>Bxy|Bu\_scaffold100\_cov122\_len1285729\_144.3\_1185

MLLIPLLLFIITANSEDLDDCPTPASNLRDKCIYYNADSVFAKNKCFIIDQLYSTNPNVSRCNHLHGFNGKMANNDAEVLKYLELRNYIKSGETLITRETKGESYTTEARVLCEYSDIFSCEDGYRLHGIHCYKVIRKETYWAEALRTCQQQGTTLAVPHNDKDSQFIASVVSKENILNDNDNSFFWVGMFVKEHKHLKFVDQTTPNYFRWLPIGHKRLLTKAYNTPNTVIAVGSSASNKGNVGQFGYYQVINGNFHRLPFLCQKLANGEYGPIYYPKRD\*

>Bxy|Bu\_scaffold100\_cov122\_len1285729\_217.5\_842

MKVLLCSAWFDALPITITWKLRCSQIPYRSAYISGYCFVYKDAGHYNCSTVKETASGLYAPKLVSLSSVEERIVSHLKKINIFSSVNEQDLCVLNMGFRCPSGYDLFEDFCYKAFKDKKTFAEARSVCQSDGGDLPEVHSDTVNARLAEYVYYNTKSPIWLGIHIIGSYWNYDRKRVNNNHNHEQPYYFRWMFQDYGNTHAVLDYGIYAGYWRSLKPTESHSFVCQIRAY\*

>Bxy|Bu\_scaffold11\_cov92\_len918884\_265\_11124

MRVVLRLTLFLHLAYSDLVRRCEDKDLCQHGGECFLTAARQSSAKCPDGRYSEVDESCLHYSPIKKTFNDAYNFCRTRYDGHLVWLESKEKRAFVEEWIGKSAWIGLQRDGQSKARWHPGGEATMMDVEDGTAEKSGTHCGVLYHNHGQPKILTEFCDESHGFVCESNISRFKGADDWIAQCSCPSGYGGRQCETKLAAEKTENSSDKELCGIRRFEESCQENEVLMIDYAIYGYSPLLKYDGLCPLTSNLDHDCIESAGLLKLAQRCQYRQKCVIEDLAKFFENPTCSNGARLKYRVRCVEKKELACPHGMKILGDRCIAISDNKEKKTYADARAECTQKGGDLAYFDPSIDFTSILKGITPLPSSEYWIHNSSEKTNHFGRRKSECLTASWWSPNVGQVPCFAMLGWICEFVPNGIADRVLVDKLNQRKHIEEDTKDRSGEKDKENPRFCKDFKFHGQKIPETKACYDFEAECPQGLSGKIILTCDCASADWTGLEDHSRCMSPSLSALKDLVRTDDPFITVGKYEHVIYNLMGNSKLTSGDIFGFLESGDSMMAMALQRLEKEANAERKKIYSKKFAKSIGNTGDYLMDKRAEKAWYNMTDDHRVARAARLMQMLQNVLVLQSHGMANGSEDFKFSHFASKLEVKPEVQYAPGTPSIRIAQDVPEPETVSFDGFQKAASMEMPSSDLLSFAVKWSHDSKQMSGGLIPRMRTLNPSSNPPQADNTLKVGHFMFSNLGNLMSSTTSKRRVNSYIMGAFVNDPAISVDLMNEHVSFTFYHLVKDGVKNPKCVFWNLTTSSWDDKGCEMSFTNDEYTKCTCSHLTSFAILMDFTNSLGELRGREDGFLPAKFVDETLDWLTIIGCALSIISLTFCVLIFTIFRSLYNSRTTIHRNLCLSLLMAEIFFLFGIEETEPAILCSGVAIALHYFFLCAFAWMLLEGYQLYLMLIKVFDARSRTLWYYCCGYLIPAIIVLLSVLVAAENYGTANYCWIDVTSPTIWTFVGPIGLIVLFNSGVLVLALRTVLAVRNRDRSLAAKVLGWLKGSAMLLFLLGITWVFGFLSAIHVLQPYVAYIFTILNSLQGTFIFFLHVVMNDKARQCVLRCLKEGVCCQSPVTSSSHSKNGIRPDSSSTFNKTNNFFALRKDKILQWWPLKSSASNSKNSNSNEENRRSSEVASPPPSLKTPKEVESPRESDSKEEEDETVTRRRLLSPVREATVTVERF\*

>Bxy|Bu\_scaffold825\_cov96\_len158809\_16.1\_18638

MWPPGAGTSILALICLFAACSTQEIDPAVAKFAEQQQLLLKQFKADKSLRPDAFHGTPPNNTVTRRKREIKEEHPEGPEHCPPGYTGHLCESPICWNQTRLDHHSGDFPGELIELDFFDQCIGGLVVHVDRHIKDLVVVVTTEQAGYPSGKLFNAHGRLLFPNFEEIHPHLRQMHYENVQDEGTGKFYFTADSDDNEDCVVAVRAHTDLVLDGGFVESPHDDRVQEFVGEYHELQRDPTEFVPGYLAFKPSRLEFPETVTTVTFYRSQHEQQYAPMLVGTRYNCNANVFAGPYVCLEYGIYFVKIRGTDRGGNVWQRVYQFACNANPGPGPGPGPTPEPTPAPDHCLNGGTFVNNETHSYCYCGHHYEGRICETKILLGIDETLEIGAANFYRNSPIIVFTDALPDDPPSTRFDILQRLNEQSNPIYIIAYGGLGFKCNPDIHTEAYEQFRVLAQFSGGLVVKATETVDEHLSWIIWRVAYTLSVGLYNEHLLAANDLLDSCQYAPNEQVFFVDDSIEELIVAFVGRADYDVNVVNTIEEEVDAFYIMKGGDLTNKVYRNLEFGNYRLVIKKGQNSSETELPCHYRVYAKSKYEVFTGASIDIDHDLTLDQPRYNEEMHIVARVNNIEFPDPENVFAEALIWHNSIFQHDKREVLYASNGVYRDGCDYNLYFGTWKCERPNQFFYVEVYVEDATGLTVKRTSVGHCTVRDPNPPDQGCRNGGVRSGDRCLCVPGYEGKNCENIVCYNEGRSHSTHCECYAPWSGPHCTEPKCGYKNQWVDFRPRGVGLSFVIQGSSDVQSTLVELNRLAPEIVRDFKFNDPYWISHYSIHSFDDKQVKLYLQTDHPDDLIHGFEALQQDTQNTESVCKDLLIYEAIIEALTSSRATAHEVVYLVVSGGIKLNEHKEKETFQLIDALGAKINIIQYPINKCRIEIDQEASTAISTLAHYSGGSLYQTNRGTAFITLPLQYDEATVFDEIRDNCDKEQTFYFPISGNAQTVSITSLGDLRRGYPKISAAENTYVDARKVYDSAMSRLNIVYKDCPDGWQPYEQNCYLLEVREIPWDDAKATCMMQGGHLLHIANKGLDDLMSLYIGGTPTWIGLNDQNSHDWGWDQGAHDDLPLGNAFKHWAAGEPKSGKHCAILTSGGWVSEACNATKPFICQKHAYDLGYNPGGKEHGHLARGIWSVKLRTYNNEFTTCGIRVNVQSATQVFRQFTKKLDDDFGNGALVWKSKNNRIIAHLESHVNGHSSEARLEYAHLYPSETANLGDVVAFHKRDQCSYDYISNPFTASNLGYYVGFTGFDAYGYPFQRVLPAVSEDSIPTCKNGGVLSRRTEECVCPPEFRGRECQIPNCKFGYAAPNGVSCKCFHDYEGPLCQYAICLRNDTDHPPPPMDVYGKSFIIVLDGSNTANNAKVAQNFNKIIAEILDRLGNTEHQMYHNYIGILAYDKAQGEVEPVSKLVVETDRSKFLNELQTLINDNYQSRGQKRDYLFALAKVISSKDVIPGSAVYVIGDSGVEDAKTWNDQLYNHIAEKHVTIHTIILNDQVPPGNASNYRDPSIQHLLGLPFVTDGFIYQVDPDRFKDLFYIQLGSRFRGYSLTHQMYRECSDKIEYFQTGGDYGLLVVDLFTAHMDLEFDVIDPNGNSTDKAEHLFLTGTNVLFTIETNIPGIWTIQIHHKNKPSACFVSVREVANTAPAIGFNTDIRGDNGLHSRSAQYYPQDGLNAIIANSDTDHLTYAQVYTHDAHTLAFASPLVRRHDCAWNYISSEPFKCPASTFTVAVVGYDRGGHPYRRTYKTHCVGYKGPRTPTLTAFSDEGTSLDFPIGLAQF\*

>Bxy|Bu\_scaffold2034\_cov104\_len350705\_270.3\_2162

MGSPISNILLFLCVSVYADYENKLIIDFNNPPPSRRNSRGPVRDDAGVLNEVKEIVFRMEHVFNERIKNLSDRVSRLENRQILHDGDPHIDWKPLGTNGKKIKVFSTEATWSDAKRTCTSHGGKLLEIQSDNENRKITDYLQNFETNLFWIDAQVSVSVRLPAGRYQNFQNNRTEKDCTALNVLGKWVRMDCTERHGFVCQF\*

>Bxy|Bu\_scaffold26\_cov103\_len1649090\_1086\_3303

MQHVFLLDSCPYLLLFVVTLSLTAFAQNGPQPCPENAIVLTGSDYPQFVYSPYDELRQYPPNTDCRFVLVARSMQHRIHLSVIESKLEEPLFTECEDYVSIRDGGLPTSDEVLRWCGSYFPPSLTSSGDSLYIHFHSDNIVQSRGFNLSFVDYLIPGCPADWIRSDDNMYCYKMFSSAHGYTFIDAQRNCFYERSNLLTIENAREYQFIVGKYSDSHKFPWIGYNDANKEGEFDAIDPNVPIWPEDLSSSLRGDHKDKDCLFLDWNSIKDGPAHTVDDCRTRHSYICKKRQDGTTVPIQLSATLLRHGFEDPVFNYTLILLILLLLLVLLIILWIIYQKCKKRNVVAASEGSRLVQSAPHPDTTARAATAAATINLAPVPEEKKKKERAKTAATDAVKNVLAISASRTTEARDLALQKTDDDQTFQLDDTLFEKSKPEDNAVAATNYQQVSAESPRIRTSPNQAAPPVQDSEFARAQRRDSNPVLSDESEAELGVGETPIPFSPVKGDKASPAVHSPPDRSHLYESGPVTVTTKDETKDAKDSGVTSKTLSSTLPPVGEPSGPSREATIQTGITAPSSHRSRGTQPSHGFDRPHVGTLENVSAISLDEFWQESK\*

>Bxy|Bu\_scaffold301\_cov119\_len910634\_867.3\_1991

MNALLCPFGWHYYQDKCYFLTISNSMTYDNAEHECNTRYGGNLATIQSEGEDQFVHFLKESSHKHPAFLNKDEIRINLCFQSIENTLKISTETIILNNIPSSSLCKQECVRLRFDLGFECNSVVWISNENECLLNIGNITKNVIVSEELQYYEDSCFDKPSEEPSDIPLAMPVSQVRNCFAKTRFATLQGVVGKVYDRISLNDCLGECWNCEDCFEENKCQTAIYYEEDAMCIITNVSAKITRERVVKEDMSSLYEKRVKCLENNCEDLEVHLVFGIDPAVYNETITKQIMIEIFSSVSRITEFVRVTAVLLSSSPSNLFDDLQYENENDFKFKLETLKVSADSSDFEAGLIEFLNGVDEHWTTTDDVDVTWVLVLTDTAFQSRLGLFLDLKEGFRRFPLFSIGVGENLDFEKLEMIASSVDNIVHIQDPVTIGKALAPRICHQKPLRRFVTSRKLKKTKTDHSFTWLGLHRNDYGKMEWSDKSVFGEYENEILKYLSVTQEDGDCILRKGTTNWAFANCTEKHNFMCTLEPRNKLEDIIKRRLNIKKLY\*

>Bxy|Bu\_scaffold30\_cov118\_len1940649\_1786\_6499

MKLDDGGAIIDVAFSSCFLICILTFICSFMLSEYRICNVSCDYYLSEQTPYSAGNRSELPVIRVFGIDKNGQKCCAHIHGTSPCIWMRTNCQLSSSQRLLLSQTLSQRLQNAGIQLRADPIIEISECKARSMYGYYDNKDYFIRISLRNPVHTRTLTKILQDEALHDFKLQPYMSHIPFILQFFIEYSIFGMGQIGFRKVLFRKAPNSSSGYNLSSLPPASNMSVEFDAHVEDILNPWEEVNCKYINSGLEYIWNDEEHRRKLLKIPMFRPGHPSINTFTIAKNERMNLAKLRDKVTDAATNVPDTQKIKLSDLPPFYDNLSFDPDAVRTDIEDAEADDESQHDESIHDELSEMSSTSLSDDETGYSEMIGPFKDVDDFVGWETEGINTQFFEVSNSYEKKVTLQKIKKAREKKAKDPGDIKQNDISQIRSFEYCGNLRDVTIYTRLIKRHNHNVSPVKGSVKIQSSSTVDNLCVMAVELIADPVSNSRVPDPASDPVMVLSCALCTDISNWTSKTPFSYIRSIVVRGGVSCGPTRDVDYVDSEMELFQKFAEIVQRFDPDILVGYDLHRESWTYLERRTSFTKHPLCKMISRVKDVSIFEKSGAGIDAGRIKLEVWKTARRDSPMRSYEFGYVVGQVLDLPFMELDFEMLKELSNSTNPDCKLLLVDICMKRAQYDIQILEKLDIFVKTSQMARVYGIQFIEVLTRGSQFRVESMLLRLARKRGMIPPSVGVKQRSLMGSPETIPLNLEPESGIYRDPVVVLDFQSLYPSVCIAYNYCFTTCLGKMSRLLNADLGDQIKLGALSYTSLTSDKLKELIDNDNIHISPTGGVFVKANVQKSMLAEMLMELLDTRVMVKDSMKNFKGDAILRRTLDAQQLALKLVANVTYGYTAANWSGRMPCEEVADAIVSKGREALEGVIHMVDGNAERYKHAEVIYGDTDSVFVLFRGCSRNEAFKLGRLIAEDVTKMNPNPMKLKFEKVMQPCILVTKKRYVGRSYEKEEDAGVFDAKGIETVRRDGSLFVSQMLEKCLNILFDFGQTAVIRYLQSKLANPESFPLSSFIINAEYRGEYAEKAQVPAKKLAMQRKEMCERFEPIRGERLPFVIIRPEPHSKTKMIDCVVGWEEFLKDSCLQLHYNYYMGKQLMSALTRFFDLTPYGLRYHSLYFDICQSCGKSTNDSEFCEDCSEDDNVDQIRLAKYFVLQRRLLRTYRSCKNCIKMDTVDIDVRNLKCFNFNCNINNTRLKLERNLENEDDIELNDDTATPSWEEKMRTLDEKWQIRLGQQVAYLRERIEKLETTMNSLNHVMESDWNHFGDQKFKFFDRNVDWNEAQVFCRLHNAQLINVDDSQKNKIISEFLTRADPAITEVWIDLKTQTQMETDSYKYDNFSEKGLIEGCTVVDIRGKWKIRPCSRQRPFICERK\*

>Bxy|Bu\_scaffold37\_cov107\_len2094627\_1113.4\_7847

MGQPNMALFWAIVLYSILVQAEKSQNVTEIPYILTGVSMNCPAGWDLVGDKCFRAFNSEKSWPQALIFCERYGALLAKVESAAENEFLGRIISRPTKSSALSKHWIGLITEKSTEDEGSFVWSDGSVVSRFVGFWAKQQPDFGNGNCVQAGVNSEKLAEWQMEMCNLMSPFVCQLNACVSGSFHCGNGKCVSEKAHCNGHNECGDYSDELNCPAPHGQVACLHYEKSENGKIESPNFPSSYGPNLDCRWVIEGPINSRIMVTFDQFETELNQDLVTVLDGGPSENSTLVLDHLSGSPQSSRLSLITSTNMLTVQFRSDALVQARGFKASWRAVPFSCGGSLKAHLFSQTFSSPRPYPAGGECVWKIEAPEDQVISLNIEEFDIKPGKDQLIIYDGPHPSSPILSRLAGNLSNQLVISTQNFLYIYFYSSQADSTNGFTIHYKKGCNNTIKYNHGNLLSPGNGIIPYPASQICRYVIDLGEGMSDRPISIDFNTFDVQNDDVLKMFDGDVNATVLHEGKGFTEGRNPPKKLHSTKGKVAIVFETNAMKQANGWNLTFSANCPPLKAPKTVFLTTQSTSFGTKVTVSCQTGYEFTNGIGHRFDISCDLGGKWSNDYIPNCQPVYCSAVPQIANGYAVAATNVSYGGIAKFKCYDGFHFKSGKDTEEIYCKTEGWTETPKCLAEICPALPTFLNGERTLKFGDATGYGTVYEFSCAPGYRHNGPNTILCQSDGKWSAQQPVCKKRICPNIPQIENGRIVVPPTGALEFGDSARVECNPGFRSTGADSVKCLANQTLSEVPECRDVDECVEAIASCVTKSTKCLNLEGGYTCQCLDGFKPQLTCPSFHVLSPSLVKTSSSAIFNMSSVTFCAEKSDDKRYLEFEFPAPKVLERIRFEKTEDGVPLAISVSYSPDLKSRLRSIEDLLEIPLKNVDMAGSQVVVLKTPVEAQRVRVRLDRFKDSACARIELMGCQKTNCVDIDECEVANGYCDHQCHNTVGGFKCSCRDGYDLFVENGQGGAMLKEGETGLDNLDMIRYNKTCVPRKCPKVEAPAHGKVINLGKEFAHPNVLEFRCDHGYQIRGSPFLQCTSDGVWNGTVPTCTPAVCEGVQNNTSIGMFVTEDKPYVPYGDNVTVVCTQQNRPIKQSPLGGLRQCIYDPRPDGMDYWLSGPEATCPLVECGPPPALAGAFYEGEDANFKVGSSLAFNCRPPYSLLGKSSYDDRIARCNVDGSWDLGDMRCEGPVCVDPGHPEAGQTFLNSVEEGAVAKFTCDRPGYKPYAYDAINCTLGTSCLLSEDVGISNGYIPDGAFSDSDTKTMWGYEPHKARMSSTGWCGSKDAFIFLSVDLQRIYTLNTLRIAGVAGSGYLRGHVTKLQLFYKVQFSQNYDTYPVEFETAPGNHNKMYQFHLEPPIKARYVLLGVTEYEENPCLKFDMHGCLAPLSTAHEIPSHLQVGWNASVPQCIDAEPPQFINCPANPIFAQTDEFGQILPIKYNVPDVHDNSGVVAYVKVEPKDVQPPFHIHAPLDVKYTAYDEAGNFAECTVQLRVPDTQPPAMKCPESYSVYTSGNETSKHVVFNESTVHVVMHDSSNITEFTISPSETEINLFSAVDVEAVATDSHNNRASCKFQVALLPEPCTEASLRTDDHTIKKCSTENNQTSCIIKCKSGYRFVNSSIEEVKYSCSPSLEWSPKSHPPACVRKSEEPARYEFQVSVDYSSSIPARDECMKPYADAVANAFETLDASLTQKCSSSVQVYVRFLGARFMVDPSNNKMVKANFTVQILPTVLQEVFYELCGLTLSTIFDLKIPGATLPIKTLLQLPNGGLNAPTCMPMNAVSTKIHQGFACSKGEILNKEGTDLPECIPCAKGSVFAGSSCVLCPPGSYQDKDGQQECKKCPEGTFTRTSGTTSRSGCLAVCGNGMFSESGLIPCQLCPRHTFAGPPLPGGYKTCDACPEGTYTANLGATGPSHCKQPCKPGFFSESGLEPCSPCPLNFYQTSLGQQRCIECANNTITHEVGRAIEEECKPLECTGVKCQNKGVCAIANHKTICECRPGFTGEFCEEQVPICDTNPCLNGATCENVAGTFRCICPQNFTGSRCQFGPDECIGVNCPNGGVCQDLPGVGTYKCVCRTGFIGHDCSEIADLCQSDNPCKNGADCVPLQLGRYKCKCLPGWEGPTCERNIGGLFLVPLRDVFEIWGRNVMLGVVKSKFFLQ\*

>Bxy|Bu\_scaffold40\_cov119\_len2195569\_814.4\_717

MNTSLVLCVLALVLGYCSANTSPCPDGWRYSPFTSKCYKLFEDKTSWTTAEYKCAFQGAHHISVHDAADNQFVSELARQANIVWLGAVQYGTDRDYTWADHTAYGAFENWENGRRPSYHKGKKCSKFDGLSGKWIQSCCKVPAAFICSKPAAVLPAAIIEDDTGINEDFRRTRLAFRRRV\*

>Bxy|Bu\_scaffold40\_cov119\_len2195569\_1517.1\_1341

MTSSWLSRLTLLIGCVVAQQAPCPPGWTYKSHTNQCYLLSSINLPYNEAVEYCKKDGGSLVSLKTQDEYDYVRELYNNNTKGFYPPWIGLKRDSRWYSPVWRWSDGFVAYFTKWLKEEPTKTADNACVAWRTIENHGWKTLGCKYAQRFICKQASANCPTRNYERPEGVLSSPNFPTNYPNNLNCFYHIKVKPGYRIKLEFHDFYTENYFDKVVLYDDYNGNLTNKIDTIYGTYLFKKIYESSENVLTLNFITDHIITRQGWNATYTSVHKEPTQELHDPTGTITSPNYPKNYPNDIDQLYLISTLPDKVLNITITDFNLEKNYDYLAIQDGKDIIKSKQLTRLTGTDVKTPLSFLTSQNYALVRFFTDPSLNYRGFSLNYEAVEKY\*

>Bxy|Bu\_scaffold62\_cov110\_len994864\_936.5\_4785

MLRSTALAVFVLGCFCLSNAITQESLEDEDSQQTRRGYKFHNPVPATPHSPWLSGPNEKKYSFHIGQQSWVAAREICLTNNADLATISSEEELEWILSHYKPQLRHSKDRQIQVGLYAEIEEDEPMREWKWVTGEAVNSSILSWASGEPFDHANGKERCGLLNINSKTLDDVDCELGGSPLRFYRFICERTFNQHLKHEELNNPMWKKLEDILVFFGISDRTKAKNSNSTDSNESLKATPLEDEDYDEKKDLKKVNATEIKKESKVERAPVKPDEKPLKDDKIVEDKDKKLQTHSQAFAAKTIETAPTRDDSDLLVITNLEPLRDAGKFDGVTESSIRTTRPDPLAHLADTLEQAVESDAPGDDDAKMKNLERIINAVQKMVGDDDKDKVGWETVRARIHSEKRPKFGPTIESENENSNSERSNSNSERSDDPTYKSDNGNSKSENPNSKTENSHFPSENRNSKSVDPSDSSEVHHISHHDSHRHPHFSFPDIFDEILGPMLPRPFRPRPFDRPEHRDTRKWQHPDKSHLQNREMSEINRQYGQKTVESTTLIPKTGEIEGSGQDIEIPIEVFTKAKAEVSTTRPNLSNIEPHWVVRKTFYAQPHQKRKIKVTEPHRNPDRETLPESFEFDRDEPEPQEQTTKTPAEKIQFVESKQKTEIEQNAVEATEPVNPTEQFQIALSLDEDFKQAQKEQQAHPGVNSGDLLIIPKSSEEIVGCGAKNLKKESTVSTTPSPAQIEERNLHINAFLNNLRDLLNRSDSTVLSNLFEANYTDSAENLADKLERASQLARTTQSVPPSPEELERLRKNIENDVLKSIEELGETEDREFKSMEVAEKDLEAIGSGLEPPAEKLISLTPVALTAHQQIIVEKKTESPEEANVSGYTPKTTVELAKEKKTKKFFVLSSAEAAENAAETEGFLAKNEEEKPVEIEASTKQTATSIIPESEEDSAEAIEGSGQAPVGTRRTEVKEQGKQHKKPRQSLFPDLDFSLLNNKKLAEEAAESSKKQKAQADEAYKALAKLDQNSLAARIAASEAQRKKAEQKTDEIKDPIQVKKIQVQPALMKNKKPEDVAKQLEKMFFDWSNGAFGVLNG\*

>Bma|Bm13532.1

MICIIKCFITILLFKGIIGRLCPEGWLYSKQTKYCYHLVTIPTTFNNAQFACLLQNAYLLSIHSEAENRFISAMFAKNGHSIWLGAAIFGNSRKYEYVDSTPFDYTNWQNGTQPIYKKSRKCVKISSENWKWFDDCCYYRPVSYVCKKLAGKYEQLYWKTIADKTSNIKKNHNHRHLKLFNYKFSNEKNNIVMKENERRNKVSNMVTSSANKIYDNKMRDKLRTRK\*

>Bma|Bm1543.1

MPRFAIRTVCNLLDSEIVKIRNKEEAHTAYGLAGGKSFWLGLRRGKRDWYWDTSTYGTRAHFFFWRTGQPDITDNKNCVYAAYAGEWMTADCDNFRSPKMFVCQSPSYKN\*

>Bma|Bm17253.1

EFHCLIQNGHQLSVHNSRENRFAKEIARDAPEVWLGSAKFGRTAQFEWSDKTPFNFKGWKNGQIPVSKLIRPCTKMNVTSGEWFQSCCRIVAPYICQKDSQPNKSYTSNIQKSYDTIRTNDKYSIVNQQWRFLVRK\*

>Bma|Bm17612.1

MFSVPAFYLLQFNSAKYLGFTNFMPRFAIRTVCNLLDSEIVKIRNKEEAHTAYGLAGGKSFWLGLRRGKRDWYWDTSTYGTRTHFFFWRTGQPDITDNKNCVYAAYAGEWMAADCDNFRSPKMVGSRVAQNPEHRTISDVLVYLEREPVMLRALQEYMREREQIEDLLLTCLEDTERRSEVEGQDGEEPVPQEQAFYEEEAEWAPLPETNDADEAENWPTEAEWAPLPESDEETEAPVAPNAVAEPVESVRELVLRTRTINIPVLATHTSVAAAPEEFHPADLGDLPEQLRRELLVPQAEPYTVVQANEERNIVCGICGRQFATLKGWRIHASRMHKQDGKFLRSLWPLPPAATRIHGRAKESGDRSSRSRLVPESVCGRDQRKAGQAPQT\*

>Bma|Bm18080.1

MKNSKMLYGKFFVKFYELYCLFTLLLLDENVESAYIGLQSVPYDVTQRYFCTGETIDYTNWLSGKPDNKNLKDNGCVILNAKNGKWIDYSCDANDELGPWATICQIKDTREEYDELKCPKGFEYCSNTKNCYKVIIPLLIFIGNNKGKGMNQTEAQNECKTYNAHLVSIDSEEENQFVSDLSMKHPLSAMRIFIGLELHQTDDISEQHWLDGTTIDYTKWDYMKPDKERVRPEHECVIMIPERHGVWSNWSCADSCCAKHAIYGAVCEIDHDDKII\*

>Bma|Bm2733.1

MAVHAQACPAEPIILQAKSNAQQVYFHTIGYETGRYANNMRCSWILMGSSSRKRIMLTVHDSDIDDALFSECDDYCSIHDGDTSKSPEVVRWCGDKHPNAVISTTDSLYVYFHSDEAFQGKGINMSFIEFDIPGCPPSWIFSSVGYCYTLKRPVHGLTWLEAQKECNLVRSNLLTLTSAIEYSFVAAIYKKSKTLPWIGYMEDSSEGKFMPVDPNSGPWLEDLPKLTGSSPGQNCAYIDWRNRNGYILAMDDCRNRHEYICKRHQDGNTIPYLPQEEMMRSSVAKSPIRFTVWLFIILLILLMLILLYLCYRKCRKQHALSRIGSSDVNQRLVAGIDVQRAATSTTVSHIESSEVQRIDGANSDARVTTVTENAFNAVLDGGSSRQTIEQNTPNQNSHSAQQLNLQRIEPTVLTIEPCFNARQTSEERLSVPSRSKQNLPFGLRENTMGSTTREEALLKIRRGELFERPRVSVLDHTSAISLDEFWNKNEMSTINRN\*

>Bma|Bm2925.1

MFYQLSSIWLHILLSTIWFHILELIQRCNGCLATSAVTKPKSHPSTYNPRTPTTTIAPNIQCFPVARQKRNSLSSTSSASNNLLVNNLPANCLPIDYLKTAMAEMKAGLVQQSDSFNFEHKLEESSLFPSTISKHPAIAIEHHTINDNSDNHQLLSSQHQTEKLCRDFEWDGPIYLYNQSLKIKVPYCYKYVASIDDDTDELTMLTQKSAREKCRSYSDINGGSSDLVSIHSNDENYDLQSTLAFFGWQSAWIGLAYDDVHTTWHWTDGTTLSFSKLSLRNPSQHCAILLTNGSWISEDCKSNTVSHFVCKKQAFA\*

>Bma|Bm3563.1

MNNYSIALFTICFTVALCAICDEGWRFSPHSKKCYKFFPKKITWTEAEFHCLIQNGHQLSVHNSRENRFAKEIARDAPEVWLGSAKFGRTAQFEWSDKTPFNFKGWKNGQIPVSKLIRPCTKMNVTSGEWFQSCCRIVAPYICQKDSQPNKSYTSNIQKSYDTIRTNDKYSIVNQQWRFLVRK\*

>Bma|Bm3770.1

MSRWWFVRLIVAIVILLAQIVGSHSTVKARQIFISPVQNYGTSWIADPEGHHYQFHLSEQSWNIAREICLALASDLVVIKSLQQINWLISHYPLRNSIMPERTIQIGLVLVDKENSAEKEWKWVDNTPLNATYLEWEILVRNTTEKALDPTERGRCALLSIDNRMLKAIPCDQRPDFDYTNRFICQRNDEQHREHERKNNPFYEFFAQWISELRKDTLVKSQPRTVQLQGVRTQIANVQGKVEDLSPISGKKENVVGEDKEDSFSGSQKIIAEKTLTTADPDVEGTDVDFATKQMEKEKQKVAKNETSTGNKHELQSKNFTAKRKSIVRKENIKNNEDVPLHNGKENGLISSLNPLKQKSQQSSELCDENETAQKDSRTWYEQFGDIFRNLNLFLKQEKSSDLRALLDNNDTNKTLVERLKETLHAKSSKEPSKHDVIENKRVLQKMNDQQQFDDSIHEVHDISNTLAHESDINSVVPYKKNTGIVLQKVDGRPVIDHTYGTAKLNRTEIYRKEELAKRSEVNEGEIYELLGKKLQSIFTERIQNVSNLDNNATIMSNEISKDIKSNISEEQINRNEIQIYYDVANEQKPGSPSLLPADQHNNITEETASVPRNFINNIQQIIKRPPESSNETETPLEFLNGNIILLEERKVDRTKTNIKLDIEKAISNMKQNLENASEEIRRLFSKSRSWL\*

>Bma|Bm3839.1

MLYELIYLFFASTIQAATSPCSDEFSATKCLNEMDDVICQETFPINEAFPVVNAHCTNFKSHKVEKCRKQCRSCCQHPDFMCTDKKDSALNCRTIAEKGHCTTTDVTFKAILAVECAGSCGLCRHAGCMDNNYLLCSMLQKLCDLSDYYELMVKKCKRTCNSCAIDMQYPGWVYNKETKAHYKFIDAISQSENISAVKYERMCVEEDAHLVSIHSETENAFVYGLAGCERVFIGLRGQTSDQFGWLDGSRVDFKNFFPGFPLGTQYCAYMTGDSMFWYTDSCFTKGCAVCKKVN\*

>Bma|Bm5701.1

MEKMNSLILMLLFAGSTAWTRLKFVNSGSERLQQNVMDRTACNHHNCLKNRKFLLTMMQSPLRIINIAVDPPVNILIRNSDECKYNEDCKDENFCWNGYCMPRGNPGDSCLSDDQCSSGLMCSNQTGSNDGICISDLTEKNIKNVSDKSGMNWIPKDQVIKTNAKMGKKLETIFTHKDEGDIKNRTSSELTSNFMDGTMIVGKNNMTEYLLPPITGINTFGGMMGEFSSLSITTDNTLNTTKAPSSPETEITTEGTLSTFPSFSAAEITTEDSLSMSLPSPETEITTEGTLSTFPSFSAAEITTEDSLSMSLPSPETEITTEGTLSTFPSFSAAEITTEDSLSMSLSSPETEIITEGTLSTFPSFSAAEITTEDSLSMSLSSPETEIITEGTLSTFSSIEITAQNSLSRVTEIITDNALATKSSSSPMSEDSIEDAVMGPSFFSPENSGEGKTTVKFAFTATIGKSNISEAEKDIPTVPSNQSDVTNMNTVDSHRGILFEVENNSKSYSEIADMISSYSSHPSNDSTTTGLNTTDISSYLLPQPQYWCDDGWKLFRGRCYIQMNDGNYTYHEAKKKCMNMGALLVAIVNEDVTGFLYSNFYFKHPFWIGLFNDGKGWKWSDGTKLKYQLWGKNEPNTIYSCVFAETEKNGRNWYTANCDDTILHDSVIGCVCQQ\*

>Bma|Bm6131.1

MIIFQQYHLFVTPQKQRLRLSLSLILLLLLQQNVVTATIFTDNNTTTITDTAVSISSIISATIISTTTTTITTTTATITITTQQENGLKNVTDAKYTVSDIGLECAQGWEKCRSKCFRVYTIERSWPQALLFCSRYGSQLARIESFGENSFLHRLVNRQQKNLPINRNEFWIGVVAQQTEDENAFFLWSDGTVISRYVGFWNDGQPDYRTGTCAKVSITTTNELRWSLEMCNTLLPFICVLPACIKGSFFCQNGKCVPHSAHCDGINDCGDYSDEFNCPASPKVITCLKYEKGESGKIQSPNFPSPYNANANCRWVVEGPINSRIYITFDAFETEEYEDFVTILDGGPAENSSVVMAILSGSKKPETLISSTNVMVVRFSSDTQIQARGFEANWRATSISCGGILKAQPYGQIFTSPDYPKNYPSGVECVWKIDADPGQLISLDIEELDLERANDFLQIYDGGTPLAPILARLTGTFSNPQLIISTQSQLYIYFYSNFARNGRGFSITYKRGCSNRIRLDKGIITSPGYTRISYPNSQRCIYTVELPDRNSEQPTAFAINSFDVAEDDRLMMFEEVEGGRALHPGDGFSAISRPPKSIFAQTGIVQIVFTTNSIRNGLGWNITFSTNCPPLQTPKLVSLSTKASAFGTKVTASCPRGYEFRTGRGQMFDITCQLGGKWTEDHIPDCQPVYCSTVPQIANGFASSATNVSYGGSAKYTCYDGFDFSTGKDSGEIYCTDEGRWTLTPSCKAMTCPALAPFLNGERILEFGDGTGYGTVFRFECTAGFRRIGAATLLCLSTGEWSFAQPYCKKLTCTNVPLITNGVVVTGERFEFGDLARVECQPGFRTVGADSLKCLANQTLSDVPECQDIDECAEGSAICSIQSTKCINMPGGYHCQCLSGFQAQLSCNTASVLNSLSAEGSSEMDGFRAEDYATTGWCANPNDSNRKITFVFAVPKVIERIRIEKTTNGAYPIVISLKYSNRTGVPLIPFVAANITKLITRNVAIVGGELLVLPQAIEVRVLELTIEEFFNNACMKLDILGCHKTNCFDVNECEQNNGNCEQICINSQGSYRCACEIGFDLLTEDGQGGVHIKDGETGLNALDVIRYNQTCVPRLCANLSSPKNGLLLSTAKTFHYPMIIQFQCDFAYQMMGASHLKCMQDGSWNGTAPLCLPATCQGVRNNSAIGLFVAPENSTIAYGRNVSIVCSQQNRPASSSLLSSFRQCIYDPQEDGRDYWLSGPEIDCPLVDCGPPPSLAGAIYEGDDYSYKVGSAFTFSCRPPYSLIGKSSYDDRTIRCNVDGNWDLGDLRCEGPVCVDPGFPDDGQIQLESVEEGAQAKFTCNRAGYKPFPSDTINCTLGTACVLAEDVGISSGFIPDGAFADNSDSTTWGYEPHKARLSSTGWCGSKDAFIFLSVDLQRIYTLTTLRMAGVAGSGHLRGHITKMQLFYKVQYSQNYDTYPIEFETPSGNHNAMHQFELNPPLRARYILLGVTEYEQNPCIRFDMQGCLAPLSIAHEIPSHLQVGWNASVPQCVDSESPTFHNCPTNPIYILTDDNGQLLPATYEIPTAADNSGSVAYIRVTPDGFEPPKMITNDMDIIYVAFDDAGNAAECTVQLRIPDTQPPVMKCPDSYIVPANDGEFEKLIRFNESTVHMVIQDTSNITDVTFEPSEALLTLSSHVTVEVIATDSASNRNKCKFQVSLQPKPCSSWSLIGEENVEKECQIKGATTICSAKCARKFTFVNGKNGTRQFTCTNGIWSPSNVIPACVPIALEPARYELTVSIDYATLTPVGNDCLKGYSEYVGTFFNNLDATLSQRCSSSIEVFVRFLDVKFINTVNGVTANYTIQILPTVLQNVFYELCGLTLRTIFDLRIPGVTVPVQNLLYVNGETIATQSVGCPSMNATKTVVVQGFGCADGEVLREGNAETLPECLQCPKGTVHINNTCELCPAGSYQDEVAQITCKPCPEQTFTQFPGSQTFNACLPICGNGMYSETGLIPCQLCPRHTFAGPPIFGGYKQCEQCPQGSYTAKLGSTGPSQCKLPCPAGHFSLTGLEPCSPCPINWYQPVLGQQRCIECHNDTITRDVGTIEGTDCMPVDCSAVKCENKGTCMVDNHKALCFCRPGFTGKYCEEQMPLCNTQPCFNEGICETAAGTFRCICAQNYTGSRCQFGPDECIGMSCPNGGVCHDLPGLGTTKCICRTGFTGPDCSQIVDPCFMDNPCKHGADCVPLQLGRFKCKCLPGWTGPTCSININDCAENPCAMNATCTDLVNDFRCECPPGFTGKRCHEKINLCAQNPCINGLCVDMLHTQRCICEPGWTGEICDIKIDQCASHPCLNGATCKDQIDGFICQCAPGFHGFLCQHMTDHCASSPCRNHATCINQGAQYLCECSLGFEGAHCEHNRNECDLLHKCSQEGTELCEDLINGYKCNCRHGYTGELCEIHIDQCASEPCLNNGTCVDTGSQFRCDCPRGWKGNRCEEEDGLCALNPCHNDAHCVNLVADYFCVCPEGVSGKDCEIAPNRCLGEPCHNGGVCGDFGSHLECTCPKDFIGVGCQYELDACQEGVCQNDAICELLEGGNYRCICEPGFTGQNCETNINDCSPSPCPLAAICIDQVDGFFCQCPFNMTGLNCDKVIDEDYDFHFYDPILSAAAALSVPFKFTSSAFTISLWVKFDVPLTRGTVLTLYSSRESNYPSKISELLRISADNIHLNLLHDETPLNLHFPPTQRLNDGNWNNLVITWQSIGGSYSLIWNAVRIYADIGYGTGKILDINAWISLGEPINEFSSEPKFVGSITRVNIWKRAIDFEAEIPSIVHQCQQQQVIYDDLTLRFAGYTRLSGKVEKVVRSTCGRDYTQQPAKKIDIFGCPSDIFVVSYQKEVNITWQEPVFTSVHGYVEVKRNLKPGQVFTWGEYLVVYLAKDNYSIAECIFKIYVSREFCPTLQDPFHGVQACESWGPQLRYKACSVECENGYEFSIEPPVFYTCSSDGQWRPRPINAYTFRYPQCTKAHQAIRVAEVSINYPTVSICNAAGRNTLAEKLSQRIELLNSKWNIYSTSNISDHSVFNISVQCFAGNEETTVTAIDMTVRLRREAQNFFNVKISIPITNDILENSKTGQRAKVSDVLENEILLEDIFGLEQVIPNGRPDLNSFELKERHLCEIGTVSVRNLCVPCAPGSFYDLTTHTCKLCMTDEYQPRAAQTSCLPCPRGYITTAPGSALLTDCKNACDAGSMFNISSGICEPCGFGFYQPAPGAFSCIPCGVGKTTLKETSIAEDECRDECPDGEHLTQVGVCLPCPQGTYRTRGVHKSCVDCPPGTTTEGIASVRRMQCNTPKCSAGQFLVTTTKQCQFCPRGTFQDEEIQTVCKLCPPDHTTASQGATQASQCYSTNQCATGEDNCSWHAVCIDLPDDNDIPSYQCKCKPGYKGNGTHCQDACNNFCLNDGTCKKNPIGYVECICKENFSGDRCEVRFQARTQKVALITAGIGGVVTILVIIVIIIWMISYRFNRVEESSEPEKCPVEENTHTNFLYGRIPSEQPRPIGYYYEDDDEYDMKTMFVGEEEKEMAERVRHAQAHMYTPSNNRLD\*

>Bma|Bm6657.2

MSPEIILVNYYFLLLIFNLVPLRYVSTKIITANVNSRYHNVEQLSNKHETECPRGWTRYERTKSCFHVIERRMRWSEAERACANFGGHLASITDEYENMFAFNLAKDANLSTPTLWLGRLVKLTRTGAYEWNDGAIGRHTDGFRGELPSGTDLCLTMWLDFDRPEGSWNEWDCNYVSGYSALCKRSLKRTPITTTATSNTRSGSHSGLSYYSRRCCLISSLCHNTSQSCTPEERCIPDDLDCWAKICPNGGIGWCLPLPKI\*

>Bma|Bm8663.1

MLILFLLSTFDIIDKINGKKENIAEAKIQIERNKLSCHNGWVPYASTGSVKYTHCLKILTVFRMTWQQAEESCRQVGKDAHLVSIQTMEQISWLTEAIDREMQIKGKSLYTLFPKNSPWFDSGWWIGLGQLCPKSQSDQMPSFRWTDGKLFANDKLIIGDVKLTVPKSNKWDNHYCVFYDFQKSPTGLATHRTFNITTCSDRRRFICQMPAFSQDQLSSGGSAIVTEEEVEITESANSELTADFPCGVDPLFCPLKTSQGTVCYRLQTEPFYWEQAMKECDAKHQSDLTSIHSKEEANFIYEMVQLQPSISGETKYWIGLHRRNAQSQYEWSDGSSFDYLLERLRNDDPDEERGICVAIQFNVSTKLLQKQPLYNLFGVPIQVTKNTPAYFWTHQRCDNRHLAICRKPGFDYHSRFELSAKEERRLKKQSNWKCSNGYKLFRGMCYKLYGTNNNGVTFSEAIQRCKNEKANLVSLTDMYENGFVTSMLQNLNSNAWIGMDMTDGRVRWLDGEPLKLIRFGPDNRVIRIGGDRHIFQNVGEPGFSNEACVALDATNMVGYWNIIFNKTNYVFPSGSTKADNKSNQCDTMELPYICETYADESANVIQNKKTCNEIDDITYCFLLNDPNKHINGHFNFVDASEICATLPTKYTNYGRKYGQLAQADNIFEWLFLTAMALENDYDEFFMGIRFRKSVGFERTDNLRLRLAPWDIGEPNLKNGNCVVLKIGRNGPAWYIDDCMKRKPIVCRLTNEEPMSMVPQTVRCPDGKEDWILGETHCYHLVSNTSMFSSGFKADHDCFKYFNATLASFETQKDFELFKSHILHNELSVSNALIGLIRQQHGSYAWKDLSPVTFLNWAEDEPADTKGRIIQQCVKMQLNGNYTWHSLSCWQSTHFLCSTPVVNVNYNPSARENDKNEGFSSQQLSYDKERNSRKKLPNDYDSYSSKTDQSLLPVPSTQSISAISTFGEICLVLIVALSIVGGIQLWKRKRRLRLSSQRIVQFDQLQNEEENTM\*

>Bma|Bm8932.1

MNGICVQSFEHLATTNDLETLIVPPFKLKPIKFDAKEKINNQPTNTTEFQTLKMAKSDEQSESEELEETETEELSETVAEATDVTASQIPNEEITEVMNVTEFETIIETGTVSDYHTSNMETDSWTLEKCDSSADCKKSQICQDGLCHNSHSYTKLCDSLWWQFRQKCYLPIHGRFTHSEGSDYCAKFGAHLVTIRDTQQANYVNYIYDIGGSGTYWIGLIKDINGTLKWQSDESMIYTNWSEGEPEPRIGCVIINTVIHNGKWSITDCSDLQYPDQGFVCEMDIRNN\*

>Bmu|BmChr1\_8922.9\_8095.mRNA1

MVGKVVVLLGMILRVGCASKVKYDENFIKEVSSRSDNEIEYGFDNMVPAKPYDQRLELNVSKILDSLIASHDRRIRPNYGGAPTEVNVTAHIITISAISEVTMDYTIDLYLRQFWRDTRLAFTSVRDDDTTKLTVGIDMVKSIWTPDTFFPNEKKSFFHDTTSHNSFLRIDNRGNVMRSIRLTVTANCPMNLHTFPLDEQLCALEIESYGYSTADIIYHWHHHKAVIIDENVHLAHFTIEDHFHVERTISLSTGNYSRLTTYFKFKRNIGFYLIQVYLPSSLIVVISWVSFWLNREATQARVAIGVTTVLTQTTLMTSTNASLPKVSYVKSLDIFLGVCFFIVFASLLEYAAVGYLMKRQRSSACRRANSQLVYYYEFEDQSQVRLGSAREKRRGASFRRTHSPQVHNGGVVEQGLPLMGLSPTHSHPSRCYAPCCPLMQHVFLLDSCPYFLLFVVILSFTAFAQNGPQPCPENAIVLTGSDYPQFVYSPYDEWRQYPPNTDCRFVLIARSMQHRIHLSVIESKLEEPLFTECEDYVSIRDGGLPTSDEVLRWCGSYFPPSLTSSGDSLYIHFHSDNIVQSRGFNLSFVDYLIPGCPADWIRSDDSMYCYKMFSSAHGYTFLDAQRNCFYERSNLLTIENAREYQFIVGKYSDSHKFPWIGYNDANKEGEFDAIDPNVPIWPEDLSSSLRGDHKDKDCVFLDWNSIKEGPAHTVDDCRNRHAFICKKRQDGTTVPIQLSATLLRHGFEDPVFNYTLILLILLVLLVLLIILWIIYQKCKKRNVVAASEGSRLVQSAPHPDTAARAATAAATITLAPVPEEKRKKERAKTAATDAVKNVLAISASRTTEARDLALQKTDDDQTFQLDDSLFVKSKPDVNSVTPTEYQPISAESPRIRTSPNQRAPQAIDSEFARAQRRDSNPVLSDESEAELGLGETPVPFSPVKGDNASPAMHSPPDRSHLYESGPVTVTTKDETKDAKDSGVASKTLSSTLPPVGEPSGPSREATIQTGITGPSSHRSRGTQPSHGFDRPHVGTLENVSAISLDEFWQESK\*

>Bmu|BmChr2\_4399.2\_6301.mRNA1

MGKIERSSTLIQRCHGGGGEEQGSMDGRRAFARLSNYLSRRSFSTAKGDGKRKTMARYQRPIDGQQERWNDRINSTRWNKMEEGWINEMLRETALVGFVLGCICLSNAITQESLEDEDSQQTKRGYRFHNPVPATPHSPWLSGPNEKKYSFHLGQQSWVAAREICLTNNADLATISSEEELEWILSHYKPQLRHSKDRQIQIGLYAEIEENEPMREWKWVTGEAVNSSVLSWASGEPFDHANGKERCGLLNINSKTLDDVDCELGGSPLRFYRFICERTFNQHLKHEELNNPMWKKLEDILVFFGISDRTKAKNSNSTDSNESLKATPLEDEDYDEKKDLKKVNTTEIKEESKVERATVRLDEKSLKDEKIVEDKDKKLQKAHSHAFAAKIVETAPTRDDSDLLVITNLEPLRDAGKFDVVTESNVRTTRPDPLAHLADTLEQAVESDAPGDDDAKMKNLERIINAVQKMVGDDDKDKVGWETVRARVHSEKRPKFGPTIESENVNSNLERPTSKAEKSDNPNSKSGNLNSKTENSHFPSENRNAKSIDASDSSEIPHIPHHDSHRHPHFSFPDIFDEILSPMLPRPFRPRPFDKPEHRDTRKWQNPDKSYLQNREMNEINRQYGQKTVESTTLISKIGEIEGSGQDIAIPIEVFTKAKAEVSTAKPNLSNIEPHWVVRKTFYAQPHQKRKIKVAEPHRNPDRKTLPESFEFDQDEPEPQEQTTKTPVEKIQYVESKQKTEIEQNAVEATERLNPTEQFQIALSLDEDFKQAQKEQQAHLGVNSGDLLIIPKSSEEVVGCGAKNLKKESTISTTPSPAQIEERNLKINAFLNNLRDLLNGSDSTVLSNLFEANYTDLAENLADKLERASQLARTTQSVPPSPEELERLRKNIEKDVLKSIEELGETEDREFKSMEVTEKDLEPIGSGLEPPTEKLISLTPVALTAHQQIVVEKKTESPEEANVSGYTPKTTMELAKERKTKKFFVLSSAEAAENAAETEGFLAKSEEERPVKIETSTKLTLTSIIPESEEDSAEVIEGSGETPLVAKINEQKEQAKKQKKPRQSLFPDLDFSLLNNKKLAKEAAESSQKQKAQADEAYEALAKLDQNSLAARIAASEAQRKKTEQKADEVKDTIKVKKIQVQPALMKNKKPEDVAKQLEKMFYDWSNGAFGVFNG\*

>Bmu|BmChr2\_4653.1\_7908.mRNA1

MGHPNMALFWAIVFYSILVQAEKSQNVTEIPYILTGVSMNCPAGWDLVGDKCFRAFNSEKSWPQALIFCERYGALLAKVESAAENEFFGRIISRPTKSSALSKHWIGLITEKSTEDEGSFVWSDGSVVSRFVGFWAKQQPDFGNGNCVQAGVNLEKSVEWQMEMCNLMSPFVCQLNACVSGLFHCGNGKCVPEKAHCNGHNECGDFSDELNCPVPHGQVACLHYEKSENGKIESPNFPSSYGPNLDCRWVIEGPINSRVMITFDQFETELNQDLVTVLDGGPSENSTVVLDHLSGSPQSSRLSLITSTNMLTVQFRSDALVQARGFKASWRAVPFACGGSLKAHLFSQTFSSPRPYPAGGECVWKIEAPEDQVISLNIEEFDIKPGKDQLIIFDGPHPSSPILSRLAGNLSNQLVVSTQNFLYIYFYSSQADSTNGFTIHYKKGCNNTIKYSHGDILSPGNGIIPYPASQKCRYVIDLGEGMSDRPISIDFNTFDVQNDDLLKMFDGDVNTTALHEGKGFTEGRNPPKKLHSTKGKVSIVFETNAMKQANGWNLTFSANCPPLKAPKTVFLTTQSTSFGTKVTVSCQTGYEFTNGIGHRFDISCDLGGKWSNDYIPNCQPVYCSAVPQIANGYAFTASNVSYGGIAKFKCYDGFHFNSGKDTEEIYCKTEGWTETPKCIAEICPALPTFLNGERTLKFGDATGYGTVYEFSCAPGYRHNGPNTILCKSDGKWSAQQPVCKKRICPNIPQIENGKIVLPPTGGLEFGDSARVECNPGFRSTGADSVKCLANQTLSEVPECRDVDECSEAIASCVTKSTKCLNLEGGYTCQCLDGFKPQLTCPSFHVLSASLVKTSSSAIFNMSSVTFCAERFDDQRYLEFEFPAPKVLERIRFEKTEDGVPLAISVSYSPDLKSRLRSIQDLLEIPLKNVDMAGSQVVVLKMPVEAQRVRVRLDRFKDSACARIELMGCQKTNCVDIDECEVANGYCDHQCHNTVGGFKCLCRDGYHLFAENGQGDVMLKEGETGFDNLDMIRYNKTCVPRKCPKVEAPANGKVINLNKEFAHPNVLEFRCDHGYQIRGSPFLQCTSDGVWNGTVPTCTPAVCEGVQNNTSIGMFVTEDKPYVPYGDNITVVCTQQNRPIKQSPLGGLRQCIYDPRPDGMDYWLSGPEATCPLVECGPPPALAGAFYEGEDANFKVGSSLAFNCRPPYSLLGKSSYDDRIARCNVDGSWDLGDMRCEGPVCVDPGHPEAGQTHLNSVEEGAVAKFTCDRPGYKPYAYDAINCTLGTSCLLSEDVGISNGYIPDGAFSDSDTKTMWGYEPHKARMSSTGWCGSKDAFIFLSVDLQRIYTLNTLRIAGVAGSGYLRGHVTKLQLFYKVQFSQNYDTYPVEFEAAPGNHNKMYQFHLEPPIKARYVLLGVTEYEENPCLKFDMHGCLAPLSTAHEIPSHLQVGWNASVPQCIDAEPPQFINCPANPIFAQTDEFGQILPVKYNVPDVQDNSGVVAYVKVEPKDLQPPFHIHAPLDVKYTAYDEAGNFAECTVQLRVPDTQPPAMKCPESYSVYTSGNETSKHVVFNDSSVHVVMHDLSNITEFSISPSETEINLFSAVDVEAVATDSHNNRASCKFQVALLPEPCTEASLRTDDHAIKKCSAVNNQTICIIKCKTGYRFVNSSIDEVKYSCTPSLEWSPKSHPPACVHKSEEPARYEFQVSVDYSSSIPARDECMKPYADAVANAFETLDASLTQKCSSSVQVYVRFLGARFMVDPSNNKMVKANFTVQILPTVLQEVFYELCGLTLSTIFDLKIPGATLPIKTLLQLPNGGLNAPTCMPMNAVSTKIHQGFACSKGEILNKDGIDLPECIPCAKGSVFAGSSCVLCPPGSYQDKDGQQECKKCPEGTFTRTPGTISRSECLTVCGNGMFSESGLIPCQLCPRHTFAGPPLPGGYKTCDACPEGTYTANLGATGPSHCKQPCKPGFFSESGLEPCSPCPINFYQTSLGQQRCIECDNNTITHEVGRATEEECKPLECTGVKCQNKGVCAIANHKTICECRPGFTGEFCEEQVPICDTNPCLNGATCENVAGTFRCICPQNFTGSRCQFGPDECIGVNCPNGGVCQDLPGVGTYKCVCRTGFIGHDCSEIADFCQSDNPCKNGADCVPLQLGRYKCKCLPGWEGLTCERNIGGLFLLLLRDIAHNIRKFEGGMSYQP\*

>Bmu|BmChr3\_5799.8\_4634.mRNA2

MFSQPPGPPQFPQQPGFPPIQPQYPVPTSQSQPPNGYFPQNAGPPQNFGPPSMYGPPGFPSGASGGPGIAPGSPGMPPTGVMPPGMGPPSGMPGIPGPTGMPLGLPGMGPPSGMPGPAGMPPGPPGMGPPSGMPGIHGPTGVPPGMGSPSGMPGIPGPVGMPPGPPGMQRPQQRLDPNAMPSIVQVVQDDRALYSDTAFQTGFTEAALPPLVTTEFTAYDTGNANPKFIRSSVYTMPVSNDMIKSYQLPITLSLTPFAELNPNELQPPIVDLGELGPIRCQRCKAYISSFMEFIDGGRRFRCPFCHATTPVEDAYFAHLDHTGKRTDVQQRPELMYGSYEFVATKAYCSNSLLPLEPAFVFLLDVSYNSVRSGLLETFCSNIVDILKHLPKDTNAEKPTIKIALATYDQQIHFYDLSSSNQTNMCVVSDIEDVFVPFVEGFFVDYETAAENLERCLRDIRQTFSDTRVTETILGPAIKVGLESLKAARRSGKLLVFHTNLPTVEAPGKLKNREDRKLLGTDKEKQVLSPGTEYYGRLGEECVKNGVGIDLFFFPNAHIDLASIAPVATITGGSIYKYQYFDAHRDGKRFLSDLKRDVSRLIAFDVMMRVRTSTGIRPTGFFGSFFMQNVTAIEMGTLDADKSLQVEIKYDDKLNENERAYVQVATLFTSPNGQRRLRVQNLTLKVVSDHAELFRNVDYTAVVTHMFKLCEKIVREQSPKDMRDELINASAKILAGYREKCSDGAPIGQLILPEALKLLPLFACCISKSDALVAGGEITVDDRTWMMNLVRSMRPDDVIRYLYPSVYPLTQVNVESIRESLPVSVRASFQYFQQEEAYLVDNGMIAFIWIGPQVNKDWLQNVFGVHAVENLDSEKSEVPLRENPDSQALHALLERLNRQRPRVLKVVLVKAGDGLESWMKKFLVEDRYAITWKLRCSQIPYRSAYISGYCFVYKDTGHYNCSTVKETASGLYAPKLVSLSSVEERIVNHLKKINIFSSVNEQDLCVLNMGFRCPSGYDLFEDFCYKAFKEKKTFAKARSVCQSDGGDLPEVHSDTVNARLGEYVYYNTKSPIWLGIRIIGSYWNYDRKRVNNDHNHEQPYYFRWMFQDYGNTHAVLDHGIYAGYWRSLKPTESHSFVCQVRAY\*

>Bmu|BmChr3\_5879.8\_10386.mRNA1

MTSNLRTKCIYYNADSVFAKNKCFIIDQLYSRNPNASQCNHLHGFNGKMAKNDAEVLKYLKLRNYIKSGETLTTSETKGESYTTEARVLCEYSDIFSCENGYRLHGIHCYKVIRKERYWAEALRTCQQQDSTLAVPHNDRDTQFIASVVSKENILNDNDNSFFWVGMFVKDHKHLKFVDQTTPDYFRWLPIGHKRFMTKAYNTPNTVIAVGSSASNKGNVGQFGYYQSVMGHWYSPVQALGISICFAVLDVVICILGLAWDGKFFTFDNIVHWFDFQSYNFTRNPIDFLAVCVIRICLLLGGAIGVYANPTSGAQACSKYSNLTFAAVLLMIAFSPSKLLAFYEHPNPLAVGDWILMIWSMTACLFVQGIWVSVLGKVRDDAYRRLDDRNFYESDNEYYAELQRREAKEQEEKRETFTMLLRLFSYMAKEWMFYMVAFTFLLLYSFSRVFAPYYTGEVVGAVFGEGASYAQLHKKVLIMAGLCISSAIFGGLRGGFFTYSQARVDRRIRNDLFRSLVRQEIGFYDANKTGEIVSRLNADCQTMSNTLSLYVNVLTRNTTMLFGSLIFMFTLSWRLCMVTLIAVPIIFLVSKVYGVYYDRLAEESQASIAKANDVAEEVLSAVRTVKSFACENFESLRFLGFLNVTLGIGARRAIAHIGFLWTTEFLQMGILTVVLFYGGHLVIQGEISSGLLVSFLLYQFQLGENLRELGEVWNGLMQAVGASRKVFELIDREPKVINDGRIAPDGRNAQIEGRIEFRHVNFSYPTRPDLPIMNDLSFTVNPGEVVALVGPSGGGKSSCIAMLEHFYEPDSGEVLLDGVPIRDYDHKFLHNKIALVGQEPVLYARSVHENITYGYEPAYNNTEMVQKSAKMANAHNFIMETTEGYETDVGEKGSQMSGGQKQRIAIARALVRDPVVLLLDEATSALDSESEHSVQEAIQKNLNGRTVIMIAHRLSTVENADKIVVIAGGKVVQQGVHKDLIQQDGLYKQLVQRQMLNGNIQEAPPKPVPAPARSRQIRQSRESTSQAQSFLGTSLAKTEMSVEIDNVDGVDAHYAYFRSVYGQLSDSTVGMRLRNIYEYTKNSNQIVQKSLDGVETRLYDVSDNFLAPLYERYCYPTTERLAKASVTGYDKSQNLIHSAKDLAQAGTALGLGVAVVSAQVGLIISASMTNLLLDGVILTKDVGVGIVAKTKAYEKQIEAKIFSTVENCKSIAGVPVNKAAEYTNSLLDVMNAFLDNFLHLPVEEIENPESSIPQRIRHLTSRVSQAIVSRTVQPAQQQIAVLLENLRAKLTLMDTLKKQGGNVKSQMLSTSLSDLYGRIEKEANEFKVHPSEALLKSIQNCAKRLNASLNDIAQKSSKTLPSAASDRLQSAISYIENLDRTFEDAESIHAIRDEVIVEAKQKLSDLLQIVRLSPRNPDDKIDLNEELSD\*

>Bmu|BmChr4\_284.4\_1821.mRNA1

MMIPQLSNILLLLCVCVYADYENKLIIDLNNPPPSRRNSRGPVRDDAGVLNEVKEIVYRMEHVFNERIKNLSDRVSRIENRQILHDGNPHIDWKPLGTSGKKIKVFSSEATWSDARRTCSSNGGKLLEIQSDNENRKITDYLQNFETNLFWIDAQVSVSVRIPTGRYQNFQNNRTEKDCTALNVLGKWIRMDCAERHGFVCQF\*

>Bmu|BmChr4\_1934\_14178.mRNA1

MWPPGAGTSILALICLFAAYSTQEIDPAVAQFAEHQQLLLKQFKADKNSRPDAFHGTPPNNTVTRTKREITDEHPKAQNIALQAIRDISAKAVSLEYCDKKAICWNQTQLDHHSGEFPGELLELDFFDQCIGGLVVHVDRHVQDLVVVITTERSGYPSGKLFNAHGRRLFPNFEVIHPHIRELHFENVQDEGTGRFFFVAESNDNEDCVVAVRATTDLVLDGGFVESPHDDRVQEFVGEYHELQRDPTELVPGYLAFKPSRLEFPETVTTVTFYRSQHEQQYAPLLVGTRYNCNANVFAGPYVCLEYGIYFVKIRGTDRGGNVWQRVYQFACNAKPGPGPGPGPTPEPTPQPDHCLNGGTFVNNETHRYCYCGHHFEGPICENKLCDHGGDIGSDGKCVCYGSWDGEFCEHLTCKERSGRTFDTTDETALNFVIRSHEDGRIRSQVLESISLIINTFEAFSENVVKAYTATFILDGRTKLYFESDDPTVFLEEISEIEDHWLPSDKCTDKIFLGIDEALEIGAASYYRNSPIIVFTDALPDDPASTRFDILQRLNKQNNPIYIISYGGLGFKCNPDIHTEAYEGFRILAQFSGGLAVKATETEDEHLSWAIGRVAYTVAVGLYQEHLLAANDLLDSCQYAPNEQLFFVDDSAEELTVAFVGREDYEVNVVNTIEEEVPAFYVMKGGDLTSKVYKNLEFGNYRLVIKKGRNSTETELPCHYRVYAKSKYEVFTGASIDIDHDVTLDQPRFNEEMHIVARVNNIEFPDPENVFAEALIWHNSVIEHDKREVLYASNGVYRDGCDYNLYFGTWKCERANQFFYIEVYVEDATGLTVKRTTVGHCTVRDPNPPDQGCRNGGVRSGDRCLCVPGYEGEKCENIVCYNGGRSHVTHCECYAPWSGPHCSEPKCGYQNRWASFKPQGVGLSFVIQGSSDVQSTLVELNRLAPEIVRDVKFNDPYWISHYSIHSFDDKEVKLYLRTDHPDDLIHGFEALQQDTQNTESVCKDLLIYEAIIEALTSSRATEHEVVYLVVSGGIKLNEKREKETFELIDALGAKINIIQYPINKCRIEMDQEASTAIIQLAHYSGGSLYQTNRGTAFITLPLQYDEATVFDEVRDNCEKEQTFYFPISGNAQTVSITSLGDLRKEYPKIAGAQKQFVDDRKIYDSAMSRLNIVYKDCPDGWVPYEQNCYLLEVREATWDDAKATCMVQGGHLLHIPNKGLDDLMSLYTGSRATWMGLNDQNSHQWGWDQGTHDDLPLGNAYKNWATGEPKSGKHCATLQVSGWATANCNETYPIICQKHAYDLGYNPGGREHGHLSRGIWSVKLRTYNDGFTTCGIRVNVQSATQVFRKFTKKLDDDFGNGALVWKSKNNRIIAHLESHVNGHSSEARLEYAHLYPSETANLGDVVAFHKRDQCSYDYISNTFTASNLGYYVGFTGFDAYGYPFQRILPAVSEDSIPTCKNGGVLSKRTEECVCPPAFRGRECQIPNCKYGYPAPNGVSCRCFPDYEGPLCQYAVCLRNDTDHPPPPMDVYGKSFIVVLDGSNTANNAKVAQDFTKIINEILDRLGNTEHQMYHNYIGILAYDDAQDQPSSPLVVETARPKFLSELQSLINKNYQSKGQKRDYLYALAKLIRHKDVIPGSAVYVIGDSGVEDVKTWDAELYNRIAEKHVTIHTIILNDQVPPGNASNYRDPSIQHLIGLPFVTDGFIYQVNPDHFKDLFYIQLGSRFRGYSLTHQMYRECSDKIEYFQTGGDYGLLVVDLFTAHMDLDFDVIDPNGNSTDKAEHLFITGTNVLFTIETNIPGIWTIQIHHKEKPSACFVSVREVANSAPAIGFNTDIQGDNGIHSRSAQYYPQDGLNAIIANSDSDPLTYAQVYTHDAHTLVFASPLVRRHDCAWNYISSEPFKCPASTFTVAVEGFDQGGHPYRRTYKTHCVGYKGPRAPISTAFSDEETSIDLPIGLAQF\*

>Bmu|BmChr5\_6207.1\_774.mRNA1

MLSTPKQMKLEGDLKVSTLDDEKNSFFCGISLNRKNFEDDIEISYYTTTPSWEENMRTLDEKWQIRLGQQVAYLRERIEKLETTMNSLNHIMESDWNHFGDQKFKFFDRNVDWNEAQVICRLHNAQLINVDDSEKNKIISEFLTRSEQAITEVWIGLKTQTQMETDSYKYDNFSEKGLIEGCTVVNIRGKWKIRPCSRPRPFICERK\*

>Bmu|BmChr6\_6706.5\_1338.mRNA1

MAFSLLTRLAVLIGCTVAQQAPCPTGWTYKSHTNQCYLLSSINLPYNEAVEYCKKDGGSLVSLKNQDEYDYVKELYNNNTRGFYPPWIGLKRDSRWYSPVWRWPDGFVAYFTKWLKEEPSKTEDNACVAWRTIENHGWKTLGCKYAQRFICKQASANCPTRNYERPEGVLSSPNFPTNYPNNLNCFYHIKVKPGYRIRLVFHNFYTENYFDKVVLYDDYNGNLTNQIDTVYGTYLFKKIYESSENVLTLNFITDHIITRQGWNATYTSVHKEPTQELNDPTGTITSPNYPKNYPNDIDQLFLISTLPDKVLNITITDFNLERNYDYLAIQDGKDIIKSRQLTRLTGAEVTTPLSFLTSQNYALIRFFTDPSLNYRGFSLNYEAVEKY\*

>Bmu|BmChr6\_7424.4\_718.mRNA1

MNSSIVLCVLVLFLGYCSATTSPCPEGWRFSPFTSKCYKLFNDQTSWTTAEYKCAFQGAHHISVHDAADNQFVSELARQANIVWLGAVQYGTDRDYTWADHTAYGAFENWENGRRPSYHKGKKCSKFDGLSGKWIQSCCKVPAAFICSKPAAVLPSAIIEDDTGINEDFRRTRLAFRRRV\*

>Cbn|CBN00312.1

MWTVLIIAIVTMAYGLTETTLYFLSTGACGSQEPRKPPMKYGDCDSDWVTVNRTKTGQKYCHKFFSDRLTYEEAEKKCQEYEAHLSGFTDQNELDILDKMLDKAKSEGVRFDNGDNVWIGARRRTACSTREGIGAEEGGFNPDPTHPCSRLQAFEWVNGVAQNPPDFEDRWIAEVEPLFYDNAENCVELLKGVKNWELWPKDVVGDKKLNDVHCGRDLYYLCGKEAPIVKTDK\*

>Cbn|CBN00344.1

MRTRPWPYWFSILYVFCSSEVVAQDSNTCSGTVVLNATKQIQYLTTPNYGTSYKYPPFLDCKFLIKAPDKARISIEIIDMEMEPRIFDDCSDYVGFSEENVEKNISTLTTLCEDSHKRQFLSASNAITVIFHTDQLVENRGARLSYRYYDITSCPPDWTELSNHTCVRIETNQKLDWIGAQKRCLEQQSNLITFSNIEKANELQEKYESINMKLWIGNNDALVEGKLVDFTNKEAPRLSKVGHAVLIDNNEDNDCMVLQFQEADEFRMDQCQNYNGYICEMEKNGSSVLYPPPVKEIQEGTNMRAGQYTLWLLLFLIGILFLTVLAFLCFMCWKHKEGARIHTESTTIQQNAFMSDSSQRVEHSRSSAGASNNIPVSNDVNRTSRSSPVTVPIENNTRAPPKKFPMAPVPNRLPMNEEISGSEPAVETAILGGDEDIETVSAAPKPQPRTLPPMPAREGTFHSINTREGSTMRTRRNKELFERPVMNVLDNVSAISLDEFWSNKKS\*

>Cbn|CBN00378.1

MKNQILFFLFSLFLLGCLADSDLTCPAGFKLVNQSKCLKIFPTSLKHLEAETTCRGFGGTLVTVKNAIDNRNIVNMAANSGASYTWLGIFCFGNDTSSCYHDDGTGALTYNSFQSGYPKSGLGGCVYMPTIGKTAGQWVNGQCEVSSHAFICEVPTTFIDPLCTHNFDGYCYLPSHEFSSDTLQNTTFEEAMVICEEQGGAKLVSIHSQKENDFIKSIYKYINFPQIFIGAKVYIGFSWVDDTRWDYDYTNPVASSDGKCLKMDTSGKIENGGMWSPVDCKEANFFLCKRPMFGVSEKEINPKFKRQLTVPASTDFPDFSHCNTTLYLAPGIITSFGYPEKSVPTYCTWNLAVLGPYRLGLFFNDFSTASELNITDEYGKVLSNPMGNLSPFQVLAPTNIVSMSYNSKMDAPDGYHGFSVTILPF\*

>Cbn|CBN00416.1

MKQEMETTLPKDTCPFSLQSIDLTYSPDPSFYSYTWTPTETGWSFPGCRDGWHLSIRSSDLSVCIKVFLLDSNQNEAKDFCKKQDSVLIRVQTVEESHWMKKTVQSLVSSNQFFWIDGIRNCTGREEYCNNFDYSDGLTTGNAALTSDGNALLSFTSNGYIENCLIIMSNWESNATINDVQCVTEYSGMFCGYQLA\*

>Cbn|CBN00560.1

MIFFSIVCYFLAAFGVVNADCAPGDIKNTQENCVHVENLASTWQEAENFCVAHNGHLASVHNAFDMTALRKVGSMCVNFWLGGQCQKGSNCNWVDGTTFDYTNFRNGNPGTDNCVVADTKSGTWTTQPCTATSCIACEIKGKMQDCQDWMKAGFTDSGKYTILVNGKETEVWCDMQTYGGGWVLFQNRLDETESYWDRNWNEYKNGFGDTDENVNFWLGNEALYQLTNGKHVTLRVELYGDRTPNSKNATDFWFEHYFEFKVGSESENYPLLNVEMDWAHPVGNASTAWYDLTCSIGSPFSTVDNIHDPVKECVTKFQMGGWWLKNCALSTLNGAYIPKDWNNGYGMFWIWDGSETILHPRKTRMLLRNTV\*

>Cbn|CBN00683.1

MSNNQNSNQSLFQRHWFSANPDQIDQADNSKPSDLLSKHWFSATSDQLRLANPVESSQNGEEFAEVRYRDPSVSRRARIVRVQNDNVPPPPLYENTPIEVLETPEPPSGVPTPRALSAVESSAPRRPPQRPQPETSFLEVSINFFLDHWKIILSLGGSLILFLVAFFLVLFFVIIPPTAKTTVVSNTTTTAPNTTTVTVTTRLPATLPTTVITTRPTTVVTTTRITTTEQTFTMKPTTLAAGTTCTNNFVLVNTKCLKLITGLSNRVLADNQCRNLAGGAALVSIKSSDENEMLYGFLRYQTEKRIWIGLQCDRNKCAWDYGRGNIALYNNFAEGSPSVDVGKCVYYLVSDQKWVSGDCEQDFMGYVCELPPTVPDDCTYNYNNNCYAKIGNVISVGEAEQICSNACSHVVSIHSELENQFLKSIVNETVLLGGVAPANNLILWEDESHGGFLNFHETGYDPNHVCIFMKHTTGHWKTESDLLIDFENVPEISEKSVPTIVAVSSDSEPKTEFEPVERQRHFGILQYVIRTRLQRVMLIGLVNIILIAALFVFIVTLVTGQHNSPDTDVTTLETTATTITTKTKTSCAYEFQGNCYLKIGYSTSVPEAEQICISACAHVISILSEQENQFLMSIVQETTLLGGAAPSKHWIFWEDRSFGNFSNFQETGYNPNHVCILMDSQSGNWRTDSVCTGLTWCKRGVEEICNRF\*

>Cbn|CBN00859.1

MSNTSILLFFLFLVTVSANVCDDLREKEGETNGCGKGWKRFQRPSGGWCIKVFFEELVTQAEAEKRCQAEKATLTGFQNQTEVFHVTTTATTHLKPATGSLWVGLKRNQKCLKLKITKNCTTMNSFDWTDKLTTGTHGFIWNGGEPLNYGWNQDCVVLTVGNTGYVETLFQVGTFDDVGCEMTYKNSARAIKGFVCGKKSEK\*

>Cbn|CBN01197.1

MTHLKLLVGFSILLTVSAADFGDSSCDSSEEHGGGGHGGRPPRPPGPRPPRPPGPPGPAPPSGPDNSNRPRCEQGWYTSYRPQGIWCFRVGIGKMDYNGAISECATYGGVLSGIQNEWERWRMAEEALRQTAAYNVQYAGIWLGAQRVNGAFQWTDGHTTGTGGMVFGPGQPDNNNMGGRGPENCLQMIALAPGYWNNPGTWAAWTNGMIDDQWCNQVDDPPTRMYVCGKR\*GPQG

>Cbn|CBN01228.1

MDYFRQIILFTLLAVGLAADNTFDPLILARSNEEPHQRPTFYNWDGRDLGTTAFENLPHQTSQSTPLPINQSEHCPDGWLKFFDSCYFFETEALGFAKAEKNCQDKQATLFVANSLDEWETVRAHTKKSQFSWIGLVRFSQYERYEKLPRWQTTGSINPSKINWLINPYQPLGNGWSTVANCVALFEFPSTIESSSYAFFYPCTQHFNSICERNSTILNARN\*

>Cbn|CBN01396.1

MQRRTTIWFLLLFQPLLVFTQNRTEPYDCKIGSLNPLAATSLNACFKLYDSPKSYQAARRHCVSLGGQLADKINKDDSSLYSANADLEVTNGTKFWVGASNLKCNIAWENGGEIEYNEMWAPDSRYYGVAIEKMSLGGLWHTIPVGQKLPFVCTFQGKSKDAPAPVHAMRAPAKKRTAKVEKAKEDDIDESLNAALADEKKKQEANSNNKQDSKKDEEDINESLNAALSDEKKKSEAMALSASDKKESSSKDEDSNTEEASMSAQQALNASAAMSASMAASSSSSNSSSDESLDETYDSAEMAMRKEIGKTVVAMKSQEMASQSEDYDKYTDEDLVSAAASLIGGYTVNANWADSRTRNSSSFDSDTDEESMSMSMTVADQMAMGMQSSNKRESSSESSDSMSESSSDQMSEQASMAMNAAMQASEKSSKKSESSSKDESEDSASMSMEQKAEANAKMAAASASASKSESNQNSQDETVEEADVASAASIFGKEKQKSGDPKPTTKVPTTTEEPDIDESLNAALANQRSTTTNSIDLSTVLTTVNPINPLIVAAKPSEKLPGCPAEWTQFSTNATAPSLCFKRFEKPMNFEDARLFCVSKGGHLASIHNERQLLLLSALLHNNGPDALSDQTWIGLNRIHQKYYVYEDETPMDFTRWLPGAPNINDCTVFTGNELPNYPHKGTQYKFGDFPCEETQKSVLCEVTLGKDKTKTQPTCEDGWSYYSHDGTAKSGKCYKRIDQSKTFTEAREVCKQENSYVASVQNEGEARFVSALVQTEKNYTVDEQTWIGYVKYDRDFGWEDGNQGLHFDPWTEKMPREKKCTVFTGNEIHEDCRSQYRFVSVECNKKQRSILCSKPPMVNGVPTVFKVTDNSSKKLSTQGTTWPEAQNACSKIRNNSASYLHSEFSREKRDFVRRQASDIEYYIGLHKVGGVWRWDQPNGSFCPGLSGFESWDENYPTTYSDSIAVVNIVKNGESKWQNTRRYEEFYYFCETIAFDTDTKL\*

