPNIIFLVAEILRLWDDLGCAQSLKDENQNGYDGSYVECYLRENEGSSYQSAREHVMKLISKLWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQDHMKSL

>EglobTPS140

DDSRIKHDEKTKSLIDFLNKVVNEPVESLIIVDMIQRLGVKSLFREQIKAILRWQYTHFSSLNHGKDDVYEIALRFRLLRQEGYHVPAGLFADVFEYFNDKGKGFVMKLEGNIKGMMELYEASQMSMEGEDILDEAGCFSSNCLNALLTCDLDHEQARMIESTLQYPYRKSFARLLAPQSFVNDMPGANLWMEDLLEVANRKRRIDQYVHQEEIHQINKWKELGLGEKMEFARDQPLKWYMWSMAILTDPSLSELRVELIKPISLVYIIDDIFDVHGTVDELILFTEVIKRYTIRWDNACAEQLPEYMKICFKVLNDIANDFGKIIFEKHGWNPTRFLKQWANLCNAFLVEFQWNASGKLPKADDYLKNAIITSGVPLVLTHLFFLMGQNIANQSMDSKKEEVQLPNIIFLVAEILRLWDDLGCARSLKDENQNGYDGSYVECYLRENEGSSYQSAREHVMKLISKWWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQHHMKSL

>EglobTPS141

FQEDIRGRHERRLEEQVRGDSLESLVMVDALQRLAVDYHFEDEIEAILQRHLLISTSQSHSRTIDADNLHEAALRFRLLRQGGYPVPSDVFQRFLHKMNDGTQNEKPQDNDILGFTSLFEASQLGIEGEDALDQVGESTRQRLHSSLADLDRFVRNSLGNPFHKSLARFTANDFLRNFVGHSYSWTKNLGELAHLDMNIVRSVHQREILQVSKWWKELGMAKELKCARDQPMKWYMWPMAILTETGLSQERVLVTKPISFIYIIDDIFDVYGTIEDLTAFTDVVNRYIIWSYRWECTEKDNIPDYMRMCFHALDDITNEFSLAVYKNHGWNPLCSLRKWASLLNAFLVEARWLASGHSPTTQDYLDNAIVSSGVHVLLVHLFFILGERIAPESVDHLENIPEIVSSTASILRLWDDLGSAKQDEFQDGRDGSYVECYKREFQGSSEEAARDHVKKMISEAWKRLNKACLYPQPFTNSFSKASLNTARMVPLMYNYDDSHSLPLLEHHMKSLLFK

>EgranTPS001

MSARFSVIPSSSLPQETGCVEGRRSANFHPSIWGDYFLKYASDSNSLEERIDRLKGEVRKMLTSAMYKPAEKLNLIDQIQRLGIAHFELEIDKELEQIRRGYFEFHCDDNNNDLDTIALLFRLLRQRGSHVSCIFNKFKDGDGNFGKSLIPDVQGLLSLFEACHLRYHGDDNLEDALAFTTTHLESVDKRKASLDLKKKVSHALNQPIHKGMSRLEMRCYIPLYQEESSHNEVLLSLAKLDFNLVQEQHRKELGNLTRWWKGLDVQRKFPFARDRLVELYVWWLGEYYEPEHEAAREILTKLSSVSSIIDDIYDVYGTWEELELFTETIQRWDVDAKDGLPEYMQECYKIVLDLYDEIGYEFSRKGHSYRLFYAKEVMKNQVRAYFVEAKCFHQNHVLTMEEYMSIALPSSGFVSILAWSFLGMGDIVTKDVFDWLLFNDPKMVKASSIICRLLNDIAGHFEQERGHVASAVECFMKQYRVTEEEAKEELRKQVTDAWKDINEELRRPTVVPMPILVRILNLTQALHMMYNGEIDNYTHAGTKMKEHVTSLLVNPLPM

>EgranTPS002

MSARFSVIPSSSLPQETGCVEGRRSANFHPSIWGDYFLKYASDSNSMEERIERLKGEVGKMLTSAMYKPAEKLNLIDQIQRLGITYHFELEIDKELEQIRKGYFEYHCDDNDNDLDTVALLFRLLRQRGYRVSCEIFNKFKDGDGNFGKSLIADVQGLLSLFEACHLRYHGDDNLEDALAFTTTHLESVDKRKASLHLEKKVSHALNQPIHKGMSRLEARHYIPLYQEEPSHNEVLLSLAKLDFNLVQEQHRKELGNLTRWWKGLDVQRKFPFARDRLVEMYVWWLGEYYEPEHEAAREILTKLSSVGSIIDDIYDVYGTWEELELFTEAIERWDVDAKDGLPEYMQECYKIVLDLYDEIGYEFSQKGRSYRLFYAKEVMKNQARAYLVEAKCFHQNHVPTMEEYMSIALPSSGIVSILAWSFLGMGDIVTKDVFDWLLFNDPKMVKASSIIGRLLNDIAGHFEKERGHVASAVECFMKQYRVTEEEAKEELRKQVTNAWKDINEELCRPTVVPMPILVRILNLTQALHMMYTGETDHYTNAGTKMKEVVTSLLVDPLPM

>EgranTPS003

MSFQISAVPSSSPRLGTGHVIQRRSAGYHPSIWGDYFVKYASPSTSMEEQIEELKGEVRKMLTNVVDKSSQMLHLIDQIQRLGIYYHFEHEIDEHLEEIHKHYSRLDHGNFKGDDLRMVALIFRLLRQQGYDVSSEVFNKFKDSEGNFRASLTSDVCGLLSLYEACHLRCHGDTILEEALPFAITHLESINESKVSTSLAKQVSHALKQPLRKGLPRLEARHYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKDIDVPRNFPFARDRIVELFFWVSGVYFEPEFVEARDILTKVIALTSILDDVYDVYGTLEELVLITEAIQKWDVDAMDVLLEYMQVYYKELLHLYEEIGNEVAAKGRSYRLVYAKETMKRQARAFFQEAKWFQTNYTPTMEEYMPLQLKTTGYGMLATTSLVGMGNVVTKHAFEWSLSDCKIVKAAETICRLMDDISSHHFEQKRGHLVSSVELLMKEHGFSEQEAEKKLRKRVNDAWKDTNEEFLRPTAVPTPILTRVLNLSRAMDVLYSDGDNYTHSGTKLKGYVTSLFVSPLPM

>EgranTPS004

MSFQISAIPSSSPRLGTGHVIQRRSAGYHPSIWGDYFVKYASPSTSMVCGFSEEQIEELKGEVRKMLTNVVDKSSQMLHLIDQIQRLGIDYHFEHDIDEHLEEIHKHYSRLDHGDFKGDDLHMVALIFRLLRQQGYDVSSEVFNEFKDSEGNFRASLTSDVCGLLSLYEACHLRCHGDTILEEALPFAITHLESINESKVSTSLAKQVSHALKQPLRKGLPRLEARHYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKDIDVPRNFPFARDRIVELFFWVSGVYFEPQFVEARDILIKVIALTSILDDVYDVYGTLEELVLITEAIQKWDVDAMDVLPEYMQVYYKELLHLYEEIGNEVAAKGRSYRLVYAKETMKRQARAFFQEAKWFQTNYTPTMEEYMPLQLKTTGYGMLATTSLVGMGDVVTKHAFEWSLSDCKIVKAAETICRLMDDISSHHFEQKRGHLISSVELLMKEHGFSEQEAEKELQKRVNDAWKDTNEEFLRPTAVPTPLTRVLNLSRATVMRYYTHSGTKLKGYVTSLFVSPPM

>EgranTPS005

DDGIEGLKGELRKMLVGAMDKPSQKLNLIDQIQRLGIAYHFEIEIYQQLEQIHKSYYELHDGDNDNDLHTIALLFRLLRQQGYAISSKVFSIVTIDDIYDVYGTLEDTFTEAIERWDVEVKDGLPEYMQVCYKIVLDLYDEIGYEVTRKGRSNYLLYAKEAMKNQVRAYFTEAKWFHQNHIPMMEEYMPIALSTIAIELLLVMLLLLGMGDTVTKDVFDWLLYSKPKIVNAMKIVCRLMDDIAGHFEQERGHGPSSMECFMKQYGVTEEEAKEELHKQVANAWKDINEGLCCSTNVPRQLLVRILNFTRVVHVVYKDEIDLYTHAGTKLKEHVTNLYVNPLPM

>EgranTPS006

MSLQILAIPSSSPAQETSRVVERRLANFHPSIWGDYFLKYASDSNSMSSAIADDRIEGLKGELRKMLAGAMDKPSQKLNLIDQIQRLGIAYHFEIEIYQQLEQIHKSYYELHDGDNDNDLHTIALLFRLLRQQGYAISCEIFNKFKDINGNFSESLIVDVQGLLSLFEACHMRFHGDDVLNDALAFAMTHLEAIDKGKASPNLKRQVRHALKQPIHKGIPRLEARHYISLYQEEPLHNEVLLSLTKLDFNLLQEQHQKELGNLTRWWKDLDVERKFPFARDRLVEMYLWMSGVYFEPEYEATRELLTKVFSIVTIIDDIYDVYGTLEELELFTEAIERWDAEVKDGLPEYMQACYKIVLDFYDEIGYEVTRKGRSDYLFYAKEAMKNQVRAYFTEAKWFHQNHIPTMEEYKSIALPTTAIELLLVMLLLGMGDTVTKDVFDWLLYSDPKMVNALKVVCRLMDDIAGHKFEQERGHGPSSMECFMKQYRVTEEEAKEELHKQVANAWKDINEGLCCSTNVPRQLLVRILNFTRVVHVVYKDEIDLYTHAGTKLKEHVTNLYINPLPM

>EgranTPS007

MSLQILAIPSSSPAHETSRVAERRLANFHPSIWGDYFLKYASDSNSVSSPAIAEDRIEGLKGELRKMLIGAMDKPSQKLNLIDQIQRLGIAYHFEIEIYQQLEQIHKSYFELHDGDNDNDLHTIALLFRLLRQQGYAISCVRHALKQPIHKGIPRLEARRYISLYQEEPLHNEVLLSFTKLDFNLLQEQHQKELGNLTRWWKDLDVERKFPFARDRLVEMYLWMSGVYFELEYEATREILTKVFSIVTIIDDIYDVYGTLEELELFTEAIERWDVEAKDGLPEYMQACYKIVLDLYDEIGYEVTRKGRSDCLFYAKEAMKNQVRAYFTEAKWFHQNHIPTMEEYMPIALPTTAVELLLVMLLLGMGDTVTKDVFDWLLYSNPKMVNAVKVVCRLMDDIAGHKFEQERGHGPSSVECFMKQYGVTEEEAKEELHNQVANAWKDINEGLCCSTNVSRQLLVRILNFTRVVHVVYRDEIDLYTHAGTKLKEHVTNLYVNPLPM

>EgranTPS008

DSSHVPERRSANFHPSIWRDYFLKYASDSNSMDDRIEKLKGEVRKMLIDAIDKPSQKLNLIDQIQHVGIADHFEIEINQQLEQIHESYFNFHSGDKDSDLHTTALLFRLLRQQGYTISCEIFNKFKDNNGNFNESLIADVQGLLSLFEACHTRFHGDDVLNDALAFTMTHLKSIDEGKASPNLKKQVSHALNQPIHKGIPRLEARQYIPLYQEKPSHNEVLLALAKLDFNLLQEQHQKELGNLTRWWKNLDIERKFPFARDRLVEMYLWMSIVYFESDYEAAREILTKVASMVSIIDDIYDVNGTLEELGLFTEAIERWDINAKEGLPEYMQACYKTVLDLYDEIGYEVTSKGQSYQLFYAKEAMKNLVRAYFAEAKWFHLNHVPTMEEYMPIALTSAAVELLLVTSLLGMEDFVTKDAFDWLLYGNSKMVKAVKLVGRLMDDIAGHFEQERGHGPSSVECFMKQYKVTEEEAKVELRKQVADAWKDINEGLCCPAIVPRPLLVRILNFVRAMHVMYKDEIDIYTHAGTKLKEYVTSLYVNPLPM

>EgranTPS009

MSLPIMAISSSSPAQETSHVPERRSANFPPSTWRDHFLKYASDSNSDDRIEKLKGEVRKMLTDAIDKPSQKLNLIDQIQRVGIAYHFEIEINQQLEQIHDSYFNFHNSNKDSHLHTIALLFRLLRQQGYTISCEIFNKFKDSNGNFSESLIADVQGLLSLFEACHTRFHGDDILNDALAFTMTHLKSIDEGKASPNLKKQVSHALNQPIHKGIPRLEARHYIPLYQEEPSHNEVLLALAKLDFNLLQEQHQKELGNLTRWWKNLDVERKFPFARDRLVEMYLWMSIIYFESDYEAARKILTKVASMVSIIDDIYDVHGTLEELRLFTEAIERWDIKAKEGLPEYMQACYKTVLDLYDEIGYEVTRKGRSYRLFYAKEAMKNQVRAYFAEAKWFHQNYVPTMEEYMPIALATAAIELLLVTLLLGMEDFVTKDAFDWLLYGNSKMVKAVKLVGRLMDDIAGHFEQERGHGPSSVECFMKQYEVTEEEAKEELRKQVADAWKDINEGLRCPTIVPRPLLVRILNFARAMHVVYKDEIDIYTHAGTKLEEHVTSLYVNPLPM

>EgranTPS010

MSLPIMAISSSSPAQDSSHVPERRSANFHPSIWRDYFLKYASDSNSMDDRIEKLKGEVRKMLTDAMDKPSQKLNLIDQIQRVGIAYHFKIEINQQLEQIHESCFNFHNGDKDSHLHTTALLFRLLRQEGYTISCEIFNKFKDSNGNFNESLIADVQGLLSLFEACHTRFHGDDVLNDALAFTMTHLKSIDEGKASPNLKKQVSHALNQPIHKGIPRLEARQYIPLYQEKPSHNEVLLALAKLDFNLLQEQHQKELGNLTRWWKNLDIERKFPFARDRLVEMYLWMSIVYFESDYEAAREILTKVASMVSIIDDIYDVNGTLEELGLFTEAIERWDINAKEGLPEYMQACYKTVLDFYDEIGYEVTSKGQSYRLFYAKEAMKNLVRAYFAEAKWFHLNHVPTMEEYMPIALTSAAVELLLVTSLLGMEDFVTKDAFDWLLYGDSKMVKAVKLVGRLMDDIAGHFEQERGHGPSSVECFMKQYKVTEKEAKVELRKQVANAWKDINEGLCCTAIVPRPLLVRILNFVRAMHVMYKDEIDIYTHAGTKFKDYVTSLYVNPLPM

>EgranTPS011

MSVQVPAIPSSSPSKGRSGGVERPLAEFHASVWGDHFIKYASPSYSTKFKFLGRVEEQVEELKGEVRKMVINAVDKPSQMLHLIDQIQRLGIDYHFEQEIDAQLERIHKSYSQLDHGDFKGDDLHMVALMFRLLRQQGFNISSEVFNNFKDNEGNFKKSLITDVRGLLSLYEACHLRCHGDAILEEALPFAITHLESIDERKVSTSLAKQVSHALKQPLCKGLPRFEARHYIIFYQEEPSHDEVLLTMAKLDFNLLQEQHQKELGAITRWWKNIDVARKFPFARDKIAEMFFWMVGVYFQPEFAVARNILTRVTALISILDDIYDAYGTLEELVPYTEAIEKWDVDAMDGLPEYMQAHYKEILNLYDEIGSDLATKGRSYRLTYAKEAMKKQAKWYFHEAKWFHTGYTPTLEEYIPLALLTTGYEALSITSLVGMGDVVTRDAFEWLLGDCKILRASQIICRFMDDISSHKFEQKRGHVASSVELFMKENHASEQEAEEELQKRVVDAWKDINEEFLRPITAPMPVLTAILNLSRVMDLLYSNGGDHYTHSKTELKEHITSLFVSPLPI

>EgranTPS012

MSVQILTIPSSSPSKGRSGGVVRWPNFMRAYGAITSSNTLPPATQWLEEQVEELKGEVRKMVINAVDKPSQMLHLIDQIQRLGIDYHFEQEIDAQLERIHKSYSQLDHGDFKGDDLHMVALMFRLLRQQGFNISSEVFNNFKDNEGNFKKSLITDVRGLLSLYEACHLRCHGDAILEEALPFAITHLESIDERKVSTSLAKQVSHALKQPLRKGLPRLEARHYIIFYQEEPSHDEVLLTMAKLDFNLLQEQHQKELGVITRWWKNIDVARKFPFARDRIAEMFFWMVGVYFQPEFAMARNILTRVTALISILDDIYDAYGTLEELVPYTEAIEKWDADAMDGLPEYMQAHYKEILNLYDEIGNDLATKGRSYRLTYAKEAMKKQAKWYFHKAKWFHTGYTPTLEEYIPLALLTTGYEALSITSLVGMGDVVTRYAFEWLLGDCKILRASQIICRFMDDISSHKFEQKRGHVASSVELFMKENHASEQEAEEELQKRVVDAWKDINEEFVRPTTAPMPVLTAIINLSRVMDLLYNNRGDHYTHSKTELKEHITSLFVSPLPI

>EgranTPS013

MSFQVSANPSSSPSKGRSGGIERPLAEYHESVWGDHFIKYASPSYSTKFKFLGRVEEQVEELKGEVRKMVTNAMYKPSQMLHLIDQIQRLGIDYHFEREIDEQLEGIHKSYSQLDHGDFKGDDLHMVALMFRLLRQQGFNISSEVFNNFKDNEGNFKKSLITDVRGLLSLYEACHLRCHGDAILEEALPFAITHLESIDEMKVSTSLAKQVSHALKHPLRKGLPRLEAMHYIILYQEKPSHDEVLLTLAKLDFNLLQEQHQKELGGITRWWKNIDVARKFPFARDRIAELFFWMVGAYFQPEFAMARNILTRVTGLISILDDIYDAYGTLEELVPYTEAIEKWDVDAMDGLPEYMQAHYKELLNLYDEIGNDLATKGRSYRLAYAKEAMKKQAKGYFHEAKWFHSGYTPTLEEYMPLALLTTGYEALSITALVGMGDVVTRDAFEWLLSDCKILRASQIICRFMDDISSHKFEQKRGHVASSVELLMKENRISEQEAEEELQKRVVDAWKDINEEFLHPTAGPISVLTLILNLSRVIDVLYTKGDHYTHSKTKLKEHITSLFVSPLPI

>EgranTPS014

MSFQVSANPSSSPSKGRSGGVERPLAEYHESVWGDHFIKYASPSYSTEEQVEELKGEVRKMVTNAVDKPSQMLHLIDQIQRLGIDYHFEREIDEQLEGIQKSYSQLDHGDFKGDDLHMVALMFQLMRQQGFNISSEVFNNFKDNEGNFKKSLITDVPGLLSLYEACHLRCHGDAILEEALPFAITHLESIDEMKVSTSLAKQVSHALKHPLRKGLPRLEAMHYIILYQEKPSHDEVLLTLAKLDFNLLQEQHQKELGGITRWWKNIDVARKFPLARDRIAELFFWMVGAYFQPEFAMARNILTRVTGLISILDDIYDAYGTLEELGPYTEAIEKWDVDAMDGLPYMQAHYKELLNLYDEIGNDLATKGRSYRLAYAKEAMKKQAKGYFHEAKWFHSGYTPTLEEYMPLALLTTGYEALSITALVGMGDVVTRDAFEWLLSDCKILRASQIICRFMDDISSHKFEQKRGHVASSVELLMKENRISEQEVEEELQKRVVDASNRRPNVGSHLDSQSLTGDRCVIHQGRSLHPLQDAQRAYHITLCSPADL

>EgranTPS015

MSVQVSAIPSSSPSKGRSGGVERRLAEYHESVWGDHFIKYASPSYSTEEQVEELKGEVRKMVTNAMDKPSQMLHLIDQIQRLGIDYHFEREIDEQLERIHKSYSQLDHGDFKGDDLHMVALMFLLRQQGFNISSEVFNNFKDNEGNFKKSLIIDVRGLLSLYEACHLRCHGDAILEEALPFAITHLESIDERKVSTSLAKQVSHTLKQPLRKGLPRLEARHYIILYQEKPSHDEVLLTLAKLDFNLLQEQHQKELGGITRWWKNIDVARKFPFARDRIVELFFWMVGAYFQPEFAMARNILTRVTGLISILDDIYDAYGTLEELVTYTEAIEKWNVDAMDGLPEYMHEIGNDLATKGRSYRLAYAKEAVSIVGTFYMHPMKKQAKGYFHEAKWFHSSYTPTLEEYMPLALLTTGYEALSITALVGMGDVITRDAFEWLLSDCKILRASQFICRLWMTLVLTRFEQKRGHVASSVELLMKENCISEQDAEEELQKRVVDAWKDINEEFLRPTVGPMPVLTLILNLSRVIDVLYTNGDHYTHSKTKLKEHIASLFVNPLPI

>EgranTPS016

MSVPVSAIPSSSPNKESSRVVERRRADYHPSIWGDYFLVYASPTNSMEFKYVGRVEEQIEGLKGEVRKMLTNVVNKPSQVLQLIDQIQRLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQQGYNVSSVVFNKFKNSERNFRESLITDVRGLLSLYEACHLRCHGDSILEEALPFAITHLESINESKVSTSLAKQVKHALRQPLRKGLPRLEARYYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFAVARDILTKVTALTSILDDMYDVYGTLEELVILTEAIEKWDVDAMDGLPDYMQAWYKVLLDVYDAVGNEVATKERSYRLTYVKEAMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTSGYEMLAITSLVGMGDVVTKHAFEWLLGDCKILKASQIICRLMDDIASHQFEQKRGHIASSVELFMKEHNVSEQETEKELRKQVVDAWKDINEAFLRPTAVPMPILMRILNISRVIHVLYSDGDNYTHSGTLLKDHVTSLFISPLPVSHLSRGAQEGTRQDYGGR

>EgranTPS017

MAAPVSAIPSSSPNKGSSRVVERRWADYHPSIWGDYFLAYASPTNSVELKYVGRVEEQIEGLKGEVRKMLTDVVNKPSQVLHLIDQIQRLGIFYHFKREIDEQLEQIHKSYSRLVYRDFKGDHLHMIALIFRLLRQQGYNVSSEVFNKFKDGEGNFRESLITDVQGLLSLYEACHLRCHGDSILEEALLFAITHLESLNESKVSTSLAKQVKHALRQPLHKGLPRLEARRYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRWWKDIDVARKFPFARDRIVELFFWISGAYFEPKFAVARDILTKVIALTSILDDMYDVYGTLEELVILTEAIEKWDVDAMDGLPEYMQAWYKVLLDVYDAVGNEVATKERSYRLTYAKEAMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLAITSLVGMGDVVTKHAFEWLLGDCKILKASQIICRLMDDIASHQFEQKRGHVASSVELFMKEHDVSEQETEKELHKRVVDAWKDINEAFLRPTAVPMPILMRILNLSRVIHVLYSDGDNYTHSGALLKDHVTSLFISPLPVSHLSRGAQEGTRQDYGGPCPQIDGMHFFRPAANEDAMRKKQEKGKQAMERL

>EgranTPS018

MSVPVSAIPSSSPNKESSRVVERRRADYHPSIWGDYFLVYASPTNSMEFKYVGRVEEQIEGLKGEVRKMLTDAVNKPSQVLHLIDQIERLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQQGYNVSSVVFNKFKNSEGNFRESLITDVRGLLSLYEACHLRCHGDSILEEALPFAITHLESINESKVSTSLAKQVKRALRQPLRKGLPRLEARYYVPFYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFAVARDILTKVIALTSILDDMYDVYGTLEELVILTEAIEKWDVDAMDRLPKYMQAWYKVLLNVYDAIGNEVATKGRSYRFTYAKEAMKKQARVFFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLAITSLVGMGDVVTKHAFEWLLGDCKILKASQIICRLMDDIASHQFEQKRGHVASSVELFMKEHNVSEQETEKELRKQVVDAWKDINEALLRPTAVPMPILMRTLNLSRVIHVLYSDGDNYTHSGTSLKDHVTSLFISPLPVSHLSRGAQEGTRQDYG

>EgranTPS019

MHQRSIQKKGDMSVPVSAIPSSSPNKGSSRVVERRSADYHPSIWGDYFLVYASPTNSMELKYVGRAEEQIEGLKGEVRKMLTDAVNKPSQVLPLIDQIERLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQRGYNVSSVVFNKFKNSEGNFRESLITDVRGLLSLYEACHLRCHGDSILEEALPFAITHLESINESKVSTSLAKQVKRALRQPLHKGLPRLEARYYVPLYQEEPSHDQVLLALAKLDFNLLQEQHQKELGNITRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFAVARDIFTKVIALTSILDDMYDIYGTLEELVIFTEAIEKWDVDAMDGLPEYMQAWYKVLLNVYDAIGNEVATKGRSYRLTYAKEAMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLAITSLVGMGDVVTKHAFEWLLGDCKILKASQIICRLMDDIASHQFEQKRGHVASSVELFMKEHNVSEQEAEKELRKRVVDAWKDINEAFLRPTVVPLPILMRTLNLSRVIHVLYSDGDNYTHSGTSLKDHVTSLFISPLPVSHLSRGAQEGTQQDYGGK

>EgranTPS020

MLSINNTLQLLIFCNADEGQIEELKREVNKMLTDVVDKPLQKLHLIDQIQRLGIEYHFECEVDEHLEQIHKSYSRLDHEDFKVDDLHTVALIFRLLRQHGYNISSEVFDKFKDSKGNFRESLISDVQGLLSLYEACHLRCHGDSILDEALPFSTTHLESINESKVSTSLAKQVSHALKQPLRKGLPRLEASHYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKNLDVPRKFPFARDRIVELFFWTTGIYFEPEFATAREILTKVISLTSIMDDIYDVYGTLEELALLNEAIQKWDFDAMDGLPEYMQAYFKEFLQLYEYIGNQLAAKGKSYRLIYAKEVMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLIGMGDVVTEHVLKWSVGDCKSVKATQSICRLMDDVSSHEFEQKRGHVVSAVELLMKYRGISEQEAAEELHKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDVLYSDGDNYTHSKTKLKDYVTSLFINPLSM

>EgranTPS021

MSLPISTIPSSLATQDKSHVVERHSANFHPSIWGDYFLKYASCSCSMENGHDQHAEQEIQKLDDEVKRMLCADADKPSLKLDMIDQIQRLGIAHHFASDIDHVLKQLSETCFACNNGDRDIDDLYTAALLFRLLRQQGYRVSSDIFNKFKDPSGKFSEKHASDVRGLLSLYEASHLSVHGEDVLDQALSFSLTHLESVKEQLSPPLATQVRHALKQTIRKGVPRLEARQYISMYEAEPLHNEVLLSLAKLDFNRLQKQHQKELFDITRWWMGLDFKRKLPFARDRLVEGYFWIVGVHFEPELAVARRMMTKVIAVTSVLDDIYDVYGTYEELELFTQAIQRWDIDCIHELPEYMQVFYKALINIYVEIEEILACTGKSYCLCYAVEAMKRQARSYFAEAKWLHQQHKPTMDEYMSIALVSSGYPLLAVTSFVGMPDIVTKDDLDWLFNDPKILKASTIICRLMDDLATHKFEQSRGHVDSAVQCYMKQYGVTEQEAENNLRKQVNDSWKDINEECLRPTAVAMPLLVGILNLSRVMDVLYKDGGDHYTNPHIALKDYIHSVLIDPVQ

>EgranTPS022

PDLQVSTIPRSSPNIGTNHVIERRSAGYHPSIWGDYFLKYAFPSNSVRLLRQQGYNVSSEIFNKFKDSEGNFQESLVTDARGLLSLYEACHLRCHGDSILDEALPFATTHLESIDESKVSTSLAKQVSHALEQPLRKGLPRLEARRYIPLYQEEPSHDEVLLALAKLDFDLLQEQHQKELGEITRWWKEIDVPRKFPFARDRIVELFFWISGIYFEPEFAMARNILTRVISLTSILDDIYDVYGTLEELALLTEAIQKWDVDAMDGLPVYMQAYYKELLHLYEYIGNELATKERSYRLVYAKEVMKKLARAYFQEAKWFHTNYIPTLEEYMSLQLITTGYGMLATTSLVGMGDVVTKHALEWSVSDCKIVKAAQTISRLMDDIASHQFEQKRGHVVSAMELLMKYHGVSEQEAGEELQKGVIDSWKDINEEFLRPTAVPMPILTRMLNFSRVMDVLYSDGDNYTHSETKLKDYVMLLFVSPLLM

>EgranTPS023

MSLQISRVPSSSPAEKTSQVPEGRSEIFHLTIWGDYFLKYASDSNLTVAFKLLRLLRQQGYNVSCEIFNRFKDSEGNFNKSSIADVQGMLSLFEACHLSYHGDDILNDALAFTISHLESIEKKKVSPNLVKQVSHALHQPIQKGLPRLEARRYIQFYQEEPLHNEVLLSLAKLDFNSLQEQHQKELGNLTRWWKDINIEEFPFARDRLGELYVWMLGIYFEPEYEIARGIVTKMMVILSILDDIYDVYGTLEELELFTEAIERWDVDAKEGLPKCMQVFYKTLLDFYDEISNELARKGRSYRLFYAKEVMKIQVRAYLAEAKWFHHSHVPTMEEYMPIALISIGTQLTFVTAFLGMGDIVTKDAFDWLLSSDPRIVKASQVIGRLMNDIAGHFEQERGHVASSVECFMKQYSVTEEEAKKELCKQVANAWKDINEELRRPTAVPMVLLMRIINLARATHAVYEDETDHYVNAGTNFKEFVTLLLVNPCQCDGSEEHG

>EgranTPS024

VLFRRSPARTCRLVTGACAAPAGHSQRFGRVAPTRSGLWPRVWARVASSGDARHVAGLEGQIEELKGEVNKMLTDVVDKPLQKLHLINQIQRLGIEYHFEREVDEQLEQIHKSYSRLDHEDFKVDDLHTIALIFRLLRQHGYYISSEVFYKFKDSEGNFRESLISDVCGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSTSLVKQVSHALKQPLRMGLPRLEASRYIPLYQEEPSHDEVLLTLAKLNFNLLQEQHQKELGKITMWWKNIDVPRNFPFTRDRIVELLFTTGVYFEPEFVMAREILTKVISLTSIMDDIYDVYGTLEELALLNEAIQKWDVDAMDGLPENIQAYFKEFLQLYKYIGNQLAAKGRSYRLIYAKEVMKKLVRAYYQEAKWFHTNIPTLEEYMSLQLITTGYGMLVTLVRMGDVVTEHVLKWSVGDYKIMKAAQTICRLMDDVSSHEFEQKRGHVVSIVELLMKYHGISKQEAGEELLKRVIDAWKDINEEFLCLTIVPMSVLMRILNFSRVVDVLYSDGDNYTHSKTKLKNYVTSLFVNPLPM

>EgranTPS025

MTCQGLHFVDLLRFPSVPPHLLYGNNRPHINTCSLEGQIEELKGEVKKMLIDAVDKPLPKLHLIDQIQRLGIEYHFEREVDEQLEQVHKSYSRLDHEDFKVDDLHTVALIFRLLRQHGYNISLEVFDKFKDSKGNFRESLISDVQGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSTSLAKQVSHALKQPLRKGLPRLEASCYIPLYQEEHSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKNIDVPRKFPFARDRIVELFFWTTGIYFEPEFAMAREILTKVISLTSIMDDIYDVYGTLEELALLNEAIQKWDFDAMDGLPKYMQAYFKEFLQLYEYIGNQLAAKGKSHRLIYAKEVMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLIGMGDVVTEHVLKWSVGDCKSVKATQTICRLMDDVSSHEFEQKRGHVVSAVELLMKYRGISEQEAAEELHKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDVLYSDGDNYTHSNTKLKDYVTSLFINPLPM

>EgranTPS026

MSQVSATPCAPSNKGTGHVIERRSAGYHPSVWGDYFLKYDSPSNSVKFKFLGRVEGQIEELKGEVKKMLTDIMDKPLQKLHLIDQIQRLGIEYHFEREIDEQLEQIHKSYSRLDHEDFKVDDLHIVALIFRLLRQHGYNISSEVFDKFKDSGGNFRESLISNVLGLLSLYEACHLRCHGDSILDEALLFATTHLESINESKVSTNLAKQVSHALKQPLRKGLPRLEARHYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKNIDVPRKFLFARDRLVELFFWTTGVYFEPEFAMARDILTKVISLTSIIDDVYDVYGTLEELALFNEAVQKWDVDAMDGLPEYMQALFKEFIQLYEYIGNELATKGRSYYLVYAKEVMKKLVSAYFQEAKWFHTNYIPTLEEYMSLQLITSGYEMLATTSLMGMGNVVTEHALKWSISDCKIRKAAQTIGRLMDDIVSHEFEQKRGHVVSAVELLIKYRGVSEQEAVEELQKRVIDAWKDTNEEFLRPTAVPMPILTRVLNLSRVVDVLYSDGDNYTHSETKLKDYVTSLFVNPLPM