>Cbn|CBN01470.1

MTSTTIPTSKTVSTAVYQSTHGSTRLVSTKLSTSTTSTPALNFTTPSPTTTISTVICTEGFTLINNKCWMLVNTKDYRGNANKVCFSNKGSTLVTIKSYDENEALAIFVKVKNISKIWLGLKCEGQGGSTCKWDYGQGPLGAYSNFGSGSPNVTVGDCIYYAVSTKQWISHSCSDKNVNIVCELPTNKDDEKNRQTDGQILYL\*

>Cbn|CBN01630.1

MRFSIIVASALTALLLVHAAPTPSNNDFESSGEAPVTLPQNSEEEPHRRLRFYNWDFKDLGTTAFEDIPYPARQPPSAVNQTEKCADGWLRFADSCYYIESALMGFAKAERNCFQKQSTLFVANSIEEWDAISSHAKEAYFSWIGLVRFTHYEKTEQLPRWQTEGAINPAKINWLIKPFKPVSNGWTQFANCAASYKSPAKLESASYTFFYPCTYLLYSICERNSTIVNVMQ\*

>Cbn|CBN02556.1

MPFLNLSSRIRRNNHSQQNEPLLLSRRFEEFLQSQNPKRQFIVLILFLAVVAYLLTKGVFELYGFLENREKNGVLIRDPLLEYGLCGADWVTVNRTKTGHKYCHRFFSEKLAHDDAEKKCQEHGAHLSGFSDQSELDILDKMLDDAKRNGTRFDNLDAVWIGARRRKRCWTRKGIGERKGFNPNDKHPCSRRLVFEWENRAAQNPPDFEGRWITEMEPSFSGEAEMCVELL\*KGVKYRDN

>Cbn|CBN02609.1

MRLLLLLLVFGMTATLGHFIEGKSSISFGNPSFHSSSSSESSSNEGRSSHRHRHSGRHGRRPPRPIQNDHSHSHEYDGGEDGGENRGCGRGWKRFDRPTGGWCIKVAQGQFSQAQAESKCQVEGGTLSGLQDTNEISYITSTAIRLFPERTGSLWVGARRSPACSRAPLSSSCNRMTSFTWTDGSTTGTAGFQWAANQPDNSHFKTQHCAVLLASSPSSDPTWNWLTNKLDDEACVNPTGSYQRIVRGYVCGKRANERRRK\*

>Cbn|CBN02629.1

MRTWVLVAALAVICLAAERELSHGERAKAVLKSWNPRNEIKYFEPIREQKYRTTDEADLNLETHHISKRSVGQPHFLAGMATRGCNLPGYTGDTCQYPLCSARNPYIPNNQNTDDVSIDATNLANCSTPYVIVVDETMWDIKIQLETDSPLNPTFYLQAENGDLVYPDSDSQRPTSYVAQYQFLAPGQYQLGPRADTGSEFCTMLMSSRTQIQVTGGFASGAQAERNDYPTLKYVYFDTESVVAVHAQGLDFPGQIQAIGFTGAENHISRYIPIGTRYNCTYPYILERYTCNKNTNNDRGENFLQVEGMSNSGYRFRRILSYTCILPPVPTSTVPVPITTPAPLTTCKNGGQLLKDTDGSSYCYCFGLFAGNDCSQMICANGGFLPEPTSERCQCPEGFTGFHCQNIVCSDTSGFDFNAENPTLTLVLRSRTELSAVIEQATTSVQGMVDLLSSEPGYLTNFIVVLFDNGKLLINKRYDSWDLAMVDLTKAINSAPSNGGCSDVVFSSVAAALSLYPTNKSPIYVITDASPNDSTEKDAIFQLESYWRAPIYFIYVTPLPNENCNSSPDNTGYRDMVDVAARSGGNTFYFSNRTIVSNFFYQHMLNTLFRSQLILSGDYSQCSSQNVYKSAAIDLTADMVIVVATGSDLSLIVTNPAGGTPDFDVVYTDGTNYIWSYNKQVSGQWFFNLKSSQPNSACTFKVYQKKYNFGGMSQYNPDYDVFWSFATTLSSAAGVLRQPVAGFDAAPVFHISNYPAFISMDRVHANLQIYAIRDGVQTEVYGSSGMWRDACEFNFYFPPFTCRVPDEVLYFNFFARDNNDMTLQRAGTMYCANVHPNPPPDHQCQNGGVMNPSNTTCFCTPEFTGTYCQNVVCYNGGTPNGASCLCPPGYAGESCEMAKCLETGPDPEYIRYGVDMVFAVEITSQSLASLVMLDTNFQEILRDVLMQDRMWIRNFVLVGFNSTWGGTIASSPANNLTAITAALHNLATSVPADTGCRVKLWEALNDAIFGRQIVPGSFIEIFQTTPEDEMDQRSLGLFYDMSRAMNINIYGFLSARPQALPNGFACNANLTDYYILFGIVTGSTGTTYILQAPEISNAVRLIPLQFSNGQVNINAMTDCRHDSGMITYFPVDAYTQTIQLTVFGYGTQIQVYNGNGVLADALELFYDDFTGQSVYEVRKTCDDGWESFGQYCVKFLATTDELMAFPQARNFCATAGGYLVDDLGDDKNNFLSSIAAKTQFWIGLAKGNDGQFYWDRGQGITPDLLNQPNTYWAPNEPSNDPTRQCVYFDGRGADTHKAWTTDSCSTPRAFMCQKHRYDADHKPNVIGNADLPAGHWYATVKTNPTNGNSPSCSLSVRVQSSLQIVTGFTASIGDDNPQIDPIQDSSNNRLIAYIHSADNENRVPILTDAMLWDFYNGTFYNGMKYQPRYGCQYGWVSQNFPCPNSDNQNNEFGVLHVGEDEFGNTFQRLTFGHCSPAQITCGNGGIRQGGQCVCTDYWTGSRCTVPFCVNGGTRNDDQASCSCPSGYTGPNCQYEVCQPNIPQLFSDDRKTLLLVVETTRQNSATVNQLIANLKAIVTSATSSTPLWFTNFGLVTFDTTGRTFEKFNYTTIDALITDLTAQSNAISTDGACSMPYLGVLAHLLEHDDVIAMPNSEIFLITPAGPSDLNKYGETMDTLFNTQAHLHYILSKTANCPTFDGVNNVKDMTWLGYGSSGNILFTDSDNLVSLLNVYLPSLYGASVLQDPTGAANYTCSDGSLPWFVPVDANTTFIYVSTSAEFGSLSVKDPLGLAHNIAPAYSVGDQKIYKIEVDRIGGIWTLQLVNPPGLCLAHVYSTGGAKVYTKFSLPMPVGSNTDLTGAHQDGRYVQPVAGFENVAVFHLSGNAFHAGQLQYVEIFDIDNNGGATNILRSELYRREQCSYEYYSDLFTCNGDMIIAFIHGVDENNQKFRRQEVVICNGRNPTTGQPVTGTMSPVTQGTVTQGPATQATNTQGPVTQQPPATTQTPPQTMPTATSPQNGLAFDIVFLIDGSQSAQNSFDQFTKFIQTMMVSFDVGMAGARVGLVVVAPDLDDQAPPAAQLNSITSQTILNSNLALLKDNYADFDHAGQVLTYNLQVVTSAEYMDPTAGYRPDISNHVLVYITTTTSFYTDPTPSAQSIIAKKQYGIITVGYGAGFDNGKLQTISGGAACSFTATDFTTLNNQIKPIQQLISNAATNGGVYCKNN\*

>Cbn|CBN02677.1

MGSIQFFKTTKLAFEGSFPGFCGEENLVRFLLVFYFFGLFCLRLLEDKIMAYFDSNINSVKKVGPSNSDYYGAMTRCTALGAALTGLQSNEERFWIDQEVNRQTMSSTIRDAGTWLGAQKIAGTNQFQWTDGHTTGLVTMGWGPKQPDNSNMRGRGSQDCVHIISLNTGYTRGWTLLGFVTGQLDDINCGYNDDPPQNFYACGKKPS\*

>Cbn|CBN03026.1

MLLRFSIFSLLLLHLVSSIFIKEPYGSDSESRERSYSGRRRHKHKYYDGGYYDDDDNRPPRPPPRPTCEDGWTFFQRPSGGWCMKVYPGTLNQYNSETMCGSQGAVLSGLQNIAEVNWLVSSALTVIAPQTSGGVWIGTRRRPECIGSGQTATCTKTNTFYWTDNSTTGIEGMIFQQGEPNNGNSPNGQQDCALMTVATTPTINAVSTYWSGQMDDIMCIASGTINWPSGTLPRANRAYVCGKKAGR\*

>Cbn|CBN03092.1

MSTSKDELPAFQENTEPLLTSAAQRKRRNDFMLGFFVSSIIFLILIGVGAAAFVLYGLNNKIDQLINCTATFPVETMTTTVPTTVETTTENSINREMEEMEKSMEQAFKMMGMIIKGLQGLSVEENTTKSTVSTTSSENSSSELRVPELKYGDCDSEWVTVNRTETGKKYCHRFFPHKLTYEEAEKKCQVHGAHLSGFTGQSELDVLDKMLDKAKSEGVQFDNGDSVWIGARRRAACSTRQGIGEKEHGFNSDPTHPCSRRQVFEWVNGVAQNPPEFQKLWLTDFEPNFAGDVENCVVLLKGVKNIGYWPRDILGDKKLNDVPCYLKYYYFCGKEAPIVKTDE\*

>Cbn|CBN03103.1

MIRLPIFLFFAGLIGLTVGAECPLGWTFNPVSSECYLISTRLFTFDESVQYCNSIGGKSVSIGSYSEKDAIVAFTNSTLLQPWIGSRRNTTTTKFYNLNGSYFYTLMWTTNEPSVNGDCVTFKGATPSGLQVTQCYQLQPAFCKQTPALCNSAVIGGSTTWSGTFQSPGYPTQYYNNLDCRYLIIAPNNTYITIEFYPYVVEEWYDYVDLYEGNSTSFADHIAEVSSTGWARGYESEGNVMNVRFKTNYAITDKGWLATWKAKKDMPVISQSGTNGTMVSPNYPNNYDSNDEQKYQISVGFGAQVNLTIDDFRTESRFDYLNIYNSSTQSNSTLVATLSGASVAPFNYISPKSYMSMKFVSDGSLQYKGWHAYWSIC\*

>Cbn|CBN03222.1

MKLFLLFTFLTTAYADIACPSGFTLVLDKCLKVIPNPLTHTKAEVDCTYLGGTLAAVYSAINKTWLGLFCFSEQNSSSCYHDDNSGTASVYNNFAPGYPLINGIYGGCVYMSTEGSLAGKWVSMNCKAETLPFVCEVPSTIYDPTCTHNYDGYCYYPSTELKTTQAKFSNAQSICQQEFNGNLASIHSKRENDYFVSLFRKIRYADNILLGAQELLPDTFSWNDGSNYADFDNRNPLDTGSKGCLVLVSSTGLWERVDCSFERVFLCKRPLSETTTPTPIAELVTSNPSDFSNCNTTFLMAPGVITSYGYLSLSADTTYCTWRIVTLGAYRIRLSFVDFNSPNPVYVYDEYGKRTDRISSGTCVISPTNIMNVTFQNSGIAGYRGFRAVAQPY\*

>Cbn|CBN03938.1

MKLLIFFTAIGGLYAQTCNTGGIYSAQFNRCYQYFTAPAQFEFAEEQCALLGGHLVSIQNGAENALIQSNGANSFKKSNYSDYWIGANDLETSGQWKWTDPSVTWNYQNWALGEPQSGSDCAIQDKGDGTWSAIGCTSYRPFVCVTPVIITATCPPITTPKPAICPTYAPCPVKNCVPSCDQGWTYFAPTDFCYRVYHGAKFDDAEAACVLLGGHLASIHSLTENTFVNNLASCGIKEGKYQNLAWIGMHQVGKDWVWTDGTTTDYINWAPKQPDNPGKELCVQTAPDVSHDSWYENWNNLACNTIMRAYICKKQSVHS\*

>Cbn|CBN04142.1

MMPRVLFYIFLLTTFAYSKAPCGSSWLHIAHLDSCFLSAPQPAEFSEAEEYCNNLGSSLVVINSEEEGSIVREFFARENPSFFNWIGMRWNERKSEFRWIDDKKRNYTYFLPDEPNASGECIAWVLDQNVDGWQSISCHYSQFFMCQKAAEGIITTWHRNDEGIITSPNFPNQYDNLEYDTHIIKSEQGTRILMYFEHVETELNCDIITVSDDYGISGRTLFRLSGSYHNYSVISNRNYVMINFKSDEDGTGKGFFMRYKIIRPLPTKVFSSNSYGTVTSNNYPNSPDSFLIQYYLVQCPLETHVTLTVKAINLDRNDRVKVYDGGDETSKKLRIFRQFSSKSTVPIRTSQNNMFISYDTGEQFNGSNHWAFEYNCEPDGNLGDEIII\*

>Cbn|CBN04543.1

MRSILLIVSLACFIAVESASTPVCTNGFTLISNKCLKLFPSAVTHKVAERSCMDWGATLVTVKNANDNHAITAIAASSSLVWMGLFCLDNDPARCLWDDATGSAEMYSTFASGFPHIDVGKCVYYSVKGALAGQWLSGDCEKDTKAYICELPVTVADNCPNNYNGHCYTFHPPSSFVQAQTTCEKECGNLASINSANENRYINTLSNRQASGNLYIGATWPTKDVFNWIDGSLWTYNNIDLSYSHGATCVAMINGANIGSSGMWFSIDCNMQYSSVCKRPAGIKCNGAAPAVTVTPVPKNPSYCNAGVQLTPGVVTSPDYPYQYDNNQNCVYQLATLGSYNVLLRFSDFGTESKKDIVTVYDGDSVNSPVIGTYSGELNAFSLVSTGNTMTLSFKSDAKNGGRGFSARFTSYAYGK\*

>Cbn|CBN04672.1

MKLFLLTTLLTSAYAHLACPSGFTLVLDECLKIIPNPLTHTQAEVDCTYLGGTLVNVHSAIKNRAVSEFASKSGLNKIWLGLFCFSNQNSSSCYHDDNSGTASVYNNFAPGYPLINGIYGGCVYMSTEGSLAGKWVSVECEAESMPFVCEVPSTRYDPTCTHNYGGHCYYPSTELNTTSATFSNAQSICQQEFNGNLASIHSKRENDYVVSLFRGKSDADYVLLGAQDLLPNTFSWIDGSNYAAFDYRDPLDPGTADCLGMEMGTGLWKRVGCTAKIVFLCKRSISKTVISTPKAHLVTSNPSDFSNCNTTFLMAPGVITSYGYLSTTPSATSCTWKIVTLGAYHIRLSFVDYSSPDPFSSNRAVVSPTNIMNVTFQDRGIAGFRGFKAVAQPY\*

>Cbn|CBN04817.1

MRVTLVSALVLLLGGPSLQGPIVAQKPRKVSPGYNVFERPDGTVVTHSYHDTLATFDEAEKICDAEGASLSGIGSMEEANFLKGLVKPVNSEGQYWIGGRRNPSCFHVKGYVNKSGDPCSRENVVTWQNNVAKTIKEDWWRDHLCDSKDCVKIPNPTSEVYDEEKGNKGFQACLGFVAGNPSWADKNSSQFLDDKECDSTFGFFCQRPLVASYRLFTDPVTPIEAEENCEATGGLLAGINTEKDAVDITELAKEEGSVNGLFWLGATRNPSCFNVSGYIDQVGHPCSRLNVMQWSRGVGTRVKEDWWRDHYISTVKNPSSNAGQQDGDHGFQRCLVFVHGSHQWAKDNSSQFLDDSECNQKRGYVCAYM\*

>Cbn|CBN05279.1

MRLTLVIALISYHTVTNALECYDSSERLIGDACFSLVNERKNFYDAQRHCQHNMKTWSNLAVENNKSQMIFLTRYAKTDFDETTGWFWLGVLRMETNENFKTVTGLPLYWQNFKDINPSMNYVAARLADGSWDTKPLEEKLPFACSYVPLPRKQAREAESTSSNWLRESVYRSIDS\*

>Cbn|CBN05294.1

MRLLLLLLVFGMTATLGHVIEGKSSISFDNPSFHSSSSSESSSNEGRGTNRHRHLGRHGRRPPRPIQNDHSHSHGSHSHEHGGGDNDGGGENRGCGRGWKRFDRPTGGWCIKVAQGQFSQAQAESKCQSEGGTLSGLQDTNEISYITSAALLLFPERTGSLWVGARRSPACSSAPLSSSCNRMTSFTWTDGSTTGTAGFQWAANQPDNSHFKTQHCAVLLASSPSSDPTWNWLTDKLDDEACVNPTGSYQRIVRGYVCGKKANERRRK\*

>Cbn|CBN05330.1

MWIPLLILCFWTMGISTLAPPREPDYSRIAGDPKTSYFCTNNFTLVFAKCLRHFPEPTTRMTAMKTCRRYSGNLVTIKTRDEQASVKHHLGAEPRKYWIGLYCFTDNVSQCVWDNGNATAQALRHFPPFSPSVKLGNCVHSQINGDGKEVWLSTNCEEEKLEFYCEIPVTLEDHCELNFNQHCYFPSVLAEKGIQNARNSCKQPFGADLVSIGSREEHLFIKNYYKTLNVSSIFIGARAWLGRYFKWMDGTSWTYTASDRYNIILGDCMVMNLKSDGNRTEGYWYGEDCMATRHFMCKRKAGQRFLIQKPLYKPPRWSLRLVSSYMNYGTITSPDYPEGYGPNVTAVYKLWTLGSQRIQLHFLEIQTEKDHDFVRVYDGMSEESKLIGNLSGQHRDLFLESSSNRMHVVFKTDLQGNDLGFQANFKSIV\*

>Cbn|CBN05589.1

MFNRISQIYQARQDRLSRQFENQESLASNRNSQHSEEIQSASLENAAATSTEGTQDAEPKTEFEPVERQRHFGILHYTMNNRFKKIMLIGLANLLIILAFFLFMFFFMMRFRCGTLDISTTTTIAPTTTYTTRAPSSTNAPQLKTCMNGFQLVGSKCWWINVRVYNRDTAVETCRTYGSILFTIDNEAEDLAWKAFMNNQHHRCWMGLLCKNSNKETCEWDNSVKWPFAYSAFAEDSPSDTLPCIYYNVSDSLGAPWTSSDCSLNLSSVCELPPTGESDCLYNYKGFCYYYYATPVTFSEAQDACKTKCGNLASVGSHLEYIFLSSIEGVQDISIYLGGVVVNQNLFYWLDGSPTNYNNIQKYDEKSSCLVLNMGQKANNGNWSTVPCTSKNPYVCKVPNDVICN\*

>Cbn|CBN05591.1

MLRALLLLLFFLISPSFSLVCPPEYILVNEQKCLKIVWTPATHWEATQNCTAVSGTLVTIKNAIDNRAIVNLLSGTEIQEIWLGLSCFGNTSSTCFWDNGSGSPILYNNFMGPNITSLYGRCVYMPVANWYGSNQGKWRNIECFNGITPSVLTVLPYICEAPPTTPSQMFPYSCMNNYNGYCYYTQNYRQTYNIAFTSCVMGAVPNLISIHSKMEIDYIRNVYKGTNTTMIYIGAQVDSNGRFYWADGSVWDFDYIDPLDFGEGKCLVMDVQGFGLWSRVDCDQQFEFMCKQKIMVPPTSAPVVSDANVFDEKENAEHPKQLYDASNCNSTLYLAPGSISSFGYPAYTASYCTWQLVALGPYRLGIYFDFWATYGTLTIYDEYGNNIGQFMGTYDRTPFPRYTPFNIATVTFEPMPKTGSGVDKGFHAVILPL\*

>Cbn|CBN06047.1

MITLEDAQAKCKTEGAVVAGTQNLDEINWMADTVKALQPSSVSIWIGATRTNACKDVRITAECTALSSFYWTDGSVVGVSGFKWQLGEPNNTGLGQACVQLYMADKTMDDVV\*

>Cbn|CBN06110.1

MLRNLLILLWLSLPILGQNYTCPPNYTMVLNKCLQVFPTTAWGNHSAAEQICRKDGGTLVTIRSAIENRAVATFAAGNNRIWIGTFCFGNDTSQCVYDDYSGPLSGYSGFERGYPLVTNHNDGCVLMVTQGSTAGNWLSSWCNPYEPVSPVCEVPPFIDYQIPTPSCVNKYNGFCYALLQGTYEYGTGCGSSFLSIHSNRENDYIQNNLFPPGQNLILLGAKRKYLVNYDWSDTTNWDFDNRDPMDFNLNHLDCLAMNRSTGLWNYVACNVSQPLICKYPIPDNHPIESHCNANSLLMAPLTITSNGYPRNNNGSPCSYKIGTTGAYRVKISIVDIWGIQLTIKDFDGNLIVQTGIQGTYVSPSSYISVTQTGTGVFRAIVIPY\*

>Cbn|CBN06265.1

MAKIYGKVESGPNATFTQGGITLEDCIDRGFTHTNIILVTWIDGVCSGYNSGPITTPILVVETEEDSGNYVAIKTFNANTCPATFNDIDLTFVQVNGDTYPWVKTADGVSFSGCRSGWTRFDRANGRSVCLQAFKLSFRVTKATAISACQQASADIVGVETKEELTWMFEQKNSLVGRDNSFWVDGERVPECLPPINQKELGCNNFKWSNDLTSNVANLSDKNLADMSYYDPYESKAENCLVLFSFHGQLNDASCTQFNSAEGVICGYKLF\*

>Cbn|CBN06522.1

MHNFLFSVFLLPLCFNSLLAATCRGEEKLDPSGKYCYVIHKGFASFHDAEKACYDYGGYHLATVPTMIDNRFVYNLSSHANVFSNYYWLGLTDMTADGSWEWIDGSDLNFMNWASDSINGYCGAMRAYDGKWQAQDCAKQYPFICYGAAQGAPTDSPNPPKTTIRPTRKEENMIKFMADSESVGNPNTDPNAVNFYNKEREYIRAVTDVLFANPSSNGNICKFYMSVSFYGYTKYDQQFDHSAAWSQGQFDNLLESNVWDDGKTDQAYNITDAITGAQKFQWSPSMDDIGYTTLVFLTARKDFTNIPSLFNPFPQFDEVVVVSLDGANMPGVPAGVANIPVSKEFNNVDINNLVSVLKCH\*

>Cbn|CBN06550.1

MTKELMAHEEAEAHCAKQEQKSTIAFMHREALPFRIYKHFTGVYSLWLEASVAITRDLIYDVKGGHLLLAIDGYPYNLPNIALARVAPTEKAMVLCEYTPRMNQAESNYLLRRYGEIYYPTIFTSDSAYVRTASVLQRNDKDPSMDHKYCKHVLRPFLQTDDAQAAVPTREFLDRSSPAGLEAMSDARAAPIYCQTTFDVMEYGDCPENYKPFYRKETGQKFCHDFIDKPRFYDEAEADCAGDGAHISGFTGREELDFLDSLLDAAQEEDDVPFGHENSIWLGARRREACNRKGIQGKEGGFNSDPTHPCSRLRVFEWVHGVAQNPPDFESRWIGPLEPNFVSDDEKCVELLKGEQTRWDDKDGDKKLNDVPCDPDRGKYYFCGKEAPIVSKKNNL\*

>Cbn|CBN06705.1

MFAALLTTLFLALTLKDVTSANLCPTGWTFANETSYCYLISDRYMTYPETASYCQSLGASQMFISVSKELTFLNYFTVGLFAQPWLAITRNVTSNKWYNSDGTTPFSTWWSTGEPGLNGDCATFKSVDPQGMKATPCYSIQPAMCKQMPALCPTTTSYGGLYTRSGTIKSPGYPDQYYNNLDCWYSITAPNNTYITLEFNPYLVEKTFDYCMIYDGANGTGTYLGKTDEYTNPRYEFESSSNHVSFKFHTDRTITSNGWLLTWNAKVYSAPVIQNGTSGNFTSPNYPNNYDPYTEQLYYINAPDGFHVNVTIDDFLTEAKYDVLEVYNTSSVIANNLVANLSGNSTAPWSWVSPSNVVTMRFKTDGSVQKRGFDVLCGSIIAGHGDKISKIDQKTGQIETIRSEKNVKLLTTLGSRWISIDLSNAISVFDADMKRSAIFEYKTVNFTSLLQAESYRNKVCVATDDETIRIINTINGDFISVSEPFGSEIRKVQQSSTTDVLAIGLSSGDIIFHRLNGHTEIGRVKMGAPVAAQEFK\*

>Cbn|CBN07064.1

MILRSLLLILIAQVTWCQIGQPGQAPGQVPLDPGYRQPLEPIKNILQGSYGNNVTLYYRNSPYRVSGDLTVEYGVTMDIETGTRIYFDTGIGLIIKGTLRAIGNEFAHIEMLPYQQQINYDDEMPKFRLVDGPTVRQGRLQVQFRERWRSVCTMVTNWTSIDTGTACRSMGYSDGGFWKWYLRNNDTYPFVMPKPDCHGSAKNLWDCPSFSDPNRIRLSENLCQGEDDIGIYCWGPPTFTGWARHWKGIQILNSPFHYVNSDPDLVAVNRESNSRLEFVDILYAGYDGVNKNTTSALYIEGVPPIMNGLRIEHSARDGLQLLDTNGPAIIANSTFSHNRGHGIFVVNTTDARIFVNNSRIQGNWGDGIWYKQKTGINLIDYGLREKRGIGSGRLEEEKPRIDMCSEHRIDDNHFFPHLILVNLKNRTFLDPTQPPICWMTVSLPSRLPYTYSIQWLHVRDRNPRTSRTTLLVCDSNNPDDNTCSTPRFRIPIKNEVYPQSISLKSSGKPLYLAVEHVLDGEQAGYVQGDVNLLFNIHASVLDKAYYGLNVTNCIIEKNTGNGVFANDIRERTALTNVTLDENQGYAGFLVRDGAADIWLNETRIFRNWGDGMNISYAGGSIIVNGTRIEKNRWRGAAIHYNQTLPFLPLYNEVIFKGRPSNNKFYLPTVISENEWGGLLVGNFCAYGNESWWGYRNPPLNMVYPRIEPKILISWVEFLKNQYHPAMEIFSCRDPSVTQNIVDITGNRVDGNMGFGMRIAPAVNMHMLISSNQFLHNNDTTLYVRNAQWPELGKLPGEVTISKNVFKFNFAKYIISIGMNEDAQRQFLTFNQQNEIRANTVFDPFPSLPPRSTPYAALVVSSSNVKIHRNCFNNERAKYEIATELERHAKWIDARENNWGFQEIPRFIDKFFDQFNRYSLASIDIDPYMAACNQRMPYISLLNGAFRQFKKASEPNRLGGIIYENHDLLKGRYTVTKDLQVVPGAKLTIASGSILEFQHGIGMIVQGDLIRNEYDQDEKVIFTSTPFTLEKRPQIRLVNPDGNDEVTEGRLEVLVDDQWGTVCNRSWTPQLTILACNQLGLVADVQYFENWRIFPEEGDLPMVMDNIRCEEQEVDLTKCRHDGVERNCAAGCRRTEVVGLRCLEPRWAGVRYSLLANPPTVTGQTTMDNWRIEKGGLFNFRTSEFCAAFKIDWNYHTFHRLEIRNNFWDGIDVVYNDLVKKPAIRNSLIYNNRRNGFHIRSAGITVENVTISHSAQSGMRYNPSVSALEQNDIVSWLSLKEQPELEANNIFRIPDQRLDLIEVMESNLNQRKFLVAAETEDCPEDPLQECVYNLMIRSVGYQYGLASKMAIQIVNPPSNISDEDAIFTEVSTGKSWSARKDQIYFPVVSTENAMRMRYTRSYGTPKLVVLVLFLDTQEYVDRFIHLYQSRVEDNQYGFSAVHYSNLTFSDGRLSNRWNNERIWLQKVNFTRNTEAVLWLHSPQHVVPQGTPLAEITYHFDNCSVVDNTGPIIESHRDLYASANIFHWILWSNTFANNSRSGIAVALPDTYDLLAKQQHSFWLTENRFERNDDFKILLDGYYAFANISSNNFTSNIAPHRFGMLEIRGMEKKLVCERNRFFFNWGHWMIKIDATSQYLRQIDVPSFIQYNYIEKNKFIRQRADYVDMWPRSYAVGVFGAQKIDVHFNRFYNELMDFELVSGSRYTDIYDTMNATFNWWGTGNEAVISQRVFDFDDWNTYTRAQWSPFYVSNDLSINFWWKPYRDGQLANATYVEPTVHDLHGRVYEDKNLTLITERWYEFPHYYRPFRPYRITRDVTIMPGATLYIQENVEVHIWPNVRILVLGNLVARGSYWQPIRFKPINTTELAEIKGRIPTEFRKKRGIVWVSREEESERAGPEGAPRLNNRLDQPSQPDQPDQPKKALHPEEPNLPNQLTQPDKPKKALHPEEPTRPKRASDRSKPDLVYRDFPTLHRDDPYYQRFTVSLTANGSDYGRSGFLQIYNKTIGETVPSCDRQFTIRNAQVVCRELGLETQNVYHWLTPRWDYNPQLRLIKTYMEPRECRGDEPSLDRCNLRLSGNDSQWMCMDSEHFNYIYCGSNRSLSNEYIGNWGGVTFAQASLEHEFGEKRGSRKEKSILQNVEIVGGGAGHNDSWQSAGLQIFHRSPILDHVNVTNCSVNGVQVISPNDRITLANLNVTFNQGQGVSIMTTFVQAPSTSQDAMRKPMSIPYYSQGMLDMCAAVKRFDVKNRIMLYYKYDSYPVDCVKIFTSSGRRVAFRIVQYHLYSSPTDLGRSDALRLYSSESFAPMSLLAEFRSDYHSVDPSQAVSSEEIAVHLRATAADGVYGFIAEVSALPSNSEQHTVGEVIIRGSRMDNNDRGAIEYSNLGEMSPNLVIESSSFSFNGIHLFGNISTSSQAIQLHLHNTVFFLFRSNSIAHNRGGLYISATSSSPVVRLGALVKNCVFVYNSNSTTLALSGNNYQSISLLNNIISHNFALYHDTIVAHDVAINMTRNTLFSNTGLHTLDIHANSKTSADKNVFFYNHFYDNLALGHGHQYMEKFGYQPLRENNEFLNRPRREARDRRQVLTQQGVSFDWWTHVDNETTRYRSTIIAGSSQEIFKFNTFNDPLNDYELTTGQQSQYEIGSIDAKENYWGYPGTVGVATGKIRDQEDYPALVKVDFMPVLESNTSLIEGDCPAGWFQAGHNEFKSCFLFVAAAVTYPRAVEYCKDLGAFVPYLRVEDILQTQLAQRVEKFSIDLITDQERLKAYGVEDDIHLWISSVNIPNTQCGWLGARSKRIGEVNCNILLPFICEKGTHPYSEPILWRPGIIIPIIIAGVIVFVLFTLVVCWCWKSRKRNEVMIERKNIVRASLKLQKREQEYQKRKMQQMQSGSEHTHTSAHASLDGGSTLSAYDWRSGRIPPRPMLRTPSDTLSTATSDHTFSYTGYTPHGGPTTGTTPSSRYRSRYVSTNPNGGYSDLTTTVPTTVTTSTETTVVRMRPHEMRSETSATESCSTCPTSDSERTSTATDISSYTSDAGSESTVRSTVVNNRRSLLPPARSPIPALRRGGSNGFLNMTNNFQPLPTEPPPRLPPTNHQPSLNRFVELHAPPRTGGGGSLNRTKKPVIETSM\*

>Cbn|CBN07304.1

MATPYHFVFLFLVGAPLVTPTVHDRSCGNDTNNYWLDVVLVIDNSENMINTNVYETISSIFGPKSQIGTGYKDPRSSRVGIITYNYNATMVANLKAIKSLQQLQNQLTTLKNAGNQVFEDSDQTNLDTYAMTSPDAIARALRSNFVNIITVNTGKDKTVSKQLATLASNKMAYIMSENITAELQNALAAINCFCPDGWVPYKHYGVCLYTSSQTKHRANANQVCQSLGVPASLPTEFNQKKREFNYELLNSGNLRVNSYWNGLTNQNGSWYWDQPKGKPLIPLDPSCGTVPPNSVCVADVEFSDKTVHWSSVNCANTFYFLCEAATCDTDNYCD\*

>Cbn|CBN07397.1

MDNVVGDRPPSKFSFGYARLHWKCYLVGMSFIVLLIIAFFLILFLAILKHPSTPPPITPTVLPNVASTVTSRMTTATTHTVAPRKTTVTKTTQTLGTRTTTRIRTIPTRTSPTSTKTVPILTKSSPIPTKTLPTSTHTLPISTKTLSSSTGTVPLSTNTLPLSTKTLPFLTETGPTSTVTPVPSTTVTMTPAIATSASTKSEISTIMSTRESTAENPCIYQYNDHCYFPVNTSMKFGDAQKYCSKNCANLPSINSALENQYINTLFKTETVVMLGAVATSKTNIIWTEKMDHGYNNIQNFTKENCVFTTLNSNDGHTGHNNDNTSSLHSVSKESLPDEIQNERTVVEVVTTEGAPDFSPREQQGFFGLLHSTVNNRFKRILLVGVANVMLILSFLLFMLFFVLKIKCAKPEVIFETIQCPTSSVFVSTTVATTKKPTVLLICPDGFTLVGQICWKIFPDYLDRTSAAEMCKTYNESYLFGIYSAEQNQQFIDFMTIKDHPCWLGLMCTNGNQGNCSFDNGLHAPFPYTNFATGSPDASTECLYYDSFHVTETLWISEKCERTLPFVCEFRPKVVTVNAICDHTYHDYCYSVHDTRLSYSDAQDACRNECGNLPSVIDENENKFLISIKDDSEIWLGGTVMSQNSVIWGDGTSMAYTNLTYYDSKQSCIMMESSGSWSTSPCGALYRFVCKVPIDANC\*

>Cbn|CBN07565.1

MLLRFSIILLLLLPLVASIFYGGDSGSDSESRERSYSGRRRHKHKYYDGGYYDDDNNRPPRPPPRPTCEEGWTFFQRPSGGWCMKVYPGTLNQYNSETMCVSHGAVLSGLQNTAEINWLVSSALSVIAPQTSGGVWIGTRRRPECVGYGQTATCTKTNTFYWTDNSTTGIEGMIFQQGEPNNGNSANGQQDCALMTVATTPTINAVSTYWSGQMDDIMCIASGTINWPSGTLPRANRAYVCGKKARQ\*

>Cbn|CBN07604.1

MYTLVLLFTLFQNALGQCVLGDDAYVGGLCYTASTYKATYSEAEFTCNGKAQSLAIIRNTAQANVLATLVNKITKEPNGLFWIGLKRKTMGSRWQWEDGTPFSWSNFDSNYLQNNLYVAESTMNGKWRTLDGEESHYFVCSYDPNLVNPTTSQSETTYYPSGSTDYPYETTPYPYTDSTYYPGETTSYVYPDGTTSYEDPGTTSYVFETTSYEDPGTTSYADPGTTSYEDPGTTSYVYETTDYPDYDSTVPDVDDSTPNPFDSTTDFPRLKKQLNKLPEGIKQLLRKYNF\*

>Cbn|CBN07748.1

MADLNKIQSINDLKNTLFNGTISETYESNLAKGLEAAEDMLYYGSVDKKRDYYQRAIIVYASVFNSQFDPTGVANRLKADGINIITIAFDEENQVSGELDWELSKVASPRYNFSNFEDENILDQIRGALLESNCFCPNEWLQYRNSFIDEYSKPFGTCLHYLSLTASWTAARFACRHIHNNSHLATEFDKAKHDYIFQMVQNSEQPEIYHIGLNMVKGVWKWDQPPGLDQPNLQGWEGWDKGYPLTSSTKNAVMNKIGAAGTVWQNVQAMSVGGYVCEVAACDTDNFCDRDDVN\*

>Cbn|CBN07901.1

MKSLVLFLLTLAIAYGYDNTICKNGFNLVNNKCWKLFQDPANHTTAENTCTQYGGSLFMAKNAIDNRAILSFVGGYQIDSLWMGIFCIGSDKSQCYWDDQTGTTMMYDNFATGFPNSGTGRCVYYSLSGYPRGQWLNEDCTEKMQYICELPTTHSDICDLNFNDNCYFRLDAQPFNVAQKQCEQMCGDMVSIHSAEENRFIASIYQDLPYDYIRIGGVATSPDFIVWTDGSTMDYNNLEKIGVNGICLYMALKNTYYSTRGAWYAFDCSTPYNYVCKRPVGAPNCRSTPAPPPPPQPTATATCTSGVHVAPGVISSPGYPHYYTSGCQYTLTTFGPNKIRLTFDYCNISPNDYIYIYDGESEYAPLISKAYTQAGKDPCLHQYDGHCYFPVNKSMNFGNAQDYCAKNCANLPSISSALENQYLNSIFKTETVTVLGAVAMSKTNIIWADLSEQRYNNIQNFGKENCVFTTLNSYNGQTGQWFTDDCTRETFFVCKRSIGVECNGGDF\*

>Cbn|CBN08074.1

MKLLILLIPLFQQISTEDICTSGFSYFPTFNKCWKAMTEELAQPDADEACRKLNGATLAMINSQIEYNALKSFLNNVVDNYNWIGLMCNGTTTASCHWTHDRGAAEDYYFKTGSLDPKTGECVYFDKSNRKLASMMCSYKTQFVCELPPTTTDSCNNNYNRNCYYVIQNSANYTDAQATCEESCGNLVSIHSELENRYVLSLFSSAGVVSLGGMAASKNYIIWNDFSVQLYNKIGEFEDGGCLFMNVGDDNSGVWHIDVCRPPSKFSFGYVRLHWKYFLAGAIFIALLITAFFLILFLVILKPSSSPSPVASTILPDVFSTVTNLLTVSTISTGTPVTVAQTTQTVVASTAKNPLPTVPTSTRTAVPLTTTVNKGSPGATTTVVPTASTQSVLSTVTSTLAPTVQSTSTKSIGNSTTAMGSTQHILSTLIPDSPTVTSTISMNISTTPGPTPDPNKVCATGFKLVNNKCWFLGPYTVYRDLGDSLCFNQAGSSLLSIKSAEENEKVAEFVAGQGIDKIWTGLKCFTNDTSSCVWDYGQGDVSGYSNFAVGSPNITIGTCVYYLAADKKWYSGVCDSDNWRYQMFCELPSTMRDTCKNNWNNNCYIENGQALFFSDAEDYCKQQCGTLLSIHTPLENRYVSSIYQLYYESRGGSLILGCVAPSQDMIIYNDYTPINTYNNLKNFTMDQNCVFFDIPSSNWYSGDYAEEECRGYNGATLVKVDSITKLKGIQQYLGDMLYRETWIGLYCNGTQPTDCYWTHDRGILDFDVFGKWSPNATTGNCVVMNVKDGIWSSRDCNQRTDSFCELPATTQDDCANNYDHHCYTLNQTSLSFSDAQRTCQQSCGNLVSIHSELENRYVSSVISQENGTVSLGGVAPSSRTILWSDSSMPAYNNINQYGHGYCLFTNVSSSYDGYGYWFSDLCSKKSWFVCKRSTGIKC\*

>Cbn|CBN08581.1

MRPFLLVIGAFLHFTSAATPVCTNGFTLVNDKCLRLFTSTVTHKVAERTCMNYGATLVTIKNAIDNRGIQTVTGTFSYTLWMGLYCFGNDVTKCLWDDASGDASLYSSFMSGYPQVQTGKCVFYSSQSSTMGKWYSSDCENTTRSFICELPTTYQDDCGNNYNGFCYTHNSAAPFITAQETCEASCGNLVSIHSANENRYLNSLFLQSGSGSILIGATRTSRNSYSWFDGSLWSYNNFDVTALQTGNCVAMSFGTSNNVSAGSWYTVDCGSSYGYMCKRPAGVQCPANPPPVTVTPVPSNPSYCNSTLLMAPGTITTPNYPRYYDNNVYCTYQLATLGAYNILLKFTSFVTEAKFDYVAVYDGDNFNSHLFGNYSGTPGPFSLVSTGNTMLVTFRSDKTNTFAGFSASFSSYVFHS\*

>Cbn|CBN08626.1

MKSLIVFLVLCFVSTHASNNTICAKGYNLVNNKCWKLFQDAAIHADAERNCSADGGTLFMAKNAIDNRAIASFVSTHGIDHLWMGVFCIGNGRNLCYYDDQSGSTLLYDNFAAGFPSSAAGRCVYYSVPGHPAGQWLNGYCNQKLSYVYICDLNFNDNCYFTIDAFSFSDGQQQCEQLCANMASIHSSEENRYITSLYSKTSYDFILIGGMAVNGFVLWNDGSVMDYSNLQTSDSTGCLCMSVNNSTRGSWYLADCSTPKHILCKRPIGVPNCRGAPVPITSPPVTPPTCNSGVHVAPGWITSPMYPSNYNAGCQYTLTTYGSNRIHVYFPIAVLEGGYDYVYIYDGDSKDAPRLDYWTGTNQAKGYYSTGNTMFIDFVYRSGSTKNQGFNATFISIF\*

>Cbn|CBN08960.1

MVTSMFLLISALILMVNAQCRFEDSPIGDLIFFIFRCYSFSKTPKTYTDASNYCHSINQNLAVVHNSQQNNFLFLKVFNSPRFPDNVRARSESSNGKFWIGLSRSSINSPFVWDDGTSLGWTNFDQNLPKDSLFVFESTVNGKWATLDGTQVLDTVCSYQLNSTTKPSVTCLFMVDMQSSGITQTAISTYQAYYIFAQTVAGKLNDQSNFSGYLDNFGYSGGLADHQEYPADLYTDFSNIAFPIDGIDDDIDLDLKDVDASLNTAQWTPHVDDQTCMIFFSAAPEAMYGGSSIQHTYDSFTTVIGVLFGAATSIPGLTDPIVASTLSDADAEAVVQKLLESLPSL\*

>Cbn|CBN09305.1

MKILQLALLFCFTIYAYGSTKVCAPGYKLVNGNKCWKLMNNGKTRDDAHNDCGVNQHGGLLAMPENSGDNEALKNLVKNSGHSNLWFGLYCWSGDKSQCQWDNIDSMGYDNFNSGQPNGNTNCVNFLSATGRWGSRDCGHTLPYVCELPTTTQDCGANCDTNFHNHCYKLVHSSKNFNDAESQCKSYGMHLVSIHSTLELEFVAHMYADKGTYWLGGKMPVDNQITWLDGTPQDFSPGTRVLDGACMQINIDSSHNDINWLGKNCGYTPSKFLCKRSVQAC\*

>Cbn|CBN09354.1

MIRLIVLLQLVGLALAGPISVTTVAPARCPDGFSLLNDITCVKLLETPRLYQDALNSCKNFDGGNLASVKSEMVASLFFELCLTFIFEENSFLVNLAAVKNSVHPIWLGLICYSSANSSCNWADATGTTAGYSNFARGNPKSSSGNNVYLLTAGSSSGKWVSADGNVVTLNYFCEVPATGVETPCPNEFNESCYIYNQTLLSEADARISCQNQFFGELVSIHSQEENDHVQALIRNTSLVRIGVRTNGVGMYWDDGSYFDFNNFASFRPDTENCSAMQILQGSVDPGKWLSDSCDEKIGFVCKRLKGHSSRSPNPGPTFNPNNCYGTHYFSGQGEIVSPNYPNSYFGMGTPCTYIFTVPSNQIAQIKFRVLKLDDQSTISLYTGIEGTVPIIELTGSTSAGSGSYSSGSNVLKMVFKNEKRKYDATTKWSANYGWNL\*

>Cbn|CBN09565.1

MKRFFTLIFVFLALLPVILTTPSCPSGFKLVNKNKCLKVFSEYDKHFEAESVCRGYGGTFATAHNAIDNRAIVSFAGNAALAYIWMGMFCFGNQSSTCYHDDGSGVVKYNNFAPGMPKVDSTIRDGGCVYTPAFGNDAGKWYSGPCEWTGIEYVCEVPVTKNDTCTYNYNGNCYFPSNLLPIEDVDRNFYDALNICHTHSMELLSIHSRREIDFIKSIYKNSGIVELTLGAQAIQKNLFDWTDGTNFDYDNFDPLSTTNGSCLQMDLSERDDIGMWYQTDCLTVKYFMCVRPAGSTTGAIEISTKEKRVNPKFQATRFTPPKILDLSDSSNCNTTLLLAPGVITSLGYSDNKPLIAYCSWKVAVLGPYRLGLYFTDFSVKNPVNVYSDNNTLLDSFDDNKTPFSLLAPSNLVTLTHDSVNDGVNNYHGFSATVLPY\*

>Cbn|CBN09662.1

MSTVPKDINVGRWLSGPCEVAGFAFVCEVPNAVADPTCTHNYNGYCYLPSHEIPNITATATFSQAQVICQSLSSNLSSVHSQRENDFIKSLYKNSGFNSSYLGGASFSSLGAKWLDETNFDYNYTDPIGYSNGTCLVMDISSRVNNGMWSGMDCQTPNHFVCKRQIQDTTANVKTKRLELTEGLVATASPDLSHCNSTIYLAPGVVTSFEYPNSNVPATYCTWKLAVLGPYCAGLYFTDFSFF\*

>Cbn|CBN10037.1

MKTDPTTIATTTIPTTTKPVVFSIVDPGALLIDCPDACATGWQYYNSKCYKKFNTAGTYAQAISACQAQGAELVTINDFDENDALRKAFDTNALVTEAQETWIGLKATSGVYAWSDGSSASYTNWAQNQPAAGSGQCVQMITDALSNKTYQYQRGGWKTYGCGKTSASYICEAPAGGPSISLVGR\*

>Cbn|CBN10379.1

MKSLIILFSLLLLHVSAQSLKCPDGYTMVLKKCLQAYPAPTRGNHSAAEEKCRKDGGTLANIRSVIENRATSVFASNNNLDKFWIGTFCFGNDTSKCVYDDDSGSVSDYNSFAVGNPQVTGVSDGCVYMLATGPQAGRWISSKCKTDEAVGSVCELPAYVDNPGYLQRSGCSYFNGYCYIRKSGPVSTMASTCSQIKGFPLSIRSKRENDFVYGLNSHNYDLLLGATRIAYDENKSISKYAWMDGAGWNEFENIDVTAHNYNGNACLGMDRWTGLWKSVYCGTSYFYYCKVPLPPNPAVDTSNCNSTVLMAPAVITSFGYPDNNSPPPCTWKIATVGAYQLRIAFKKGYDSIVTVYDGYGNNIGTASPDSSIVAPTNYITVVQTGGGPFYADILPY\*

>Cbn|CBN10724.1

MLRLFFFVALCIFGSVAPNCLPGDVSFEQYCFSFNRVFGTFNDTNALCNKMVGGSLVKINNMIENNWIQKWAVVNLDADYNLFWIGASDEGHTKDWRWRDNSALNFNNWNRGEPLEDRHCGAMALSSGKWFSALCTEKHQFLCQYPNSNYPTGAPYTCPPCPSFSK\*

>Cbn|CBN10901.1

MPTGFTYSWTANTTSWSFNGCRDGWTRFDREDSVSVCMQIFLQNNIAYNTSKEVCSAQSAVLTGLASLEECKWVQARVFQITTEDWMGFWIDGVRNCTDGQTCQTFAWTDGYTTNYDVLYDSTNADLAVSPAGPAYECCLTVGYTSPQTINDDKYCLMAYLDESVECYHYRYTSRPKTIVVKELKDERVVAIKAIIPPDLLSTCPSTHDSLDFSMTIPSGDTYSWTKSLDGYSLNPCRDTWKSFSRTDGNMVCLQIFQVNNIDQPAAKKFCMDREANLTGVASVEETSWMHETLEEIPPVNEFDSFWIDGERQCAEDYQCDVSGV\*

>Cbn|CBN11122.1

MKSLLLLLFFIAVSSAQNCLSSADRLINKRCFTFVNQQLSYQDARDWCHFRNPVTFSYLATVPDANTANFLASIAHTLFNNNGGYFWIGLSRYNNKFQWDDGTPVSWTNFQLQNSQNYVAESITNAKWTTYPNDNKYNFICSYDPNGSQTGRPTYPPDTSVAPWGTTAETETPPGPTPTGKPR\*

>Cbn|CBN11239.1

MMNKVLLATVLFGAVAAFDFSSSSESCEDDSHGHGGGRPPRPPGGGNNGGGNGGCPAGWRRFNRPNGGWCMKAFGGALTQANADAQCRSYGGVLSGLQNMEEARFVSRSALSVISRPSGSIWIGARRRSACLRQRITSSCTALNSFQWTDGSASGTAGFVWSDRQPDNAYDLTQECVVLTAAADTLKVKNVDWPVAMLDDTPCVLPLTDPSPRTIAGYVCGKAASRR\*

>Cbn|CBN11518.1

MKLFLLSTLLTTAYANIACPSGFTLVLDKCLKVMPNPLTHTEAEVDCTYFGGTLVNIHSAIENRAVSEFASKSGLNKTWLGLFCFSEQNSSSCYHDDNSGTASVYNNFAPGYPLINGIYGGCVYMSTGGSLAGKWVSVKCEAESMPYVCEVPSTIYDPTCTHNYGGYCYYPSTELSTTSATFSDAQSICQQEFNGNLASIHSKRENDYVVSLFRGNPNANYVLLGAQELLPKTFSWNDGSNYADFDNRDPMDASNMNCLAMVTGTGLWTRMGCTGRIVFLCKRPISETVTPTPKAELVISNPSDFSNCNTTFLMAPGAITSYGYLSLTPSTTSCTWRIVTLGAYRIRLSFVDVDTKNPVYVYDEYGREIRRVSYNTAAYSPTNIMNVTFQDSGLAGYRGFRAVAQPY\*

>Cbn|CBN11562.1

MLQHVFLASLSFLLVCSYPYTMIVTYGKPSNYTGYNRVLNVLSWEKCVMHCYNLPFCLFAYSPSSTPLECYSFYAKHMLFEVEKTTSANNLLVAFKVVDDKGYCPVGDNAPTFGGAPNYGSVSLGKSNTSYVITPEPGPSWKIRYNATLACQYDWGMFTRPTTKWCIRVFGNAWSESYTQEAALAFCKTQNATLTGLDSIEERDFVAKVALIRITSYNRFAGFWVSGIRKPECYFDGWENIPYCTGANPQQFNHTDNYLTSYSGYTWDPSQPDRSGNCVQMWIRDPALNPDHDYPHGNSDDYDCSTLNRGFACGKLPELTFN\*

>Cbn|CBN12021.1

MQNKDQIFKQLPTTQKQRTRLGKHICNIKTRVKEGSEDEYGMTFYNWDGRDLGTTAFEDLPHQASQSTPLPINQSEHCPDGWLKFFDSCYFFETEALGFAKAQKNCQDKQATLFVANSLDEWETVRAHTKKSQFSWIGLVRFSQYERYEKLPRWQTTGSINPSKINWLINPYQPLGNGWSTVANCVALFEFPSTIESSSYTFFYPCTQHFNSICERNSTILNARN\*

>Cbn|CBN12109.1

MKCYQFFLLLLSVSVGSALYDPSSYTDRPCGNDISNLWLDVVAVVDNSIGMTTEHLNNIAANIGTLFADTRIGTRPSEPRTTRLGLVTYNSLATTNADLNKFQSLDDVYNGLFSALDRTSNTNTAYLATGLQAAGQLFATQSIGSLRNHYKRVIIVYTSKYQGSGELDPVPMAARFRADGIYIITVAYGDDSKALSDNLQKIATPGFNFTYTSQSLVRDIQGALLQSNCFCPNDWIHYRQSYLDMNSYRYGSCLKPVNLPGSWKQAQLSCHSRHSNSYLVTEFNSNKHDFILTAVKNTFDQPISYHIGLNYINGIWVWDQPTGLPPVPMNGSSWDNWIPGYPKNPHANSGVQNIQTGFGVDWQNIPVYIAMSNYICETYSCDSDNFCDASDVKH\*

>Cbn|CBN12236.1

MQKSTLILVLCAVSAMADCPAAYRALLNSQMEESTSNGCAADWKFVNRPSGGWCMKVFTGYYESKAEAEKACQAVDATLSGLQTADEALYIQAAILAQVSESSGSLWTGIQRTKKCIGQKLTATCTNLTSFEWTDGATTGTGGMVFQVGQPDNQGLNQNCALFLASKTPTISARGTYYAATYEDVGCALTTFTPENVGRKTLGYVCGKKANE\*

>Cbn|CBN12378.1

MKSLIILFSLILLHVSGQSLKCPDGYTMVLNKCLQAYPALTRGNHSAAEETCRQDGGTLASIRSVIENRATSVFASNNNLDKFWIGTFCFGNDTSKCVYDDNSGSVSDYNSFAAGMPLVTGIIDGCVYMLATGPQAGRWVSSKCKTDEAVGSVCELPAFVDNPGYLQRSGCSYFDGYCYIRRSGPVSTMASTCSQIKGFPLSIRSKRENDFIYGLNSNFNDILLGATRIAYDENKSISKYAWMDGAG\*

>Cbn|CBN12459.1

MQTVDPRMILIHNFLDINKETIKNAKTDQVLPQAIQSNLIQNSQSSALQDDSANSLVLMDSTAACDSGWTKSSVNGMCYKIATSDTTWYAAEDWCYNQRYGSHLTSVHSQAEAKWIAATYVTGGSWFPFMDNWVGLRRSCDNTSYVWTDGTPVDFLWWQPGYPGSKDPEQSCVTIWVNTLLKLNPQYVMGQFDDIWDCGTNLATPTCRYDPTSTAPHIKYDTSYTCRDSTTEAAKITTTTMPLTTTTTTETTTTTETTTTPTTTTTTTTTPTTTTETTTTRTTTTETTTTATTTTTTPTTTTTTKTTTTPITTTTTPTTTTTTQITSTTTPIVQGTANFNTAKRGCQAFGGEMATISDSEMNEALRLAFSTNNDSTIAHQAWVGASSYSNWAPGKPNQAQGSEYTEYCNVMTLSVVNSGLDFGFSRGVWSDYPCNFTQEFVICKQS\*

>Cbn|CBN12487.1

MMQVPDTVIDEPSGSSMDILTCVTGCLLDSECFLVYSKADGECIRLDVLTPYQVNVTSDGRFVAFKTNLTTCPTTYLGLSFSVIMPSGFTYSWTANSTSWSFTGCRDGWTRFDRADSVSVCMKIFLQNYIAYNTSREMCANQSAVLTGLASSEECKWVQARVFQLTATAWVGFWIDGVRNCTEGQTCQTFAWTDGYTTNYDVLYNSTNADLSISPATSANECCLTVGYISPQTINDINCAASLNLILGYVCGYKV\*

>Cbn|CBN12528.1

MKQLIALLCLSSPLVFSFSNIPICTNGFTLINNKCLKLFDYSVPHGVAEKICRHSGATLVTAKSLSDNQAISTIAAKSVALIWIGLYCADSDSSKCLWDDASGAANMYNSFAADDCTFNYNGNCYTFNGTNATFIDAQTTCEQECGNLVSINSELENRYISAMAERLWTPRAAYIGATITAASVSWLYSWTDGSRWTYSNIDNMMYKPCFTMMIGNNYLQASGAWFGYVCEWETSFVCKRPAGLSCDRSQPVVPVTDPPARSSFCNSSLLFAPGVISSPNYPDNYENNVDCEYHLSTIGSYNIALSFLGDFVTEECCDKVYVYDGDSTSSPLIGVYSGTLDTFNLVSTGNTMTVVFKTNSEGVARGFNARFVSYSG\*

>Cbn|CBN12533.1

MAASAGVTNIWIGVYCFATGNTTTCYHDDGSGTISYKSFASGNPAVQSGGCVYMSVTGKSAGQWVSAPCEVIALPFVCESPPTVADPSCNLNYNGYCYMPSHAIPYSPSITNYTNAQSICQANGGFLASLHSKPEIDYVRGIYRNAEYSALFLGAQAFLPDTFDWDDGSHWDYDYTDPLSKTKGNCLLMNLPVNDPVRGLWSETNRTFEYPFLCKKKILEQTPVSTMSPVQVKERNLEETLHINKNNLPHHQKLIDFSNCNTTLYMAPGTITSFGYPNSKPPVSYCTWTVATLGPYRLGVYFTDFSTCLNVYLYDELGNQLSNPSGNQRPFRVLGSSNIVKITHDSSYDAMYGYHGFSATLLSF\*

>Cbn|CBN12739.1

MIFKLFLLSTLVGLASSACFDNGDKEIGGSCYKFVAQKLSFEDARNWCHYKNPVTASYLAYVPNQFTSNFLASYARSAFGTNDGSFWIGLSRKSGGSWSWDAGFPIGYTNFGDQVGQNYVAESIVNAKWNTFGASDTNFFVCGYDPAAPPTFAPQTAGPSGPTPTMRATTQPVPTTTD\*

>Cbn|CBN12850.1

MRFCLLLLICTAVPITHQLLSYDWSLKKACEKMNGQFNQREKDTSTTGDTCSLKFKVATRDDDDSRAFCELYAPWRLLKVSRETVSGRHFTTCHVEATLTCEKGWWQMFGHCLMIPNKGMTYTRQEAEELCKITNPNAGIAFMHHKYIVGIWRRYFKGTGQIWVDATETWDQYIQKTKTVDGTALALAFTGKHYDFSVQSNSLIKIDPNVKLEVLCQYKPEMNPAEINYLGRRYSEIYYPTIPVNNGILVRTTSSYTRTSSNFEVCQKITKPFMFKPIAPFVPDENALEELGMHPKHLIYLTRSGAELPYEKAKMDETICDISKDPLTVKHPNASIGSFRIKNFKEKSQCQNMLSTAIVHGKSPAELRFMSDSRSLPIWCKLGYAQAFIKDNFTTVDGFESFARENGEVIAHKLFTTRMKYWDAKEACKKNGAMLSGINSKEEADKLGELVKKAGTNEDQFWLGGKRRPECQNIDGYDKDPKSICSRNKVIVWEDNVAQEFFDDWWKDGDYHTNPSYWKGEQDCLTYVYGTPGWASSKSEGFLDDVRCDINSMFFCAKKLKFDEKAPDGWV\*

>Cbn|CBN13087.1

MRLLLALFLLVTAVAAAPSYDSAFQHLPNYYPELKHQDAIHIRAKRAIFAALGIANSCEDGWTGDGCKNPICTDPRPVPTTGQTALIELLFLKGGCGGSYYIPVDSDVGKTTQTIQIHISAAGIPYVNLTDSKGVVFTPTYANNGDGYSLSIYGDLPSGGYSLTIDNQGVPTTECIVEVNSDTVLKVTEGFVNSPQSDDTPYGESAVDGVPMYVVAHVDSQQAPAQVHSITIRQGNSLTPVYRAPLTRRYQCGYEYYAGQWQCQLGNSYYYHVDGIDSNGFAFRRTGKFACMQHLTSPAPPTTTRAPLTTCFNNGTLLNVVNQGQTCFCTELFTGTQCEKVNCMNAGFPDPDGNECACAAGYHGTNCQDVTCPLNWEPYLTDYKTLVVVIRSVTSMNQNLAAISNAVYKELTSNAANNYEVYKGFVLVKFGNGVYTNTYYPAYDQTKFLTDINLASAAAGQCSDATFDSIASIFTEVAIYQKSPIYFFTDAIASDVEKWQTVIEMNTRQKFPIYTHFFVQDNCLFDDMSQGFQAIEYASYYSGGLILRPTPDTLQHIFQNVIKATAYKMNSVLIDDLGSCATPTRVFFVDTSTTEIMILAIGESLIVSVTDPNGATTTALQIVNSGTTQMYEIANPVVGEHLITVVSNVKNTPCSYRVQARSEYDLFIGTSTGVNDDASDSEPVVGQSAHIVAQLTGLKKNVADPFRLFSEISITSNVNLDNTYQKPMYYSSGKYRDGCGFHMYFGASDFCDFMSQPFYATVYADDGKGFTIQRTTTGFCSGTPTTPYPPNTCQNGGVSDPTNNATCICPPGFYGKYCENIQCVNGGTARGGSCVCPVGTAGTFCEQYMCTTFNNNPDVSFDGQSIAFVISTRSTMKNAVATIATNVQTMTRDMQQASDKWIDKWILIAVNSNTSYLLVNSNRPADFVAGVNNLNGNFTNYAADETSCQIQIEQAMLGAALLSERRSSVWVFTDSDGPNDLNYIQLFDTAQEYQISLNLVGVGSSICTTPENNGQFPYYLKSLSETTLGEVYMTDKLDQIMFFIISLYKSAVSHRYYVPDCKAGTSYYMPVDGWTQSLTLAVTGTDLRSVQITFPDGTLGQNSDYELVAINDPELKLNQYVAACEGSFWNHRKQNCFEFTAEKYDWLDGWNMCHSQKAYLLHIDSQDINDFVFSQITGYRVWIGLAFLNGKWYWDVPDNNFEQPLSGYTNWADGVDPANPKFNHAVMNANGKWEPADPAEMNFGGCMKHRYGQGYYPGEGANIVPAGLWKVTVQSNSGSCEIQARSQSEIQVFFGFVTDPRVDKPNTYANIQSSNNYLIAYPTGVYPYTPDTKPSMEGKLNYAVLSSNRTITNSLPLGNRVCTYATISAPFSCPDTDGSISDFSIKFTGLDQYGYAFERYADALCTKTVISCGNGGFINNGVCVCRAGWVGTTCNTPVCQNGGIEKNGKCDCSSVPQFSGQFCELAHCEPPYPTAFNDKDRTLAIVLETSYNMGSSIFQLRKNLKASLDSINNDPTLQGWFTNFVLYPFDSTSNQASWYPVTVSRNSDDIVAAVKNISTMSCPGNAPCSSQCPRPIVSVLQNVLSMDALASPNSVVLVITRSSPEDYEQVGRIAQVLQDKKAYINFVFPAIDSPCGEGWNNPNVDALYRIISYSQGNTFTMNPVELSKNFLTQYIPTLYSSGGIAASSGNCMNDEIIFQVEHEMYEFSIDFYHPLMETIKVFDPSGDQITIPDNIITSDSNYIGIFPVNETGATRAGTYRILLTGTGGNNCFATVRGRSNLELFLGFVDSNSDSNNGATNDAAHHAPVNLQQNTVVVHATGLGQGIVRYVQIVMPGFGLLHTTEMRKRDTECSYEWYATTPFQFDYDSYWIVIYGSSEFGSNWKRNFYVSTVGSRPPLPPPPANCDLQSVKQDTLFLIDSSLKDTNVTFTILKQFAVTAMQPYNYVNSLAQVAAGSVADKGYWGFSYNAGENSFDRVSELLYDMQYIGVNGQNVTAGLQLVLDFFDLPAQGYRSDPDVRHLLVYVTQTNPTDADPSELVRAIKRSGRYEIIVVALDMQPSDQLTNMVAPRCFYYAQDFHDLMNYGVNFVQGQSCLRWNFCNY\*

>Cbn|CBN13470.1

MFQLLLLSILLPLISAQCGPGAVYQASGSRCLTFFRTATDFDSAESICATLNGHLVSIHNTIDNNWVSSQAQKYFSGSSWLGAKTTAPDVTNPLNWYWTDGSNFDYQNYRVGEPSAQGATACMQMQTATTKWLTANCTMQLPFICSYSSSVTPTCPTVTIPSHCPSGYTWYDETDFCYKSTVRFTNFNDARSACQADGGDLASIHSLNENTFLVELSKAGITNKDKSHNDDVFIGLIYQNSKWQWTDGTPVTFLNWGDGEPNNMEKEWWTSLVADPHEDKNTENTRWNNVAQIDMRAFICKRAPLH\*

>Cbn|CBN13670.1

MCEFWGGGSTYKPREGQKSLRGDTCSFTLPFASDTKESARMICEEYVPYHINEAVPGVPDTVCKAEATLVCKNGWIQNFGRCYKMWKEMMTRDDAGKHCEKEGATVAFMHREALPFRIKEYFTNVYQFWIDASIAITKDLIHDVENGNLLLAIDGYPYNLPNIALARVAPDVKAMVLCEYTPPMTQSESSYLLRKYGQVYFPTIETSQATYVRTASSLNRNINNPTADDDYCTRVLKPFIPDGKAQSAIPTQEFMNKLVEMRAGGAAIVRTSAFSGNANDKDRKSKSCVNYDKNSLFRMYSKDMKGKYLTIDSSNWKKNEPNEQCDAATYSSGIVLSREGKPGLEAMSDARYAPLYCQSVVSEYKYGGCPDGFKEFHRKQLGQKWCHMFIGNNMKNYADAQAHCQTMGAWLSGYSSQEELDFMDQLITVDGDTLIGARRRDQCSRFGTDYSRGYDEDPSSPCSRKWVFEWKNGVAPNPPDFEPNWAHAVEPNHGTYDEECLIVMKGIRPYIGSNQFNGDKKLNDHRCSDEFNFFCGMEALIVVVN\*

>Cbn|CBN13677.1

MLQHVFLASLSFSLVYSYPYTMIVTYGKPTNYTGYNRVLNVLSWEKCVMHCYNLPFCLFAYSPSSTPLECYSFYAKHMLFEVEKTTSANNSLVAFKVVDDKRYCPIGDNAPTFGNAPNYGSVSFGKSNTSYVITPEPGPSWKIHYNATLGCQYDWGMFTRPTTKWCIRVFGNAWSESYTQEAALAFCKTQNATLTGLDSIEERDFVAKVALTRITGYNKFAGFWVSGTRRPECYFDGWENIPYCTGANPQQFNHTDPYLTNYSGYTWDPSQPDWSGNCVQMWIRDPALNPEYDYPHGNSDDYDCSTLNRGFACGKLPELTFN\*

>Cbn|CBN14296.1

MSQKDAEAKCKTEGATLSGVQNKEEMKWMGDELIAISGKNGRIWIGLHRTDQCMSGGLTATCTPLSSFYWTDGSTVGVSGFKWGAGEPNNMNGQACGIVWAAAQTMDDMGCDQTVTEALVCGKIATF\*

>Cbn|CBN14384.1

MNGQFNLREKDTSTTGDTCALKFKVATRDDDDSRAFCELYAPWRLLKVSRETVSGRHFTTCHVEATLTCEKGWWQMFGHCLMIPNKGMTYTRQEAEELCKITNPNAGIAFMHHKYIVGIWRRYFKGTGQIWVDATETWDQYIQKTKTVDGTALALAFTGKHYDFSVQSNSLIKIDPNVKLEVLCQYKPEMNPAEINYLGRRYSEIYYPTIPVNNGILVRTTSSYTRTSSNFEVCQKITKPFMFKPIAPFVPDENALEELGMHPKHLIYLTRSGAELPYDQAKMDETMCDISKDPLTVKHPNASIGSFKIKNFKEKSQCQNMLSTAIVHGKSPAKLRFMSDSRSLPIWCKLGYAQTFIIDSFTTKDGFESFARENGEVIAHKLFTTKVNYWSARRTCQQNGAMLSGVNSKEEADKLGELAGKAGVKDDQIWLGGIRRQECRHINGYVKDRNSICSRNKVIVWEDNVAQEFFDNWWKDGDSHTNPNYFAGKQDCLTYVHGFPSWASAKSQGFLDDVGCDSWYMFFCAKKLKYDEKAPDGWV\*

>Cbn|CBN14703.1

MKQNGRCRKRRLLPEVVFILLLAVFVKPTLSSSKAAPEAQLTDVELKCPEDWIRLGTKCYLPFNIHQSWPFALTTCQRYGSTLAKIQTGNENQFIASLLSKPGKSTDIKEYWIGLTVEVLDDDELYVWSDGTPTSRYVGFWRQDQPNHLNGTCALGKVERKDLEWRLETCNLLRRFVCERAACVQGSYFCSSGSCISESKKCNGYNDCDDGSDEQNCPQAFQPNCRTYEKGESGVLSSPNYPNSYDPNLNCRHVLEGPINSRIELTIEHFETEPDFDVMTILDGGPAENSTIVIKRLSGSLDTAQTITSSTNMMIVQFRTDAQSNARGWQLKWRAVPFTCGGHYTAQAYIQSFVSPGYPKTFSNGAECVWTVETTPGQVVSLVFGHSSIV\*

>Cbn|CBN15049.1

MLLRASIFLLLLPSLVSSIFIKEPYGASDSESRERSYSAGRRYKAYGGGGRPPTCEEGWTFFQRPSGGWCMKVYPGNLNQYNSETMCVSKGAVLSGLQNIAEINWLISSALTAIAPQTSGGVWVGARRRPECIGHGITATCTKTNTFYWTDNSTTGIEGMIFQEGEPNNRPAPQNCALMTVATTPRIHALSYYYSGQMDDMICERADASWWPSSTLSRSNRAYVCGKKARR\*

>Cbn|CBN15687.1

MDYNGAISECATYGGVLSGIQNEWERWRMAEEALRQTAAYNVQYAGVWLGAQRVNGAFQWTDGHTTGTGGMVFGPGQPDNNNMGGRGPENCLQMIALAPGYWNNPGTWAAWTNGMIDDQWCNQVDDPPTRMYVCGKRGPQG\*

>Cbn|CBN15729.1

MNESSLIPTSSLSDSSSADLSVLSDAVGTAACASGWKRYSVNGMCYKESSTSMSWYAAEDWCWGQRAGAHLVSVHSQAEAQWLNSQYKVWYAPMDDWIGLKKECDMGKYFWTDGSPVDFTWWQPGYPKAQYAEQSYLEYSIVASCFWIHTGAIR\*

>Cbn|CBN15864.1

MCEYYKGEYKARTGGSKSMVGDVCKFKFSYATDNKESARTYCEEYVPYHIQVASFGPETTCLAEATLICASGWVQFFGRCYKMTKELMTHEQAVNHCATQDKKSTIAFMHREALPFRIYDYFTGVYSLWLEASIAITKDLIYDVKGGHLLLAFDGYPYNLPNIALARVAPTEKAMVLCEYTPRMNQAESNYLLKRYGEIYYPTIFTSDSAYVRTASDLQRNDGKPLRDHKYCKHVLRPFLQTDDAQAAVPTREFLDALKKERVAEIIRTSVYSGDSKVSSRSNEACSASDSRNYGMSFPTSGGSPLFKSMKDDKIWRKDEPKEVCDGASWSTGIVLSRSFSELGLEAMSDARAAPLYCQTSFDVFEYGRCDSDWNTAYRKETGQKYCHRFFSEKVTYDEAEKKCQEHGAHVSGFTGQSELDILDKMLDEAKRKGVSFEEYENVWIGAQRRAICTRLGIEGKVGGFNPDPTHPCSRRRVFEWVHGVAQNPPDFENRWVADLEPNFVGDDEKCVELLKGVKNRWNWPKDPADKKLNDVPCDLKLYYFCGREAPIVKIDA\*

>Cbn|CBN15890.1

MRFLISLFLFSTLISSAVGIVCPRGFSAVNNQKCLRAFTNNLKHLEAETDCSYLGGTLVTIKNAVENRGVANLAGLAGANNVWIGMFCFATGNTTTCYHDDNSGVVAYKSFASGNPAVQGNGGCIYMSTSGKTSGQWYSAPCEVIGMPFICEVPPTVYDATCTHNYNGYCYYPSFELTSGTTSTTYQKAQAICQSMGANMVSIHSKPEVDYIRALFLNSGVTNVFLGAQAFLPDTFDWVDGSHWDFDYTNPLAYVKGSCLQMDLSNRPNNGMWSETNCQLTNSFLCKKKISGAVAASTPQPMAGTVPAVVEARVNPKFHNALPHRQELLDFSNCNTTLYMAPGLITSFGYPNTKPPATYCTWRVVSLGPYRVALYFTDFSVYNPVYIYDEFGNLITSPGYNQSPFAILGPTNIVTLKHDSSYDGAYNYHGFSATVLPY\*

>Cbn|CBN15927.1

MNLKYILVLAFLCSLWILAIESRKVTQKPKKADPPPPPPLKKDKSWVRSKIDSAKEKYEAGKQKIKSKISSFGSKHGETKVKNAPAPIPQKTTTARRADWNHHMKTTKSYGWNPNIQGQGGVQNSLKTTKQHYGWNSNIQGSGGIQNPPQTGWNSNTNIDPAIGNPFQTTKKPLFDRIKEKAKNSEKYVGKAVGWAKKDLGIGVEGPKKPSKILKYGKKAVEYVFKKKSPKSPNIPVRIAKHPIPGYDSGSLNSNGYSGNVGSGNLGYSGSNYGQTYPESYAPSSERSSDLHQKVEFLRNRLEKMQETIQGTWNTSEAGTKYKLFEEKKNWNDAQLHCEELGSNLAYLDSESKNNYAKFLIDSQNVTMVWFGLRTEVGSEQESQDQFSNFSNLDGCGVVDRNGTWSISTCTMELPYLCQAFRFDVLVEIP\*

>Cbn|CBN15937.1

MACFHEETCIMAFEAETTCQLFYYTSKPTYLIVLDSSAGGIEGTGVVAIKANVPSCTATFNFSFIFIRSEIENEYYFWYKTFSGWSFQSCRYGWQRFDRNRGASIVCMKAVKSETLETAKEQCESLNSTLIGVASTQESDWMKSTVLQNTNDEAAMFWISGVRNVSNNEGSELVWTDGITTDNTTIALLSDITGESENCLAIQATETSSIIKVDCYSSVPTGAFCGYKFI\*

>Cbn|CBN16409.1

MKSLIVFLILCSASTCAFNITICAKGYNLVNNKCWKLFQNAATHTDAEKSCTADGGTLLMVKNETDNKAVASYLTNTGIEHLWMGVFCIGNSRNLCYYDDQTGSTLLYDNFAAGFPNSAIGRCVYYSVPGHPAGQWLNGDCTQKLSYVCELPTTHPDVCELNFNNNCYFMLDALSFSDGQQQCEQLCANMVSVHSSEENRYITSLYSKSSYDFIRLGGMAPSSSFVTWNDGSIMDYNNMETFGSTGCLYLSLKSTVTYSRGSWYTADCTTPKHILCKRPIGAPTCRSTPFPITPPPITPPTCDSGVHVAPGWIASPRYPSAYNAACQYTLTTFGSNRIRIHFNPVSTANNNNDVVNIYDGDSTDAPRLGSLSGNNFARYYTSTGNTMFIDFVYRSGSGYTGFNATFYSIF\*

>Cbn|CBN16457.1

MLLLPLALIPLLSVLTSATTPVCTNGFTLVGSKCLRLYTYPSTHQVAETTCASYGATLATPKNAVDNRAIATFVGSNPSLVWIGVYCFGSSLSKCMWDDATGSVEPYNSFASGFPLVDIGKCVYYSTQGALAGKWLSGDCDNEPRAFVCELPHTYTDICDHNYNGYCYIPIAITGFVAAQTQCERNCGNLATINSPNENRYINAFVSYDYNDGRNLMIGAIQARRSFYTWADGSIWGYNNVDPSSGYYDSCMFMSISASNVVPNGYWYSANCTSPSYFSLCKIPAGIKCNGAPPPVTVTPIPSSPSYCNSSVLIAPGVITSSHYPDNYDNNLYCVYQLTTIGSYRVQLTFTDFYTENGNDVVSVYNGDTVTSSALLGQYSGTLSTFSVKSYGNKMTVTFKTDGSVVYRGFSARFTSV\*

>Cbn|CBN16652.1

MSPTLISAFLLIATVFHSSLAASCPTGTKLYNSKCYAALGMDMTRDKALAYCKKTYGSYAVLATPLTYAENNFVTEQVQLHANWHTWLEFVADGTYIVGDDGKPPVYTNFAVGEPFSVSVGYCITIGMNGYWYAQPCADSHSALCEFALYPPTVKPTTTTTVIPSGYPSCVQKYLNFVPCQSGWEYYPPTCACFRIISNTTYYNAMNTCRSIGGTLASVHNSGEAAFINRLGVQTNSYWISTASARDNIIVGLTYNSDRGIFQWDDSTTFDYAQGFAPAEPADYTSQGQIILSNPMGYATYMRMGNCAFQTCRYAACKRYVY\*