>EgranTPS027

MSQVSATPCAPPNKGTGHVIERRSAGYHPSVWGDCFLKYDSPSNSVEGQIEKLKGEVKKMLTDIMDKPLKKLHLIDQIQRLGIEYHFEREIDEQLEQIHKSYSRLDHEDFKVDDLHIVALIFRLLRQHGYNISSEVFDKFKDSKGNFRESLISDVRGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSANLAKQVSHALKQPLRKGLPRLEASCYIPLYQEEPSHDEVLLSLAKLDFNLLQEQHQKELAKITRWWKNIDVPRKFSFARDRIVELFFWTTGIYFEPEFAMAREILTKVISLTSIMDDIYDVYGTLEELALLNEAIQKWDFDAMDGLPEYMQAYFKEFLQLYEYIGNQLAAKGRSYRLIYAKEVMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLIGMGDVVTEHVLKWSVGDCKSVKATQTICRLMDDVSSHEFEQKRGHVVSAVELLMKYRGISEQEAAEELHKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDVLYSDGDNYTHSKTKLKDYVTSLFLNPLLISL

>EgranTPS028

LDSQVSAILRSSPNKGTNHVIERRSAGYHPSIWGITSLNMLSTPEEQIKKLKGKVRKMLAGVMDKPSQMLHLIDQIQRLGIDYHFEHEVDEQLEQINKSYSQLHLEDFKVDDLHMAALIFQLLQQQGYNVSSEIFNKFKDSEGNFRESLVTDARGLLSLYEACQLRCRGDSILDEALPFATTHLESIDERKMSTSLLKQVSHALEQPLRKGLPRLEARHYISLYQVELSHDEVLFTLAKLDFNLLQEQHQKELGKITRWWKEIDVPRKFPFARDRIVELFFISGLYFELEFVMAKNILTKVISLTSILNDIYDVYGTLEELALLTEAIKWDVDAMDGLPVYMQAYYKELLQLYEYIGNELATKERSYRLVYAKEVMKKLARAYFQEAKWFHTNYVPTLEEYMSLQLITTSYGMLATTSLVRMGDVVTEHALEWSIGDCKIVKTAQIICRLMDDIASHQFEQKRGHVVSAVELLMKYHGVLEQEAGEELQKGVIDAWKDINEEFLCLTAVLMPILTRMLNFSWVMDVLYSDGDNYTHSETKLKYYVTLLFVSPLPM

>EgranTPS029

MLKFIYKINRTCRFQQFHVLSPNKGTYHVIERRSAGYHPSIWGDFFLKYAFPSSLEEQIEELKGKVRKMLAGAVDKPSQMLHLIDQIQHLGIDYHFEHEVVEQLEQIHKSYSQLHLEDFKVDDLHMVALIFQLLQQQGYNVSSEIFNKFKDSEGNFRESLVTNARGLLSLYEACHLRCHSDSILDEALPFATTHLESIDESKVSTSLAKQVSHALEQPLRKGLSRLEARHYIPLYQEEPSHDEVLLALAKLDFNLLQEQHQKELGEITRWWKEIDVPRKFPFARGRIVELFFWILGIYFEPEFAMARNILTKVISLTSILDDIYDVYGTLEELALLTEAIQKWDVDAMDGLPVYMQAYYKELLQLYEYIGNERSHLLVYAKEVMKKLVKAYFHEAKWFHTNYVPTLEEDMSLQLITTGYGMLATTSLVGMIDVVTEHALEWSVGDCKIVKVAQTICRLMDDIASHQAKEGHVLSAVELLMKYHGILEQEAGEELQKGVTDAWKDINEEFLHPTAVPMPILTQMLNFPRVIDVLYSDGDNYTHSETKLKDYVTSLFISPLLM

>EgranTPS030

MSLLVKTITLSFCFLPIVELHIMEWRHCVTVWSWCGFGPLTSMFPFFSEERIERLKGEVRKMLTSAMDKPSQKLNLIDQIQHFGLAYHFEFEIVEQLEQIHRSYFEFHCGDNDDNLHTIALLFRLLRQQGYNVSCKIFNRFKDSEGNFSKSVIANVQGLLSLFEACHLSYCSDDILNDALTFTITAKLDFNSLQGQHRKELGNLTRWWKDIDIEREFPFARDRLVELYTWMLGVHFEPEYEIARGFMTKMNVFLTIIDDIYDVYGTLEELELFTAIERWDVDAKEGLPECMQVIYKILLDFYDEIGYELIRKGRSHHLFYAKEAMKIQVRAYLAEAKWFHHSHVPMMEEYMPIALTTIGIQMALVASFLGMGDTVTKDVFDWLLSSDTKIVKALRVIGRLMNDIAGHFVRRFYQRKNNFDDIYIFCSLSKREVMWKMSKRLIVRNMTRS

>EgranTPS031

MSVRISRVPSSYPAEKTSLVPEGRSAIFHPTIWADYFLKHASNSNPTEEHIERLKEVRKMLMGAMDKPSQKLNLIDQIQRLGFAYHFEHEINERLEQIYRSYFEFHYGDNDDNLHTVAILFLLQQQGYNVSCIFNRFKDSEGNFNKSSIADVQGMLSLFEACHLSYHGDDILNDALAFIISHLESIEKKKVSPNLVKQVSHALHQPIQKGLLRLEARCYIQFYQEEPSHNEVLLSLAKLDFNSLQEQHQKELGNLTRWWKDIDIEREFPFARDRLGELYVWMLGIYFEPVYKIARGIVTKMMVILSILDDIYDVYGTLEELELFTEAIERWDVDAKEGLPKCMQVFYKTLLDFYDEIGNELARKGRSYCLFYAKEVMKIQVRAYLAEAKWFHHSHVPTMEEYMPIALISIGSQLTFVTAFLGMGDIVTKDAFDWLLSSDPRIVKASQVIGRLMNDIAGHFEQERGHVASSVECFMKQYSVTEEEAVGEIFLKYFEVVKTFPSV

>EgranTPS032

MSLPISGVPFPSPAEETSPVAERRSAIFHPTIWTDYFLKYASDSTSTSSEGIVEEQIKRLKGEVRKMLTGAMDKPSQKLNLIDRIQRLGLADHFEHEIDEQLEQIHRSYFAFHCEDNNNNLHTIALLFRLLRQQGYNISCEIFNRFKDNEGNFSKSIIADVQGLLSLYEACHLSYHGEDILNDALTFTITHLESIDKRKSEPNLEKQVSHALHQPIQKGLPRLEARRYIQFYQEEPSHNEVLLSLAKLDFNSLQEQHRKELGNLARWWKDIDIEREFPFARDRLGELYIWNLGVHFEPEYEISRGILTKMMAILTILDDIYDVYGTIEELELFTEAIERWDLDAKEGLPECMQVIYKILLNFYDEIGYELTRKGRSYCLFYAKEAMKIQVRAYLAEAKWFHHSHVPTMEEYLPIALTSIGIQMALVASFLGMGDTVTKDVFDWLLSSDTKIVKALRVIGRLMNDIAGHKFEQERGHVASSVECFMKQYKVTEEEAKKELCKQVADAWKDINEELCRPTAVPRVLLMRIINLAGAIHAVYEDETDNFVNAGTNFKEFVTCLLVNPCQCDVLKDEV

>EgranTPS033

MSLQISAIPSRPSAKAASPVAERRSASYHPSIWGDYFLRYASDSCSTVATLLIGLNQPCCFCNIRALAFRVNSDSEEQIEELKEEVRKMVAAIVPTSQKLELIDQIQRLGIAYHFQGVIEEQLEQIHESYFELNDGDHDHNDLHMVALLFRLLRQRGYGISCEMFEKFKDSDGNFRESLTADILGILSLYEACHLRVHGEDVLDGALSFTVTHLESIDKNQVSPTLAKQVSQALKQPIYKGLPRLEAMQYIPIYQEEPSHNEVLLSLAKLDFNLMQEQHQKELGHIARWWKELDVARNFPFARDRVVECYFWILGVYFEPEFVLARKFMTKVIAMTSIIDDIYDVYGTLEELELFTGAMERWSIDAIDGLPKYMQVCYKALLDVYDDIEKAIAENGTSYGLYHAKEAMKNLVRAFTEAKWFHQGHVPTMEEYMAVALVTSAYEMLATTSFVGMGDLATQDAFDWLLSGPKMVKASTTICRLMDDIVSHFEQKRGHVASAVECFVHQHGVTEQEAKEELWRRVVEAWKDVNEECLAPTAIPARLLTLILNLTRVIDVLYTDEDNYTNAGTKLKNYVASLLIYPLPM

>EgranTPS034

MSPQISAMPSPSPALETSHVAERRSGNFHPSIWGDYFLKYASDSGERIERLKGEVKKMLTSAMDKLSQKLNLIDQIQRLGLAYHFEIEIDKELEQIHRSYFEYHRGDNDEDLHTTALLFRLLRQQGYDVSCEIFNKFKDNEGHFSKSLIADVRGLLSLFEACHVGFHSDDILNDALAFTVTHLESIDKEKVSRNLEKEVSHALSQPIHKGLSRLEARHYIQLYQEEPLHNEVLLSLARLDFNLLQKQHQKELGNITRWWKDLDGERKFPFARDRLVELYFWMSGVYFEPKYEATREILTKMIVIVSIFDDMYDMYATLEEVEVFTEAIERWDVNAKDGLPKYMQVCYETLLDLYDEFGDKFTRKGQSYSLFYAKEVMKNHLKAYFAEAKWFHQNHMPTMEEYMPIASTSIGCELLLGTSFLGMGDIVTKNDFDWLLYSDSKMVKASKVVARLMDDIAGHSEQERGHSPSSVECFMKQYRVTEEEAKEELRKQVVNAWKDMNEELRRSSAVPKLLRTRILNFAQVFDVVYNDEKDHYSHAGTKFKEHVTSLYVDPLPM

>EgranTPS035

PNLQVSAIPHSSPNKGTDHVIERRSAGYHPSIWGDYFLKYAFPSNSVVSNSSVIFYFCFLAIAFCRLTSISEEQIEELKGEVRKMLAGIVDKPSQMLHLIDQIQRLGIDYHFEHEVDEQLEQIHKNYSQLHLEDFKVDDLHTVALIFRLLRQQGYNVSSEIFNKFKDSEGNLWESLVTDARGLLSLYEACHLRCHGDSILDEALPFATTHLESIDESKVSTSLAKQVSHALEQPLRKGLPRLEARRYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGEITRWWKEIDVPRKFPFARDRIVELFFWTSGIYFKPEFAMARNILTKVISLTSILDDIYDVYGTLEELALLTEAIQKWDVDAMDGLPMYMQAYYKELLQLYEYIGNELATKERSYRLVYAKEVMKKLARAYFQEAKWFHTNYVPALEEYMSLQLITTGYGMLATTSLVGMGDVVTEHALEWSVGDCKIVKAAQTICRLMDDIVSHQFEQKRGHVVSAVELLMKYHGVSEQEAGEELQKGVIDAWKDTNEEFLRPTMVPMPILTRMLNFSRVMDVLYSDGDNYTHSETKLKDYVTLLFISPSLM

>EgranTPS036

MSLPVSTIPSPSPAQETSQVAERRSGNFHPSIWGDYFLKYASDSNSMSSQGVAKERIEKLKGEARKMLTSAMDKPSQKLNLIDQIQRLGLAYHFEIEIDEQLEQIHRSYFEFHCGDNDSNLHTTALLFRLLRQHGYNIPCEIFNKFKDNEGNFSKSLIADVQGLLSLFEACYLGFHGDVILNDALAFTITLLESIDKGKVTGNLEKQVTHALNQPIHKGLPRVEARHYIQLYQEEPSHNEVLLSLAKLDFNLLQEQHQKELGNITRWWKDLDGERKFPFARNRLVELYFWMSGVYFEPEYEATREILTKVMVIVSIFDDVYDIYATLEELELFTKAIERWAVDAKDGLPEYMQVCYKTLLDLYDEIGYEVTRKGQSYCLFYAKEVMKNHMRTYLAQAKWFQQNYVPTMEEYLPIASLSIGCELLLGTSFLGMGDVVTKSYFDWLLLSDNKMVKASDVISRLMNDIAGHKFEQERGHTASSVECFMKQYKVTEQEAKDALRKQVINAWKDMNKELCHPTSVPKPLLVRILNFARVFHVVYNDEVDHYSHAGTKLKEFVTSLLVDPLPM

>EgranTPS037

MSLPVSTIPSPSPAHETSQVAERRSGNFHPSIWGITFSNMLLTPTQCSQGVAKERIEKLKGEVRKMLTSAMDKPSQKLNLIDQIQRLGLAYHFEIEIDEQLEQIHRSYFEFHCGDNDNNLHTTALLFRLFIFSHAPFRCIEIFNKFKDNEENFSKSLIANVQGLLSLFEACHLGFHGDVILNDALAFTITLLESIDKGKVTGNLEKQVTHALNQPIHKGLPRVEARHYIQLYQEEPSHNEVLLSLAKLDFNLLQEQHQKELGNITRWWKDLDGERKFPFARNRLVELYFWMSGVYFEPEYEATREILTKVMVIVSIFDDVYDIYATLEELELFTKAIERWAVDAKDGLPEYMQVCYETLLDLYDEIGYEVTRKDNHTPLLCKRVMKNHMRTYLAQAKWFQQNYVPTMEEYLPIASLSIGCELLLGTSFLGMGDVVTKSYFDWLLLSDNKMVKASAVISRLMNDIAGHKFEQERGHTASSVECFMKQYKVTEQEAKDALRKQVINAWKDMNKELCHPTSVPKPLLVRILNFARVFHVVYNDEVDHYSHAGTKLKEFVTSLLVDPLPM

>EgranTPS038

MSLETSANRPLPAKENSQMVERRSVDYHPSLWEDYLAKYSSPSNSMDDGHDQQAEQEIQKLKDEVKRMLCAHADKPSLKLDMIDQIQRLGIAYHFASEIDNVLKKLSQTYFVSNNGNYDNDDLYTVALLFRLLRQQGCRISCDIFNKFKDTSGKFTEKHASDVRGLLSLYEASHLSVHGEDVLDQALSFSLKHLESIDKEQLSPPLAAQVQHALKQTIRRGVPRLEARRYISMYEAEPLHNKVLLSLAKLDFNHLQKQHQEELFDLARWWMGLDFKSKLPFARDRLVEGYFWILGVHFEPELAPVRRMMTKVIAMTSVLDDIYDVYGTYEELELFTRAVQRWDIDCINELPEYMQVFYKALIDVYVEIGEKLACTGRSYGLDYAKEAMKRQARSYFAEAKWLHQQHKPTMDEYMSVALVSSGYPLLAITSFVGMQDIVTKDDLDWLFNDPKILKASTVICRLMDDLATHKFEQGREHADSAVQCYMKQYNVTEQEAENDLRKQVDDAWKDLNEECLCPTAVAKPLLMGILNLTRVMDVLYKDGGDHYTNPHIMLKDYIRSVLMDPVQTF

>EgranTPS039

DIFNKFKDTSGKFGEKHASDIRGLLSLYEASHLSVHGEDVLDQALSFSLKHLESIDKEQLSPPLAAQVQHALKQTIHRGVPRLEARQYISMYEAEPLHNKVLLSLAKLDFNHLQKQHQKELFDLARWWMSLDFKNKLPFARDRLVEGYFWILGVHFEPELALVRRMMTKVIAMTSVLDDIYDVYGTYEELELFTRAVQRWDFDCINELPEYMQVFYKALIDVYVEIGEKLASAGRSYGLDYAKEAMKRQDRSYFAEAKWLHRQHKPTMDEYMSVALVSSGYHLLAITSFVGMQDIVTKDDLDWLFNDPKILKASTVICRLMDDLATHKFEQGREHADSAVQCYMKQYNVTEQEAENDLRKQVDDAWKDLNEECLCPTAVAKPLLMGILNLTRVMDV

>EgranTPS040

MSLETSANRPLPAKGNSQMVERRSVDYHPSLWEDYLAKYSSPSNSMDDGHDQQAEQEIQKLKDEVKWMLCAHADKPSLKRDMIDQIQRLGIAYHFASEIDNVLIKLSETYFVSNNGDHDNDDLYTVALLFRLLRQQGYRISCDIFNKFKDTSGKFGEKHASDIRGLLSLYEASHLSVHGEDVLDQALSFSLKHLESIDKEQLSPPLAAQVQHALKQTIHRGVPRLEARQYISIYEAEPLHNKVLLSLAKLDFNHLQKQHQKELFDLARWWMGLDFKNKLPFARDRLVEGYFWILGVHFEPELALVRRMMTKVIAMTSVLDDIYDVYGTYEELELFTRAVQRWDIDCINELPEYMQVFYKALIDVYVEIGEKLASAGRSYGLDYAKEAMKRQDRSYFAEAKWLHRQHKPTMDEYMSVALVSSGYHLLAITSFVGMQDIVTKDDLDWLFNDPKILKASTVICRLMDDLATHKFEQGREHADSAVQCYMKQYNVTEQEAENDLRKQVDDAWKDLNEECLCPTAVAKPLLMGILNLTRVMDVLYKDGGDHYTNPHIMLKDYIRSVLMDPVQTF