>Cbn|CBN16661.1

MKLVVFTCFLLFGIVSARFDLSSSESCEDSHSHSHGSHSHEHGGGGGGGANRGCGRGWRRFNRPSGGWCIKVAQGQFSQAQAESKCQEEGGTLSGLQDTNEISYITSTALRLFPERTGSLWVGARRTPACSSAPISASCNAMNSFTWTDGSTSGTAGFQWNRKQPDNSHGQTQQCVVLLATGTQVVRDAWTWNTNQLDDVRCVNPGGSQQRIVRGYVCGKRATERRRK\*

>Cbn|CBN16694.1

MTNTNVLQPWIGARRNTTTNKFYNIDGSYLTTLAWTTNEPSANGDCVTLKGAAPSGLQVTQCYQMQPAFCKQTPALCNSAVLGGPTTWSGTFQSPGYPTQYYNNLDCRYLINAPNNTYITIDFYPFVIEEWYDSVELFEESPHMTGYVAMSQMEM\*

>Cbn|CBN17504.1

MKLFLLTTLLTSAYAHLACPSGFTLVLDECLKIIPNPLTHTQAEVDCTYLGGTLVNVHSAIKNRAVSEFASKSRLNKIWLGLFCFSNQNSSSCYHDDNSGTASVYNNFAPGYPLINGIYGGCVYMSTEGSLAGKWVSVECEAESMPFVCEVPSTHYDPTCTHNYGGYCYYPSTELNTTFATFPNAQSICQQEFNGNLASIHSKRENDYVISLFRGNIDAEYVLLGAQDLLPNTFSWIDGSNYAAFDYRDPLDPGTADCLGMEMGTGLWKRVGCTARIVFLCKRSISKTVTSTPKTHLVTSNPSDFSNCNTTFLMAPGVITSYGYLSTTPSTTFCTWKIVTLGAYRIRLSFVDYSSPDPVYLYDEYGREITYVVSSNRAVVSPTNIMNVTFQDRGIAGFRGFKAVAQPY\*

>Cbn|CBN17513.1

MQKSTLILVLCAVSAMADCPAAYRALLNSQMKESTANGCAADWKFVNRPSGGWCMKVFTGYYESKAEAEKACQTVDATLSGLQTADEALYIQAAILAQVPESSGSLWTGIQRTKKCIGQKLTATCTNLTSFEWTDGATTGTGGMVFQVGQPDNQGLNQNCALFLASKTPTISARGTYYAATYEDVGCALTTFTPENIGRKTLGYVCGKKADK\*

>Cbn|CBN17994.1

MRTWVLIAALAVICLTAEQELSQKDIIKNVLKTWDHSSEKKFFEPIRQQKYRTLDDADFNLETHHISKRSIAQPHVFAGQATRGCNLPGYTGATCEIPLCAARNPYVPNDQSSDDVAIDAVNLANCSETYIIVVDETMWDIKIELETQSPLNPTFFLQSENGNLIYPDSDRQTPSTYQATYIGMPPGQYQLGPRADTGNEFCTMLMSSRSYIKVSGGFVSGSQAERSDYPTLKFAYFDTESVVAVHAQGLEFPGQIQAIGFTGAENHISRYVPIATRYNCTYPYILERYTCRRSADTDRGYNMMQVEGISNAGYLFRRIISYQCVLPPVTTTMAPAPTTPVTPITSCQNGGQLLTDANGAAYCYCFGLYSGNDCSQMLCANGGFLPTPTSERCQCPEGFTGFHCQNIVCTDTSGFDFNAENPTITLVIRSRTQLSAVIEQATDAVTSIVDLLASEPGYLTNFIVVLFDNGKLLVNKRYDSWGAAMVDLTKAIHSAPSDGGCDDVVFSSVAAALSQYPTNKSPVYIITDANPNDSIEKETVFHLESYWRAPLYFVYVQPAPADGCNTSPDNAGYRDMMDMAARSSGNTFYFSNRTNINSFFYQHMLNTLFRSQLILSGDYSHCSNQNVYKSAAIDLTADLVVVVATGTDLTLLVTSPTGDRPTFDVSYNDGVNYIWTYNRHVSGQWFFNIISSSSSSSCTFKVYQKKFNFGGMTKYNPDYDIFWSFATTLTSAAGLLRQPVLGFDASPVFHVSNYPAFVSMDRVHANLQIYAIRDGVQTEVYGSSGMWRDACEFNFYFTPFTCRRPDELLYFNFFARDNNDMALQRAGTMFCASVHPTPPPDHQCQNGGVMNPSNTTCFCTPEWSGTYCTDIVCYNGGTPAGDHCVCSPGYAGESCELARCIETGPNPEFIRYGVDMVFAVEITQNSLASLVMLDVNFQEILRDVLMQDRGWIRNFVLVGYNSTWGGPIAESPASNLTAITNALHSLASTVPSDTGCTVKLWDALNHAIFARELPPGSFVEIFQTTPEDDTDTRSLGLFYDMSRSMDLVLYGFLAAVPRLQPSGFVCNATIENYYTLLGIVSGSTGTTYTLQAAEISNAVRLIPLQFSNGQVNFNYLDDCSHDNGMITYFPVDAYTQTIQIGTFGYGTNIQVYTGDGVLAEALELFYDDFTGQSVYEVRKACPDGWDPNGQYCMKFVSANDDILPMPQARAFCASAGGYLVDDVSEDKHNFLISAAHRTQFWIGLFRNTDDGQFYWDRGLGNDPSLLNQPQTYWGVNQPSADPVDQCVYFDGQQGDNTKVWITDSCSTPRPFACQRHRYDADHRPNEIGDDDLPAGHWYAFLKSNPSATQSPSCYMDIRVQSSLQIVTGYTTNIGSDMPQPDPIQDSPSNRLITYVHSKDNENRVPILTDAYLWDAYNGTFYNGLKYQARFACQYAWVSQDFPCPNGDNQANEFGVLHVGEDEFGNTFQRLTYGHCSRAEISCGNGGIRQNGVCVCTDYWTGSRCTVPICVNGGTRNADQATCNCTDGYTGQNCQFELCYTNSQELFSNDRKTMLLVVETTRQNSATVTQLIANLKAIVTSATSSAPLWFTNFGLVTFDTTGRTFEKFDYANIDALITDLTTQSNAISTDGACSLPYLGVLAHLLEHDDLIAKPNSEIFLVTAAGPSDLASYVETMDNLFNTQVHLHYVVSKSASCPTFDGLNNVQDMTWLGYGSSGNILFTDSDNIVNLLNNYLPTLYGASVLQDPTGNTGYDCSDGSLPWFVPVDINTTYIYVTTSAEFGSLSIKDPLGLSHNVAPIYNVQNQKLYQIEVARLGGIWTLQLVNPPGLCLAHVYSTGGAKVYTKFALPNPTGGKADPLGSHQDGMMAQPVAGFDNVAVFHIAGDPFHRGQLQYVEIFDVGQNSVTNILRSELYRRYECSYEYYSDLFTCNGDMVVVFVHGVDENNQKFRRQEVVVCNGRNPSTGLPVTGTAGPVTQPTQGPNTQPQTQGPVTTTQVPQTALQFDVVFLIDGSSTAQTSFDSFTKFIQTFMVSFNVGLAGARVGLVVVAPDLDDQAPPAAQLITITSQTILNSYLALLKDNYADFDHAGQVLTYNLQVVTSTDFMQASAGYRSNINNHVLIYLTTTTNFYTDPTPSAQTILAQKQYGIITIGYGAGFDNAKLQSISGGAACSFTATDFAGLNNQIRTIQQLIINANSNGGVYCTGN\*

>Cbn|CBN18069.1

MILVFLLFALFPHATGIACQRGLTAVNDQKCLMMNKMELKHLWAENSCAQYGGTLVPIKNAVDNRAVANMAASAGATNIWIGIFCFATGNTTTCYHDDGSGTISYNNFASGNPAVQNGGCVYMSVTGQSAGQWVSGNCEVSLPFVCESPTTVADPSCKLNYNGYCYLRSHEIPSTSNITTFTKAQAICQANGGFLLSLHSKPEIDYVRNIYKNTRYSSIFLGAQKFLPNTFDWDDESNWDYDYTDPLSKTKGDCLLMTLPSFKDQTAGLWSRTNCSFKYPFMCKRKILEPTAVRSLKPVQLKETSIEKTVYHSQKNLPHRQELVDFSNCNTTLYMAPGTITSYGYPNIKPPVTYCTWTVATLGPYQLGVYFTDFSVSKSVYLYDEHGNQLGNPSGNQSPFRVLGPSNIVKITHDSSYDAVYGYHGFSATLLPF\*

>Cbn|CBN18172.1

MKEWNTTESGSKYRLFEERKNWDNAERHCQGFGAHLAIIDNEAKNTFVTNLINSSETSDFAWIGMKTKTTTQTSTPFTNFDAESPIDGCAVMDAKGVWSIRSCIQLRPFICQIIKSDISI\*

>Cbn|CBN18283.1

MMNFNQFFIFSLLPLVINAQCDPGAIYSPERNKCYQYHTIDEDFKTAESICENSNGHLISVHTAIDNTYFAQQAQKNLYNGLVWLGANADSPVLSNPDNWKWMDKTPFNYQNYQSGQPSVLGSSACMVFNASTGKWLTPSCQNSYPFICASDPVNTVQTTCAPQKANKCPSRYAWLEETNACYKLVSSKKNFTEANAACKQEGAELASIHSKLENDFLVEMSTTSANSSIPSGHSFVYIGLVYLQNKWQWTDGSESEHYRNWAVGEPNYLNREFWTVLMPDPCRADYNPTGTQWNNIENMEQRAFICKKPAN\*

>Cbn|CBN18295.1

MLRLFFFVALCFFGSVAPNCLPGDVSFEQYCFSFNRVFGAFNDTNALCYKTVGGSLVKINNMIENNWIQKWAVVNLDADYNLFWIGASDEGHTKDWRWRDNSALNFNNWNRGEPLEDRHCGAMALSSGKWFSAVCTEKHQFLCQYPNSNYPTGASYTCPPCPSFSK\*

>Cbn|CBN18469.1

MQLLLTFLFTYVSLVASTSSTPVCTNGFTLINNKCLKLFPDPVTHRVAERTCMNLGATLATVKNANDNQAITTVAGSTTSLMWLGLYCFDNDDTKCIWDDGSGVTNKYNNFANGFPLAIIGKCVYYTTQGVFAGQWLSGDCDTDLHAFVCELPFTFADTCDYNYDGNCYTFHNTLTPFVQAQQACEQECGNLVSITSEMENRYIAIITNRLWGVFGIYLGATWSMYDMFTWVDGSRWNYNRIDRSFIDRPCVALLSGPGQTPSADSWYGVSCTSARYFICKRPAGSQCNSPQPTVTVTPISSSPSYCNSSMLLAPGVITSPNFPNNYDNNVYCTYHLSTIGSYYISLQFLAFSTEADFDRVFVYDGDSTSNTLLATYSGTSAPLLVSSGNSMTVVFKTDRSNVAQGFKARFMSYAR\*

>Cbn|CBN18475.1

MHLLLSLLIFLPSISYSQTAICTNGFTLVNNKCLKLFTEPATRKDASKTCGKYGGTLATIKTSQDNSDVVTIVANTKRRVWIGLYCLMNDPPTCFWDNDRVSVAKYNNFAPNFPYVEIGRCVTFKTDGKLAGKWLNVECEEDLRPFVCEIPSTFEDDCALNYNGYCYIPSEGEAIGFDNARRSCQAVCADLISLHSDNEVRFIESYYESSNVSSIQIGGRAAPSKYYKWVDQSEFDFNNYDRLAGVHGDCLFLALSTDGKLSKGSWYGDNCLESRSFMCKLKIGTQCDGTNTTTPATVDPVKLQSVNCKYQWTS\*

>Cbn|CBN18529.1

MSTSKDELPTHQETAEPLLNPAAQRKRRNDFMLGFLVSCIIFLILIGVGVAAFMLFGEKNKTDQLISCTPISPVEGMTTTIPTTAATTTKASIDREMEEMGKSMEQAFSIMGMMIKGLQGLAVGDLQKPAMEHIDKDSDWVTVNRTESGRKFLHRFFPEKLTYEEAEKKCQEHGAHLSGFTGQSELDVLDKMLDEAISKGVRYDGSDNVWIGARRRDACSTREGIGAEKGGFNPDPTHPCSRSRVFEWVNGVAQNPPDFQNLWITDFEPSFAGDSESCVVLMKGPKNIPGWPRNVAGDKKLNDVPCELEYYFFCGKEIVKTDE\*

>Cbn|CBN18842.1

MFKPEGPKCLDVVGHFMVDYDDSHGGEDDENDFFNVENDDTPEAETPVVNAPAASNPVVVSKVETADVACRKMEVGNCEEGWKSFKRPNGEWCMKVFYENWVNQIESEKRCNEQNATLSGFHDQLEKQFVTTTVTDHLYPSTGSVWIGLKRTPNCLNSKLTKNCTTLNSFEWSDKFTKGSDGMLWTWGQPANVGGKQDCAMLTTGYNGYIQYFQTGTFDDVGCDIRYKDTTRGVRGFVCGKQAKH\*

>Cbn|CBN19186.1

MACFYEETCIMAFEAETTCQLFYYTSKPTYLIVLDSSADGIEETGVVAIKSNVSSCSTTFNFSFIFIPSEIENENYFWYKTFTGWAFQSCRFGWQRFDRNNGASIVCMKTVVSGTLEAAKQQCESLNSTLIGVASTQENDWMRNTVLQITNDETAMFWISGLRNVSKDEGSELIWTDGITTDNTTIALLNDITGESENCLAIQATETSSIINMNCGSGAPTGAFCGYKFI\*

>Cbn|CBN19332.1

MKSISTLLLAVVIGSVVSHRDNYGFGGGRPGSGGRPGSGGRPGGSRPGNSNRGCGSGWERFNRPSGGWCIKVFRGEHSQANAEARCQNIGARLSGVQNQAEINYITRSALSLISQSSGSVWLGAKRTSACSTAPLSNTCNSMNSFQWTDRATTGTAGLIWNTNQPDNAHAQTQQCMVALASRSAMVQDSWGWQANRLDDVGCGVVAGENGPRTVRAYACGKRA\*

>Cbn|CBN19745.1

MLKNLLILSWLSLPILGQNYICPPNYTMVLNKCLQVFPTTAWGNHSAAEQICRKDGGTLVTIRSAIENRAVATFAAGNNRIWIGTFCFGNDTSQCVYDDYSGPLSGFSGFERGYPLVTNHNDGCVLMVTQGSTAGNWLSSWCNPYEPVSPVCEVPRFVDYQIPTPSCVNKYDGFCYFLWQGTYQDGTSCGSSFLSIHSKRENDYIQNNLFPPGQNQILIGTKRQYLVYYAWTDTTNWDFDNRDPMDFNLNRLDCLAINRSTGLWNSVACNVSLPLVCKYPIPDNHPIESHCNANSLLMAPLTITSNGYPHNNNGSSCSYKIGTTGAYRVKISIVDIWGVQLTIRDFDGNLIAQTGLQGTYVSPSSYISVTQTGTGGFKAMVIPY\*

>Cbn|CBN19898.1

MIFLILSFFTSVVVGTTPAPPTCPDGWTVLNDDTCVRDNRILTNLAISNGQTHPVWLGLTCPGSSWGTCAWDDQSGYTSDYNCFASGSPSSDIGPNAYILTTGNSIGRWVSADGDILSLAYFCEIPTNNQPAFCPNEFNGSCYTMHISLANETIARETCHQECGELASIHSQDENDHIFALYPRTTNQYQYRIGGRTTPDGTGRYWVDGTDFDYQNFDYFNEFNGQCVSVALVFDIIDAEGWMSNPCDEEIPFVCKRPKSAVSCGAVPPTVSPKVVTVPTVAPPPTVTPYPEMCRHTMFDVGNGTVFSPYYPESFNPIMSWDCKYVFTTPPGTKAQMRFSPDSNLIDTPLFYQDALEYCKAYPGGNLVSIHNAIDNRALVTIANDQGYTKPVWLGMTCMDWEYVTCVWEDQTGYSTSYSSFASGYPSLDIGVNSYMITTGNSIGKWVSADGTVQTLSFFCEVPTNGAKMFCPNEVNSFCYSFIAPSPFLPFQQARDYCTSQCGDLASLHSDYENFFIKNLVPYTFYQKNQFWIGAQTDGNALYWTDNSQFDYNNFGFLNPDIGNCSSLSIYTDTVASGQWVSSSCDQKLPFVCKRPKNVTSCTGISPTVIPNGVPLPTVAPRPTVSPNDPEQCHRGAQFFSGSGTIYSPFYPNNYNSLDGGPCVYVITVPHGQIAQVQFTQDTFIKNSWIEFYAQLEDGKQFGNFSGNAPVVPFYSSTNVIKMVFHLFWEYRDANEHWVANYGVKV\*

>Cbn|CBN19996.1

MPDNSCPELFTDVDMKVPNTDVAWKKSGRRWTLMKCMDGWELFQRPGDIFVCMKFFQTEFGANRSTAQNTCTKNEAKLSGVANRKKSEWMEKQAEYLNTGAWDGAWLDGVRSCDASEPNCHNYIWSDGFTSGNDAFGGNLWSPNHTATVQSCLTALSILSGYQRLNAVSCEKYDRAVGVICGYQLK\*

>Cbn|CBN20166.1

MRHSVLVGVLLSLATVETVSVAKSTDSDIVLKVSTDKQSTRDGHHFSGEWLESPWGDLYQFRAGDQNWLTAREHCLSLNADLAAIRNVEQLDWILSHYAPLSSRFAQRLVQIGLYAPEGQTHEWKWLNGEEINKTLQWSSGEPYDHSMEGRERCGLLNVEKRLLDDVDCESTIPDHRAQRYICQRTSENHKQQQRSNNYIWQKIENLFSFFGIGGSPTPHNATAPATNDYEDEVLKNETSTAKTVAKFSDSNEETSSEEEESVAKTLAALPKIEGSGESTSLKELQEPEGSGQIVDKKAIEAADLIPGVDEKKLDKMIDKMEEMIKSIDDLTVQPSSLERTTVSTVVLKKEKKDEEVTEEKKVEEKVKEKVKEKDQELNDNKISESIEGDFDHAQSKDMPKADIEPPKEEEEDVDCDEEGSGSGEEEQNEEETTEKLELAPEKEDKIKEFLGVLRLFLDRAEHGDLRKLLDDQSGKTLLERMKNAVREANKREFEMLEKLESSKKTGDKDELVKIMKKDQMSTEEQKDLYKKISSAVMKAAKLHKIEEKEEKSEEKVQEEQAMEKFAIAKEKADSEESEGTLEVLKSAREGKAEKKEKVGDDDYYGDYLDDNNVIKVQNREKSDVVEGKKEEKKETKKEEKKEEEKVAEKADEVKKETAAHDEPKKEEDAKKEESNEVKEEVEKDSKEEKEKTGETTTIAKVESDEAENDDKLKEKKDDESTTVASESENSSESTNSTTEKSETVVSIKPAEAEENDAELEASGQEEISTTTESTTVALKQIPAEEIEKIAKLEAKQLTEDEPVTEETKVETTTTPTSSSTTEINKESTSSSSATTTTTQATSSSKTTTTEAVTTTKAVTVPVKTVSPEEMEKLSKMEATEKVTLLPPLPTFTFPTLAPFTFPTLPTHATAKPTPAPKVPTLEEILGNLNDQFKKLLSPPKPLPPK\*

>Cbn|CBN20395.1

MRFSIIVASALTALLLVHAAPTPSNNDIESSGEAPVTLPQNSEEEPHRRLRFYNWDFKDLGTTAFEDIPYPARQPPSAVNQTEKCADGWLRFADSCYFIESEPMGFAKAERNCFQKQSTLFVANSIEEWDAISSHAKEAYFSWIGLVRFTHYEKTEQLPRWQTEGAINPAKINWLIKPFKPVSNGWTQFANCAASYKSPAKLESASYTFFYPCTYLLYSICERNSTIVNVMQ\*

>Cbn|CBN20633.1

MKLIVFTCLFLLGLVAARFDSSSSESCEDSHSHSHGSHSHEHGGGGGRGANRGCERGWRRFNRPSGGWCIKVAQGQFSQAQAESKCQVEGGTLSGLQDTNEISYITSAALRLFPERTGSLWVGAKRTPACSSSPISASCNAMNSFTWTDGSTSGTAGFQWNKNQPDNAHSKTQQCVVLLASSTQVVTDSWTWNTNQLDDVRCVNPGGSQQRIVRGYVCGKRATERRRK\*

>Cbn|CBN21163.1

MAPRVVFLTILALVGGAAAQTCNTGGIYSAQFNRCYQYFTAPAQFEFAEEQCALLGGHLVSIQNGAENALIQSNGANSFKKSNYSDYWIGANDLETSGQWKWTDPSVTWNYQNWALGEPQSGSDCAIQDKGDGTWSAIGCTSYRPFVCVTPVIITATCPPITTPKPTVCPTPTPCPVKNCVPSCDQGWTYFAPTDFCYRVYHNAKWDDAEAACVLLGAHLASVHSETENTFVNNLASCGIKEGNPKDLAWIGLHKVGQDWVWTDGSKSDYINWAPKQPDNPGKENCVETAPDLSHDKWYENWNNEACSTEMRAYVCKKGSIHV\*

>Cbn|CBN21227.1

MKSLVLLLLISSIAYGYDNTICKNGFNLVNNKCWKLFQDPANHTTAENTCTQYGGSLFMAKNAIDNRAILSFVGGYQIDSLWMGIFCIGSDKSQCYWDDQTGTTVIYDNFATGFPNSGIGRCVYYSLSGSPRGQWLNEDCTEKMPYICELPTTHTDVCDLNFNDNCYFRLDAQPFNVAQKQCEQMCGDMVSIHSAEENRFIASIYQDLPYDYIRIGGVATFSDFIVWTDGTTMDYNNLERIGVNGICLYMALKNTYNSTRGAWYAFDCSTPYNYVCKRPVGEPNCRSTPAPPPPPQPIATATCTSGVHVAPGVISSPGYPHYYTSGCQYTLTTFGPNKIRLFFNYCNISPNDYIYMYDGESAYAPLIPGKGTWTFTSTGNTMFINFKYGSNKPAPGFNATFYSVF\*

>Cbn|CBN21611.1

MVLAIIALVVSAFFIPDVLADPCGDSNWRYFPQTNSCYKLIDENLPWTIAEFKCLFQGAHHVSIDSPEENQFVHELSNWSEIWTGAAFFGKDMHYVNSDGSRYGNFENWKDGRKPPMNRARRCIKMDQNGEWFQSCCKKKTYTICEKKAAYSASSYSGSTNTVNGFRFMRHRS\*

>Cbn|CBN21668.1

MVLQMLLYTWSFFFIYSILPAIISANECYVTPCTRDIIIVVDGSSSMQTSTYVSQEINMITKLTYSWTLDESKVRLALVGAYFGNEFNGLDYFTDSSLVEKRLQSFRLAAMQYGLFSGNFNTTVRFLDERYVGKRANFGPRINVQKRIVIFSSHSGTSDISSTKNTLEQFSQQGYEVTIVGIGVDESVYKGTYYHKFVSVQWFELGVVAQSIIDTITEEGICFLDKGWTTPKPQTCTTTTTTTTTRAPTTTTAKGVTAKTVTSKPTTSPKPVPPTHPPFPVGDYQECSCTTQSLYIDIVFVVDTSAGMGLGGLMMVKAEINTLTVFKPSDYDNEDEFTEDLWTDPRLEDVDETIDEVNLHAGLQQAAKMLGSMRNGVKKVVVVYAASYNDEGNDDPRQIAANIRGSGHKIITVAFVEPESSSLVLKMAEIASPRMNFTSYRDDLLVEELEDAFCQVRKKEFILFLFHKFQVNCYCPRGWRQLTLENRTYGECFFPTKIDASWTATKYECPILSKEHTGNGHLVYVNSALKNTFLNNFYMENWDKENQEKPNYDIGYYYDKTTQKYIWVNGVTNNPYANWAENHPDLSKGECVMAKQVEGTTTDFKWISINCQVDSGRGLCQEAACDSDFYCPPEN\*

>Cbn|CBN21835.1

MFKLVTLALAYLAFASAQTGYTDWFDSTGTVVPTPYPTPGGTNVDRECGGDLSNLWLDVVVVVDNSKGMTNEGITEIAANIVTVFGNGTKIGNQYSDPRSTRLGIVTYNKQATIVADLNLLQSIDDLYQTIFSVLNTVSNTDDSFLAKGIGAAESVLQNGRANGVRSNYKRLVVVYASAYKGEGENDPIPVSDRLKSSGVILSTVAFDQDGDESLLAGLAVIASPNYAFTSKDLNLVGELQGVALQSEFSSKYKPPNCFIPANCFCPNLWTQYKANFDDEYSYKYGVCIRAATISSSWTAAKFACQNLAKNGFLATEYDGQKHNFLFRVAQNNTAFTAPYIYHIGLSYVNGGWNWQQPAGYPLKPMSGYSTWNPSYPKSFSSNIGVLEQQFSSDLTVGWQNINAYSVAEYYMCEVASCDTEKYCS\*

>Cbn|CBN21895.1

MFFLPRSFSLPSFLIFLNFLVIFAYSKKTNGHCPKDWKNVTRPSGEWCMKIIYENYLIHSEAEKRCQEEGATLSGFQNQMESMWVTTTVASKIYPNTGSVWVGYRRIKDCLKSGVTANCTRLNSFEWTDKVTTGSHGVVWTCGQPSNYAYAQECVTLTVGYTGYTEDGYQVGTLDDAYCGTRFKGTPRDVRAIVCGKTPEC\*

>Cbn|CBN22240.1

MRQSSVFILLLCVSSALATVEVATKCPDGWKWFKRSRGGWCMKVFAEMITLEDAQAKCKTEGAVVAGTQNLDELNWMADTVQTLQPSSVSIWIGATRTNACKDVRITAECTALSSFYWTDGSVVGVSGFKWQPGEPNNTGLGQACVQLYIDKKLMDDVVCSGHKLGGYACGKIASF\*

>Cbn|CBN22241.1

MILNKCLQAFPAPTKGTHSAAEELCRNDGGTLVNIRSVIDNRATSVFASNHNLDKFWIGTFCFGNDTSKCVYDDYSGSVSDYNSFAAGMPLVTGISDGCVYMLATGSQAGRWISSKCKTDESIGSVCEVPAYMYDPEYSNKNQCSYFDGYCYIKQGGEISTMVRTCSQIGGFPLSIRSKRENDFVYGLNSNNYEDLLLGATRIAYNREESVSKYAWMDGAGWNEFENIDISADNSDNDARACLAMDRWTGLWKSVYCGTVYNYYCKVPLPPNPAVDISNCNSTVLMAPAVITSFGYPDNSSPPPCTWKIATVGAYKLRIAFKNGFSSGVTVYDGDGNNIGTAIYKSIVAPTNYITVVQTGRGQFYADILPY\*

>Cbn|CBN22337.1

MFPLFLSVLFGVLLTCDGLSTTEAPYSCQQGYTLLNNDVCVKLFESPLRLDDAIRQCGNEGLFYYGYGKLVSIHTKDELDTLLSIAKAQNVVSPVWIGLTCPSTQAMDCLWVDRSSVYYHPFSYGNPKPENGDNVYMLTSGSSAGQWVSVNGAVASFGYFCAIHSITSKTFCPNQWNDYCYTYHNESLNEADSRSVCQKECGDLVSVHSDAENNHVSLVVPYDPLLTEIRLGGRVDGNQKYWVDGSEFSFSKFGYLDTNIGNCFGLQVKNDLVYRDWWLSNNCADEMPFVCKRLINATSCPYVPSTTPNSPYVNFDCGVVKHLTGTGTLYAPPYLYSGEYGPCVYVISQPKGSIAKVQFLPNSEIKNSRFTLYSQLEGGQPFANLTGTLPLTVFSSPTNVLKMIYTGEPTYPTQLLNYSANYWST\*

>Cbn|CBN22358.1

MKLLVFLSLVVYTVSDTPVCNNGFSLVNSAKCLKLVTTPTKHRTAEANCASYGGTLVTIRNAIDNRAVSTFVGNIGLSFWIGVYCVTNDPTTCYFDDDLGTASAYNNFARGFPNTDLGGCVYSASSGSLAGQWISSECEDVEMAYVCEAPTTKTDSCAHNYNGYCYLTSHENATSPALPFTAAQDACRQNCGELVSIHSRRENNYVQNLYTNTNISAFLIGALTTAPLTPYWIDQSRWDYGHVNPRSGSTGSCFQMTTGTDGTWYQVDCKASQYFLCKRPAGTVCNSTPPPPVIVTPAPTNPSGCNSTSLFSSGTFTSPNYPSAYGVTWCVYKLTTLGAYRISLYFTDFYVYQYTFVNVYDSNGARLAQLTGTSLPSPYYSSSNTMTVSFSSTPGTPGYRGFNAKFLSF\*

>Cbn|CBN22634.1

MEKIQSKLRWMVYESELNPLLFSSEYSSKVFSGTNIEYTDAASACANNNAVLSGIQDSNEMRYLARTASSNLASSTGSLWIGAKRTAACAHSKLTAICSKTTSFYWTDGATTGTAGFSWLDGSQPDNALGGNQDCIAFFFAPSNTRIATVNWFPGAMDDVNCDASQFNSIPQRKIQGYVCGKDASS\*

>Cbn|CBN22819.1

MLILELSFFALLDCYFLLITLWTQAKVMPKTSFSLLLFSSFVIICSAQVQNGTCEPGWTWFSRPNGGWCMKVFYGSHTWWHAAGRCQSHGARLSGISGEVVFPLPADIERNFIKQSILNLTAGMNSDIQPNVWLGARRSALCMYKQYFVGGPPCLPQFAFQWTDGFTTGVNGFGFGTGEPNNIGGLEDCAAYRPVGGANDFNCDDETATSGYVCGKEDIDP\*

>Cbn|CBN23042.1

MKTLIVFLVLCLALTHASNNTICAKGYNLVNNKCWKLFQDAASHANAERSCSADGGTLFMAKNAIDNRAVASFVSSSGVDHLWMGVFCIGNSRNVCYYDDQTGSTLLYDNFAAGFPNSATGRCVYYSVPGYPTGQWLNGDCLQKLSYVCELPTTHPDVCELNFNDNCYFTLDAFPFSDGQQQCEQLCANMVSVHSSEENRYITSLYSTSSYDFIRLGGMAPSSNFVTWNDGSIMDYNNMERFDSTGCLYMSLKNDYYHSTGSWYTADCTTPKHILCKRPIGAPNCRSTPVPITPPPITPPTCNSGVHVAPGWIATPRYPSAYNAACQYTLTTFGSNRIRIYFFYGVYTPNSNDQVNIYDGDSTDAPRLATLYGKVGDQLYTSTGNTMFIDFVYRSGSTSTYSGFNATFFSIF\*

>Cbn|CBN23248.1

MQLFIALIATCVSLVFTSNTPVCTDEFRLVSGKCLRLFTSEVIHSVAERTCMNYGATLVTIKNAVDNRGIQTVAKNFNNTVWMGLYCFGDDVTKCLWDDASGDSSLYSSFMAGNPQVQTGKCVYYSNVNESSTLGKWYSSDCENTARPFICELPSTYEDDCGNNYNGFCYTHNPAATFTVAQATCEASCGNLVSIHSANENRYLNSLFLQSGSGIFYIGAIRTSRNSYSWFDGSLWSYNNFDVTALRPAGVQCPANPPPVIVTPVPSNPSYCNSALLMAPGTITSPNFLNNYDNYLNCTYQLATLGSYNILLKFTSFYTEGCCDIVRVYDDDNVNSPLLGTYSGSLGSFSVVSTGNSMLITFKTDGSITFYGFSASFSSYVFHT\*

>Cbn|CBN23527.1

MRIKIFIAFTFLILTTVAQDFDWSFKKMCAFWGGKDTFKPREGGSKAMAGDKCSFTFPMATDTELSARTYCETYVPYHIISVVPGPNTVCNAEATLICASGWVQMFGRCYKMTKELMTHEQAEEHCAKQEQKSTIAFMHREALPFRIYDYFTGVYSLWLEASIAITQDLIYDVAGGHLLLAIDGYPYNLPNVALARVAPTEKAMVLCEYTPRMNQAESNYLLKRYGEIYYPTIFTSDSAYVRTASVLQRNDKDPSMDHEYCKHVLRPFLQTDDAQAAVPTREFLDALKKERVAEIIRTSVYSGDSKVASRSNPACSVSDSRNYGMEFPGDGKNFFKTMKDEPIWSEDQPKEVCDGASWSTGIVLSRSSPAGLEVMSDARAAPIYCQTTFDVMEYGDCPENYKPFYRKETGQKFCHDFIDKPRSYDEAEADCAGDGAHISGFTGQEELDFLDSLLDAAQEEDDVPFGHENSIWLGAKRREACNRKGIQGKEGGFNPEPTHPCSRLRVFEWVHGVAQNPPDFENRWIGPLEPNFVSDDEKCVELLKGEQTVWDDKNGDKKLNDIPCNDRRLYYFCGKEAPIVSKKNIL\*

>Cbn|CBN23542.1

MKLLLLAGILFTISFYAYADIICAPGYTLVNESKCWQLFNNQTAESDADESCRQNGGGILATLTTAIDNRALLTMFNGTDVSRVWIGLKCTGLSLSTCQWDDQSQVKYSSFASGFPNDRFGQCVYYSADGSPQGQWANGPCEDKLPYVCELPTTSSDFLNCTNNYNNNCYTADNTTIEFSWAQKDCQTQLGNLASVHSYLENRYLTSLFDFDGSVWLGGLAPGAGLIVWTDGSNNNYYNLRTTGNGTCVSMDLHTDSSNGNWTSVDCNSQLGYLCKRYTCSSDGHCP\*

>Cbn|CBN23669.1

MKHFVSILLLIALTGSAIGITCPRGFSAVNNQKCLRLFNNNMKHLEAENDCSYLGGTLVTIKTAIDNRAVTNMAASASAQNVWIGVYCFAVGNTTTCYHDDNSGVLNYTSFAAGNPAVQANGGCVYMATTGKNAGQWFSAPCEVIGMPFVCEVPPTFADKNCTRNYYGYCYMPSHEIKSSSTNTTSYDEAESICEANGGTLASIHSKPELDYIRAIYRNTNIQKIFLGAQAFLPDTFDWQDGTNWDYDYTNPLATTSGDCLQMDLTAGKPNNGMWSETDCGSNLYFLCKRRITPTPGVMAQEVKKQGRVNPKFRKSRKALPHRQELLDFSNCNSTLYMSPGVITSFGYPNSKPPVAYCTWTVAALGPYRVGIYFTDFSVYQDVYIYDEFGNVVSAPSGTQRPFQVLGDTNLLRLVHDSRYDANYGYTGFSATVLPF\*

>Cbn|CBN24093.1

MNKFLLISIFSLLFSGVASVACPRGFSLVKSNKCLKLVTSKLKHLEAELECSYLGGTLATVKTAIDNRAITNLAASASATTVWLGMFCYTNGTTIPCYHDDDSGPVIYNNFASGNPKIQGAGGCVYMTTTGKTAGQWTSSICENVGMPYICEVPTTVADSTCTRNYNGYCYLPSHELKLPLSTYPNAQAACKANGGNLASIHSKTEIDYIRAMYKGTGISDLFIGAQSVKANTFKWEDGSAWDFDYRDPLSTTLGTCLLMDMYPNIINNGLWGATDCQNAFNFLCKRKIVAKSVEENEERYMDHPKNLAIPHELLDTSNCNTTLFMAPGVITSYGYPSTKPPKTSCTWTIVTLGPYRVGLYFTKFSTGSAVEIYDEYGGIINSPSGDQSPFYNLAPTNWVKIVHNSKSDTGHAGFSTTILPY\*

>Cbn|CBN24189.1

MKSISTLLLAIIIGSVVSHRDNYGFGGGRPGSGGRPGSGRPGNSNRGCDSGWERFNRPSGGWCIKVFRGEHSQANAEARCQNIGARLSGVQNQAEINYITRSALSLISQSSGSVWLGAKRTSACSTAPLSNTCNSMNSFQWTDRATTGTAGLIWNTNQPDNAHAQTQQCMVALASRSAMVQDSWGWQANRLDDVGCGVVAGENGPRTVRAYACGKRA\*

>Cbn|CBN24248.1

MSSVLLRFKLFNWSYKDFGTSAFTDISLDQRQRFADFPTGLCPDGWVRFSDSCYWIEQHKQSFAEAEKRCYEKNATLFVVNSQDEWDAVREHFPQVGFTWIGLVRFTHRERSEDFPTWQTEGAVNPTRLNWLIRPYKPVSNGWSILANCAAHYSAALNWEASAYTYYQPCSFKHFSICERNSTILDFLNRKFDIQS\*

>Cbn|CBN24249.1

MKLILLALLCFITYAYGSTKICAPGYTMIDGHKCWKLMNGAKNRQDAHNDCGLNQHGALLAMTESSDDKEALKKFVASTGQSNFWFGLKCSSDDKSNCKWDNGDHLEYDNFNSGQPSGNFGCVNFLSATGRWGSRDCGHTLPYVCELPTTTKAPQQNIPDCGNNCDTNFQNECYKLVHSSKNFNDAESQCKSFGMHLVSVHNALESGFVAHMYADKGTYWLGGKMPSDNQINWLDGSSVDYKAKMRVLDGQCMQISVNDNHSTDMWQGKNCGYTPSKFLCKRSVQAC\*

>Cbn|CBN24453.1

MKTDPTTTPTTTVPTTTTTVVDTTTTVKRYITFRRTSVGARLTDCAAACPDGWKYWNSKCYKKFNEWGTYYDATLSCSTIGAQLVSISSESENGALWRAFDSNVLVDESEVSWIGLKYVSGNWMNTDGYISGYFNWAPTQPAMGSGQCVQMITDSLKNATYLWQRGGWKTFDCTSVSASYICEMDANI\*

>Cbn|CBN24497.1

MISKAVAVFLIFLVKFGVSDDPCPLNATLLHDNSCVKLFESPLRYQNASDVCKSLNGSLVSIHDSINDNALLLLAQSRYVVSPIWIGLSCIGIHREDCNWDDGTGSSAEYFHFASGNPSLQAGNNVYMLTSSYRAGQWVSVDGRLASFGYFCQFPPIVPLKFCPNLFNGYCYTLHTDELNEADARKVCQNDCGDLASIHSHEENVHINSLSPYGANAIDTARLGGRADQKVKTWFDGTPFNYTHFGHLESSRTCFAMNMVTNANLDAGQWESFDCDAKVPFVCKRAMSSTQC\*

>Cbn|CBN24657.1

MSNTSILLFFFFLVTVSANVCDDLREKEEEINGCGKGWKRFQRPSGGWCIKVFFEELLTQAEAEKRCQAEKATLTGFQNQTEVFHVTTTATTHLKPATGSLWVGLKRNQKCLKLKITKNCTTMNTFDWTDKFTTGTHGFIWNGGEPLNYGWNQDCVVLTVGNTGYVETLFQVGTFDDVGCEMTYKNSARAIKGFVCGKKSEK\*

>Cbn|CBN24871.1

MSFGYILLVLCAILFFGNAVNGHPKIKSCPKGWLQFEKTCYFRQPDILNFEDASKSCERRESKLFDYDDAFEFEAIRKLFPNYYYTWIRANVEEELEWLYEPYEEIINGKNSVATCIAFYSSPTRSYSYYHPCSALFHSICKKSLDTFHQWMD\*

>Cbn|CBN25294.1

MKSFISLFLLFVLFSNVAAMVCPRGFSVVNNQKCLRVFSNKLKHLEAEIDCSYLGGTLVTVKTAIDNRGVANLASMSGATQVWIGMFCYPTGNTTTCYHDDNSGPLTYTSFAAGNPLYEGNGGCVYMSTSGKTSGQWFSAPCEVIGMPFVCEVPPTVYDATCTRNYNGYCYMPSHEMDIDTANTDYAKAQATCQDNGANLVSIHSKPEIDYIRAIYQSSSITRVYLGAQAFLPDTFDWQDGTQYDYDYTDPLATTKGDCLMMDLSKKDNNGMWSEISCTNIEYFLCKKKLVEPTAAPVVTTAGTMNTSPAAGDVEQKEVEKVNPKFHRVRSALPHRQELLDFSNCNTTIYMAPGVITSFGYPNTKPPATYCTWNVATLGPYRVGIYFTDFSVYNAVNVYDEYGNLITTAAYNKNPFQVLGTSNIVKITHDSRYDAIYSYTGFSATILPY\*

>Cbn|CBN25378.1

MRLKILFFAIFLFVVNAQDFDWSFHKMCEYYKGDYKARTGGSKSMVGDVCKFKFPYATDNKESARTYCEEYVPYHIQVASFGPETTCLAEATLICASGWVQFFGRCYKMTKELMTHEQAVNHCATQDKKSTIAFMHREALPFRIYDYFTGVYSLWLEASIAITKDLIYDVAGGHLLLAIDGYPYNLPNIALARVAPTVKAMVLCEYTPRMNQAESNYLLKRYGEIYYPTIFTSDSAFVRTASDLQRNDGKPLRDHEYCKHVLRPFLQTDDAQAAVPTREFLDALKKERVAEIIRTSVYSGDSKVSSRSNEACSASDSRNYGMSFPTSGGSPLFKSMKDDKIWRKDEPKEVCDGASWSTGIVLSRSSPELGLEAMSDARAAPLYCQTSFDVFEYGRCDSDWNTAYRKETGQKYCHRFFSEKVTYDEAEKKCQEHGAHVSGFTGQSELDILDKMLDEAKRKGVTFGNDETVWIGARRRPTCTRLGIEGKEGGFNKDPTHPCSRRRVFEWVHGVAQNPPDFENRWVADLEPNFVGDDEKCVELLKGVKNRWNWPKDPADKKLNDVPCDLKLYYFCGREAPIVKIDA\*

>Cbn|CBN25828.1

MSQKDAEAKCKTEGATLSGVQNKEEMKWMGDELIAISGKNGRIWIGLHRTDQCMSGGLTATCTALSSFYWTDGSTVGVSGFKWGAGEPNNMNGQACGIVWAQAQTMDDMGCDQTVTEALVCGKIATF\*

>Cbn|CBN25876.1

MLEGKFEKKFYEMKMKTEYDIEKEVGKLRDQFNTDLRDYERITTKDIIQIKREESWYTASEKCIGYGAHLASIHSRLENGFVSKLIPANETVWIGVNDIQKENVFKNPDGTAVDFLRWAQHQPNNEEHNENCVEVDHNGYWHDKLCIITRPFVCKKKIK\*

>Cbn|CBN26332.1

INGKCIAVTTGRYSGSSQQCKSISCNPKQYVFTFLSIDSKAENDHVMDGLSTNNVAAAYIGLAQSSSGWGWQNGDTSIYNNWAKPPVTQPPTIGPTTTPFRSTLPPSEQRRSTAVQVDFITSLSHYIADRGPAEFAFFAYGCTQTSPYIYQYPNFVSTFEDTDKMIETLKTTINENCVRSSPLDFRSMFRDQTVYYNRYSTSYRPFKSKFLSMIYFTSSTDADNIKAASALYPMANSSVITINVGTTSIDVSRLSIPIGKYGLRVNTPEDITNLVPKVDSMIFGATGVSSAGVKVDVMKEDQWDFDVRKSEPSVFASSDYTDCAYMNTTDGLWYSDGTCATKRQVLCQYVLPLPPQPPTPNPTIAWQDPCYNEYTNFTYFEILSNAKCYRMSSSKKQFAEAENVCLSDHPLFLHVPKLVSIETREEEEQLKTLITGIPNEGMFWFGLKRDPTNSSNWYFINGDTYDASYSNWRDGYPRDADGCDCVALVVNDSSWINTDCNKPLYSICSYRFNGTEPTVKPF\*

>Cbn|CBN28123.1

MWFHSTFILALLVYVSADTSDTCPKGFSILGSTNKCVKLITDVARHADASANCSSYGGHLISVHTAIDNRAYVNLASSSSTPFWLGLKCSASGVPASCLWDDQSGNAGSYNAFANGYPVVEVGNCVYVSTTGSFAGKWLSGDCNTMSLNFICEAPANTPVTDTCSFQYNGNCYYPSLSSLSEQEAEFACEQECANLVSIHSIEENNYVQSLFTNNAPTYIRIGATSNNQNVKSWIDGSNWDYSNIGYENSNLGLCWSMALLNDIVSTGKWISSKCDTSVPFVCKRKVGSQCGSTAGPTLAPGQCNGPQFYDNSGTFYSPSWPYSYIGQQNPCSYVLDTPVGSLAQIQFPIMVLDSQASIALYSRIEDSTPLVVLQGNSASNQWYSSTTNTMKVVFRPCVSNCAPVNGVVYRWQANFQPSNQVTQAPPVTITPNPNNPSGCNATILAAPGYITSPNYPNLYPNFSECLYHLSTNGGYRIRVDFGQIDTEQCCDNIVIRDGPLLSSPVLGSISGSWPAHSKIYQSSTNSMLVTFTSDASGQATGFSATFTAY\*

>Cbn|CBN28656.1

MKIQILIILLPVVTSAQLDLNSIRPCNVGCQDGWVPYSGNCYKKMFNVLTQSTAEQECLNLGSHLASFETTEEATAIRSLVLIAPLFSTNLLSYSSTSQDSWIGLSKTSNGAWKWTDSSEVEFTNLPDGTSVTGASCVSMNISGVWQPNECSSTVSSFICKRASASSA\*

>Cbn|CBN28738.1

MIAVVLTALLLASASQIVTADDNNHCPSGWTFSTNTSFCYIQSPQYLTYAEADPFCQSIGGSQVFVFTARELTWLTDFTKASFALPWLATTRNVTSGLWYNSDKTTPTSSWWTTGEPSANGDCATFKGTGQSGLKATPCYSIQPALCRQMPALCPTTTNYGGTSTRSGTIQSPGYPVQYYNNLNCLYSITSPVNTYITLLFSPYLLEDYFDYIDVFDGPNSSYPYLGTTDDWWYTRDSFESSSNSVSFIFHTDSIITDKGWLLTWNAKSNTPPISQSGQNGSFTSPNYPNNYDPYTEQLYYITAPIGFQVNVTIPDFNTEMNYDVLEVYNSSYVSSYNLVANLTGSAVAPWNWLSPSRYVTMRFKSDPIVQKKGFYVVWTIQ\*

>Cbn|CBN28838.1

MVNVDNAIARQFLFSNFVSRNQESLKHSDGSDERFLFKLMNQNSLTLPEPVNFIGVQDFDQSSPTIISDAIGTAKCASGWVRWEGNGCCYKEMGSPMLSWYASEDWCWSQRAGAHLASVHSQAEATWLNYQYKLWWSKMDDWIGLRRNCDNTAWEWTDGSPVDFLWWQPNYPIYGGIEDSCTAVCYFLIFILFIPS

>Cbn|CBN29294.1

MKFYSFILFTTTVITIFGQLEEDWGLKKACEKTGGKYTKRVSRQSSTGDTCEMPFKVATRDEQDSRDFCELYAPWRLLKTERKKDAGRHTTICHVEATLMCEQDWWQMFGNCFRMPDKHMVFTRGEAENLCKTSAPTGTEGTIAFMHHKYIVGVWRRYFRGTPQIWVSATESWNEYIQKTKTVDGDALALAFTGKHYDFSVTANSLIRIDSSIRLNTLCQYKPPITPAEINYLGRRYSQIYYPSIPVDNGIMVRSASSYTRTAKNWDVCKKVLAPFMIEKIGDFVPDPSVLQSMRYARVERSFTYLTRSGAVRELDDNGILQRTSNGTCSSYLPEYKIKVENEKYADFLVKDIPIDQTQDCDNMLSAAINHKEKTNLQIMSDSRSLPIWCKLGRPERFQHKPPPPEYETFRRTDGKWVAHKLHKDPKTYDEAKAICESEGARLTGIDARKEADQLRDIAEKAGVKDNQLWIGGRRKPECVDQEKWNTDVNDKCYRSRVIYWEHATAREFEESWWKDGKTPETRNPDYSKKEQDCLSLVVGNPSWADPKSGGFLDDIPCKDAYGFFCSMPLEMTKTLVED\*

>Cbn|CBN30028.1

DNRAIASFVSTHGIDHLWMGVFCIGNGRNLCYYDDQSGSTLLYDNFAAGFPSSASGRCVYYSVPGHPAGQWLNGYCNQKLSYVCELPTTHPDICDLNFNDNCYFTIDAFSFNDGQQQCEQLCANMVSIHSSEENRYITSLYPKTSYDFILIGGMAVNGFVMWNDGTVMDYSNLQTSDSTGCLCMSVNNYTRGSWYLADCSTPKHILCKRPIGVPNCRGTPVPITSPPVTPPTCNSGVHVAPGWITSPRYPSNYNAGCQYTLTTYGSNRIHVYFPIAVLEGGYDYVYIYDGDSKDAPRLDYWTGTNQAKGYLSTGNTMFIDFIYRSGSTKNQGFNATFISIF\*

>Cbn|CBN30206.1

MKTDPTTIATTTIPTTTKSVVFSIVDPGALLIDCPDACATGWQYYNSKCYKKFDTAGTYAQAISACQAQGAELVTIDDFDENDALRKAFDTNALVTEAQETWIGLKATSGVYAWSDGSSASYTNWAQNQPAAGSGQCVQMITDALSNKTYQYQRGGWKTYGCGKTSASYICEAPAGGPSISLVGR\*

>Cbn|CBN30616.1

MTKVLVFFLLGFFITEIRAQCGIGSIVDEHNNKCYHFHKAEVDFKAAESVCSTRNSHLVSVHNNLIIPYLTEKSTQHLFENGYAWLGGQRGFPIESNQQWEWTDGTPFDYQNFTNEKTDSSEIYGCMKFSVETGKWLTASCTEKHQFVCASDRKQKVTALLDSCPTGTANRCPSRYVYFEATQSCYKIIIGLFYNTTSNSFENTDGTPVDYTNWSQGQPNPSNFNTYTTIMSDAHGSINAGEWFNVVNENERGFICKKAATLY\*

>Cbn|CBN31237.1

MEGDKCTFKFPMATETEESARTYCEEYVPYHIITAVPGSPTTECRAEATLICHSGWVQMFGRCYRMVKQMMTKDEGKQRCEKERKGSKIGFMHREALPFRIAEYYTAVYQYWIDASEAITGNLIYDVPDGNLLIANDGYPYSLPNIALARVDKSTKAMVLCEYTPEMTQSESNWLLEKYGQIYYPTVRTSEGSYVRTASSLNRNENDNTADNKYCERVMRPFVPGGMAQSAFPTREFMNKVKEVNKNDRSLIVRTSAFSKNSQKAERQNKRCVSRAAADFHMIVTKPSGGSIAKTVEQSSWKYSKRQEVCDAATWSSAIVLSHEGSPGLELMSDARYAPIYCQSITNTYRYGPCPSGFAQYDRKSTGQRWCHKFVKSSKNYDSAEDNCQTMGAHLSAFTEGEEVDFLDKLMAGASLDTWIGAKRRKQCMKKGSFLEDGFDRDVTSPCSRVRVFEWLNEVAPNPPAVEDDYWRTPTEPNYIAEGEDCLSIVPGSPRRQLNENACPRRFYSFCGLEAPIVKV\*

>Cbn|CBN31606.1

MRSIFVVLLMAAVVQTQFNFHGMSSFFSTDEEFPTQLQNFEGRTQTEIRTLKEKVEKLEKLVEGLQSILMKEWNTTESGSKYRLFEERKNWDNAERHCQGFGAHLAIIDNEAKNTFVTNLINSSETSDFAWIGMKTKTTTQTSTPFTNFDAESPIDGCAVMDAKGVWSIRSCIQLRPFICQIIKSDISI\*

>Cbn|CBN31672.1

MRLLLLLLYSTTINTIFGQLEEDWGLRKACEKTGGKYTKRASRQSSTGDTCEMPFKVATRDEQDSRDFCELYAPWRLLKTERKKDAGRHTTICHVEATLMCEENWWQMFGHCFRMPDKHMVFTRGEAENLCKTSAPTGTEGTIAFMHHKYIVGVWRRYFRGTPQIWVSATESWNEYIQKTKTVDGDALALAFTGKHYDFSVTANSLIRIDASIRLNTLCQYKPPITPAEINYLGRRYSQIYYPSIPVDNGIMVRSASSYTRTAKNWDVCKKVLAPFMIEKIGDFVPEDYVLERMSRVNLGLTYLTRSGAIRELDGNGEHQQKNDATCHAYLPEYKIKVQEDRRADFPIKNITIDQNQDCDNMLSAAINHKDKAKLQIMSDSRSLPIWCKLGRPERFQHKPPPPGFIPFLRSDGKYMAHKLHKELKKYDEAKTICEAEGARLTGIDARKEAEHLIKIAQNEGINHKQMWVGGRRKKECMDQERWNDNKDHICYRSRVIYWEHAMAREFEESWWKDGPTEGTKNPDYASGGQDCLTLVVGTPGWADPKSGGFLDDISCRDVHAFFCSIPLEMTKVLVED\*

>Cbn|CBN31834.1

MGKYRYLLIFFALFDVMYSIAELLTPIAVINTGYGFVTFITDGPFFDDVMSGQHGVASRCTFISLSYAILIIHFVYRYLLLFNPDHVRRFFEPAGVLILTLYFIFHGVSWTYICEHCLAPNEEIRDIIRPAFQEVYHVDADTVPCLTGQYMNASDYVVYKSWIGISSLTLFSSYCMTLYFVLGYKILTKINGLSTNNVAAAYIGLAQSSSGWGWQNGDTSTYNNWAKPPVTQPPTIGPTTTPFRSTLPPSEQRRSTAVVIGVDASLFSTNQLTFAQVDFITSLSHYIADRGPAEFAFFAYGCTQTSPYIYQYPNFVSTFEDTDKMIQTLKTTINQNCVRSSPLDFRSDADNIKAASALYPMANSSVITINVGATSIDVSRLSIPIGKYGLRVNTPEDITNLVPKVDSMIFGATGVSSAGVKVDVMKEDQWDFDVRKSEPSVFASSDYTDCAYMNTTDGLWYSDGTCATKRQVLCQYVLPLPPQPPTPNPTIAWQDPCYNEYTNFTYFEILSNAKCYRMSSSKKQFAEAENVCLSDHPLFLHVPKLVSIETREEEEQLKTLITGIPNEGMFWFGLKRDPTNSTNWYFINGDTYDASYSNWRDGYPRDADGCDCVALVVNDSSWINTDCNKPLYSICSYRFNGTEPTVKPF\*

>Cbn|CBN32010.1

MKFVVFILAVTLCSAQVDRDWSFQAFCGHWQGNATYKPREGYSSLSGDSCSLKFPMATADEESARQYCEEQVPYHINEAVPGSETICKAEATLICKAEWVQMFGRCYKMKKVMMTREEADAHCKKEQASIAYLHRHALPFRFYEYFTHVSQIWLEASEAITSDLIYDTPGGNLILAFDGYPYNLPNIALARVDPTQKAMVLCEYTPAMTQAESTYLLRRYGEIYYPTVFTSEGAYVRTASSLNRNENDNMADNKYCSRVLAPFVPGGKAQSAIPTREFLDEVKRVNRNDKALIIRTSAFSQKADKSKRVQSSCVNDQSSVFHIYSLEKAGSIKIGKSEWMAGEPTGMCDAASWSSAVVMSREGSPGLEAMSDARYAPIYCQSITDVYAYGDCPAGFSVYERKELGQRWCHKLVVDLMTYDDAERNCQTMGAHLSGFSSEDEYKFLAQLMGPRYSKHYGTMEVFLGAKRREQCMKLGTGKSRGYEKDVNHTCSRNRVFEWKNNVAPNPPVTDNFWMSSAEPNYYHIDEICLVMIKRKQGDKGTLNDIGCAYKLAHFCGKEAPIVKVSS\*

>Cbn|CBN32585.1

MKIQILIILLPVVTSAQLDLNSIRPCNVGCQDGWVPYSGNCYKKMFDVLTQSTAEQECVNLGSHLASFETTEEATAIRNLVLIAPLFSTDLLSYSSTSQDSWIGLSKTSNGAWKWTDSSEVEFTNLPDGTSVTGASCVSMNISGVWQPNECSSTVSSFICKRASATTA\*

>Cbn|CBN32741.1

MRLAEAHSYCHKLIGDGSAHVLRVECGGENDYISGMVKGHSDKVWIDARARFDIVDGAAGLFGPGFVYRWPNGKIVRYSNWADGNGLEEIGTSNKCVTIKNDGHWINANCSSTAAVICEKKLHRPYSKFCPKHWVYNKETQSCYRTISKTNMTILEADNKCFDYGFEHRQDAMLTSIGSEDENQFVMDLAKEKDANFEFIYLGGYGRSRNGNKWHWMDGSDFTYMNWDRGMPFGRRALAVLVMNKRGKWINHYADKILSQYNAVAVCKFKS\*

>Cre|FL81\_00190

RDMFPMRVIVETVRSQHCLTCSHEGHMITDTYAIVAGTTTLNQLVDTVLAALGHSSMANSARGLIQVNNWKPLPFDQITENLDETVENLFKDISSHVVLKILSKPTTDTNAVQCISEVKNKLLKAAVNKTPNVLTNVENQQVKDVINTIISGDETLLNSEQLGAVNEWLDTLDTAEDRRSPTQVQRFNTLFEIPRLEKWFKQDANPSKQKMNNYLSQLNQSPFRRNNSKISYQQMCNWFSQKRSSNRSAAPTDPVQVTPAQTTASQLLPGLQLNLLQSLFGVGVEPRPKFDFSLMNEKLDDNRILGGSDSPSPADDEIHSNSDETIQDNMFVMNIKPEPETFQESTASSPDMSNSMRESLSSTSPKLISGLDLGSFSNHSSSTNSMPNVNSSAARSRLMFDPLTELPVLEKWFEENPHPTWMQIDQYTQCLNNCAYRENYPHISQHNVKIWFKNRRAKCKRLLNGMQEKMEQKLFVKMLKFAFLALVLLGLVSGLDVDSQNKISERLSSKLLQYNSFGLPEVSQRFQPEFAAKSAVAATNAPISCYNRSIDILPHDGTAQYGDLVESDFSSTCSDTFTFYVDNFIDEFFVIITTLDALNPRATVYNPIGGEVSSCKDYASSATQSIHLICNGKNIHGTGAYTVKLAADMNKPCIFEIRAPTKLTVDGGFVEDIRDDDVQQIILSTANQGIFRFPLENQASYLAFKVESEEFPIHPEEVHLYTNGQFDIKMDLNLRYGCNTPHITQQSYNCTSQNLYHAKFRGYDSDGNRFQRIYDFNCDIGDVVFTTPSVDISTTPARFCENGGILYNDTGCYCGEFFAGVNCEIPLCLNGGTSTDGGCICDIGYSGDHCQHISCLQLSDDNFEEAQSALAFVVRASSSMKAQLNEIAEAADRIVKYYEVHYPIFFQKFVLTVVSNNGVTFSHDYDSGKDFVASIRNLTAPATETECDDALLAGVSATIDNNAFKKYPIVNTRTQIFFMITDSASGSCNVDVSTNTFDQLRSISRLSGGLLIQTTLLQLSDATFSVAQDIWQYDSILTNDLEDCRKAPQFQPFFVDQSIDYLTLRATGYNLSPILTLPNNTQLSLQLFYSNGDFYVWRTAKPPVGAYFLNINTNSTHNSICQYRLMGRSTYRLYTSITDNIGTDDTYHAPVFQTTSHLVARMDGLYLDDPLDTTIEAIVWYNDPQTSQRQILYASSGTYRDQCQYEMYFGMFSCPQPYLPLYINIYTNDGYGQVVLRTATSYCSATIPNPVDSNCLNGGVYYNNTCQCPTHFIGDKCQQILCENGGNTLFGACQCPSGFSGQFCEVTKCYEYNGYGFWGFNHRSLTVMIHDSLTTRSTLRTLNDAAPRVINDILYQHPKWISNYQLVEFNATGHTLLVDSESGQDLVTGISSLYDQNRNHTSYSCLGLNFYSTLLDTISHDNVQWGGIVYVFLYGQPVQDLDSYEKILQRIEINKIQINIVQSSLNPCGQDIALDGLISLTQFSGGAFITATTPNAGNVFNQLPTHYMSSLIYENTALDCTDTTFYVPIDVGTQTFTAYVQGYLNADPVYTPPTDSLSTVTNVFNDLGTNARIDHIVRVCDDGWTVDGSHCFKFSFEEKSWFAALADCHSEQAVLTGVFNQAEQDGLNYGTDGAQFWIGLNDVLGGQWEWDTLDDKLNLTLQDTQYTNWETGQPSADPTKKCVVDSNKGAKNPSSRGWFTEDCTKQYYYVCQKHAYSADYIASDPEINSNRLVVYTYGVKNPSGAEYAHFYYDNFTMLEAQTLRYRDNCMYNFISTPFKCPNFYFQMLITGIDDAGYLYQRVVPAACIGGVNEDSCTNGGVYYKGKCLCTPNFYGDACEYAYCQNGGYLSATLDQCSCPSNYGGQFCQTPICDRNQLNVPAIGDVQRTFIVILDGTNNDAMKTVNDNFEKTLNGVLNSIQTQDPSWFTTFVGVVFRDAESVKANPSVPSTSQVFTSKNSADFASMLATEVKNNPYTAQQQKRDVFTGIVKAIINSNVVPNSKVFVITAGNAEDTIDRQTVISALALSHSSVNFLFIGDTKPPGDANTYDDPTVTSLFEAAHITGGASYQLTSPDDLQTTWLSILASLHQSYYVAIVDIFAQQAPQIAVLDTDNKQVESFSIVQSKTNTVRAFKQNGEQPGVWTIDVDYGMTNSGPCTLNIRSQSKLEVDLGFTQDVASDGGYHDGGAVLFPRGGDFVNAVVADISTGGTLTYAQIFDLAETRIAWASPMIKRDGCAYPFVSEYTFQCYRNQFVVALDGFDFEGHPFRRTFTIHCDGDIRPPPTEPSFSTTPEVTTPAGPTPKACDATTATVDIIVAFDSSDTITEDMYYATIGALKSIGNAINIGQDRSRIIMGTYDATSHFNGDLNTIDSFDKYQEEIADLFSLGYTGINGNNIQSVFDYIVAENNTAPLRPAPARKLLVLLSSQGWDKGNVSDGKENGYPDPTASAKALQQIGFETFAIAVGPTANLSQLTAIAKCTSQVTTPTALDKTVAQIISSLCGTTPVC\*

>Cre|FL81\_01778

MRLLLALFLLVTAVAAAPNHDSAFQNLPNYYPELKHQEPIHIRAKRAIFAAIGISNTCEDGWTGDGCKNPICTDPRPAPSSGQSELIELLFLKGSCAGSYYIPVDSDVGKTTQTIQIHVSASGVPYVNLTDSKGMVFTPTYTNNGDGYALTVFGDLPSGGYSLTVDNQNVPTTECIIEVNAGTSLKVSQGFVYSPQSDYTPQGESGIDGVPMYAVVHIASQQAPAQVHSITIRQGNSLEPIYRAALTRRYQCGYEFYAGQWQCQLKNSYYYHIDGVDSNGFNFRRTGRIQCMEHLTSPVPPTTTQAPLTSCFNNGTLLNVADQGQTCFCPELFSGRQCESVNCMNAGFPDPDMNECVCAAGYHGTNCQDVTCPLNWESFLTNYKTLVVVIRNTVSMNKYLDAISTAIYKELTSQAGNNYEVYKGFVLVKFGNGVYTNTYYPAYSQDKLLSDIKIASTTVGQCSDATFDSIASIFTEVAIYQKSPIYFFTDAIASDVEKWQTVIEMNTRQKFPIYTHYFVQDNCGFDDMSQGFQAIEYASYYSGGLILQPAPDALEFIFQNVIKATAYKMNSVLIDDLASCSTPTRVFFVDSSTTELMILAIGQSLTVSVTDPNGNTNTALKIVDSGTTQLYEISNPVIGEHLITVVSNVQNTPCSYRVQARSEYDLFIGTSTGVNDDASDSEPVVGQSTHIVAQLTGLKGKVADPFRLFSEISITSNVNLDNTYQKPMYYSSGKYRDGCGFHMYFGAASFCDFMSQPFYATVYADDGNGYTIQRTTTGFCSGTPTTPYPPNSCQNGGVTDPTNNATCICPPGFYGKYCENIQCTNGGTARGGQCVCPVGTAGTFCEQYMCTTMNNNPDVSFNGQSIAFVISTRSTMKDSVAKIAANVQTMTRDMQIASDKWINTWILIAVNSNTSTLLVKSNRPEDFVAGVVNLSANFSNYAADETSCQIQIEQAMLGAALLSEKRSSVWIFADSDGPNDSSYIQLFDVAQEYQIVLNLVGVGSSICTAAENNGQFPYYLKSLTETTLGSVYMTDKLDQVMLFIVSMYKSAVSHRYYVPDCTKATSYYMPVDGWTQSLTLSVIGTDLYNVEVMFPDGTKGQNSDYELVSINDPELKLNQYVAACEGSFWNHQQQNCFEFTATKYAWLDGWDFCHSQKAYLIHIDNADVNKFVFSQVNGYRAWIGLAFNAGQWYWDVPDGNFPQPLTGYTNWAPDVDPANPKYNHAVMNSNGFWEPADPNEENFGACMKHRYGQGYYPGEGVNIVPAGLWKVTVQSNSGSCEIQARSQSDIQVFFGFVTDPRNDKPSTYANIQSSNNYLIAYPTGVLPYTPDTKPSMEGKLNYAVLSSNRTITNSLPLGNRVCTYATISAPFSCPVTDGSISEFSIKFTGIDQYGYAFERYGDALCTKTVISCANGGFVNNGVCVCRAGWVGTTCSTPVCQNGGIEKNGACDCSSVPQFTGQFCQLAHCEPPYPTSFNDKGRTLAIVLETSYNMGSSIFQLKRNLKASLDSINNDATLQGWFNNFVLYPFDSTSNQASWYPPTISRNSDDIVAAVKNISTMSCPGSAPCSSQCPRPIVSVLKNVLDMDALASPNSVILVITRSSPEDYLQVGQIAQKLQDKKAYINFAFPAIDSPCGEGWNTPNVDSLYQIISYSQGNTFTMNAVDLSKNFLTQYIPTLYSSGGIAASSGNCNNDEIIFQVEHEMYEFSIDFYHPLMENIRVFDPSGDELTKPDSVIASDTNYIGVFPVNETGATRAGTYRILLTGTGGNNCFATVRGRSNLEIFLGFVDSAADSNNGATIDAAHHAPINLENNTIVVHANGLGQGIVRYVQIVMPGFGLMHTTEMRRRDAECSYEWYATTPFSFDYDSYYVIVYGSSEFGSNWKRNFYVSTVGSRPPLPPPPASCDLQQVKQDTLFLIDSSLKDTNVTFTILKQFAVTAMQPYNYMNGLAQVASILVYGQAQGGFSFNAGENSYDRVSGLLNNLTYIAQPGQNVTAGLQYALDYYDMPSQGYRTDPDVKHLLVYVTNTNPTDADPSELIRTMKRSGLYDVVVVALDMQPSEQLTNMVSSRCYYYAQDYHDLMNYGVNLVQGQSCMRFNFCNY\*

>Cre|FL81\_01910

MRSRLWPFWFSLLYFLSLSEVVAQRNATCSGTVVLNATKDFQYLTTPNYETSYKYPAFLDCKFFIKAPDKSRVVIDIIDLEMEPRIFEECSDFVGLSEDVTEKNFSRIITLCESLRMRQFISTSNTITVIFQSDELFEFRGARLSYRYYELPSCPPGWTELSNETCVRLETDQKTDWVRAQNRCLDQRSNLLMLENDAKVNELEKLYKAVPTKLWTGNNDAAIEGKLVDISSREAPHLISQTFSSLTDNNDDNDCMTLQFGDTEMLRMDSCASLNGYICEMKKDGTSVLYDPPIEEIKGGSFSKTSQYTLWILLFLIGLLFLTILAFLCFICWKQKDARVHTENATIQQNAFMSDSAHRADQPRVAAPGQNTVHIANDTNRTARSSPVVVPIENNRPPPKKFPMAPVPNRLPMHEEPSGSEPAVETAILGGDNDIETVSAAPQPQPRTLPPMPTREGTFQSINTRDGSTMRTRRNKELFERPIMHVLDNVSAISLDEFWSNKKP\*

>Cre|FL81\_01945.1

MRTWVLIAALAVVCLAAEQELSHKERVRAVLKSWDPKADTKFFEPIRQQKYRTTDESDLFLDTHHISKRSIAQPHVFAGQATRGCNLPGYTGETCQYPLCSARNPYVPTNQASDDVQIDAVNIANCSVPYIIVVDETMWDIKIELESEVPLNPTFFLQYENGDIISPDSDRQLPTSYTATYAFLAPGQYQLGSMLPGSTGQEYCTMQMSARTPMKISGGFISGNQPERNDYPNLKVAYFDTESVVAVHVQALEFPGQIQGIGFTGAENHISRYIPIGTRYNCTYPYILERYTCKRTSNNDVGRNFLQVEGISNGGYLFRRILSYQCVLPPVSTTIAPSPTTPTPPLTTCQNGGQLLTDASGAPYCYCFGLWSGNDCSQMICANGGFLPTPTSDRCQCPEGFMGFHCQNIICTDTSGFDFNAENPTLTFVIRSRYQLSDVIEQVTNATDEIVQELASEPGYLSNFIVVLFDNGKLLLNKRYDSWDGAKVDLLKAIHSAPTDGGCDDVVFSAVASALSLYPTNKSPIYVITDANPNDNAEKETVFHLESYWRAPVYFIYVQPGPADGCNTSPDSSAYRDMVDIASRTGGNTFYFSNRTNISPFFYQHMLNTLFRSQLVLSGDYSHCVNQNIYKTAAIDLTADLIVVVATGTDLKLVATSPLGSYPDFNIAFTDGVNYIWTYNNAVNGQWFFTLLSGSPNAACTLKVYQKKFNFGGMTQYSPDYDIFWSFATTLTSAAGILRQPVLGFDASPVFHVSNYPAFISMDRVHANLQIYAIRDGLQTEVYGASGMWRDACEFNFYFPPFTCRVPDEVLYFNFFARDNNDMSLQRAGTMYCASIHPTPPPDHQCQNGGVMNPSNTTCFCTPEFSGTYCQDLVCYNGGTNKGDHCVCPPGYGGESCELARCIETGPTPEFIRYGVDMIFAVEITQNSQTTLMMLDTQFGNILRDIQMQDRRWIRNFVLVGFNSTWGGPIAEAPADNLTAITDAMDKIRSSGSTDTGCTVKLWDALNHAIFSRELIPGSFVEIFQTTPEDDTDTRSLGLFYDMSRRMDLVLYGFLVTNPLLKPAGFVCNAQIENYYTLLGIVGGSTGTTYVIQAFEILNAVKTIPIQFSSGQVTFNYDNDCRHDDGLITYFPIDAYSQTIQIDTFGYGTNIAIYTGDGVLYSAYQIMYDSFTGQGIYEVRKGCDKDWEEYGQYCLRFILGNDNVLPVPQAMKFCASAGGYLVDDMDAGQNEFLNGAAAYTQFWIGLYRNNDGQFVWDRGTGVTPAPLSQTETYWADNEPSNDPMNQCVYYDGRADPKKAWVTDSCSTPRPFACHKNRYDPEHRPNTIGEDDLPAGQWYVMVKSNPGDGYPSNCSVSVRVQSSLQIVTGYSTSIGDDIPQPDPIQDSPNNRLISYVHSLDNENRVPILTDAILWDAYTGNFYNGLKYQPRFACQYQWVSQDFPCPNGDNPANEFGVLHVGEDEFGNTFQRLTYGHCSKAQITCGNGGIRQNGVCVCSEYYVGSRCTVPICVNGGTRNSDEATCSCPDGYAGPNCQFELCQPTLPQLFSNDRKSLLFVVETTRQNSDTVNQLIANIKSIVSSATSSTPLWFTNFGLVTFDTTGRTFEEFDYTNIDDLIVDLKAQSNGINTDGACSMPYLGVLAHLLEHDDVIAMPNSEIFLVTAAGPADLDKYVEAMTTLFNAQAHLHYVVSKSAGCPTFNGVNNVEDMTWLGYGSSGNILFTNPTNLVNLLNNYLPTLYGASVLQDPTGNTNYTCSNSKWLVPVDMNTTFIYVTVSSEFGSLSANSPLSTGVTPEIIYNVDDQKVYRIEVDRLGGIWQLGVNSPGLCLAHIYSTGGAKVYTKFAQPNSAGGKPDPLGAHKDGSSVQPAAGFDNTAVFHIAGDPFHNGQLQYVEIFDIGSNTITNILRSELYRRAECSYEYYSDLFTCNGDMIAVFVHGVDEYNQKFRRQEIVICNGRAPVTNAPVTGTIVPVTQLTQGPVTQVTQGPVTSTTPVPHTALQFDIVFLIDGSQTAQDSFDWLTKFVQTFMVSFNVGLNGARVGLIVVAPDLDDQPPPAAQFNSITSQASLISNLNLLKENYADFDHAGQVLTYNLQIVTSNDYKSAGYRSNIDNHVLVYITTNTAFYTDPTPTAQTIIAQQQYGIITIGYGTGFDNNKLQTISGGAACSFTAPDFARMRTWVLIAALAVVCLAVEQELSHKDRARAVLKSWNPKNDLKYFEPIRERTYSISDDFIVETHRSKRSIAQPHVFAGLATRGCNKPGYTGDTCQYPLCAVRNPYIPNSQNSDDISIDATNLANCTQPYVIVVDETMWDIKIELETESPLKPIFFLQAENGDLIYPDSASERPTSYTAKYEMLPPGQYMLGPMAATGEEYCTMMMTARTNIQVTGGFISGDQAERSDYPTLKYTFFDTESVVALHAQGLDFPGQIQGIGFTGAENHISRYIPIGTRYNCTYPYILERYTCRRTSNNDVGHNFLQVEGTSNAGYRFRRILSYQCILPPVSTTTVPAPTTTAAPLTSCQNGGQLLKDASGSPYCYCFGLFTGNDCSQMLCANGGFLPTPTSERCQCPEGFTGYHCQNIVCTDTSGFDFNAENPTLTLVIRSRSELSSVIESAAGSVQSIVDLLSSEPGYLTNFIVVLFDSGKLLINKRYDSWDAAMVDLLKAINSAPSDGGCDDVVFSAVAAALSLYPTNKSPIYVITDGTPNDNGEKETVFHLESYWRAPIYFIYVQPTTAENCNSSPDNSAYRDMVDVASRTGGNTFYFSDRTTISTFFYQHMFNTLFRSQLVLSGDYSHCVNQNVYKSVAIDLTADMVVVVATGTNLTLQVTSPTSDRPTFNTAFTDGVNYIWTYNQQVAGQWFFNLVSGSPNAACTLKIYQKKFNFGGVSQYSPDYDIFWSFATTLTSAAGVLRQPVAGFDAAPVFHVSNYPAFVSMDRVHANLQIYAIRDGVQTEVYGSSGMWRDACEFNFYFPPFTCRVPDEVLYFNFFARDNNDMSLQRAGTMYCASVHPTPAPANQCQNGGVMNPTNTTCFCTPEFTGTYCQNLVCYNGGTNKGDHCVCPPGYAGESCELARCLETGPNPEFIRYGVDMIFAVEITQQSLASLVMLDSNFQEILRDVQMQNRGWIRNFVLVGFNSTWGGPIATSPANNLTAISAALHSLATTIPSDTGCRVQLWDALNHAVFARDVVPGSFIEIFQTTPEDVLDQRSLGIFYTMSRSMDLSIYGFLSARPQSQPVGFVCNATLPDYYVLFGIVTGSTGTTYILQSAEISNAVRLIPLQFSNGQVTINELDDCRHDNGMTTFFPVDAYTQTIQLTVFGYGTSIQVYNGNGVLAEALELFSDDFTGQSVYEVRKNCDNGFEPFGQYCIKFLAKSEDTMSMPQARNFCATAGGYLADDLGDDKNNFFKTGSANTQFWIGLFKGSDGQFYWDRGQGVAPDLLNPANTYWADNEPSNDPTRQCVFFNGQAGDVHKTWVTDSCATVRPFICQKHRYDADHRPNTIGDADLPAGNWYVNIITTPPANMPNYCTLSVRVQSSLQIVTGYTTSVSDDNPQIDPVQDSSANRLISYVHSTDNENRVPILTDAILWDAGNGTFYNGLKYQNRFGCEYSWVSQNFPCPNSDNANNEFGVLHVGEDEFGNTFQRITWGHCSPAEITCGNGGIRQGGQCICTDYWVGAQCTVPICVNGGTKNDDERSCSCPDGYTGLNCQYEVCTPALPQLFSDDRKTLLLVVETTRQNSATVTQLIANLKSIVTSATSFAPLWFANYGLVTFDSTGRTFENFNYTNIDDLITDLTAQSAAISTDGTCSLPYLGVLAHLLEHDNVIAMPNSEIFLFTAAGPSDLNKYGETMDTLFNTQAHLHYVVSQSANCPTFDGVNNVRDMTWLGYGSSGNILFTDSNNIVSLLNNYLPSLYGASVLQDPTGPTNYTCSDGSLPWFVPVDANTTFIYVTVSSEFGSLSVKDPLGLAHNVNPAYSVNNQKMYKIEVDRLGGIWTLQLVNPPGLCLAHVYSTGGAKVYTKFSLPMLVGKNTDPTGSHQDGRNPVPIAGFENVATFHLSGNTFHAGQLQYVEIFDIGNNGGATNILRSELYRREKCSFEYYSDLFTCNGDMIIVFIHGVDENNQKFRRQQVVICNGMNPSTGQPVTGTMAPITQATQQTQGPITQQTQGPNTQPTPQPGQSTTQPPVTASPSPSPSSALQFDIVFLIDGSQSAQSSFDSFTKFIQTMMVTFDVGLNGARVGLVVVAPDLEDQAPPAAQLNSISSQSSLNSNLALLKDNYADFDHPGQVLTYNLQVVTSNDYMSATAGYRSNINNHVLVYITTTTAFYTDPTPSAQTIIAQKQYGIITVGYGASFDNNKLQTISGGAACSFTATDFATLNNQIKPIQQLIINANTNGGNYCKSN\*