>EgranTPS041

MSQVSATPCAPPNKGTGHVIERRSAGYHPSVWGDYFLKYDSPSNSVVRNPSVIFFFCFLAIARLLRQHGYNISSEVFDKFKDSKGNFRESLTSDVRGLLSLYEACHLRCHGDSILDEALPFATTHLESSNKSKVSTSLAKQVSHALKQPLRKGLPRLEASRYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKNIDVPRKFPFARDRIVELFFWTTGIYFEPEFAMAREILTKVISLTSIMDDIYDVYGTVEELALLNEVIQKWDVDAMDGLPEYMQTYFKEFLQLYEYIGNQLAAKGRSYRLIYAKEVMKKLVRAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLATTSLVGMGDVVTEHVLKWSVSDCKSVKATQTICRLMDDVSSHEFDIQFEQKRGHVVSAVELLMKYHGVSEQEAGEELLKGVIDAWKDTNEEFLRPTAVPMSVLTRMLNFSRVIDVLYSDGDNYTHSKTKLKDYVTLLFVNPLPM

>EgranTPS042

MSARFSVIPSSSLPQETGCVEGRRSANFHPSIWGDYFLKYASDSNSLHSHVIAEERIERLKGEVGKMLTSAMYKPAEKLNLIDQIQRLGIAYHFELEIDKELEQIRRGYFEYQCDDNDNDLDTVALLFRLLRQRGYHVSCEIFNKFKDGDGNFGKSLIADVQGLLSLFEACHLRYHGDDNLEDALAFTTTHLESVDKRKASLHLGKKVSHALNQPIHKGMSRLEARRYIPLYQEEPSHNEVLLSLAKLDFNLVQEQHRKELGNLTRWWKGLDVQRKFPFARDRLVEMYVWWLGEYYEPEHEVAREILTKLSSVISIIDDIYDVYGTWEELELFTEAIERWDVDAKDGLPEYMQECYKIVLDLYDEIGYEFSRKGHSYRLFYAKEVMKNQARAYLVEAKCFHRNHVPTMEEYMSIALPSSGVVSILAWSFLGMGDIVTKDVFDWLLFNDPKMVKASSVIGRLMDDIAGHKFEQERGHVASAVECFMKQYRVTEEEAKEELRKQVTNAWKDINEELRRPTVIPMPILVRILNLTQAMHMMYNGETDNYTHAGTKMKEHVTSLLVNPLPM

>EgranTPS043

MPSPSPALETSHVAERRSGNFHPSIWGDYFLKYASDSSSKSSQDIAGERIERLKGEVKKMLTSAMDKLLQKLNLIDQIQRLGLAYHFEIEIDKELEQIHRSYFEFHCGDNDDDLHMTALLFRLLRQQGYDVSCEIFNKFKDNEGHFSKSLIADVRGLLSLFEACHVGFHGDDILNDALAFTVTHLESIDKGKVSRNLEKEVSHALSQPIHKGLSRLEARHYIQLYQEEPLHNEVLLSLARLDFNLLQKQHQKELGNITRWWRDLDGERKFPFARDRLVELYFWMSGVYFEPKYEATREILTKMIVIVSIFDDMYDVYATLEEIEVFTEAIERWDVDAKDGLPKYMQVCYETLLDLYDEFGNKFTRKGQSYCLFYAKEVMKNHLKAYFAEAKWFHQNHMPTMEEYMPIASTSIGCELLLGTSFLGMGDIVTKNDFDWLLYSDSKMVKASKVVARLMDDIAGHKSEQERGHSPSSVECFMKQYRVTEEEAKEELRKQVVNAWKDMNEELRRSSAVPKLLRTRILNFAQVFDVVYNDEKDHYSHAGTKFKEHVTSLYVDPLPM

>EgranTPS044

MSVPVSAIPSPSPNKESSRVVERSRADYHPSIWGDYFLVYASPTNSMEFKYVGRVEEQIEGLKGEVRKMLTDAVNKPSQVLHLIDQIERLGIFYHFKREIDEQLEQIHKSYSQLVHGDFKGDDLHMIALIFRLLRQQAYNVSSVVFNKFKNSEGNFRESLITDVRGLLSLYEACHLRCHGDSILEEALPFAITHLESINESKVSTSLAKQVKRALRQPLRKGLPRLEARYYVPFYQEEPSHDQVLLALAKLDFNLLQEQHQKELSNITRWWKDIDVATKFPFARDRIVELFFWISGAYFEPEFAVARDILTKVIALTSILDDMYDVYGTLEELVILTEAIEKWDVDAMDGLPEYMQAWYKVLLDVYDAVGNEVATKERSYHLTYAKEAMKKQARVYFHEAKWFHTNYTPTLEEYMPLALLTTGYEMLVITSLVGMGDVVTKHAFEWLLGDYKILKASQIICRLMDDIASHQFEQKRGHVASSVELFMKEHDVSEQETEKELRRRVVDAWKDINEAFLRPTAVPVPILVRILNLSRVIHVLYSDGDNYTHSGTLLKDHVTSLFISPLPVSNLSRGAQEGTRQDYR

>EgranTPS045

MSLPISRVPSSSPAEKTSLVPEGGSAIFHPTIWADYFLKHASNSNSTRLLRQQGYNVPCEIFNRFKDSEGNFNKSSIADVQGMLSLFEACHLSYHGDDILNDALAFTISHLESIEKKKVSPNLVKQVSHALHQPIQKGLPRLEARRYIQFYQEEPSHNEVLLSLAKLDFNSLQEQHQKELGNLTRWWKDIDIEREFPFARDRLGELYVWMLGIYFEPVYEIARGIVTKMMVILSILDDIYDVYGTLEELELFTEAIERWDVDAKEGLPKCMQVFYKTLLDFYDEIGNELARKGRSYRLFYAKEVMKIQVRAYLAEAKWFHHSHVPTMEEYMPIALISIGSQLTFVTAFLGMGDIVTKDAFDWLLSSDPRIVKASQVIGRLMNDIAGHGVWFHVASSVECFMKQYSVTEEEAKKELCKQVANAWKDINEELCRPTAVPMILLMRIINLARATHAVYEDETDHYVNAGTNFKEFVTLLLVNPCQCDGLEEQG

>EgranTPS046

MSLQISAIRSSSQAQEKSGVVERQWANFHPSIWGDYFLKHASHSYSMEQEIQKLKDEVKRMLYADADKLSLKLDMIDQIQRLGIAHHFTTDIDHVLKQLNETCFVCNNGDRDIDDLYTAALLFRLLRQQGYRVSFDIFNKFKDPSGKFSEKHGSDVRGLLSLYEASHLSVHGEDVLDQALSFSLTHLKSIKEQLSPPLATQVGHALKQTIHRGVPRLEARWYISMYEAEPSHNEVLLSLAKLDFNRLQKQHQKELFDLARWWIGLDFKRKLPFARDRLMEGYFWIMGVHFKPELVVARRMMTKVIAVTSVLDDIYDVHGTYEELELFTQAIQRWDIDCIHELPEYMQEFYRALIDIYVEIEEILACTGKSYCLYYAVEAMKRQTRYYFAEAKWLHQQHKPTMDEYMSIALVSSGYPLLAMTSFVGMPDIVTKDDLDWLFNDPKILKASTIICRLMDDLATHKFEHSRGHVDSAVQCYMKQYGVTEQEAENNLHKQVNDAWKDIDEECLRLTAVAMPLLMGILNLSRVMDVLYKDGGDHYTNPHITLKDYIHLVLIDPVH

>EgranTPS047

MSQVSATPCAPPNKGTGHVIERRSAGYHPSVWGDYFLIYDSPSNSVEELKREVNKMLTDVVDKPLQKLHLIDQIQRLGIEYHFECEVDEQLEQIHKSYSRLDHEDFKVDDLHTVALIFRLASRYIPLYQEEPSHDEVLLTLAKLNFNLLQEQHQKELGKITRWWKNIDIPIKFPFARDRIVELFFTTGVYFEPEFAMAREILTKVISLTSIMDDIYDVYGTLEELALLNEAIQKWDVDAMDGLPEHMQAYFKEFLQLYEYIGNQLAAKGRSYRLSTQKKLMKKLVRAYYEAKWFHTNYIPTLEEYMSLQLITTGYGLLATTSLVGMDDVVTEHVLKWSVGDYKIMKAAQTICRLMDDVSSHEFEQKRGHVVSTVELLMKYHGISEQEAREELLKRVIDAWKDINEEFLHPTIVPMSVLMRILNFSRVVDVLYSDGDNYTHSKTKLKNYVTSLFVNPLPM

>EgranTPS048

MSLPLSGVPSSSPAKRTSPNAERRSAIFHPTIWTDYFLKYASDSNSMEERIKRLKGEVRKMLTSAMNKPSQKLNLIDQIQQLGLAYHFEFEIAEQLEQIHRSYFEFHCGDNDDNLHTIALLFRLLRQQGYNVSCEIFNRFKDSEGNFSKSVIANVQGLLSLFEACHLSYRSDDILNDALTFTITHLESIDKRKVSPNLEKQVSHALNHPIRKGLPRLEVRRYIQFYQEEPSHNEVLLSLAKLDFNSLQGQHRKELGNLTRWWKDIDIEREFPFARDRLVELYTWMLGVHFEPEYEIARGFMTKMNVFLTIIDDIYDVYGTLEELELFTKAIERWDVDAKEGLLECMQVIYKMLLDFYDEIGYELTRKGRSHHLFYAKEAMKIQVRAYLAEAKWFHHSHVPTMEEYLPIALTSIGIQMALVASFLGMGDTVTKDVFDWLLSSDTKIVKALRVIGRLMNDIAGHFEQERGHVASSVECFMKQYKVTEEEAKKELCKQVADAWKDINEELCRPTAVPRVLLIRIINFAGAIHAVYEAETDHFVNAGTNFKEFVTCLLVNPCQCDGLNDEV

>EgranTPS049

MSQVSATPCAPPNKGTGHVIERRSAGYHPSVWGDYFLKYDSPSNSVKFKFLGRVEGQIEELKGEVKKMLIDVVDKPLPKLHLIDQIQRLGIEYHFEREVDEQLEQIHKSYSRLDHEDFKVDDLHMVALIFRLLRQHGYNISSEIFDKFKDSKGNFRESLISDVRGLLSLYEACHLRCHGDSILDEALPFATTHLESINESKVSTSLAKQVSHALKQPLRKGLPRLEASRYIPLYQEEPSHDEVLLTLAKLDFNLLQEQHQKELGKITRWWKNIDVPRKFPFARDRIVELFFWTTGIYFEPEFAMAREILTKVISLASIMDDIYDVYGTLEELALLNEAIQKWDFDAMDGLPEYMQAYFKEFLQLYEYIGNQLAAKGRSYRLIYAKEVMKKLVGAYFQEAKWFHTNYIPTLEEYMPLQLITTGYGMLSTTSLVGMGDVVTEHVLKWSVSDCKSVKATQTICRLMDDVSSHEFEQKRGHVVSAVELLMKYRGVSEQEAAEELQKGVIDAWKDTNEEFLRPTAVPMSILTRMLNFSRVIDVLYSDGDNYTHSNTKLKDYVTSLFVNPLPK

>EgranTPS050

ISLTAEQHQKELGAITRWWKNIDVARKFPFARDRIAEMFFWMVGVYFQPEFAVARNILTRVTALISILDDIYDAYGTLEELVPYTEAIEKWDVDAMDGLPEYMQAHYKEILNLYDEIGNDLATKGRSYRLTYAKEAMKKQAKWYFHEAKWFHTGYTPTLEEYIPLALLTTGYEALSITSLVGMGDVVTRDAFEWLLVDCKILRASQIICRFMDDISSHKFEQKRGHVASSVELFMKENHASEQEAEEELQKRVVDAWKDINEEFLRPTTAPMPVLTAILNLSRVMDVLYSNGGDHYTHSKTELKEHITSLFVSPLPI

>EgranTPS051

MIIWTIPVLFYHKKSRQLVTVYDYLDYPVLFYHKKSRTCPRNSSPFRTNFKFPLLFQEIQKLDDEVKRMLCADADKPSLKLDMIDQIQRLGIAHRFASDIDHVLKQLSETCFVCNNGDRDIDDLYTAALLFRLLRQQGYRVSSEIFNKFKDPSGKFSEKHASDVRGLLSLYEASHLSVHGEDVLDQALSFSLTHLKSVKEQLSPPLATQVHHALKQTIRKGVPRLEARRYISMYEAEPLHNEVLLSLAKLDFNRLQKQHQKELFDITRWWMGLDFKRKLPFARDRLVEGYFWILGVHFEPELAVARRMMTKVIAVTSVLDDIYDVYGTYEELELFTQAIQRWDIDCIHELPEYMQVFYKALINIYVEIEEILACTGKSYCLCYAVEAMKRQARYYFAEAKWLHQQHKPTMDEYMSIALVSSGYPLLAVTSFVGMPDIVTKDDLDWLFNDPKILKASTIICRLMDDLATHKFEQSRGHVDSAVQCYMKLYGVTEQEAENNLRKQVNDSWKDINEECLRPTAVAMPLLVGILNLSRVMDVLYKDGGDHYTNPHIALKDYIHSVLIDPVQ

>EgranTPS052

NDALTFITHLESIDKRKVSPNLEKQVSHALNHPIRKGLPRLEARRYIQFYQEEPSHNEVLLSLAKLDFNSLQGQHQKELGNLTRWWKDLDIKREFPFTRDRLAELYVWMLGVHFEPDYEIARGIVTKMMVIISILDDIYDVYGTLEKLEIFTEAIEKWDVDAIEGLPECMQVYKIIFEFYDEIGYELTRKGRSYCLFYAKEAMKIQVRAYLVEAKWFHKSHIPTMEEYMPIALTTIGNQMAFVASFLGMRDIVTKDTFDWLLSSNHKIVKASKVIGRLMNDIAGHFEQERGHVASSVECFMKQYKVTEEEAKKEIRKLVADAWKDIDEELRHPTAVPMVVLMRIVNLAGAIHAVYEDETDHYVNAGTNFKEFVTCLLVNPCQCDGLEEQV

>EgranTPS053

MEQVQRLKEEVRGLFDREINQVAKLEFIDVVQRLGLGYHFEMEIKNALSSIYNNTEDAQISDNLYATSLRFRLLRQHGYNVPQDVFQRFMSKMGTFNELLHEDVKGLLGLYEASFHGLEGETILDEGWNFASKHLNDLNLDKVPTNIASHVSHALDMPIHWRPNRLEAQWFMDMYGKQQDMIPSLLRLAKIDFNLVQSIHRKEVSNLARWWVELGANKMTFSRDRLVENYFWSCLFVFEPQYTAFRELSTRIGCMVSLIDDIYDIYGTPEELELLTDLILRWDITNIDKLPPTIRDGFMVLYNTTNKLGYWTMRERGINPIPYLRKLWADECKAYMKEVYWYNKGIKPTLKEYMDVGVDSIGGLILLLDSYFLTTDKLTEEGLDYVSKIPGVMHSSAKILRFNDDLSTSSHELARGDNSKALECYMNETGASEEAAREHIRHLVRETWKKMNKEVFEDYPFSGFGPFLSACLNLARASHCFYDYGDGHGLPGHQTKDHVVSTIFEYVPL

>EgranTPS054

TCAVTIENPEIVRRSANWKPTVWDYEFLKRLLRQHGYKIPQDVFQQFMNKTGTFNESLNKDVRGLLSLYEASFHGLEGETILDEARNFASKHLKDLNLDKVPTMLASYVRHALDMPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARWWVELGANKMTFFRDRLVEHYFWCCAMVFEPQYTAYREMTTKLTCMVTLIDDVYDVYGTQEELELLTDFLVRWDITEIDKLPPIIRDSYMALYNTTNEIGYWTMRELGINTIPYMQKVWADECKAYIKEVHWYNKGIKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSAKILRLNNDLSTSSYELARGDNFKALECYMNETGASEQATREHVKQMVHETWKRMNKDVFEDYPYSGFGPFLGACLNLARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPL

>EgranTPS055

TCALKIEDQEIARRSANWEPSVWDYGVVMEQVQRLKEEVRGLFDREINQVAKLEFIDVVQRLGLGYHFETEIKNALSSIYNNTEDAQISDNLYAASLRFRLLRQHGYNIPQDVFQRFMSKMGTFNESLHEDVKGLLGLYEASFHGLEGETILDEGWKFASKHLKDLNLNEVPTDIASNVSHALDMPIHWRPNRLEARWFMDMYGKQQDTIPSLLRLAKIDFNLVQSIHRKEVSNLARWWVELGANKMTFFRDRLVENYFWSCIFVFEPQYTAFRELNTRIGCLVTLIDDVYDIYGTPEELELLTDFILRWDITNIDKLPPTIRESFMVLYNTTNEVGYWTMRERGINPIPRKVWADECKAYMKEVYWYNKGIKPTLKEYMDVAVDSIGGLILMLDSYFLTTDEVTEEGLDYVSKIPGVMHSSARILRFNDDLSTSSHELARGDNSKALECYMNETGASEEAAREHIKHLVLETWKKMNKEVFEDYPFSGFKPFLGACLNLARASHCFYDYGDGHGLPGHQTKDHLVSTIFKSVPL

>EgranTPS056

TCAVTIENPEIVRRSANWKPNVWDYEFLAEQVPRLKEEIRGLFNREMNQVAKLEFIDAVQRLGLGYHFETEIKNALSSIYDNAGYAQLLNDLHAVSLGFRLLRQHGYKISQDVFQQFMNKMDTFNESLNKDARGLLGLYEASFHGLEGETILDEARNFASKHLKDLNLDKVPAMLASYVSHALDMPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARWWVELGANKMTFFRDRLVEHYFWTCAMVFEPQYTAYREMTTKLTCMVTLIDDVYDVYGTQEELELLTDFLVRWDITEIDKLPPTIRDSYMALYNTTNEIGYWTMRELGINTIPYMQKVWADECKAYIKEVHWYNKGIKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSAKILRLNNDLSTSSYELARGDNFKALECYMNETGASEEATREHVRQMVHETWKRMNKDVFEDYPYSGFGPFLGACLNLARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPL

>EgranTPS057

TCAVTIENPKIVRRLANWKPNVWDYEFLAEQVQRLKEEIRGLFNREMNRVAKLEFIDAVQRLGLGYRFETEIKNALSSIYDNTGYAQLLNDLHAVSLGFRLLRQHGYKIPQDVFQQFMNKTGTFNESLNKDVRGLLGLYEASFHGLEGETILDEARNFASKHLKDLNIDKVPAMLASYVSHTLDMPIHWRPNRLEARWFMDMYETQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMAKWWVELGTNKMTFFRDRLVEHYFWCCAMVDEPQYTAYREMTTKLTCMVTLIDDVYDVYWTQEELELLTNFLVRWDITEIDKLPPIIRDSYMALYNMTNEIGHWTMRELGINTIPYLQKVWADECKAYIKEVHWYNKGIKPTLKEYMDNAVDSIGGLIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSAKILRLNNDLSTSLYELAGDNFKALECYMNETGASEEATREHVRQMVHKTWKRMNKDVFEDYPPSGFGPFLGACLNLAQASKCFYQYEDRHGLPDNETKDHLVRALFDPVPL

>EgranTPS058

TCASKIEDQEIARRSANWEPSVWDYGVVQSLSRLLRQHGYNVPQDVFQRFMSKMGTFNESIHEDVKGLLGLYEASFHGLEGETILDEGWKFASKHLKDLNLNEVPTNIASNVSHALDMPIHWRPNRLEARWFMDMYGKQQDMIPSLLRLAKIDFNLVQSIHRKEVSNLARWWVELGANKMTFFRDRLVENYFWSCIFVFEPQYTAFRELNTRIGCLVTLIDDVYDIYGTPEELELLTDFILRWDITNIDKLPPTIRDSFMVLYNTTNEVGYWTMRERGINPIPYLRKVWADECKAYMKEVYWYNKGIKPTLKEYMDVAVDSIGGLILMLDSYFLTTDEVTEEGLDYVSKIPGVMHSSARILRFNDDLSTSSHELARGDNSKALECYMNETGASEEAAREHIKHLVRKTWKKMNKEVFEDYPFSGFKPFLGACLNMARASHCFYDYGDGHGLPGHQTKDHLVSTIFESVPL

>EgranTPS059

TCTLKIEAQEIGRRSANWQPNVFDYDFLNRLLRQHGFNISQDVFQRFMSKSGTFNESLNEDVKGLLGLYEASFHVLEGETILDEAWTFASKHLKDLNLDKIPTNLATHVDHALEMPIHWRPNRLEARWFIDMCEKQQDMIPSLLRLAKLDFNSVQSIYRKEVSTLARWWVELGANKMTFGRDRLMENYFWSMIMVFEPQHIAFREMNGKIASMVTLIDDVYDVYGTPEELELLTDFIVRWDITDVDRLPPIIRDSFMALYNTTNEIGYWTMRERGINPIPHLQKLWAEECKAYLKEVHWCSKGIKPTLKEYMDVATYSTGGLVMLLASYFLTTDKLTEEGLNYVSKIPSIMHCSCKMLRLINDFSTSSYELARGDNLKALECYMNETGASEEAAREHIMHKVREGWKLMNRAVFEDYPIPGLRPFLGACLNQARVSHTFYRYGDGFGRPDNDTKDYLASAIYKPVPL

>EgranTPS060

TCAVTIENPEIVRRSANWKPNVWDYEFLAEQVQRLKEEIKGLFNREMNQVAKLEFIDVVQRLGLGYHFETEIKNALSSIYDNTGYAQLLNDLYAISLGFRLLRQHGYNIRQDVFQQFMNKTGTFNESLNKDVKGLLGLYEASFHGLEGETMLDEARNFASKHLKDLNLDKVPTMLASYVSHTLDIPIHWRPNKLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARWWVELGANKMTFFRDRLVEHYFWNCTMVFEPQYTAYREMTMKLACMVTLIDNVYDVYGTLEELELLTDFLVRWDITEIDKLPPTIRDSYMALYNTTNEIGYWTMRELGINTIPYMRKVWADECAYIKEAHWYNKGIKPTLKEYMDNALDSIGGPIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSAKILRLNNDLSTSSYELARGDNFKALECYMNETGASEEAAREHVKQMVHETWKRMNKDVFEDYPYFGLGPFLDACLNFARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPL

>EgranTPS061

TCTLKIEAQEIGRRSANWQPSVWDYDFVSEEAQRLKKEVKGQFDREMNSVAKLEFIDVVQRLGLGYQFETEIKNALSSIYNNTEVAQLLDDLDAVSLRFRLLRQHGFNVSQDVFQRFMSKSGTFNESLNEDVKGLLGLYEASFHVLEGETILDEAWTFASKHLKDLNLDEIPTNLVSQVDHALEMPIHWRPNRLEARWFIDMCEKQQDMIPSLLRLAKLDFNLVQSIYRKEVSGLARWWVELGANKMTFCRDRLVENYFWSSIMVFEPQHTAFREMNGKIASMVTLIDDVYDVYGTLEELELLTDFIVRWDITDIDRLPPTIRDSFMALYNTTNEIGYWTMRERGINPIPHLQKVWADECKAYLKEVHWCSKGIKPTLKEYMDVATYSAGGLVMLLASYFLTTDKLTEEGLNYVSKIPSIMHCSSKMLRLINDFSTSSYELARGDNLKALECYMNETGTSEEAAREHIMHMVREAWKWMNRAVFEDYPIPGLRPFLGACLNLARVSHTFYRYGDGFGLPNNDTKDYLVSAIYKPVPL

>EgranTPS062

VDPNTNEQSPVARRSANYMPSVWDYDILSRLLRQHGYDLSQDAFQRFINKTGTFEESLKKDVKGLLGLYEASFHGLEGENILDEAQDFASKHLKNLNLNEIPTCLAKQVLHALDMPIRWRPNRLEARWFMDMYGKQQDMIPSLLRLAKLDFNLVQTIHRKEVSNLARWWVELGANNMTFSRDRLVENYFWSCLMVFEPQYTAYREMTTKIGCMVTLIDDVYDVYGTLEELVLLTDFIVRWDITDIDNLPPTIRNSFMALYNTTNEIGHWTMREQGINPIPYMRKVWADECRAYIKEVHWYNEGIKPTLKEYMSNAVDSIGGLIMLLHSYFLTTDNLTKEGLDYMSKIPRIMHCSAKILRLNDDLGTSSYELARGDNFKALECYMNETGASTEAAQQHIKHLVRETWKTMNKDVFEDYPFPGFKPFLGACLNLARASQCFYQYGDGHGLPGHETRDHIVSTLFKPVPL

>EgranTPS063

KCSLTIEDQDTARRSANWKPSVWDYGSVTEQVQRLKEEVKGLFHREINQVAKLEFIDVVQRLGLGYHFETDIKNALSSIYNNTEDAQLSDDLYAVSLRFRLLRQHGYNLQQDVFQRFMNKMGTFNESLKEDVRGLLSLYEASFHGLEGETIVDEAWNFASKHLKDLNLDEVPANLASNVSHALDMPIHWRPNRLEARWFMDTYEKQQDKIPCLLRFAKVDFNIVQSIHKKEVSNMARWWVELGANKMTFFRDRLVEHYFWCCAMVFEPQYTEFREMTTKLTCMVTLIDDVYDVYGTLEELEVLTDFIVRWDITDVDKLPLKIRACFLALYNTTNEIGYWMMRERGINPIPHMRKVWADECKAYIKEARWYNKGIKPTLDEYVDNGVTSIGGLIMLLGSYFLTTDKPTEEGLDYVSNIPSVMHCSAKILRLNNDLSTSSYELARGDNFKALECHMNETGASEEATREHIKHLVRKTWKRMNRDVFEDYPYSGFGPFLGACLNLARASQCFYQYGDGHGLPDHETRAHIVSALFDPVPL

>EgranTPS064

TCASKIEVQEIGRCPANWQPSIWDYDFVSEEVQRLKKEVKGLFDREMNQVAKLEFIDMVQRLGLGYQFKMEIKNALSSIYTEDAQLSDDLEAVSLRFRLLKQHGYNVPQDVFQRFMSKTDTFNESLNEDVKGLLGLYEASFHGLEGETILDEAWTFASKHLKDLNLDEIPTNLASHVSHALDMPIHWRPNRLEARWFIDMYKKQQDMIPSLLRLAKLDFNLVQSIYRMEVSRLARWWVELGANKMTFCRDRLVESYFWSNTMVFEPQHTAVREMNGKIASMVVLIDDVYDIYGTLEELELLTDFIVRWDITNIDSLPPTIRDSFMALYNTTNEIGYWTMRERGINPIPYLQKVWADECKAFLKEVHWCSNGIKPTVKEYMDVATYSAGGLVLLLASYFLTTDKLTKEGLDYVSKIPSIMHCSSKMLRLINDFSTSSYEVARGDNLNALECYMNETGASEEAAREHITHMVREAWKWMNRAVFEDYPIPGIGPFLGACLNLARVCHTFYRYGDGFGHPSNDTKHYLVSAIYEPVPL

>EgranTPS065

ANQPEVVDQMHQRRSANYKPNIWNYDFLEEVKPMLSEAVDSLAKLELIDCMTKLGLSNLFENEMKEALETVASIHNGVFTMEEHLYASALRFRLLRQHGHIVSQDELRRFKEGSILFNRSNGEDVKTMIELLEASHLALEGENILHEAKAFSTGILRERVSSLDGRLFKRTVHALELPLHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRWWRDLGLMEHVDFTRDRLVESFLCALGLSQETRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAINRWDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHRLPHLAKAWADFCKALLTEAKWDNKGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDLADLLERNKDLIYNVSMIIRLCNDLGTSTSERDRGDAPSSVVCYMQEANVPEDVARKHIKELINQAWKSINAHCFGNVETPFVRTFIDVTVNASRVAHMLYQFGDGFGVQDGDIRRQILSAVIHPIAL

>EgranTPS066

ANLPEVVGTMNQRRTANYKPNIWNYDFLKERIEGLVEEVKRILSEVVDSLAKLELIDSMTKLGLSNLFENEMKEALETVASINNGVFTMEEHLYASALWFRLLRQHGHIISQDELRSFKEGSILFNRSNCEDVEYVELLEASHLALEGENILHEAKTFSTGILRKRVSSLDGRLFKRAVHALELPMHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRWWRDLGLMEHVDFTRDRLVESFLCALGLSQEPRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAITRRDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHRLPHLAKWEDFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNWEDVADLLERNKDLIYNVSMIIRLCNDLGTSTAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAYCFSNADTPFVRTFIDVTANAARVAHMLYQFGDGFGVQDGDIRRQILSAVIHPLAL

>EgranTPS067

HQRRSANYKPNIWNYDFLKERMEGLVEEVKPMLSKSVDSLAKLELIDSMTKLGLSNLFENEMKEALERVASNNNGVFTMEEHLYASALRFRLLRQHGHIVSQNELRRFKEGSILFNRSNCEDVEAMIELLEASHLALEGENILHEAKAFSTGILRERVSSLDGRLFKCTVHALEIPLHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRWWRDLGLMEHVEFTRDRLVESFLCALGLSQETRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAITRWDSEQIQQLPECMKWADFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDVADLLERNKDLIYNVSMIIRLCNDLGTSTAERDRGDAPSSVVCYMREANVPQDVARKHIKELINQAWKSINAHCFGNVETPFVRTFIDVTVNASRVAHMLYQFGDGFGVQDGDIRRQILSAVIHPVAL

>EgranTPS068

AHLQQVVGTMHQRRSANYKPSIWNYNFLEEVKRMLSEVVNSLAKLELIDIMTKLGLSNLFENEMKEALETVASINNGVFTMEEHLYANALRFRLLRQHGHIISQDELRSFKEGSILFNRSYCEDVEAMIELLEASHLALEGENILHEAKTFSTGILRKRVSSLDGRLFKRAVHALELPMHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLAEISRWWRDLGLMEHVEFTRDRLVESFLCALGLSQEPRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAITRRDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDWHRLPHLAKAWADFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLEDVADLLERNKDLIYNVSMIIRLCNDLGTSTAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAYCFSNAETPFVRTFIDVTVNAARVAHMLYQFGDGFGVQDGDIRRQILSAVIHPLAL

>EgranTPS069

ANLPEVVGTMHQRRTANYKPNIWNYDFLKERMEGLVEEVKRILSEEVDSLAKLELIDSMTKLGLSNLFENEMKEALETVASINNGVFTMEEHLYASALRFRLLRQHGHIISQDELRSFKEGSILFNRSNCEDVEAMIELLEASHLALEGENILHEAKAFSTGILRKRVSSLDGRLFKRAVHALELPMHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQAAHQRDLREISRWWRDLGLMEHVDFTRDRLVESFLCALGLSQEPRFSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTCAITRRDSEQIQQLPECMKACCRVLNDVIHEIAYVIGKDEDWHRLPHLWAEFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFWEGVNWEDVAEGLERNKDLIYNVSMIIRLCNDLGTAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAHCYSNAETPFVRTFIDVTVNAARVAHMLYQFGDGFGVQDGDIRRQILSAVIHPLAL

>EgranTPS070

ANLPEVVGTMHQRRSANYKPNIWNYDFLDLVREGLVEEVKPMLSEVVDSLAKLELIDSMTKLGLSNLFENEMKEALETVASINNGVFTMEEHLYASALQFRLLRQHGHIISQDELRSFKEGSILFNRSNCEDVEAMIELLEASHLALEGENILHEAKAFSTGILRERVSDLDGRLFKRTVHALELPLHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDLREISRWWRDLGLMEHVDFTRDRLVESFLCALGLAQEPRLSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTSAITRRDSEQIQQLPECMKVCFRALNDVIHEIAYDIGKDEDSHRLPHLWADFCKALLTEAKWDNMGYTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNLKDVADLLERNKDLIYNVSMIIRLCNDLGTSTAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAYCFSNAETPFVRTFIDVTVNAARVAHMLYQFGDGFGVQDGDIRRQILSSVIHPLAL

>EgranTPS071

HQRRSANYRPNLWKYDFLKEQVERLVEEVKPTLSEAVNSLLKLELIDKMKKLGLSNLFGNEIKEVLQTVASTNNGVFNMEDHLYASALQFRLLRQHGHVVSQDALRSFRDGRNTLSGSNCGDVEAMIELLEASYLAMEGENILEEAKAFSTGILQERVSGLDGQLLKRAVHALELPMHWRVQWFDIKWQIDLYEQQEDKQSSLLPLAKLNFNIVQATHQRDLRDISRWWRDLGLIEHVDFARDRLVESFFCALGLSQEPQFSSFRKSLTKVIILILVIDDLYDLYGSLEELECFTDAITRWDLEQIQQLPECIKVCFQALRDVSYEIAHEIGKDEDWHQVPHLMKVWADFCKALLNEAKWDKMGYTPSLEEYLSNAWTSSSGPLILSHAYYLMGQMKLEDAADFLKRNKDLIYNVSIIIRLCNDLGTSTAERERGDAPSSVACYMREANVSEDIARKHIPILINQAWNSINAHCFGNAEKPFLRPFINVTVNAARVVHMLYQFGDGFAIPDGDIQQQILSIVIKPLAL