>Cre|FL81\_01976

MSPTLISVFLLVLIGLHSSVSAASCPAGTKIYNSKCYAALGMDMTRDNALAYCKKTYGSYARLTTPLTYAENNFVTEQVQLHANWHTWLEFVADGTYIVGDDGRPPVYTNFAVGEPFSVSLGYCITIGMNGYWYAQPCTDSHSALCEFDLVPPTVKPTIAPTLAPSGYPSCVQKYLNFVPCLSGWDYYPPTCSCFKIITNTTYYNAMNVCRSIGGTLASVHNAGEAAFITRLGAQANSYWTLTATARDNIIVGLTYNSDRKIFQWDDSTVFDYAQGFAPAEPADYTSQGQIVLSNPMGYATYMRMGNCAFQTCRYAACKRYVY\*

>Cre|FL81\_02592

MIFHFSESSNLHYSPQPLDLYPLILHLVIKLFNWSYKDFGTSAFSDISLEQRQRFADFPAETGTCPDGWIRFSDSCYWVEQHKQSFAEAEKRCYEKNATLFVVNSQDEWDAVREHFPQIGYTWIGLVRFTHRERSEDTPTWQTEGAVNPAKLNWLIRPYKPVSNGWSILSNCAAHYSASLNLDASAYTYYQPCSFKYYSICERNSTILDFLNRKFDIQA\*

>Cre|FL81\_02666

MLRVLCLTIACFLALVAGGCLPGDASFESYCFSFNRLQGRFDDAQAHCVKSVGGSLVTIYNMIENNWIQKLAVDNLDADYDLFWIGASDAIKTNDWRWRDNSKLNFTNWNRGQPLEDRHCAAMSVASGTWFTEVCTIQHQFMCQYPNGDYPTGAPYTCPPCQACRFF\*

>Cre|FL81\_04478

MNLLFLIASLFSSFLIVNSTVTCNYGDTEYDGYCYTFVDQQLQFPDAQAYCVSLGGVLVRFRGNADGRWLTSTAATKFHATYGNFWIGLHYVKNENNENKTLIWDDGHDVNYTNWSSGSPFSGYDYVGARLADTKWVSLLAETPLPFICYYQKGQNRNQPTTPVPSELPTGICDGAELLLGHRCFFFNPTLLNYDLAKQECEKARKTLAIFDDFSQINFVTSTAISKFSMTYGSFWISLRKNSNDENDKKFYWADGSVNTLNNWTPGYPFQNQFVVSLQVSNSKWKTSDNSTYMPSVCSGYVQ\*

>Cre|FL81\_04479

MIVSHFYVIINNEFESQFVINVTFFRFKMTSMDLIGRESGKDKTLIYLLSQTAIKNKIKCHTNIIKNRKQHQETTLQDHFNIMILSLSLFILGFIGLSETATCRYPHEKFIGKRCYSFVSKRHPYAAAEEYCHSHGYALATVDTAITANFLASTAATEFGSNNGQFWIGLSRKKDYSLFYWDDGTNVAYTNFEAGFPNTKDYVAENTLAEHKELEFVCSYDPLSTTTPAPTTTPTTVKTTTVTTTTTVKKTTATTMTTPKPTTTVSTTTTTTVPPTTTAKACPRGFTLFEPTQKCYIVLVYGNDSDYPVVPDDAPFLTKENQRCAKYGATVATVHSSGLNDILRSLIYERFNDTRYATIGLRNIDMKTIGGKWAWFDGSATDYLNFGNMFPKTGDFIAQTSSQGFWVTYTHTAPNEGVVCSVDF\*

>Cre|FL81\_04694

MTGSTDDSAPDTSGVSRIFWNYEMTPYYGAWCYEIGLHYLEEGRDDQLNQVLSTPYDLAIVDETYTSLQGAISLKLKENHGTKIIAFATTELMPVAANMRGYARNPVNVPNTFLLSSEVYENNRNGFFSRTRRIYEYLVDQIYSGPIASRNSEASGKLLGLESATKSRIFENSLLTVNDFPDTFSFIQSRGNDLIPVGEHCASSENLPSDFRNFVEDPISKGTIYVAFGSYLNLEDGPEGTVESFVEALNYFEDYRVIWSHKGNVTGAKCHVKFVNWAPQKELLAHENTVAFITHGGLKSAKEGVCSGVPMLFLPFYGDQPRNAHRFVTNGIAEALYKKSITAVDIKQKLEKLLEDPSYKENVVKTRSYYLDSPMSSLNLGAFHISRVLRRPESQFIRFKRRSISMTHLQYLNIDIIFYSFCYLMSPLISYNFPSSTTNDHGLGVSEKYHRAKYLETQQKLSDASQPSLVLAADGAILPCDANWHQYPDTGCCYRISDEKSDWYGGTNICKALNSDAQMASFHSQAESLFFANKYSSIHAWTGLSQTEVPNTWTYTDGTPDWHWFPALTSASSAADSSCVEMMDGLLGLLFALSLQKGQTNPYSCTEVNQIICKYCPKETTSSTTTTTTTTTATTTTKTTTKTTTPTTTTKATTKKTTTLPSASVTCTSNCPAQSVNFNGKCYKKCRGSVKFEDSCNECGGTMITISNKAEKDFVSRVFGENDGTVSQIWIGNTESNGYLDWEYGQPSKPDNSLDYCISMDLTAVDHVDEFLQNKTFNDILEMSQKFQRARYLETQQKLSDASQPDLVLAAEGAVLPCEAGWHQYSGTGCCYKKTDAISAWYGGTDLCKALHPEAQMASFHSQGESEFGTPGVWTYTDGTPDWHWFFAQSSTMKPESSCVEMLDGVLVYLFSWSAKKGQTQPYSCTEEIAILPERNNFNEYNYNYNNDNFNYHNNSHHYNRNYN\*

>Cre|FL81\_04696

MTNFQKCRGSVKFDESSDWCGGTMVTISNKEENDFISRVFGENDGTVSQIWIGNTESNGYLDWEYGQPSKPNSALDYCISMDLTAGPWRGKYKYLPCESTVVSSITSMNP\*

>Cre|FL81\_04698

MLFLTSILLLVFANLCSSVEVNPCDSTWHYYNKTGCCYKTSTDLGTWFDGSAICAKMHVGAHLASLRNEDESKFVAKTHRNGLDGIHAWTGLSQTQNANNWTFTDGSKPWSSFMTPYIFPNNHTSCVEIVDNWLVELFQNTGKTQPTFCYHYRKSLCKYCPVPVVPTIITTTTVRTPAARIEKAHPRSNQPELVSGCSSGLAANQVPVIPVSNATTPVPTTTKTTKAGIISAASLHTQNGNQSNKTRSI\*

>Cre|FL81\_04714

MRFYFLVATIFSGLLFSQAAPVDVVDGSGEAPDTLLQNTEEQPHQRLRFHNWDYKDLGTTAFEDIAFPARQPPAAVNQTEQCPDGWVRFADSCYWIETELLGFAKAERKCFEKQSTLFVANSLEEWDTVRSHSKEAYFSWLGLIRFTHYEKTEQNWLIKPYKPLSNGWTQFANCAASYKSPASLESASYTFFYPCTYLLYSICERNSTIVNALQ\*

>Cre|FL81\_04808

MSKILMKILIMFNILVFTNGQVDRDPSFQSMCEFWNGKDSYRPRDNGYKSMSGDKCSFVFEVATDTEASARRYCEVNVPYHINDAIPGERTTCKAEATLICKNQWVQMFGRCYKITKELMTRKDAGEHCEKEKATIAFLHREDLAFRINDYFKFVSRLWIDASEAITKDVIQNVQGGNLLLALDGFMYNLPNIALAIVDSSEMAMVLCEYTPPMNQAESNYLLKKYGEIYHPTIVTSHSSYIRTTSSLNRNVDDETANNRYCTNVLKPFIPDGKAQAAIPTRDFLNELARKKVGGIVRTSAFSARTTKTDRQNRQCVRNSNSIFHTYVSGLNNKGGYEPVESSEWRQNEPNEMCDGATSSTAIVLSVVDAYEYTNCPNGYQMFYRKELGQRWCHKYYNGPGVPMLNYDEAQAKCASEGAALTGYTSPEELAFLDDLLTKGNNLNRDTLIGAKRRDDCPQYGNKYSGGFSPDVTHRCSRKNVFEWKNGVAPNPPNIEADWAYPDEPNHGYDDEKCLVLLKGANSDHFRADMTKKLNDHSCTKKYHYICGMEAPIVKQ\*

>Cre|FL81\_04978

MSNLVPVHKSLESSLVDVPLLSKEVDDSDVFETSHSSQFQMFQLKHLVTLSVLLIGVASRGCFDADDKEISGFCYKFVNQKLTFEDARDWCHYKDPVTQSYLAYIQNQFTANFLASYGKTIFGSTDATFWIGLSRERNWMPFTWDNGYQLGQSWSNFDGQIKQNYVAERVSNAKWTTFAENQTNYFVCSYDPTDPPTFAPKTPTRPTTTTTTTTTTIGPTTTGK\*

>Cre|FL81\_05261

MFQPMLLVSLLLLPLISAQCGPGAVFQSSSSRCFTFFRTGVDFQSAEAICATLNGHLVSIHNAIDNAFVSSQAQKYFDGSAWLGAKTTAPDVTNPLNWYWTDGSNFDYQNYRVGEPSAQGATACMQLQTGTAKWLTTNCSTQLPFICSYSSSVTPTCPTVTIPSHCPSGYTWYDETDFCYKARKSTVRFTNFNDARSACQADGGDLASIHSQAENQFLVELSKAGITNKDKGHNDDVFIGLIYQNSKWQWTDGTAVNYLNWGDGEPNNMEKEWWTSLVADPHEDRNTEDTRWNNVAQVDMRAFICKRAPLH\*

>Cre|FL81\_05393

MKTALILAVSLVFCHLIPSDGGQCQMGWSPLYPYCYKAFHQRAIFGEAEGICTANSAHLVSIHSLEENDLVKMLTKTGHLPVSYWENYVRIGLFYNTATNLWAWTDGSPTSYLNWAPRAPEYMYNMQYHAALMPDRSYNDSDYNKEGGQWYNIQNWPTRAFVCKKLNYEH\*

>Cre|FL81\_05692

MRPSILVGFFLLTLSGIGAVSVAKSTDNDIVLKVSTDKQTSRDGHHFTGEWLESPWGDLYQFRAGDQNWLVAREHCLSLNADLAAIRNVEQLDWILSHYAPLSSRFGQRLVQIGLYAPEGQTHEWKWLNGNEINKTLQWSSGEPYDHSMEGRERCGLLNVEKRLLDDVDCESTSPDHHAQRYICQRTSESHKQQQRSNNYIWQKIENLFSFFGIGGSPTPHNATVTNTNDYEDEVVKNETSTAKPAVKFSDSEETSSEEEESVAKTLAALPKIEGSGESTSLKELQEPEGSGQIVDKKAIEAADLIPGVDEKKLDKMIDKMEEMIKSIDDLTVPPAGLERTTVSTIVVKKEEKFEEKKKTDDKKEEEHKKDKELNDNKISESIEGDFDHEQSKDMPKADIEPPKEEDCDEEDGSGSGEEEAAEEEESGEKLELAPEKEDKIKEFLGVLRLFLDRAEHGDLRKLLDDQSGKTLLERMKNAVREANKREFEMLEKLEISKKKGEQDEFVTKKDQMSTEEQKDLYKKISSAVMKAAKLHKIEEKVQDEQAMEKFNIAKVKADSEEESEGTLEVLKSAREGKAEKKEKVGDDDYYGDYLDDNNVIKVQNREKKDAKKGSKEKNASEDKKESGEKKELKKKNEQSHDEPKKEEVEKKKKEKKVEEKVESEEKKKEEESMKEEKPTEELKKDQEVNAEEKNVLKQKEEEEKTTEETTTMTTEEQEKETTISVEQSSSVSSIKPAEAEEDEAELEASGQEDIVTTTESTTVAIKEVPSEEIEKIAKLEAKQLVEDEKVTEETKEEATTSIPSSSTESEKTSPSTTTSEATTPTSTTPVTTTKPVTVAIKTVSPEEMEKLSKIEATEKVTLLPPLPTFTFPTLAPFTFPTLPTLATAKPTPAPKVPTLEEILGNLNDQFKKLLSPPKPLPPK\*

>Cre|FL81\_06741

MVLFLLTIILILPELARAQLKCPPGYTLVNDKCLMIIETPLTHSRAEANCTFNGGTLVNIRNAITNRAVTQFAATAGIDKTWIGLFCFENKNTSMCYYDDNTGPILDYNSFASGYPMVDGIYGGCVYMPTSGSLAGKWVSVKCEAESIPVMCEVPVSVYDSNCAHNFNGYCYTPSSELPITTAKFADARKICQDKKSDIVSIHSKREVDYIKSLYRGSKSQVLIGAQQILPNTYTWLDGYDWNTFDYRDPLDQQRTDYNCLTMDSATAPQNPSDFSNCNTTLLMTPGTITSDGYLSTSPPEPAVYCTWRIVTTGPYRVRLLGIAVGVFICLRRRKGKSGGGGGKGKK\*

>Cre|FL81\_06742

DVNKTYMNLLLAIFLILPVLARPQDQLECPSGYTLVIDKCLMVIKTPMRHLEAESACTYNGGTLVNIKDAITNRAVTQFAATTGIDKTWIGLFCFENKNTSMCYYDDNTGSILDYNSFASGYPMVDGIYGGCVYMPTTGSLAGKWVSVKCEAESIPVMCEVPVSVYDPTCAHNFNGYCYTPSSELPITTAKFADARRICQDKNADLVSIHSKREVDYIKSLYRGSKSQVLIGAQQILPNTYTWLDGHDWNSFDYRDPLDQQRTDFNCLTMDSATGLWNRASCDYEYAFLCKRPIAWSTVKPPTETVLAQNPSDFSNCNTTLLMTPGTITSYGYLSTSPPEPAVYCTWRIVTTGPYRVRLSFTDISTYNDIYVYNEDGTTFARVRTTSNFEQGMSIPQELQAFMAYGFGKELPPSEVEKGHKFCNDLTSEQHDKLYEAFKGTCEKYLDTESYKSGKTNTAGYIICCDSFGMCGMSGWMIFLIILIVLLCLAGAAAAFWNLVEAKQYFANHDFIRPLSAAEMERGKKFYNELSSKEQNELYSLFDASCNTYLDSKSYNSAIREPDMYSTLCLAGAAAAFWFFYYKRKMGGRDEEKEIESTADTANTGHDISVETY\*

>Cre|FL81\_06749

MYLSRSSESTRAQWVTTWCNNDRNSMMSLYPYICEAPPTEEGTVAFSCEFIYNGNCYFRSAGLGFGYSPSNATEAAYACPHYNGILTSIHSKMEVDYIKNIYRGTNISRIYIGAQSALMTDRLSWIDGTDWDFDYMNPLDTNRGMCLVMDVQGDGFWSRVDCNLQFDFLCRQKIIPFTPEVSSKETHPEIVLDSSNCNSTFVLSPGSFSTFRWPQVPDVMSYCTWRVASLGPYRVGIFFDYWGTYGSLTIYDEFGTNIGEFSGIYEREPFASFTPFNYATVKYEPGNATGGNRDTGFHAVIRPV\*

>Cre|FL81\_06791

DNRAVSTFAASAGATTVWLGMFCFATGNTTTCYHDDNSGPLSYNSFAAGNPAIAGNGGCVYMQTSGKTAGQWLSAPCEVVGMPFICEVPLTNADPTCTHNYNGWCYMASHEMQLATVNTTYVRAQSICQSNGGNMVSFHSKPEVDYVRAIYRTSGIQQIFVGAMAFLPDTFDWSDGSVWDFDYTDPLATSKGNCMTMDLSSRPNNGMWSETNCQNINYFLCKRKAGAAQPASTAKSMVEDEDNSVVEQEKPVNPKFVRTLKGTITSFGYPNTRPPITSCTWNIAALGPYRVGIYFTDFSVYNAVYIYDEFGNLITSPNGNMRPFQVLGATNVVKITHDSRYDAAYNYHGFTATILPF\*

>Cre|FL81\_06792

ELSDAKIACPTGFALVNQQKCLKIFPNHLKHLEAELDCTHFGGTLATIHNAIDNRAVSNFAANAGVQNAWIGVFCFENQTTSCYYDDNSGRLSYNNFIPGHPRLDNGYGGCVYMTTSGKNAGQWSNPTCLHNFNGNCYLPSHELTGSPPNATYSDARGICHSNSAELASIHSHQEVDFIRTIYKDLDFYSVLIGGQVSADGNNVTWVDGSDFDYNYMNPIGQTDGNCLQMNTIKSQTNNGLWSKFKCERINYFLCKRKIGDAVNPKFKITTLGYPNSVEGIFCTWKIGVLGAYRVGIYFTDFSINGALNIYDEYGNLIEAPSISRYPFQALGPTNLVSMTHDSRYDKPGLYHGFSATILPY\*

>Cre|FL81\_06793

MNSHILFALFSLFCSTYAASTPVCRDGFKLVNRKKCLKSFPDYKLHDEAEADNRAVSDLAGGHSNPFVWLGVYCFSNVTTSCYLDDNSGPLTYSNFATGYPKRDAQYGGCVYMTTYGPDVGKWFSSPCEYTGLEYVCEVPSTVDDKACTHNYNGNCYLPSHELSINTPNTTYQTAQNICKSINARLVSIHSKSEIDYIKSLYTNSGIQQITLGAQAFMQDTFDWTDGSSFDFDNFDPLATTKGNCLQMDLSSRVDNGMWSQINCQTVNYFVCKRKAGVAVTVAKKEEQEEEEEEKDVNPKFKFQMVTEKRELPIQHLDLSDLCNSTLFIAPGVITSFGYPAAQPPITYCTWKVAVVGAYRLGIYFTDFSVMYPVNIYVEKNNLLASPKYEMKPFSVLAPYNMVTLTHDSAKDAELQFHGFSATILPY\*

>Cre|FL81\_06795

MPKLYSLFFLFFNLFSIIHASEIVCPSGFQLINQNKCLKLFSTNLKHLEAELTCTSYGGTLVNINNAIDNRAVSNLAASTSATSIWIGTFCFSSRDISTCYNDNGSGNLTYTNFAAGYPNVGEGYGGCVSMQTSGPTAGKWISAPCEVAGMPFVCEVPATVAEKICFNGGSKMVSIHSKREIDYIREIYKDSEVTNQITLGAFSYDSDVFNWVDSSRWNFDYFDPLDMSFGDCLGMDLSEEPNTPGQITSLGYPISKPPAAYCTWKLATVGAYRLGIYFTDISVAKSVYIYDEYGNLLADPSGNLSPFKVLAPTNIMTITHDGSSGDHGFSATFLSY\*

>Cre|FL81\_06952

MFQNSIIGINGTSGRQVYIEYTISYDQTSQSWNFQSMRPLRCFSAAYKMFKRALGPWCITMPVTTPRKYTESASICARTSNSVLSGLDTPEEFEYIKGPLEQVARKRWLNASYPLYASWLSGAFSFADPTLSANPTGYLFNPGKPDGTGEDCLAFRVNSDRTCGIDDIPCDQDRTSDNSTWMRGLISVDSVMIVTKGTPEVYINYSSLAMKWDQCLTWCTQNDLCTVKRSNDIESKFAYKVKNENASTCPADDTIGETNFIFGTNRTSGRQVYVDYTISFDQTSQSWNFQSTRPLLCPSAGYKMFKRPLGPWCIQLTSNSDCQNYTAIESICTKTPTMESIHLSGIDTPEKSDLPRIKCKESDSKKAFSFADPTLSANPTGYLFNTGKPNGTGADCLAFRVNSDRTCGIDNILWLKSRCDQGRTSDNSTCLDMNLLLPIILILPVIVNSQLSCPPNYTLVIDKCLMIIKTPLTHSQAETDCTYNGGTLVNIDSAIINRAVTQFASNAGINKTWIGLFCFENRNTSMCYYDDASGTLLDYNSFASGYPMVDGIYGGCVYMPTTGSLAGKWDNNSDLVSIHSKREVDYIKSLYRGTIEPVDILLGAQQILPNIYTWVDGYPWEKFDYRDPMDRGAQDIDCLTMNSVTGLWTRAVCDRPLLFVCKRYITGNPSQTEVAPTENPSDFSNCNTTFLMTPGTITSYGYLSTSPLEVNCTWRIVTLGPYRVRLFFTDVDTYNTIYVYNEYGIQIEAVRYSRSVISRSNIVTVSWQGIINGKPETYTNSRILPLSWDQCLSYCTQNASCLSVYMENNVCQKFEGGDLQTVKRSNNVLTKFAYKLSNVAACPKDDNVDGKTYIFTTNVTSGRQSYLEYTITYDPSLQSWKSAKQIGRFRALKPMATSWISGVRKPECIGNATCQGLSATVYCPMIVTNGVPEVYSTPNSLALNWDQCLTNCSGTVSCMAVYSNAEGNCQLFDVGQLQTVKRSIQSNSKFAFKIKDENLSTCPVDDRVEGKGSYIGYNATRSQRFYKGYTVNFDPASLSWIFNSTESLYCSDKTYQFFMRPLGPWCMKIVISTDCRISSDIADTCGMIPGGMLSGIESQLEIQYIEQRTGGWDVYKNPYNAIWISGIRKTECIGNTSCQGASAFSFSDPTLSSNLPGYQFKPNKPDGTGADCLAYSIEGDISRGIENFHSLDLGWEDCLNYCTENATCVAIHEEDTVCRMFEIGQLQTVGRSVSVESKFAYKINNDDLLSCPADDTIGGKGYFFGIDTSTGLSTSGRQIYENYTITYDSSTQTWNFLTNGPLMCPSAGHQMFLRPLGPWCMIFYPNSPCQDNAKIVSICASSVNKYLSGIESPEEFEWVRARAYGANWFDPSIRLNAAWVSGAHAPPPIPQMFVWAVKFVASGLHK\*

>Cre|FL81\_06997

MISKSVSIFLLLALFSIKYSEGQSCPTGFQLVNQNKCLRVFAQKLKHLEAETDCSYLGGTLVTIKTAIDNRVIANIAANAGASSIWIGIFCFATGNTTTCYHDDNSGELTYNSFASGNPAVTGNGGCVYMQTSGKTSGQWLSAPCAVVGMPFVCEVPMTVADPTCSHNYNGYCYTGSTEMHLATINTTYERAQSICQSKNSDLVSIHSKQELDFIRAIYRNSGIQQIFVGAQAFLPDTFDWSDGSNWDFDYTDPLATSKGNCLVMDLSDRPNNGMWSQTDCQNVNFFLCKRKIGDATVATTVATAETTEAVNPKFKRASRAAIRNELLDFSNCNSTLILAPGTITSFGYPNTKPPITTCTWNIGALGPYRVGVYFTDFSVYNAVYVYDEYGNIISSVTGNXRPFQVLGTSNVVTITHDSRFDAAYNYNGFSATILPY\*

>Cre|FL81\_07002

MPFVCEVPMTVADPTCSHNYNGYCYTGSTEMHLATINTTYXRAQSXCQSKNSDLVSIHSKQELDFIRAIYRNSGIQQIFVGAQAFLPDTFDWSDGSNWDFDYTDPLATSKGNCLVMDLSDRPNNGMWSQTDCQNVNFFLCKRKIGDATVATTVATTEAVNPKFKRASRAAIRNEFLDFSNCNSTLVLAPGTITSFGYPNTKPPITTCTWNIGTLGPYRVGVYFTDFSVYNAVYVYDEYGNIISSVTGNXRPXQVLGTSNVVTITHDSRFDAAYNYNGFSATILPY\*

>Cre|FL81\_07268

MKSSVLVFLLCISSALAYVEVAMKCPDGWDWFKRSRGGWCMKVFSGPVTQGEGETKCKAEGAVLAGVQNGDEVKWMGESLVKVAGGGSLWIGAKRSIPCIPIRGLTALCTPLTSFYWTDASTTGFLGFKKWLAGEPNNYGGNQGCVQLFSASGLMDDAACNIYSTGYVCGKSSTFVLLLCVVSALADCPAAWKTILNAQREESTSNGCEADWKFFKRPSGGWCMRVFPGYYEAQADAEKACKTVDATLSGLQNKKEGIYIQSAILAQVPQTSGSLWTGLQRTKKCMGQKLTATCNNLTSFEWTDNATTGTEGFLFQDAQPDNKNLDQNCALFLASKAASIVARGTYFAGTYEDVNCVTGFNSENIARKTFGYVCGKKASSLWNGGKRSKACIPIRGLTDVCTSLTTFYWTDASTTGCLGFKKWMVGEPNNAGQDCIQLFKNTGLMDDLGYFKK\*

>Cre|FL81\_07269

MKSSVLVFLLCISSALAYVEVAMNCTDGWDWFKRSRGGWCMKVFSEKINQGEAEAKCNEEGAVLAGVXNXDEVXWMAESLVKLVGKGNIWIGAKRSIPCRSVSGFTALCTDLTSFYWTDASTTGFLGFKKWLVGEPTNWGLYQHCIVLSSTARLMDDVACNIKATGYVCGKVASF\*

>Cre|FL81\_07448

MNFKFPTLFFLIFHHPKMPRHMPLTVFLLLNVLLIPVFSMFAPVNSGRSCIDAKSYFAVSEDESNEQNEESEDDFFHVENLEVQQDQQNNKNRLVSVVQSDVSQAVTCPKVANGNCEEGWKNFTRPSGEWCMKIFYENSVTQPAAKERCKAQGALLSGLQNQMESQFVFSTVTAHIYPETGSIWVGLERRAECRDVQWSWNCTQTTSFEWIDKSATGTDGLAWACNQPDNSRNRTQQCATLTASYQGSVLGFQTGQLDDVGCDFDYIKMNKKARDIKAYVCGKKPKA\*

>Cre|FL81\_07450

MSSFWSLLILLNFLVIAVSSGKTNGHCQKGWTKFTRPSGDWCIKIFYETLVTQPEAEAKCQAADATLSSFQNQVESLWVAATSVAHIYPKTGSIWIGAKRTKACLKSQLTEKCTRFNSFEWTDKSANGTDGFLWDAREPSNTRSIQDCLIMTIGSTGYVSGYDIQVGTLNDNKCDLKLNSKDPQQIQAMKSSVLVFLLCISSALTYVEVAMKCPDGWDWFKRSRGEAEAKCNEEGAVLAGVLNQDEVNWMAESLVKVSGGGSLWTGAKRSSACIPIRELTAF\*

>Cre|FL81\_07595

MLRQFIACLALLILPQLTLATAGTPICTNGFTLINGKCWRFFATGASHRSAERTCMNYGATLVTVKNAIDNRAVQTIVGTSTYSIWMGLYCFGNDVTKCLWDDASGSSELYDNFLSAYPQIETGKCVVYSLQSSMVGRWYSADCQNETRAFVCELPTSYAEHCGNLVSIRSANENRYINSLFLQSGTGSILIGATKTSKNSYSWFDGSLWSYNNFDTTALQTGNCVAMSFGTSNNVSAGTWYTVDCGASYGYMCKRPAGVQCPANPPAVTVTPVPSNPSYCNSTLLMAPGTITSPNYPRYYDNNVLCTYQLTTLGAYNILLKFTSFVTEAKFDYVTVYDGDNTNSYLFGNYSGPVPAFSLVSTGNSMLVTFRSDKTNNYQGFTASFSSYVYHS\*

>Cre|FL81\_07599

MQLAVIPFFLHSFFYTSFAASTPVCTNGFTLINNKCLKLYTTLASYSVAEESCRNVGATLMTAKNANENQAFTTIVGSTVSLVWMGLYCMDSDPSKCLWDDTTGAAGMYSNFASGFPLVDIGKCVYYSVQEALAGKWISGDCDNDPKAYITVLTIKTDFVIPFIARGLHLFKHKRYVNMNTGILFQ\*

>Cre|FL81\_07600

MQLFIVAIFSFCIAFVSCSTPVCMHGFTLANNKCLKLYTNETTYKLAEQSCKTFGATLVTPKNLNDNRAITTFLGSSASLVWMGLYCFDSNPSKCLWDDASGSADSYNSFASGFPLVDIGKCVYFSAQGALAGKWLSGDCEKETRAYVCELPHTYADSCQFNYNGHCYTIHDSTTFVQAQSICEQECGNLASITSANENRYLQTLTNKLVMDSNLIGGMWPSLNVFNWIDGSPTSYNNIDRSATYNANCMAVSNSASLSVPPGYWYSVSCNSPRNFICKRPAGVKCSGTPPPVTMTPVPSNPSLCNSTLLLAPGVITSPNYPQNYANNQSCSYQLATLGSYQILLKFDGFITEATYDVVNVYDGDFTNKPLLGSYSGNLGSFHVDSTGNAMYVTFKSDRSNVAQGFSASFQTESFDHASVYDGDSTSSRCVLNWKHNVCHIPVGRE\*

>Cre|FL81\_07703

MRSIFVVLLLAAVVQTQFNFHGMSRSFFSTDEEFPTQLQNFEGRTQTEIRTLKEKVEKLEKLIEGLQSILMKEWNQTESGSKYRLFEERKNWDNAEKHCQGFGAHLAIIDNEAKNTFVTNLINSSETSDFAWIGMKTKTTTQTSTPFTNFDSESPIDGCAVMDSKGVWAIRSCIQLRPFVCQIIRNDYSILFCFFLALWITQIETRKVTQKPKPPPPPPPPPKKDISWVRSKIDSAKEKYEAGKQKIKSKFSFGSKSDDTKPKETFAQKTTSRKPDLHLKTTKKYGWNSNVQANYAVPNTMFTTKKPLFDRVKEKVKGSEKYVGKAVGWAKKDLGIGVEGPKKPSKILTYGKKAAEYVFKKKSKKTAIAAYSTGRSNSNDYSRDFGNSGSYSGGGNSEVSSDLHQKVEYLKNRLEIMQNTIKGTWNTSEAGTKYKLFEEKKTWNDAQVAQKRESQLRHGFYSYIVKSWEVISHIWTANQRITSRNFCCILKISQWFGLDLEQKLELNQYPHLKINSQISHIWMVVELLIAMGHGAFHHVPWNSRIFVKLFVSMFWSRYHEIL\*

>Cre|FL81\_07917

MTLETIYRRIGKFGLADFEFQKPAFTETIAVSVALVLIAIYVYVSFFIYSGVFGSPIPQNSDVYADPLCPGNIKNLWLDVVVRNTISQVFGAVSNIGPTKWPADPRSTCVGVVTYDNSSTVNAEVDASKSFSDLYNVIQSSLVAVDTTNTSYLSSGLLAAEKAFKDSRQRTYRYKFQQVVIAFAADYQGSGTIKDAKPVANRLKNNGVSIITVSCTNDPNASNEIQSLASPGFNFIDEMNTAKLVKQLTNALLSVNCFCPSDYTQYRADYHDPTSTQYGICIKGYIETGGIIDPYQHAIDWCEYEATNGILVNEFTKQKHDFITYYMNDAFGVNKPQEYYIGLRYLKNQWVWEQPTGQERIPLDPNGWTNWAPGYPQANSTGQVIADQPWTKGSSEFVWAPPQTDDFYFVCQAVASSTENFTGQL\*

>Cre|FL81\_08198

MSQKITACVPSRNPLKSIAFQALFESKMVMNLLIIWSLLVYTNAQNFDKSFKEMCEFLDGKDSYRQRENISQPMEGDKCTVVFPISFDDKNSAQRYCEDNVPFHIHGSDFEREPGKLFCDAEASLICKDGWVQMFGRCYQITRQMMNHPDAVKHCGDKKSKIAFMHREALPFRINDYFSGVSQVWLNASEAITNDLIYNVDGGNLLLALDGYRYGLPNIALARVETNEKAMALCEYTPPMNQAESNHLLRRYGEIYYPTLFTEDKAYVRSFSSLQRSSDRMRDHNYCKKVLMPFLQTDSAQSAYPTPEFLELLTKHREPTIIRTSVYSADSSLLNRVSSNCTTSTSKNYGFDRTNSNGSALFTTLTSANIWRKDEPKEQCDGASWSTGIVLSREKGEARLEAMSDARYAPIYCQTNFDTFDYGKCPDKWRPYYRKERGQLWCHRLAVNEKYEPIQESFDGAEKWCKLQGAAVTGFTNAEELALLDDIINKGIWITDNVKDQFRTWLGAKRRPQCDKVLKGKKGFIPEKSHACSRLRVFEWLNGVAQNPPDFEDHWVAPSEPNNWQKNTEGCIELLKGDEMKRWKVKDASKMLNDNDCSQQKYFICGKEAPIKSNSNV\*

>Cre|FL81\_08596

MRHIALLFAILPAILASASPYCTNGFSMVNNKCLRLFTSPMVHKDAVATCSTQSVCESLCGNLVSIHSGNEMRYIKNYYAARSTESIYIGAITVSGKYNSWTDGTAWDYNNIDNSQSWQATSNCMMVSLSSNGTQTNDAWYHTSCDTARPFMCKRKVGTECSSDYSTTTQDSTSVDPSGPPITPTCNSFLMSRGTFFSPGYPGNYYNNLNCSFTLATLGAYRIRLSFNSFQTESCCDRVKIYDGDSADSRLVAQLSGAQNTPLYHESTGNMMYVTFTTDGSVVQQGFTANFLSLI\*

>Cre|FL81\_08597

MWRHVFLLLALLPSIQATQTITCTNGFTLVGNKCLKLFTAPTSRRNASKTCAEYAGNLVAIQNQEENDALASFVGDGVRSVWLGLYCFGTSNCLWDDASGSNDGFSSFVYIYDIYKCVTYKVTGSWSGRWFRGDCSYDLRPFVCQIPTTYEDECALNYNGNCYLPSENFFSSQVIGIDSARQWCLNNCAGLVSIHSANELRLIQNYYKTKDHESILVGAVTNSGKSFLWTDGSTWDYGSVVGSEQSSGTCVKLALKTSGSRVKGSFYVTKCEESNYYMCKRPAGISCVGEPAPSGETPPVTPNCNEFLMNSGSFSSPNYPETYSDGESCTYGLGTLGSQRIRVTFSNIVVKDHEDHIRIYDGDSVESPLAMIITGRHSEPVYYESSSNRVFVTYNTADNLDAEFARTGFKADFVTIENEALASFVGDGVSSVWLGLYCFEGGTRNCLWDDASGSIEGFSNFVYNSNAYNIYKCATYKVTGSWRGRWFCGDCSYDLRPFVCQIPTTYEDDCALNYNGSCYLPSENFTSPQTIGIDSARQWCLTNCADLVSIHSANELRLIQNYYKTKDHESILVGAVTNSGKSFLWTDGSTWDLGHFVGSGQSFGTCVKLALKTSGSRVKGSLYVTKCEESNYYMCKRPAGISCVGEPVAIVEALPVTSHCNESLMNSGSFSSPNYPETYSDGENCTYDLGTLRSDRIRVTFSNITVKDREDYIRIYDGDSVESPLALIITGNHSETVYFESSSNRLFVTFNSVTNNDTEPARTGFKANFVTIV\*

>Cre|FL81\_08599

MRHILLLLALLSYIPVTQSITCTNDFTLVGNKCLRLFNTPTSRTNASRTCAEYAGNLVTIRNHDDNFLLSAFVGNATDDDIWIGLYCFDKNVTNCLWDGGQGSAEVYNNFVSSRSEGNPFFGFYKCVYYKVGDPWNGHWLSADCKWLRYSFVCEIPTTFDDDCALNFNGSCYIPSEELINSTQSLGLDSVQKICQENDGDLISIHSANENRFILNYYEGLGLDSVLLGAVVTKHFFWMDDSHWDFSNIDHTNDEYGTCLKMALQNNITISKGSWYITPCDGSHYFMCKRPAGNSDLIHVPKVAKTPPSQCNKVLLMSGTFSSPTYPENCMYTLKTLDGQRIQITFQKFHVTNGYIEIVEEYQGAEVKQKFSGTNKNLRYKSLTNELKVLFITEDLENMDSEFVAKFFSVFENE\*

>Cre|FL81\_08602

MHSFQSFSITFLSFLVVFSVSDPICNNGFTLVNSAKCLRLFTGPVRHRAAEAIVDLGGCVYSAAAGTLAGQWISAECEDVEMAYVCEIPTTKTDPCAHNYNGYCYLMSHENSTFPTMPFTSAEDSCHQNCAELVSIHSRRELTYIQSLYSTPNISAVLIGALTTSPLTPYWVDQSRWDYGHVSPRSGSTGSCFQMAVKTDGTWYQVDCKTSQYFLCKRPTGVTCNSTPAPPVIVTPAPTNPTGCNSTSLFDSGRITSPNYPSAYPIPSLCNYRLSTLGAYRIGLYFTGVSTYTNYGYVYVYDSNGARLAALTGSAGANTYYSTANTMTVTFTSGTYGSGYSGFAANFLSF\*

>Cre|FL81\_09841

MHSLIFLFSLLALLSDGLLAAVVCPGEEKLDPSGRYCYVVHKGALSFHDAEKACYDYGGYHLATVPTMIDNRFLYNLSSHSNVYANYFWLGLTDMTADGTWQWIDGSDLNFVNWAPDSAQGYCGAMRESDGRWQAQDCAKAYPFFCYGSIGDPNTDTNALNFYNMERDFIRAVTDSLFANPSFNGNVCTFYMSVSFYGYTKYDQQFDHSAAWSQRQFDNFAITGAQRFQWSPSMDDIGYTTLVFLTARKDFTNVPSLFNPFPKFDEVVVVSLNGAQMPGIPDGVQNVPVSNKFTNVDINNLVSALKCH\*

>Cre|FL81\_10016

MLTVLSVLFSLLCVPVTSFLPTFPPNNKNPCERFGLDSEFFDLNTWFKKRKQLFNWAAEIRCLRDIINKCEDGEEKSRGGRSLQDPYSNNYPTEASTTDYGNPYSYPRPYSRTYYRHSISPIRPPIPQPITTAKPAGECSCQQELEKLEAKFEKKLYEVKMKAAYETETAVGELRKQFEQDLRSYERITTKDVVEIKRTLDYMQAPRVMNNDVEYFLIQREESWYTASEKCIGYGAHLASVHSRLDNGLLAKLIPANETVWIGVNDIQKEN\*

>Cre|FL81\_10194

MGQTQPVWIGLTCSLSGSPSSCYWADDSGSAYSYSNFASGNPFVDVGQKVYMLISGGSAGKWVSGDGDLISISSRSICESTCGDLVSIHSSAENNHILWIYNQYPSNYYSGDYLRIGGFSDGVGKYWLDGTAWDYSNLEYFNPQIGSCMTMAVKDDIVPRGTWMSNNCAVQTGFVCKRKMGATC\*

>Cre|FL81\_10290

MYAELQSRRGGTINTDSASGSSSPGINEESTTVEIINTNPPSEFGLVDKQRHFGILRYTVTNRFRKLMLIALVNLVVFAAFFLFVFFLIVHLDKKHEDILVSSTNNCQSSYDVYSYARLDVNSDLKNHGYSTSLDDIEDDIKSDLPDPKESYPSYYFGSNILTCIRTMFTSDMTLCGAKMYFLVKRLPNDTDVSDLVFLLRKFHISITFVVSEKPSGGMNQQVLYTLATQTNGFCVFAEDHKFHDTPAWVPSFWPLYLVYSANAGVRSTGSLTLPVFNAPLLGEYHICMTLQDHGAMQKFRMVHLKWNNSESSSSGFFKETLESHAVKFGETTYIIKGPYTLDAVPYNMTLGFEYSDDEINILQIRIYSVSAVDCWVPYSIMTSQIPESYDEPSHKPHSSGIVSIIMKNRLLILIVFLPRSHSGYLETTTPSKSSFTTTIPFGHIDCTPNQTSTFFFAYSNDLTPDQVLNTWHTLRNNSQGSYDIYSYARFDVNSDFKNHAYSSSIENIEDDIKSDLPDPKESYPRYYFGSNILTCIRDMFMSDINLCGAKMYFLVKRLPNDTDVSDLVDLLGTFHISVTFVVSEKPSGGMNQQVLYTLATKTNGICIFAEDYMLQETPTWLPSIWPLYLVYSVNAEVKSTGSLTLPVFNSSLAGDYHICMTLQDHGTIDILGLIDKWNCRSLGKIQNGAFDMGNTTYIIKGPYTLNAVPYNMTLGFEYSDYEINILLIRIYNGFDSVGNNCWKYVHKFMDQSGADTECLQYNGASLIKIYDKYENDHLQSYLILKNANDRVWLGMTCNESTVAASCNWSYDRGTAAEYNNFGNNYPNVTKGPCVYIIKYNKQWFSSDCEQRRAVMCEVPQTSEDPCPYNYNHNCYFPSDVNASFADAVRSCSNMCADLVSIHSALENRYLITIPDIQARWWLGGVGPAPDIIVWSDFSPVTYSTFQFYHTQISGCLYTDINYNTKVDRLWFTDYCYKTARFFCKRPTETPPIASVEKSPDRVFKYCKIATFVLLGLLILGVVVFLILFFVVPKHGDQSASSTVVPSISTIGSTTVTKLATTTKPSSELYDSSTVPLVTNVTAEHSTTSKHLPTNGPITNTTASGLSTTSPSNRCSLITNTTFLFAYSNDLQSSLIQKALGDIKTFIVNPKITTFANNRFDTIKEDPIHFHGSKDNFTDSVNALLPDSKLKLPNTKDGSNVLNVIEKFLEQPTCGAIVYILMKRLPDTVDVTDLIQELRLNHISVFPVIDSAYIGSKDQSIMCKLAHTTNGFCDYQIASRLENEVYETMWIVSRVHVFVSQSYQVSGKGSIKVPSFVRPPQGNENGSMGLVVTYQNHARDTNFKALNLTITDDQNKVVLTGQTKSTNGNALLKHPVLKNNVTYQIGIDYEYARTDWFEKIDVRMYSISVPSLYKAKNEANQGLEVIELEEEVPENDADELEEEELVRYCFWIWILLLDIAFGKCVFYVLEVGEESGQWGNGLCKDDRYPFICEFPPTFDDTCGFNYNNHCYTKLNFQFTFTDAQDACQRYCSILLSIHSELKNRLVVSMFNTTGSILLAGVAPSENLVIWADRTAQDYNNLKSFDMELSCIHMDFQSGDWSSALCNKASWIVCKRRVGINAFGNRPSVSRIVDVPTYNDDPTTEMEPINKQNYFTLLNQVGDSQFQKVILIGLLNIVIIGVFVAILFSLFFLNHKDPHASSPTKSSTSSYPTTNTKPTVTTTTSTQNATDCTPTTPATLLFAYSNDIFSGHIQDACDWITEYFTSLKIIYFANIRFDTTTDDPIYFHANKSNFTVSVNTYLPDSSLSFPSQRTESNVLNVIRKFLSNQEYPLCGSILYILIKRLPNTKDVSDLIQQLQQHHIFVYTVTDTNSFGGTDQGLMCEITHATNGFCDFQSTDMRNEYYQTAYEISRTYQFVSQSYQVSGQGVINVTSFVRPKQGNQAGTMSLVITFQNHGTDDNLKSVSFSILDDEDKVVKSDHYKSTNGNSFLEHPVLKNDVTYKIVINYEYGEQRKEIIEVRQQHHLALFHRVANSQLQKIVLIGLLNVIILSIFAGVLLVLVFTEDKPHINNKEGSSTTAAQSKSTDVAQLTSTTVKSFSPSYPDACTPRSNSTFLFAYSNDLPSDLIDKARDWIVNLLPNRRPVCYANRRFDSTDDIIHYHNSNQQVKSSLSQSVKAHMPNSTLKFPSRANGSDVLNLIRSFLTNEECPLCGAVVYIIMKRWPNYEDPSELIQQLRQHHVFVYTNTDTTPSGGIDPNFMCKITHATNGFCGLQSSAKMDDDIFHTVRLISRPFQIVSESYQVSGKGSKRTPKFQIPLQEYADDFISMVIVFQNHILDDNYKYINYTFLNDNQEVVIAHYLKPEQSNTDIEQRRLAVGVTYQVILDYDYGTAQEDLMEIRLSSSKTSPKSRSLLIKIGQPQFALHFCKTYKMINRISQIYAERQARKRQFQNDISRASVSKDSRYQSTTTNTRERTIVEVANQEPRPDFEPVERQRHFGILRYNMKNRFYKVMLIGLMNVILIVIFFLLMFFFAFKSKCSSDEGSTTVSPREHFITKAIGSGALLLTCPDGYDLVGKNCLQLYTTLLTWSDAKDRCHLSSSYLLTIKTKQEDKEFRAYMQEHHQYNRTWLGLTCTSSKLTSCEWEDQPFPYSAFANGSPNGGCMFYNVSDTLGTPWVSGDCDEKLVSVCKTRPTATCKNNFGSYCYYYYSQEASFSEAADFCKLQCGNLVSVLSEDENNFLLSMDEIKRGLIVSEDKIMWADGSAMLYNNIVEYRKQDLCLIMRMGSNAGIWTSTTCSKTYSYVCKVPAQ\*

>Cre|FL81\_10496

MARSAVFLAIVALAGGVAAQTCNTGATTCPTPAPCPAKTCVPSCDQGWTYFAPTDFCYKVFHGAKFNDAEAACVLLGAHLTSIHSLTENTFVNNIASCGIKESKYENLAWIGMHQENGKDWVWTDGTPTDYINWAPKQPDNPGKELCVQTAPDVSHDSWYENWNNLACNTVMRAYICKK\*

>Cre|FL81\_11286

MQLLLLLSLILSAFSITFDRGSDSSESCEDTSEYHPRPHRPRPHRPRPPPHKPRPPPTELTKCPDTWMLFRRPQGNWCVTLFHKSQTWQGADNMCKTYGGRLTGLQTGQERMRLAEAARRIVQPLTPRNASVWIGARRKPECPRAGVCQDQNSFYWTDGHTTGTAGFHWAASQPDGQVEGNFGVQSCARLAVFSGGSAASPRHGAYDDYTCEYLPSRVTLVACGKKATRY\*

>Cre|FL81\_11297

MSHLKLLLTISLLFLISTSSARDFGDDSSCESSEEHGGGHGGRPRPPRPPQPTPRPDDAHRPRCAQEWFTSYRPQGIWCIRVGIGKLDYNQAAAQCATYGGVLSGIQNDWERWLISNEANRQTLAYNIQYSGIWLGAQRNPGSNTFSWTDGHTTGVQGMVFGPGQPDNKNRDNRGPQNCLQLIALTPGFWNNPGSQVWVSYQSGQIDDYWCDQVEDPEQRMYACGKLGPRE\*

>Cre|FL81\_11313

MTKIIFLFFFFLFATVFAIFRPSDSDGSCEDESRHHGGHGHKHHHRDDSSDEGGYGGGGYQDPEPRCPSGWLKFNRPTGLWCVKVFSGVLTQPDAETACQAQGATLSGVQDENEITQITAQALPLLPSQSSFSIWIGATRTTACSPCTPLTSFQWTDGSTTGTSGFLWNLLQPDNNFGGTQSCVVLLASTSLVIRDQWTWNANRLDDESCVGERGGALRGVKAYVCGKRGE\*

>Cre|FL81\_11327

MVRGCGRGWHRFDRPSGGWCMRVFKGNVSQMEAESRCRREGAALSGLLNENEIGRVAGHALRTLRPLTSGSIWLGAKRTSQCSTSPISSTCTPLNSFLWTDGSTQGSSGFQWNTKQPDNNYAKTQQCVVLLASRSTVIQDQWTWNSNRLDDVACVNPGGSEQRAQKEMRTLLLLLALIIGSVVTQREYRGGRGDNGNSNNNNRGCESGWQRFNRPTGGYCIKVYRGEHTQPQAEARCQSVGAKLTGVVSQEEISWITKSALSLISQSSGSIWLGAKRTNTCNSSPLSSKCTSMNSFYWSDRITIGTSGLIWNTNQPDNSHAQSQQCVVLLAARSTVIQDKWTWYSNRLDDVACGLPSGDNNGPRAIRAYACGKGA\*

>Cre|FL81\_11543

IAVLITKIFGESRIGTSIPNQPKTTRLGLVTYNWNATIQAGLDKFQSQQDVFENIFNDLNSVSSSSESYLANGLVAAENVLARGPNRGNNYQKVIVLFAASYSSHSNPIAIADRLKQAGITIITMGYNNVGDPNFYQNLGNIASPNKSFTERSLSQIGDIQGALLDSNCFCPPNWLQYRTPFTKLGECISPVSLQAVWNAARLSCRNQRPNAYMVNEYSQAKHDFVLQLVKNTSGFQQPYTYFIGLAYSSSGNWQWDQPNGWPQPVLQNWTNWDHGYPVSSSSMGAVQNQQKGEGAVWRNVGVWNSAAPYVCEVAACDTDNYCVDEDS\*

>Cre|FL81\_11778

MIFHLILVYFLISFVQAQNKCINNNDDRYIDGACFTFFNIPLNFTAAQEYCQHHAPSAWSILAKETSDTQAIWLAKIAVTEFEMNSGYFWIGVYRETTYDNFKTMDGFYLRYQRFAVMNPSMNYVAARTSDGKWYTLPEERRLPFVCSYYPTNVVQAAANAPRVLKSLKELFYL\*

>Cre|FL81\_11779

MTTQSFFLLPVFLLSFVNAQCYNAEDSAIGDLCYSFPRFQMNFQDAQNYCHSQNQNLAVIHTSTQSSFLATIVRTRSNTTNAKFWIGLSRSSANSSYVWDDRTPLSWSNFNPNGRYVVESTANAKWQTETASSLLDFVCSYDPFTTGFYTTEEPMTTTGETMASVTCLFMVDLQSAGIDQSAITTYRSFYNFAQLVGSKLNDASDFSGYLDTFGYSSYLGNHDMFSSLNYDDFKNIPFPIDGTDDDIDMDLKDVDSTLANAVWSPPSQDQTCLIFFSAAPVAEFGGTTIKSSYNSFTTVVGVLLGGATSIPGLTNSISVSSMTDADAQASHMKHLYFLSTLLLAIATTAQNCADSSDHLIKGRCFKLVNKQLSYQDARNWCRYSNPVGFTYLATVADQYMDNFLASYARTTFNSNEGNFWIGLTRTSGKWQWEDETPVAWTNFRVQNSQNYAAESITDGKWTGYSPDTKMNFVCTYWPGVTPGPTPTPEVGTSDTPTWTTVSEAYPTPTGIFLMLLKQLVLTFTISIGLASSACFDNGDKEIQGGCYKFVPQKLTWDDARNWCHYQNPVTATYARSAFGTDDGNFWIGLSRSSNGSWTWDNGFPVGWTNFGPQNGQNYGAESIVNAKWNAYGSSDKYFFVCSYDPAAPPTFPPPQSTTTSSPVAVSTQAVPTTTGKKS\*

>Cre|FL81\_12618

MSSSLTSILLFLIFLIPSTSAKTPCSPSWLHIAHLDSCFLSAPQPAEFSEAQDYCSQMNSSLVVINSEDEGSIVREFFARENPSFFNWIGMRWDERRAEFEWVDGKKRNYTYFLPDEPGVSGECIAWVLDDNLDGWQAISCHYSQFFMCQKPAEGIVTTWHRDDEGVITSPNYPEPYENLEYDTHIIKSEPGTRILMYFENVETEQNCDVITVSDDYGISGRTLFSRPLPLKVFSSNSYGTVTSNNYPTSPDSFLIQYYLIQCPMEFHVALTAKAMQLDKNDRVKVHNGADEKAKKLRIFRQFSPQSADAIKSTQNSMFISYDTGEQYMPTNHWAFEYQCVPDGNLGAEIEI\*

>Cre|FL81\_12734

MVLFPLLFLLFFRRVAHTLTFPPSSSSTTTVLFCLQPFVPENAHVIFNEPGPYARDTVAKYSCALGFDLIGSEERTCLSDGSWSDEPPICAIDVAFNKPVTQSSGNVAIALGGNMCTMTNDESKSFWEVDLLGDYSIRSLSMRLGTKSSPIVSVEAIETGGAQCIVDSSLFTINTTTSISCLYDNISRLRITATRRLHLCQVNVYAVNAVFGGMCYAASRDEQTDWLGAQRKCLDRGSTLPLRIDDSTRRGLRASLSASSSAKAFYWIGASSSMTEWRWVDGEGVGDSADWPGQPSPIPSASEAVLLARPLDWKWVPASQTAWNSFLCQSKPKFCTSPGVGEATKVSFSSHSYAIGTLCFYSCDAGYDLHGIRQRELNTNAQTVGTLPTPRRPPTDHSVEFVNPTEHGAVLSQLVNLSIVEDRRLSRMEELTSNRRLTNRWPITQIKGSTSHEQQNGGGSDSTIAMAVLASVIVAILCYGITKFAKSTNHGANGDLSISRDKLNASNAAIYATPSIPPQRPDSVIYYAPTVAHMEVPPHLLQLQQLPNGNIHVTLPIGRQMGRPSLPSSMLFNSSMPPPSPTPSQILYSFDHEPIYDTPPDTHVYQS\*

>Cre|FL81\_12970

MTYFYFISLFITSLLLLLPTFGLSIPPTTFPNCPKGWHHDEPGRTCYHLARRKMRLPEAHAYCHKLIPDGSAHVLRVECGGENDYISGLVKVHSDKVWIDARARFDIVDGSAGLFGPGFVYRWPNGKMVRYSNWADGNGLEEIGTSDKCVFIKNDGHWINANCSSTAAVICEKKLHRPYSKFCPKHWVYNKETQSCYRTISKTNMTILEADNKCFDYGFEHRQDAMLTSIQSESENQFVMNLAKERDANFEFIYLGGYGRSRNGNKWHWMDGSEFNYLNWDRGMPFGRRALAVLVMNKRGKWINHYADKILSQYNAVAVCKFKS\*

>Cre|FL81\_13197

MIRYHSLLLLILPVFVNAQCDLGSVYNSDKNVCFTFYNASVDFKTAESICTISSGHLASVHNIIDNNYLAKQAQQYISANGIIWLGAKSTSPNVTDPNSWNWSDGTPFDYQNYQSGEPSSLQTAACMQFSAATAKWKTASCINYAPFICEYQPDNFPVTCPPTIIKSCPSGYYYLQETQYCYKLVIARGNFDDARSGCWSMGAELVSILSPTENGFIHDISQTGHDVWNKEQTNNIYIGLIYQNGHWQWTDGSSAYYLNWASGEPNFMKKEHWTTYMPDGHSDKYNPYGDEWNNIENDQQRVFPIPFVRFCRHSASQKCVAVDVWLGQHSDKRLFPMKCLNDTCPEGTFCDEDGKCWEVIKFGDGSRYYEMKLIDGKWK\*

>Cre|FL81\_13198

MILPFFLLSLPFLVNAQCGVGAIYNEKNNLCYRLYKAAVDFNTAEMICSTLNGHLASVHNLDDNNFLTQQASKLIYDNGPVWLGAQTSSPNVRDPNNWKWTDETPFDYQNYRIGQPSSLGTSACMQFLTSDGTWLTATCTDEFPFICASEPKKITTVSGVTCPPTKVYRCPSRYVWFQYTQSCYRVFIGSYSFESANQYCKNDGAELASVHSYTENQFLAQISTTGLGETSTGNNIWIGLIKNGTHWQWTDGSPVDFVNWESSYPQGYLATAMISDGDQRWYNTIYPERGFICKRPAIH\*

>Cre|FL81\_13257

MLLYSLLSFYFISITVDAYCEYGTEYKNATGCFQFFRTPLNFTNAVRFCRVNMKSTLVRPVSFIRNQQLQQAAMKLGIEEYWIGASNVDNDWEWLDGSMLTYSNFDVGSGYPKKTESQIGAVSMGSLSGLWYTKLDAMMLPFVCEFPISTQFDNGVLYRAPKLQSLIFPSAGTKAPMLLVESVDQSSLFNKIGPKKNEMETGEKVYLKPIDMSAAGMSGFSGQPIVIMNTFKRKVKVKPVVVSQTETEMARSLKEKEEIEDSTNAKSVLNVGGNAAARNGTSMTEEMSSNSKAKREREENESIRSKTIQISRG\*

>Cre|FL81\_13514

MLLTLSLVLLFAVPTSAQLGNGTCDEGWKWFHRTGGGWCMKLFTGSYSWFHAAGLCQTQGARLSGIGGDTGVNPQQRIEQQWIKDTLLNLTSHITDVQPNVWIGARRKPECMYKQLNVAALCIPVLAFEWTDGKTIGVNGFQWAPGEPNNVGGIEDCGALRTDMNKSNDFDCYSTHNTRGYVCGKPQIDP\*

>Cre|FL81\_14185

MILSNNYFLLTLVVFIICIIHVESSCPVGYDQVNSKCITITPQRFTHHKALLTCKEKNGHLVFVQNAIDNTAIVNYASNITSPMWIGAICKVNKQPKECTWDDGSTLDYSNFLPGYPVTNIGTCVYIDSPNQPLKGRWIILSVSAEKDPNAPSECLSKCLTPLAKLQRSFSYVFNNFEKVCDLLEDGAFCSRKCNQEDQTKFYQYTTFYRIHCIDYEEDIQEHLTCIAKASEDADLVCKDKCKQAHKVEKTASKETKMKKECLTLECSTLCYFDELAESCPEARNVLLKINIGQVHSMASGVHPITMEKMLPECRNLHNTEYMRAKLLASSSSLLMDHTPSEMETEEKPVITA\*

>Cre|FL81\_14186

MYWTLLLLTFLVSVSADTCPNGFTLLDATQKCVKLITTAAKHADASASCSQYGGHLISVHNAIDNRAYLALASASTTPYWLGIKCSLSGSPQSCLWDDQSGNAGTYNGFANGYPLVEVGSCVYSPTQGSFAGKWLSGDCDTMVLNFICEASTNTPVTDTCSFQYNGNCYFPTLSSLSEQEARFACQQECADLVSIHSVEENNYVQALFTNNAPSYIRIGAMTTDQNVNTWTDGTNWDYSNVGYSDTKLGYCWSMSLTNDIVSAGKWISSKCDTPIPFVCKRKVGQQCGSTAGPTLAPGQCNSPQFYDNSGTFYSPSWPYSYIGQLTPCSYILDTPVGSLAEIRFPVMNLDNQASIAIYSRIEDTTPLVVLQGNNAGNQWYTSTTNTMRVVFRPCVNNCPTDGGVYRWQANFQPSNQVTQPPPVTVTPNPNNPSGCNSTILVTPGYITSPNYPGLYPNFLECFYHLSTNGGYRIKLDFGAVDTEQCCDNIVVRDGPLLGSPVLGVVSGSWPAHAKIFQSTSNSMFVSFTTDASGQGMGFSATFNAY\*

>Cre|FL81\_14266

MVFAVIALVVSAILIPEALADPCGDSNWRYFPQTNSCYKLIDENLPWTIAEFKCLFQGAHHVSIDSPEENQFVHELSHWSEIWTGAAFFGKDMHYVNSDGSRYGNFENWKDGRKPPMNRARRCIKMDANGEWFQSCCKKKTYTICEKKAAYSASSYSGANNSVNGFRFMRHRS\*

>Cre|FL81\_14806

MIFFSIVCYFLATFGVVDGDCAPGDVKNTQENCVHVENLASTWQEAENFCVAHNGHLASVHNAFDMTSLRKVAGICTNFWLGGQCQAGSNCKWVDGTDFDYKNFRNGNQGTDNCVVADTKSGTWSTQPCTATSCIACEIKGAMQDCQDWMKAGYTDSGKYTILVNGKETEVWCDMQTYGGGWVLFQNRLDDSESYWDRKWDEYKNGFGDTDENVNFWLGNEALYTLTNDKHVTLRVEMYGDRTPNSKNATDFWFGHYFEFKVGPETQNYPLVNLEMDWAHPIGNASTAWYDLTCSIGSPFSTVDNIHDPVKECVTKFQMGGWWLKNCALSTLNGAYTPKDWNNGYGMFWIWDGSDTILHPRKTRMLLRNTVV\*

>Cre|FL81\_15127

MTTLRFIIFTLFVYGVTSDNTTDGPYILALSDEQPHQRLQFYNWDHKDLGTNAFEDLPPLAEQPTPLPINQTEKCPDGWVRFSDSCYFYETELLGFAKAERKCYDKQATLFVANSFEEWDLVRTRTEKSHFSWIGLVRFSHFERSEQLPRWQTTGSINPSKLNWIIKPFNPIANGWSSIANCAATYQSPSPVESTSYTYFYPCTLLLNSICERNSTIVNARN\*

>Cre|FL81\_15604

MSKNAMTQINIENDKSDSRERRRRLGRKRRKRRRLCDQIGEDKWIKRVIMRERKERITDCLMVFAPLPIGFIVANWLCCLLVHSANCNGKRTVEGEEDDEEAEAVTSDRSGKITELFSDLIIEEMKFTILVLCVCLLKIANSLNLNDIKKVRTNPTTIATTTTMKPTTTTKTTTTTTVYTSTTKPVEHSVVDPGPMLIECPDACPTGWQYYNSNCYKKFDSGVTYSQAVSACSGLGAQLVTIDNFDENDALRKAFDTNTLFYESQETWIGLKFVSGSWTWSGGSEASYINWAPTQPASGQCVQMITDALINETYKYQRGGWKTYDCSKISAIEMKCLTAVFCLQLLTFSSALDLNDIKKMRTDPTTLATTPTTTTPTTTTTKPTTTTKTTTTTPTTTTVTTTTTKPVEFSIVDPGAIMIDCPDACPKAFDTNALVDESRETWIGLKASVTGGSWIWTDGSTASYTNWAPTQPSSASQCVQMITDALSDATYLYQRGGWKTYDCSKTSASYICEQSASEAFDTNALVDEPKETWIGLRSTSGSWKWTDGSSASFTNWAQTQPSSSQCVQMITDALSNATYQYQRGGWKTYDCSKTSASYICQRWATI\*

>Cre|FL81\_16165

MDSETENVLFFSQKLHMNLYSLTTFFLLPAYLSAGPSCPAGFSLLNQNKCIKVFTSSAKRSDATTQCISLGGTLVTIKNAIDNRAISTIAASAGLQNIWIGIYCYNFHNVTCYHDDSTGVISYNSFRPGYPKEAYDIGQSVYMQTNGAEWHTGYRDQMSLPFLCELPTTVSDPTCTHNYNGYCYLPSHEIPGIDSSTTYSKAQAICKANSANLASIHSKQEIDYIKSIYTNPNEISQITLGAEARQLHVFNWVDGSNFDYNYFDPLVNSTGNCLQMDLSYRYDRGLWSEISCQSVNNFLCKRKIGATEQIMEPSQPINHFDLSDPSNCNTTLLMAPGVFTSFGYGTSPLPNTYCYWRLATVGAYKVGIYFTDFSVWFNMNIMDQYGETIARSTGNLQPFSVLASTAIATVTHLQTDDTPSYNRHGFRAVVLPY\*

>Cre|FL81\_16206

MFLLGLLLLNLFGNLSAAGTGPTCPDGFTLLNDSKCVKLYETAMTYAKAVKTCRSIIKGDIVSVHKNTDNQALLNLINSHHSVRPIWLGLTCVTSNPNSCSWDDNSGAASYYNNFAKSNPNLSAGKNVYMLVSGSSTGKWISADGNLVSLSFVCETPSSLVPDDESCSPASPTTFLFAYSNDLNPTDVLEVWSHFDQHREEISNKSVVFANVRFDLRKAEDIFYHTNFSDVMDSVEAHLPDSDLGFTDVGTGSDIISIIQKFMNDGQKAPICGSAMLILLKRYTNEQNIDDIVAKLRKHHIYIYVVTHEAPSGGLYSQTMYNVATRTNGYCSFGIDQNFLYAATNGGAYYSHYLFYSTNIPVSGKNGTVALPLMTVPDLETDYLIMTIQDHGPLTSFIRQEIDWNAVGTDLSGGEAENIWDFGWVKGNGTFYELSWQPRPNYVYNMTYSFAFTDRRSQVLQFRAFTEDENVINTWIPYDN\*

>Cre|FL81\_16497

MKMLMKILIIFGLLASITNAQVDRDWSFQRMCEFWDGGSSYRPRPNGFNSIEGDKCTFEYPVATDSRESAKRYCEENVPYHINDVTAGERTKCSAEATLICKNEWIQLFGRCYKMTKELMTRDNAVEHCKTQKXDATIAFLHRETLPFRIYDYFTRVSRLWIDASEAITXDLIDENVNGNLLLAIDGYMYNLPNVALTRVDSSETAMVLCEYTPPMNRAESNXLLKKYGEIYYPTVSTSEGAXIRTTXSLNRIDEDLFKDNRYCSRVMNPFIXNSNARSAIPTREFLDEVNKVQNGLIIRTAAFSKNSRKDERIGATCSAKKGATHRVLWRGSDGNDVSVPVDKSLWRSDEPNEICDAGSWSSALVSGRDGSPGLEAMSDARYAPIYCQNTVDSYSYGDCPAGFTEYYRKSIGQKFCHRFFSEKKTQPDAEAHCQTFGAHLTGYTDSEELKLIGTLNVLGIWETLIGGRRRSECITNGAKNEPGYSREESSPCSRKRVYEWKNGVAPNPPTIENDWSFDYEPNYVAYKEECLTIVRHKGVSLNDNECDWPFPFVCGMEAPIVKLLSS\*

>Cre|FL81\_16649

MHCSLLLILIIPVIVNAQCELGSVYNSDKNVCFTFYNASVDFQTAESICTVSSGHLASVHNIIDNNYLAKQAQQYISSNGMIWLGAKSISQNVTDWNWSDGTPFDWQYWQSGEPSSLETTACMQFSAATSKWRTASCINYAPFICEYPPGEVAVTCPPSIIKSCPSEYYYLEETQKCYKVVIDRGNYDNARSGCLNDGAELVSIHSYTENSFIHDISQTGHDVWYDTNEDQTNDIYIGLIYNGYWRWTDGTSFDYSSWASGEPNNMNREFWTTYMPDAHTDNLRPNYNPNGLQWNNVINEQQRGYICQRSMIS\*

>Cre|FL81\_17156

MADARATTCYLNGLSLRTINEVEKILRSLPREGDPCEIQCSQPSIGSLKIHEDPKPLVLSPPTKQEXPKKSKGKQTISEYSCVSLKSEEMKKREVIASSVSGTGSKIQCKVLTDQIQVNPIMSCNGVVLSLDVEVTIPDRQEKKKMRLEIECPDFMPARIKIGNKWKSIIIENSLLLNNALESCRTYTDGTLVSIHNAIDNRALINLAVAQQTVRPIWIGLTCLTTSCVWLDQSQTDYTNFVSGNPQPDVGINVYMLTSGNSAGKWVSADGSLVSLNYICEVPAIIVPDLCSNPFNDYCYTFNQDVRNEINARIYCQKDCGDLVSIHSEKENRHVLSLFNFTSPPPQVRIGAGTDGIGKYWVDGTVFDYSNFGYFNVDIGKCSTMQIPYGVLDAGQWLSNNCDDELPFVCKRLNGITSCPPSPTPTYNPNMCYGSHFFTGNGTIYSPNYPESYYGQFYPCTFIFTVPSGNIAQVMFTLLNIDDQSKISLYSGIEGTEPIIELTGQFFSPPPFNSSTNLVEIPSLISDDMESCRNLTFGSLVTIDNAIDNRALINLATAQNTTRPIWIGLECYGFPCYWLDQGGTNYSNFASGLGVNDKRAEDRKQWKGANKLGKILEKVRDELWENEEFRRDRELIEKEDEEKRCESLEKS\*

>Cre|FL81\_17187

MFNLTHSRTSADGICFLHNGATLVSIKSANENRALVDFVKNEHLDTVWTGLLCNNGTNITSCIWDIQAGTAARYSNFEAGYPDVTYGGCVYFTASGKAIGQWGSAQCSQSMAFVCELPATVLDETCIFNYNGNCYTRFDNYWNFSGAQRECESRCSNLVSIHSANEMRFIQTIYSDVQSAFIRIGGIAMSQDFLIWTDGSPGDFDNIQYFQPGSCIIMATGTSKSGYWYTHPCDQGYVMSFILDHWKHLLIGGISVLVLIVSVFLITFFAVRGSFHCEKENVMITTTASNIITETTNFKVKTTTTSTRTPFKATSTTLKPTTTATPQNLTCTNDFTMVHGKCWRWFNENSTRADADQKCKWHNGATLVSIRNYEENQALADFIKEKNIDSLWIGLYCTEWTNIDSCIWDIQAGSAANYNSTCDFNYNSHCYSPFPYRKYVTDAQNFCVSRCSNLVSIHSANENRFIQSMYPDVPYMYTMIGALAPSLDYIIWIDGSESDYNNMRQTTESPRGSCVAMATGSVDTGYWFVFPCTEYWYYTLLCKQDSASIPGDRDASKTRFQNIITFVMDHWKPLLIGGISILVLIVAVFLITFFAVRGSLDCESDYTSSTFSSSIGTESSVRTTASTAIPSTVSTQKQFPTSLNLSSTAVYSTTPDLETSVQLFDLVPQVPICTNNFTMVEGKCWKLFNHGEIRSDADKICKTYSGSTLVSIKNYDENKLLIDFVKDSHIDTLWTGLFCNNGTNSTSCFWDVQAGSAEQYSNFGTGYPNLNYGGCVYFTASGNTIGQWGSAQCSQNMPFVCELPPTIIESGCKYIYNNNCYIRTDYGYTTTQAQRYCVSNCANLVSIHSGNENRFIQAMYDMSYAYILIGALAPSRDYLIWLDGSPTDYNNLNVINPGVCVLMSLSNGSPAIWYTKECGYPSWFLCKRPVGAKC\*

>Cre|FL81\_17188

MEEKESVIKTHFEKFITFIRDHWKLISIGGVIILLLMISVFLITFFAVRGSYESGVHFGVREILIMHVSSLHNDSLDNGNDDYLEFPTTTVKTAKPSSTTTLKSLTNPVFTTTSAPLTCTNNFTMVNGKCWMLINNSSIRSDADKMCKTYNGATLVSIRNADENQALTDFLKDENINTLWTGLYCFGETNITACIWDIQAGSAANYSSFKVGYPDADYGRCVFYIGNGTDIGQWENEECGETMPFVCELPPTVHEGTSDFLYNSHCYFRIDMMKNITDSQHFCLSRCSNLVSIHSANENRFIQSIYDTNFTNIAIGGFASSKDYMIWMDGSPTDYNNIQFSYAGSCVIMAAGTTDTGYWYTRPCNETFWFFDDATTLEENDNGALQTHFENSVAFVMDHWKPLLIGGISVFVLLVSVFLITFFATSLLLRVHPKRRRKRVQNLKLRQKLVYFLFLNSVNFSFIHSENSTTITSVTPPDSYTTTLGINPVQITSHL\*

>Cre|FL81\_17189

MNAKTKILERLSQVFSRETSERAGTSTPSVSTISDEFEGPEQTIVDMYDAPPKTEFEPIERQRHFGILHYTVNNRFRKMMLIGVINVILIVSFFLFIFFFVIQPKTGGGGDGFQSSTLHRGAVTTSSPPALMCTNDFVLINEKCLKLNVTAYSKPTAETICNEVGATLLSINSLKENQEVVDYLKTQNVSSVWMRLVCNNNDKSSCHWNTGDNVTYSNFTKGNPTSDAKCVSLLLSGDTTGQWKSEYCNQQLSFVCELPTTSPDNCPYNYNHHCYLRFDQSLSFSDAQSTCQKHCANLPSVHSSSENLYLTSIYGFQNQNLFLGGFASSQNCIYWIDGSPTDYINLNSFHSNFACVISHMGDGGEWETVDCSQPISSFICKRPTDGNHKKLDPMLTEGDIQFSSQVGMYSKKRESAMKHG\*

>Cre|FL81\_17241

MIHLILLFLKCWMLVSQTADEPTADEYCRLNGGGVIATLKNAIDNRGLLTILNGTSVSRLWIGMICTGLSPSTCRWADTTTVQYTSFSSGFPNDRFGQCVYYSADGYPAGQWASGPYVTGDCLDYANYNNYCYMKEEDVQSFSWAQKDCARHNANLVSIHSYLENRFITSLFQEGKMDLWIGALAPGSALIVWTDGTPNNYYNLKNSGNGSCVSMGFDPNTNSTGDWSSDERCRENGGGILVTMKNAIDNRALLTVLNGTGIHRLWMGMTCRESSVSWCQWADKTDVQYNSFSSGYPNSQVGKCVYYNSYGDLTGQWTSEPCEEKLPFVCEILSSTPEIVGSDCYSQYNNFCYTRVRDKLSFKSAQQNCVLKNSSLISIHSYLENRYITTLFNIDGSVWLGGQITPYDTLEWTDMTPYDYSNLKHVGNGTCVSIGLVKYTNAMDWSTGNCESTYPSICKRPLTI\*

>Cre|FL81\_17267

MKILIIFGLLASFANAQVDRDWSFQRMYEFWDGGSSYRPRSNGFNSIEGDKCTFEYPVATDSQESAKRYCEENVPYHINDVTPGERTKCSAEATLICKNEWIQLFGRCYKMTKELMTRDNAVEHCKTQKXDATIAFLHRETLPFRIYDYFTRVSRLWIDASEAITXDLIDENVNGNLLLAIDGYMYNLPNVALTRVDSSETAMNGLIIRTAAFSKSSRKSERIGATCSANKGSIYHVLWMGSDGNAVSQPIDKSLWRSDEPNEICDAGSWSSALVSGRDGSPGLEAMSDARYAPIYCQNIVDSYSYGDCPAGFTEYYRKSLGQKWCHRFFPDKMVNEDAEAHCQKHGAHLTGYTNQEELKLLADLIGDNYEKLYHNLDTWIGARRRSECITTGTDNEPGYDRDPASKCSRVRVFEWINGVAPNPPDIEPDWNHDGEPNFAENREQCLAVMKGNKLTGTLNDVPCTMKYNFICGTEAPIIIKSP\*

>Cre|FL81\_17412

MKLLFVLFLKFVFISAQLDLNSIKKQQTYPATGPTTISTSAASTVGPCVGCQYGWVPYGGSCYKKMLDVLTQSTAEQECITLGAHLASFETNDKATAIKNLVLSAPLFSTDLFSYSSSSQESWIGLSKTSNGAWKWTDASEVEFANLPTGTSVTGASCVSMNTSGVWKPNDCTSTVTSFICKRLSSPL\*

>Cre|FL81\_17436

MKLIILYSCLFQLIVSQTLKCDPGFTMVLDKCLQIFSEPQNHTFAENKCRSNGGTLVIIQNAIQNRAISKFASDNNLSKVWIGVYCFGNSTSSCFYDDFSGPVSIGNNFAPGFPYSGCVSMVTTGSQSGKWYSYNCNDVDGINSYICEMPTTRNGTINGAESCVNYDGYCYYMTHDAPLEVAERICQENNGHVASINSQHENDFIKNTFASVYFLMLGAREYFPNVYAWSDGSKFEDFDNRYPFDIADNTRPCLVMATNTGLWQRAGCDIQQSFVCKVPLEPKTIEGNSHCNSTMLMAPTTITSYDYNIGSEVFTPCTWQIISPGPYLIQIYFVDIQNSTVEVFDENGKQIALVTSRITVYAPSNFVTVVHKNGGGFKAKIQKYESYFPTLVFYIIHPIAKSNMHCLRYYGSDNQIHSEIYECRLFGGTLVTINNAIENRAVVQYASDQGQERIWLGSYCFGNSSSSCYNDDYSDSSYSNFAPGNPLVNGSEGSCVSMITKGSHVGRWFSSNCNHNFYSYICQLPATLNGSMYKSDGKWLEVFNNSAYYVVEGSIDQAEIECQKKNGHVVSIHSKQENDFILNRMALVPENVRLGAKRVFNNSYAWADGTLWDFDFRDQLDDMPESLDCLEIFTVHQLWSRTDCDTTASNICKIPLPPIEDNSHCNTTLLMSPSTFTSYGYGMQGLQSPCTWKIVAPGPYQVNLQFLEMRNSSVTVLDASGKLIASVNSTVKVLAESNIVTVVHNGQGTFKASALAF\*

>Cre|FL81\_17908

MFVRTWILLLVFPVIVSTNECYVTPCTRDIIIVVDGSSSMQTSTYVSQEINMITKLTYSWTLDESKVRLALVGAYFGNEFNGLDYFTDGSLVEKRLQSFRLAAMQYGLFNGDFNTFFVSVQLFELGVVAQSIIDSITEDGICFLDQGWTTPKPEICTTSTTTTRAPTTTTKKTASVKPATTPKPVPPTQPPFPVGDYQDCSCTTQSLYIDIVFVIDVSEGMGLGGLMMVKAEINTLVGQMSLDPNIQKHVQVGLIKYSNEAEIVFKPSDYDDEDEFTEDLWSDPRLQDVDKVDEVNLHLGLQKAAKMIGSMRRGVRKVVVIYAASYNDEGNDDARQIAANIRESGYEIITVAFVEPESSNLVMKIGEIASPRMNFTSFRDDLLVEEMEDAFCQVNCYCPNGWKQLVLENRKYGECFFPTKIDASWTATKFECPILSKDHTGNGHLVYVNSALKNQFLNDFYMNHWDPENQEKPNYDIGYYYDKTTNKFIWVNGVTNNPYSNWAEGYPDITKGECVMAKRVDGTQEDFRWVSVNCQTDYGRGLCQEAACDSDFYCPPEYN\*

>Cre|FL81\_18659

MLKIARIQSPSKNNSLHLQIPCEVCKIQMSHGNHFGVNSCRACAAFFRRTVHSRWSQLKCQGGSCNKMTFFCKPCRLQRCFEMGMVTANFQYNRDGIVTPSVPTTISTVSHITPSLEQYLGRPHFVILSDKNPKKTIIDLHRLLGEATKILNLGPATPIFCDGSQLKKLSFGMKNEFDLRKLKIATRMTQTEIAGNWEFYVKKVATWLTHFDEFKKLPVGMKMKILQTIWHIWSRLEKLSTTAKYRRSSGRNKRSEIVVQSGVLIDISEVDFDSKWMSDYPTDQVRRFMMHSSCDQFTVTDHLTEMELSDVELTFMLAQLCFQYAGNRYQGEIQEVCDRLMTILSDDLHDYYVNELNMPRYFKRLAKMMQINNEIQVAQHPSRSRSNGSDPHVSNSEVGVHTSRNDNRAVGTYVSSYGIDRIWMGVFCIGNSKSQCYFDDQVGSTAIYDNFATGFPNAENGGCVYYSVPGSPSGQWMNFYCREVLPYVCELPITHNDNCDYNFNDHCYFPFVELPFSSAQLQCQNLCSNLVSIHSPEENRYITSIYSQSSYDFIWIGGIATSSDFVVWADGSVMDYSNLETFSTGGNCLKMALKSTDYHSRGGWYTDDCSTLAHFVCKRPIGAVDCSGTPPPPTPTPPPINPPTCTTGDHWAPGTISSPNYPNSYRSGCAYTLTTYGSNKIRLIFDYKQIYVTDSVDIYDVNMKFIIYLFLFIAACHAASNNTICTNGFNLINNKCWKLFQEPANHTMAERTCTGYGGTLFMARTAIDNRAVGNYVNSFGIDRIWMGVFCIGNVKNQCYFDDQVGSTVIYDNFAPGFPNAGTGRCVYYSVPGSPSGLWINADCTEQLSYVCELPTTHSDYCDFNFNDHCYFRNDELPFSAAQLQCQNLCGNLVSIHSAEENRYITSIYSQFSYDFIRIGGIATSNDFVVWADGSVMDYSNLETFGTGGNCLKMALKSTDSHSRGAWYTDDCYSPGHFVCKRPIGAVDCSGTPPPPTAPPPPITPPTCTTGVYVAPGVISSPNYPSPYHSSCAYTLTTYGSNKIRLTFNYVYPYPNYDFVDIYDGGSTDTPKITSLTGYYGGSYTCTSTGNIMYINFRVTSSNSPGYIGFNATFYSVF\*

>Cre|FL81\_18956

MSCSNRRSNSSLATEFSQAKHDFIFNVVQNTTGFSPPYQYHVGLNYVSGLWVWTQPTGRQQVPLQKPFMWLSGNPQRSSTQSAVMNMQSGHGTGWQNIATMTLSANFICETYSCDTDNYCADYSPLSYVDRPCGTDLSNLWLDVIAVVDNSRGMTNKGLSNVASSILSVFGENTRIGSNSVEPRTTRLGLVTYNSVASQKADLNQYQSIADAYTGVFDALSTTVDTIQSYLATGLALAERMLVDQTVNSTRAHYKRVMIVYASEYNGNGESDPLPLAERLKLSNINIITVAYEQPGSVGLLQGLTQIASPGFSFSTNCFCPDWIQYRGSYSDPASSRYGVCLLPVGVPVVWAAAKIECSNRWNNSYLATEFNQAKHDFIFNAAQGSYFQQNPYQYHIGLNFVNGAWVWDQPAGQPQVNLKSWFNWGTGFPNSPASQSAVSNIQSALTTKWNNVGTFTTPATDSYSPLSYVDRPCGDDLTNLWLDVIAVVDNSRGMTVNGLNYIASNIASVFGFGTRIGLNASEPRTTRLGLVTYNSVATQMADLNQYQSLHDAFNRIFDDLSNTVDTTESYLSTGLTLAEKMFNDQSVNSTRAHYQKVVIVYASKYQTNGESNPESIADRLKLSGVKIITVAYGNAYGLMKSLSIIASPGFAFSNLVVSPGNLVGQVQTSLLESNCFCPDGWVQYRESYFDPASSRYGVCVQLVSLQANWLSAKMSCINRNSNLATEFNQDKHDFIFNVARNTKGFAPPYKYHIGLNYVSASWAWTQPTDRQQVPLQQPLMWLSGNPKPASTQSGVMNMQSGQGTGWISIAEMTGSANYVCETYSCDTDNYCCSADEVCGGSVTGIWLDIVIVADNSQRVHQYNFVSDVQNSIYYIFKGVNFPYTRVGFVTYNYVATVNADLNKFKSPSALSQGVYNSYNLDNISPEKTSFLGTGLTTAGDILTVQGSADGRVNNPKVIIVYASVLNGTGFVDPLLVANTLKSAGITIITIPLDTDHNGVIQKQLVSIASPGFAFDYLNPIYSDPVRNALRDVNCFCPPGWTQRRESYNNETRKFISCFQFIGAPTSWNTAKQGCRNLWPDNSYLAMENEPSKQDYIQGAVRNNSAFQQTPLQYHIGLNMMQGNWIWDQPYGLPRKILNWDDWMPNYPVVSSSMTAVMNVQNSTSSGWQNIDPIKVSAGYVCEAVACSVNNFCDANWNTKKQT\*

>Cre|FL81\_18957

NCFCPSNWIQYHTSYSDPASSRYGVCLQLVGVLANWVAAKNGCRMKSNTNLATEFNQAKHDFILEAVKDNSGFQRNPYQYHIGLNYINDDWVWDQPAGQPPVKLQSWFNWGTGFPNAPASQSAVSNIQSGVTTKWTNVAMYTGAANYVCETYSRRILSYVDRPCSTELSNLWLDVIIVVDNSQGMGIVRLTNVAANILDVFFNTSIGSNSSEPKTTCIGFITYNSNATLNVDLNKFQSSDSLFVDRVFNFLSNVAYSRDSFMGTGLPMAEQLLGRQGFGIGRDQYQNVIIVYASTYQNNKEFDPESIADRLKKTCSAQYSPQSYVDRQCGTDLNNLWLDVIAVVDNSHGMTNGGVQSVAANIASVFSSGTRIGSNSTEPRTTRVGLVTYNSXAKLDAXLNKFQDLDGLYNGVFKDLSDVVDTTDSFLATGLNAAEELLQSQSLNTTRDHYKKVIIVYASEYKGSGELDPVPVANXLKGSGVVIVTVAYDQGGDEGLLRDLANIASPGFAYSNAPNNAGNLVGQIQDSLLQTNCFCPNDWTQYRASYSDQKSFRYGVCFLPVNLPAVWNAAKMACRMKSNHAHLAAEFDQSKHDFIFNLAQDSNFKPNPFTYHIGLNFVNGAWVWDQPAGQSPVNLKSWTNWQSSYPKSPASLSGVSNIQTGLTTQWNNVALFVGAQDYVCETYSFSVYADSYSPLSYVDRPCGTDLSNLWLDVIAVVDNSRGMTVAGLNEVAANIASVFGSGTRIGLNASEPRTTRLGLVTYNSVATQKADLNQYQSIGDVFHGIFDALSNIVDTNESYLATGLELAERMLIDQSVNSTRAHYQKVVIVYASEYDGNGELDPLPIAERLKLSGVKIITVAYGNAYGLTKSFSNIASPGFAFSNSDNQGKLIGQIQGSLLQANCFCPSDWIQYRTSYSDPAAYRYGVCILPVTTPQVWRAAKMSCSHRWNNSNLATEFNQPKHDFILSAVRNTQGFSPPYQYHIGLNYASGSWVWTQPSGRQQVPLRQPLMWLSDYPQLASDKSVVMNQQNGHETGWINIASMNVVANSVSDYSPLSYVDRPCGEDLTNLWLDVIAVVDNSRGMTVDGLNEIASNIASVFGFGTRIGLNASEPRTTRLGLVTYNSVATQKADLNQYQSIGDVFHGIFYALSNTVDTTESYLATGLELAEKMFNDQSVNSIRAHYQKVVIVYAATYQTKGEMDPESIADRLKMSGVKIITVAYGDAYGLMKSLSVIASPRFALSNLADSPGNLIVQIQISLLEANCFCPDGWVQYRESYFDPASSRYGVCIQAVYSS\*

>Cre|FL81\_18958

MKHHSLLLALLGVYACSADYDPASYVDRRCGEDLSNLWLDVVAVVDNSQGMTNPGLINVASDIYSVFSSGTRIGSNSSEPRTTRVGLVTYNSNATQKADLNKYQSIDDVLNEIYDDISTVVNTADSYLATGLQLAEKMLIDQSENTNRAHYKRVVIVYASEYKGEGELDPLNVANRLKLSDINIITVAYEQKGDDGLFHDLSQIASPGFSFVNNASDTGNLVTNVQNALLQSNCFCPSDWIQYRTSYSDPASSRYGVCLQAVNIPSNWLGAKMSCSHRWIKSNLATEFNQAKHDFILSVAKITDGFAPPYQYHIGLNYASGSWVWAQPTGLQQVPLQQPLMWLSGYPQLASDKSAVMNQQSGLGTGWQNIATMTGNYNYFCETYSCDTDNYCFAQN\*

>Cre|FL81\_18959

MKLHTPLLALLGVYSCSADYDFASYVDRRCGEDLSNLWLDVVAVVDNSQGMTNEGLSNVAADIFSVFSSGTRIGSNSSEPRTTRLGLVTYNSAATQKADLNKFQSIGDVANGIGNALSTVVDTTDSYLATGLILAAKMFNEQSVNTNRGHYKRVVIVFASEYKGIGELDPLPVANRLKLSGVNIITVAYQQAGDDGLLQGLSQVASPGFSFVNNPLNLVTNVQNALLQSNCFCPSGWIQYRTSYSDPASYRSGVCLQLVGIPASWAAAKNGCRMKSNTNLATEFNQAKHDFIFNAVQDINSGFQRNPYQYHIGLNFINGDWVWDQPAGQPPVKLQSWFNWGTGYPNSPSSQSAVSNIQSGVTTKWTNVAMYMSAANYSCSYVLADHYTPYSSLSYVDRPCGTDLSNLWLDVVLVVDNSEEMGSQRLFDVAANIIDVFGANTRIGSNSSEPITTRVGLITYNFNATLNANLSQFQSYDDLSNGVFHSLSNVTNSTDSFIGTGLAMAEQLLRRQNFNTTRDHYKKVIIVYASAFQRNEDETPEWIADRLKGSGVKIITVGYGNSHGLIKSLSNIASPGLSFNSSGDGNLINQIQTSLLQANCYCPSTWIQYTSSYSNSSSYHYGLCIQPVPTLTTWRMAHYACIFLGNHSSLATEYNQDKHDFLLDAVKDTSGFSPPYQYHIGLMSNSYYWGWDPPTGSSGPTLQSWSNWILGFQGDTEARSVINIESENLKEGTTGWLNIDDTRTKAGYMKIANMKLHTLSLALIGVYACSADYDPASYVDRSCGTDLSNLWLDVIAVVDNSRGMTNKGLSYVASSIISVFGKNTRIGSSSAEPRTTRLGLVTYNSVATQNADLNQYQSIEDAYYGIYGALSTTVNTTESYLTTGLNAAVELFSRQSFRSNRQHYRKVIIVYASEYNGRGEFDPVPIANRLKASGVNIITIAYEQPGSAGLLQGLSQIASPGFSFSGDNIAGNLVKEIQTALLQSNCFCPNDWTQYRGSYSDPTSYRYGVCLLPVNLPKVWASAKMACSMKSNRTHLATEFTQAKHDFIFNLAQHSNFKQNPYTYHIGLNFVNGAWIWDQPAGQSPVNLKSWSNWQTGFPIGSPASQSVVSNIQNGVTTKWNNIAMYTAAADYVCETYSCDTDNYCDADFVYDN\*

>Cre|FL81\_18960

DTYSPLSYVDRPCGTDLSNLWLDVVLVVDNSQEMGSQRLHDVTSNILSVFGADTRIGSNSVEPRTTRVGLVTYNSAATLNADLNQFQSFSDLRNGVISFLKVAANTKDSYLATGLAMAAQVLNVQGLRDHYQKVIIVYASKYSGYGDLDPQPIADRLKGSGVKIITVAYGDETVLESLSSPRFGFNSASGYPQIQNALLESNCYCPHTWIQYRTDYSDRSSSPYGVCILPVNLAANWFAAKYQCSNSWNNSHLATEFNQAKHDFIFNVAKDYLRQNPYQYHIGLHYANGDWVWDQPAGQPQVNLQRWSNWQAGFPIGSPASQSGVSNIQNGVTTKWNNVPLYTMTADFFCETYSFRSADEECGGTVLDLWLDIVIVADNSQRVNQNNSVVDIQNSISNIFEIVPIPINRVGFVTYNSLATINADLNKFKSWGDLSQGVNDSYNNMNLSSENTSFIGTGLITAGELLQVQGSAIGRVYYPKVIIVYASAFNGTGLLDPLSVANTLKSAGITIITVAVDTDNNGVIQKQLASIASPGSAFSLDPDDDHWPVREALINANCFCPPGWTQRQEFYRNKFKKYASCFQFIGTPSAWNFAYFRCLILWSDGSYLAMENEPSKQKFILEAVRNNSAFQQTPLQYHIGLNMIGEKWVWETSDGPQQELGWNDWMDSYPVISSSMTSVMNVQNGASSGWQNIDPDEVMAGYVCEAKACSASRFCYIKTSNT\*

>Cre|FL81\_18975

MILRTLLLILIAEVTWCQIGQPGQAPGQVPLDPGYQQPLEPIKNILQGAYGSNVTLYFRNSPYRVMGDLTVEYGVTMDIETGTRIYFDTGVGLIVKGTLRAIGNEFAHIEMLPYQQQINYDSEMPKFRLVDGPTVRQGRLQAQFRDRWRSVCTMVTNWTSIDTGTACRSMGYSDGGFWKWYRRNNDTYPFVMPKPDCHGSAKNLWDCPAFSDPQKIRLSENLCQGEDDIGIYCWGPPTFTGWARHWKGIQILNSPFHYVNSDPDLVAVNRESNSRLEFVDILYAGYDGVNKNTTSALYIEGVPPIMNGLRIEHSARDGLQLLDTNGPAIIANSTFSFNRGHGIFVVNTTDARIFVNNTRIEGNWGDGIWYKQRTGVNLIDYGMREKRGVGSGRLDEEKPRIDMCSEHRIDDNHFFPHLISVNLKNRTFLDPSQPPSCWMTVSLPPRLPYTYSIQWLHIRDLNPVTSRTTLLICDSNNPDENSCSTQRFRIPIRNEIYPQSISLKSSGKPLYLALEHVLDGDQAGYVQGDVYLLFNIHASVLDKAYYGLNVTNCIIEKNTGNGVFANDIRERTALTNVTLDENQGYAGFMVRDGAADIWLNETRILRNWGDGMNISYAGGSIMVNGTRIEKNRWRGAAIHYNQTIPFFPLYNEVIFKGRPSNNKFYLPTIISENEWGGLLVGNYCAYGNESSWRWNSRNPPIQGLYPKLESKILISWVEFLKNQYHPAMEIFSCRDPHVTTNIVDITGNRVDGNLGFGMRISPAVNMHTLINSNQYLHNNDTALYVRNGQWPELVNLPAEVTISKNVFKFNHAKYIISIGMNEDGPRQFLTFNQQNEIRANTVFDPFPSLPPRSTPYAALVVSSSNVKIHRNCFNNERAKYEIATELERHAKWIDARENNWGFQEIPRFIDKFFDQFNRYSLASIDIDPYMAACNQRMPYISLLNGAFRQFKKTSEPNKLGGIIYENHDLLKGRYTVTEDLQVVPGAKLTIASGSVLEFNHGIGMIVQGDLIRNEYDQDEKVIFTSSPFTLAKRQNIRLVDVDGNDEVTEGRLEVLVDDQWGTVCNRSWTPQLTILACNQLGLVADIQYFENWRIFPEAGDLPMVMDNIRCEENEVDLTRCRHDGVERNCAAGCRSSEVVGLRCLEPRWAGVRYSLLANPPTVTGQTTMDNWRIEKGGLFNFRTSEFCAAFKIDWNYHTFHRLEVKNNFWDGVDVVYNDLVKKPAIRNSIISNNRNNGFHIRSAGITVENVTISFSGQSGMRYNPSVSALEQDDIVSWLSLKEQPELEANNIFRIPDQKLDLIEVMESNLNQRKFLVAAETDDCPDDPLQECVYNLMIRSVGYQYGLPSKMAIQIVNAPSNVSDEDAIFTEVSTGKSWSARKDQIYFPVVSTENAMRMRYTRSYGKPKLVILVLFLDTQEYVDRFIHLYQSRVEDNQYGFSAVHYSNLTFSDGRLSNRWNNEKIWLQKVNFTRNSEAVVWLHSPQHAVIPGTPIAEITYHFDNCSVVDNTGPIIESHRDLYASANVFHWILWSNTFANNSRSGIAVALPDTYDLLAKQTHSFWLTENRFERNDDFKILVDGYYAFANISSNNFTQNYAPKQFGMLELRGMEKKLICERNRFFFNWGHWMIKIDATSQYLKQVDVPSYVRYNYIEKNTFIRQRADYVDMWPRSYALGVFGSQKIDYTDIYDTMNATYNWWGTGNEAVISQRVFDFDDWNTYTRAQWSPFYVSNDLSINFWWNPYRDGQLANATYIEPTVHDLHGRVYEDKNLTLITERWYEFPHYYRPFRPYRITRDVTIMPGATLYIQENVEVHIWPNVRILVLGNLVAEGSYWQPIRFKPINTTEYNEIKGRIPTEYRKRRGIVFDGEPTNSEKPRPKRASDRSKPDLVFRDFPTLHRDDPYYQRFTVSLTANGSDYGRSGFLQIYNATTGETIPSCDRQFTIRNAQVVCRELGMETQNVYHWLTPRWDYNPQLKILKTYMEPRECRGDEPSLDRCNLRLSGNDSQWMCMDSENFNYIYCGTNRSLSREYIGNWGGITFAQPTLEHEYGEKRGTRKEKSILQNVEIVGGGAGHNDSWQSAGLQIFHRSPILDHVNVTNCSVHGVQVISPNDRITLLNLNVTFNQGQGVNIMTTFVQAPSTSQDAMKKPMSIPYYSQGMMDMCAAVKRFEVKNRILLYYKYDSFPVDCVKIFTSHGRRVAFRIVQYHLYSSPTDLGRSDALRLYSSESFTPMSLLADFRSDYQSVDPSVAVSSEEIAVHLRATAADGVYGFIAEVSALPSNSEQHTVGEVVIRGSRMDNNDRGAIEYSNLGEMSPNLVIESSSFSYNGIHLFGNISTSSQAIQLHLHNTVFFLFRSNSIAHNRGGLYILATSSSPVVRLGALVKNCMFVYNSNSTTVALSGNNYQSISLLNNVISHNFALYHDTVVAHDVAINMTRNTLFSNTGLHTLDIHANSKISADKNVFFYNHFYDNLALGHGHQYMEKFGYQPQKENNEFLNRPRREIGKSEVNRNRKKRQVLTQQGISFDWWTHVDNETTRYRSTIIAGSSQEIFKFNTFNDPLNDYELTTGRQSQYEIGSIDAKENYWGYPGTIGVASGKIRDHEDYPELVKVDYTPVMESNTSLIEGDCPAGWFQAGHEEFKSCFLFVPSAVTYTKAVEYCKELGAFVPYLRIDDILQTQLAQRIEKFSIDMITDQERLKAYGVEDDIHLWISSVNIPNTQCGWLSARTRRIGDVNCNILLPFVCEKGTHPYSEPILWRPGIIIPLVIFCIVLALLVLLVVCWCCKSRKRNEVLIERKQAARASLKLQKRHQEHQKKKMQTGSEHTHTSAHASLDGGSTISAYDWRAGRQPPRQVARSPTDTLSTATSDHTYSYAAYTPHGGPTTTTGTFQSRRNNRYVSTNPNGYSEITTPTVTTVPYTGATSSTGTTVKMRLHQLRSDTSDATSCSTCPSDSERTSTATDISSSYTSEASESTLQSTVVNNRRSPLPPAKSPIPALRKGNSNGFLNMTNNFQPLPTDPPRSQPPALQSQSSLNRFVELHAPPRTGGSLKHKKPVIETSM\*

>Cre|FL81\_20271

RQGAHLHSDSNDSSFGFSCFQLHWLHRLFTFDESVQYCNSIGGKSVSISSYSERDALVALTKTNILQPWLGARRNTTTNKFYNLDGTYFYTLMWSTNEPSVNGDCVTFKGASPSGLQVTQCYQLQPAFCKQTXALCNSAVIGGPNTWSGTFQSPGYPTQYYNNLDCRYLINSPNNTFITVTFYPFLIEEWYDSVDIYEGNSTSYANWIGQPSSYSSGRGFESSGNMMNVRFKTNYAITDKGWLATWKAKKDMPVITQSGTNGTMTSPNYPNNYDTYDEQVYQISVAYGMQVNLTIDDFRTXSKYDYLNIYNSSVQSNSTLVYTLSGTSVAPFNWISPRSYMSMKFVSDGXIQYKGWHAFWNATAADNNHCPSGWTFSTNTSYCYIQSSQYMTYSEADPYCQSIGGSQVFVFTTRELTWLTDFTSSSLVQPWIATTRNTTTNIWYNSDKTTPPRSYWTTGEPGVNGDCATFKGITTAGLKATQCYSLQPALCRQMPALCPTIKDYGGSSTRSGTIQSPGYPVQYYNNLDCWYTITSPKNTYITLLFNPYMVQDYVDYIDVYDGPNSSYPFLGTTDYWYFLRFDFESSNNSVSFKFHTDNIITDKGWQLTWNAKSNTPPISQSGQNGSFTSPNYPNDYDPYTEQLYYITAPLGFQVNVSITDFVTELNFDILEIYNSSYVSSNYLVANLSGPSIAPWSWVSPSRYVTMRFKSDYMVQKKGFSLLCPSGWTFANETSYCYIVSDRYMAYSETAGYCQSLGGSQVFVSLSKEFTFLNYFTAGLFAQPWLAITRNVTTNKWYNSDGTTPFSTWWSPGEPGPNGDCATLRGSDPSGMKATPCYSIQPAMCKQMPALCPTTTNYGGLYTRSGTIQSPGYPAQYYNNLDCWYTITAPNNTYITLQFSPYLVEKTFDYVTVYDGPNSTYPYLGKTDEYLNPRYDFESSSNYVSFKFHTDRTITKNGVYSAPINQTGINGTFTSPNYPNNYDPYTEQLYYITAPDGFHVNVTIDDFLTEARFDVLEIYNTSTVIANNLVANLSGNATAPWWWVSPDKFVTMRFKSDGSIQKRGFEGSWYIL\*

>Cre|FL81\_20821

MQLFLLFLFIIPAVYGLSCPPEYILVSGIKCLKMFSTPANHWEAEKNCTSVEGTLANIKNAIDNRVVTEFVRNASVNAVWIGLTCYGNNKYSCYWDDASGMPSLYDNFNYNEPSDKENGNCIVMSAETNWKWESKVCMDPAWPYVCEAPTTVEKSSCSQKYNYNNNCYTKSLQVANGSLAAYNCQNKSDTLVSIHSKMEVDYIRNLYKGTNTTSIYIGATVDANDKITWLDGTPFDFDYRNPLDTQKGDCVVMDVHGYGLWSRVDCSQNFEYLCKNPLHGGSGPEVLEDKPEIFPTQSGCNSSTVLAPGFISTFEYPLNGLNIFACYYDIVALGPYSVGIYFDFIDTYGELTVFDYRGLKIGDFGGIDNRDQVAVYAPYNTATVYYEPRHKNGTEKDRGFHAVILPL\*

>Cre|FL81\_21016

LFVISVELVVPEKQQTYPATAPTTVSTSAPSTVGPCNVGCQDGWVPYGGSCYKKMLDVLTQSTAEQECITLGAHLASFETNDEATAIKNLVLSAPLFSTDLLSYSSSSQESWIGLSKTSNGAWKWTDASEVEFTNLPTGTSVNGASCVSMNTSGIWKPNDCTSTVTSFICKRSSSTL\*

>Cre|FL81\_21460

MIRSILILSVVFVAIQAMMAPCIDKPVCPDGWKKFEDRTNGQWCMKVFPGNMTWWEAERECRCTTKGAHLSGIESSSEKQWVEGQGQEVLDKIQDKNGAIWIGAYRRKECPSGATSSDVNCHAEKLFQFTDQHTCKTFIFQNWADNQPTNNAGDDCGAILVSTESSGDNVDASGKTVAKNCLQTTGTTPIMTSVGYVCGVKPAYPGNDYGGGYNTGYGGGDGGYGFGGGEMVVIGAGKPEKKKN\*

>Cre|FL81\_21470

MRAVIIFFTIIVGSLTVENDMDDLLNRVNITKMFELSSGDAAILNELNMIRKLIAEGFMNNPFENIGKLIFDGAIQWIKNVYDKAFSQAEYIAEYGLKVFEFADLDFGAALIDTQEALTNLAGQALDGLEDLGNGAKDFFSNNFPSFGKRKKRYIVKFIEEKVTAFRETIEKPKNVFGAATNMNMLTWNRRLAQLAMVEKENIENGKRVVEYEGKRYRVNLYGTLATYVIANTGIQWIVRTGYLAAKLWFDKIDIPNQKEIDTKDKTHEMLFADRSEVGCFFTWPNTICIIGPLNATTGYLYQKGDDACLDCKYGCTEALCNPPPHYFFALREKYKKHLRQKIEKFEIVEGFDGQKPILGKNFMIDSANYSNNSLIPPESSKPSGLQDASQSGPVILSDTIGTAKCASGWIRWEGNGCCYKEMGSPMLSWYASEDWCWSQRAGAHLTSIHSQAEAVWLNYQYKLWWSKMDDWIGLRRNCDNTDWEWTDGTPVDFLWWQPGYPIYGGIEDSCTALWDSSVLRGMYGFLPGQFDDGRSCTGSVAWAVCNNYRTKVCQKRLYYYFNYNHHINNDNDNSHDNNNDNLEARKELAGNFLKDNQNLYRGAEDERWMFKFLNQNSLIPPETKSSSLSDSSSANLVVLSDAVETAACASGWKRYTVNGMCYKESTASMSWYAAEDWCWSQRAGAHLASIHTQAEAQWLNSQYKLWYAPMDDWIGLKKECDMTAYYWTDGTPVDFQWWQPGYPQAQYAEQSCTTIWNTALLFLVSGYTPGQFDDMKECGMATGSYALCKYDPNTYYYGNDDDTYNNYDNSNHNNNITYNDYHNSDHNYCNHYNNDSLHNSNDYNHNTYHNYDNSNHDNYNTNNYNNNHHNTYHNNNQVSTTTSKTTSKATTPFDTSKCANNCPTGWVSYNGLCYAKIKGPAKSSDFNTECVRLGGQMAEVSGSGVNEALRSFSTNTASTTLEEAWMNLSGGFTNMAPGYSAATGSCYTIVLSQSDNGVYTQRGLWRTQLCTSLKEFGICQKAS\*

>Cre|FL81\_21471

MCYKLSEYDMSWYKSEEYCWNQRAGAHLASIHSEAESRWLNAQFRDKYGQMDAWIGLRRDCDNVTYVWTDKSPTDFLWWQPEYPRSEFAEFSCVTLWEQSFLLDVDGYVPGQYDDMKECSSSGGSVALCKYDPNTSIIGEKYVKKTCSLIPETTSTTTSTTSTTTTTTTTTTPTTTASFYRLLKI\*

>Cre|FL81\_21528

MLWAVLLLVLAVTTPTQSQLVTDRSCGNDLSRLWLDIVFVVDNSKNMNMYKVFDTISSLFSPYVQIGTGYDDPRSTRVGFITYNWNATDVADFYKLQSYSDLSNQIQQLSTTPLSRRDESYIDTGLAAAIRMVNATQGLRDNYKKVVVFFTSQYNYYNTYPEDQAKLLKSWGATLITVNTGGDDNTQENLHDKIANKGMAFLMSDGNTTQELQRALLATNCFCRPDWYQYHYPLKSTDIFSNYGVCVYRPAVAMNRISAQNYCHQLTDTSYLVSELDEQKRAFNWEYLNSKGSDPTHAFYNGLTSFNGTWWWDQPNGMPMWPLSPYSGAAPQRAGCVADMKYSDGTYSWTPISCTNLFRFLCESVACDTDNYCEF\*

>Cre|FL81\_21530

MFKLVTLALTFTALVSAQTGWTDSWGTTGAGPTYGPSTPRPTPGGSNVDRECGGDLANLWLDIVVVVDNSKGMTNAGITQVAANIATVFGNGTRIGNQYTDPRSTRVGLVTYNKVATEVADLNHIQSIDDLYSVVFSTLTSVSSEDDSYLATGIGAAEKVFQNGRNGNVRSNYKRLVLVYASAYKGDGQNDPIPVSDRLKSSGVVISTIAFDQDGDEALLAGLAQIASPNYAFTSEDLNLANFDDENSYKYGVCIRAATISSSWTAAKFACQNLAQSGFLATEYDGQKHNFLFRIAQNNTAFSAPYIYHIGLSYVNGGWNWQQPAGYPLRPLSGYTAWNPSYPKSFSSNTGVVEQQFSSDLTVGWQNINGYSVAEYYMCEVASCDTEKYCP\*

>Cre|FL81\_21536

MKPYLLLLLLIPIVLFSYIDAEQVCRDGYTMVNNKCLAFMQTPQKYDDAEKTCRFNSGGVVVLSKNAVDNRALVNFLSVWNVANVFIGLKCSNGDTSTCQWDDLDGLNDYNNFAAGYPLSSQECVILDSQSGKWTSQSCDQPMQYVCELPPTERDCNSNCEVNYNNNCYIRIITPKSFADAENTCKKLNSHLTSVLSYLEFRLIAEMYRTPGQYWIGGLCASNDSPIEWLDQSQGEFSFGKTIIDGNCLQYGMKPLLILLPLLAYTSISTAEKVCASGFKMVNNRCLALVRQYKSYSNAEKWDDVDMLGGYNNFNGGIPSGDVCVQLNVGSGKWQSESCDKTLPFICELQETQKDCHSNCDYNYQNHCYTLVKQQKNFQDAENHCKSINAHMTSIHSFLEGRFVAQLYADWGLYWLGGTLTSADAKIKWLDGSSDDFETTKHHKDGNCLQYRVDSIGIGHDWFADNCGDESIFICKRPASC\*

>Cre|FL81\_21802

MTNLRWFLQVLSCLIVLGYCTDPRYNDSDMYDDCFQGAPGWYHLTATCIFPLTQFERNYSTAAQMCGAVNHSIGYRETNWLIAQQLLEMFTNEKSRDLMKLYWTGLSVRNGSIVVESEDATNDTVANVASLSSNELDGSCIALDLRNSSNFGWRSLPCSSQLPILCQNYACLPGTFRCADNSKCIPSSFQHDGFNDCLDGSDEMPVTQSIPLSSSTPNSLLSNVLRENPVYEWPMIVSSGGILSPTTVRYGRGECTHRWTVLSPNDQHFIIWIKWMSPTTSTAIYVEGKDQNGRIYLNSRNATSSFTLLSSSFVLTASDTDTRKIEFQVHYQEADKTICRITENNQLFFNSESIPMSCNYRFTTKIPSSYVAILIRKCEGPSPIVSTIQFNNSTVSLTRRQSKKLLIIPSNSLNIHVNSTWPGSETQLDFQFFELRPGEESVDVFMIDSDFEIEWIPKSSEICMEGQFRTLTVNMILTSSDESENSSQSSTWNVERFLKSCSEDNVQIVSKNQSAYVSNLGSVTGFGPTTVVIHQSAEPFEFYSIYALQGIARDGSGWAFDEGVSTTTISTTLSTTDIISTTTSSPSSGTKCKLPTINNGYIKAVSDHAYSVGTIVSVNCDEGYMLDSLPYNIQCSDNGTWIDGENRAYPPVHPIVKCLHINCPSETGYEIDNSMTPDTYETSYGTVRRYQNRSTYGYQPFCICGDDKKWLADWMCYNTEHLTKYEIPNGCIIPEVHDAIFVTQLPNDQYVAPSGYTIEMDCMVCPTVKKTYRCLDGLWRASNGSVQAYDSFECRCQDEPGWIDPCLPHGTYVQYQGYYSCQCENGWKYGDGTCVDIDECNETSSFCDPFAKCVNTNGSYYCECPINYHLFNASNFNPSQWGSIQRYLIDGYSCVETTCIYDIEWSQWNIQVIKPPTLSPYYKSGNSMGYLYATNMCDSDYKCLLQFKETCLNGDWLPRPNPLVACKALDQSVYSFQPVAPYFHVFQTIDLACNQESKIMI\*

>Cre|FL81\_21849

MRFATSLIFVSIILLVSGNRRFGFGVKTCPKGWLQFQRHCYIRQPDTLDFKGAMESCARQGATLFQFDSTFEFAAVRNLFPDYMFTWLQAEIEEELEWLYEPYEEKINGKNTVATCIAFYSSPTKSYNYYYPCTSRFHSICEKPLDAFHVWVA\*

>Cre|FL81\_22637

MHLCGYPEYPRWSSTKFTVASRNGVFEGSEGSEGTESFGESADDFISKYMQGVGVTRLWLGLYCDHSTPESCLWDYGQGNALLTNRFLSDSPDISKGKCVYMDGKSGNWSSVDCEEKMPYMCELPQTLEDPSCDHNYYGYCYIPHSTLLAYGDAQKVCTQNNADLISIHSEFENVFVSNIFKTPGAILIGGVALSKGTIIWTDFSLSSGYNNIQSFNTGNCLFMNVYTDNDTDGFWYVDQTVPITLTCTATTITVNLCHSYVQAIQEINKDYIWLGGFAASKNFVSWMDGTPMNYNVFNSRKDLLQDKESCNDK\*

>Cre|FL81\_22643

MKLNTELFCFFLLISLFFDVISSTCTNGFSEIYKNCYKILPESLTKADAKTRCERDYGAAILTIHNAADDFISKYMQGVGVTRLWLGLYCDHSTPESCLWDYGQGNALLTNRFLSDSPDISKGRCVYMDAKTGNWSSVDCGEKMPYMCELPQTLEDPSCDHNYYGYCYFPHSAPLAYGDAQKVCTQNNADLISIHSEFENVFVSIIFKTPGAVLIGGVALSRDDIIWTDFSLSSGYNNIQSFNTGHCLFMNVYTDNDTDGFWFVDTNHYNSSVSHPSTTQNFSKQRTLPARYNCY\*

>Cre|FL81\_22646

MISRIKNIYAEFQSRRGGIINNDSASVSSAPGTNEEPTTVEIIDTNPPSEFGLVDKQRHFGILRYTVTNRFRKLLLIALVNLVVVFAALIIFVFFLILHLNKKHEDIHISSTSHNHLETTTTSTPTTSAQTTKTDTTSHSYSCVTTTELFDNTAAKSVDDTGCSPNQKSTFFFAYSYDLTIDQVLNTWQSISNNSNFFFEKYALGIFDMMNSNNNITGIYDTLLSGLPNSTESLKDPSEGGGVLSIIDIFFFEDITHCGATLFIITKRLPTDTSISELVSMLQKYHTYVTFVVSNNSFGGLSPESLYRLASETNGLCIFTDDDRIQEFRSTSFWHQTPTWLPSIWPSYLVYSFNANVTNSGSVTLPIFNSPLVGCYYICMTLQDHGSLDTFRMVKLTWYNAKSSKSGYFEETVESHADYGNTTYVKKGPYTLDAVPYNMTLGFEYSDDKIKILQIRIYSVSIMTMPYRGEFVLAKTFGKTKIPDFSESPPEEPKNVLRKYWKAILFGFMCFLMICLIFFLILFLVYWKQTDSITSSTVLPTSGTTTDSNATTEVSTTPLPIIINTTSKPHPAPFLEGSTTVGFSTGSQTTNRLITELNSVPQSTVTELSTPFALRSSYSTSGTTKSVTTAPAIVTTPEQSTTFGLTTTLEDSTTSKPLTTKSISTTPLTTPKYSSSSTQKTTMSSTTLSTSELTTSQVTESTEVSEPSLSSTVSSTETTIFTNPSTVTIISTTAKPSESPTTSKSRTTANPERSTTSETLKSSTTVLKDLTTIKHIPSSLFTTSETPTKPSEGSSTSKSQTTADLTTIKYLPTTETTSVQYMLFTTSTTSKPSERSSTSKSRVTSDSKITTETTEVSTTVSQGTSRSWATVTTPSVLTTPTSPFSGIQIETSTGSSTTFTTTPGLKSTKPASTLPQSTSSSLKTTEGSASTVSQSTSTTAMKTSTTPKPELTSDVRTSSAPETTTETSTVTTTESTTPKSTTVEITTVTNPSFSSTTASTSTVPLASTSSVSSSTTPPVTVTTTVTSQSVGSTTGSTTAVPTTPDKSTVSTIRAESTTARTSDRSTSSAYKTTGVSTNTPVESTLSSTTTGLWRTTTPKYLSTTVTTPSSTLPEFTTTKTKQYSTTSQHIPTSGYQSSGTIRTTEFSTTRVTTPSTSVITTTASWGTTETSEHSTTSDESSSTSTVSAKSISTTPSTSTQETTMSSTAINTSKLTTPQSTTTTTVSEPSLSTVSSTETTIPTSEKTQTLSTTSETSNVLTTVLKDLTTIKHLPTTETTILTSPSIMSSNVITTTVPLSNTTIEKTTTYKSSPISSSSTAETTKSTSTSATSQQSTTVSTDGTTTTSPLETTTFLKYTSTSEILKSTSGTTIPEATTTTPWLSSISTTTVPLTTTEKTTSEPPENDQVESNTNFILKHWKSILLVILGLVLIALVIFLIVFFVILKPADQSTSSTVVSSGTTIGSTTVTKLATTTKPSSKSTVPSVTTVTEKRLTNPLHTNGPITNTAASEFSTKPSSITTAKLVPTNSHITTKSTGNPWTTVATSKTATTPVELKTSTQILTTVSSTEKSTMSSSTTFKKISTTEATTPTSTTVEITTSTVPLASTSSPTTVINTKSSAPSTATSTPSTTEHVSTSGATTTIATSKPPPTTREQTTSESPEPPARSSNFIMNHWKTILLVLMGLLILSIAIFLIIFFVILKPAGHTTVSPSTTRSSIGTTKLLTAVSSTTSKSTNGLTTVIKSTSTVPPINSTTRNKTTETPPIASVQKQKSPDPVFKYCKIVFVVLLGLLTLGLIVFLILFFVVLKPADQSASSTVVPSISTTGSTTVTTKLATTTKPAICSPITNTTFLFAYSNDLTSTLIKKALGDVKKYIVNPKITTFANNRFDTSKEDPIHFHGSKEDFDNSVNALLPDSKLKLPSTNDGSNVLNLLRKFLEQPTCGAIVYILMKRLPNTVDVTDLIQELRENHISVFPIIDSAYIGSKDQSIMCKLAHTTNGFCDYQIASRLENEVYETMWIVSRVHVFVSQSYQVSGKGSIKVPSFVRPPQGNEKGSMGLVFTYQNHVRDTNFKALSFTIKTDTNTVVLKGQTNQNNGNALLAHPSLNNNVTYLIDINYEYEKTNTLEKIEPARHMDSISNLSKCFNYQCLDSLFDVIAGSEVTRDTESSREAVLVYQNVGFEEEESELPGSQLEVITTSALASASLRESDQSTPILQSTGQVEEESEVPGSQSQDATTSGPASASSRELDQSTPILGRIGLGQVLSSIREDIEPNEQTKPSEPPIENLPRYENLENLELSNEAISSSESCQVRASTSSRESPILESIGHVEEESEVPGSQSQDVSSSGPASASSRESDQSTSILGSVGQVDQEPNEPTRTSEPPAENLPRYENLEHLESFRVIRQLVPVYQYMDCRAEEPVRFRPQPEEIPIETPCLDFTVNFVLDYWKFILIGFFILGIVIFLIVFFTTSKHGSVAPTFGTTTSFATVTTTVDTVTTTEAEPMQFTISTTSMNTTVADNFTSPSVDGCSPITNTTFLFAYSNDLPSSLIQKSLGDIRRFIVNPKITTFANNRLDTTKEDPIHFHASKDDFDKSVNALLPDSKLKLPNTKEGSNVLNMLKKFLEQPTCGAIVYILMKRLPDTVDVTDLIQELRENHISVFPIIDSAYIGSKDQSIMCKLAHSTNGFCDYQIASRLENEVYETMWIVSRVHVFVSQSYQVSGKGSIKVPSFVRPPQRNEQGSMGLVVTYQNHVRDTNFEALSFTIKNDQNTVVLKGQTNQNNGNALLEHPVLKNNVPYQIDINYEYEKTNTXEKIEPTRHMDSISNLSKCFNYQGLDSLFDVIAGSEVTRNTESSREAILVYQNVGSPGEGESELPIPQSQVFSTPGAASGSSRESDTPILRSIAQVEEESEVPGSQSQDVTTSLAASGCSRESDQSTPILGSVGQVDMEPIEPTRPSAENLPRYENLENLESFRVIRQLVPVYQYVDCRAEEPVRFRPQPEEIPIETPCLDFTVNFVLDYWKFILIGFFILGIVIFLIVFFTTSKHGSVAPTFGTTTSFATVTTTVDTVTTTEAEPMQFTISTTVASKLTSPPVDVNSQYPMSSVEINIEVVPSEDSDESIFTYCRVFFFVMLAILIICIVLFVVFMSSKPAESSTISTRSKTTITTTSLPVQNCTPKTDTTFLFAYSNNLSPSVVEKGRDLIVQYFQTPKIVNFANIRFDTTTDDLIYFHSSKEEFQKSVTNNLPDSKLSFPSTNTGSDVLNVLRKFLANQESPLCGAIVYILMKRWPNTQDVSELISQLRQRHIFVYTVSDTSQSGGENQSLICEVTHGTNGFCDFQSTGYMKDDMYQSLQCISNTFQIISQSYEVTGKGVIQVPAFVRPYQNNGLEPMALVITYQNHKRDGNLKSVGYRILDDKNENVWMNSLKSWDGNVFLDHPVLKNDVTYQIVINYEYGGVREEKIEVRRSGVLVAVFLLYAFGNRPSVSRIVDVPTYNDDPTTEMEPINKQNYFTLLNQVGDSQFQKVILIGLLNIVIIGVFVAILFSLFFLNHKDPHTPPDNLSTAVSLGSTVSAHTTNTTLLIPTTSAPTTFATTISAPTTRTDTTTHSPSSDTTTYPFDHTDCSPNHKSTFFFAYSNDLTADQVLNTWTSISNNTNFFFETYALGRFDNMYSRLNETFSTFDSSDSFDDITDALLSNLPNPADSFNDPSRGGTVLGIIDSFFCSDVIHCGATLFILTKRFPTETSSYIDYLVSLLKKYHSYITFVVSENSLGGLSPESMYKLASETNGLCIFTGDDKIQEVWITVLVSKYLFFASDTLLATIHLAFIFVNAEVTRSGTLTLPVFNAPLLGKYHISMTLQDHGPLDTFRMVHLTWYNAGTPNSGSFEETLESHAGYGNTTYIMKGPFTLYADPYNMALEFEYSDNKINILQIRIYSVSIPDTCDYNYNNYCYTKLNFQFTFTDAQDACQRDCSSLSIHSKLENRLVVSMFNMTRSLLLGGVAPSENLGTRADRTTEDYNNLKLFDMELSCIHMHFQSDDWNSALCNKPSWIVYAFGNRPASSNEDPTTEMEEIPKQKHFALLNRIVDSQFRKIVLIGLFNIIILGVFAVALFFLLFLNHKDSHTPSDSVSTAVSTGTTASGPTKSSSLTTNTVSSGTTVSAHPTNTKPTGTTTTITRNPSDCTPTTPATLLFAYSNDISTSLIQHGRSWITDYFTSLKIVYFANVRFDTTTGDPIYFNTNKSDFTDSVSANLPDSTLSFPSQRTESNVLNVIRKFLSHQEYPLCGSILYILMKRLPNTKDVSDLIQQLRELHIFVYTVTDTNSFGGNDQGLMCEITHATNGFCDFQSTDMRNEIYQTVLEISRTYQFVSQSYLVSGSGVINVPSFVRPVQGNQSGTMSLVITFQNHGTDDNLKSVSFSMLDDQNNEVLSDHYKSTNGNSFLRHPVLKNDVTYNIVINYEYGEERKEIIEVRRMKYFITITVLLVFLFNLMESLTICPNGFDPSTQFMKMESCWKYMPDLLDQEAADAECLKNNGAALVMISSCETTHALQQYLRDKGVSRIWTGLTCNQTGVPTSCYWSDGRPSTSVLQADPGANDFAPGSPNVTVGECISYEESSRHWISTNCGVSMTFVCEKNDSNSLHNKSTNGNSFLNHPVLKNDVTYNIVINYEYEEERKEIIEVWFYSFSRMKSFFFTITCVFIFFVFNPTESLEVCPEGFNATTQYKKVHTCWKYIPHELDQAAANAECLKNNGAALVMINSCTTTNALQKYLRERGVSRIWIGLTCNETAVKTSCYWSDGRSTSSIQADPGYNEFAPGSPNVTVGKCISYEESSRHWIRSQFHVTLEREASAKSENVEDSHRVELEEENYQHVMNPDDPDESYNHPIRFVRNPRLSREARGEPPEYELGRETELEEEEPVRFRQPRQEEEQEPANPPEEPPEDPQNTPFLDVAVNFILDYWKMISLGLLALLILGLVIFLIVFFVTLKPAGHATVAPNSTTSTVTGSTVTTVTKPTAVTIPTVSTTTTTTTVTQAPTTTTKTTTATTAVTSLPTTTTTLSPAPTPTADPNSICTDGYTLFYNKCLKVITQPATQASAYEICSKTGASLVVIKSGGENREIGEFLKLQGLRKIWIGLQCNENDKSSCLWDFGQGDLTSYSNFVTGSPNIGYGRCVFYLYNESLPDAGQWGNGNCDVDQLSYLCEVPPTINDYCDFNYNKHCYTRIDYGFTFTDAQDACQRICSNLISIHSELENRFVTSMFNITGYLMLGGVAPAKDLVMWIDGTPRDYNNLKLFIADQNCMYMNYITGDWSSVDCASAAWPVCKRKAGARC\*

>Cre|FL81\_23076

LSPNFITRCYSFPRFQLNFQDARTYCHSQNKYLAVIHDTTQSSFLATIVRTRSTNANAKFWIGLTRSSANSSYVWDDGTPLLWPNFNPNAPQDGRYVVENSDNSQWQTETACVLLDFYFNFAQLVAASLNNASDFSGYIDTFGYNAGLSDHDYFSPYSYNEFKSTPFPIDSTDDEIDLDLKDVDSTLTTATWVPPTNDQTCLIFFSAACHFNPRTN\*

>Cre|FL81\_24087

MKPNVGRCRKRRLLEFPVVFILILAALVKPSTSSSKTPESVVTDVELKCPDEWIRLGTKCYLPFSIHQSWPFALTTCQRYGSTLAKIQTGSENQFIASLLSKPAKSSQEVKEYWIGLTVELYIWSDGTPTSRYVGFWRQDQPNFLNGTCAMGRVERKDLEWRLETCNLLRKFVCERPACVQGSYFCSSGACISESKKCNGYADCDDGSDEHNCPSAFHPTCRTSEKAENGQLSSPNYPNSYEPNLNCRHVLEGPINSRIELTIEHFETEPDFDVLTVLSEDICERSRVCVDGGNDARTSRLFNYA\*

>Cre|FL81\_24231

MMRKLSLFFLVLLFAVNALDFGSDSSSCEDDDGHGGGHGHGVFSGSNIEYDAASTACSNNNAVLSGIQNSEEKNYISRSASSHLSSSTGSLWIGAKRTATCARSKLTATCSKTTSFSWTDGSTTGTDGFSWLDGSQPDNALGGNQNCIVFFFARSNTVIARVNWFPGALDDVNCDAAQFNSIPQRKIQGYVCGKDASS\*

>Cre|FL81\_24443

MLIVTLILSAFLIYSVEGQCSSTEDSYIGDLCYTIYNQQLSFQNAQSYCYGLNKNLGVIHTTLQSNFLASLVRTKTGSNEALFWIGLSRPSMNSRFQWDDGTTMSWNNFDSNFPKDNLNVAESVLNGKWRTMNGQEALPFVCSYDPRKVTPGTAGPTTTGYYTDGSTTSTDWPASTQTQSSSSGSTSDYITDSTS\*

>Cre|FL81\_24444

MLRFILALSLIHIVAGQCNQNDRLIGDLCYSVSTQKVSAENAGSLCLLYNQYLAVIHTTLQANFLASIVRSQTGADKFWIGLRRASLNSRFQWSDGTTMTWSNFDSSLPKNDYYVAESTTNGKWQTVNGGQQLYYVCSYTPGSVTGIPVSYPPSETPAVSYPPSGAPVSYPASGAPVSYPPTGVPVSYPASEGPVSYPPSGAPVSYQPTGEPVSYPASGAPVSYPASGAPVSYPPSGAPVSYPASGAPVSYPASEMPVSYPASGAPVSYPASGAPVSYPASGAPVSYPPSGAPVSYPASGAPVSYPASGAPVSYPAYTPDNYPSYAPTVM\*

>Cre|FL81\_24900

MLRFILALSLIHSVIGQCNQNDRLIGDLCYTVSTSKQTPEESEGICLVSGRYLAVIHTSIQANFLATLVKSQTGADKFWIGLHRVSGTSNFRWTDGTPMTWSNFDSSRVFQRGLPKDEHYVAESTSNGKWQTVDEAHEFYYVCITRSPTTGKCFDNQDIEIQGECYKFVPLKLTFEDARKWCHYQNPVTASYLAYVPNQT\*

>Cre|FL81\_25024

MQQFQMIKQFILLFIIFIVGVHTTCLDPNEKELKGICFHYVKQKMTFENARYWCHYKNPVTQSNLAIVQNQFTANFLASYARSAFGINDGTFWIGLSRAHNWNQWSWDNGTLLDGWIMIRTVLQHSLQVHRLVPQPLQLQLLVNQQLQLSLIESGMRAFQLVLLVGALLVTSLAVPQRPAGEPASRRPPPPPSDSPKYLSNPSRRPPPRGTGTPPPPPTGEPQELIEDGNASRGPPPPRGTGTPPPPSADEPRELAAGNASRRPPPPPRGTGTPPPPPTGEPQQMIGDNNASRRPPLPPRGTGAPPPPPTGEPVE\*

>Cre|FL81\_25050

MRNLKQFIIIFHVFLFEIAFNTNRLNHVYKSKRLFQIVLYLVLIATLIISTFLIYSVEGQCSGTDDRYIGDLCYTIYNQQLSFQNAQNYCYGLNTNLAVIHTTLQANFLASIVRTETGSNEALFWIGLSRPSLNSRFQWDDGTTMSWSNFDSNFPKDNLTVAESVVNGKWRTL\*

>Cre|FL81\_25262

MLILLLALFPTVFSQCFLGDDAYIGGLCYTTSNYKTTYQTAQLTCHWKSQNLAVIQNSLQANYLASLVHRLTNEQDGKFWIGLSRQSVGSRYQWDDGTPLTWSNFDSKYTQNKLNVVESTTNGKWQTVDVQESHYFVCSYDPSKYSTTLEPPSTYYPDSSTVPPVSESTYYPWSTDYPDVSTSYPPYGSTDYPWGTTDYPWGTTDY\*

>Cre|FL81\_25310

MSCMNRWSNSSLATEFCQPKHDFILSAVQNTQGFSPPYQYHIGLIYASGSWVWTQPTGFQQVPLQQPLMWSSGYPQLASDKSAVMNQQSWLGTGWQNIATMNVVANYVCETYSCDTDNYCDENMNKKQ\*

>Egra|EgrG\_000677600

MLTRLVIWLSLLCCGIAHGSPDSNCIQSGSSRWCFTFYSEPMPFGDANRKCEEVNSSLATVPNRYVKEFVLNYLNKTNNRTETFWIGLHWSHSMLRWISGYPAVVDVFWNKSSEDLSFKCVVASADGLWDSRVCTEPHPFLCSSEVKDSTESVRFLPHFKYECPRNFHLVGRRCLRFFFDEMATRAEAESTCTGLGAYLPTIRSFRENDLLVAMLADHPSTFWLGLSYGANGHWWANSGETEVAFTNWMAGEPSGDISNNCTVIHTDLYFLGKWSEVNCLSTAHFVCEAEPKLVPAHADSHLHGGLFVQGRCSSGFYEYRSACYMIIDLPPEVTRTSSLSSDSVTMACQNTVLDVDCSPSNVGGVLCPMVASPRDQFDAAFLRSLVDKFAHPPNAAWVGLKADRSHVYSDIPKFLESTNLLNYSILNALSNSIVCFSLHADKTLLSNNPCDSHLAALCGYELDARPLLPSWPQIPDVKPEVLKCPGDAWKLFDTNCYRLEGAGNEGRSWHDAELACIQFGGHLTSIASMTEDNFVRSLLPTTQPLKPWIGLKVLIDAGEDGSTVVKWSDDSPVNHLPLYVDGHGEGDEECFQLGSVQGKQFWTRANGCEELAPFVCKTPAFPISVEWKPQGSDHCLPGSHPQFCFSVNHTAVKFADAVSFCQAAGKHVATILDDSQQDFVLRALRQLASLELGRNTIQRYWIGLLRSRGTLHWVSGYPAVPNVYWKRGAEDSKEICVYVDVDLGNMLSWGTANCEEVNPFLCSNTPPLPPLLPSPKRPPIVPLKTSCPLGFLYVNGKCYKVEGDSRNNFTFAEAIAKCSRSGGHLATISSMYEQDIISVLLAERSFPFWIGLNTTTEGRKWANGASITYTNWMEEYPKWLNPRNPLCTYVHNQPTRTDGQWAETACNTKMGFICETRPTEVQMQQMFTPRLFSQDDCASGFLHYRGACYMLLRPSSSLPGRSASQLYDDVSAACAATSPIPLDCEKARGLAGCPVTITPHSHTEAAFMRLLIGEVADGNYVTEVWTGLKILSNSSLDITQTEDRVPLGSLDIDFGHLNNAAGAGYTCFSLRRDHTFLSSRHCSLPAPAICGYYHDTHPLHPHLTNADDFACPTVTERVGRSCFYRVDPTMKMSWVEAEEYCMIAGHEMNAAADGSVVGHLPSVHDPFTLRFIGQLNGNGLVWLGLTSTQELQGSTNGSWIDSQFQWSDGSPVDYLVFDPTTKKNYNRAALIGNLKTCVALDPQSGYWVKVDCFKRLAFTCQFPIEAFPKTHLVSGSKYLPAVKQCPSSFKIETENACYVVVKTQLSAKKALAFCGTLHPYASLASLHSEKEERDLLARLVDQHLEKAYWFGLSQSDLQYAWADSSVVDHISKTGVTVESSHFWHFQDCFTFNPLRNGPNASLTAAWYETNCSAERPFICQVYRGVHGPPSLEPAHPPRSDLPPLQCPQGYRQHEDRCFRFFPTLLSFDDAEGVCRKAVEGTGFMGFLARISNSREQDFVAGLFAAEAPRQPSMAWIGLRQGEKRWTDGTEVTFFRGSLDFPVPVPRDEESMCTLLLYSSNVHFYGLWSRSVCSISDQMYFVCQAVPISPTAVTVDNTAKANTMESTALTCADGYTLGFFNRTALALGESLSPPHCLQLVSTTPMTWQDARSLCKEQSASLPSIDTLADLSFFRAWLQTPRSLGGAGFPSNAAVWLDLRVPACPQCYSNWRWHAGEWDESPVRLTDWFNAPPDPSGCYLFGVAPPARNSTIASHLRSIRPAISCTNISLPVVCQRNLRLPSNSIGFAVNRCVRNPTPELSNVTAFHTNHSVAISGRACIRWDLVQHDFNRSDAVLPRNWRIFTAEIAYSEHASPFWEEHCAHLAIQDAAGKTIYRYACYTSTDPDSGLEDCDMDSCVTSLIPLGWIIFIALTCLALSVGITLCVVRVWNRQRFFLPRGRWLSPIKMTASSSVFGGAVAVHRQQFQQHGVLYSNGDGDPAAPYVRMFDNPASLPPLHSLVPSLTFKHNVYRPLHDQNPLLLDEPDNADEFTGPQMVNPEATALLLVTLTMPRPLTVPFLHDHKFLAYDWLCWKRF\*

>Egra|EgrG\_000176400

MEELAPIFSVVGHLEPKKFDCSFRDGEVRYYHEGNPLLNMDTVRVTIFFFRNNHSIIQTADIPVDIMDLPEKGGEMDQTFPRPRIHGPLELNVKSIKAASQAISASVLKIDYNPEEEECCLSFTRPDILSPGEQRRKQNQLESQIGRPLVTPWWEANWGLWTPRLGRPSASGPAIGASRRWPLFGHIIAAAFNRTAVDHFEHECHEALLKGYRYLHRKSDSSEADYIPLQVNIWRKVPDGGREFVTREARYLRVSIAGARKLEPPVIRIFRQVNLTHIGGSFSVLPKDCIHVVNPDLEDLLEVNVTKVQGPLYAQLVNLRDPTRPVLSFRIAELRKGLIALQLLNYAEMIEKIFTLTLVAIDPFMQVSEPVNLRLVSRLQPVFPTRLLGSSMGHKPFVFQVFSLPLFSYTGALSIVQRYNLQVVGYIDESMVRFQVLPNREEEEYFKLFNTTGMGGGHLQLLGMPLVDGGATTPTTSASTASWTLNEIAGQQLLYAHPGSLHPTVDRFRLHPMLDIQRAGYHQWMRVARQRIRRNAGVSESELELPVRVVRLYENARESALKKDITINLHHGAAHCFTSEELITPSALEAVRSDFIDLKFHVKFHPSQGRLMRRSMLLRFAFNNSTQQRRRKPLISLTKEGVEAVDGDGGVGTADAKGISQISVISMIDLEAEEICYLGLRRDSRADMFGLQQTGQNNFPTVAVNINILPKPKYQLIRRTDPNQEPLEVAESVNFAVLESTNLCYVVRPTRQWLRSSAHNLIPLMPNTTGVLYSLTSQPRFLITPSAATLESSTSAVSGQHGAADAGRLVSLATMSASQMEGDMALRPGLTNLLRELEPTGLSHFTQAQIDAGDIVYVPPVKDLGPSDQIVEFRYTVSAPGITPFNEESFQFKVLAEDNQKPDLKLLKSLEVHRDGELMIDNSVLYLSDEDTYFDRLALRVTRAPKHGNLFQMMQHPMFNNTNANYKTTATTAPLANRRKISEGEEIPAGLMRAGKLSYKQDGSNVKEDSFNLTATDGRQDSEVVNLKVAIRPRVLLEPVWNLLVNNSIIVEENSTVMLHPSVFPPLTLPAMRGPRFFVVVPPTKGKLLLDKKRKTAQFSTSDVANSRISYRHGPAEIGTEDKVDLVRVWDFKTGKIFSLNFTLLPVNSQPPTITALAPLQVNEGSAVVLSHQIISVRDPDTVDSQIKVKLVTHPKWGHLELRPENNTSIGSTEFAFTGRDLITGRVFYANSRHQDGLESVSDIFSLRAYDEMFPSRESTPIHVSIHPVNDEVPSVRLVEYFAVPLNGRRVLTPYLFTISDRDVPRDILQISFPRLPRFGHLTVHWQHGEQYTITEASAPIAESYLGMMNIVYIQNGSVQLPARDSFTVSVSDGLHVVKKSAYVLLRQENRYAPEIRVTEEGGLVLEGLAWRQLTSVLTISDMDTPGEDLVIIVVRAPKLGQVERLQRQDVTGVPAQEDLIEAAMDQYEAEVDGEKRNTRNLKEGDRFTRRQLDTGRIYYTYTGEYTQAYVYDLITLSVSDGQFEAGPVDLPIRIRATKGRTNPMVQSQSSLYELLDKGRFDSDTLLSDAASELWETKEQKTEEPSIFLDNFKVTVAEKIEVAAGERRTLTVDEHIRIEPIGVDGSLENVKETLATANFQHLESEMSRRGCILLARANTSSNYALTEFTYKDVVHGQIMLNAESCFGKSPLEGAISLLLSIPLQKPVSFTIPIRIIGEVDHFPRPTVAIGQPISIIPGADIPLTLTHLNLFYTGMDPTKVYFYSSNGRFHWKHDCNVTAKVFSFFNIIHDDIVYHHTADATAPRLILVNLNHLEVDFNAIQIERFIESIIPLTESSPLLQYLRADSPDHITSEPITLRITTDDLYTHVISSGRIFIRAPGPEELTRVRAGEMGFFLTPKHLLASDASVVYSLDTKMRDKWVIIDVKSGEAMNRFTQEDVNRLRLALVVFSHPLQTKITSFGRQKTRIETRVNVGLSLFEPKSRATENITLSVYWAQVGFDRKRYRICVSSGVLALPLVRHGALGHHVEVYVDEVIKQVRMRVTLSSEMSSEKQFFTVAVKAPSGAVLDGNSEAHIVMLGKRKCRNSPYFTAFNTSNGVGTGDEVGHSRRVSLHDWLASNVIPDSNALNKAYLISMQRRKRAPAFSCDSSWTLYQSRCYRFFHHENLTWLEARDHCENERGYLASVPDASTSTWLKTLLGSYSSRLWIGLHKPVANGAWLWHSMEQTNFVNWESGYPKNLRGKLPRQTSHLRRRLFRRHPSPPLKTAEHTVWRSTSAYGYSRSPRSASNGWHQREALGQELGLQRLCVNLDSGRGMVWRNAACVRMPQLPFVCMKNPN\*

>Egra|EgrG\_000699700

MPPDIMKLIILLIYLNTVPPTLGLGQCSSVWKAFTTPSTLHTGVGEVKCVDLCYFKSYTKLTYAEGAALCNSLNTKMVYLKNEAENNALKSLVDEPIYLLTRVVGSAFFNDGDPVTYGKWDCDIFSKKDNRCVKRLKSGFMTTTSCNERLTVLCDLY\*

>Egra|EgrG\_001157000

MRILAVSRSEECPNGFFRISNSCYFVYNGTKELFSWSEARKQCKGLHSDADLMEIHDQSTQDSLNVVISLVAWPVWIGLQSSAAYSMDRSSYKWITSNRTPNYSNWAPDAFSYLEISSKQGCAFLSTANLRVGAWDHSDCDKTRIGFGCEVPLNSVSSLNSTIRLEGAQPAWTKENNAAGQICYLGTCYRLLPSFPMELGFDEAKELCGDAAVALPRNPLELIFLVDRLANASVSTRAWIGVEVTNTQDRLEFPRTSSVTPWLTAAIHRSHPAFLIPPSNQSETFCLQVHVNFTSTSPFLVMPCVGDDDEEAEEEEDATLVTAFCATPEPSYPGSCPDGEGSGESVEWHAFGDKCFAVMRDCEGDSVPASLKTPELDAFAAWLLPSNLRSDDEVLIGGIVNTTSPLTITWLDGSVTEGFNRLKPSFLQHPVSRDGLCLAIQPGSGWWVLRQCKGQSAPRLTLCSIPIKPQNHTTTIGPPVRESEPMCPEDYFPHHRNNGSVVCYRVVLGGARSHGHDWRAAERACRAVALGGDQKVRWRGNLASLPNKETSDDVIALLQQNAFTVGIWDGTNNLPAHMLRPSEFIWLGLSKSEDKLFWNNWTDGSTGNPTFYDNRTRQNQSFFSDSSGYFFDYGTCIALHLLSGYWYPLRCTLDLGYICQATLAPDSETEGGVDHFDIPSCLISSKSRNAGPSVETGFIHDPNVDCVVPGFTYFNGQCFRTFHDKFMTFAEAQAHCHDIGSPYSRNGKAGLAIFRSEADQLFVASQLSRLPRMPASPGFYGRGSAIYDRLEVIWRRYHWVGLFHYRHTFHSVDERVPCYIAHELNRPLASSAGGPLCVSITGVPDTEHFASLTFDIGCNESLPFVCSFEPSPTRLTTKSSTSVCPKGYATHNAATGDHCYRFMGEWMGSYEEATAMCAQTAAGARLAALTTPFTVAWMRAHLPSDYTATGMLPWESVPHWIGLKLRARDESSWRWANGLPVTHTRWSSQPVDVVNSATDMCFAFAKSISMTSYELDMITVNCSRRLSPLCEADPLVELPISMSKPDESYLAADQHDYIGRLAKSASGKACIRWDLISPTNTSEMDALQRAFHNFTLAAVAAALDVNSSTDGDIYSPAFQPVFSSVCNWCRNPASLRDHAFCYIDVDKWEFCTLPPPSISSSPSSPSTSQIRTTLPFSVIFSIVVIFLGVFFLFPLCLLFIFCLHRKSRTGWVSTSPVQEILLQRLPFSWRWRWSRTASQPCLLADNVSYSAGAVQEDTIRDPAA\*

>Eve|EVEC\_0000124501-mRNA-1

MASYAFYYDNDISIYILIMTTLLLTSTLLFYYEFEISIYMRTHRTQNVTKNKTSSFHLLLPSKMQIFIPVKILKFINVFSSVSIHGGSRIAKSFLCITIRFFTFSVAEQLAKNQFWLGLVKKSDNWYWSDGSDFSYTKFLPMPSVDEKTEMCISGSLSGWKLEESSVKVLSFLRFGVDYKYKNLYINVLQLPMKVELGIAEQICLARDSSLVWITSEAEQKFLNGELNL\*

>Eve|EVEC\_0000124701-mRNA-1

MPTFDPSEFSEEHHIVVFNKSRLFVVNSSIYALAICKFPKFDRIQCPTKWQEYNGNCYFREKNVHSREFAKTVCQQKGAHLVSITSPKERDFLYDLARKLPFHTGLTTRHTEVPVFLTTSRNLFNYVNSVKVLDDAKGKTYPIQYKKEFARMTTITHENQSHPLCEYRVYHCRHDWYPVGEYCFKTVSISNSFWLKNYRSIIVVIKVRTALFYDDAVKTCIANGAFLASFQSNTEEDIAKDLVPSRYYWIGAQMYNGKWVWQDGSEWRYGKVKLEDDYPHKLPVVADRKTKFWIGISPNSRFPALCKYHGA\*

>Eve|EVEC\_0000135401-mRNA-1

MIRTFFRFQLGFEVRAFLCFSLLLLFTEVYSNRTSGEALEEGLCNYGYQNFQDKCYYFSCLNCRKNFYDALQHCREEGGDLASIHSEEVYKFLKNQTNNFLIGMRYDSGKEQFYWSDNTTINFDKLRVDFSKWHPYFGSCVRVNDGVWENAVCERKYRWLQSPGYPSNYHVGDSACYFKLVVKVDELIVVVFNETDLFYNFDNTYLEEDVIEVFEGFEDNERLIARFENAFNTLQHVINSHKRFYFTYTTTNCPIVEL\*

>Eve|EVEC\_0000159201-mRNA-1

MVIGKAVTVKTCPHYPYANYLGIPRMIEGYKPLKSYCFYPVSARVANFYNVNPENEGKISYAITTLWAPQTFNQADEYCQTRFGGQLASFKDARERILLHKAVFPSFDERSHKSLGFLVGLKSYFHAYPIFTDGTDGSYGFNRSETESDKLPRCHGIVRSYKYPIDSMQAVKCTHFFKFVCKGRIFSIPKEVQKYMVDDTTKQADSNDICEEERELLYFFHATKVVDIRDGSSYCIHDFFVSRKVHITDFQEAEELCRTHLGGHLLSISNSEELRFLSGLLFPPLNGSMVELELRPLGLHYSHGDISNFTDGSNGLYAIKEGYKEKNSLDLLGKCFVFVHLYNENRSAIWRSNCKAETVYKRITCKVRNEPISNGKSKRFAASGIGRDSTQSKRNWEQFLIMGSIGAVSGLIIIALYISRSER\*

>Eve|EVEC\_0000169201-mRNA-1

MKELSSDLTARFSRQILAVQDRIEYLEKELDGLKKAVTYDWKRTDSGSLYNVFFINKNFDDAQIPKSLSLYFPSDILTDALNETEIEQEVWFGTKTKTSTMSSPDSTYSNFDEKQPLKGCTSITSDGKWHIKDCSELKPFICQRIFLR\*

>Eve|EVEC\_0000203301-mRNA-1

MQEVLKPMTFEEAERNCEILGSHLASFSSVQQFKNIRNRFPRTNWWIGLKQVNQEWAWTDAKNVDYGIWSKYGLSKIIIDVQKCMRATERGSWERSSCELDSSSLCKLDPLESCRPGFNEFQGFCYNIETKRVAYEVAQNFCLANGADIVWVTSSKEQGFLNGLASSHPFWLSLVLESGSWVWKAEESPSFLNWKHGEPNHCCPEEEASNAFSEPSGWSDTSYLSKYAVVCKYKKGILLNSEVDFESDSSLSRRSPEDQSRLIAILPLSPFYATGIVLLVMVAITITAILCRKKPVVIVEYAKVPEIFEDDSYSAKVYYHNPTIIREYDA\*

>Eve|EVEC\_0000203401-mRNA-1

MVYFQGPRCVDRSTAADFCEDHGGILPTIKTDEESADALRHSENGFWLGVERIGSRLTWLDGLNSSASLFVGPKKDSGNFAVMTTNGHWRVVEHENETCGKPVCFMRDVVTSTKCPWYSEEENYNIYDSVVVSESNGKWYYCLIDVGTKDGKTTTLASSQKYCHNAFKGRLLSFPPIREYIFLHGHFYSSIKRGKPRVTLGPVEKELVQHLADANINTLTMAHLADTFFVAMESKTDIKYLCRPLWTYLDGVCYKKGTKKLTYSQSSEYCRTMERSRLATLYDDNSLVKFLDIPNDKRQNYWIGLDYQDNNYFWGNGRQYTLKSLKKPQPNFRVAITPDGFELFHETSKFLPICEYKSSILLTDSGTVRRFACKKYFKPVEELSNESFTGLETRSLRGQAHYG\*

>Eve|EVEC\_0000203501-mRNA-1

MRLYQLLTFQIAQPVIFEDAERYCEVLGGNLASFSSVEQFKRVQTVFPGTKWWIGLKQVNEEWGWVDSQTVDYNTWGSYGLTQEIISTQKCICATERGKWERVSCELELASVCRLNRITNEVKHKQLIRKLQGVERVEYETARNYCIAKGAELVHVASSNEQEFLNDLSDFHPFWLSLILHSGEWVWQFGEQVTFLNWKKGQPDQCCPKKEATHAASESGVWSDTSPLSKAAVICKYRKSALYKNKIVLEPDKGAVAKRIVWSETEKLLAIDVSPMYIIVGVLAISVALISLAIFCKQRSLTMQYVQYAEVPRYDEVYFGRY\*

>Eve|EVEC\_0000203601-mRNA-1

MQHFNKRNKISCKAEQNLQPTVQHDKGLDTSRKCPWYAEQKIHEIYSSEVIAENYGKWHYCLIDVRVKNGETTSLDNSVKYCHNAFNGRLLSFTSIREYIFLHGYFYSPIKRGRPHVTTGPVEKELLYHLADSNITTLSVDPAVETFLVPLPPETTFFFLRDTPNFIMVFYLPDVKHLCRPLWTYFDGMCYKAGEENYHHYNAKKYCSFMDKSRLAILYEEKSLHKFLSLATPGKRYWIGLKYEGDRYVWEDGRPYTLKPLPPPSNSEQLVQLTSEGFQLANKGAIAQPLCEYKSSVSLVDKSSIQRFACKKYFKPVKEFEDETFSGLKSRSQRGQLHYG\*

>Eve|EVEC\_0000212101-mRNA-1

MGPPDGYPASDAWIGLTTYGDRRRYFIDGNACPFRKWYPGIDPENRPKSAHRNKNCTLIDSEGEWDVEDCNLNDTVRAFVCKKRAGFRKWQPPKRLHL\*

>Eve|EVEC\_0000212201-mRNA-1

MIDREDASNCHCVKLDLTSGKRFWLGLRKSKSNGNWSWDDGSEYSYKNWDIGEPNSCCPMDPIPIHSYVGGNGLWYDTGELHYPLPDGYVCKYKHQCAEDWNIVWNRCYKYVNATVNSFTVPETYTVASTICQGYNATLTSIGSTVEELYLKTLTGGVPFWVGLQRDSDRWFWTDGTDSASLPWKSKEFSNCCENDEVTVIYNQGLQVVTVEDWQTGFVCKIDGDADYSPPAEMHIAKTILLPKKLEQQYPSATITTDSKKISDNCSFEN\*

>Eve|EVEC\_0000217001-mRNA-1

MINRYYLRENLDRNFPLAQEINEPMAFEYARAYCRAWHRGQLASFLDSVQIETFKTLIREGMKAWIGLFYNGSDYVFDDGRKYWENSQLKSKVGTPDYQACFGVEKSGNLGATRSS\*

>Eve|EVEC\_0000217101-mRNA-1

MRHNVTKTVSPGRKCMSVDGIGNMIRENCEREMSFLCRFEQKLIIVIILFATFYQLCFCNCSEDKSPKAVEWNVARKFCFARGSELVWIDSEAEQKFLNTLAGMDPFWISFVKNGDKWEWLYMDNVPYTKWKSGEPDQCCPVGKANRAFSAHNGWSDVGPTFKTGVMCKYEIKLPYFCTYFKID\*