>EgranTPS072

ANSRQAVDSMHQRRSANYKPNIWKYDFLEDVKAMLAEAVDSLTKLELIDWMRKMGLSNLFDKEMKEALETVASINNGIFAKEDHVYASALRFKLLRQQGHVVSQDELRSFKEESDTFNRSNCEDIEAMMQLLEASHLALEGEDILDEGKAFSAEILRERVSSLDGPLLKGAVHALELPMHWRVQWFDIKWQIDLYEQQEDKQSNLLELAKLNFNTVQATHQRDLIEISRWWRDLGLIERVDFTRDRPVESFLYALGLSQEPRFSSLRKSLTKVVIFILLIDDVYDLYGSLEELECFTSAVTRWDSESIQQLPECMKVCFRALQDVTYEIAHEIGKEEDWHRLPHLTKAWADFCKALLTEAKWDLLGYTPSLGEYLSNAWTSSSGPLLLSHAYFFVGHMKLEDAAESVERNKDLIYNASMIIRLCNDLRTSKAEIERGDAPSSMVCYMREANVSEDIARKHIKGLIDQAWKNINAHCFVNAETPFLRPYIDVTVNAARAAYMIYQSGDGFGVQDGTIGQQMLSAVIEPLAL

>EgranTPS073

TCASRIEVQEIGRHSANWQPSVWDYDYLSEEVQRLKKEVKVLLDGEMNQVAKLKLIDAVQRLGLGYQFEMEIRNALSSIYNNTEDAQLSENLDVVSLRFRLLRQHGYNIPQDVFQRFMSKTGTFNESLNEDVKGLLGLYEASFHGLKGETIIDEAWTFASKHLKDLNLNEIPTNLASHVSHALVMPIHWRLNRLEARWFIDMYKKQQDMIPSLLRLAKLDFNLVQSVYRKEVSNLARWWVELGANKMTFCRDRMVESYFWSNSMVFEPQHTAFREMNGKIASMVVLIDDVYDIYGTLEELELLTDFIVRWDITDIDRLPPIIRDSFMAMYNMTNEIGYWTMRERGINPIPYLRKVWADQCKAYLKEVHWRSKGIKPTLKEYIDVATNSSGGLVLLLPSYFLTTDKLTEEGLDYVSKIPSIMRCSCKMTRLINDFSTSSHELARGDNLKALECYMNETGVSEEAAREHIMHMVREAWKWMNRAVFEDYQIPGLRPFLGACLNMARICHTFYGCGDGFGQPSNDTKDSLASAIYEPVPL

>EgranTPS074

TCASKIEVQEIGRHSANWQPSVWDYDFLTRLLRQHGYNTPQDVFQRFMSKTGTFNESLNEDVKGLLGLYEASFHGLEGETILDEAWTFASKHLKDLNLNEIPTNLASHVSHALDMPIHWRLNRLEARWFIDMYKKQQDMIPSLLRLAKLDFNLVQSVYTKEVSNLARWWVELGANKMTFCRDRIVESYFWSNSMVFEPQHTAYREMNGKLASMVVLIDDVYDIYGTPEELELLTDFIVRWDITDIDRLPPIVRDSFMAMYNTTNEIGYWTMRERGINPIPYLRKVWAEECKAYLKEVHWRSKGIKPTLKEYIDVATNSSGGVVLMLPSYFLTTDKLTEEGLDYVSKIPSIMRCSSKMLRLINDLSTSSHEVARGDNLKALECYMNETGVSEEAAREHIMHMVREAWKWMNRAMFEDYRIPGLGPFLGACVNTVRICHTFYGCGDGFGQPSNITKDSLASAIYDPVPL

>EgranTPS075

TCASKIEVQEIGRHSANWQPSVWDYDFLSEEVQRLKKEVKGLFDREMNQVAKLKFIDVVQRLGLGYQFETEIKNALSSIYNNTEDAQLSDNLDVVSLQFRLLRQHGYNIPQDVFQRFMSKTGTFNESLNEDVMGLLGLYEASFHGLEGETIIDEAWTFASKHLKDLNLNEIPTNLVSHVSHALDMPIHWRLNRLEARWFIDMYKKQEDMIPSLLRLAKLDFNLVQSVYRKEISNLARWWVELGANKMTFCRDRIVESYFWSNSMVFEPQHTAYREMNGKIASMVVLIDDVYDIYGTPEELELLTDFIVRWDITDIDRLPPIIRDSFMAMYNTTNEIGYWTMRERGINPIPYLRKVWAEECKAYLKEVHWRSKGIKPTLKEYVDVATNSSGGVVLMLPSYFLTTDKLTEEGLDYVSKIPSVMRCSSKMLRLINDLSTSSHEVARGDNLKALECYMNETDASEEAAREHIMHMVREAWKWMNRAVFEDYRIPGLGPFLGACVNTARICHTFYGCGDGFGQPSNITKDSLASAIYEPVPL

>EgranTPS076

VCPVRSIWEPPCRGLCSGDESWGLRFQNGRVQMLEQEVRSAMKDESAELSTILALVDDIQRLGLVFLFEEDVKRALRRYHSPDGGYKNRDQKTLHGTALFFRILRQNGFEVSPDVFRIFMDERGTFMESLGRDVEGLLSLYEASHLAFEEEGILLEAKEFAVKHLKRLNDIDISKDLEYRVNHGSVPPLHQRMPLLEARQSIEAYSPQRDAERRLLELAVYNFNMVQSILQRDLQEMSRWWNDVSLANELSFARDRLMECFFWTVGMAYEPQFSNLRKGLTKVTALVTTIDDVYDVYGSLDELELFTDAVHRWDVNALSNLPSCMKLCFLALYNAVHEMAYDVLKQNGENIIPCLTKVWSDMFKAFLQEAKWKHDKVTPTFEEYMNNGWISVSGLVILIHAFFLSTPDVRKEEIESIETHGHDLLKSPAIIFRLCNDLGTSSAELERGETANSILCYMQDTGVSENVAREHIKELIDIEWKNMNRYQVDYSMFGKSFVRLAFNLARIAHYTYQDGDAHGDPDDRAKYRIHSLLIDPISL

>EgranTPS077

MLEQEVRSAMKDENAELSTILALVDDIQRLGLIFLFEEDVKRALRRYHSLDGGYKNRDQKTLHGTALYFRILRQNGFEVSPDVFWIFMDEQGTFMESLGRDVEGLLSLFEASHLAFEDEDILHEAKAFAIEHLKRLNNIDVNKDLEYQVNWGLALPLHQRMPLLEARRSIEAYRTRRDADHRLLELAVYNFNMVQSILQRDLQEMSRWWNDVSLANKLSFARDRLMECFFWTVGMAYEPQFSNLRRGLTKVTALVTTIDDVYDVYGSLDELELFTDAVHRWDVDAVSSLPGCMKLCFLALYNAVHEMAYDVLKQNGENIIPCLTKAWSDMLKAFLQEAKWKHNKVTPTFEEYMNNGWISVSGLVILIHAFFLSTPHIRKEELELIETYGHDLLKSPSIIFRLCNDLGTSSAELERGETANSILCYMQDTGVCENVAREHIKELIDTAWKKMNRYQVDNSLFGKSFVRLAFNLARIAHYTYRDGDAHGAPDDRSKYRIHSLLIDPISL

>EgranTPS078

STSTKAAFPQGGRRSANYQPSVWTHNDLQREKAQMVEEVRGALHDENAELITIFALVDDIQRLGLGRHFEEDISRALHRCLSVYKGLQKSLHGTALSFRILRQHGFEVSQDVFKIFMDESGSFMKNLGNDVQGMLSLYEASHLAFEEEDILHEAETFTIEHLKNHNRDINKDLQGEVNHELEWPLHRRMSLLEARRFIEAYSRRRYTSHRILKFSATNFNTLQSTLQGDLQEVFRWWDNVGLANELNFARDRLVECFFAAVAVADEHPLSNCRKGLTKANILNVIIDDVYDIYGTLDELELFTDAVRRWEINAVEDLPGYMKLCFLALYNCVNELAYDTLKETRENVIPYLTKVWYDACEAFLQEAKWSHNKITPRVEEYLNNGWISVSGHVMLIHAYFLSSPSMRKEELESLEHYHDLLRLPSMIFRLTNDLATSSAELERGETTNSIWCYMQEMGVSELEARKYVIKMIDTTWKKLNKYLVNDSTFNQSFVRMAFNLARMAHCMYHDGDAVGAPDDLSMNRVHSLIIDPVSL

>EgranTPS079

MALQIFSLPNVCSKRIPAQVPRSASAKAAVSQGGGRSPQYQPTLWTYDYLQSLPIGVHRRVVINSHFVRSQSEQQNGRVQMLEQEVRSAMKDENAELSTILALVDDIQRLGLIFLFEEDVKRALRRYHSLDGGYKNRDQKTLHGTALYFRILRQNGFEVSPDVFWIFMDEQGTFMESLGRDVEGLLSLYEASHLAFEEEDILHEAKAFAIEHLKRLNNIDVSKDLEYFQVNWGLALPLHLRMPLLEARRSIEAYSTRRDADRRLLELAVYNFNMVQSILQRDLQEMSRWWNDVSLANKLSFARDRLMECFFWTVGMAYEPQFSNLRRGLTKVTALVTTIDDVYDVYGSLDELELFTDAVHRWDVDAVSSLPGCMKLCFLALYNAVHEMAYDVLKQNGENIIPCLTKAVWSDMLKAFLQEAKWKHNKVTPTFEEYMNNGWISVSGLVILIHAFFLSTPHIRKEELELIETYGHDLLKSPSIIFRLCNDLGTSSAELERGETANSILCYMQDTGVCENVAREHIKELIDTAWKKMNRYQVNNSLFGKSFVRLAFNLARIAHYTYQDGDAHGAPNDRSKYRIHSLLIDPISLE

>EgranTPS080

STSTKAAFPQGGRRSANYQPSVWTHNDLQREKAQMVEEVRGALHDENAELITIFALVDDIQRLGLGRHFEEDISRALHRCLSVYKGLQKSLHGTALSFRILRQHGFEVSPDVFKIFMDESGSFMKTLGNDVQGVLSLYEASRLAFEDEDILHEAETFTIEHLKNHNRDINKDLQGEVNHELEWPLHRRMSLLEARRFIEAYSRRRYTSHRILKFSATNFNTLQSTLQGDLQEVFRWWDNVGLANELNFARDRLVECFFAAVAVADEHPLSNCRKGLTKANILNVIIDDVYDIYGTLDELELFTDAVRRWDINAVEDLPGYMKLCFLALYNCVNELAYDTLKETRENVIPYLTKAWYDACEAFLQEAKWSHNKITPRVEEYLNNGWISVSGHVMLIHAYFLSSPSMRKEELESLEHYHDLLRLPSMIFRLTNDLATSSAELERGETTNSIWCYMQEMGVSELEARKYVIKMIDTTWKKLNKYLVNDSTFNQSFVRMAFNLARMAHCMYHDGDAVGAPDDLSMNRVHSLIIDPVSL

>EgranTPS081

SGSTQVSDTQGGRRSANYQPTVWTHNYLQREKAQMLEEVRGALNDEKAEPMTIFALVDDFQRLGLGQHFKEDISRALRRCLSNDAVNKSRQKSLHSTALSFRILRQHGFEVSQDDFKIFMDKSGNFMKTLGGDVQGMLSLHEASHLAFEEEDILQEARSFAIEHLRNLNCKVDKDLQDQVKHELELPLHCRMPMLEARRSIEAYRRCGYTNHRIPEFAATNFDTLQSILQRDLQEMSRWWNDVSLARNLNFVRDRLTECFFWAAGVADEPTLTNCRKRLTKVTSLITIMDDVYDVYGTLDELELFTDAVRRWDINAVDDLPGYMKLCFLALFNSVNEIAYDTLKETGKIVIPYLAKSWYDLCKSFLQEAKWSYKKTNPRFEEYLNNGWISSSGHVILIHAYFLSGPSMGREELESLEHYHDILRLPSMIFRLTNDLVTLSAELERGETTNSITCYMQEMGVSESEARDYVMKLIDTSWKQMNKYLVNGSTFDQSFVRMAYNLARTTHFMYQDGDAHGSPDNRSRNRMHSLIIEPISL

>EgranTPS082

PSPTANVESIQARRSLILKKDGDRPIQREKAQMLEEVRGVLNDEKAEPMTIFALVDDIQRLGLGRHFEEGISRALRRCLSKNAVNKSRQKSLHGTALSFRILRQHGFEVSQDVLRIFMDESGSFMKTLGGDVQGMLSLHEASHLAFEEEEILHGARSFAIEHLRNLNRKVNKDLQDRVKHELELPLHCRMPLLEARQSIEAYSRGYTNHRILEFVVMNFNMSQPILQRDLQEMSRWWNNVGLANNLNFARDRLVECFAAVAVADEHPLSNCRKGLTKVNMLIVIIDDVYDIYGTLDELELLTDAVRRWDINAVEDLPGYRKLCFLALYNSVNELAYDTLKETRENVIPYLTKVWYDSCKAFLQEAKWSHNKITPRVEEYLNNGWISISGHVMLIHAYFLSSPSMRKEELESLEHYHDLLRLPSMIFHLTNDLATSSAELERGEATNSIWCYMQEMGVSELEAGQYVIKRIDTTWKKLNKYLVSDSTFNQSFVRMAFNLARMAHCIEEPCALTNN

>EgranTPS083

SASTQVSDTQGGRRSANYQPTVWTHNYLQREKAQMLEEVRGALNDEKAEPMTIFALVDDIQRLGLGQHFEEDISRALRRCLSNDAVNKSRQKSLHGTALSFRILRQHGFEVSQDVFKILMDESGSFMKTLGGDVQGMLSLHEASHLAFEEEDILQEARSFAIEHLRNLNCNVDKDLQDQVKHELELPLHCRMPLLEARWSIEAYRRCRYPDHRIPEFAAMNFNTLQSILQRDLQEMSRWWNDVSLARNLNFVRDRLMECFFWAAGVADEPTLANCRKRLTKVTSLITIIDDVYDVYGTLDELELFTDAVRRWDINAVDDLPGYMKLCFLVLFNSVNEIAYDTLKETGKIVIPYLAKSWYDLCKSFLQEAKWSYNKTNPRFEEYLNNGWISSSGHVILIHAYFLSSPSMRREELESLEHYHDILRLPSMIFRLTNDLVTSSAELERGETTNSIMCYMQEMEVSESEARDYVMKLIDTSWKQMNKCLVNGSTFDQSFVRMAYNLARTTHFMYQDGDAHGAPDNRSRNRMHSLIIEPISL

>EgranTPS084

SASTQISDPQEGRRSANYQPSVWTYNYLKEKVQILEEEVRGALNDEKAETFTIFATVDDIQRLGLGDHFEEDISNVLRRCVSVFMSLQKSLHGTALGFRLLRQHGYEVSQDVFKIFLDESGSFVKTLGGDVQGVLSLYEASHLAFEEEDILHKARSFAIKHLENLNSDVDKDLQDQVKHELELPLHRRMPLLEARRSIEAYSRRGYTNPQILELALTDFNVSQSTLQRDLQEMLGWWNNTGLAKRLSFARDRLIECFFWAVGIAHEPSLSICRKAVTKAFALILVLDDVYDVFGTLEELELFTDAVRRWDLNAVEDLPVYMKLCYLALYNSVNEMAYETLKEKGENVIPYLAKAWYDLCKAFLQEAKWSNSRIIPGVEEYLNNGWVSSSGSVMLIHAYFLASPSMRKEELESLEHYHDLLRLPSLIFRLTNDIASSSAELERGETTNSIRCFMQEKGISELEARECVKEEIDTAWKKMNKYMVDRSTFNQSFVRMTYNLARMAHCVYQDGDAIGSPDDLSWNRVHSLIIKPIPA

>EgranTPS085

TRALKIEGQEIVRRSANWQPSIWDYGLVQSLGRLLRQHGYHVPQDVFQRFMNMTGTFNESLSKDAKGLLGLYEASFHGLDGETILDEAWNFASKHLKDLNLDKVPSNLASNVSHALDMPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKIDFNLVQSIHRKEVGNLARWWVELGANKMTFFRDRLVESYFWTCIMVFEPQYTAFREMCTKIGFMVTLIDDVYDIYGTPEELELLTDFIIRWDITDIDKLPPTIRNSFMVLYNTTNEVGYQTMRDQGINPIPYLRKVWADECKAYMKEVHWYNSGIKPALKEYMDVAVDSIGGLILLLHSYFLTTDKLTKEGLDHVSKIPSVMHSSTKILRFNDDLSTSLHELARGDNSKALECYMNESGASEEVAREHIRHLVRNIWKKMNKDVFEDYPFSGFGPFLGACLNLARASHCFYEYGDGHGLPGHQTKDHLVSTIFESVPL