>Eve|EVEC\_0000217401-mRNA-1

MNASWFVTLALTLFLAIGKLRAACPPGKTGPDCDIPICDTPGSVEHHDGMEGYGDYIFWEVSFGCNQEYPVNIDEYVNDITVSAYGNGQRFSCGLYKDEKLIIPSDVSSTGTGWESGHYDGIGLAHGYGQYTVKLSTESTTQCEISVSAVTAVVVNGGFITDLSDSNVQQLAPRPHQGVGQYPKVNVSTYFAFEVSDALRRPGSATSVTTYMAEGFEHTELVSGYDTMYNQWDRVYPFMCEGGTSPTTGPWVPPTECYNGGILINGGTQNAECYCGYYYEGKSCETIRCFHDGYAWAADSCACAEGYSGTYCQDVNCRDKSYVDGLHYRAIVFVIRTGRSMIDHITQITTAAENIASYYALIDPTYIQQWVLVTVSQGTVKMTTYDSSIVFISAINTLPTTEDTICNDVLFEGISAYLSSSYAEAYKRSSIFVFSDGLPDDSEETRFGLYHQFSFFRGQIFFILADSSIGRCYIDKSAEEYRSLRSIAQFTHGHVTYVDINYISQSKLLEEKRIPSEMVEEDSLQFILFNLAILFEAENLVVIMLQIVKRSMKINVCSIGTLFGIAVDDGKAAYLLAATMHQAVQVMTNDFLDSCLKAPKYQSFFIDESLKSFYVTGVGDSLVATVITPDRTVLELDTLYSQGDLHIWKLENATVGGYLLSLKSAGAGPCSIRVYGSAETALWFGTTDNVNDDFELTLPTTTKEAHIVAYIKGVEIPDTFQTHAEATLWSNEGPEDKRVVKYASNGIYRDNCAYNLYFGAYQCERPFSFVYINIYMTSKSGSIVQRSATAYCSTTPPTSTPQTDCLNGGLPVGINNTCLCPAHYTGDKCQRIQCLNLGTAVGGTCTCVNGFTGKFCQTASCTRRNDEVYFIPNGRSLSLIIQDSISTRSAIKAISNQLPGLYQDLIHQHKDWISNYQLWRFNDTTFTNVMSSSNPNDFLNGMKTLKNSNAEHSDPSCRNLYVLPGLLNALLHTGLTYDGIMYLFISGYMKFSTTDMSASAAVYEMLQATRVKLNVVLMSPAPCGQDLNSPESTVLMNLAAFSGGEFTMVMPPRAGNVIRSIPTLYRGSYIYENYAVNCSQQQNFYFPVDSQMQSFTAYILGDLDQTSIAYYQPNGFAKAPYTLWSDIGMGSRMDQIIKECDDGWELLSNRCWLFVLRSQPWDVAQAMCHANNAVLITLFNEYEQSYVNQHTMKETYWIGLRRGSTGFVWDTINDKQLTLESTGYTNWAAGEPTSDSNKICVTDKAAVGWKMNDCSERHSFICVKHAYNADYEPDAAEIGERLARGIWKLSMRTLEGSCYVQIYSQSGIELYTKFTTNVHDDFGEAQPITNADDNRFVAHVTNQLSTSTGNAGELKYAHLYQENLKIIQAQTYSRRDQDKCSYEFISTSFKCPADNFLSMSSGIDRFGYLYQRIQPVACYSGAVAEDCINGVYHNGRCICEPYYSGDFCTIPSCQHGTLDSVLQHCTCSDEYTGPTEYEKEYTPTTDERSIMNAVSRVMESDFIRYRSLMWIVTAGVPEDANRLSLALDAVARRHVYVNFLIIGDKSGPANVQYNDSRLLACFDLVTETGGQFYQVSEEEGKLSKFWQGLLSELYDVYYISTKRLISCPAGIDEYIQVGSKTITLIVDVYGQGTMNVFSPNGTVASYTKAASSRTNLVVVVEADVPGLWRIVITGNKAFCGISVRGQSDFEVYVAFTWDMSTDNGLHSNDGEAYPVAHGMPNALVAHSSFGKLNFAQVFSNDERSLLWSSPLVARQNCVYQYISTNVFICPQHSLAVSVDGEDENGYPVRRMFHIHCVGTILTIAPLPTITTRQPVITTGYPTIQPPDCDKSGKFDMVAVMQELPSTVPIDQSHTRFILSTYTDAYHTVNPNFEMIKSSDDFLKYLDVLRRVEYEGTIGNNIQSIFDVANNLTWRSDAVKVIVFTSSMGWDKSNTGQPFPDPTASATAFKRNGGKIIPLGFGPNADQSQLVAIGNGCTKMSMNLDYFHSVIIPWLSGSICNVAGALFEILGIGLERISFRSTSRLP\*

>Eve|EVEC\_0000268101-mRNA-1

MKIRSYAKNECEKTWIATEDYCYSKELRRHNFDEAQQVCKKKGARLPVFLSEKEFADFRNMTKEPHDFWIGIRQQTRRMWRWLDGAPLHLSEISLPISFTDGFRCAVLSKRGVGFRSFDCPSYWQEFEENCYLLVCFKAFNEASIFSKEEEDFLKELVGDKTAYIGLDFMYLARDTYLPVEFELANEYERVFIKRAYFNVRYQECLQLDWKATMMAYQACEHTAEFTCQKESMVMWQPQFLLTEDISKSIYRERNEKVRK\*

>Eve|EVEC\_0000268301-mRNA-1

MLLGLQVTNKFRKESEILSTGNQTEMYIKADKFCINRLNGRLLYAENVDEFKYLYKIFYEHPEFSRIPVSMSISNNELNVYAETDLLNENIHYGAGVHQFLVSSENKGKYWIGATYKSGKWVWEDDEVLDPIKFSLTSGSSFECLAVVNGKLQYYRSCSENNEFVCEYSSNFNYVKSNEIKRVVCKGYYNLAELQAAIEDDTEDTVELEDTTDSGMLGYLKEYI\*

>Eve|EVEC\_0000275201-mRNA-1

MAVAFVSELKSVEQERSCPKLWFEFEGRCYYHIKSKLSAHKAWEKCRRHWGSDLVSIHDRYLNEFIANLEEDGLLIGLYYNEGKNAYQWTDETPVDFVSSGT\*

>Eve|EVEC\_0000280501-mRNA-1

MFRLLEVLALVLSLRGSGGTSDCVGNAIYNSHINKCIQFFSTAANWLDAERTCEKLDGRLVSIASTYEGNFINAEAQKNLPSNDYWTSGSNILHENFWTWIDQSRIIHTNWDSFYPTYNDTMMCVYAMKAGGSWRTDSCLKSQKAFACQIKPLTKVDLTEWTYYEETKSFYKPLSSGFGWNRYEEDCKTEGGHLASIHSELEATIVIQVGLGIPGCLQWAIGFKRVTPESNFTWTDNSDDDYTDWRGSNPQDNFQCTFVRYYDEGWMSYQCYSAILNSCAVCKKPAK\*

>Eve|EVEC\_0000290901-mRNA-1

MSFTIRLKSFKFHRYFQFELQAKMFFIFIILSIGTKLSRAQSCFNGGIYGQQFNKCYHFFYSPLIAEEAEAVCASIGGQLVSIASPAEQAFVAGSTLSVSTQLKSVILVPSVSNQKLKNGNKGSQQLEANNCVAATLVHGNWYNTNCDLATNYFVCQTEPIVVAPASKLLI\*

>Eve|EVEC\_0000291001-mRNA-1

MYSQVALVEGFLKAIPTMATKSWEDYEKECTAQGAHLASIHSGYENSFVYGIAFGDDLCQYAAIGLKSVSGNLNSFQWNDGTSLDFNYWDSGKPPYENKFCTFMRYHVKGPWYNFGCDDTAWSFCAVCKKPATQI\*

>Eve|EVEC\_0000292601-mRNA-1

MRQAVIFIALSVTFTQAMVCPVGWERYTGTADTCIAAYKKEMSWLDANNFCKSLRADLVSIHNSFQNLHAATIAEKKFEACRYWIGLYNIDKDKKFKWTDKSSVDYTNWLQGEPPSVAEATTVYMSLQSRFRWVTTTEVAENNCFICEKRFNEPSTNPESTTETFESPSTGAPTETIVETFKPNYSTEKKLTTENPESSSTGAAPVETNAGTSKP\*

>Eve|EVEC\_0000337201-mRNA-1

MREEMRQYYKSLIDEEKDATHFGYGGQCPTNRNAVLYSDGTQFICLGLVRDSDVSNFEDAEAFCEKHYNGHLLSIRNLKEHDFLLSILSQTRSITDDILQLIPLGLKGDPNMAVAFTDGTDASYVLEWYKPYNDSGNFDDYSDKPCYFLMFSTLAYWQGRQKPPAETFVIDWFSTVLVIVSGGVIVGSIIVVLYVTYVTRALPYVSKGVLSDYGVLVKPKVVRPYEEISDKSSRTYDIADSGN\*

>Eve|EVEC\_0000346901-mRNA-1

MGDVRFIELDYSRKCPQSFIQGELDVKQTRVVNERNGRWRYCLFDVNVKGNTVTSYESSRKYCSSTFHGRFLSTSSVREFIFLQGVLYNKSEDGRPNVVIAPVEKNFLRYLADAKVKRMSAEYGRFKFRVNIEEKWYFHDRFCRTWQDATLATFYDVEHLHRVASMQQVTRNYIGVTFNSTQNRYVFDDGRPYFSGGPDNVKHFCHLIRRTYTAITECKDFHYSVCEYKSQLLFTDEVSIQRFACKKYFDTEEAFEKQINQPKNFEDSQRYCETVDSTLASFSSEQQYKMLKERYAKAKYWIGLKQVNEEWEWLDATTVDYKVWYLYNVTKRKFGIEKCMSVDEAGDWRRKNCEEKLNFLCKFEPKLWCRPGFTEFNSFCYKFFNASVPWSTARVTCRGYGSSLVWITSGREQKFLNEFTESKPFWLLPLFYSGKWRWPFSKVPKFTNWKRNEPDQCCPKEEILAARSESGKWSDTSPLFKGTTVCKYEKGQLYVGSEEETYAAIVKKLETKLGLEEELPDEEVPTDTPVN\*

>Eve|EVEC\_0000350801-mRNA-1

MTTGKKNSGFLPPNSEFILGVARNSDHFYDGTDAKYARKNARRWNAAASPSDCLAVTRVSIGEGFISKNCPSQSGDRKTDKVEIRNIWYISAENGRSKYCICQDTEAIEKSHKEEWQKKDDKKKNSKNDNRNGSSGKITTTKAESSRRFDFEEAEETCITKYGGHLLSVRNAEEMMFIIDTLLPGGAEYEKQKYYIPLGFRLLSEYRISRFTDGLSAEYIVKRADNSADFRSSDISTKCYALVRDTKIKRSSVEIIPCEGEEIWKGIVCKTLESTLPDDVYSLFHPFLM\*

>Eve|EVEC\_0000353901-mRNA-1

MKYDKAYELCWRQHSVLAYIEDSAEDEYIKREFGNQTYWIGINCQKDRWLMTNSELAFHTNWIHRQAKGCPLNEKAVYETDYPGGWNITDKNSSHYYACKHKIVWISATLAILLSTAIFLLVLRLCLKEDDTETIMPKVIAGTAAHTCRAPVPDVTAPTTMIPTTASAHTITPASTSLSLITATTTIPTNATTSSISTTTMTTIPTTLDPNQSTSLVISLTSLSHSESSTSDTVSTTFASSELSTESSTIS\*

>Eve|EVEC\_0000358901-mRNA-1

MPNMKYWVGLQRSGNDWQWVDSSTSVYRNWANNVTPTRGCVVANAPGTVAGSWSGMACNQRYQITVAATVFNVYLFATTQSTTVI\*

>Eve|EVEC\_0000376501-mRNA-1

MVYSRIAIISAGAKATVVANLTRSSSELHKLIYQTNFCKADLFNFTDAVQLAERIFADDRTRSNVPKVVVLFSSRTITCLPTSRCYILRSAKNYEDTYGCSLVAKMSRTYGVTFIGLSVGNHGLNMDFVRGCSLIPFDGFHSYSRIYRTLCYELIVANALKNFKNSKDFSVNCNCETKSLSQLSFGGSDVCSRRNLCVESRNLRLSFDDAAEHCRSRGFSLAIPTDKHTSSFIEGQITSRNKAEEYWIGLRKHGDKLYYLTSYKVLSEVGSLQTDWCPDANIKNDGCVYRRRCQARSGYGWDVGPCGPLTPLRHFACETTACSTIKYCDDQPGREYCRKGESDALRC\*

>Eve|EVEC\_0000382001-mRNA-1

MSKTETGTGEILTSVSNRGFWSGHEKINGSWRWLDGTEDEGDRRCADTEGPSNERCYNELYKRYFLFEIVPASKNLRIFGEYPLHDDIFGAAVYFLLNCATVVVSKVKGKKSISFEDSQKYCYRHFRSRFLSISLVREFIFLHEQLYGSSRSEQPNVVIGSVERDFLRYLADANLKRTSVKYGELKFRLPHPKEGMNQTINHYIGFKKTKSGYLYDDERAAHYLSHSESRECHRFMMDQYIFSSCFTPANSICEYKSQVLFTDEKSVKRFACKKYFVSQETSGRQSVPTVFKINEKNETFKNVQRYCETMDSMLASFSSKTEFRTVQEAYAPANYWIGLKQVNEKWNWMDATTVNYTDWNKYNVTEEYDKKVDWSVAQGICIAYGSYLVWITSNDEQNFLNDFTESNPFWLFPLSYSGNWTLPTAEKSKFENWKAGEPDQRYLYGQLFFAYSEPGGWNATSPSFSAVIVCKYEKGQLHRRYPEEQYEVALNESRGSGRTSEVASKTKYTTQQSKESREPHASTVRQSEGGTLAFQALLFIAKD\*

>Eve|EVEC\_0000406201-mRNA-1

MEMALAALLPLLFTSVFCVSASNEAVKAGNSCPEGWTGNNCDAPICYEQKIIERHEGGSYGDYLFWEQSSRCSGEFYFYVDEFVQNITLYVEGGENFFGEVRKNEKRVQAHGTPPVVSPDIHVSEFDEIASFYGYGVYTIVVQSDGTESCTIYVRSATSLMIDGGFVQDRRDDSAQYVVPQINQGVGRYPIVNNNSYFAFQYPVALSHPGRANFVYINSGSGYGSRIAVKDRYGCGASYISNAVQCEEDLSLTYHLKVEGVDTKGNTWQRVYIYMCETYATPSPPPTEPPPEQCLNGGILVNAGTAQQECYCGNDYEGRMCETKRCFNNGQVGKYGRCTCAVGYTGESCEHVFCQNPTEGYGDSKYKAIVFIVRSGLSMAGHIEEIAGAARTIASYYQSDSYIQRWVLVTVFNGMVDVQSTTRADEFVNAIRAIKIEQDTICNDAIYTAISTAIDTPAVQMYKRSMFFIFTDGMPDDNTEERLTLLHQLSFFRGQMFFMLANSVSGRCNIDTASEGYRGLRYLAQFSFGQVTYVDLEDLGSASLLTLLFNLKMQWATVVLAITAHKADHIFSNDLMDSCKRAPKYQSFFVDHSLRNVFISATGSNLNLYLTDPSRNRTEATLFYSSSDHLYVWQIENLMYGGYLMELESQSYNPCSLRVFGYGDTSLWVGISTGLAEDATVTQPIYQQTSHMVARINDVNYPDPTQILAEATIWTNEGTSDKRTVLYASGGIYRDSCNFNLYFGEWECAYPNEFFYMNVYVTASNGAVIQRSYTGFCSIVETTQTPPGQCMNGGVETTLSNGTQTCICPAHYTGKKCEKIQCLNLGTAIGNKCECVSGFTGQFCETSVCHQRNEDFDFGPNKRSLTLIIQDSISTRTSMRSIKNQLPSLVQDLTHQHAEWISTYQLYRFNDSTFTKVASTPNANEFLQGMDALYSANLAASDPSCRDLRVLPGLLGVLMNHQLTLNGVVYLFINGYMKLDVTTSEVEAVYELLERTKVMFNVVLMSGSPCGRDLSENETLVLMNFAGYTGGQFIMVMPPRAGSVIRSTPTLYRANYIYETYKENCTEPEPIYFPIDSQTQSFTAYVVGDMEDNAIKYYRPDGSKKEPFTIWKDLGMGSRMDQIIRECDDGWELSGNRCWHFGIVPRTWSEARDLCHNNNAVLITIFNQAEQDYIDSLARGEPYWTGLKYDSTSSAYVWDTTEGTPLTVFISKDDFKLSYNKKTRHMALSSTGYNNFPGGNVPAFNLTTQCVFDKHPVGWSLAACSERRSYVCVKHACSKNICVSKYLEKNVVSSTSVANSRISLTSAEETNNADYEPDFQDLGDLLARGIWKMTVQTISGACSVQIYSQSAIQMFMEFSSDIHSDFGSQQPYVQASDNRIIAHVTKQTSTSAGLTGSLQYAHLYKISSNITIVQAQTFSKRDMATCAFEYLSTSFKCPSEHFLSLNTGIDRFGYLYQRIQPISCFKGPVPGDCVNGVYNQGHCVCDPYYEGELCETPICQKGTLDSLRENCKCFAGYAGVVCDIPVCNRGTSQNMPSINNRTFVLLLDGSKTGRMKNIASSLEDLLTSVFDESNEPEYRGWFTHYTGVVFRDSSVGEQSVSEVIESDDSTDFVKKMLAERDKSYTPSGESRSVMAAIVRAMQSTYVQPRSYVFVLTGADAEDYERKTAAIEALARTHCYVEFLIVGDEEAPGGGKNYTKPQLVAYYDIVRETSGQLYQVQDNEGNVDVFKTFWRSLFSTYYDTFFVTTVQKQDCSSGIDEYVQLGYNASTLIIDAVGSGQVSIFDPQNRQVNNINSIKGSRTNRVNTVSVNMTGLWKITLPEYKGFCRLQVKGKSNIEIFIGYVHDGTDGGLHSRDVDYRPLTDGVNAVVAKSDVAKINFVQIFSLDERKLLWSSPMIARRSCTYQYVSSRTFTCTEPSLSVAVEGEDDRGYPIRRMIHTHCVGNFATTAAPGTTATLLTTTPVVTLKPLQCDDNAKFDIILMFDGSDGFNANDFEDVVKAFESVPEKMNISQNGIRFAIGTYAESAEIFSTFENTDVTEFHNTLQRLVSFGHEGVTANNISDIFTKIENLNFRDSVPRVLVMFSSLRLDVGLGEAYPDPKQQAEEFRAKGKILPIGYGKYVDADLLKNLGNNCAKFAGDMLEMKALLPWVTSSLCRFVIGYLKKLPLLWLTG\*

>Eve|EVEC\_0000407001-mRNA-1

MDEQSRHYNRRIGQQRNFGKMSEKNPLKSNECTGYDTAADFCEDHGGKLPSILSKEENNILSCISTYGFWSGHEKVNGSWRWLDGNKSNLTFWKSGHPGINGRHIKVNKDGEWVSVSDGECAEAICIIRAEDEGERRCADPKGPSNERRATALLKSSKHTNYETKATASLNAAVHPQPFLSVEHSKRCLPSFSGETDATRSIAVAERYGRWHYCLFDVKVKGRKAASLEESRKYCYHTFHGRFLSIGSVREFIFLHGVLYKELEDRRPNVVIAPVERNFLRHLADANLKKTSVEKKGNWWSADKYCRTWHRGLLGTFYKVSDSARVLRTDNKEYYYLGASFNYSANDYYFDDGRHLLTSGLDSANNQSCLAQLKDSVVFVDCQILFTNEKSIERFACKKYFDTEEDYGGQIEELLSFEDSERHCETIESTLASFSSEQEFKMIQEKYASKKYWIGLKQINENWEWMDTTAVDYTVWKKYNLTDEEFSVQKCMFVDGTGSWGRENCDFHTEVSWIVAQKMCAEYGSNLAWITSNDEQAFLEEFTDLKPFWLSLVFNTDKWILPIAESPDFVNWKPGELDKCCSDEQISAAYNAPEGWRHAPPFFKAAAVCKYESEF\*

>Eve|EVEC\_0000410501-mRNA-1

MCKRTNFASLLTVDSQAEQSFAISCFIISSYVTRYETYNYQIQSLLGFTYHKYWIALRRSGSGWVWENGRPLTYSNFGGGGSGDCVMSINRRWTLMNCRYISPTTQPATRPPPLRLFLATPLTCQDRVGPNGRTDCSERRSFCNDRIYYHYISYQCPRTCNRCWLANTGAPSVHYC\*

>Eve|EVEC\_0000437301-mRNA-1

MLSDDYEDQNIPIIQQLPGLLTPGSMGSGSNAFSGSSLLEPGSSRWISHHMKRVFAPDVFDVHFEGQQNAQTHLSDSLSGQPIPETPPERPLEKLPHTPAEQLSYANLKSTQAKRFELQKRATITSWNKTKTSTPIISQQLAAFAEEVTYNEALLRCLKLSSNLVTIRSQQENDYVTGISKVKNVWTGLFRRKTGWFWSDYTVPNFFNWARGQPRGGSGPNVRCVGINALWTSGTWFDADCNSHFGYICKYDPQSKSSFLSHNLAITTKMHLHRPVITAVAPNLFAQKPLIYLRPPAATANLYAYYYYALMQQLAHQMYRNIAI\*

>Eve|EVEC\_0000461501-mRNA-1

MLTTQKLLSNDVEEGAELIFLLLLEKLACFEISSNITRKRKGRSCFLTFSFSEKVTWDEAQRHCEARRSYLATFDSALQYRDISKELARNPFWFGFRKNAKGWEWVDLQTPVYSEMPTESNDVLAEFHCAYGTQTGAWNTALCSERMEYICEFRR\*

>Eve|EVEC\_0000461601-mRNA-1

MKIRSYEGFIIYILLLLCHVFAEEPENECPEWWHRTENYCYSRIEDRYTYDDAEEHCKKKEARLPTFLNKKEFDALLRYLRAPRNYWFGAKLQDKLLWNWTDGTPLQLSEISLPIFGLGNFSCAVLSQKGVQTVECTTYQNAICKRPKRKLFNQLNNLEYPKLNCFPGWDELEQNCYLLSTQGFVHGAAVKFCENNEANLATVFSKEEEEFLKTLLGNKSAYIGLDHISTRKNAWIPNVPDRLDRIYINLTKKRNPNGKCLQLYYATKQMDSQICDEIAELTCQQESSVIY\*

>Eve|EVEC\_0000469601-mRNA-1

MLRSLASKGYDAKANIKVPYDYASSICSALNAHLVSIHSEIENSFINKVHNIRSIWLGLKLTKNFDWKWEDGSVYNYSSWDILQPNGCCGANVRCAKMNWIIKNGKWHDLSCQDESGVVCKYDPKNRNVNGQNMAEDETQGLPKRRIKGPLSQEATTTEAGVKAENEKQSKNNSQQKNDNRFSSKTKWPSNIIADYSFRRSVKQPKTVTTTSEETQTPNFEEAISDDISATNSAKKTSVNAKTLLATVLEIPANDTAPSKIEMKPKNESLEKSTISSASERNYGFDGTITEPSDVKESQSITRGYGFNSTTFDITKQISTNFAIDKESSSTAVPEENMLLTRPKDELTCSSEAPSTYNSIKKLATSHEDTSAKAIAVETSERRNGTMVDQQFVTQTDFKTSTTAITTAAEKSFSVSTIRNYVDKRIFLEKNSFTTPSIPLAESATTDFNTPSNSENNAFRLLSNTSTPKKNVDKRKRCVPKTVGDGNIVCVCNATYCDEFPSVGKLHSHQAVILQTTKSGKRFEKSSGNFCYKRRKDRASKEIIITVDARKKYQEFIGFGGSFTDAVGINLNALTQPTVDNLLKSYFTSDKGLHYTHLSIPIASNSFSTTPYSYDDEDGDFELKHFNLTEEDYELKIPYIKEAKKLAQNKLKLFATPWSAPGWMKVSENMLINSPLKNDTKYYQTWAKYLSRFLEEYSKNGLNVWALAVQNRPYSNATKSWQQMRYSTQTKRDFIINYLKPMLQKSKSGKNVELLIFNDIYQFLPSAVDQVLKDSQTSNFTSGIAVQCDQNSFNEDSYTVFSEVHKKHPEKFILLTETAAGRLNPTHDDWSNAEIYANSMIGSLLNYVSGWTDFNLCLDQEGGPNLLDLSVSAPILVNTAADEFYKQPLYYFLAHFRYRLIFELSKIPSSPSVNFYTYIAIKITA\*

>Eve|EVEC\_0000475201-mRNA-1

MILTFESKAEYENFRAIKTDFKKKIWLGNVKHSSFLEWDYDTPRFINDESRSYECYSFNATTINPTDCKEQLPFVCKKSTVKQDEKIWVGRRKIKQLVHQSPDPQELRKPITPSNLKSCPAVVGEELLRRKCSKTYDVYFEEYMGKDKCPPYTMKYGEYCYFAIFSLAIFSKMPKRKPKNLESLVRLYQAKVKKFSRVEKFWVSELQTDEWERVKIFYYGSLVRYETAVQICANEGGFLASFVDEKEERVLEKLAVTRYFWLGLSQNDNTWEWHDGLNGDYIEKQIENNRFHTMRGNEENTRVFADRETMAWYETGSDQDEFSVLCKFHEVDQNKCPTYFSLQDYFLQPPESVSVNDGERHYCLYDFKLSKEMFGETEVINETVTFETAENFCIDKMNSEFLRPESADEFVFLHQSRICYPSWEKGDSTCYRIYSTYKNKTSAEKICESMANGYLAFKELTRDQTSVKEYIRDDCYYVGIYKDPYQKLKWIFPDGTEVPQSVMSSQRANYDCACIKATDTIKYFHSKCDGMRPFICEYKSRFYAQNYHLTLIILHNSFHRLGDRTH\*

>Eve|EVEC\_0000552301-mRNA-1

MFRIVLLAAIQLAFVTAKCPTGWTNLPGSLKCYKGFAERKTFAEADTYCRENFATNAGKIANELDKSCDFWIGLHYNEREGVQMWTDGSYLGFQMWDSGYPTGDIQKRVTYLPQDSRSHKWRSTTVADDRKCFFCQQRPAENDVRISENAAQAFCSAWKANLVSVHSAEENAFLNKLSQGKQYWLGLKYSTKWNWIDGTAMDYMNWNGQVTSGSKDTVCADANEPDFYGKWSKQGCYKRLRSICKQTRMLVAIIL\*

>Eve|EVEC\_0000564001-mRNA-1

LLIERFLVKLECQTGYERFREACYHIFNYTLNFIEAEQFCVNDGGHLASVHDNEEAAFLVQMIKEKSALMIGYNGRNWTDGSSTSYIANQSLLLNYLIPSPVFEDRSVAQQLYLVADSNNFFFSYSVVEHPSVPFACERPAYYNTDRSCPQNNIFAGFSTVTSPGYPKKYHAGYNLNCTYYFAAESGHLGHIQFKDVDLNGDYVKVYDGWNPLERRAIGIVTGNNKNTATSFKTTMTSLISIEFIGNYTGKWLANFTSEKALSGGTKNGISSESDERAETSDEQSDSKQYEEETAFMSAEDNDDQVLTSPATLGSAENILSQEDVASEEQIPDYDYEKS\*

>Eve|EVEC\_0000712301-mRNA-1

MNSTLVTYLSEGENLVARAVGNSGDFWIGLKKTDGEWQWDDGYPLIYQNWLNDNVTNLKRKKLDCVQDKFYKIWVDRPCSEKASFICQYEAQFTCPEGWREYNGDCYIFERTAIALPEAEKYCALNGAEVTDVVSKEERLFLKEVSEQNPHWVQFRTQGGNQKNAKRLDNRRSENDSLTENNREIKHVIATSEGWKIPHKYTLTAAVICKYKSGHLPSGETQL\*

>Eve|EVEC\_0000769101-mRNA-1

MNKKCFQSHLAKIENDADRNFLSQFFQVEVSNLTAAFRNIGIWIGGHSVLNYTEATYVWKPENYLITKFYWKNDEPNIYIDYTNVCVYIDDRSLYLDWATTLCTDEKYYICQRDVTDTEKKEMFAQCYCPPEYSGTFCEKAVETGNAKELQQVICSNEKLNFSCSSGEIIQVDFATFGNIGEVPSHCKSLTSEMLLVPQSDFCANPESLQRITALCEGLRECTIPSIPSHFPKSPCFGTPTSLTYRFQCVEESQSKCPGDGIYYNGRCYRAYFATAENERLTWEQAQQSCLKKSGILASITDETLHELVVNSARTYSDSADYWVAVWTNDDSDIIVGNNKTLGFVPGGSTIVGKNKCVAYKITETEAIWMSEECNSTKNWICESPPERETRAVEEYKEREREGTVFIGTPP\*

>Eve|EVEC\_0000787601-mRNA-1

MDFDTAVDFCEDHNAELPSISNDKQNDILASTSIHGFWIGYEKVSGEWKWLDGSTSNFSLLSKDKSGGKHVMVNKKGIWTLANEDSCAESICIIKDLEHSEMCPVAIPTGRRDNIKVERYVVSERNGKWQYCLFDVNVARMSWEDSKEYCYHKFQGRILSITSAREFIFLHSILYSQKLDGIHNVVVAPVERDFLRHLADANLTRKSVEYGELKFRIMHPKEGHMKGTYATHHGHSSKEYATSWLDLKGFLYIYAEALADVTAIGSRDN\*

>Eve|EVEC\_0000800001-mRNA-1

MEQSDVFEITFTVYSHQGPLENSKADAVCGTYAAFLTSVTSDDERAFFLERSVSKKFWVGLYWIPHNVWESVDGNRVVYISKQKDLIATEGGFRCLLRTNLQNETFSSKKFLQFTRTNAQNHGFGLASTVTQLLVFGHKSLEGRMLDVATFEEAVEICAEEGAFLPSIPGKYEEDVIFAMSPTRYLWLGLLSDTAAQMMWMDGSNTSYALSKLQSSRSSKVRSEFSKIVGDRNKKNWIDVEGTAHKVSVICQYDSIDINKCPQHPNLEPYYMQPPKSISVDGGKHYYCIYDFQVHKTLFSGLPVRNGEASFIAVEKFCLDKVHGTQIQPRNEDEFIFFHELFEKNVSLIALSQRTDHLWRYGETELRTNNNRKFLAFFDSRKPKSLRNTWYWMGFQKYEDAWYADAGNELNVSFQTVRTIDKKGAVCAVYNRLQNSVLGVECEEEHQFFCEYTSMVKWSRKRLKRFVCKQPYIPENEMITSEKFKELLFFAEQSVDAPSKNLNSTLPTALEHPFQFSHSVPWDESADFCQVEHGTLAVFSSYKTYLLVLGNKINIS\*

>Eve|EVEC\_0000800101-mRNA-1

MVQWGDNKIKRVLCKHYYDSKKYLLSSKDVEDFLDEREKLILHYREYLCPYEWISIHDLCYKYVSFSIPKPWNDAAEQCQMEHGTLAVLRDYETYRHILQEIKKSYFWVGKRRWKLEWEWYDFAPAGPIKILGEIDENDDCAHARNEDGLGATECFNELPFLCQFDPKKYCRAGFTEYEGFCYMFQRTKQPLRIAEEVCDARGSRIVWIDSEEELQFLENLYWGGKRVGGDKTILFRKERLQRVFMEENAINKIPQISEAVFKLDNYPDLGKFKPNVVTLREEVRGLSSKRTFWIALRYIHGSWSFPDQEKPKLLKWATNEPDGCCASQVMSHAAHEPGKGWSDRNEQQVENFICKYKKGFRDLPSSVFEGSPGGFQYEGNRIKLRRASPRSSPGVLLGGLDSRDNVVKMTFIMGMLTSTLVICSVGSVILYYSTRRAKLDSNILALYDMVTKSDAARYNMALYDQTYCEGYARHLREVNIPKQRSDLEVTEWVGKVQGAQFQGKQEARGKEEAMEKTEEKREGPKGKSKSQGVQELPAIDPVATEEVCHEAYIKQAVPAEESFDAGSVWRKCPL\*

>Eve|EVEC\_0000819401-mRNA-1

MCLYKVYSNLEELGSCFNGDGRLTVFNTSIGVYFCYYLRKLHIAEFEVAENLCEENHAHIVSVKDAVEEEFLKATFLQEVTPNGSEFWLLLGLQLNNSIPRWTDGSGISFIANRLQLYSHQYQSNCFALVRILTNSGFSDNYVSISCDEIPIKEVLCKADIRTLVLSRKSRTLQGKLPLAALKKIPDYEFLENYFSTGPLMEAVTESSFMGGDHKSDTNDEETEPKCDILRVIEDLNYLVYSERETIAASGGSAKSQSESLPLLPGCAEHLLKLVEAAYEEEFRKVSSCVLFSAAVKFGEIRFFIGNWLDDFNGLTFIPFLGLIVTILVVIIMAIQMCTRDRKTPLSEDSYCVPSIQSSPSEAVDTPSNKFQVRCDQTRYALVATRDSE\*

>Eve|EVEC\_0000835001-mRNA-1

MKFQFSAEVERGGLNYGLDIQSNSAVKATTVFTNVAEVEMTDTCDEGWKAFGDSCYLVVSESLEECLSYSSTLVSILSKEEEEFLERLVENEKFWLGAQKSENEWIWLDSGKTVDSKYWSESFSSSDSVLNEGGLCLGYPEPDVTMCNRTSDMIKSFLHAFMISLNLNGSDVGTRPESKVKCLAKKQSQLTTVLSDAEGKFLTDLRCSLFNFIVGNANQVVIGCLEITGGKEVWTGLTYSAGQWAWDSGQEQLNYTNWAEKTESEAIEISGVAFMYLANDKWQVTTMESEIRGYVCKRLGSRVRRALVPKETKVNK\*

>Eve|EVEC\_0000839701-mRNA-1

MRDICSCQLQPSEAAPDDFATKKVESFEEAESACVMQGSMSYESHLLSISNKNEHAILTELITGSILGKALLGLHKKVEGAVEFTDGSDVNYVRKNLQIFKDDCFYIASKTGNLSNSACESGVQDVFCQARPRGNYEEESPKTYGCTSNKCQRLWESIEEKLSVLDIVRSRRQAEKSKEKLKESINLASFQNAVIQISLLENVLGGHCSCTGNEESDDFRGGEALLGIIVGIFGVGILMILRVAKTTVRKLRPTYDIVSTRAYYSKTGSGEEYYSRVSRQFDDAPIYTM\*

>Eve|EVEC\_0000856001-mRNA-1

MFAQYFYPILLAILWLTSPNYGYRGHVCTLSNLELDVVFVLDASAGVDQHGYAGEKAAIYGLFNELTIGQRTEMTRVVTLNMGSQTNNEKVSLGMYRAGDQAKKDLLELPYKGGEVNLQSGLAAAYGLFKTESDRPSKPNVVVLFSSTAVNCANGGLTQSGACKQAFRMKNESIILISVDLRYHEDPNEETMNLGEYSLQNNETLFDKLKEIFCEVSPTRPPTLTPNACPCVLHGVWLDIVVMFDSSDGASTVGFAGQRGAITGLLHRLFIKQKGEQFSRIGFVNVGSTATLVSDLNKYSHGTEAIMDMMAMKPMKGEYNFGNGIVQAKTIFQKKMSRRERQNVKDLLIVFTNTIVKCETGKEGCQVAKWLTENGVTILTIDISVYGVPNGDPNQGSSFGDRCFRLSNNKYFLENLEDLICKANCFCKPPTIQFKTDECGIYGQCVYLEESPAASESAKVGCGLVGMTLVDVYSDEKDKFLTDIAKAEKTDKYIVGLQYINDELIWSSGETMDKDDYNIYAPGEPDARRGECTYADLYSSKNSIWKTMKCSYTSPAMRYFCQKDTCDSEHYCQ\*

>Eve|EVEC\_0000885401-mRNA-1

MILLQLSYGDNSDWSCDHDFTQIGSWCYKLVDTSATFDTAVNLCKTQYGANLASIHDDKENVGLRHLGDSFLIGLRYYEVASDLKWADESEIYSPGWPREYHLSNKTCKYNLAAKPNSTIDATIQLFSFGTTDECRDTLQVYEGWNLISIPDAQLVYLTLLFNFKL\*

>Eve|EVEC\_0000915701-mRNA-1

MTNLSENFKTPNVSETVKKPISLETVKKISKVDVIPKSSKSPKVDTVLKKIRKNEVRLTPEKETLDYSTSTIATDTVRIFFIDLSKCGSDKKFGKKKLMANATFTLVLKVEYCDNCVWGDTNNCKLASIHNEQEDICIGRLVRDTKTNAWLGLRRPKFTWENRAAVNFENWSDGKPNFLGGHCTMIRYDLLWDNYFCTMKNPAICQWKRTPTNGCGNYSNIYSGDHWCYHVTKSRMSWLRASSYCKRRFPNGRLASISTKDEMKHFRKMKQNFSTMFLWIGYNRLKLYWSDHSPVDYQDFNNRQRYVGNFDYCAFMPPSTLGLYGRTLWSQKPCNHTLQARVCQRTKL\*

>Eve|EVEC\_0000962501-mRNA-1

MIRKKLFGIDTQNQCPVCPNIRRFYLQPPKSISVDNGKQHYCIYDVQVNRKYFDLDNSLKRLASFESGEKFCITKMHGSVVFPENEEEYWFLRESFSANISRIGFSLRTPRAWFYGELPLRGSKETDTDLIPKFKVFDSQGKREEINFYYDYMYEEALMFCESLLDTHLSTTLHQLNSTQQKEVLYPYIGDYWLGLQKSEGHWRWSDGVIANLGDNIFESLRNVNNTQEHTFYNSRNGHFYTSEKIKRYPFVCEYKSKIHWFKNKLGRFLCKRPYDPSKKLIKSDDVDQLLSISQDALRYRSKSFAQYQLDTDC\*

>Eve|EVEC\_0000971501-mRNA-1

MQYDVAADFCEDHGGKLPSIISEKENTLLSRSSHYGFWNGFERSYSSSKWGWIDGINGNVSFWKNGQPSEIVGHVKVDQRGRWEVVSDETCAEAVCMIRDIENSIKCPQYFREGQMEVRRTTVVNVRDGKWHYCLFDIQTKYNKRTTLDESRKYCYRTFHGQFLSTSSVREFIFLHSELYKVSDEKRPNVVIAPVERSFLRHLADANLTRTSAEYGHLKFRLPHPEEDQKYLCRPGWTFVGGICYQSISRTGDWYALDGYCRSWNYGLLATFYTKDDLEQLKTKWKYPASSDELYIGCKREGAKTCVFEDKRLAPFLNCKDTKNYCTFGSNGVYLSDGRKSIRGICEYKSQIFFTDEKSIQRFACKKYFDKKIIFENQGQSTSGNKTYYGQINQRLNFENAQRHCEAEDSMLASFSTVEEFKTIKRKTSSLLGNAKKYKSASYWIGLKQVNEKWQWMDTTTVDYIAWNSFNVTAETFGVLKCMFVDEAGSWNRENCDVEHDFLCKYEYFTESKPFWLSLVLYSNDWLWPFRDRPTFGNWKSGEPDQCCPSSKIYAAYSEKGEWSDTSPSFKATTVCKYRKGQLYKDVEKPYAAAYNEVEEEMREAEKLRTEDDYMGEDGKLRQRKQTEQEAMKHTYMLYTAVAFLMFATIFSILIAIIRTRLKTVFDVKPPLYDEFYEPFVATPLTQESTQYEDVKDRSQDYQLKLLSMSH\*

>Eve|EVEC\_0000973001-mRNA-1

MHPKCNMFLLLLIGLYICLLKATAILAQQCQTVPVSLTAKDSLQSFTTPDYFVGSYPNNADCFWLLTARSVDRRIYLRVDDSQLDDALFYTCDDFCAIYSGKTNTSTKLKQWCGDEKPYAIISPSDSLFVHFHSDARFQRHGVKMSFTDYEIPGCPPGWVSNTALGTCYTLIYSGGGLTWAEAQNECLNQRSNLLTLSSQEEYSFIIDTFTEDEAMFWLGYTDAAVEGTFKSIDPNEKIWPDQFPTFFKNHDFEDCVCINAHSYEGIAYEVTNCMSRFPFVCKMSRDGQTIPYAPDLNAIRKGLAEEHTVRFNWALWILIILLLIAAILAILYFCYKCQQKRSKQRVGSADDNNRLTHTSTQLSAATGNEHTNVRYVQQISHRSSQPIENYPMNEGLSPTDRRRAAEHVNRFVETFERDLDRNFDTPGTANAAQNPQRLDAPLPRRPLEQMCPTVLTVVPSRDRFPHDFVNENIEPVNGSIRNEAFLKNRRDDLFERPHVTLLDNVSAISLDDFWNKSAPSGSR\*

>Eve|EVEC\_0001035701-mRNA-1

MLQLLLLSIFLPIFSGQQLSLCSSATWTTYNGNEYCAFTGYATYAAATVLCKKFNSNVVSLLSQAEQNFIDSRYTSPKKAYWIGLEKSGSTWEWADRNAYSYNNFRTTQATPDEQCVMVGANNPVDSFWDIKNCNFHRMDQIVVCKKSGSAPKGCTSDSQCSVYELCQNGQCLTHGNKQCQADTDCSTGETCRYGYCGFPAGKACTADGECGITELCQNGQCLPYGSTPGSSPQQQKCADDGECDPTTLCQSGTCLPPTAECPNGNECQATEECRFGFCALREQFLTVAAAGGGGGGGGAGGNPGP\*

>Eve|EVEC\_0001043201-mRNA-1

MSWKLNVVVYLLSLIGSTLSNLCDINNCYEIFPEDNIPGATVNEAMEFCAAGVGGFLASIHNAEVNSMIAKHLSENEENGSALIGIRYYPSEKKFFWLGDNSMVKYTNFDENFVTSAPTKGHCAVITAAGLWINIHCNNTRNYPALCAIPKRKRSEKPCTYLLAVGQEYRIEIQVIDAAFSENSYINLYRGWDPSEDYLVERQ\*

>Eve|EVEC\_0001054601-mRNA-1

MNSQKCYALLIEKPKTFEESERYCETIGGTLVSFSSENEFKILKGRHSKKKFWIGLKQVNEDWEWMDTTAIVYSQWKERNVTRDVFKDQKCMFVSGTGDWHRENCEKKLYFLCKFNRMRLT\*

>Eve|EVEC\_0001077901-mRNA-1

MPLSCRSVNYEEAEAACATLGAKITTARTEAENTRLNKIANGKKFWLGLKRIKSSRWKWVDEGPLIFNSWSGGKPSTTHDCALAANYGLWHTYPCQKKIENSIGQDKKNRREAFLSCSGKSATLLQLEDLEEENFIKDFLVGQSFSNKDKKDKDGPVAVWLGAEKKDNNWVWDDNQDFKYTHWEMGQPDGCCGSNVIYATLNVTKQGSFWDDTDVEVQHNFICKYTIQEPDEPTPFITDQTIVISVTKPSTTAFATVTIDEKAQKGQVGLGTLIMIIAGILLAITIAMTACFSRREIIVAPQPFYYEIPLEADEGPMLVNEPLHSAELFTQSTQPNIQIAPEDRLYDQYAKRPV\*

>Eve|EVEC\_0001112401-mRNA-1

MRSIWIALRRASVDNHTIWKWSDGSPFVYENWQLFQPNDCCGDDVTCAKMNWLLLSGAWFDTSCLEKLGVVCKYDPSMRTVPITTTEANSVLRENPNPLDGESIKFTCDAVTQNLAVLR\*

>Eve|EVEC\_0001112501-mRNA-1

MSSSVGRQTLAGAQPIWLGLKAARGGWLWADGTEVKYVNWYTTQPDKCCGEDVSCATTNWIFDNGKWFDTSCQALSGVVCKYNPKSRRTPLPAEMIEYKTTIRADSGLAEYNPIWIGLNRIKNRWFWNDLTDMKHKNWQQFQPDMCCGSHVNCAELRWIHNKAKWFDTCYFDVNSPASTPVPIWCRCPRNWVVYNEHCYQIYKSSAGPLTTPIAAAKCRRLGAELAEACTDTEFSLFEKMVEPFETQNPLFGMMVDKLFGGCSVSPAHGKTVCCHINWLYGTPAFGALYSTTCPTSNQDVYLCHTMSTSIEAPVFCSKTASWLGNKFYQVDTRLDSSHHIAPQK\*

>Eve|EVEC\_0001114301-mRNA-1

MYFSPLTKTCRNTLRAQHENEELEPPQVDLCDPGWSRLENKCYKVHLCGGCTWTETNECPLASIHSDKENMFVTDLVRRSGVDSWIGAIRLTFGIDDITLTSYFNWDRGEPSSKHNLAAYCVAMKTNGKWASYPCHTRMSIICKFRTKNVETAIRPFTKYWIGINRNSVRWSDETPVDYQAFSKYQDLPGDVRFCTYIKADLNRYAPPIWMQKPCKETLRAKICSRPAQQRVDLPELDSHFPRAKHPSRDKYYNIGETSLSLSKVSEIDEFKHSEERY\*

>Eve|EVEC\_0001176101-mRNA-1

MLHSWVLPLPQMTVAFKGRNINISLVFVSECPLGWHQYESTRSCFQVNKKTLSWSEAERECNQEGGHLASIVDEFENVQVFDIVKQANLSVLTVWLGRLVKLSETGEYEWNDGSVGRHSEGFKGGEPLSAKFYFDSPPSGTNKCLTMWLDSGRAEGSWLEWSCTYRPGYASLCKKPYKSVPSSAPSIHQSSRCCVTARCTTKCPPRQRCIPDDLNCWTKYCPDNGPGWCLPNP\*

>Eve|EVEC\_0001176701-mRNA-1

MLEDDIKQAKSFFFEVFEVGLKYEEVIDKCLLHNSTPVSILSSEEDDFVRGIAKSKDYWLGAYRTEHDWAWLDPPTAVAYTNWYGIGEPKSFDKCISAPIDCEPEWQKLSPYCYFYGNDVTSRDGAKAKCMAKDGSYLTSLLTEKEEQFVKNMTGAKPFWIGLMYSNGRWMWDDDIQRLKYANWANILDVDAAGKSSTAYVYANPKWRVTTLGKENYGYVCKKLGFRPRPPEEASRAQRSRSGFSQWMIDVDKESSGMVLITTIVIVAVLFSGVTLVCLLTTLFKAEKMVPIYAEVRDGNVYYNRPYTERPHQYYVSVPPEYEEVIVEKTADLKTLPDDIPPLTRTPYPAPL\*

>Eve|EVEC\_0000017301-mRNA-1

MTSRLQVCFAKSLRCYVFCKALCSHHPHDAAALLLDSFGCRSVHFKNIGRLLERNLQCHNRNKAVFQVVFAIPVNVTVVTASAIVMYYEKLQNYSECRSTCKSIGAVPLVPFDEPSLSAFGTFGYEEEIFWVGVSAERCHWQWDNGPFLCNYDGNFSKHINQCASFRENKITETPCNSTLRFVCKKSRIYATLSLLDFSLDLLKFIKAIESAVLLTSVFRNKAGNITGLLDLVCPEGWKYFNGDCYIFYPDKTNYYNARMKCDNGKGYLTTAVTKMEREYLENISEGNEIWLGMHESKKVLWKGEDGNLLVYHLDGARFKDAQQCLIVQQKQYFNYNCSEEAKCICSRLG\*

>Eve|EVEC\_0001190401-mRNA-1

MTWDDAQRHCETQRSHLATFDTEQEYLDVSNALEGDSFWFGLRKIAGLWKWVDLQTVSYGKLPSESEGALRNSDCVHGKRFERWSATVCSEKMGYICEFLR\*

>Eve|EVEC\_0000019701-mRNA-1

MQCSILTVVLLYFFLMTIHSSNQYSISPLQKKPNHFPSQLHPDFENSLQKLLTKSITEVYETTPNCCNTTATPTATSTTTATTPGEHSLVKHLNCGCEDESLTRGVNYWLDIVFVVDSTDAVRDLDFSDVKSFVSLFGNLQIGTASNGDPRYSRIAVVNTGAEAEIIADLNRFKSGTDLQNTVAQKLVKKGGTKFNLYAGLTAAQDILTSEDNASRRINVPKVVIVFSTIPTNCGLLARNSSTTGDRKVDRLCSLATYLQQQATLITIGLKMAGATSYPHIDIANNCNRFQNSFDMTMNVLRALCRANCHCPKSYDQFATGDQCDSSGECVTVHQLSVPYASAVEICLQDGAVVADAATHRKELFLQSLYKEAYFSPFWIGLNFIDGRYIWSNNQSISEYNYNNWCTADHQPKISGGNCVYEDRCGEYSTGWFTAECGMMLPTFYFACQKDACESSGFKN\*

>Eve|EVEC\_0000019801-mRNA-1

NPTTRDQWWKSTTKSPWWNPTTTGQTGQWWKSTTRDQWWNPTKTGPWQNPTTAYPTKSTTTAPYPGIKSSTCGCEDESLIRGVNYWLDVVFVVDSTDVVRDEDFYDIKTFISLFGNLQIGTASYGDPRYSRIAIVNAGAEAETIADLDRFESGTDLKNAVAQELNKKGGTKFNIQAGKVNLTRSEKKVDGMCSLAAYLQETTTLITIGLKMAGTKNFPQIDIADNCNRFENSVDMMMNVLRAFCRANCHCPTSYKQFATEDRCEPSGECVAVHQLSLPYRSATEICHQDGAVVADAATYKKERFLQSLHATATFSPFWIGLNYINGKYVWSNNETLNYYDYNNWCTADYQPKISSGKNCVYEDRCGEYATGWFTAECGMMLPTYYFACQKNACSVNSYCE\*

>Eve|EVEC\_0001202201-mRNA-1

MILITDGEDSTNVGVEHNLAWENDIDVYALGVTNDPPEPVPVSTTCGCDKIGQMIYNNYWLDMIFVVDTSDGVARQDFASTKVLAKLEERTTKEMQSIISNFKQTGGQGVDVQKGLELAQDMITKEQEAKRRLNVRKVVVLITTESIDCRRQQTKFLKNKATDTETHVICQLVSIMETNCYCLDDYTQLTKNTDNCAKYAECYRVNSFSLPQNMAQTTCGEVGGTLPNIVGSEKEEFINELHKTAGFFPFWIDGTCTSADTCRYSDNSLVKYKNWCTAKKQPNFGNGNCVYEDQCVGFNVGWFTGSCDDFMTDRFFTCQVPACSVNHYCDYNTMGKKINKKPKLHLKRH\*

>Eve|EVEC\_0000020501-mRNA-1

MSRSCLTGWTMIDEMCLLQSTRCLDYDRAADFCEDNGGKLPSVLSKRENDIMFHFSKHGFWTGYEKINGSWQWLDGNKSNFTFWGVGHPRNNRAHVMVNETGEWISVDNGKCAYAVCTNRGINPFNASTEARKGDLMHHNSSKNLLSAHSRLEF\*

>Eve|EVEC\_0000033201-mRNA-1

MKAVILLIVYAVTLVRGSSCPPGWEPYAGTSDRCIAAFRNESSWFDSLRNCQRYGASLVSIHNSFQNLHVATLAEKTFESCKYWIGLYNIDADKKFRWTDNSPTNYSNWLQGQPPQVSEATTVYMSLQSRFKWATTTEVAENSCFVCEITLNSSTVGTFAPPTTKRTTVAPCSQQENRDVCGESDHLGKCEQIGNSCDYHCCCTDGTYSWHCE\*

>Eve|EVEC\_0001272501-mRNA-1

MYICHITWARTYPCSTFGRNWAAEIRCLRNLLSHCEKSLKDSSRRTSRDLEEVPEGPEKMIDSNSHSYTTQRCVITDTPSFDCNHCCTKRLLELEIQFNKKINELNKKLDEAALRHNRKFAKEILSLNKTMRLMTSRIYSNGGNEFIVVDEHVSWYHAEENCIKWGGHLASISNEEENEFIKGLIRGQSWIGVNDVAKENKFVWTDGSRYAYSKWRKAKNYAVFLSQAVIKLKRSFGTEVSTAPKILQHLCRFNMRTVQNQPEQTEALSPTGT\*

>Eve|EVEC\_0000036601-mRNA-1

MPLPETSEFEEMLNSYNFTVVPGNITNGKNEPSSGEPFFNYKTAVELCRTYGADAVSLNSADEEDFVKKLAFYTSISKLNPNELETPRRVLLGLHGSSTKNLVWSDSSSTDYIVQRLAEEKITLSEDRSCLELQRRYLAQQIYYGITVL\*

>Eve|EVEC\_0001284501-mRNA-1

MELLTIHNDLCYTASRLETLHWKAAQGRCLSLGGTLPIRVTHDTNTVLRYALSHSNLKSSFYWFGLMKTGYQWRWADGDVIDPDQQDWAETPNDDNGEAMAAVFSRPESWHWISMSQSVYNAWICQTKPKFCTSPGVSEFGRVTFSSQSYAVGTTCYYSCEEGFELSGESRRECLSSGRWSHTIPICKRVDCGPLEDWSNGTVLLLNGTTTFGSLAEYRCKKGMVISESSPSYRVCEFDSRWSSVIPFCTDIDCGKPPELSNGKVDFEGTTQNSTATYSCNNNFKLIGHKKIYCSENGQWQPSSPVCYDLETLREMKESSGESNVILAIVVVLLLLLLAFLSFRLTRRGFSPLAIHTFNEGKRTSPRPLVYSTPSQQQDSVIYYASTGASMTHVEVPPELLQLHQLSNGNIHITLPSLKPIVRPALSLSMTQPIEVAENNSRNVPETSTSPTPSQLLYSFDDDPVYDSPSEDNVYEELSQAHDVK\*

>Eve|EVEC\_0000038301-mRNA-1

KSAKLYFNQTGRSRRQDDLLSAIQFKKNFWQQKLLFKEFWIGLEKQSNERWSWTDNSPFDFKQWGFMQPDNCCGTNVKWHWFDVSCGLTHGFLCKYNPLCRRYCAYQYRQVL\*

>Eve|EVEC\_0000069701-mRNA-1

MDGKAIVYRTLVIGIILQNLFVVAEYDCHKLTSQWNNHCYFKVNGAYVTYPKAQFLCKAVNASIVSIESAEENNFVRNLSDPYSTYWIDIKPNINANKNAQQTADNSGYSNWDISKTMDAGNGNCTIFNSVTGFWESVNCTNYASVICEKDFVPIIDEQKPSEIYLSSTASTPSPPSPSAALISQSSEILTKKLSPAMDRYCSQRKRPKTVLQLSTNRRFILGPLIPTVQLFGNKFFAF\*

>Eve|EVEC\_0001369501-mRNA-1

MRWERGMEEEGKSVYPSTKLLSQYGSQLARIESQRENSFVSRLINRPLRSASLVQKTQFWIGMIARRTEDEDALFLWSDGSIVSRYIGFWEIGQPDYKSGTCTRVDAHSLYFIYLFIFLITYIRLI\*

>Eve|EVEC\_0000092501-mRNA-1

LLPSFSVCSADRCDEGWRYSPHSGKCYKFYPKDSSWALAEFKCFFNGGHHVSLHSVYDNQFARELAKGAKTIWLGNAQFGKSVDYVWTDHSPYNYESWPHGIRPPRISGRQCTKMNIVTGEWFQSCCKVPSPYICQKDARLGSQYDSHHQKLHNIVDNSNVPLS\*

>Eve|EVEC\_0000096601-mRNA-1

KQQAANCSYPHISVPEIPACYFEVKETGNYSEVSNRCQEHGMHVASVLSKKENDFLLTFLMGKYGNSFEHFLGLTEQGTWEDGSPVSFINGSSRCNVALTRFGWKCRMYTEHSAICKRIKVD\*

>Eve|EVEC\_0000098101-mRNA-1

MCNLYNGTVVSILSAAEQNFIDSKAVAGKYANPRKAYWLGLTRNGSTWQWTDGSPFSYSNFRAMQTFPNEQCVMVGASEPTDSFWDIRHCNFSKVQQLVVCKRRNPGN\*

>Eve|EVEC\_0000099201-mRNA-1

KQQATNCSHPHISAPEIPACYFEVEKNLNYSEISKICQQHGMHVTSVLSKKENDFLTTFLTRKYGDSFKHFLGLTEQGTWEDGSPISFINGSFEHPVGITMFGWENLSNGPYYGMCKRFSCD\*

>Llo|EN70\_10316

MRNILLSTIWFHVLEVIPRCNGCLATSTVTTPKAPLKVTTYNPRTPTTTVAPNVQCFPIARQKRDFPSSASSASDSLSTTCLPTDYLETAVAEMKAGLIKSDSSNSERKVEENALFPLAISKHPAIAIEHRTINDHSNNGELSSSNHPAKKLCQDFEWDGPIYLYNQSLGVKIPYCYKYVASIDEETDELTRLTQKSAREKCRSYSGQSDGPSDLVSIHSSDENYDLQSTLSFFGWESVWIGLAYDNVRSTWRWIDGTTLSFSKLSLRDPSQHCAILLTNGSWVSEDCKSSAVSHFVCKKRAIT\*

>Llo|EN70\_11733

MPIAGGTSKSPEIVRWCGVKHPDVIISTTDSLYVYFHSDEAFQRKGINMSFIEFDMPGCPPNWISSSIGYCYILTEATHGLTWLEAQEECSLVRSNLLTLTSAIEYSSVAAIYTKSKTTPWIGYMDYSGEGRFTPVDPNSQPWPEEFVDGHLSNTENKKFLSGTPSAVLISAVMFSATSSRGTAKTDLIGTTVQITTSSKLLHSQANKLRQSIHLPKLIGSRSGQECAYIDWRNRKGEILAVDDCRNRHEYICKRRQDGTTIPYLPQKEMMRNGLAKSPISFNIWLFIILLVLLTLILLFVCYRKCKKQRALSRIGSSDANQRLVTGIDVQRAATSATVLHIGSSEIQKTNSVAINNNGARNDARVPTVTENASSVVQYRDSSRQAKEQNTPSQNSHSIRQLNLERIEPTVLTIEPRFNARQASEERLSVPSRSKQNLPFGIRESTMSSTTREETLLKIRRGELFERPRVSVLDHTSAISLDEFWNKNEMSTINRN\*

>Llo|EN70\_11756

MDIDIVINIYNASGNGTYWIGLLKDINGIFKWQSGESLNYTNWNKGEPEPRIGCVIASIMECNGKWLIINCNEMLYPDQGFVCEKDIRRS\*

>Llo|EN70\_1372

MFRSPKDQFPNDGVIVAEEEVKVAENENNELTEEFPCGKDPLFCPLKTNQGTVCYRLQTEPFYWEQAVKECDAKHQSDLISIHSKEEANFIYEMVQLQPSISGEKKYWIGLHRRNARSQYEWSDGSSLDYLVERLSNEDPDEERGVCVAIQFNISNKLLQKQSLYNLFGIPIQMSRKVPAYFWTHQRCDNRHLSICRKPGFDYHARSELSAKEERRLIKQNNWECSNGYKLFRGMCYKLYGTNANGVTFSEAIQRCKIDKANLVSLTDIYENGFVTSMLQNLNSNAWIGMDMTDGRVRWLDGEPLKLIRFGPDNRVIRIGGDRHIYQNVGQAGFSNEACVALDATNMIGYWDIIFNKTSKLYLFSA\*

>Llo|EN70\_325

MYVTNSTNHMKVENVSLFCAKENATLTTVNSNAERDFLYDLISHSTYYPSIASYKVLIDVQNDKWVDSNILLYTDCETKYPSSSECTAIRVESNGIMAKIGKWTRMNCDESVFAFLCKTKANKLPVLHRQCLKGYVYRPRTGLCYAIKSPKTNTTAYETAAISCQDELGMLVSVHSTEETEFITRELVPQRSNVTRIYLALIYNFDKNGGYSWADGTIFDYQNWNPTKARQNAENSCVEMDPKTGFWDQIPCIRKSKHDNTHTADNAGIICQTLPIFH\*

>Llo|EN70\_3335

MYLVSLLCSSLLLCLFPIVDSLSPCPPGFSYHVNSEKCFMVVKWLDEPMNQTNARLTCAKENAFLASIESDDENNFIKDLLVDKNAEIAYIGLQSVPYNVAHRYFSDGTTLGYTNWAPGKPDNDNLMDDGCVVIDAAEGQWDDWTCSANMVTGPWATVCQTRYLEKEDQKEEANCPTGFAYDSISTKCYKVIIKAEGITAWNAKIECANYNSQLVAINSKEENQFISNLAMKHPLSAMRVFIGLESDRTNLDARNRYWIDDTWVEQRYVNWEYDKPDNVPYYLNDCVVMIPERNGVWDDWACNLPRYLEHAVYGAVCEFRNE\*

>Llo|EN70\_4319

MFSEKCRTNNDCGSGRCEWRRCVGKLGKVISDRMEIENCYVDDDCPIKQVCRGGSCQERLPLISDVVNVRPDHCYTDANCPLGFKCGFYKKCYNMSDGRYVVESFMHIPCKHEAPSFCAEATGFENAICREIYFEHENVRSYICQFPPPFMYAEHKSCDEKGGCSRYGTCIRGTCYQPFWVTVRQRCKSNDECTFRATCNSDGGCEEGRWALRYRTCRVSSECGNGGSGSVMRYVCRRFECTYRRSVPAECDACRFDEFCDLYENCLRVQRFSELNCDGDNWFYWYSAFYCSSTTEKTYKDALLECMELKAKLVYSPDRGSETSLSPENALLSYLAIRAGWVKEENDEIEKNFVNWNFDSEKMKKSRFFCKKEVPRSSVPNNATAYIGQKCQTSFVYRHDYCYLAGFTNFMPRFAIRTICNLMDSEIVKIKNKEEAHTVYGLAGGKSFWLGLRKGKRDWYWDTSTYGTRAHFFFWRTGQPDITDNKNCAYAAYAGEWMSADCDSFRSPKIFVCQSPSYKN\*

>Llo|EN70\_4739

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>Llo|EN70\_7414

MNTETYYWVQVIVRETNGGSKLGPCPEKWLPLIPTNNYALLEKCIAHVNVTLLQSKVTEVNGAINACSHVFGNESTIATIFRPNNKRELKNFLTYASEEALEGMIDIFVEGSAPYDHFGNDLRQLGDAVLNPLSTALDKQCAWNLQKYRTTARNARDVCKEKKAELVTISNIGEWSYVTRLANTLAPNTRDRSLLLGYTRCSTDPPEWRTMEGGISSGIFPFPNATTANDAECCLEMNIEHKINCKEYFYR\*

>Llo|EN70\_9690

MRWSDAERACINLGGHLASIMDEYENMFAFNVAKEANLSTPTLWLGRLVKLTQTGAYEWNDGAVGRHINGFRGELPSGTDLCLTMWLDFDRPEGSWNEWDCNYASGYSALCKRSLKRIPITTTVKPNIRSGTGSILLYHSRRCCLISSLCHNTSQSCTSDERCIPDDLDCWTNICRDGGIGWCLPLPKSHLYPE\*

>Mar|M.Arenaria\_Scaff10221g073326

MRYNLHIRIFHPKKVLGPPYGFSIFNRLYLGSKIFPRANFDATPVSDDTRTDLTTLIGTEGTTSTPNTSCPPDYTFFKEGNCCIQISSPEKKPLTWKEASEEAKKNGARMASIHFKKEDDFIRDLVAKQPKVEGKDNPVYFTGLNVNATNGKINNFAWSDNTRVNYGSPKDIKPNTDPWGPKTTFNGNTGFGGISKDPSGKASWGLYDPNQKGGYVWKIDLSKKVPEPGNPTGGSPEEGIVKGLPAGYKCTTGCNPSSIKLKAEKGQPSPVDEGPTEKNGCQTDVLSCTTNQPIATITFGTQGSLKSNQRDKRNVRAQVFCANEEATGKKGWVRNGLDNNPKLIFVEEAHCEQQSS\*

>Mar|M.Arenaria\_Scaff1022g018209

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>Mar|M.Arenaria\_Scaff1022g018210

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>Mar|M.Arenaria\_Scaff103g003034

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>Mar|M.Arenaria\_Scaff11047g075792

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>Mar|M.Arenaria\_Scaff1136g019637

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>Mar|M.Arenaria\_Scaff1141g019702

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>Mar|M.Arenaria\_Scaff114g003306

MLHQQQQQQQQQKPKFRLQLEDVGNPQPCPDNPIRLLASRTPQYIYSPYDENKLYPPDTDCQFLIEATDKFHRIHLTIIESDLEEALFTDCNDYVSVRDREGNETSIKEVARWCGQDYPAAIASASDSLLVHFHSDSIIQKRGFNISFVQFDIDTCPPDWISDGISSPYCYKQFVLPHILPWYEAQKECNFERANLATFQNEADYAFIVESYSQTHSFPWVGYSDANVEGIYESIDRNVPLWPENFPLKHENEMKDCVYLDWNKRDQIVVYEIDDCRNRRPFLCKKRRDGTEVPVILPAGMIRRGFRDFTMDYTLLVVVVIFALLALVVGCVLFHKYKERNNRIINIDMNQRLVQQQQGQQPGNKDKAAAALARQKAKERERRELREQKYAETSNNNSNRGGGRGGGGGIAATTKSPFESQDSNASFPLQTFQSTFAQRMTTTTTGNVEPLDTAAALAEASASASQQMREHEATKLHPQQLSAEILSVDSPPEDDLNSSPRIRMSPNQPSFVEEGRKISEKKIRKGWMGAGVSGGGTTDREEEEEEKDRHNMGYEPDSEEEEHEENERQKIRRASKINGEGEGEGEENFLMELNDEGGRKNTGENEELEQYTQHNHVEEELEQYSGGEQFKQYKHKNVIETEQYINSQQFKQLESADGGEIQQKVVQVELHGENGEEGGLGQFKDKRTKEERINNFDEKMMDSYAIGDHFKAAKVATSAIASAAAIAATEHPIRPPIELMRTRTTSTDKAKSPPPLKEAKESEKIGESGKSSREATREGKEETREEKETFPEKVSGKVNIPSSTATNIVKTEGEGTGTRIRIKRKTFDRPPPVGPLDNVSAISLDEFWQQQK\*

>Mar|M.Arenaria\_Scaff12243g079028

MKKRESYINEENIGKTKLSSNSIEKRLVRLEANQQNLRRATLADWPAFSVDKRVRIFDHTRSTWIDAQRECSEHAGTLLEIDSESENERINEMLTNSGSNNRPNDHYWIGVQIMLQFSNGSSIIGNYSNFEEQNNSENTQNQKLPKGLVMKRCAAISASQTTKSEGRWLSLECSEKHGFICQL\*

>Mar|M.Arenaria\_Scaff14882g085346

MKLNFVFLISLFIFLFFSYTTEAYFGCNCQYPNNHYVPWYLSGNVENRLTFLERQTSQKINMLIARIEALERELGLIHRISMQEWNNSGAGNIYKIFNTSKTWEEAKNTCMTFGARLASIDSDYKNAFVRNMIERSFGKDESAEVWIGLKTRAELTNNPNSHFTNFGEEEKIDGCAAMGIKGKWKIRSCSNLKPFVCEQILM\*

>Mar|M.Arenaria\_Scaff14g000640

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>Mar|M.Arenaria\_Scaff14g000646

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>Mar|M.Arenaria\_Scaff1513g024059

MAVPVCKANGGIIASLYSSDESAFIAQMVGNDTPVWVGAVMKNNGDGSFSCKMLDGGDCPSEIQNSFQNQQTDTETPIYGTQLISGKWNVVNCTERVYAVACKMSCDQ\*

>Mar|M.Arenaria\_Scaff1555g024489

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>Mar|M.Arenaria\_Scaff17036g089683

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>Mar|M.Arenaria\_Scaff17036g089684

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>Mar|M.Arenaria\_Scaff171g004614

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>Mar|M.Arenaria\_Scaff171g004615

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>Mar|M.Arenaria\_Scaff17210g089981

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>Mar|M.Arenaria\_Scaff1802g027090

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>Mar|M.Arenaria\_Scaff1808g027149

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>Mar|M.Arenaria\_Scaff1830g027373

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>Mar|M.Arenaria\_Scaff18594g092419

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>Mar|M.Arenaria\_Scaff20685g095772

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>Mar|M.Arenaria\_Scaff20871g096061

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>Mar|M.Arenaria\_Scaff20891g096089

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>Mar|M.Arenaria\_Scaff21037g096304

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>Mar|M.Arenaria\_Scaff21711g097276

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>Mar|M.Arenaria\_Scaff249g006304

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>Mar|M.Arenaria\_Scaff249g006305

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>Mar|M.Arenaria\_Scaff24g000943

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>Mar|M.Arenaria\_Scaff24g000947

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>Mar|M.Arenaria\_Scaff250g006344

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>Mar|M.Arenaria\_Scaff25127g101748

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>Mar|M.Arenaria\_Scaff25773g102522

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>Mar|M.Arenaria\_Scaff2581g034484

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>Mar|M.Arenaria\_Scaff2628g034872

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>Mar|M.Arenaria\_Scaff2637g034970

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>Mar|M.Arenaria\_Scaff2835g036573

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>Mar|M.Arenaria\_Scaff2868g036863

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>Mar|M.Arenaria\_Scaff2906g037202

MITLTYVSLFYLSLPALIAGQCSSDWQTNVGSDGFTYGYKAIVSDMVNFFEAHDVCAALGAQVASIHSAQENAFMISIASSLLDQCENNNAVCKQRVDRSTTSSLRLDRLLRSFWIGMHRVQYAPFYNTSVDCCWSDGTQCDYGRFDGVADPNQNIPPWSTGNPSGSSSSVTSAGWNVEDCVEITNDNGVLWNDIGCYHKLGGVVCKKNCTNTCPPVTTQAPAITSKPITTIPVVTTTTDDDTGGYICGSDDWQWKNNGNGKAYAYKWFNQSGSFWQLHNLCYDSCATPCSIESEEENQHIVNNICAGAFSSSSSGRKKRATDSECIYTGFHRYQESPPNGPIGCSCDDGKSCDYGNDDTTTTTSKTSTTKAATTTTKAITTPRPSTSTIRATTKATTIITSTTKPNNPWAPGCPANSTTGLGDSDGYGTKNCVGFDSNGKWRDQACERPGKGIVCKKPCIPPTGS\*

>Mar|M.Arenaria\_Scaff307g007449

MKNIHTGHKRPRNRKIKLYISYLNLLINIFVITTLFVNINGTESDEHLLGLKDNDASYSSSTSVDDEEPVFSQSAQHLFKNENSNEDAEKHPSLEASSPSKNHRQHRKNPPPFVLADVQLSCAEGWERFEGKCYKLVSIEKSWPQALAFCSRFGAKLVRLESSEENKFLAKYLMRPHLTSGPTTSPSEYWIGLLYRPLMMDSSISSSSSHSKSLMDGSFLWSDGSQTSRYVGFWSYGQPDPANGSCTKILVDGLQVEGPTWQLDVCNQLRPFTCEQNACIKGSFFCQNGVCLPERAHCNGIDECGDSSDEFNCPSAHSEMSCQRYEKGESGRIETPNFPASYRQGTNCRWVIEGPLNSKIQLNFDSFETEERHDLVTVLDGGPSENSTFALSTISGTPRNTEKLSFESSTNRMIVQFRADQSIQARGFQASWRTVPISCGNQQLKASSIGQQFHSPEWPRNYPKGLECVWRIEAPSGQLISLFIDEFNTEAETDFLTIYDGPSPSEPILAKFSGHMKEPQLIISTQSQVHIYFFSSETVSQKGFTITYKKGCDNSIRRSHGVLTSPGNAHLPYAPSQICRWSIELPSQQIENFEAAAEIPSLFLVLNSWDVADLGDKLQIYEGGEDGSSNGRPLHESDGFTVNNAPPKTIYAKQGRVELVWRSNVLNSGTGWNISFSTSCPPLSLPSRRVLLSTKNTAYGTHVTISCERGFEFSTGLGRHFETECELGGLWSNYAPVPDCQPVYCSAIPQIANGFAVSATNVSYAGMARYQCYEGFSFASGKQHEEIFCTDEGRWTQSPKCKTDACPALPSFVSGERILQFGDGIGFGSVFQFHCAKGYFIEGPLSIVCRPNGEWSSPQPLCKKLTCTDIPVVENGELHLLPSNNMVMDEKSNKDKKLKDQTKNFGSKQKMEFKTKRNMVVRELQFGDSLRVECHSGFQSVGAETLKCLANQTLSGIPKCRDIDECELQSAGNCAAKSTTCVNMPGGFHCQCQSGYKPKLDCSGPLTIIPTKILTSHGVPIPVQTLNSKNGWCADSAITNAQMLEKRIMPFNESITSSFPSTILTLIFTFPVPKIIEKLHLEKVVVPNAVAPSGIAGAIAATPEAWPQRFTLSYSIEEGMPFEVYNGGLAELGGNNNITSTNENKKSNEKKLNIPNTKEIRTRALGAIGSEILVLAKPIEARTLQIEFLEFHGGVPCMKFEFLGCQRTSCEDINECEDGRNGGCEQHCHNTQGGHRCSCEEGFDLFVEPGQSGVRLREGETGYGEFDSLRFNHSCIPRHCAPLMTPENGQLIAQNLYKNFKTEANNTNNKSEFFSSSFAFPSIVEFRCTFGYQMRGPSHLKCLADGTWNGTVPSCIPASCSGVKNSTAVGLFVQPETVSIPFGQNLSFVCSQTNRPPKHSALGEIRQCIYDPRTDGLEYWLSGPEVDCPLVDCGPPPALSGAYYEGDEGHHGGNFKVGSVYLFQCRAPYSLVGKSSYDDRMVRCNVDGTWDLGDLRCEGPVCVDPGHPDDGQTFLDSVEEGAVASFSCNRPGFKPFPAETISCSLGTPCVLSEDVGISSGFIPDGAFSDNSDKVIWGYEPHKSRMSSSGWCGSKDAFIFLSVDLQRIYTLTTLRLTGVAGNGHLSGHVTKMQLFYKVQFSQNYDNYPMEFSTPSGNHRKIYQFTLNPPLRARYILLGITEYEKNPCLRFDMHGCLAPLSTTHEVPAHLQVGWNASIPQCLDAEPPTFKNCPQSPIIVQTDENGQLFPANYVIPEATDNSGRITYMLTKPEDFHPPYPVSQDTDIIYQAFDDAGNMAECAVRLRIPDTVPPILKCPDSYAIWAQENQTELHMHFNESLVRLVVQDQSPITQISYDPPEARIKLDSHVTVEASVLDAHSNRNKCKFQVALLPEPCSPWSLRIDEATVQKQCQRHASGTVCQVQCRKGYRFLESFPQQKSEVKKQQNSTNTLPQRYSCSMEHQSGKWLPSPTPPACVPMAMEPARYEMRVHMNYSLTSPLPSDCAKSYELLVGSLFDSIDQVLSQRCSSTVQIYVRFLDAKFSQMGEKTVSFFKKFFYKHLLQMSANFTVQILPTVLQQVFYELCSLTLRTIFDLRIPGATIPIRSLLTLSGDSVPAILNLGCPPINASSISVSQGFSCSQGELLKLQTPNVGSDDFLSAAPGLPECFPCPKGTAFVNNSCIQCPMGSFQDQEGQIRCKPCIENTYTLQSGAQSNESCLDVCGNGMFSATGMIPCQLCPRHTFAGPPPIGGYKECEPCPEGTYTARLGSVGPSHCKQPCAPGHFSVTGLEPCSPCPINFYQPNIGQQRCLQCSNDSFTAETGRSADEHCKKLDCQTLKCQNRGQCVVANHKEVCECRPGFMGSHCEQQIPLCDSHPCLNGGTCELHNGAFRCICPQNYTGSRCQFGPDECISSVHCPNGGVCQDLPGLGTTKCICRTGFTGPDCSQISDPCQSDQPCKNGAQCIPLQLGRYKCKCLPGWEGTNCDKNIDDCTENPCALGAKCHDLINDFECECPHGFSGKRCQIKDNLCDPSPCLNGGQCVDTLFDRHCICKRGWNGTFCEQEVNECSQKPCQNGATCRDQEDDYSCECAPGFHGYQCQYMIDHCAVKPCRNNGTCINRGPIYDCQCPLGYEGDHCEHNVDECEMMTPCDAVGTGRCEDLVNGFKCHCHPGYEGTFCEQHVSQCEDEPCMNNGTCTDLGAGFQCECQLGWKGDRCQEMETQCDRKPCMNEGKCVPLVDDYFCVCPEGVSGKNCELAPNRCLGEPCHNGGVCGDFGSRSDCQCPKGYSGNGCQFRFDGCHEGLCKNGGTCVNNNDLSKHQMSKIENIAVEQNSEANGFKCICAPGFYGNECEIDINECQPSPCPLASHCVDLVNGYYCKCPFNMTGANCEKRIDPDYDLRFLESSSQPASASLGIPFNFVSSALTLNIWVKFEKNHQTDVLKEQRKSPPIFFTLYSSSSANQPTNLTELLTISSEAINIRLFPELDKQPLVLHFPIHQRPDTQLAWNNIIFMWDSQQQGSYSLLWNAVRLYSDKGYAPDRRLDINAWINLGDPKGIEQQQNQHLMTNKIISTDLPKGNEKIIGTKFVGSITRVNMWNRVLDFETEIPSIVQRCQGSPDLYEGLSLRFANYDRLQGKVERIAKSTCGRIDLLSPTCHSSGDENKNLKDHQCRSKIPSNMNDYFKEELVEVEGCPMEPINVQTPLKELNISWKEPKFYETSSRVQIAKIEQNLKPGQVFTWGQYSAIYLALDNQSSPLATCQFKINVVREFCPDPEIPVNGVQRCEQWGPGLRYKACSVHCQNGYGFSRPPAAFYSCVEDGKWRPNEGKQRPFRYPQCTRQSPAEHLARIQLSYPQLALCNPAGKSTVTEKIIERINQINNKWHICANNEESSDCSGVQVQINCQDIFALSRLKRQTTLQQFDVIIDVPIREVQRMDPVEIIRDEAMAHGLFSLEQVIPNGRPDIGAFRVENAFRCPIGYLLNNGSCVPCAPGTFYFVPTSECKLCPIGQYQPEEAQNQCIECPTDFPMTVGMGSIKQNECRKEAQNQCIECPTDFPMTVGMGSIKQNECRIRCLPGHHLNISTGQCEPCSYGFFQPDSGAFDCIPCGIGKTTLERTAINEDQCRDECPDGQQLTASGSCQPCPQGMYRTRGQDKQCVECPSGTTTEGVGAGNKALCNTPKCGAGQFLLADIKRCQFCPRGTFQDQQLQFVCKKCPPSFNTAEEGATRESQCYSTDQCALGQDNCSWNAQCIDLPDDNDVASWRCVCNPGFRGNGINCTDACLNFCLNDGICRKNKLGHVECSCKENFSGERCEIRFQPRSQKLVYWTGAIVAVVFLLIVIVVVIWMISLRFSRSSNNSFLSSPLDKPALSFTQSTTDSPLASNFLYGRPPPILDRSHSSSLGGGGSNSIIHPIGFYYEDEQSPYDGGVVGAVGRHGRENSQEMKSIFLASTVPDNNNEVVGGSSSASHSPGQQNNGGIKVTGTTNTTNSSGGSPGSATRALEQRLRHIQQHMYRPMGDG\*