>EgranTPS086

TCAATIENPEIVRRSANWKPNVWDYEFLAEQVQRLKEEIKGLFNREMNQVAKLEFIDVVQRLGLGYHFETEIKNALSSIYDNTGYAQLLNDLYAISLGFRLLRQHGYNIRQDVFQQFMNKTGTFNESLNKDVKGLLGLYEASFHGLEGETMLDEARNFASKHLKDLNLDKVPTMLASYVSHTLDIPIHWRPNRLEARWFMDMYEKQQDMIPSLLRLAKLDFNLVQSVHKKEVSNMARWWVELGANKMTFFRDRLVEHYFWNCTMVFEPQYTAYREMTTKLACMVTLIDDVYDVYGTLEELELLTDFLVRWDITEIDKLPPTIRDSYMALYNTTNEIGYWTMRELGINTIPYMRKVWADECKAYIKEAHWYNKGIKPTLKEYMDNAVDSIGGSIMLLGSYFLTTDKLTEEGLDYVSKIPSVMHCSTKILRLNNDLSTSSYELARGDNFKALECYMNETGASEEAAREHVKQMVHETWKRMNKDVFEDYPYSGLGPFLDACLNFARASQCFYQYGDGHGLPDNETKDHLVRALFDPVPL

>EgranTPS087

QAVDQTHQRRSANYKPNIWKYDFLEQRMERLMEDVKPMFPKAVDSLAKLELIDRMRKMGLSNLFDNEMKEALETVASTKNGIFDMENHVYARALRFRLLRQHGYVVSQDEMRSFKEESKTFNRSNCEDVEAMMQLLEASHLAVEGENILDEGKAFSTGILRERVSSLDGRLLKCAVHALELPMHRRLQWFDVKWQIDLYEQQEDKQSNLLELAKLNFNTVQATHRRDLIEISRWWRDLGLIEHVDFTRDRPVESFLCALGLSQEPRFSSLRKSLTKVIIFILVIDDVYDLYGSLEELECFTSVVTRWDSEPIQQLPECMKFCFRALHDLTYEIAHEIGKEEDWHRLPYLMKAWADFCKALLTEAKWDHLGYTPSLEEYLSNAWTSSSGPLLLSHAYFFVGHMKLEDAAELAEIERGDAPSSMVCYMREANVSEDIARKHIKGLIDQAWKNINAHCFVNAETPFLRPYIDVTVNAARAAYMIYQSGDGFGVQDGTIGQQMLSAVIEPLAL

>EgranTPS088

VNLPEAVGTMHQRRSANYKPNIWNYDFLKERMQRLVEEVKPMLSEVVDSLAKLELIDSMTKLGLSNLFENEMKEALETVASINNGVFTMEEHLYASALQFILLRQHGHIISQDELRSFKEGSILFNRSNCEDVEAMIELLEASHLALEGENILHEAKAFSTGILHERVSGLDSRLFKCAVHALELPMHWRVQWFDIKWQISLYEQREDKQSNLLELAKLNFNTVQATHQRDFREISRWWRDLGLMEHVDFTRDRLVESFLCALGLSQEPRFSSLRKSLTKVVILILVIDDVYDLYGSLEELECFTCAITRRDSEQIQQLPECMKVCFRVLNDVIHEIAYDIGKDEDWHRLPHLWAEFCKALLTEAKWDNMGSTPSLEEYLSNAWTSSSGPLIMSHASFFVGHMNWEDVADLLERNKDLIYNVSMIIRLCNDLGTSRAERDRGDAPSSVVCYMREANVPEDIARKHIKELINQEWKSINAHCYSNAETPFVRTFIDVTVNAARVAHMLYQFGDGFGVQDGDIRRQILSAVIHPLAL

>EgranTPS089

MTDGEISISAYDTAWVALVEDVSGSGSPQFPEALRWIVDNQLPDGSWGDDLIFSPHDRIINTLACVNNLEGMEGLNWEKLLKLQSADGSFLFSPSSTAFALMQTKDANCLDYLSRAVQRFNGGVPNVYPVDLFEHLWAVDRLQRLGVSRYFKDEIKGCMSYVQRYWSEKGICWARNSRISDIDDTAMGFRLLRLHGHEVSADVFEQFKRGDVFSTFMGQSTEAVTGMFNLYRASELIFPGEKILEDAKSHAVKFLRRKREANELLDKWIRTKDLPGEVGYALDVPWYASLPRVETRFYIDQYGGENDVWIGKTLYRMGYVNNNVYLELAKLDYNNCQALHLSEWDNFQRWYCESKLVDFGTSGKTLLYSYFTAAASIYEPERARERLAWAKTSVLVDAIASYLEGEGTSRERRRGFVREFQQFSKKQKHINGRKYCSRSSIPSKGGQGLIAALLGTLDQLSLEVLVARGKDIGHALRTAWEKWLVGYEEEGDKYKGVVELLVQMIALGSGNSSFSDGRSSHPQYRHLCNLTNTICRHLAHRQTQKACENEDLPIQMAMQELVQLVLQDSAHRLDRDVKDAFFSVTRSFYYTAHCDPATIKSHIAKVLYER

>EgranTPS090

IDVPIMKWQEIGEDDLGVEGVKVASPSSEIGERVKAIKLMFWSMSDGKISTSAYDTAWVALVEDVGGNGNPQFPEALQWIANNQHPDGSWGDDLLFCPHDRILNTLACVVALKYWKIHPDKCDKGMSFFKDNISKLAEEKPEHMPIGFEVTFPSLIETAWKLEIEICDDSPVFREIYANRNTKLNKIPSDLLHQVPTSLLHSLEGMKELKWEKLLKLKNADGSFLFSPSATAFAFLQTRDLNCLNYLSRTVQRFHGGVPNVYPVDLFEHLWAVDRLQRLGVSRYFKEEIKECMSYVYRYWSDKGISWARNSNVADIDDTSMGFKLLRLHGYEVSAEVFENFKSGKEFFSFMGQLIVPVTGMLNLYKASELIFPGEKILEDANRHAAKFLRRKQEANELFDKWIITKDLPGEVGYALDVPWYANLPRVESRFYIDQCGGQNDVWIGKTLYRMEYVDNDVYLELAKLDYNNCQALHLSEWDNFQGWYCESKLVDFGISGKTLLYSYFTAAASIYEPERAGERLAWAKTRVLVDAIASYLEREGATREQRGAFVRAFQQFSRKQKHTSGRSSILDERGEGLIAALLGTVDQLSLEVLEARGKDISHPLRAAWEKWLVGYGEEGDKYKGVVELLVQMIALGACNSLLSDDLSSHPECHRLCNLTSTICRQLAHHQTQKVRKNENDQIEMAMQELAQLVLQNSTRGLNRDVKDAFFAVTRSFYYTAHCDTGTINSHIAKVLFERVN

>EgranTPS091

MSVLLLQLSEVSKERVRDMSNKVELSISSYDTAWVAMVPSPGSPKSHRFPRSLILGVSPTIIRNRHRLLIKDALLSTIACVLALEQWGVGERQINCGLEFNILLSSMIEQAGRLNLNLPLRSANLDSMSYERNLELKRNGESDWEMIKKHQRKNGSLFNLPSTSAAALTHLQNVGCLRYLKLVVEKFGDAAPTIYPLGIYARLCMTENLERLGINCHFRKEIIDTLDDTYRCWLPGEENIFLDVATSAMAFRILRSHGYDVSSDALSQFAEEDQFYNTLEGHEKDAGWVKLAYCYFSAAETFLARQLLDTHISWAKNSVVVTVADDLFDVSGSAEGNEVLIRLLRKWNVNLSADGCSEQCQQWMNTLLMHVSFGLGPTVLPALYLVGPKLSEKQVESPEYHNLFRLMSTCRRLLNDIQSYERESKQGKLHAVTLQMLDGSGTSEREAIERISSIIISMRRELLKLVLQEKDSIIPRVCKDLSWKMSAVMHLFYMDADGFAPDEKTSAVKALLDQPITFNEL

>EgranTPS092

MSFSSYGNGQLTDAGCRGEEEIFQHIATSAMAFRILCSHGYNVSSDNLFSCAIDQWKVDDALRFPLEESLTRAANRRNIQLHNTNSTRILKCKLRSHNFHNKDFLNLAMHDFNMCQAICQDMETWGGDVSADCCSEETGCKLIAWQGRDVTGHRRTKAVPKMDEYMAHPSHLVWALSFSWLAGPRLSEKLIKSLEFHYFFGAVSTFGHLWNNRWGAEEGKPTAVMMQMLDGSSTSQEEAIQRISQMAVDETRKLLKLVLQEKESIVPRPCKDLFWNLIAVLHFFYREEDGFSSP

>EgranTPS093

MTHSHFSSLGLSAPISGAFPLDFGLKSVKQSSSCVAVALGEGSKERISDMFNKVELSLSSYDTAWVAMVPSPCSPQSPLFPRSVSWLMNNQLCDGSWGLPDHHPLLIKDALLSTLACVLALKQWGVGERQINKGLEYIASNSASVIDDRQHTPIGFNILLSGMIEQADCLNLNLPLRPADVDSVSYKRNLEVKRGLSGISGRYLSYVAEGMGSSADWEMIMKYQRKNGSLFNSPSTTAAALTHLQNASCLHYLESVLEKFGDAVPTIYPLEIYARLCMIENLERLGIDRYFRKEVIHVLDDTYRCWLQGKEEIFLDIATTAMAFRMLRSHGYDVSSDALNQYAEEDQFCNTLEGYVKDAGSVLELYRASQLIINDDKIILDKINSWTYDFLRKGLHTGKMHANRLESYICGEVDDALKFPLHANLERVANRRNIELYNIDSTRVLKCGLRSCNFCNKDFLNLAVNDFNNCQAIYQEELKYLERWVKEKRLDKLKFARQKLAYCYFSAAASFSPPQLSEARISWAKNGVLTTVVDDFFDVGGSAEELENFIWLVKRWNVNLSADCCSEQVQIIFSALHSTISEIGDKAVTWQGRNVTGHVAQIWLELLESMLTEAKWTRKKAVPTMDEYMANAYVSFALGPIVLPALYLVGPKLSEEQVESLEYHKLFKLMSTCGRLLNDMQGFKRESREGKLNAVTLQMLDRSSTSEREATERISSIIISKRRELLKLVLQERDSIVPRACKDLFWKMSTVLHFFYMDDDGFTSDEKTSAVKALLDQPITLNELELP

>EgranTPS094

MESQKSSIQSLINMIKRDLLSVIGSHSFLSPSPYDTAWLAMIPDPRRHDRPMFEGCLNWVLHNQNEEGFWGYHDCDRHEMPDGVGCLASTLVCMIVLKKWYAGSPLIEKGLKFIHKNAELLLSRYTHGKFSRWIAIVLPGMVELARASSLEVVFPESVDRALEDLFINRRQILKMEELVDKNQYCPLLSYLEALPSTYKISHETILKHLDSDGSLFQSPSATSRAYLSTGNEACLAYLQSLASNCASSGIPSFYPVDEDLTKLSMVHQLVRLGLTEYFDRENDEILAKIYRLLYKDCLEFWLLRMHGYRVSPSSFCWFLDHEEIEHELGLPWMARLDHLEHRTWMEEKDACVLWMGKFQYNRPSFVHNQDIVQLALQNYVLRQSVYRMELDVVKRWSETTGLRKMGFGREKTLYSYFAVAASISLPCNSDVRVLVAKSAIMITVADDFFDMEGSLEDLEKLTNAVQRWDGEGLTAHAKTIFEALDDLVTDFRMKCFKQSGKDIKKNLQEIWGETFHSWLMEAKWSKSGGAPPTQEYLDVGMTSIAAHILVLPSSCLASPTTPLHQLWSNAYQPITKLLMVITRLLNDIQSYEAKAKSGRCSLSGACLLLLLLWTYIHSLILSPCFYDFLTLQKEEKQGKLNFVLLYLKENPEASIEDSINFVQLLLEQLKKEFLLHVLEELCNLPEPSRRLHLGCLKVFHMFFNSSNRYDSETGMLHDIQKALVVPPRVPKLKPLRPLPEQLGPKPREFVTKSLYGQVGLERFPRKSFVGYRISSRTGPVDRWEKMYKSSNFKLCFA

>EgranTPS095

MEFQKPSIQSLVQMIKREILPNMSSHSFLSSSPYNTAWLAMIHNPHQHDLPMFKGCLNWVLHNQNEEGFWGDYDHDEDEMSNKVECLASTLICMTMLKKWHVGLPSIEKGLKFIHENVELLLPGNKHGKFPRWIAIVLPGMVDLARASGLEVIFPESAEHIIADLFSNRQQILKREKLVDKKQYFPLLSYLEALPPTYKVSHETILKHLDSDGSLFQSPSATASAYLATGNEACLAYLQSLALNCASNGVPSLYLVDEELTKLSMVYQLVRLGLTEYFDREKDEFLAQIYRNYKHEKPIVKSIHSIAAELYKDCLGFWLLRMHGYKVSPSSVCWFLDREEVRDHIEKHYEYFSSVLLNIYRASNLMLPNEHELEKARTFSKKFLEKIASRGTRDSSIISSSHCRMIKHELGLPWMAHLDHLEHRMWMEEKDACVLWMGKFSCHRSSLVHNQDILQLALQNFEQRQSIYRMELDVLKRWSETTGLSKMGFGREKTVYSYFAVAASVSVPCNSDVRVLVAKGAVILTVADDFFDMEGSLEDLEKLTEAVQRWDGEGLSAHAKTIFEALDDLVTDFRMKCFKQLGKDIKKNLQNIWGETFHSWLIEAKWSRSGDVRPTQEYLDVAMTSVGAHVLVLPPSCLASPTTSLHQLWSNPYQPITKLLMVISRLLNDIQTYEKEEKQGKLNFVLLYLKENPGASIEDSINFVQLLLDQLKKEFLQHVLEEPCSVPELSRLLHLACLKVFNMFFNSSNRYDSDTDMLHDIQKALVVPPRVPKLKPLRPLPEKLRLKPRVFETKSLSGQYGLEHFPRKSFFGYQMSSRTGPVNRWEKMYKSSSFKLCFA

>EgranTPS096

MRGQIFLIESLVNTIKREILLSNIVSSSFLSPSPYNTAWLVMIPDPHWHDCPMLNVCLNWVLHNQNEEGFWGDYDYEEHEMSDGGECLASTLVCMTVLKKWHVGSTLIEKGLKFIHGNAELLFSRNKRGNSPRWIAIILPGMIDLARAVGLEIIFPESTESAIVDLFRNRQRILEREKLVDRNQYYPLLSYLEALPPTYKISNETILKHVDGDGSLFQSPSATASAYLSTGHKACLAYLQSLASNCASNGIPSIYLVDKKLAKLSLVYQLVRLGLTEYFDQEKDDILAQIYRLEKPITKTVHWIATELYKDCLEFWLLRMHGYSVSPSSFCWFLDREEVRDHIEKHYEYFSSVLLNVYRASNLMLSDEQQLERVRTFSRKLLEKILSGETRDECIISSSHRRMIEHELGLPWMARLDHLEHRMWLEEKDACVLWMGKLSWHRSSLVHNQDILQLALQDFVLRQSTYRMELDVVKGWSETTGLSKMEFCREKTTYSYFAVAASISLPCNSDIREVVAKSAIIVTVADDFFDMEGSLEDLEQLTDAVQRWDGEGLSGHAETIFKALVDLVTDFRWGETFHSWLMEAKWSRSGGAPPMQEYLHVGMKSIATHILPITKFLMVITRLLNDIQSYQKEEKQGKLNFVLLYLKENPEASIEDSINFVQHLLHQLKKEFLQHVLAEPCSLPKPSRQLHLGCLKVFHMFFNSSNRYDSDMDMFHDIQKALVVPPRVPKLKSLMPLPEQPGPKPRVSVTKDLSSQFRLGRFPRKSFVGCQMPPHSGPATRWEKMYKLSSFKLCFA

>EgranTPS097

MVDLAHASGLEVVFPESVERIIADLFSNRQRILKREKLVDKKQYFPLLSYLEALPPTYKVSHETILKHLDSDGSLFQSPSATASAYLATGNEACLAYLQSLALNCASNGAVPSLYLVDEELTKLSMVYQLVRLGLTEYFDQEKDEILAQIYRNYKHEKSIVKSIHSIAAELYKDCLGFWLLRMHGYRVSPSSVCWFLDREEVRDHIEKHYEYFSSVLLNIYRASNLMLPNEHELEKARTFSKKFLEKIASRGTRDSSIISSSHCRMVSGNIQHFLSFSIIKHELGLPWMARLDHLEHRMWMEEKDACVLWMGKFSCHRSSLVQNQDILQLALQNFEQRQSIYRMELDVLKRWSETTGLSKMGFGREKTVYSYFAVAASVSVPCNSDVRVLVAKGAVILTVADDFFDMEGSLEDLEKLTEAVQRWDGEGLSAHAKTIFEALDDLVTDFRMKCFKQLGKDIKKNLQNIWGETFHSWLIEAKWSRSGDVRPTQEYLDVAMTSVGAHVLVLPPSCLASPTTSLHQLWSNPYQPITKLLMVITRLLNDIQTYEKEEKQGKLNFVLLYLKENPGASIEDSINFVQLLLHQLKKEFLQHVLEEPCSVPELSRLLHFACLKVFHMFFNSSNRYDSDTDMLPDIQKALVVPPRVPKLKPLRPLPQQPGPKPRVFETKSLSGQYGLERFPRKSFIGYRMSSQTGPVNRWEKMYKSSSFKLCFA

>EgranTPS098

MGSSSFLSPSSYDTAWLAMNPNLHQPNCPMFKGCLNWVLHNQNEEGFWGDYDYEEHEMSDGGKCLASTLVCRTVLKKWHVGSPLIEKGLKFIHENAELLCPKNKHGKFPRWIAIILPGMVDLARAVGLEIIFPESTERVVADLFSNRQRILEREKLVDRNQYYPLLSYLEALPPTYQISHETILKNLDSDGTLFQSPSATASAYLSTGNEACLAYLQSLASNCASNGAVPSLYLMDEELTKLSVVYQLMRLGLTEYFEQEKDEILAQIFRNCKYEKPIVKSIHLITTELYKDCLEFWLLRMHGYRVSPSSFCWFLDHEEVRDHTEKHYEYFSSVLLNIYRASNLMLPNEHELEKARTFSKKFLEKIAFRGTRDSSIILLSHRGMIKHELGLPWMARLDHLEHMMWMEEKDACVLWMGKFSCHRSSLVHNQDILQLALQNFVQRQSITRMELDVLKRWSETTGLSKMGFGREKTLYSYFAVAASVSVPRNSDVRVLVAKSAIIVTVADDFFDMEGSLEDLEKLTEAVQRWDGEGLSAHAKTIFEALDDLVTNIRTFHSWLIEAKWSRSGDVRPTQEYLDVAMTSVGAHVLVLPPSCLASPTTSLHQLWSNPYQPITKLLMVITRLLNDIQTYEKEEKQGKLNFVLLYLKENPGASIEDSINFVQLLLDQLKKEFIQHVLEEPCSVPELSRLLHLACLKVFHMFFNSSNRYDSDTDMLHDIQKVLVVPPRVPKLKPLRPLPEKLRLKPRVFETKSLSGQYGLEPFPRKSFFGYQMSSQTGPVNRWEKMYKSSSFKLRFA

>EgranTPS099

MVYQLVRLGLTEYFDQEKDEILARIYRNYKHEKPITKSIHGIAVELYKDCLEFWLLRMHGYCVSPLSFCWFLDHEEVRDHIEKHYEYFSNVLLNVYRASNLMLPDEHKLEKVRTFSKKFLEKIASGGTRGESIISSSHRKMIEHELSLPWMARLDHLEHRMWLEEKDAFILWMGKLSCHRSSLVHNQDILQLALHNFVLRQSIYRMELDVVKGWSETTGLSKMGFGREKTTYSYFAVATSVSLPCNSDIREVVAKSAIIITVAEDFFDMEGSLEDLEKLTNAVQRWDGEGLSGHAKTIFKAVVDLVTDFRVKCFKQSGKDIKKILQDIWGETFHSWLMEAKWSRSGGAPSTQEYLDMGMTSIAAHILVLPSSCLASPTTLLHQLCSSPYQPITKLLMVITRLLNDIQSYQKEEKQGKLNFVLLYLKENPKASIEDSINFVQYLLEQLKKEFLKHVLEEPCSLPKPSRRLHLGCLKVFHMFFNSSNRYDSDMDMFHDIQKALVVPPLIPKLKSPMPLPEQLGPKPR

>EgranTPS100

MIDLARAVGLEIIFHESTECAIVDLFRNRQQILEREKLVDRNQYYPLLSYLEALPPTYKISNETILKRVDGDGSLFQSPSATASAYLSTGHKACLAYLQSLASNCASNGIPSIYLVDEKLAKLSLVYQLVRLGLTEYFDREKDDILAQIYSFCWFLDREEVRDHIEKHYEYFSSVLLNVYRASNLMLSDEQQLERARTFSRKLLEKILSGETRDECIISSSHRRMIEHELGLPWMARLDHLEHRMWLEEKDACVLWMGKLSWHRSSLVQNQDILQLALQDFVLRQSAYRMELDVVKGWSETTGLSKMEFCREKTTYSYFAVSTSISLPCNSDMREVVAKSAIIVTVADDFFDMEGSLEDLEKLTNAVQRWDGEGLSGHAETIFKALVDLVTDFRAKCFKQSGKDIKKNLQDIWSETFHSWLMEAKWSRSGGAPTMQEYLDVGMTSIATHILVLPSSCLASPTTPLHQLWSSPYQPITKLLMVITRLLNDIQSYQKEEKQGKLNFVLLYLKENPQASIEDSINFVQHLLDQLKKEFLQHVLEEPCSLPKPSRRLHLGCLKVFHMFFNSSNRYDSDMDMFHDIQKALVVPPRVPKLKSPMPLPEQPRPKPRVSVTKDLSGQFRLGRFPRKSFVGCQMPSHSGPANRWEKMYKLSSFKLCFA

>EgranTPS101

RGRHERRLEEVKQLLKQVRGDSLESLVTVDALRRLAIDYHFEDEIEAILQRHLLISSSRSHSRPIDADNLHEAALRFRLLRQAGYPGNDILGFTSLFEASQLGIEGEDALDQVGESTRQRLHSSLADLDHVQTRFVRNSLGNPFHKSLARFTANDFLRNFVGHSSWTKNLGELAHLDMNIVRSVHQREILQVSNWWKELGMAKELKYARNQPMKWYIWPMAILTETGLSQERVLVTKPISFIYIIDDIFDVYGTIGDLTAFTDVVNRWECTEKDNIPDYMRTCFHALDDITNEFSLAVYKNQGGNPLCPLRKPWASLLNAFLVEARWLASGHSPTTQDYLDNAIVSSGVHVLLVHLFFILGERITPESVDHLENIPEIVSSTASILRLWDDLGSAEDEFQDGRDGSYVECYKREFGSSEEAARDHVKKMISEAWKRLNKACLYPQTFTKSFSRASLNTARMVPLMYNYDDSHSLPLLEHHMKSLLFGGPTF

>EgranTPS102

RGRHERRLEEVKQLLKQVRGDSLESLVTVDALQRLAIDYHFEDEIEAILQRHLLISSSRSHSRPIDADNLHEAALRFRLLRQGGYPVPSDVFQRFLHKGTQNKKPQGNDILGFTSLFEASQLGIEGEDALDQVGESTRQRLHSSLADLDHVQARFVRNSLGNPFHKSLARFTANDFLRNFVGHSSWTKNLGELAHLDMNIVRSVHQREILQVSSWWKELGMAKELKYARNQPMKWYMWPMAILTETGLSQERVLVTKPISFIYIIDDIFDVYGTIGDLTAFTDVVNRWECTEKDNIPDYMRMCFHALDDITNEFSLAVYKNHGWNPLCSLRKTTTQDSLDYAIVSSGVHVVFVQAFFILGERITESVDHLENIPEIVSSTASILRLWDDLGSAEFQDGRDGSYVECYKREFGSSEEAARDHVKKMISEAWKRLNKACLYPQPFTNSFSKASLNTARMVPLMYNYDDSHSLPLLEHHMKSLLFKGPTF

>EgranTPS103

GIKHDQKIKSLIDFLNKVVNEPVESLIIVDMIQRLGVKSLFREQIKAILAWQYTHFSSLNHGKDDVYEIALRFRLLRQEGYCVPADVFEYFNEKGKGFVMKLEGNIKGMMELYEASQMSTEGEDILDEAECFSSKCLNALLTCDLDNEQARMIESTLQYPYRKSFARLAPQSFVNDMQGANSWMEDLLEVANRKRRIDQYVHQKEIHQINRWWKELGLGEKMEFARDQPLKWYMWSMAILTDPSLSELRVELSKPISLVYIIDDIFDVHGTVDELILFTELIKWDNACAEQLPEYMKICFKVLNDIANDFGRIIFEKHGWNPTRFLKQMWANLCNAFLVEFQWNASGKLPKADDYLKNAIITSGVPLVLTHLLFLMGQNIANQSMDSKKEELPNIIFLIAEILRLWDDLGSMKDENQNGYDGSYVDCYLGENGSSYQSAREHVMKLISKLWKLLNKECLSPCPSSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQDHMKSLTCDHETL

>EgranTPS104

LPRTILAQLERETLPPRFVCPFFSCNSFCSAHRRFRKFHSRLLRQGGYPVPSDVFQRFLHKGTQNKKPQGNDILGFTSLFEASQLGIEGEDALDQVGESTRQRLHSSLADLDHVQARFVSNSLGNPFHKSLARFTANDFLRNFVGHSSWTKNLGELAHLDMNIVRSVHQREILQVSSWWKELGMAKELKYARDQPMKWYMWPMAILTETGLSQERVLVTKPISFIYIIDDIFDVYGTIEDLTAFTDVVDRWECTEKDNIPDYMRMCFHALDDITNEFSLAVYKNHGWNPLCSLRKTWASLLNAFLVEARWLASGHSPTTQDYLDNAIVSSGVHVLLVHLFFILGERITPESVDHLENIPEIVSSTASILRLWDDLGSAEFQDGRDGSYVECYKREFGSSEEAARDHVKKMISEAWKRLNKACLYPQPFTKSFSKASLNTARMVPLMYNYDDSHSLPLLEHHMKSLLFKGPTF

>EgranTPS105

GTKHEEKIKSIIGFLNNVGGEPVESLIIVDMIQRLGIKPLFQEQIKAILRWQYTHFTSLNQGKDNVYEIALRFRLRQEGYDVPCDVFEYFKDKGKGFIMKVEGNVKGMMELYEASQMSIEGDDILDEAKCFSSKCLNELLTCDLDPEQVRMIESTLRYPYRKSFARLAPLSFVNDMPGVNSWIEDLLEVANRERRIVQSMHQKENHQINRWWKESGLGEEMKFARDQPLKWYLWSIAILTDPGLSELRVELVKPISLVYIIDDIFDVYGKVDELILFTGVIKWDDACAEQLPEYMKKCFKVLSDITNDFGNIIFEKHGWNPTRFLKQMWANLCNAFLVEFQWNASGTLPKADDYLKNGIITSGVPLVLAHLFFQMGQNIANQSMDSKKEELPNTIFLVAEILRLWDDLGSSKNENQNGYDGSYVECYLRENGSSYQSAREHVMELISKSWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKNGLGLLQDHMKSLTCDHETL

>EgranTPS106

GIKHDEKTKSLIDFLNKVVNEPVESLIIVDMIQRLGVESLFREQIKAILKWQYTHFSSLNHGKDDVYEIALWFRLLRQEGYRVPADVFEYFNDKGKGFVMKLEGNIKGMMELYKASQMSTEEEDILDEAECFSSKCLNALLTCDLDHEQARMIESTLQYPYRKSFARLAPQSFVNDMPGANSWMEDLLEVANKKRRIDQFVHQKEIHQINRWWKELGLGEKMKCARDQPLKWYMWSMAILTDPSLSELRVELIKPISLVYIIDDIFDVHGTVDGLILFTEAIKWDIACAEQLPEYMKKCFKVLNDIANDFGKIIFEKHRWNPTRFLKHMWANLCNAFLVEFQWNASGKLPKADDYLKNAIITSGVPLVLTHLFFLMGQNIANQSMDSKKEELPNIIFLMAEILRLWDDLGSLKDENQNGYDGSYVDCYLRENGSSYQSASEHVMKLISKLWKLLNKECLSPCPFSVPFLEACVNAAKMVSLMYNYEDKHGLGLLQDHMKSLTCDHETL

>EgranTPS107

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>EgranTPS108

RLLRQEGYYVPADVFEYFKDKGKGFIMKLEGNAKGMMELYEASQMSIEGVDILDEAECFSSKCLNELLTCDLDPEQVRMIESTLRYPYRKSFARLAPLSFVNDMLVANSWMEDLLEVANRERRIIQSLHRKEIHQINRWWKELGLGEEMEFVRDQPLKWYMWSMAILTDPSLSELRVELIKPISLVYIIDDIFDVYGKADELILFTEVIERWDNACAEQLPQYMKKCFKVLSDITNDLGNIIFEKHGRNPTRFLKQMWANLCNAFLVEFQWNASGKMPKADDYLKNAIITSGVPLVLAHLFFLMGQNIANQSMDSKKEELPNTIFLVAEILRLWDDLGSLKDENQNGYDGSYVECYLRENGSSYQSARKHVMELISKSWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQDHMKSLTCDHETL

>EgranTPS109

GIKHEEKIKSIIGFLNNVGGEPVESLIIVNMIQRLGIKPLFQEQIKAILRWQYTHFTSLNHGKDNVYEIALRFRLLRQEGYDVPADVFEYFKDKGKGFIMKVEGNVKGMMELYEASQMSIEGEDILDEAECFSSKCLNELLTCDLDPEQVRMIESTLRYPYRKSFARLAPLSFVNDMLGLNSWIEDLLEVANRERRIVQSVHQKENHQINRWWKESGLGEEMKFARDQPLKWYLWSIAILTDPSLSELRVELVKPISLVYIIDDIFDVYGKVDELILFTGVIKWDDACAEQLPEYMKKCFKVLSDITNDFGNIIFEKHGWNPTRFLKQMWANLCNAFLVEFQWNASGTLPKADDYLKNGIITSGVPLVLTHLFFLMGQNIANQSMDSKKEELPNTIFLVAEILRLWDDLGSSKDENQNGYDGSYVECYLRENGSSYQSAREHVMELISKSWKLLNKECLSPCPFSAPFLEACVNAAKMVSLMYNYEDKHGLGLLQTI

>EgranTPS110

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>EgranTPS111

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>EgranTPS112

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>EgranTPS113

MIESALQYPYRKSFARLAPQSFVNDMSGVKSWMEDLLEVANRNRRIDQSVHQKEIHQINKWWKELGLGEKMKFARDQPLKWYMWSMAILTNPSLSELRVELIKPISLVYIIDDIFDVHGMVDELILFTEVIKRWDYACAEQLPEYMKKCFKVLNDIANDFGKIIFEKHGWNPTRFLKHMWANLCNAFLVEFQWNASGKLPKADDYLKNGIITSGVPLVLTHLFFLMGQNIANQSMDSKKEELPNIIFLIAEILRLWDDLGCAQDENQNGYDGSYVDCYLGENGSSYQSAREHVMKLISKLWKLLNKECLSPCPSSAPFLEACVNAAKMVSLMYNYEDKRGLGLLQDHMKSLTCDHETI

>Os01g23530

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>Os01g42610

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>Os02g02930

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>Os02g17780

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>Os02g36140

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>Os02g36210

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>Os02g36220

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>Os02g36264

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>Os03g22634

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>Os03g24640

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>Os03g24680

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>Os03g24690

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>Os03g31430

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>Os04g09900

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>Os04g10060

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>Os04g26960

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>Os04g27070

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>Os04g27190

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>Os04g27340

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>Os04g27400

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>Os04g27540

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>Os04g27720

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>Os04g27790

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>Os04g52210

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>Os04g52230

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>Os04g52240

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>Os07g11790

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>Os08g04500

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>Os08g07080

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>Os08g07100

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>Os11g28530

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>Os12g30824

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>Pt0001s31550

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>Pt0001s31570

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>Pt0001s31580

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>Pt0001s44080

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>Pt0002s05300

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>Pt0004s02970

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>Pt0004s02990

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>Pt0004s03810

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>Pt0005s09830

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>Pt0005s23190

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>Pt0007s02810

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>Pt0007s02920

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>Pt0007s07360

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>Pt0007s07410

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>Pt0008s08190

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>Pt0008s08220

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>Pt0011s03440

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>Pt0011s14600

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>Pt0015s05270

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>Pt0015s09710

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>Pt0017s06920

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>Pt0019s01270

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>Pt0019s01290

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>Pt0019s01320

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>Pt0019s01340

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>Pt0019s03350

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>Pt0019s03980

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>Pt0019s03990

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>Pt0019s06190

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>Pt0019s06220

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>Pt0092s00200

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>Pt0121s00250

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