>Mar|M.Arenaria\_Scaff3125g039029

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>Mar|M.Arenaria\_Scaff314g007604

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>Mar|M.Arenaria\_Scaff318g007688

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>Mar|M.Arenaria\_Scaff3282g040286

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>Mar|M.Arenaria\_Scaff3501g041912

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>Mar|M.Arenaria\_Scaff3557g042312

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>Mar|M.Arenaria\_Scaff3761g043744

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>Mar|M.Arenaria\_Scaff3816g044124

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>Mar|M.Arenaria\_Scaff3854g044370

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>Mar|M.Arenaria\_Scaff3976g045190

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>Mar|M.Arenaria\_Scaff4203g046670

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>Mar|M.Arenaria\_Scaff435g009786

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>Mar|M.Arenaria\_Scaff4940g051102

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>Mar|M.Arenaria\_Scaff4940g051104

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>Mar|M.Arenaria\_Scaff4981g051339

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>Mar|M.Arenaria\_Scaff5003g051475

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>Mar|M.Arenaria\_Scaff5003g051476

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>Mar|M.Arenaria\_Scaff5343g053330

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>Mar|M.Arenaria\_Scaff5658g055026

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>Mar|M.Arenaria\_Scaff583g012096

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>Mar|M.Arenaria\_Scaff603g012386

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>Mar|M.Arenaria\_Scaff6289g058096

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>Mar|M.Arenaria\_Scaff649g013106

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>Mar|M.Arenaria\_Scaff6528g059216

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>Mar|M.Arenaria\_Scaff656g013200

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>Mar|M.Arenaria\_Scaff656g013207

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>Mar|M.Arenaria\_Scaff656g013211

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>Mar|M.Arenaria\_Scaff6696g059989

MITLSFVSLFYLSLPALIAGQCSSDWQTNVGSDGFTYGYKAIVSDMVNFFEAHDVCAALGAQVASIHSAQENSFVISIASSLLDQCENNNAVCKQRVDRSTTSSLRLDRLLRSFWIGMHRVQYAPFYNTSVDCCWSDGTQCDYGRFDGVADPNQNIPPWSTGNPSGSSSSITSAGWNVEDCVEITNDNGVLWNDIGCYHKLGGVVCKKNCTNTCPPVTTQAPAVTSKPITTAPVVTTTTDDDTGGYICGSDDWQWKNNGNGKAYAYKWFNQSGSFWQLHDLCYDSCATPCSIESEEENQHIVNHVCAGAFSSSSSGRKKRATDSQCIYTA\*

>Mar|M.Arenaria\_Scaff682g013606

MIILSFVSLFYLSLPALIAGQCSSDWQTNVGSDGFTYGYKAVVSDMVNFFEAHDVCAALGAQVASIHSAQENAFVISIASSLLDQCENNNAVCKQRVDRSTTSSLRLDRLLRSFWIGMHRVQYAPFYNTSVDCCWSDGTQCDYGRFDGVADPNQNIPPWSTGNPSGSSSSITSAGWNVEDCVEITNDNGVLWNDIGCYHKLGGVVCKKNCTNTCPPVATQAPAVTSKPITTIPVVTTTTDDETGGYICGSDEWQWRNNGNGKAYAYKWFNQSGSFWQLHDLCYDSCATPCSIESEEENQHIVNHVCAGAFSSSSSGRKKRATDSQCIYTGFHRYQESPPNGPIGCSCDDGKSCDYGNDDTTTTTSTTSTTKAATTTAKAITTPRPPTSTIRATTKATTIITSTTKPNNPWAPGCPANSTTGLGDSGGYGTKNCVGFDSNGKWRDQACERPGKGIVCKKPCIPPAGS\*

>Mar|M.Arenaria\_Scaff7342g062916

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>Mar|M.Arenaria\_Scaff7585g063931

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>Mar|M.Arenaria\_Scaff7862g065029

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>Mar|M.Arenaria\_Scaff82g002512

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>Mar|M.Arenaria\_Scaff897g016596

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>Ppa|PPA00415

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>Ppa|PPA01120

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>Ppa|PPA01181

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>Ppa|PPA02713

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>Ppa|PPA03201

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>Ppa|PPA03617

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>Ppa|PPA03637

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>Ppa|PPA04072

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>Ppa|PPA04265

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>Ppa|PPA04644

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>Ppa|PPA04648

MLRLSLLASLCYSAWAVCPSGFELVRNGECHRQLYDGQTTYAPNGALQAIDFCNDYGAIPVNIVNQEDHDYWVSVSRKDKKNGNQYGNIILGIYCDNTNHWMWADGREVYYEWKPEDYDEDLHERCGENGQYCMWTINPTTNNWQKWCNTYQTTDNYCLILPTSKPEEPDRDCTNFDHDDDNDVCYQVGKYPANWTEANTICHSFGANVASIHNDLENSFIRRLSVSKGLINGMLLGGSLNAKKNAYKWADGTKWDYDNFAPGFPLNGFGECVAMETNNVGGQWINVDCTTELPFACIRAPDDSDPVCDGSVKKENDIIYNPGFPSDASIPCDFMLKVDPGMLVEVEILMLEANSCCDRLVLSEGTLGGQEIAILTGELYDGWTFRTTSQNVMRASWQPKGGVNVKGMMITFLHSSPSSRLTRSSRPRAEWSLLLLLRSLSTLPHLLASTTLGVMGPQLLLHCIVALNCLQTGWELFLIYRQRRKHESTVKRPAGVESIISEEDYTKARSYSIDRLSFKVFRMVIECALMITMLYSGYYHYLWTTATSTWAPLSVFLILHNLVSFLLDLPLSLYENFVIEELHGFNKYTGSFYIVDAIKKLVLSTAITIPLASGAVWLIENGGDLFFIYLWVFISIVILLAMTIYPAYIAPLFDQYSPLPDGDLKKSIEELAAKLEYPLKKIFVVDGSTRSGHSNAYLFGFWKNKQIVLYDTLLSGEEKRKVYEALGKKVDEDKEEKEGKKKDDDKGMGVEEVVAVVGHELGHWALSHTVRQLGVAELNILLTLFCFSHFYTNETLGAAFGFTGGAPTVISLLVVMQYVMGVYNEIFGLISVSLTRRMEFEADAFAASLGLGSKLTTALIRLSKDNLSVPVNDSLYSLCRHTHPPVTERIEALKKKQ

>Ppa|PPA04669

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>Ppa|PPA04672

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>Ppa|PPA04770

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>Ppa|PPA04790

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>Ppa|PPA04810

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>Ppa|PPA04842

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>Ppa|PPA04844

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>Ppa|PPA04853

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>Ppa|PPA04854

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>Ppa|PPA05204

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>Ppa|PPA05209

MWRLFLCFALLQLASCTCPGTFDLVKDGECRGLVSIETLTFDQAAKTAIEKCNTVPGQPVIIHNEEHQTYWKGKAPATSEGFLILGIICNTTTRKYVWADGSAIDYKPSNGYNEELDSNYCQPDYCWDIHPDGFWSYGGPGAFIKASIYCTMQLEQPPLNTDGCDNFEDDTDDGVCYQVAATAQNYQDAQVLCKKAGADLASIHNSQENAFVRRLAVSRGAVNGVFLGASADKNGRFGWADGSKMDFVNYYPGFPKKNFGECLAMDTSLSAGQWMNVDCAAPLPAACVRDQRPGQAPVCSGDDYDEGQIIVSPGFPNSAATPCDYFLAVPSGKKVELTIILLEANTCCDSLVLYDGTLGATVIAKLSGSIQNQVYTSKTSNIMRVSWQPNGGVNVKGMVASDQEIVHYPSHKLALTICPPNFDLVRDGECRGFVSVEKLTFDQAAPTAIELCAALPSKVQGQPVIIRNQEQQQYWKDRAPATTTDGYLILGIVCNPATKKFEWADGSPIDFRPKEGYNGGELDALCYTEYGWYMRADGYWNFATRGAYVQADIFCTVQLLQPPLNPDGCDNYEDDMGDGVCYHVGAYAEDWQDAYMVCKKEGAELASIHNSQENSFVRRLAVSAGAVNGVYLGASSFFAQEEGAFGWADGTPMDYQNYYNGFPKKDFGDCIAMDTSSTAGQWMNNDCTKAIPAACIRRQKVDPAPICSGQDYYEGQIIVSPGFPNSAATPCDWFLEVPAGKRVQLQVIMLEANSCCDSLVLYDGSLGSKPLATLSGSQHNMTYTTKDSNIMKVSWEPNGGVNVRGMAKMWRLHLAFAILGLAHCSCPKGFDLVADEQCRGFVGKFYLPFELAAPYALEKCVSVQAQAVSIHNEEQQSYWSSKAPATTDGFLDWSAIPSRRSGSGPTGPHWTTNRPPTFAIRAAPKAIEKCADVQAQAVIIHNEEQQSYWSSKAPATSDGFLVLGLVCNSKSKKWEWSDGSALDYKPPTNLRNPELDKPCTPNYTWDIHPDGYWSYGGPGNYIQAYIFCTTDLPPLPTFTDGCENFGQDAGNGQCYQVGVTAASWQDAENICQQAGAHLASLHNKDENAFLRRMAVANGAVNGVFLGASARDNEPFRWVDGTNMDYEPYAPGFPKPNIGYCVAMDTSSANGQWMNVNCAAKMPFACRRKQRNDVEQPTCYDEEWKENTIITSPGFPSSAVTPCDYLLSVAPGKKVSVEIQLEANSCCDSLTIYDGYMGGSVIAILTGDINNGTYTTKTSNIMKVSWQPKGGVNVKGLAMTFRANEHRHLCCLRLSHGSNDQARAVPDRRATPFALAQPITPDQNDENRNETAVTPTRSVPSEVDEAFRKFATSPPSALSTVDSTPSAFHAPRLGLQGLQGFGHALPDALMMTPTSPLSPSPTTVFAPLPATPMLPRVPPLTNNAFWQQMLYNNLVLSLAANQQRLAALAQSSSVLLTPSCPSTPKQTTSPYSFSSAESLARSDAVPSPPSFFSTPKRRASSADHSTPVTGKEVRCPTCGKAFTRPWLLQNHMRVHTGEKPYACDTCGKAFADKSNLRAHTQTHSGLKPYGCTRCGKSFALKAYLSKHEESAYAVTGFSVSSPKPAVSGSPLKTSPAPVRPSGSPVGSTGFFYPTTKGFGNPSVKPVTGGPVSGSPKPAASTGFFYPTTRGFGNPSVKPVTGGPVSGSPKPQGFTGFFYPTTRGFGNPSVKPVTGGPVSGSPKPQGSTGFFYPTTRGFGSPSVKPVTGSPVSGSPKPQGSTGFFYPTTRGFGNPSFKPWWPCLGNHPRMVRTPQNLSDMPVESDSFFAIVNERVSFLFILYFVTREMGVFSTSTSASRNSLPSPLSSFESKTTTEAPVTSEVPVTDGVTPSEAPVEPSESATAADAPAASSPLPDAPVVQSEAPLTSDPVTDSPAPSDAPVVQSEAPLTCDPVTDSPAPSDAPVVQSEAPLTCDPVTNSPAPSDAPVVQSEAPLTSDPVTDSPAPSDAPVVHEEIMLKHLVLFAILQNIRSSCPTGFELVKNGECRGKAPSYYTLSWNTAMSDVGAKCALVCNTATSRWEWSDGSVLDYKPQSYDKVCSAGSANFEIGCTTHLAQPKPAGDGCENFADDNEDGVCYQIGNTTASSEDAKVTCRSFGADVASIHNDKENSFVRRLAVSRGAFNGVYLGATGVGNEFSWIDGSTWDYSNFYNTFPLDGYGKCLAMDTSGTSGQWVNVDCSSKLAVACMGQQNYSAPLCSPGPWKEGQIIYSPGFPDDASIPCDYLFSVNTGKKIEVEVLFVEANSCCDRLVLIENYIGGTVIAKVSWQPDGGVNVRGFMNNITILSDIVNATCRSGFELFRNGECRGNYTRLTPYWDASPNPSIASCKQIQAQPIIIRDAMDQSYWSSKATGGYALLGLVCNSTSKQWNWADGTVLNYKTPSGYATDLDKDCVPSMNWAIQSNGYWYSGAAHNTFTADVFCSIPDSQPVPSPNGCESFDDDSDDAICYQIATTAENFRNAQMVCKNVGGDLASIHNDRENSFVRRLAVSRQALNGVLIGGLLSGNDKAWTDGSAWDYDNFYPGFPINGLGQCLVLDTQGTSGEWMNVDCNNTVAVACERQQNFTTPFCPTEPPKERQLVVSPGFPFDASTPCDYMLMVDAGKKVQMEILMLEANTCCDRLIVYEDYFAGKVIANVTGEFKERVYTTSTSNFMKVSWQPNGGVNVRGMMITFRGVVVSVVSVFESIALIRVDKNRRSLRIELVFRAESIPGYSTSTMLLLILFSILRKHLSLRVPKALNWFAMASAGGFTLLYILVATKNLTSPSQNAQKSMAHQSYLTRHVHGGAYSKILLGLMCNSSSTKWEWVDKSPSDYKPPGDYDAALNKACKLGCVWYLTTNGVWACENSTPQLDVFCTTQLQQPVPAGEGCEGFDDDVEDGACYEVGDSAESWQDAQMNCAKLGANPASIHNSQENSFVRRLAVSKGAVNGLYLGATMSGKGKDFGWVDGTEWDYANFHQGFPMDGLGECLAMDTSSSAGLWMNIDCSVQLPVACVRQQNAIIHPNCSSGPFVEGALITSPGFPYSASTFCDFFLTVEAGKKVEAEILFLEANTCCDSLVLYDGYLGGQVIATLSGEMRNATFTTTTSNVMRVNWQPQGGVNVMGLAVNDLPWSVIPLGVYIREIVLGACPDGFKLTAEGQCSQITPTQVYAGYSQATDTAISKCKEKAAEPIIIHYAEQQSYWDSQYRTNYNLPLGLICNTSSLKWQWTDGSALDYKPSEYDAALNSNCKTGCVWHMASTNGSWNYACSNSGVYFNVFCTIQLPQPIFSDDGCENFNDDSEDGGNEFGWIDGSQWDYDNFFPGFPIAGLGDCLVIDTDGTSGQWANVDCSAQLSVACTKSQNYSPPTCTTGPWKEGQIIISLEANPCCDYVTIIENYFCGNFLANLTGEIERKLITTSSSNFMRVSWQPNGGVNVRGMMSGLDCGEEEKIEETFIRGACPDGFKLYAGGQCELITPLYYTGVRYDQAVNTAISKCKDKHAQPIIIHYAEQNSYFAGKYSSYAQPLGKCIQILSMKLRQAVLVCGLVCNTSSLKWQWSDHSALDYKPSAGYSSGIVTFYDILSALNSNCYTGAVWYIARTDGYWSVASGSSTSSFNVYCTIQLPQPIYSEDGCEYFYDDSEDGVCYRVGEDAETWQEAQLNCKKVGANLASVHNQQENNYLRRLSVSQNAITGLFLGATISGKENNFGWIDGTPWDYQNFYPGFPLPGFGDCVAMDTSSTAGLWMNFDCNSKLPVACIRDKMTNLVANYTCSAGPWEEDTLITSPGFPYNASTPCEFFLMADDGKHVELEILPLEANPCCDNLVLYDGYMSGSKIATVTGIHTNVTYTTTQTNFMRVSWEPKGGYNVMGLANIEKVGNDFYAVLSFCPPGLDLVRGGQCRGFYTTVTVPDDVAENIAANKCKEINGLPIIIHDDEEQAYWKSRATGAYDLVLGLVCSSSRWMWADGSQVDYHPPSFIPRCGDDQDTFQVYCTTQMPPLPVPSPDGCDGFKDNGDDGVCYQVSTTAESWNDAELICRKLGANLASIHNDHENSFIRHLAVSKGEVRGVFIGASSGGRGEKEADFAWVDGSPWDYSLFYNGFELTEFACENAHIRSGFPKDGFGACLTMDTSTTSGQWMNIDCAAKLPAACVRGRTSFSEIVLLNIDIFRKNRACVQFRNMEGARACMFILFQSFFIDITSPGFPYNSATPCEYFLMVESGKRVNVEILLLEANSCYDSLTIYDGYLGGDVLVSLTGEVYNVNYTTTTSNIMKVAWQPNGGINVLGLAMTFPVIHCSCPDGFELIAAGECRMLKTISLNAHDDNATDTFTSQCKNYQAQIVIIHNDEIWILIARMGVLGCDSNAHNFDVYCTAQLQQPIPSGGGCESFEDDSDDEVCYEVANAAQNWKEAQTICRSFGADVASIHNDQENSFLRRLAVSKGAVNGMYLGASPSGKGNQFGWIDGSEWDYEHFYPDDYISSGCYTGAWKEEEIAYSPSYPFDASVPCDFILSVDPGKRVELEVIVLEANSCCDYLIVHESYVGSNIIANLTGALDNTFYTTTSSNSMRVSWQPNGGVNVRGVMSNNIFSVHIQKRCRMLTPINMKIRDDQATDNVISQCKALQAQPVIIHNDEQQSYWTGKRKISSSYVPLGLVCNTSSLEWQWSDGSAVDYKPSASEGGYYEGFDKDCTNGCVALIYNSTGYWARWCGTDVEPFDVYCTVQLQQPTPSVDGCESFEDDSEDGVCYQVGATAENWQDAQILCLKLGANLASIHSSQENSFIRRIAVSRGAVSGVYLGGTISGKGSDFGWIDGSAWDFTNFHSGFPITGAGDCLAMDTSTSSGQWMNIACTEKLPIVCIRDQKPVVEPTCTDGPWEEGHIITSPGFPYNASIPCDFFLIVDEGKKVEVDVVFLEANSCCDSLIIYDGYLGGHVIATLTGEIRNSTYTATSNTMRVSWAPNGGVNVKGMANYSITTCSFMRTPVTTIKFIVFRVHIFNDKMLTLFLLLFAFSIIHCSCPDGFELVAAGECRMTTPISINIRDDQATDTTISQCKALQAQPIIIHNDEDWYATQVRSNGNGLMDRHGDSVRINTFFQENSFIRRIAVSQGAVSGVYLGGTISGKGSDFGWIDGSAWDYTNFHSGAN

>Ppa|PPA05500

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>Ppa|PPA05781

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>Ppa|PPA05905

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>Ppa|PPA05947

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>Ppa|PPA06670

MNCFCPPSTLCGSSDGSEPTLRCFKPATEPASFDRALLNCANESMEMATIHNKNDASLLILSTVKGLPRWFGLRHEYNGFHWSDEEQHSYSNWAAHEPELEKNQNCAYALKGTAKKIEWYFFSPCWIAGSKSHPLTLPPVQNKPFCPSFNHATTHTSNSQVDRPLIVDCSRSPATVIFLSTTHVLQPLVQQKSTAPKKNLPNIGVSQAKSDKSWDENTIVLDKYTSALRICPIWMQVEKSDISMKRTVWKALLMLHLPTRSGSLHNPHLFVTICSSESNDGDEKENNK

>Ppa|PPA07634

MRLSLVLSLILSFCVAVSSANLFRSTNTISGAATDAPQCRNDFDFYKGWCVYTYGWPGPYQSEVERCAEVDAHGPSLHSDEDLKFWSDAVLDLKYDYFWLDAYCPNRGNEPVVWLDGTPTDYYGPDDELAKCVYGSGYMLYSTGLTLFEYRYFGNTLCVYRPELPSTSTTSLLTTQRPITPRPTTAISPPSNETADSCPCNPGTVYLDLVFVVDASDEMTRSTVDDATATIQSTLYGLTFGTGNFQTNVAALAYAETVQKVTNFGDIISTKNISSFSIPFLGGNSAKIADAIKQASLMISVNGRNFARGVIAIFSHNLNGLEAKDMDVVNEFKDNGGVIITVDYSKNLLPSDIASPGYSIHSSSEVSGDLLYAFCDANCFCKDGLSPYNTENERGREVPDSCYHVADTFAVYDAAEANCERKNGFVATVHDDNKNFFLTSRELFELLDFDIFPTKSRYWLGLERNEESFEWADGSADGYTNWAPGNPIGGLDCVYSQQQTGFNAPWFSAPCTDPLKNSMTYACQIRPCSSEHLFEKMRNCQKTRMKIYNHWVPLYDQLVRNPLDYEGFKLIYERYLVEKRENSAWSKLSSAQPDSHQCLNMIGNENNENNDNNEWKLCNWRKNEARNLTKMSETTSEREDLYVWIQINEVPAVALIDSGFQGIPMMRYSFAAIAGLAGDIDTRHRRSFYGNYAAKTVGKIHSCEFEIDGIKYDTSADICFDEDEHDVIIGLNFLRTHNCVIDLPNNRLILNGTEIVDFLPDAEARKHRHAREDERCRNRPMSIKPNKNKRNHIMDMGFAKDDVVRALTESLNDVPGAVSSLYKCAEKEELKSGNKSKTVVDKAIVGISEAVKPKATPEDEKDNQCRKLFEEMKKPDNSFSEGFKNEYENFISAKKTKTDIMNDPESDIGKALAIREKKVQRFDNDLKKRQEKNSKLFVPNELFFIRIAVNEISTLALVETGAPTSFIPKQFAENAELESKIDIRFQNDIEGFGGKKKAAGILSCSINISKFLFDAQCIVMEGDRYAIIGLDFLRKYNSSVMTCPAPANNHTDFAKKEHLFPCLQEDSGIPTEPFLSAFQGLADFVGFMGTAFAPVKSDIAGNVTGWLKDPIGQDTLQKLIASDLKDNGGKLGIATEGLLWLKRGQEFMLLMLIFMVRDYRKDKASTESLVSYSKWPTMADPVVEDQSSSSQDEVLQIKTLTKKHIQVLYRLLILIVDNFGGGRKDLFGCEGGRREGTSTAEGRKEEREGGGWKERGVEECEEKRLEGPMGGEEKKKESEGITFNGSVHVGIVPEGKIRKWLCVQFPPSPSFEVDQQMLADLIALKFDGKDAERALKKTLNDLDGAVTMTITVSNEAKSIPNMGESSPSIDNVKYSGPGDKEQNKKCRRLFEKLRKCEKTRNKIFVHWKPLHDKFIDNHLDYDSFQTAYEAYLTVMRGKADWSKYSHLESQLIENVDEENIEWQQINRKEKKRRNKLPEKVLPRASRSLYIWIEVNGVSTIAFVDSGSGGTCMQYSFAVKVGLASDIDTIYRSTCCGLYTVKTVGDIHSCKFEIGGSTYESVVEVWTESEPDCDVLIGMDFLRRHNSIIDLPNNRLMLNGCKTVEFLPREQAREFRRERRRNKPVKINCNKEKINQIVDMGFEKDIAEKQLRKSMNDVLNAVHNLFLRAQKDTRRAELENRAKKELQINEVLIELNSLLDKEEELKCRQLYERMKKPLTKRTTYFNWPALLIQYINFPCDYDGFKQEYVAFLTMKKNRNDIMNDKSSSIGQALTLHKAKEDAFEKQSAQVRKPPLCQSRLVTFTGKIHVGGVPEGKIRRWNYRRKFTPPPSFKVDDEMLSELIAMKFDKKEAIEALEETLNDIELAVSDLYYKEHDREIMAQLLQMRLAFILVFFAAAASAHIPRPALNASALSGAAKKIVSSNSDVQCKSGFSLYNGWCLYNSAPTNYYYQDAVDICTGKGEFAPSVHNADQLDFWKTLASEVEHFWLDTYCPSAGNTYLWRDGTPTDYYGPSNELLNCKEEVGYHMHNTGFASYGYTESGASAVCAYDPQRYVDVTSDYCSCSPNTIYLDIVFVVDTSDDMTIGLVGDATATILSTLYGLTFGTGMFQANVAIVAFAETVQTVVNFGGFRTSKDITGFSLLFMGGNSDKMAEALKQASSMINSNGRDFTRGAIVLLTNSFDQRHASNINEVARAFQDDNGIIITIDYSVGTGIQGLEDITSPGYYVNDTSTNPDLDADVLYALCDANCFCKDGLSVYNVANERGRSLPKGCYHVSGFSAVYDAADDNCHNMDGFVATVHDDDKNFYMISLFPPKSRYWLGYRKNGTNYEWADHSNDRTTYWAAGNPISGQDCVYGQQQSGFNSLWYSAPCTDPLKNSMPYACQLRPYDEPAPALCVYDPQKPISSTQKGIHKQVHCFVFHINAAHITATIKSTLSGLTLGTGLYQSNIAVFAYSETVQIVVDFGSFKSSEALAVSSLQYFLSPVLGSIKQASSMISTNGRAFTKGVIVLLTNSYDEHQTVDIAEAVNAYKNHGGIFVSIVYRLMMIHILKKSFPLVKLILAACLAIVSIHLFNYFALILFFKCQSSARMRLALVLSSVVATAAAAVFNRSAARIESGVAAGNPQCREPFFAYSTGCVYIENGNKHTYQQAVDLCSSLGSFAPSLHSKQDLTFWSDMMETWNVYPYHFWLDAYCPSAGEKYKWRDGTETDYYGPENELKSCDPNIGFHVEWNGVLGNEELDQLAPALCVYDPSLTTLPPTIRPTTPKSSDVPSEFCSCNPSTVYLDIVFVVDASDSMTKDLVGDVTATIKSTLYGLTFGTGHSQSNVAAIAYGETVQTVVDFGGFQSSKDISSFSLPFLGGKSDKTAEAIKQASAMLSANGRSFTKGVIVLLTNSYDQRQAVDIAEAANLFENNGGILVSIDYSEGSGLAGLQDVASAGYYINDTASNPSLDSDMLYAFCDANCFCKDGLTPYTVTNERGRNAPDGCYRVAGFSAVYQAAKENCDEEGGIVSTVHDDFKNFFLMSLFPSKTKYWLGLQRTADGFTWADGSTDAYVNFAPGNPAPGADCVYAQQQTGFNTRWFSAPCTDPLKNSLSYACQLRPCGSDYDCSA

>Ppa|PPA09328

MSHAMRCLAVFVVLFGLAHALVKFDYSVVLQAADLDPFSNTVLFDCYTSCKVYVDRKSDKLLISHNGRVIADFTKIIGDSAFNPAGFEIAAGTYKLENRGEINPVFVFYIVDSEAANVNTQVYVPTETIGISFKGHDRYVTVLSSFDALEFSAFQGTFPAGYPRIYSTGFDAAGDSRCHPVYQARSQDNAEISLPRVASAVITVDFGFVGAHNVSVNQKSLDNPRKGQGASTVYMSPGYVGCSFNAGHNYYANVSEVYDYYQSFMNEFNLVAVYDSLTYNEPLQITMGGVEQALTGSSRYEVHNPSDALVPSYTVLWSRTTPSSSFAVQIEWNIDEAQPTIPTTTTRRAVQTTTTRAVPKTTPVPWQTTTFGAPSTRNPAIGDSYCSCAVDKFGMPHGWLSTEIWLDVVIVLDTSEAMGAESLEDAATLIESLIGDDDYDVLITDTRSQFYTRIGVVVMSDTAEVLFNLNMTKSDTITDKVHVAKGVTKIDVMHAFVTATDMFANGLITKPDRANTRQVIYYLTDSDAKLNATQIKDFKERGTIIVEQFAKKGENDKDLPQLASSGYYFKTNEESPIQNFCKANCFCAPDRSPYAGPWSDAAVIAGGGCFHAPTIGLQFGKAQKECSNNRGSGELASVHDKHKALFLNELVSDSTNKPYYFWIGYSKNDDGVWKWEDGSSDPYTNWDYNEPSSASVSKCAYVDQEQENLPWGAGNCQIVFPYRLPMAMMTDDLRMVKLDEGLS

>Ppa|PPA10019

MKDLEVVETIKTRLSFFRNCRLFKSSVHRFKNGLLILGFLVEGRRSDCLAMDTLSTSGQWMNMNCSASLAAACAGQENPKPVCSPGPWVEGQTIFSPGYPYDASVPCDYFLTSSLLMKGREWRWSDFEIHQILLLEANSCCDRLILTDDVLVGKIVANLTGEISDKTYTTSTSNLMRVSWQPNGGVNVRGMMNLSLVHALPGSNWGLYATMTMHFDDSIDPVIAKCAEIQGTPVIIHDEEHNTYYQMRVADSHHLAIFDIYCTTQLQQPTSPDFGCYDFEEDNEDGICYQVDANIESFKDAQKLCGQYGANLASIHNLQENSFIRRLAVSAGAVNGVFLGATKSGKGDSFGWTDGTTWDYSNFYPGFPVEDRGDCLAMDTLSTSGQWMNMDCSASLAAACARKENPKPVCTSGPWAEGQTIFSPGYPYDASVPCDYFLTVADGKRVQVEILLLEANTCCDRLILTDDVLGGKIVANLTGEISDKTYTTSSSNLMRVSWQPNGGVNVRGMMVDTVQCSCPPGFELASQGECRGVTARTVVVYTDDALNTVKAYCDTVNGQVPIIHNEEQNSYWLSQQNDRFLLGLKCNSSTKKWEWMDGTDVDFKPEKYSQVSGHSKTTTDVYCTTQLQQPIPANDGCQNFEDDEEDGVCYHATLQILIMKTTTLLQEAVENWQVAQMSCRNFGGNLASIHSLKENSFVRRLAVSKGAVNGLFLGASVSGKGNSFAWIDGSEWDYDYFYPYFPLEGQGDCVAMDTLAPAGERINKNCSASLAFACVRQRNTKSVCPSGPFKEGQIITSPGFPFDASTPCEFILTVSPGKNIEVEIHVLEANSCCDRVILTDDFVGGNIIANLTGEISDKTYTTSTSNLMRVSWQPNGGVNVRGMMMTFREIAHCACPDGFDLVSNGECRGKLKTMDIFWDTWMATTITECAAIQAQPIIIHNEEQQSYWASVAGQSSTKHNNVILGLVCNSTTKQWTWSDGSRLDYKPPNYTSDLDKNCCDGCTWVVEPGNFWGYACGHSGTMNRDIFCTKQLQQVDPDANEGCLYFDSDSDDGVCYQVGENADTWQDAQLNCKKLGANLASIHNTQENSFLRRLAVSNGAVNGLFLGGTYSGKGDNMGWIDGSVWDYENFSPGFPKAGFGECLAMDTFSTAGQWVNIDCGAKLPVACIRNELTIVVPNATCSSNTWKEGQIITSPGFPFSASMPCDFYLTVDSGKRVEVEIILLEANSCCDNLFLFDGYLGGSLLANVTGQVSNVTYTTTSSNIMRVVWEPNGGVNVLGLVMTFRVLPEQTKNLYNGQSQISETITVEEVDLEAALNYSCPAGFNLVRAGQCISYGQPFQTRSEDLVQRASKTCIDMGGQLIVIHDNEDQLYWIAQYKTNEILLGLACNSASSKWEWVDGSLVDYKPHSYYDGTLDKSCVKNCAWTLLPTGKWEIRCGEHDYLTVNLYCTAQLTPPPVPSGDGCEDFEVDNDDGVCYQVFPTIIIKWKYAQLLCQSVGANLASIHNSNENAFVRELAVSKGAVNGVFLGANRSIALPHFQWNDRTGWVYENFYPGFPQPDFGDYLVMDVPTGQWMNMNCGSEMPFTCIREKRSLPPPSCRSESYERAGMISSPGYPFNASMPCDYFLKVDAGRKIITLEANSCCDYLTLYDGYVSGKVIANLTDVVRDETFTTTSTNFMRVSWKPNPGKYGFLESYWDEQEKVAMMKCMELGAMPVIIHNDEQQKYWQLHVDRKGDEFVLGIVCNTATMRWEWADGSQIDYRPPQHDPNLERNCITDASWRQQLNEAGHIDDGYTDIFCIKNLMQPIPSAEGCDSFADDSTDGVCYQIGGIAMSWPDAQKICRGVGANVASIHTVSENSFVRRLAVSKGAVNGVFLGATTVGKGNDFGWIDGTAWDYENFYPGFPVAGAGDCIAMDTSSTTGQWQNFDCSSTSLPVACIREQKPVVEPMCAGPWNEGDIIILLEANTCCDSLVIYNGNLSGNVIANLTGEKMNATYTSSSNSMKVSWQPMGGVNVRGVMENEMINHIANSMDELKERDMNLVLDLNCKNSTSRLEWADGSSLSYLPDSRLEVDFDCVHAKRTLFSKPRDGQWYHVLTDYNMGWTFTESDQILGGGRDL

>Ppa|PPA10028

MGMKKLVLLLFSILQIIHASCPGGFALVRDGQCRGQYSTITKPWDDILTTSISKCSEIQGQPVIIRNEEEQSYWSAQKSENQYFVLALTCNSKSKQWEWTDGSALGYKPPKGQYHRALDDRCSTGCSWLLTTDGSGYWMQGCGRFSTLTVDVFCTTQLQQPTPADDGCESFEDDKEDGVCYQIGEIAQNWRDAQRICRNFGADLATIHRKKFQANSFVRRLAVSRGQVSGLFLGAMSGSDNKFGWIDGSDMDYNNFYPGFPIAGLGTCLAMDTQGTSGQWVNTDCSTKQSVACIRPQNFPTPACTSGPWNEGDIIFSPGFPFDASTPCDFLLMVDEGKRILLLEANSCCDNLVLFDNYISGKVVANVTGEINDKTYTTDSSNFVRVSWQPNGGVNVRGINVCAHFALASCDMLGLLVFLSVLQLDLADVRACPQGFDVVANGQCRGYYKTLNLYWDERAVNTAISSCGEIDALPVTIHNAEQNQYWAARGWLVIGLVCAKGETKWRWTDGTPLDYRPPKYHAALDKQCKGGCSWDILEDGSWDFICNGQQTYKTNIYCTTQLDQPFPSPDGCDAFLDDRDDGICFEVAKTPTNFQEAQKICRSFGGFVASIHNDRENSFIRRVAVSKGATNGVYLGATVAPNAQSVKWLDGSVWNYKNFYSGFPLANAGQCVVMDTQGTSGQWVNTDCNAKQAVACERRQYYNDTTCNAGPFKEGDIIYSPGFPMTSNIPCDFLLSVDAGRRIAVEVLFLEANSCCDKLVLTENYIGGPVLATLTGEVSNKVFTTSSSNFMRVSWQPRGGYNVMGMMEQAHVVEYVTSRDLYWYERAVNTAISTCGAMGDDVDAVTIHNAEQQQYWTERGWLVIALICANGETKWRWTDGTPLDYKPPKGMYHSALDQQCKGGCSWDIKEDGYWNFICNGQETFTTKIYCTMQLEQPKPNPDGCDAFQDDRDDGICFEVAKAPSAFNEAQRICRSFGGFVASIHNDKENSFVRRIAVSKGATSGVYLGASVAANAQSVKWLDGSVWNYGNFYSGFPLPGLGECVAMDTQGTSGQWVNVDCKATQAVACERRQNYSDLSCPTGPFTEGDIIYSPGFPMTSNIPCDYLLSVEAGKRIAVEVLFLEANSCCDRLVLTENYIGGQVLATLTGEVSNQIYTTSSSNFMRVSWQPQGGWNVMGMMVTFRAV

>Ppa|PPA10030

MLTLLALASVLNFALVDANLCPDGFDLVANGQCRGLYKTLSLYWDERAVNTAIHTCEEIDADPIMIHNEEQQQYWTSLSQKGLELVIAIVCAEGETKWRWTDGTKLDYKPPKGMYHSVCNGSQKFTTKIYCTTQVEQPKPSPDGCDAFQDDKDDGICYEVAKVPTDFQEAQRICRSFGGFVASIHNDKENSFIRRVAVSKGATNGVYIGASVAPNGQSVKWLDGSIWNYGNFYSGFPLPGAGECVAMDTQGTSGQWVNVDCNATQAVACERRQNYTDLSCPTGTFTEGDIIYSPGFPFSSNIPCDYLLSVAAGKRISVEVIYLEANSCCDKLVLTENYIGGQVLATLTGEVSNKVYTTSSSNFMRVSWQPQGGWNVMGMMVTFRAV

>Ppa|PPA11288

MVQHKPSIHYIILVYSKELCPKDLDSNRDDIMAHGTCEEVPLKRELVLKDAYSKSDFFWIGFSKSDGVWRWEDKSTDSYTNWEVDEPNSAAVARCAYVDSSTKALAWGSGNCNVAFPFVCEDVPCSVGNKDC

>Ppa|PPA11506

MLQTTLLLSLVIIHATLGCTPPYNTWIDGNCYYSYSSYTTISWPAAAENCKGRDATLASIHGSQENADFLKLAKEDTLQETKRGYWIGLRCDGKKFYWEDGSFVDYTNFGDSTYKCNTTSTDLHFYMNWDDGKWYRDVNWDWYGRAYVCKKNYRPEDSICEEYELVSDTKTCLSLRSDSMDSKDAENSCTYTGGHLAAIHDNTVNDYIRRSAVSNNLLNGVLIGLKQSGNDLTWNDNTTVNYTNFAKNFPNSSLGSCFAMQTSSLAGEWVNVQCGGTSATPTKLPYACTMPAYDLPDEMETSECPIDTYYSDGDMIYSPSFPSPNNTNSCEYLIVGPEGAKNMQVEVVFFETNRCCDSLTIYEGIAGAQKIATLAGSTYNGNIYKSANGPAMRLVYNVQSGAHVRGWQLKVKAIK

>Ppa|PPA11619

MGKWIHTTPRMRLILLLSCLPALTNACAAGYNTVYDGLCFKNFGSGVHYDVAKNTCDSDDGHLPRLYSQAEQDQYWSVFHGYYAWTGLICDGERFIWDDGTVATYTNFDGTVTCNSGNTLNTYINPSYGKWYQSDGSQDTNNAVCAANTRSWICDTYYLLQMGKSDDWCYLFITSLTAQPAAESNCLTQRAHIAAIHDKDFNDYLKRTAVGYGITNGLLIGLKFVNGKYEWNDGSEVDYTNFAPGFPDESFGECVTMGINLKMDELGLCHSTSIHIFSPTWGSATGPALCDYALMDLDKTKKVTVEIVFFESNSCCDTLTIYDGLVGSTVLKTLSGYYGFTSIKVTASANAIRMEWNAKSGAHVRGWHAKVTSA

>Ppa|PPA11856

MARNAEKAMTTLARWRRLKEEEEKGPVAKRPHDTKYKLRDMNDDINKMLRIKMAWEWRIKELGGPDYRKIAPRQLDREGREVSSNRGYKYFGAAKDLPGVRELFEKNTEMEGVRKTRAELMKNVDADYYGYMDDDDGLLVPLEKVAEEKAKLAIKKKFDEQGGERLKKEHEDDIDIDFYKVEEDSEENGMETRESIVVGEDGRKMTIRHVMVPSQQDIEEMILERKKQALIDKPDCFEREMAPAWIAPRNANHVKVSSVQECLAICASAHSILQWECTRIVYDNINQGCLLFGSSPGEGEKMGVDPSFDAYNNLCWMEETTKNEVNFPDKDDEEEEISLGNVQTVEDLKKNLVSMKQIDSIPTTVPSIPSIVPTEQTRKCFRRIPQGNIPGKADDIYQNISSTECLEKCMECNDCLGDDLPCMSVIYYEHVSECILLRFKEENGLSRISPIQETSSLFWRDLTCGGTNKCNPHMDLIIILDGSDSTGIKDFEKGLKVIRTVMNTIGKLTSDARVKVFQIIGGRSLLGATVSQVIKNTQSDTSIFILISDLFIEDNPKLIEIELNKYDRQMITLSLTEVFDTKIGDRLTMGRTGKMIHSIGEEEAEEKLLRLLCEEREKRGKKQTNLLETRRVWIGLRRTVEGELLWTDQSTVNDLSRLSDIPTDDKKCVSSEIEWSYTECEKEFPFVCTFTPLEKVVMVKNDKKGAGPLHQKGPVTVSALQNDHITEIARKNWAPNTKDKDADFSKDLISKIYNEEVKASKFNPRKIVLLEFSQYLECYLWPNFTPERDSNEFIMSIVVMVNEKFRERIPAWQSFNKNPKHFNFFLHRVLNLALDETQLSMIEHCSILQFLVNCFNSVEVDLVREQITRLVHIRIWNNILPKQREDMLSKNKKLRKFWNQTEAKAKTAKLTEEAAKMQEMEQVFLWKMIQRFKRTLDRIDDENSEIDVDDIRYCERFVQLMIDLEALLPTRRFFNAVLHSSHLLVHCLLSSFIKSEAGSLFCQLVDMLKFYARFEIDEITGLPLTHTEVATRHTDHVIQLQKAAFKYFKESMKDFYLLNVSGVDSRKALTKQFTSMSKSELYRFAEFLHLVPSVEEGDEKKTMDGMEKEYLMEALILHCERRVNQLQQLNEQPLYPTETVIWDENIVPYEHYSGEGVLALNKLNLQFLTLHDYLLRNFNLFQLESTYEIRQDLQDVLFRMKPWLHETNGNCVWGGWARMALTIDEFTIVEVAKPLVGEKSPAVVKAHLQLNIGKRMDIRGEWESLRKHDVLFLVTCRPKSAIGTRFNPRMPFKDQIEVAYVRGAEVEGMLDPHGNVIEEFEAYEKKPTVQGDVRRWRITLDPNQYRLDMENTVEKKTEDVYYTFNLVVRRDPKTNNFKAVLGTMRELLNTECVVPDWLHNLILGYGEPDQANYKKMTNVVDTVDMNDTFLDFDHVKESFDGYKVVGSEKDEKMLPPFSLSFKDLTTVEGMRSKERTVEVRPLSRVPVTPYSHKTNKNKIRFTPAQVEAIKSGMQPGLTMVVGPPGTGKTDVAVQIISNIYHNWPNQRTLIVTHSNQALNQLFEKIIALDVDERHLLRMGHGEEGLETEKDFSRYGRVNHVLKERIRLLGEVEKLARAMGEVGDVGYTCETAGHFFRYRVCRAWDEFLSSSKLDEGEGRDIVKNSFPFTAFFADIQPLFSGVNESDSRIAASCWEHISRIFSQLEEFRAFELLRNGRDRTEYLLVKEAKIIAMTCTHAALRRAQLVQLGFRYDNILMEEAAQILEVETFMPLLLQNPQDGRNRLKRWIMIGDHHQLPPVVQNVAFQKYCNMEQSLFGRFVRLGVPYVLLDRQGRARSDIASLYAWRYRALGNLPHVEAIPAFQRANAGFAFTFQLIDVPEFNKVGESQPSPYFYQNLGEAEYAVALFTYMRILGYPSEKISIITTYNGQAQLLRDVVQRRCADNPLIGMPHKISTVDKYQGQQNEYVILSLVRTNNIGHVRDVRRLVVALSRSRLGLFVLGRASVFENCFELTPAFEQLSRRPKKLLIIPSESYPTERKVDEKSSDKVIRIDDTAHMCNFVHEFYNSNVEMLAANYQAAMDEQERVRMRFLPPPEEEPMEEDEDVKKAEEKKIKEEKKKQEEAEDIAFEEMDFQRLENMGDNNLPVEVNGLSVKENGDAPEENGDIVTPWDVSSGSATGVDYDKLIVKFGCRKLESDLITRLEALTGKKAHPMLRRGMFFAHRDFASILDRYEKGKPFYLYTGRGPSSGSLHLGHLIPFMFTKYLQELFDVPLVVQMTDDEKFLWKNMKVEEAKKMAVENMKDIISVGFDPEKTFMFQDFDAPFYENIVKIWKCVTGNQARAIFGFVGEDSMGKAAFPAVEAAPCFPSSFPHIFGKKTDIACLIPCAIDQDPYFRMCRDVSHKLKFPKPALIYSTFLPALQGAQTKMAASDDSSCIYLSDTPNQIKNKIKKYAFSGGRQTVEEHREFGGNCDVDISFQFLKYFMESDERLEEIRQQYTCGEMLTGDLKAIAIAEVSRVVMEMQERRKNVNDETVKQFTTMAPDLERKSSQESSSSEKGDIITPWDVSAEAPTGVDYDKLIVRFGVKKVNNDLIDRLERLTGKKAHPMLRRGMFFAHRDFGLILDRYEKGEPFFLYTGRGPSSRSLHLGHLLPFFFTKYLQESLDVPLIIQMTDDEKFIWKDLTVEESKRMTKENIKDIISVGFDPEKTFIFQDFEYIPPFYENIVQIWKYVTGNQARSIFGFIGEDSMGKAAFPAIEAAPCFASSFPHIFKGRKDIACLIPCGIDQDPYFRMCRDVASKLGSPKPSLIYSKFLPALQGAQTKMAASDANSCIYLSDTPKQIKNKINKYAFSGGQPTIDEHREKGGDCEIDISYQYLTYFMEDDQRLEEIKKSYSSGELLTGELKAIAIEEVTRVITAMQSRRALISDSVLAEFMSVRPLKYSF

>Ppa|PPA12964

MSTTSRLATVSALLIAYVAANCDPGWRYLPSTQSCYKLIDDQLPWSVAEIRCLYQGGHHVSIASYEENQFVHETARHQEVWLGAAFFGSDYSYVYSDHTPFGYFEGWEFGGARPSMNRARRCIKINDRGDWFQSCCKKLAATVCKKAATPAWGNSNDLRA

>Ppa|PPA13083

MINIIQITYPIIHCSCPDGFELVAEECRMLEPITMSIRDDQATDSAISQCNAYLAQPVTIHNDEQLKYWIEKKGSNYMPLELLNDCKSGCVWFINNSTGYWGEQCNTDVRAFDVYCMAHLRQHVPSGDGCESFEDDSDDGVCYQVENMAIKNEHLPLSPSPRVPGVNIFKFGALAENWKEAQLLCGSFGAQVASIHNEKENSFIRRLAVSKGAVSGMYLGASVSGKADNFSWIDGSAWDFNNFYSGFPINGLGDCIIMDTESTGGEWANVDCSTKMSVACERKREFIELKVILLLPVQQMYSPGFPFDASTPCDFILSVDSGKKIELEPKTGEVHDKKYTTSSSNFMRVLWQPNGGNNVRGAMVSEIASMNRTALKALQGKNSDYATIKKDLSLALRVGMNNCDNYNEQIQLTTSKVLYTITDLLLAGVENIEAGKQFDLTYKLVDAYSTMNKCQNPKDPHQVCLFKFARCFILFMDNLHGKKLLKGEEAPEKKLIPSVWVDSEVAKRNNPVKQLPIRSSKSTSVGIVRNIGAQQIVIINDRPGPSGCSQTEPAPHLPVPVVVTKRRLVPAKRVMPPAPSLVKDSPALFEDPETVKKGETEEEGVAWKDMGQQPSTSAHNDAPPSFLSHPPKEEEVEDRIIPSTTYHNAAPSTSSQSIKQEVEDNYDYGDVKMEMEIKEEDEEEMDGPIADTVKLSELCSSTNGFHDPTSSTSQPSLSSSSRRKQKMTLSPPPPECAGFATAEAQKLFFQSPVNCPYCGVEIPDGKKLEQHMKINHRDHWLKYVQKCPVNICDFRSSDPSVVQRHHVMVHNRNYNTRMGNAAVNFKFVATCPFCPDPLRGLAGFVQHMEKKHPRLCTYEAKILACAECRYSTSNVYMLLTHWLKTVPMCTQGLRFNYEIAANTKINDAIDHEETVFLLCNAKFDAALSFSRDQTVKMAIQLCDELPALPQNQYYMGELPPPESTPRPIVLGLMCNPSTRKYEWADGSPTDYHPPGFSFDEACNPDCAQYMADEDGRWSTWCGPDMERVTIYCIYQLPEPAPPPSGCANFDDDTDDGSCYEVINAVEDWQDAQVTCRNIGSDLASIHNERVTELRCFFCFRKYTDCEKLEENSFIRRLAVSQGVVGWIFIGGAVTGKGNNFGWIDGSEWDYENFYPGYPVDGNGECLAMDTRVNGRIWTAQQIWLLCAGGEIVSPGYPYDASVPCDYILSVETGKRVKLELQILEANSCCDRLILTDNLIGGNIIANLTGALSNRTYTTDSSNLMTVSWQPQGGLNVRGMMRIFIFKSLLVLGNYNSDLAHSSCPSGFELVRDGECRGRYTAVNSNWNDISRTAVTRCKEIQGKAVIIHNDEHQAYWRNRVPSETLFMGIVCNSSSMRWEWGDGSSVDYRPKEGYMEELDAECKSGQSWDMHDNGYWHIGEPFHTDLLLMSRFLAYGTDMEYSLSIFCTTQLQQPTDYGCDSFEDTEDGMCYNILPSVQNWQDAQNSCRNRGSTVASIHNLQENSFIRRSAVSQGAVNGLYLGASFYSGRFSWIDGSNWDYENFFPGFPVSGQGDCLAMDTFSGSGEWMNVQCSSRLAVACARKALRIRYDFVMNRHKNRFSRPEARVHRWAVIYSPGYPYDASVPCDWFLTVPAGRRVRVQIMLLEANSCCDRLVLQDATLGGNIVANLTGEITDRVFTTSSSNLMRVSWQPQGGVNVRGAMFTFNAV

>Ppa|PPA13091

MSKLALIACFFLAAHAVSGFSVSSPKPAVSGAPLKTSPAPVRPSGSPVGSTGFFNPTTRGFGNPSVKPVTGGPVSGSPKPAGSTGFFYPTTRGFGNPSVKPVSGGPVSATTRGWLVSEANLRFSSVSTEMRRLIVFLLLLCIVNATCRSGFELYRNGECRGNYTRMTPYWDASPNPSIASCKQSQALSIIIRDAMDQTYWSSKATGGYALLGLVCNTTSKQWNWADGTVLNYKPPSGYATDLDKDCVPSMNWAIQSNGYWYSGAAHNTFTADVFCSIPAPQLVPSPNGCESFDDDSDDVICYQIATAAENFRNAQMVCKNVGGDLALIHNDRENSFVRRLAVSRQAINGVLIGGLLSGNDKAWTDGSTWDYDNFYPGFPISGLGQCLVLDTQGTSGEWMNVDCNNTVAVACERQQNFTTPVCPTEPPKEGQFVVSPGFPFDASTPCDYMLMVDEGKKVQMEILMLEANTCCDRLVIYEDYFVTGEFKERVYTTSTSNFMKVSWQPNGGVNVRGMMITFRESILSSCPEGFELVRDGECRGFYSTVTGIPPSQQLDIAHQTYLTRHVHDGSYSKIILGLMCNTSSTKWEWIDKSPSDYRPPADFVSALDEDCELGYTWFLTDNGAWDYYAHSTVSMDIFCTTQLQPPVPSGDGCDGFDNDIEDGVCYEQENSFVRRLAVSKGATNGLFLGATMSGKGKDLGWVDGTDWDYDNFHSGFPMPGLGDFLAMDTSISAGQWMNIDCAAQLPVACIREGERAIEQPTCSSGPFVEGALITSPGFPFSASTFCDFFLTVEAGKRVEAEIIVLEANTCCDSLVLYDGYLGAPVLATLSGELSNVTFTTTSSNIMRVNWQPQGGVNVMGLATRSSIVSSRLRVDMRRLLLLFFILQFVRGACPDGFELTAAGQCSLLTPITVSNVAYTAATNTAISKCKEMQAQPIIIHYAEQNSYWASQFNKNLVQPLGLVCNTSSLKWQWTDGSAVDYKPAAGYFAELNSNCKTASLWYMASTSGYWYYTESTATNTFNIFCTTQLPHPIPSGDGCESFEDDNEDGVCYQVGASAENWQEAQTICRSFNANVASIHNLKENSFLRRLAVSKGAVSGMYLGATMIGKGNDFGWIDGSEWNYDNFFNGFPMQGLGDCLIMDTEDTSGQWVNVDCSSKLAVACMRQQHYSTPSCTSGPWQEEQIIYSPAFPLNASSPCEFILTVDAGKRVEVEILLLEANSCCDNLIIYENYFGGTIIANLTGEVGDKKYTTSSSNYMRVSWQPTDGKKCEGSDVHIPKPVILPTAFTSNCPDGFILTAEGQCSQTSPIVVSSREDEAIDLVISMCNEKHAYPVIIHYAEVSTLFYPPVRRDLLMFSNCELENKIRLYQLTLPCKNGCIWFVNRDGGWDSWCFATIHDFDVYCSIQLPHPEISEDGCENFEDDTEDGVCYLVGPNAETWSDAQLNCKKLGANLASIHNQQENNFLRRVAVSRGAVDGLFLGATISGKDDHFGWIDGTDWDYQNFYPGFPLPDFGDCVAMDTSTPVGLWMNFDCSSKLPVACIREKQLNVPADYTCSAGPWAEKRLITSPGFPYDASTPCEFFLKAEDGMKVELEIVHLEANSCCDFLLLYDGYLSSTLIGNITGILTNVTYTTSLTNYMRVSWQPKGGVNVMGLAVTVMKTIIVSKYHSDEFPKSMAHCACPDGFKLTAAGQCSQITPTLISNVRADQALDKAISTCKEIHTQPVIIHYEDQQQYWITQFKSTNIVLGIVCDTSSLKWQWTDNSPINYRPTTHYDSALDKNCRTGCTWGLWDKQWEYYCDGTTTSYNVYCSVQMPQPIYSEDGCEYFDDDTADGVCYKIGEDAESWQDAQLNCKKLGGNIASVHNQQENNFLRRLAVTQNAVTALFLGATISGKEDNFGWIDGSSWDYQNFYPGFPLPGFGDCVVMDTSTTAGLWMNYDCSAKVPAACARDKRTNLVANYTCSAGPWEENTIITSPGFPYNASTPCEFFLMADGGKHVEMEILHMEANPCCDNLVLYDGYVSGSVIANVTGIQNNVTYTTTQSNYMKVSWQPKGGYNVMGLAMTFRSVGAREHAIFGEEINGKTYIPNADVAISFCPPGFDLVRGGQCRGFYTTVTVPDDVAENIAANKCKEINGLPIIIHDDEEQAYWKSRATGAYDLVLALLDECGLTARWLIIIRLLSFPVRPVSFVQSSLDEECSSGCVWMQGKDGMWREWCDDDQDTFQVYCTTQMPPLPVPSPDGCDGFEDDGDDGACYQVSTTAESWNDAELICRKLGANLASIHNDHENSFIRHLAVSKGEVRGVFIGASSGGLGEKEADFAWVDGSPWDYSLFYNGFPKDGFGDCLTMDTSTTSGQVDAEGNKAGMSC

>Ppa|PPA13095

MQNSYRAHSSIVSARVRVAMRGLLLLFFILPIVHSSCPDGFELYSGGQCLELQPTQWSGYRADQAVSPAIAKCKEKQAQPVIIHNSWASFVLISVMLTLQHNYWENQYSSHSNTVVILGIVCNTISLKYQWSDHSAIDFKPSSYNSVCDSITYTYNLYCTAQLPVPIYSEDGCEYFDDDSDDGVCYKIGAAAETWQDAQLNCKKVGANLASIHNQQENNFLRRLAVSNLAVDGLFLGATISGKEDHFGWIDGTDWDYQNFYAERQNLPTNSECGTDPYLEDTLITSPGFPYNASIPCEYFLMVDEGKNVELEIVTLEANSCCDYLLIYDGYLGSSMIANVTGAVQNVTYTTTQTSYMRVVWQPNGDVAISFCPPGFDLVRGGQCRGFYTTVTVPDDVAENIAANKCKEIMDCRLLFTMMKNKPTGKAAPPALTTSTSMQFLSSVDMGRRLVGRLSSAFVHSQTYFDTHFGESIGKDLSGSHWCDTDVEPLDVYCTAPSRQPIPSGHGCESFEDDSDDGVCYQVGAAAENWKEAQIICGSFGAQVASIHNEKGNSFLRRLAVSKGAVSGMYLGASVSGKADNFSWIDGTTWNYDNFYSGFPITGLGDCIIMDTGSTGGEWANVDCSTKIRLYCSCLHNRSLGGRADNVFSGISIRFSIATTPCDFILYVDSGKKIELEVLLVEANPLTGEVNDKKYTTSSSNFMRVSWQPTDGKNVRGAMFTYKAV

>Ppa|PPA13470

MLLIVLLSFFPLIAAQSRRECAEGAKYCDSAGGACSLVENDEWTYFAQCECYDGFDGPRCDKRIAPGDSGQRYHCEGPFHAECPKGQTLRMDYASFGTNFASSTCAFAKHTCTDDRSLAVMRQECDGRQFCSIENLDYAFPNNNCTGKKSLIYRYRCTSDALPSACPEPNSIRGSDRCFLFDDTTGKIDYREAYEVCRRKGGFLASPITARDHQQFIDAGIMNEKRSRAWIGAISNNKAIPSWNDGSNLTFVPRDSQLEWANACLSYTTSAAIPNSFFWVSENCDQLRFGLCSFVPGTTPTQPTVPIPGKSKGKVEHDLALSFTNTIYFFCPTRAKSMTKRGSLAPVANRCDEKSPSLTATVDRVSIGDSVPRRPMPFARLFESAAHCEETTWRGVIFPRTRACDTVIVDCPNPDLIEGREQSVVRASAESSRMGVREMRNAVSRGREAEIVSGETANHLKTTLSTQLYGGDITGSVDLTRSMLSLARGQYNSLDDRVVRQTRAQNFTQNLGDCGDSLLEGRALPVWEQLPSGARINQASDLMQSLEESAILLADYSYIEKQAIDYDHWAMEVEVRRTVQPQFGGGGGEGAAGAFEAAAAAPPAAVFAPTSPFAANADVMDDSGFTARGMAGRQPVSSNDVPLPKLPEYQEQKPSDPVSFSTIRKSPIISLPSTSTLSSSAGPMFSPADSPPAGPSFFSPASSSGASFRVLNFSYFVFSSLGAILSNETTRVNSQVIGATVNDASRSVQLPDSEPVTLTFFHLHTSGVANPRCVFWDTFVSDWSTRGCQLLMSNLTTSVCQCNHLTSFAILMDITGELSQLENTALDVVTVVGCAISIVCLLLSFLVFSCFRSLRGLRSTIHANLCLTLLLAELVFVLGVSRTKNTVACSVTALLLHLLFLSAFCWMLLEGVQLYMMLVQVFEPSSTHIALLYLFAYGLPAVIVGVAAGVDWKNYGTENYCWIDTTTPTIWAFAGPVAAVVAINIFFLLIALRVVLSISSRDRSRADRLRGWLKGSATLLCLLGITWVFGFLTAVHGASVVFAWIFTLLNCTQGIFIFVLHVLMNEKARTAVSRWLRHGWCCFSNAESAANYNSKEYVTSRQRFLNMIRSTAADTGDNADETSGADKRQKRMRKEDTTSSTGPSTASTDTKEKGPLTPTSKTSAWLSQIPSQDDGNDYDLPPQSPVEKEEIKDHKEIKDQREIKDQDEEDRPPPLPKSPPPPLTPPTSPRLQYLEVPPLPPPDYDDDFIVPPLSRSTRSLDLRETDNRTPVRRKKFPLGATDEERGAAAAPLHLEQDQEALSRL

>Ppa|PPA14572

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>Ppa|PPA15131

MKSSTSSSTRVSNFLLATLVSFWKVALWALRIYTCIERPNEVSWSIVSEGNVDLNCSKELSLIFTSTPPNVNEASQISPWQDFKMKNATVDENHEQIFVVPQAGIRIHAMQCLGDGNITASAGAGSGEAESRCSDLPTWIISFDNVITLSADKVTWLAVEYVWIGDNGMDVTVALSDRVAVMSSGLSDNVQNLPSAASLTEAADITMETQEGFGIKYYSALDTPENVGSRQDNFVVELTFTDIVPPILEKDPYCGCALAEDQQGPDGWDPRNIWLDVVIVLDTSEAMTQDDLDIASLVMMEIFAGPGEKYLTTNTGATFFIRVGLRTVAEEPQVRYNLNMTIDNLYHVLAQFKVTKGLDKMNFDDALNAAETMLTVSRSKLRIVKQLDKSGQLSTADRFKNSGGIIIVNNYIKEGEVHPGLFNLASPGGCFQAVPASSQFLNARKNCDQLGGGLISSIHDYHKGQFVQQLLTSASKSGFYWIGYTRTDSSTNPYTNWDEHQPSKLSHTKCAYADASSNLWGAGNCNIAYPTSCASSPQVSTQQVKSFLENYIDEMKLKREEDRKLKREEETVVNEKVYTSAMEICIFVALLALFTGGTNGYVYTCEEVKYKMINSDLEVSTDFACLVAAGNWSTEDSYRVDPLSSVYVSLGNATTSFMDIYNSTCIERPEKYSPWKIVADPAFDLNCTSAQFALIFTSSSTNINHDWINIDFRLKPAVVAELDEQVFAVPFWGQNLVMGQCLAPIGFTESDSNRLAIIASGLSDNPQNNPRFNNRADNRISIDLNFTSDGQITMDTDRYYSVYYKSAPVWPQEIRTRNDNFVFELAFTVIKPTLPPPPPPTPAPGPEDPYCSCALNRKSSGAVGWDSQEIWLDIVFVLDTSEAMSENDLYRAYILIPHILGNKGGNIGAYLTTNIESYFYSRVGLIAMSDKAEVAYNLNMTYTSSMKMYHVTKGVPKINIEDAFNAAENMLKQGHIAHRASARKIIYFVTDSDLIGSLPAADQFKANDGIIIVNNFIKAGEVRPGLFALASPGYYLTDAPFQQKEWLSLQLLCKANCYCRKEAGFTRYANYNKDPTKPASVLVDSKPEYPYFWIGYTRTDGHWNWEDQSTDTYTRWNRAFGEPSMPSLATTPALSFANSCPVKPAIRSAEAIEI

>Ppa|PPA15390

MVPMNLIFLCLLVPSVYSTFPCAQYGSDLYGEINCLRRLLNQCTSEKQNRETRTVPTVPPPTTTSTTTTTTTPRPTITTSTSTTTSTITPVPATDKWEDAVIESSDDWPTPNSALIIDALKYELSREIEEKIREANQKFDAKLASYQVQMEVEMKKMNKEMRMIKLKVHRRANYEYILSEERESWYTASEVCIQWGGHLVSIKDSKENAFVAAFLPAGESAWIGLNDIQREEVFVNHNGEKTTYRKWEEGQPDNLYHNENCVEMMGGGEGRWRDSLCLLTKRFVCRRA

>Ppa|PPA16060

MRSLLSFIVVFLLTLAIVHSFDYNYYGSRAFGEMDKRNPGMAMRNVGPQENLAGFLNQFKPSFGKRSRPYSFYPDIRRKKEEVKICPIPSNLNPHLILSSMAFVVTLSGFASATFRGPIADIYSTWDLSKETIYVKDFDHLAPLYVEKEVHEEEHSRKKRNAEEAARFIASANPITKTCDRPGYTGQYCEFPICQQTNLMIDPTQFQTGDGYLVDVADLGNCTRSQEIIVDETMYDIRILIQSADNVNPTFTVTDSNGYYGQPDGELKESDRYEAHFNELKPGFYRVTGKADSLNSRCLLQTTSQTIMTISGGFSTDERDRNDFPNPNAQVHQFNSIMVHLNGARSPAELKTISVIGTNNYVFRPRILDKRYGCGYEYYFDSMFCMVKGSYAMIVEGVDFNGNPFRRAATFQCADGPPQTTQPPTSTVTTPMPTACDNGGVFLFNGLQSSCVCQDHWAGGHCEQPLCINGGTLIEGKCFCPTGFEGVHCEDVRCEPNSDHGFGVDRPTLVLVVRVRQQMNDVMAQVLRAVDEISDNLQFEPNYFTRFQVVYFNDYTNFKSQSYKNIYEFNADFFKATISDHTDGGCTDAVIGAAATALTNLALTSNSFIYVITDALADDSPAMTDALLQWNSYFRATINFIYVEPTTDSGCQSDLSDPGFRKFDDIANTFSGLAMHVSDRTKVYDVFYNHLNSIVYKSQLMLTVDREECGNGLVKTVMIENKNENLILMSKGKGFFPVITNPMGENLGEDTLLTVANYQTPGPNQAEAFWSITTDIDQDGQLYQPLAGIDNHPVFHVDNLQDQDDWDHAFSFLNIYSWRNNQEMEIYASNGLYRDGCSYKFYFPSFRCRANEKLHYEFFLRNDYGFYIQRAGVMDCYLYIPTPVPPTDCQNGGVMFNETCLCLAHFTGDKCQTQICENGGTPGVNYQCICPNGWGGAFCQFAVCSEPGLPPTFGYHVDMAFLVEVTKSGVNQIKELIDQLPGLIRDITSQHGDWIDRLVLIGYDSKDVIRMVDAPISSPGKVFDALTAWGNSNPTDDNCVVRVWEAVFQLMRNRMDGPNRRNLPRRSIVNIFQSSLPDNQGDAIQALSTSEELLETNALTNVFQWLDTTSDSHWRCNGKQDDFQYIEQLARRGDGKMYTIENSDIKNILRMIPTLFSSSIVYKYHNEECHSSTNLVYFPIDAYTQTISAIVAGYKSTVQLFKYTGDQFTDDGRIPIHKNDMEQIVEFRNHNSAGQKIWLGLSWSATGGWVFQHDDGTTLAVPANMKKNWDGGVEPNGANGKTCAYFNPTAKNGYWFAEDCTKKYLTVCQKHMFDSSNEPSSIVDDDLAPGKYYLKVQTETPTNGWGGCDVEVRVQSDLNVEFGFVDGLRKDSPHPVANIDSNSNRVVSSISIGQAKTDLSVLEHVLLRDDSNQNVLLEAATYSYRFGCAYEYYSQELNCDLTQGKDFNVIHIGEDDTGNTFQRYSTSLCYKWNVCSNGGVYSNGACLCTDYWTGDNCRTPICQNNGVLNKDGKSCTCQPGYGGNACEFVQCDADSQTKFSNDGKVLALILEKSENTADSIRDIANNFKKIMDGINAKADKWINTFILHTFTSTGSVDDTVVLRDIDDVIAHLNQYASDADKLIGSCQQPLWDAINGLFTAFTPFLKGSEVLIITASAPLDADLSSVQSTMELFDEGAPIVDFIHIESVCQTEDWMRGLESFYWFFQTLGGTMFRVQPGIVADGLIGFLPTRYAAQSLTIQDAGACQQNTMYIQVDTRMREVYVLVGGSSGSVSVISPLGEQVIPTTVYNADVQKLWKVDIPYPGVYAVTISSNSKACFPTVYGSGGAQVFVGFVQDYSTSDKPLPYAVYGKVNFPVFHIMDRPDAPGVETLYMANMYVQSVWGKQGKMYDTDLDSRTGCSFEYIGKGFTCSNKDEVITVISSGVDDYNQPFSRESVAWCKAGTVPPPSSTTSKPTTTGPTVTSTLPPIPSSSTSTVTPPVDNPTVITSVLPSLSSTSPVTVTSTVTTTTTRKTTTKYPTTTHTNPPTSTTTLPPLSIPPTTTTTLPPTTTSASSLSALWGLTIVFLLTLYSI

>Ppa|PPA18549

MTDKIVASYRENARQIIYYLTNSAPGANMNGVDDFKTGGGIIIVNDYILEGEVADPGLQKLASDNFFFTDLSENYINSLGVFCEANCFCSPDLHPFNDDDNSPRTQANRGCFHPVNNGIPQQKARETCQKEGAALVSIHDALKEFFVNGVVSIFGPKKKFWLGYQNDGTQWIWDDKSTDPYTDWDNKQPNTNGGKNMCAYATSTFYMHITFHYCSPLQCTQLDQPTTQFVMKIHSTRCSQVYKDYSSPRYC

>Ppa|PPA18563

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>Ppa|PPA18776

MSGLRAEPSLSPVIRVLRLILLANYASSLNLPCSHSAVYHQMKFNEAVDIKTPGFDNNQTYPANMSCEYMFQGSNTSAKIQVDFISADFEQPIFSGCADYIMIKDGSSTTSKELIKFCGSDPLKSIVSTNDMIHISIVSDQTVQMRGAHMVVREFFEGSCGDDWDTKSSFPICFKFIKKRKTWLEAQRSCFAEMSNLMTTTNQEEYDFIIDTYGDNSSFNYPWFGIFDAATEGTYQSIQYKEVLWPHPQPVVANNSPIRDCVILDFTIKEGMTHVAEDCLARHPFICKKNKDGSTSAVMGPRQLIRRSQIAEKVDLTIWILIIIALILLIVLLCLFCKDCIKRKCCPNRVEPENRLMRGLEQDYRNPVPVAPPRNLQPSTNRARFVDDVDARAKESTIEAQRRNNETTANNNSTRPTEITIGSVSLPANTSPQPSFNHPLPPLIDRTPPHNQTVHVMPVDAVVHRSEEPEEVPVLLPVVHEIDEHRPLSPQELPLNVPSLRTDHQRGETIDEREPGPSNGNGYRAETAFRSGPTIKESTFISTREESFLRSKKNEGLFEKPKTKVLDNVSAISLDEFWNATKK

>Ppa|PPA18937

MLPFAMNHAFFFLFLSFYGSNAFTFTCQQVKKLIQDGTRFPTTDACISLDQFVPTSSGFTTEVFFDDGSGKGKWSFAQTASIGCVSQYSSMGAWRIVTDRPDKGEGIDCTYEFTVFFSSIQTNLVTAKNSGLHHQSYKAYNITVVAPRGGILIDFSCKDTQEPLNFYTGLGNGAAEDMYYYGSSLCDDRLSVFAWDTAITINVPNDGYIMITYTGTGAYLSLGSVSYDFILLGSGKSNAIVQHGEEDKFVWLSPSMNDDLKFHIDGFAEFDPRNGNSLVLSAQCKENNCTGSINPVPSDEIHLQLEADFLAIDYFTHVPDDQWKNSDMFFIRIASAPLNSTEPPPTIPPPKPNTDYSCGCELTNGKAEFASSIWMDIIFIVDVSKAMGNDGIAKASSMIDSIVSSLTIGNVSPSSIQFSRVGVVAVSDKAEVIYGLSNAVQSPLKLTPSTSAEADIGIGIESSLNLFLRSHRSSTRQFIYVIAASDSSNTDRNQPRSNQFYDATFDVQKFKYNGGIIAVTEADPAQTVTWFNNLASPGYFNPKFNDNVNLDLQLLCDANCMCPSGLSAFTREESERETALGGCYHSPSSTDPYALAKEACQAEGGILTTIHDQDKQLFLLQLISLYGAKVKFWIGNEYNGKEWEWIDDSNSTFSNWASGQPVSSLGRCSISQQTVGFNSGWFSEDCSDDHLYICERPPCSVDRFSVNGFVYSCNEVKQSILKKTTISASNACVALGDYSVLAGFVQDIFVQDGTGKNQWNLIEVHEAGGCVNSTVDSWRIVTNRTDGGEGIGCDEEFTLLFSSIQSTIVTARDNGRAHYSNTAGNITVVVSRGGILLEFTCNNTLQKLDFYTGLGNGEEEEMFYLGSAQCDDQLSLWALDTAITVSIPDDGYIRMINTGTGGYLSMGYYEFDMIVMGSGKSNNLIQHGDNDKFLWLDADDRVSFAIDGFYEMDQKVGNNIVLTAATDCERDPCTTKSVPLNSSSVHMTMVADLLSFDYYTKVGNADYWRDDDAFFFRIISSPLTTESPTTIPPVKGDTDYSCGCDLTNGIASFSSDLWLDVIFLVDVSKSMDSVNLNKIIADLSSPFPNSINFNPSNSPEANIGNGIDTSIDMFSRASNRTSRQLIYIITASDSSSTSFKIKFTQASALQSSPGDSFKNSGGIIAVTDVSPSKVPSLVDLSSPGYYNLGFRNNINLDLQMICDANCFCPQYQTGFSDDSDERETPSRGCYISQPITATFSLAMDYCSSSGSLLSTVHDDQKEYFLIGVISQFGAKTPFWIGYENNGKDWEWIDNSNSTYTKWASGQPNIGSCAYEIQTTGFNSAWYSDNCSNEHNFICEKSPCSVSNFCN

>Ppa|PPA21045

MGVPKFYRWLSERYPCLSEVITDAQIPEFDNLYLDMNGIIHNCSHPNDDDIHFRISEEQIFNDIFKYIENLFNIIKPQKVFFMAVDGVAPRAKMNQQRARRFMSAKNADALIEKAKRAGEEIPTEKRFDSNCITPGTQFMVELQRRLDEWVQKKVNTDGRWRGMRVYLSGHDCPGEGEHKIMDFIRSERAKEGYDPNTRHCMYGLDADLIMLGMCSHEPHFSLLREEVKFTRPSKPGGGKKKAPPPKKTESDTICFHLLHLSILREYLSWEFIKVKDSIKFDYDMERIIDDWVLMGFLIGNDFIPHLPNVHIHDDALPLLYKTYMDVLPTLDGYINEDGHLNLHRFQEFLTAFSRNDRNSFLQVMEDEEYLASKMGATGIDDDVEGTLVQFHDDDMSTASDEEGANSGDTEAAFQSSDDDDSSPALPSSRGGPSQGVLADGGIGGATDLLAQLKDDPVEDEFADQLAALQFRDMDDAEFENNVDTAKCWSRSINNDFKRHKKRYYNEKLKMGNISKGQLREQAEGYVRAIQWNLHYYYHGCCSWNWYFRHHYAPYISDVLDFTEMSMGFEMSTPFLPFEQLLAVLPAASSECLPRPLREPTLAAEDRARNVHGPHLLFTTKEAPENGNWCSRVEIEKDTFRIPITKVVHGLLPNVKLDVFFPGFPTMKHLPHKGELKEAHVKVFNMASRKLSMVLSILDRPDLNRDVESISAQLLGEEVCIDWPVLKVGLVEEIWTETHAFRRCYDETTREEVRGKVVAEKLDEDQQSQFALWRRNTKDRLMERYAIEPGTVKAMARVRRLLGTSMVVEGDKVVPRRQWTPVDIAVPVPLQLVCIGVLVNENISRVPLSIKEAFPVETKVFVMDPSWAGYGYPAIVKEIIDEGTTNCRLTVQYALPQQEMDLRPIRSEPDKFSLQWCDGYTSQRQTGLDRGLIARLTGTVFIMDCTQDELTADASFRPPKLNVGLNLKLSKRNEETPDYAKRLPEGYWIYSILTVRALAEYKNKFPEIFKYLEKNNSMDDNYYSGDIWPKEEQRKERMDELRQWLENQPSFSEQKQTGGEEYADRNAVAYIESVLAATNKDCVFRKSIVKPSLIYRPSLTSSSKKVRPDPDANFLLFDRVTFAQDNQSVPFGLTGTVIGLHGTDHVDVLFDREFPTGTKMRSTSASCARVLIAALVNTTFAKERKTAGIMKPPVPKKKEQYGSAPQKNAWEDRSKKGGDEKRGGGGGKEREKKDRKDSSGSKGKEKESPPATVLKLLKNTNAAKTVSGVAVSAPPLPNDNQKRNKAEKTAEAQQLLDMLIGGGPAPTNKKGGKKEPKKEMAKIEKKRSTDEKDEEERNKRGAKAGAAILASLMTATSSKTSSRKGDTESVQSTPSTSREERPPNRKERRMEKKEKQKQLAAQEGVAAVWSPRPKTPPVSEEVSEDGEKMKKKKNIMENTVCMQLLAMLGVNPEKEKEEEKKEERKEDKKEETAVEKENEEAIEPLSVSTPPVQQVQQQSQQARPSPRGGRAANQFWGPTRGGNSQRGGGPPHNQQHHQQQHPHVNHHMMGYGGRPGLPPMNGRGRGGGGGGGQRGYGAPPMGMPSPQEVMMHVARQQVVHGGHSLGPPPPPPHIVQQIMQQQQQQRMNNERGGFNNQDQNGRGGRRGRGGGEREAMKPEEYVRDKVTDLTPASVRGFGKGRGGGRGAQRGGGRGGGARGGRTSRTGPSPSLDAARSPVVSPTPPTAAAAAAPAASAAPAATQQQPKPRKARLAVKLAAKSDLASFSSLTPQPCATGDGPWRVVTDSPSSVDCTYEITLLFSSVPTNLIVVQPHTYEYIRGPGSDLTFVSPRGGISLNWHTQGEVTGYEEITFYTGVGYGPEEDLYPIGSLFTNDMAEGRDTDIFDPVVTVKIPSNISIEIGYDTFADKASIHRNAIKTMSVNVFGYPGYSVNVLSSGLATTFQEQNTMKVVQASYGRRASVHVTASITFDPSSDHKLKLQAYCGDDICGEKIVQQSTTVDWLLNAEKFRVNYITGLTASQIGKNVDNVFISVVSSTHNQVDGSKKCIDFLEGVRCDDDYLQLGDHCYRSRRTNTFINQLASGAPIGVFIGMKQDQGVFKWTDGSAVDYNNGHLDSFGGECVIMGSSTETWSNADCDFAFKYICEKNANE

>Ppa|PPA21410

MCFSQDTQMTVMFSGSFDARYDNYVDVAGNSSNGMQWARTFRNETSSMSTVATNFTALYVSTPVDAPDLWDSQDNFVVVMDLTDPYCGCELDKKFGMPIDWDPNGIWLDMVIILDCSEAMGKNSLVEASNLIQSFFGEGDYDVLITDPKAQLYNRIGLIAMSDVAEVFNQISVNIFAKIIWNVKTIYNLNMTKGDKVNVSIKTGVKQINVLDAFAAAQQMLQDGQTPGRSNARHVIYYMTDSDPKVDLTSLDSFKEEGVIIVNDFIDSHVIERPGLKDLASDGYYYTDIQDNYMSSIQLFCKANCFCSAEADHVPYAGHNKDEAGEAAGGCFHVAPAGVPYNSMIQICLELGGGQMVSIHDDNKAIFVNNLYKAAKLKPDYYWIGYAKSDDLWSWTDKLFYAKHTMLSVYESVHARIRLTTVLTSTRPRRIGEESVSSLGVLSLVPLTVEKARGMKRLRPDSRAGKIIDHVEKKMHRILFRGAANCNVGYPSVCEFKPCARKRSTRHSCLSACVVVISSMGLFGSVFLFFLFIGGTQAFVFSCEEVLNKLINSNLQEPTQYVCLVTQEGFTNEEALKDIYVQNDKVSTSFYTMWKEMPCVARPGSAPWRVVADLPLSLDCTQEFSLIFTSVPGDIFPVYDHENWLKAGVNALYVAPKTGIVLHKDTCEGDGQLNVYTGAGKGVGEFRFHLKSWSCADFPDWIISFENVITILPDAGVSYSVYYRTHDHTTGIDVSPSDHVAVMSSGYSDNLQNLFQERNVVVFNEKEDVEVTVNRTASFDDRYQGSVIVDYTNAGEGLEWFETIHNETGGSTTTVAQRVQVEYHTIPFAPQDIWDSYDHFVVELFFTALEKPTTAAPTIDADPYCGCALDKKFGMPDGWESTKIWLDVVIILDTSEAMGAVALTDASSLIESFIGTDDGDVLVTDKTATFYTRVGLIAMSDKPQVLYNLNMTKADKVVGKVQINSGVSYLDVVEAFNAAVQMLNDGMQEDRAYTRQVIYYMTDTDPKFDSRVLDSFKASRGKIIVNNFLEPNEVERPGLKELASPGYYYSNIQYNYMSTVQLFCKANCFCRPDIDRFPYPGHNTDPALLASGGCYRAVPAGVPFSKMRGNCEGGLIASIHDADKANFVAQQFTIAAPNSDYFWIGYSRGDAGWAWEDKARQLFNKPVHELGQSERRAQHSFGRQMGAGNCNVGFPSVCEYAPCEVLLSFVIICFYPLICLAFLRAVSRSFQVRENVEVMTFMCKIYLPAAVVSTIAFGGFGWKLYVPTEWRLSRNIAYACFDLGLELCFVVFFSCAILGNERIHREFSFASFAYLNLGSTTLTATLS

>Ppa|PPA21927

MPRRQPVKKERQSRPTSCVVCGSDAAGYNYDAPSCASCKAFFRRVVIKKQVFPACDRNALCDIDVRRCRACRYERCIKGGMNPLIVACPDNNESKTDSSDSSSVNGSEPSTSSAHAEYSPHDQSFQEDPEKIETIIEICRIKKSSPRSEPSPQSTEFDPCDPDNEAYYMNEHELSLVENPIRIEKRLDQMMHHLLLLEEACQKLRISSYVIKLVPGLSIDDFYLTQSKMGSNFEPMDSSYEPVSIVLMPVQVILDKRQVVDHSKVEQTSRRIWPIQDVAYSIEYIKALPFYNMLDDVSKKILIGSALICSNFTSAFFSYSKGADRTTYPDGSCMTWDRQVEEQSPEVARFHTVLIVAMRQVELDDREYSLLKLIIVCNPNAPKHFFRMYLRDEECGPAYFAKILSLIEVATKLTSWQKSTHILGLAMGLYKNITPDWNMRVCLILLLAFAIGEERNIVNISSHGREQTGDDNRCRSGFFYREGWCTALSPKFLSFSGAVDYCAGIGAYSPSIHSKVDLDYWAGSAFDLSPRFWLDASCPEEGEPNQWRDKTPTDYMGPLGELQMCTPNYGFIMSSKGFVNETYSDMNQAVCVYPVDPMPEPPLINVDDQYCQCNKSAIELDIVFAADTSEGMSGTDVSDITSTIQSMLCSFALGIGAHQSNVAVLSFGNEVKLVKNFGDINSNDDISKINVPVLGGENPNFEEVIDQASSMLASTGRKLTRKAIVILSKSSSSIDYTNGISRAQQFQNTGGVVLTLDLAINSNALNGLSSRGYNIKLSSNVVADSLEAFCDANCFCQDGLVPYLVPNEKDRDLPMGCYKVGQKVAIFDDAQKECRKLKGFVITIHDDAKNFFLISLFPPKAPHWIGLKEYGSEFVWTDGSNDGYTWWAPGNPVKGLACVYAQQTSGFNTGWFSAPCKDYTYSLNYACQLRPFDAGYSGIQ

>Ppa|PPA22158

MTDLSLAENNHFSMPTSAVLQSLLLLCLAVGINGYVYSCEEVRYKLINSNIAQNTTFACVFTQEGEFTLVLTSDVPTFQTPTKQPRQRAIRGRETFIQPHTYMWFHTESCLGDGDITFSTGAGVGEQEERYVLRTFQCWNMPDWIFSFDNVNTIYVDDGIVLSVEYSSEPGGSKNPTKVAKGDNIVVLTSGRADDVQNLKGRTDNRAYIQIGNKDNADVSMDMMINLDKDNSGSVAVQKAYAGTTYNYYNGTRTENFNTGYFETTTPSPTSAAATTKAPKPAGDDPYCKCGVDKFGFPAGWKYNDIWLDVVVILDTSEAMDASSLADATGLVESFIGDANDNVDFLITDTTAPFYSRVGVIAMADTAQVLYNLNMTKTDKVQAAIKKGVAQINVVDAFNAAQKMLSDNPSKVGARQVIYYLTDTDPTNNLSPLYQFKTTGVVIVNNFLQAGELEKDGLKELASYGYYYSDTNYMLTLQSFCKANCFCNPGKDALAGTDPATPSSGGCYHPSSAAVPFSKAKSTCAADGGIIAVIHDDDKGRFVQQQMAKTGTKSDYYWIGYEKSGDNIWRWQDQISIFSSRTEFDGPVHELGRGSQFQFVYGDARWASRTCASSRPAPWATRAAEPFLFSFMKSLLESEQPWSMPSYKTMVVVAVVIWMRRELYRWAVMASRSLYHLWDLKGPTNYPIVGSVYDFRWNVFALGMFKAWLGPVPIVILLRARHVKMILESNSLITKPWFYDIISEWIGRGLLTSTSEKWYSRRKIITPTFHFNILKGYREVFVAQGRVMVDELEASADTGREIDVFPIVKKCALDIIAETAMGTQLNTQTGGNADYCDAVVRMSNRMFEYMLFPLLWFKPIWLASGRGIEFYRLVKKSQEFTLQVIRERKKLMQDEGLLGGDTAVEDSKTLSKKSVFIDMLLLQQAANALTDEDIREEVDTFMFEGHDTTASAMGFTIWFLGQYPACQKLVHEEIDAVFGDDVARDPTEEDLRKLPYLERCIKESLRLMPSVPFIARVCSHDVEIEGVTLPKDLAVIVAPWIMQRDPEHWERPDEFFPDHFLPEKVAARDPYAYVPFSAGPRNCVGQKFAIAEEKTVLSWFFRRYSAESVEPFPGSPIVPELIMKPYNGFNIHRSLSSDPSITYGISKDLQTTPFWARFPVKNWTLTRNRQSVGRALPGCILAALTTHQGFRLIQHIIISPDGPGDTSDKWFSRRKIITPTFHFAVLKGYQEVFVTQGKIMVDQLESTADTGREVDVFRYIKNSTVMGTKLNSQTGESAEYSDAVVRISVNAFDYSRFPHLWLKPIWYGSGRGFEFDRLAKLTREFTLKSMKEEGLLDVDSSETLVASKKSVFIDMLLLQQAANNFTDEDIREEVDTFVFEGHDTTASAMGYTIWFLGQYPEYQCLVQEMDAVFGDDSVRDPTENDLRKLSYLERCIKESPRMVPLVPQFGRVLSHDLEIEGVTLPKGLTVFISPMATQRDVCKLGRVCKLAH

>Ppa|PPA22164

MRFIAALLQLLLLTCILERAGAQAISCTDVGAKLINSHIKPNGKVFCVIPQEGFSNFEQLKNIHVQSLFGDKSSFFDLATNNTCVEQQLALEWTITADKEFSLDCSQHFDVIIGLIQVEFVKPIKQIQEKTIAESEYRQFTVPQTGAWIRIKEANCKDASNKVTLIMGSGKDATGYNDYNKPHQWKCASVPDWIVTFDNYFTLSSDTNLLIEYSSDIESELQVSPGDKIFMFTNGINFGGKSSRALFEIGHEKRHNISVSVEMPEAPDNNPSIKLRKGQNDLLSYNAGEHKSSITGKKFEVHFNASNIPSSQLQKIEHCIRININIDNEAAPDLPDSTTTESPEETSTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTNPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTNPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGLDSETTTPEEDDEETTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTQEEDDEENTDSDVDGATTTGPDSETTTPEEDDEETTDSDVDGATTTGLDSETTTPEEDDEENTDSDVDGATTTGPDSETTTPEEDDEETTSPTDLTTRFLSTLLTTAFTTTFPLETTTTALNPWNPSSKDPYCNCAVDKFGFPIRWKHSDIWLDIVVILDTSEAMGRAALDDAAALIESFISDGVNDFLVTDESADFHTRVGVISMADTAEVLFDLNMTKTDRVRGRAAIKEGVLKINVIDAFEAALLMFNHGLKARPDREQTRQVIYYMTNSDPKNNLNPLNQFKASKGVIIVNNFLQEGAVEQPGLVHLATDGYYFSNHQYMNALQHLCKANCFCKRDRNAYAGADKAFRAAGGCYHYAPSGVPFNKAKTTCAQEGGILATIHDENKAHFLHHLTSKAPQGQFWMGYQKSAEGDWQWLDQSTDPYTNWDGLEPSEEAVAKCAYVSTANATLPWSAGNCQLGLPYICQYTPCSVGYKDC

>Ppa|PPA22169

MLLRSLLFSLLIVHSAHSFAYSCLEVADEFVGSSFDESLTYICLIAQEGYSNWQQLEKIHLTADITTVSLYDIVTSSSHCVAKGSPSARWTVQSGLFDLTCNQEFTLIFSSQKPDFIGVYHKAAQQFVARNTLVVPQTGLWIRSKGCLDGDVGSVTFYTGVGTDENEHIFEMKSWPCSSLPDLIVSFDNVVTIEVAQNVYEMECSSDIDRNIANLKPFMVSPGDRIAVLTSGRSDNLQNFKGAINAIALQLNDGQMYDVTASMDLTFDWSDTGAVWLQEYYGGPLVEFFGGKYIEYFHTNYLQVQYVPNGLSAAQIDASGDNIIVEITIGGGAPTIKPTTTAQSKTTSRAPTTKAAPTTNAQSKTTPRVTTSAPARTTALPIASTTASSSPPSESPYCNCAVDKFGFPVGWNYNDIWLDVIFILDTSEAMGEDSLGDATSLIESFISDGVNDFLITDPTAPYYTRVGVISMADTATVLFDLNMTKSDSLSGKAAINKGVSEIDVVDAFDVALRMFSDGNSADRVNTRKVIYYMTDSNPGANLNPINQFKTSQGIIIVDNFLEEGEIELPRLKELASVGYYFANSNYMEGLQAFCKANCFCKPNRDVYQGSDPAIVASGGCYHPSPAGVPFNKAKTNCMNDNGIIATVHDDDKGRYLQQLMAKSSSKSDYFWIGYEKSDAGVWQWEDQSMSSFTNWDVREPSTAAVSKCAYVDTTNAALPWGAGNCQIGFPYVCQYTPCSAGNKNCYRHDAARRKNQIKMLLQSLLLLWFSVQGVKSLAYSCLEVQDEFVGASYHKSLTYMCVVPQEDFSNWKQLQGIRVSAGTQTASLSDIANTPTRCLEKTSPEAEWTFQSTPFDLDCSQEFTLIFSKIAIDILTPVAAHAELGVGRATLVVPQTGMWIRTKSCVAQTSGNVTFYTGVGSDDNDHKFEMKSWPCTSVPNLIVSFDQVITIEADWSVTYTMEHSSYIDDFFWVYPFDEIAVLTSGRSDNLQNLQCTENLAKFWLGDNQKYEVVANLDLTFDWADDETGTVILTDYYTGQEVPFGEGKYIEYFSSDFFTIRYAPQPLLPAHIDACADNVVIQFSIGGRVQTGSTKPAPQTTTVQRKTTTRATTAALPTTTVQAKTTARATTAAPTKTTTRAAISSTTSSTKPPSEGPYCNCAVDKFGFPVGWNYNDIWLDVIFILDTSEAMGEDSLGDATSLIESFISDGVNDFLITDPTAPYYTRVGVISMADTATVLFDLNMTKSDSLSGKAAINKGVSEIDVVDAFDVALRMFSDGNSADRVNTRKVIYYMTDSNPGANLNPINQFKTSQGIIIVDNFLEEGEIELPRLKELASVGYYFANSNYMEGLQAFCKANCFCKPNRDVYQGSDPAIVASGGCYHPSPAGVPFNKAKTNCMNDNGIIATVHDDDKGRYLQQLMAKSSSKSDYFWIGYEKSDAGVWQWEDQSMSSFTNWDVREPSTAAVSKCAYVDTTNAALPWGAGNCQIGFPYVCQYTPCSAGNKNCYRHDAARRKNQIKMLLQSLLLLWFSVQGVKSLAYSCLEVQDEFVGASYHKSLTYMCVVPQEDFSNWKQLQGIRVSAGTQTASLSDIANTPTRCLEKTSPEAEWTFQSTPFDLDCSQEFTLIFSKIAIDILTPVAAHAELGVGRATLVVPQTGMWIRTKSCVAQTSGNVTFYTGVGSDDNDHKFEMKSWPCTSVPNLIVSFDQVITIEADWSVTYTMEHSSYIDDFFWVYPFDEIAVLTSGRSDNLQNLQCTENLAKFWLGDNQKYEVVANLDLTFDWADDETGTVILTDYYTGQEVPFGEGKYIEYFSSDFFTIRYAPQPLLPAHIDACADNVVIQFSIGGRVQTGSTKPAPQTTTVQRKTTTRATTAAPTKTTTRAAISSTTSSTKPPSEGPYCNCAVDKFGFPVGWNYNDIWLDVIFILDTSEAMGEDSLGDATSLIESFISDGVNDFLITDPTAPYYTRVGVISMADTATVLFDLNMTKSDSLSGKAAINKGVSEIDVVDAFDVALRMFSDGNSADRVNTRKVIYYMTDSNPGANLNPINQFKTSQGIIIVDNFLEEGEIELPRLKELASVGYYFANSNYMEGLQAFCKANCFCKPNRDVYQGSDPAIVASGGCYHPSPAGVPFNKAKTNCMNDNGIIATVHDDDKGRYLQQLMAKSSSKSDYFWIGYEKSDAGVWQWEDQSMSSFTNWDVREPSTAAVSKCAYVDTTNAALPWGAGNCQIGFPYVCQYTPCSAGNKNCYRHDAARRKNQIKMLLQSLLLLWFSVQGVKSLAYSCLEVQDEFVGASYHKSLTYMCVVPQEDFSNWKQLQGIRVSAGTQTASLSDIANTPTRCLEKTSPEAEWTFQSTPFDLDCSQEFTLIFSKIAIDILTPVAAHAELGVGRATLVVPQTGMWIRTKSCVAQTSGNVTFYTGVGSDDNDHKFEMKSWPCTSVPNLIVSFDQVITIEADWSVTYTMEHSIFWVYPFDEIAVLTSGRSDNLQNLQCTENLAKFWLGDNQKYEVVANLDLTFDWADDETGTVILTDYYTGQEVPFGEGKYIEYFSSDFFTIRYAPQPLLPAHIDACADNVVIQFSIGGRVQTGSTKPAPQTTTVQRKTTTRATTAALPTTTVQAKTTARATTAAPTKTTTRAAISSTTSSTKPPSEGPYCNCAVDKFGFPVGWNYNDIWLDVIFILDTSEAMGEDSLGDATSLIESFISDGVNDFLITDPTSPYYTRVGVISMADTATVLFDLNMTKSDSLSGKAAINKGVSEIDVVDAFDVALRMFSDGNSADRVNTRKVIYYMTDSNPCANLNPINQFKTSQGIIIVDNFLEEGEIELPRLKELASVGYYFANSNYMKGLQAFCKANCFCKPNRDVYRGSDPAIAASGGCYHPSPAGVPFNKATTNCMNDNGIIATVHDDDKGRYLQQLMAKSSSKSDYFWIGYEKSDAGVWQWEDQSMSSFTNWDVSEPSTAAVSKCAYVDTTNAALPWGAGNCQIGFPYVCQYTPCSAGNKNFQGVKSLAYSCLEVQDEGFRPSARVFRSLFWLCRKVTIPANCFCKPNRDIYRGSDPAIATSGTNKKLLGGCYHASPAGVPFNKAKTNCMNDNGIIATVHDDDKGRFLQQCGKNRSIGVLMSLLFSPLTLTPTGMGAGNCQIGFPYVCQYTPCSVGNKNC

>Ppa|PPA22639

MLPKTFLFLFFLPFIISAPRNGLRSQDEFESLSSPPSLPTNDPPSSSLTELEAKLNERMRIIYSDLSSRMDTIEEAIHQVHNSNEKGEWLERDDKSSYRLHEERRKWKEAQSICQSEGASLVTVDSEGENGFVTQIVKTKPHIDFVWLKMKNRPKVTPIDVQFSNITDKDQHNQCTVICSDSSWALRSCDQLRPFICKRDPPLPPKSDSDEEDEKKDEVSIDPTLKQPIQPWKNNQMHSALSGAESLNAQWFISPVVNIRAFKETAEEELQFTNSRMGVSDEYEPEQETLSSFLGCSSRTTSRILKDISLEKLLEPGKRSLNDDLEALDQPSLILPETLKTHRACMDRMKRFSDHSTKSCYFQKMRYYKWETFGNKMCPSDFGTYIEEGKELEKPDPKYFNISLYPSSFIFIHDTFYIDTSRPECQDISAEIREFMANKSCFGPTKVESMTGVTVMDLTLRLGQPYLFLHSGNCEHLIQFTDLRLMTKDDEQDESKYPIMTFERGGEVRCMACKKMEAGMGAYFNNRPLELRHTPMNPYTSCLAAERKMEGKLTSGTLHMAIRVKRKKKDPSVVKAECIGLVGTQFKFDSLCDFQYLPIRGKPQSDVFDDLIPRLIPTDLPSALCWWDKPELNGEETPLFLPPFQFSRYNTPSNKILCRETVFGEKTRKKALGHGHNLRVERKALSVNVHANDDFPLAPTADALADANFRCKNEGPHRMLFELFEERPLWTRVAVAYRTKLEETLLKSLLQKYAFYINNGPWGRLWCKFGYDPRKDPNSVLYQTLMVSFRQHTKIPERQRLKVSTSERKLGDEGEGTNSVNYVNFRSAQDLLRKNQSLEFVPDSGFISVATLDQIRDLIKEDVKKTSSEMEVDESDGMEITIDEEW

>Ppa|PPA22928

MLLQASLLLAFTSAVTGASPTPFVPPSTTPVPLPRECPSGARVFTPTNACYWIVRDQMTWSEAERACVRKGGKLSSVEAEDENEFLYDFTRSANLSSPTFWLGMLNKNKHSGQYVWHDGVQPRNAGAFKNFITREAGTASEMCVSMWSDYTQADGSWHPWSCAFQGYAGVCKRKFRSLNPSDVRSTISPLEDSIQANRCCTHCGKACASNERCIPDDLDCLIKECPGSEGYGWCLPAKDKN

>Ppa|PPA23636

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>Ppa|PPA25240

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>Ppa|PPA25718

MQTLSLLAVLASVAAACEWGWEKYKGSCYRLQSRTNTWTIHNFECVYEGGTLASIKSEGENEFIRRLAHGRDVYIGGASFGYSWEWADHSSFYGYSNWADESESYPPRGKPCISMNSYGQWEAHCCANPPRAAVCVRRW

>Ppa|PPA27057

MHFYAFLLLIALVGVSLSKITDYHQRSCDPGWTQVGSKCYKLIGSQLASISSAAENEAIRSIAGGREIYTGGLSYALGPWSWADHTPFGVYRNWRNGYEPSPSPYKPCIKMNPSGQWFDNCCRVPLFPVSARGVCSIF

>Ppa|PPA27097

MADNHCVNMENETRPWTIVADNPSLSCDQQFTLILKSDETKLVIPRLNAINKFFDGSGVFVVPQVGMLLERMSMSGEGIISFYSGAGTGEEEERYLLQSWKCSMLPNRIFSFESVITIVADDSCSYMLQYISNFDRNVNIFRNDRVAILSSGRSNNLQNRNGTKIIAYIEIGEWEESNVTVNMNLNFDSENTGSVGLMEQFAGPIDPYFNGTHKVEFVTDYFEIRWNPKELEPFEISNNQDIINIDIQVSHSNDEFECPDGYELISVDDERWCFTIFGPIPPSRGFSFLEAAAQCYIAGDSMPIVTSQEMNLRLAKFIYDFEVIEEAWIGLSCDPENGTWLWQDGQPLDYNALEGGTDKCSIAENVAIDKKSWRVHDHSDLMGKVVCSQRAHAAASSTTPELTTLHEFIGSTETTLAAATDQTTSVTSFAADTSTANTLTSTSTFSTITIISTLTSSNPPTTSTVDNSNGPPAWEIVLIVIGILLIIGCGIVLFLIVRRRRGLKDQILEEKLEIRKISQQVHMHYGIASDSEDEWEIDRRFVGIDYMNKLGEGAFGCVFLENADSQVERDFMSEIELMKRIGYHERLVNMLACVTSSRPILLICEYCANGDLLGFLRRRRKFMLERPEETESEEVITVKKQLMFAIQIAYGLEFLSSRGFIHRDVAARNVMVDQNEGCKIGDFGLGRSVGRENEHYHAQGGKLPLKWMSPEALDKYYFSTAADVWSYGVLLYEIVTLGGVPYAGWPAVELLSRLKRGERMDRPDNCSEMLFEIMCECWSEDPSDRPTFERLRKELGDLLENVHRDDYYLKLNAHAHYYVMESQASE

>Ppa|PPA27600

VYRIPPARMSRRRAPSLRLVLHATVCLLLLTTTVAPASGDDNSILSIDDVKLACAEGWTRQGAKCLRAIAREASWRRAEEFCKSRGATLAHIESPSENEALGAEVLRDPEVAGRANFWIGLSSDNSDRGVYHWSDGRAVSQYVGFWAIGQPEETDGDCVSVSLASSPLWSRSPCAQLLPFICQQPACVEGSNFCRNGKCSSISDICNGRDECGDGSDEENCPGTPCRAHLTAITGTIVSPGHPNHYGPAESCRWIVEVPINMRVELTFDNFDTEPSADVVTVSDGLPSSSSSNSSLLLATLSGNKQQERKFTSTGNVLTVQFRSDRSVHAHGFSASWKAVPFACGGSLTAQSFGQVLSSPAHPSLAPRGIECAWTISAPAGQLLTLSLEDLDVGSSAVDIYDGETASAALLVRFGQGNETSLEQAVSSGLEHLVSTTSRVYVVFRASRAVDVGRGFSLSYKRGCDIVVRRPFGALLSPGASGRLPYPAGADCSYTIELPDASPDHALSLAVEHFDLAGNDYLQIFEGSSKGSPLHDGEGFTQSARPPRQMTCRQSRAQLLFRSSGVRHSKHTGFNVTFSTNCPSLIKPPSVSLSTRATTHGTKVTVSCPKGFEFVTGRGVHFSTTCERAGRWSEPVVPECQPVYCSPVPQIANGFAVAATNTTFGGVARYACYEGFSFASGKKSEEIHCGDEGKWGELPVCRAASCPPLVPFMHGDRSLAFGDGSGYGSVYRYECAPGFRRMGAAALLCQNDGKWSVAQPTCARLECPSLPRISNGRLLVQKPFLFDQSAQLICNDGFEPDGVAEVHCLASQTLSHVAKCVDIDECARGDAKCDSASTRCVNRPGGYSCECLKGYQPELGCSIPSSLSTARISVSSKAPGQQLSSASSWCASPDDDDRLMRLHFSTPMVVEKLHFERENGGFPTEIALAFSSVDGMPLKAYGEGNKTVFTIKNAASSSGGYVVLPKPIEAVTLEIELLSYTGTPCLKVEVLGCHRLACADVNECKENNGGCEQICVNSLGGHTCSCRDGFDLFTEDGQGGFHIREGESGKQAGDVYRLHQSCIPRVCPPLSSPSHGLLLSTKKSFSFPDVVRFQCEFGHQMFGAEFLRCGEEGNWNGTAPRCEPALCAGVANNTEIGLFVSPSDEVVAFGESVHVHCTQQSRPIRKQPLSDSRQCIYDPREGQADYWLAGPPVDCPLVECGAPPALAGVVYDGNTNNRKVGAQLTFACRPPYQLVGRSSHEDRQIRCTMDGSWDLGDLRCEGPVCVDPGFPDDGSVEMTSVEEGAVAKFACERPGFRPFPTSAIACQLGTPCLLAEDIGISNGYVHDGAFSDNSDKPNYGYEPHKARLSSTGWCGNKDAFIFLSVDLQRIHTLTTLRLAGVAETARLRGHVTKLQLFHKIQFSHNYDTYPVEFETPSGNHNALHQFELDPPLRARFILLGVSEYEEHPCLRFDVQGCLAPSHDSPSHLQVGWNSSVPQCIDAEPPSFIDCPEEPIQVQTDSFGQLAPADYAVPKAIDNSGRVAWVRVEPEHFEPPHAISADTDVVYTAFDDAGNSAECVIKLRIPDMQPPLLRCPDSYTVHAEKGESVQLVFNSSLVPLHVQDVSNISSLVFSPTHANLKMGEHATITVTATDAAGNRAECRFQVAHKAPPCSPHSLSAGNTTLRTCTEKGEGKLECAISCAEGHRFVDEAEVVTQFTCEDGEWSPAVVAPSCAPLAEEPARYELSVRVEX

>Ppa|PPA27669

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>Ppa|PPA27907

MRSLLALTLVVSAALAAGAPRHTLTPNFYDHLEAQSPNEHHRAKRAIGGFRSPCPEGWTGQFCENPICGNEMKVDPYETDLDKTQDILYLPSGCDGEYYVPYDSTTDLLTITVTTDAMTKATAVLTGPTGDTPNAISSDYAGRTATYRFKAKPNPYVLTIKMDSHTEECLVHIQARSSLSFNGGWVASPMIDNSPFGESLYNSKPQYFIVHPFNMAAPAEVKTVTIRQAQLTQPDYRSLLTRRYDCAFEYYAGQFQCKGQDSRYLYQIEGVDSKGYAFRRSRPFLCLQDQTPTVGPPTGVPTIPTTECFNGGSLLYANETDTSFCFCPELMTGKQCEEVLCMNGGIQVDGHKDECDCIPGFVGKNCDSVVCDPDVGKLLTDTKTLAVVVRNTASMKDHIQKISAAIDTEVLHHQIDGRTVYDGFILSYVRDGVVTAKSYAMQKFAQFQADLENLAAKYGSDTACTESLRIMDQSPIFIFTDATADPGDSDQFKDLMRLNAANRMQLHTMFMNTQANCKVNPNLEFYNRLAKYTAGLVHKPPADKLEDTFQMSMRATTYHMNLVESGDLKQCSMKQKSLLVDFESATLILIATGTDLSVTVTDPDWQVSMKTTVYDDGWTHIFNIDRPTGGEWIYAIQGDDLISPCSYRFYSQSDFDLFLGTTNAVDVDERTFEPVVGQAAHLIAQVNGFYGGYVTDQFRLFAEILITSPDEDDKHQPLYYSNGIFRSSCGFHLYFGVANFCQSEDQIFYATVFVDDANGFPVQRAAVGYCNAADIDPPLPDDCQNGGVRYNETACWCPSHFAGDLCQTPECLNGGRLNNDQNQCICPGGVTGRFCEMMECTTKADEWEATFDHRTLNFVVSTRSSMKDTVKKLADGAAAFAGYYNLNHKDWIDHFAIVTVNQTSADLHLTNSPQEFADMFREISNNFDSYTNYDDDNCTVLINAGINSALAASYENSNIFIFADSQAEKLEFPNILSLLDRADELHSTVTLFGTSYDMCDGSKSFGEQEQNVVDFTGGKTFYTDNIDRVFDYVDTFYYSGVVLEQTYDKCNEGVSIDFPLEASAHSVVVTVEGKGSGIVMSTPDNFDGLYHDQLLSGNEFFIQQYIQACPDQWDTTDNQCYFWDVTEVQWITSLVACGNMDPNKGASLVTIFNDAKHDQVQAELKTAAQGVWIALYRDSQSNKWQWMQAGAQPVPLDPSLEKYFAAGQDMNDMSKRYVYMKNDGKWYIDDTTGRHWTLCQRDRYGGTYNPESQEPDLPPGFWNLQVTSSSTTCTVNVRTQSDVQIAFGFSQNPHDDFKRGTANVDSDSNYVVAKAIGLDTFDFNPDIPEGKVDYATIAADGKDLYPLVMTPRAQSCTFDTISQIPFTCPSQQGLSEIVVKFQGIDQFGYSFERSLVTRCDTYAVRCKNDGFVNNGECVCPPHYNGDDCGVPICENGGTALWDGSCKCPPLYSGKFCSYIQCDPAYPDTFKRNERTLVIALETSFTTSTPIFYLSNQLVDSLDILTQKRPDWFDTFVVVPFDSTSNKDKWYKPITTYNYKDLDDYLNDIPTATCPGDDPDANPPISCPDQNCPRPIGSVLGDILDRPDVSRPDSVVIVITNSAIEDHNNIYDIVPKLINSKAQVHFVVAPSATPCNLGWDNEMNQAMTYMASFSSGTVSSVVPKNIGKYFSDFLPSMYNAQEVVIDSQYVKDCSAKENVFQIDHSANEFNMQFFGVEADTISITGPLGDVTVPPNLLPGSSAYFGVFEVDNNVIVPGTYIVRTKSAGTNCDLKVRSSTKILVDVGFTQVHDTIGGNSQDDAHYAGVYGVPNKVMFHVEGLEEGGALMYAQVISPRGDVVATKPVLARVSDCTYAYVMDGTFSCDYTDLEIVVYGVDNQNSPFHRNFKAHCTDDRPQPIPPMPTCDLGAMKADIAFLVDTSVEQGYVNWFQLFITQMMSGKFTLGREQTQFAVMSISDKPEQGGFFSFRFGSDKSTMTQMLGSIHSDGHVGQNITSSIPAMMADIFTKNNGFRGDDKSVKKLLIYLSSTNPTDDEPDNAFFALTSNKLTGVAVATFRLANPDKKMKSLVEPHCFWDSGPDGNAFAVYGPRFMQNLLCATQPICGIPPPHNNCSAPSPTCALGSIKTDLAFLLDTSVDAASVERFRNMISAAIKEYSISSSYSQIAVMSLSDQPMQGGSFSFANGNTKTNVNSNLQTIKSDGHKGQDLTSAVPVLMREFYSKNGGYRAGNNDVKKLLVYVTATEPTDNDPTNAILTMTLSETTGFAVITSDIASPSKKLRGLADPSCTYNTASYDDLLKNAPNFINNILCAQPSASLPSPLWHFANNNSAARESQRRL

>Ppa|PPA27964

MTLLALSIGVCCLAATAAGGALHLGLAGRQQADADPCPLGYSAVNGTDDCFKVYTMAKAYADAEDFCRQDGGHLASIHSADERRNLNDLLGPNSPLIGIKCSTTTSCTWSDGTPMDYQNFIYGQPTLEYGSCAHLFADDDKWYSWNCATPMNTFICRLPATAPQCHLASIHDLTTNYGLSNLISNTTLTCDNQMQLNCNVHIGARYSQSAGYWWTDGTPYDFRNWATPEFPDTHFGQCSQMLNTDEFGAPGQWTNIPCDTKLPYVCMKAPGVSPTYAPLACPRMQYFEDQGTVYSPGFPVVIPSKLYCEYLLAGDLDTTLSITFPFFNIGDDSKLSIYDGMSAAYPNYVLSGSDFAGSTFRSTQNIMKLVFETPYNTDGEGWEAAFTTIRPYTTARPMTTAVSSTTTTLPIILSSAAGTTVNSNCPPVTAYADAQISSPGWPLGYPRNANCWFYLSTQPGKRLMIDFEYIDTKRNKDYVSIRDGPFDYSTEIARVSGKTSENTLRYVSTSNYLTLQFVSDSAKGGTGWTATVDGCVGYALANMIGLLALVSLLALSQGCPDASWTTIDGGDCFKIYEISKTYYDAEDYCVGQGGHLASIHSQYELYDLHPLIGSRAPLIGLKCSTTADCVWTDGTPYDYANFIYGIPTLEYGSCVHLYGTDDQFYSWNCATPMNSFMCKIANITDVCSPGYTPYLGSCLTVKTIYKTADDAERECAVEGGHLASIHDPAANNFLTNLLLDANLTKNAHIGIRDNADVITWTDYSAYNYRNWATYYPNTYFGYCGQLLGTEEFGYIGQWSNIPCDTKLPYICMKAQGVNPMYAPLQCPSMQYFEDAGTVYSPGFPQTVPPNSNCEYLLASQVGTTISVSFPYFAIDSSSKLKLYDGMSESYPIAVLSGALPTGTEFNTTQNILKMISSPGYPLGYPQNADCVYYVSGNPGKKLVIDFTYVNTKKDKDYISIRDGPYENSLEIGRLSGDTLQNQLRYVTSTNYVTIIFHTDGTKGGAGWVTTIYTEKFAKSECKSLNVFSRSVVYNECEEKEEPGCGDYCGRFAQTTDAICKNSKNRRGVIIKTLTSRFPRLHCVPENVHDIAKTNRADEKDDELNVASKIKTTLEKSALTTLAGSFFSIIARWMFSPSIRPTRAHTINCTVEKRTAEV

>Ppa|PPA29746

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>Ppa|PPA30435

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>Ppa|PPA30817

MKLVLLLAALPVLALSCADGFNTWLDGRCFRMNYYASAPYVTAFDQCARDNTRLPAINSQEENDQFFSALKQQNAFIDFSFWLSLTCDGSKFVWADGTEAEYTNFAANYTCTKSSMDRRYYVDTDRLWIEADQQSFYYAVNVIVCEALQRSSSPCDTYDALDATDTCYKLQKDEMSWKQAEETCNESGGHLAVIHNEIFNDFILKTAEVANLHDGVHIGIKRDDESSNYTWADGSDIDYNNFAPGFPIDDNGPCVAMQTGFIPGEWMNTDCYFTRLPFVCTKPAYSVTSQQPSGCPVKKQYAPGDEIFSPSYPLPPGVGGCQYLLLERDQNKRVAIEIDFFESNSCCDSLTIYDGLFGSNILQTITGYLSKPVTIRATSNAMRLVWNAKSGAHVRGFHAKMSTLSCGYGFDTWLDGRCFLVIDFSSAPYDTAFDRCARDDARLPAIRSHEENEQIFAALKKINAFADFSFWLSLSCDGSKFVWADGTEAEYTNFAANYTCTESSKDRLYYVDNHRLWQEAEEDFTLIYYYAVNYIVCEGLHRSSSPCDTYNLRDSTDTCYKLMRDGMTWMQAEEMCNESGGHLAVIHDQTLNDFIVQTADAANLLDRLHIGMKRDDKSGNFTWVDGSVIDYNDFVPGFPKDYNGPCVTMQTGFMPGMWMNTDCYYTRLPYVCTKNTYLTSIPQPAGCPVKTQYAPGDEAVVEIDFFESNSCCDSLTIYDGLAGSNILQTITGYLSKPVTIRGVSNAMRLVWNATSGTNVRGFHAKMSTLSCADGNETWLDGRCFRIFYPISVGYGTALDQCEGDNSRLPAIKNQQENEQIISALKKYNAFADFSFWLSLTCDGSKFVWADVIEAEYTNFAANCTCSKISKGHRYYIDKDGRWYGADGHSFDYPVNSVVCERLGFKQDLSIDNV

>Ppa|PPA31391

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>Ppa|PPA33774

MPRPPHFGRPHLVYLLLLMMKMCNGLPSTTISQYTTTQEPASTDRSDYSTQYHVDDNTDQPFEPNIRPGPNEIDTTALTTEFATTEDGIERYACPEEFLQLTIDWCFHFRYNIDDRLDFTESQDYCSIKDAILPAITSEDVTKALMLERTTVMGISPFEGFYIGLRCNTKKHRWEWMGGVEYDSSLAVFARARTNPKYCVHWNDTVEYGSEFQFDQFGTWSLPNQMSKLASLVVCATRPKGYSPPNPIDAPCTDSWTQLPGGMCYRLYTIQYPDTGLDVYDAEMSCRSMGGHLPAIRSQDQSNLIQAYLTGKGKQNSQFWIGLYCNFGEDYMPGDTGVRAWIDGTPYTNDFTNFLEDSDDTVTCNVAVVDTFLYNGALKGKWQKENYTQLLDTIMCSRPDPEPMPGTSTATTRRTIPPPKTTTNAPEDTTDDGTTSSSDEPEKPEHTTTHAPTTSGSPDKPRGLTILELVLIIILVIIIIFVLVVILVYCIKRCRRAKVQEIFYNVQKRFSRSNTNAVVRTDEWEVKRQFVGIDYSRQLGRGAFGSVYLGRVFSGNIPEMAVKTLLQLNTLKKEDDFVAVKTLHETADRQAASEFLDEINIMKKIGFHERLVNLLACVTETEPLLLVVEYCSNGDLLKFMRERRMFMLKLKDTVGHDIAGRHSVITQKQQLMFGIQIAYGMEYLSQRGFVHRDLAARNILVDANETCKIGDFGLCRQISGESEQYISRGGRLPWKWMAPEALERFYFSVESDVWSFGVLLFEIITLGGNPYPEWPAVELLHRLKTGERMPRPEGCSNGFYEIMLDCWRCVPMQRPSFEKIRRKLAHELEESSSDDYYLKLDAAAKYYQGPASISVVNLNDKLQSSPIAVYVVQKAAADKITYGIYDVINMNPESSDYPQRESNLQPNSVTARLVGFDNALDGNVDECPVAYSTTKQALSFTVYVDGPIVSLSFAEKVGITARMQFIPSFDLAYPGFITSGGWNGCKKPASGGLQSFRSLFVNTDAVYLLTSQTDKYNVSMDIEPNLDKKNAITVYDLINRRDEEVFGYEKKALQFDNTSNFNIIFSGLKGDQGFLLRYSAVVLPRPITTAAPTTTSQTSTSTALTPTTTSGSSRLESMLLTLAALVVAGLI

>Ppa|PPA34500

LINSVLEESTRFVCLVPQDGYTGLNQLEKIFAQTDKVSTSFAILLSAQCIERPNESPWRIVAGLPVDLDCTQEFSLIFTSSQPNINVIREQANSYSVSDEEAIFVSSATGMELNTNACSGDGNVTIYTGAGSGVAEFRYPMVSWSISRGTRASRGDVKRSHLQNYHAERNFVKLFTCQDTQMTVMFSGSFDARYDNYVDVAGNSSNGMQWARTFRNETSSMSTVATNFTALYVSTPVDAPDLWDSQDNFVVVMDLTDPYCGCELDKKFGMPIDWDPNGIWLDMVIILDCSEAMGKKLAGRGNAFAAAQQMLQDGQTPGRSNARHVIYYMTDSDPKVDLTSLDSFKEEGVIIVNDFIDSHVIERPGLKDLASDGYYYTDIQDNYMSSIQLFCKGIVRLKCSANEMCWLASYRLSGREAGGRKGGGGHLIYRLLPVSSFLRPLERSSKVSYEWNGNILTIHDFIDRECLWLANCFCSAEADHVPYAGHNKDEAGEAAVLRRLLPRGACRVPYNSMIQICLELGGGQMVSIHDDNKAIFVNNLYKAAKLKPDYYWIGYAKSDDLWSWTDKNTVNNCAYVDSTSTYWGAANCNVGYPSVCEFKPCAVGHKKKKA

>Ppa|PPA34980

MVYTLKYYLTVVTVVLGGSAQFYSYGVVNPAQRLIMDWINQTYYDRNGDALGVTELNLFWSFVVSSIAVGAIVGALLTRVISERCGRRNGLILNGAVNVVGAVLELLAKPTRSPELLLVGRFVLGVNMGLTSGLVPMYLMEITPASSRGVAGTLHQVAVAFSDWFSLLIGLPEVLGSAVLWPFAFAFPGLFALLLVLVLPFSPESPKYLMSTKKDRMGALDACRSLVGHDAAQHMYEELVKEHIQEQDQSSATFRELFTSPQLRVPLAAAGIVMLAQQFTGCTAVFAYSTDMFVNAKLDQCVSCRLFHRVCSFCSFRKYRNTYTTNLRVTARFATLAIGIAYFVFTCSAPLLIERVGRRPLLLFQLSACFVSLLALTIFTGLQTYSKVSWASYGMIGALVVYMCVYGVGSPIPWMITGELFNQRFRSCAVTVSVFIAWFLAFLTSTAYLPFSQLVGVTFSYLPFLVGLLVSTTVMFFLLPETRHRAPSEILEEVRERSSSLASGRPWEAVTHTRPTSRQEMQSAHVNISKFNVLGNAMRFAYLLLLLLCAGGVRTYTFTCEEMLYHFNRGTIDDEITHACVILPDGNRNVEQLKKFHLTPHMTFADIFNAPGHCVKRANGVAWQPRVDDGAVCTPEFILIEAKQQPAIITPGAEPDQHVLDGQSVVLVVPQTGMWIGKSRCVGQGNVTFSTGADIEEPGLDMQYRSWPCHSIPVRIDVFDSVVTVKVDANVQFTMQTSSYIGSYNSARSGNHFAVFSSGRSNDRQNMEGYYNHANFKMDKEDEVTVNMDLTFDSANTGSVILKKSAGGVLENFYNGQYSENFNTKYFEIQWTPKPLKPNEIYYNQDKIVVDIFIGPQATAPPPVASKNEYCNCAVDKFGLPDGWKYNDIWLDVVIVLDTSEAMGERSLVDASALIESLISDGVDDLLITDPAGAFYTRIGVIAVADTAEILYNLNMTKTDKVTASVKQGVKEMDFNAAYSSALSMFSDGLTSQPNRAGTRQVVYFLTNSDPDCKRFAKPIASATCTMTPIQAPIPRFRLREVAIVPRPRAFPSPKLRVPVQLTEESLQPFMMMRRECFCTMMTKSASKSDYYWIGYEKSNQGEWEWEDQSTNPYTNWGPHEPSLASVAKCAYVDATTKNLTWGAGNCQIGFPYVCEFVPCSVGRKNCRANSGFRPIELGAYAFAVLDCSRYLAVLSLLEFASDRGEKKGKCPYYFEL

>Ppa|PPA35254

MNTTELDPIFKAFLVNYHHVSVVRGVIVFIANSLVSIVIIMDKDSRATTYRSYLLALQITSMTTDSLLDAYTPFILLNSHLVFSDSFLAQHLDIVSFFTIALFFFSTALSSYFYCVFYRRCVVLPAGSRFCWVGCSRYSLFIGLQVNVAVVTFMLVIVIISARVPAKDVPEDLSWLCSMPSFGLLNASPYFYTAAACSLNLNIFSQWYLKKFRNGSHNSDIILPSDSFPHIRMPRNEVETELLDCPADISHLSIRWQIKHPCSDAGSIAVFVFGSLVLMIWDVQRELRRGIKHASGATQRIQKRAITALTLQAWNDSECLFRHSCNRSPSTLSALLFAVLPMHTFMHSLTILACSPSYRRTIRDAVCRNKNARQRKSTTLFISPCCVFVVNSLVSIIIILDKDSRATSYRFYLLALQLTSMSMDILIDAYTPIFIINGRLIFSDSLLAKHVDIVPFFTIAVVFIGGAISSYFYCVFYRRCVVVPIGSRFRWFGWRRYSLFLAQQANVVIVALIVGVVASSARDVPAYLSWLHSMPSYILFNTSPYFYSAAAYAAASAIITFGAVVLMIWDVQNKLRRGIKHASGATQRVQKRAITALTLQGIIPSVCFVVPEVGLSLVYFRSLSQGLEVAAHDRRASTLSALLFAVLPLHTFMHSLTILACSPSYLPSMIMDLLIHLYNPILQMNSRVVYSDSMIANHVDIVVFFSFAAVFFCQSVTAYFYCVYYRRCAVLPRGNRFCWEGWRRNSLFLALHVYVWIVLAVIYISLYSVRAPVEEVPTALNWLRYTSSFIFVREQPAFYVAVGFVLFWGFSMASVVILMIIEVNRELRTGMINASSSTRKYQKLAVTALTLQGKIPRAFYTLPIVGEVLIYLTSLSMGLEAASENATAISGGLLLSMFPVRTFVHSLTIVACTPSYRAICFLFNVLVFTVILIDKDSRAKHYRIYLASLQLSSIPMDLLIDSFTPMLLINCRAIYYNTFIAKYVDILTDIAVGTRNGRNAFALSSTRTEKWHAACKSCNEKGVIPSAFYMIPATSVDTAGAKFGSTMSVLFFSMLSLHTFAHSITILACSPAYPRKTIRNMAPWCFKGESSISATAVFLVFQSASYELSLIYTDMRFIESISILLLLVGICEAFVFSCNEVKYKLINQNLEENTRYVCLVPANGYTNLEQLKKIYAQADKVSTSFFDLLDSQCIERPNEGSWRIVADNPVSLDCTREFSLIFTSSKPAIYTTYDESAVSLSGTEVIVVNAEAGIMMRMEECVGEGNVTVYTGAGSGVQEYRYEMASWRCSDVPTWIVSFDNVITVATDSGNLIVTPKSSLYHHYNITRVSPLDRITVMSSGRSDNLQNMTPANNFIDFNMGGTVPITMNCTVTFDKRYYGSVLAYTIKPENDHSFDYDINTWNTYGQAIEVKYLTDPVAPADLWDSSDNFVCDIRFGDYIEQPTTDAPTTLTPTTRAQTTPPAPTADADPYCTCTLDPKFENPLDFDPKQIWLDVVIILDITEEMGSDSIDEATILVEQFIGDGDFDVLITDPKAPFYTRVGLIAMSDRAEVIYNLNMTKADSVSDKVAMKKGVKQIDVVAAFDAAQQMLIDGEKPERSNTKQVIYYMTDGDPKFNPTTIDVFKQYGTIIVNDFIDSGVLEHPGLKNLSSPGYYRTDIQNSYTRTIQLFCKANCFCRQDIDRKPYAGHNEDIAVQAAGGCFHAAPAGVSYSKMVSTCNNLEGGGKIVSIHDMDKAQFVNTVYNNASIAKDYYWIGYAKDDAGKWNWEDASTNPWTNWDTANGEPSLNSVSKCAYVDRTTGNLLWGAGNCQTGFPSVCEFKPCMVGNANC

>Ppa|PPA36768

MLVLLLALIGTCAALCPDGYLQISRTDCYTIYFTNQTTFVAAEADCVLDGGHLASLHSYDEQHSLAGMTYGMNPLIGMKCDDEAIANCTWTDGSVVDYQNFPGGVPVLSYGGCVRLGSNDEMWYSWNCAAPTDSFLCKVPAYDDIVTIPVEMTTAEPVPTTPIDHIKGCPKQQYTADTYVFSPNWPSPYQAGVDCLYFITAKNSRKLTIQFEYVETNDMIIVYDGSDMQSRVIANVTGKNGAAVWQYYSTGSTLTLDFIANSTTGGKGWSAAVYNV

>Ppa|PPA37151

MTSSLQLFIILSAILNSSVAVVNFTKSILYDEIDFATQVVYVPNFCSEGCRIYVSVQEASASIAKNIVVHDYIHDQFSLYDISQQVESDGQKGYSAVDVGNAQVNIINTNLGYATAPLAVWIVRKDATNFGYSRVFEADNLSTAPSSLQVVSIMSAVPFTLRTKTQGSTELISTLTGFDAVNTSEDECIQVITEMDFDTFLDVQTFVQSPLITLFFNDEKRPTTSLSTETGYGNDLDLSGVSFVASPGFIGCKGNQTFRSSLYDDYTSVNYSNHQVTIKDTTNDKEYKLISPGGTSATNITISQTNILDISWTLQDSLSSSNNSFLLRLTPSKETMITPISTTATKPVQHSTTPVSVPSTTTKPAQGSALHSCPSPLILYRDEQCRGYYASDMEYMDDSAGQVISCCIKINAHPVSIHTDEQQDYWSAQKHERYFILGLTCNSRSKHWEWADGSVLDYKPPTFDKEMDSDCNTGCNWYMESDGAWRINCTHVVQETDFFCIAQLSQPTPTTDCGSFIDGSDDSQCYEQKRRPGTKLARSVTVSELNSLPFTVNSSKIIQQNSYIRRLAVSRGAINGVLLGGTVSGKGKTFGWVDGSEWDYANFHPGFPIDGLGDCLSMDTITTAGQWMNTDCNFKMPVVCSRPFYDTPELAGCSAGSWNEGQIIYSPGFPSDASVPCEYFLTVSAGKRVQLESNRRGQRSNVHYEGHKHNEGNLATEWRRECERIDDVVHYILNISFSYHSYSFCCNKEDCARCVLRCLATIACICIIKSARHYHKAAKLLAEQAIDVEMLKAIVFLQLLILTFHSVFGGCPSQLPLYRAGQCRGWKKNDDPYMDADALNRVTSECNSIQSVPVSIHDDEQLSYWVGKKTGYKFVLGLTCNTGSKKWAWSDGSILDFKPPSSQYATDCTHNWEYTDYFCIKQLVQPTQSNDCGNFDEDSNDGTCYEIAKIAETWNDAQSICHSFGAEVASVHSEQENSYIRRLAVSQGSTNGVLLGGKVAGKGNDFGWIDNSDWDYSNFYPSFPIDGLGECLTMDTLTTAGQWMNTDCASKLPVVCKRPFYNSPELAGCTGGPWKEGQIIYSPGFPDDASVPCDYFLTVPTGKLVKLEILLLEANGCCDHLLLTDGYTGGAIIANLTGDGLGGKYYYTTVSNTMRVSWQPNGGVGVRGLMCQLLRDIEMLMVFFVALLQGVHASCPSGFELIRNGECRGTVGRQNYYYDEAMSNAVAECKSIAGQIPIIHDDEDQSYWNNKEYFYIPLGLVCNTQSKLWEWIDGSHVDYKPPAGNYDAGGRPHMRPFAVNGVYLGATLSGKAKGFGWIDGSEWDYENFYPGFPVDGLGDCLSMDTFGVAGQWMNMDCSAKLPVACVRKPNTSYADSCSAGPWKEGQIIYSPGYPYDASIPSDYFLTVDMGKRVEVKVHLLEANSCCDRLLLNDSYLAGNIVANLTGEISEKTYTTKSSNLVRVSWQPNGGVNVRGFMMSYRAV

>Ppa|PPA37162

MLIQIDSLTPGQQYRVYAAQSAIVLAGEYVGNVVIKGVDGKQFDVQSLTKPIPNTGYVLAETNVLTAPITIADSMVPGANDKLVPFVIYIVSTKIPASPVISAQLAGSHVDSSIAKMSADSCTVLSNAIRMELSELNISPNGELMVKSAGYDATSHDYTVLSVNQNAVGCKLTVEGPIASLHNPLGSSANFTFTLAFDTPPHTILAPGASAVFLSQGWLSKHESCETLHGIISSIGHPCTTVNVTIDQGLIREAPRFMVQIESVDLLDILTTTERPATNMKPDPYCNCTVDKSGAPNGWRYNDIWLDVVVIVDATAAMGVDDVANAEYLVDSLISDGVSDFLITDPTKTYSTRIGVIEMTDSARVLYNLNMTKTDKIQGKITMKMGVEGINVIDAFDAAMNMFNGASTPDRTYTRQVIFYITDSNPTQDLASLNKFKQKGIIIVNSAVHRTGLWNLASEGYFFIESSTKHVLRAFCKANCFCKPGKQAYGGSDPAITAGGGCYSSYPKGSSFSNAQSTCASEGGIATDHDGEKGAFLNRGEFAILRNHRMDDDVSALKDASSKSDYFWIGFSKSDDGSWKWEDKAGFTTEINSTDSYTNWNEGEPNSASVSKCAYVDSTTPGLSWGSGNCNVAFPFVCEDIEVDSLSPGQQYRVYATQSAQNSAGEYVGNVVITGADGTHFELSLAKPIPNTGYVLAETNILTAPITIADTTEPAKNVKLVPFVIYIVSTKISASPVISALLAGSHVDSSITKVGFLGELTVSTAGYDSFSQDYTVLSVNKYQTGSKLTVEGPIVTLNNPAASPANFTFDLSFDAAPHGHLAPGAMTVFLSQGWLSEQASYDSDYPLDTAQFSSCTLDGIIFVLEPPCTSINLTVDKALINGAPPRFMVQIETIDFLALQTTTERTPMSKPADPYCNCAVDKQWAPDGWRYNDIWLDIVIIVDASEAMDEEPLANAIYLVDTLISDGYSDFLITDTTNPFSTRIAVIEMTDTAKVLYNLNMTKADKVQGKIATKKGRLQRSHGHVQRRFNTGQGQHSPNCILPHRHGTELHFAVCFRKQDLTPLNQFKQSKGVIIVNSGLQSSSLLSLASKGYYFLNLNNKHALRAFCKANCFCKPGKQAYGGSDPAITAGGGCYSSYPKGFSFSNAQTTCASEGGIIAVDHDGKKGEFLNRGEFTTLRNNRMKDGIAVLIDSSSKSDYFWIGFSKSDDGSWKREDKSIDSYTNWNVGEPNSATVSKCVYVDTTSSNLAWGAGNCNVAFPFVCEDLPCSLSNGQPIVNQKVFPALSTHLPNLRLQEMLSSQTWNNKLTTEAEKVAAHCEPTPSSPGQNTLYFPGTVHLFSKSSMVSYSAKYWCVEMVYRAWRSMNRTVPIEDSGVTEAIQMARPETREVGCAVSFCGVDDESALVAAATPPIPRDSPSATLSRRAQVREESSRPTTKTRKEPSLIKSTDSYTNWEADEPNSAAVAKCAYVDSSTKDLACQNAVGSKLTIEGPIATLHNSLGSIANFTFTLEHNVASDRDLTPGALTSILSQGWLTLNKSYDSDYPHDPAPFGRRYNFGRPARIRFSTENNFPLGISCELWCERGKEAPIGPYTYNDIWLDVAVIVDASEAMNDAALKSAGALVDSLISDGISDFLITDTKKKFSTRIGVIEMTDSARVLYNLNMTNADKIQGKIAIKKGVKEINVIDAFNAATNMFNGAPISDRAYTRQVVFYITETNPHNSKKKIFLKVYCTSPRKIE

>Ppa|PPA37170

MRVSWQPTDGKNVRGAMVSELAMSMNRTALNALQGMNNDYATIKKDLSLALRVGTNNYDNYNEQIQLMTSKVLYAITDLLLAGFENIELGKQFDLTYKLVDAYSTMNKCQNPKDPLQICLFKFARCFILFMDNLHGKSLLKGEEAHEKRLMPSVWVDNEIAKRNAPVKQPPIRSSKSTSIGVVRNIGAQQVVVINDRPGPSGCSQIEPAPYLPVPVVVTKRRLVPAKRVMPPAPSLEKDSPSFFEDPETVKKVKTGEEDEAWMRMAEQPSTSARNDAPPSFLAHPPKEEAEDGRINQSTSYHSAAPSTSTQPIKEEVEDNYNYGDVKMEIEIKEEEEEEMDGPIADTVKLSELCSSTNGFYDPTSSTSQPVVSSSSRRKQKITLSPPQPECSGFATAEAQKLFFQSPVNCPYCGVEIPDGKKLEQHMKINHRDHWLKYVQKCPVNICDFRSSDPSVVQRHHVMVHSRNYNTRMGNVAVNFKFVATCPFCPDPLRGLAGFVNHMEKKHPRLCTYEAKILAYAECRYAASNVHMLLSHWLKKVPMCTQGLRFNYDIAANTKINDAVRERDERARMSTIVLDNHNVIQHFYLAVAEHRNAHIHDIDFYSGLMCNTNTSKFERLDGSATDFHAENFHFDTGNCNPACSMIIDENAYWFGWCGSDKAEADVYCTYQLPEPAPPPSGCANFDDDTEDGTCYEVINTVEDWQDAQLTCRSIGADLASIHNERENSFIRRLAVSQGAINGVFIGATVTGKGKQFGWIDGSDWDYENFYPGFPVDGIGECLAMDTLSKSGEWMNMDCSTNLAVVCARKEDPKPICPPGPWTEGQVISSPGYPYDASVPCDYFLSVDAGKRVQVEVGVVLCADWIRIQVLEANSCCDYVLLTDNLLGGNIVVNLTGALSNQTYTTHSSNFMRVSWQPDGGLNVRGMMITFKGVIVEPLMHYYD

>Ppa|PPA37173

MFHIHLTADDLYECFRDHSQKATRSTLSVMKRWFVLFALLHLALSSCPNPGYDLVRDGECRGLEDETTVSFNKARLFLPDLYSKGAAIEAVETCANARATPVIIHNEEHQSYWRSQAAATKNFFLILGLVCNTTTKRYTWADGSQVDFKPSEGYAKDLEGDCSPLYSWYLQSNGVWGIKGGFATGNPALVSIYCTTQLTPPVRSADGCDAFGDDGEDGVCYFVSKFASHNVQAAQSGCMMAGGNLASVHNAQENAFIRRMAVNQRANYGVFIGGSAGKDGNFSWVDGSPMDYENYKPGKFNLSFTYFLLYIGFPKAGAGDCLSLDTSAASGQWSNVDCLSGLPAACMRDQRPVTQPTCVSEGYKENTIIASPGFPFDASTPCDFLLTVDQGRKVQVNILQIEANSCCDHLVLYDGAEGGNVIANLTGGEIHGETFATRQSNVMKVSWQPNGGVNVMGFT

>Ppa|PPA37343

MRVPLLLLVHVGSVLSTLVCPPKYFSIEGRCIRPYTLNANDYLDIIMDYAQAACALDGATLPIIRSDEDNDMFTRIAQTFLQPSGTRIYLVLGVVCDEETDMTRWPENQWKRLLLGDAHLFTSLCVLEEQIATTDEVTEKPDNKCGDYERMEEGMDDETPCFKVFTEPQSWENAQKKCEADFGSLIAISSAEENSFFWNVATTHKFTGGMHIGAHQCPDDSTTWTWIDGEIPITSNTYNNFIRSFPIAGSGKCASMVTESVAAAWVNVDCYEDELPFICQRGDFSLIPSSCPNAAPKAGEEIFSPSYPKSDISCEYFLTVSEDKLVEVEIISLISEKNIDYLEIREGTSGMKLLANLTGTLEKPTKFTTSKSNVLRVNWKPVGTADGRGFKIRYTEVDKVDVGQPATVPVQDEVTTTKSATPQGIFAVIATLLFLHFVSTTAVTQLSCPPNYFFFEDKCIRPFAVMADDTLLNLLPLARESCAQDGAHLPMIRSHEENESYARLVNLLTAPPKGRMIRTNLMDLPNEVLVNIFDFCRHPQSIQIEIKHATRSGSTLRFSGNMYSNGADLPHNPPDMNAFVQDYTYFNRLRFGLQRLAQNTRVQDLRIQMQPMMTDAVNYIIRVLLSFEITNTILWCPESTWNQEIPTITKGPAHGTTMWGGHIQKAVQLWSADSQAHSCPKAAYSLTGQRGERVCEMKRRRPVFRTLHCTDDSIEDVAESCTLDLEISSDCDRGLRFHYCTMTLHKPSGELDWTRTGKWRFLLSSSPIFTLPCLARNGTSVTVVCQERHCNDMNLDANIELCTKELLRRNEAGNQHSSTCDANSASDNQTLSCLCVEGLLIVFLLQLLQYVHAKRNAAKLEKMRHKLNVSSRANGNSENYEEYDSASELHCNKEIVCGDQKYVLSEEDCNRGLVNQYCTKTLIRSSNDNQTNNVDLKFTTKELLPDYSYVWQTEKGTLYYAKFVVNWVLYVMFEGKKVTTKLPAEFGMESVSSLGVRKIIYIGQIDQEVAVEQFNADILIIKIPMTPKYKWSFGHDSSPYFYITNGESLFTINTDTRKILTTLKFRGVNSLVYIAGVFGSEISLMVNQDGWKLISAQLPDGYFVDVSIAGDNNGAIAYTEDRCASTGWKRTNGWELLLSSEPIANVPCLVMNETTMIIFCDSKQCKASHYYFFTRTFNVFKDSRLDMDIKNCADKCKERMTKMGNDEAIRAGRSIQHEDNIDVVCPLNSLHSSTHLLNAHRDAARVEKMQKEIFLNTALPEIPRSSSRQFIDNDDPNSEMVDY

>Ppa|PPA37365

MAVFLLPSQSFQCRRHSHQSTMSTNTIFLLVFTAIYPLSAQSVGTTQSSGTTQCPDQFTSYWDGACLAFKKPDTAKDFIGAQAVCQNIKGNLVTILTKPENDFIKDKVNKTFGASAVFWLGLQCSKGELEWTEDCPMNGYANFAEPDKTICNNNDAHFFVSNALDVIWRTAEDGFVTDAIVCSYRTDQGCKQPDPHTPSADDLTTLHVNELIIISTSLVVVIVLLGAVCACFWQIGRRHRLEKRKAEDDRLKKECVEYLREANIDLNIEAGKFKFQVGKAAAAAGAADKAIERTASMRYTPFPRAEGAGKDFDEWEIDRRHVSIDYTTKLGQGAFGNVYLGIVDSSNIPTTSEKSIIEQSALRKDNNAQMQFFEEIDLMKRLGYHERLVNMIACATQSEPALLIIEYCVHGDLLNYMRERRQFMLGSPEGISSIDRSKIITQKQQLMFCVQIAYGMEYLSQRGFVHRDIAARNILVDQHSSCKIGDFGLCREVERQDEHYHSRGGRLPLKWMSPEAIERYDFSIASDVWAFGVLLFEIITLGGNPYPDWPAAEILTRLKRGRRMDRPDNCTDHMFTVMNTCWQYKPENRPNFSDLRQKMGVALEEVSEDDYYLKLNARALYYCTQKTSPSDSECPDAFMQLTPDWCFHSHFDPDQIMGFKEAQNYCSQKNAALPAITSAEVTLALIRERSPAMGLSPFDVFFIDLGCDLMNHRWTWIDGPVFNSSYTHFQETLTNPQMCSLDRPFFFDHDGKWVSTSRYAGDFPTLLVVCVVRPASYMEPAFTDAPTTDAIQSTVDTDISVTSNTFSSTADGTISKHMPNTSTASISTTCTGLWTELPGGLCYRLVTLAAPVNIHDAELSCRSFGGHLPSITSNEQSNLIEAYLAGKGKQHSRIWIGLYCQVSVDLPSETDGYRAWIDNTPYSDEYTNFIDEDDDSKFCNISQTTTFIYNGVLQGKWQKAHADTELHVLMCTREYAFFSIPPSPFRILTFDYRSMCGVRKRPGGGKNPQHVSTSSTPWATNSQTTDDNDILYFTVAPQSTTNPTTTAVELSTTSASQRGAYSLHLLIAMASVSKLNSLI

>Ppa|PPA37381

MRALLLFAVLAGSALATLVCPPKYFSIEDRCIRPYTLNANDYLDIIMDYAQAACALDGAHLPIIRSDEDNDMFTRIAQTFLQPSGTWIYLVLGVVCDDETEMTRWVDGSPIEYQGPPGSDPALFNCSLSPTMPTSMLPENQWKRLLLGDAHLFTSLCVLEEQIATTEEVVTEAPDNKCGDYERMEDGMDDDTPCFKVFTEPLSWENAQKKCEADFGSLIAISSAEENSFFWNVATTHKFTGGMHIGAHQCPDDSTTWTWIDGEIPITSNTYNNFIRSFPIAGSGKCASMVTESVAAAWVNVDCYEDELPFICQRGDFSLIPSSCPNAAPKAGEEIFSPSYPKSDISCEYFLTVSEDKLVEVEIISLISEKNVDYLEIREGTSGMKSLANLTGTLQNPTKFTTSKSNVLRVNWKPVGTTDGRGFKIRYIEVDKTDIVEPATVPVHDEETTTKSATPQGIFAVIVTLLYSLTTRFAKRLPRAAPIKAFTCERIRMRALLLVALHFVSTTALTQLSWPLNYFFFEDKCIRPFAVMADDTLLNLLPLARESCAQDGAHLPMIRSHEENESYARLVNLLTAPPKGRMIRVPLDLVCDANTTLMTWADGTSVDYVPYTSDGMKFDCTQYNHSVYTEPMYVTSTVYRWTRVELDTVMSYTSLCVHDSEVVQDVTTSSATSATTLLALLVAILRYDSSRNGAPSLHTLSSVRTMIESLSMRSVFFLFGFAAIGAATPPHLSNHSSAKILPIDSVSAASDDVQCPSGFTDYLGWCAYLFHESFMYSEAAQFCSNKGTYAPSIHSESDYNFWNLFAHINEFWFDAYCPNQGEPYAWLDKTPTNYYGPKNELGNCQMDKGMQMLPSGLHAEKLTIGAYALCSAPTATSGPTTGDDVQCASGFSNFRGWCVYQSPEKMTYPEAVDVCASMGTFAPSIHSESEYNFWNLFGYTHDYWFDAYCPSEGQPYAWLDKTPTNYLGEHNELSNCQKDWGIQMMVFGLAAFPYDFDASPLCVYEASNPPANLATTTLQTVQPTATPPATSGFTTESYCDCNVDKFGLPDGWNPSEIWLDIVIVLDISMAMGQDQLDDAEVLIESLLSDGLTDFLTTDVQAKFFTRLGVITMPDNKSGATPLPDLINIIASDGYYFMDSNNMQGLQAFCKANCFCGSPDMIVNGDSASGGCYHASLSGVPFNKAKAACSNNFHGFLATVHNEDKGRFLQKLLNSSKSDYFWIGYEKTDDGVWQWEDQSSDSYTNWDEDEPSSSSVAKCAYIDSSKTTLPWGAGNCQVGFPYVCQSIPCSAGHIDCM

>Ppa|PPA37386

MWKLLLFCAIAQVVHGACPTGFDLIGNECRGTYAKTLLGLNNVTETTKKMCSGILGQPVIIHNEEEQSYWAKRVQISPSKPGDPMLVLGLTCEGNEYRWADGSPMDYLPWNYDTMLKSYPCKSNIRFYIDSDGSWLSWGGSAYTVDVSCTTKLNQPVPSGNGCDSFEDDSEDGVCYQIFETAERWEVAQNICKKYGAKVASIHNSQENSFIRRLAVSKGALNGVFLGATISENGKDFGWVDGSNVTYENYYPGFPIPGSGNCLAMDTSKSAGQWMNIDCSTSLPVACIREQKEVTEPTCNGGLSIEGTVINSPGFPYNASTPCDYFLQVNPQQRVEVEISLEANPCCDFLVIHAGFLGGEMIANITGEQRNLTFYSTSNLMRVSWEPNSGENVRGLAVVHGACPTGFDLIGNECRGTYAKTLLGLNNVTETTKKMCSGILGQPVIIHNEEEQSYWAKRVQISPSKPGDPMLVLGLTCEGTKYRWADGSPMDYLPCNYDTMLKSYPCKSNIRFYIDSDGSWLSWGGSAYTVDVSCTTKLNQPVPSGNGCDSFEDDSEDGVCYQIFETAERWEVAQNICKKYGAKVASIHNSQENSFIRRLAVSKGALNGVFLGATISENGKDFGWVDGSNVTYENYYPGFPIPGIGNCLAMDTSKSAGQWMNIDCSTSLPVACIREQKEVTEPTCNGGLSIEGTVINSPGFPYNASTPCDYFLQVNPQQRVEVEISLEANPCCDFLVIHAGFLGGEMIANITGEQRNLTFYSTSNLMRVSWEPNSGENVRGLAMKFRGV

>Ppa|PPA37408

MRYVIFSLLILSFAHCDPCPDGFFQAPNGGDCFKTIKFYDSWANYYTPTSFEEAEEACSNWNSGGLLASIHNFDENEAIQSDAMRTCGVSYATLNIGLKCKGKDCKWDDGSPVIYTNFAGDGPSENDGESCYAIYGNQGEWIRKTCGTQKADCWICRVKARTIDCVDGEIEYKGGCVSIQTSPLDQKSAEESCPGGGHPVSIHSANENKFYVNAAVDAGITGTIYIGGQYSKEMFEWADSTLQGFMKWANGFPNPVFGSCVQILLDSEFGVQGQWTNIDCSTKQPFICYRDGAVYNPADIYPKEGPSCPFGAYYEEKGEYKIGNLYSPNFPLSLQSSQDCTYVLNTVSVTLASINFTTFDCQSGVTLELRDPGDPIDPNTPFITFNSTSPPVIGQYYSSGSKEMEIQFTTDSSPVGTGWAAKYTGIYAGDN

>Ppa|PPA38230

MKVILLLAALPVLVLSCADNYDTWLDGRCFRMNYYSSVGYSTAADQCGKDSARLPAIKSQEEQEQFFAALKQYNNFGAYSFWLALSCNGSKFVWADGSEADRLQLHFHLNRSSLLHRQRSSVAGIRRTELLLWTSPCDSYELLQTGKSTDTCYKLQQQQTTWNQAETYCKGQGAHLSVIHDQTIAFPFSDASDNYTWVDGSDIDYNNFVAGFPSDSYGNCVAMETGFLPGQWMNVDCYNTRLPYMCTKPAFYATNPQPAGCPEKMQYAPGDEIFSPAYPQAPGGTGCDYLLLEPNQNKRAEITIDFFESNTCCDSLTVYDGLFGSNILKTARKLSFEKCRDQHVYKIISTITGMNAFRIAAFLGDDRLLLEPGDYQGQFKCDQTGVECDEWRTCERIPCQV

>Ppa|PPA38315

MVFYLLAVNRMLSSKTKKARFYTYDLIYSSSSVACHEQAFSARSIRSYAWWDSPGTAMPVVSDFAAVSADCPNDFDIVHDGKCAGKVPRGRCNWADPSCMAQSCNSTDLRAFNLKPVIIHSEEEQKYWTEQATSNKNGIFLDLGSCTLPPPEYYFLIWWIEKDTGRWTAERSDGSYDVFCIGQLPPLPSHDFCDDGFVSDKMKDQCYKIGSPATDFTRAQMACDDANADLASIHSTQENSFVRQLAFSSGATNGIFLGGATDENQTEFTWTDGTAWDYDNTYAGYPKEGNGECLLMDTFSSSGKWINADCSSKLPYVCVRPETLPVCAPGPWKEGDKANNYIFILKILVSLQITSPGYPYDASTACDYILSVDTGKYVEVTIEELQANSCCDQLLLTDAKFGGALVAKLSGQIITGQPKTFISASNFMRVSWQPNGGVNVKGFKMSYRAVDTREPTTTTTTTRTPKPATQPEKTTETTSYNYSDYSETTVKSTSTSETTVKSTSTTVLPTTTSGTSFVGSALMVMPLLTICLF

>Ppa|PPA38318

MRAFLLLFSAIGSTYAIVHFSNSTLIGYYDALHYSVALDQCNYGCLIYAAGSSGFHNEYPNNTDPYLSNVFVHNTRINSNIISIAKLASQVDSARRKVPLTIQNKNEKLTIVDLNGPHDSSPGFVIYVVDLATANAIADFEVYDVADVRDAELKPQSEIVTFISADPFTLSAPASEQTNQVVVRLGGLDNALANHRDDCPIALQISDDSAFPGFSIQPNTPIISMVVTKKNRLILQPSANFMKDRDLSSDGFITSPGWNGCRNPNSGGIQSFRSPKYMPSDSYRLTAKLVEHAKFSTRRVSNVYSHPFLFFFMFVHIQLRAVHSHQCGPNLDQYHPLMIQEKGDQRIDVTGTEVVAFDFDVSDDKFVDVWYENMVGDQGFLLTHTSKSTISASTALPPASTVITADSYCNCAITNGWFDHWDPSEIWVDVVFILDTSMDDKLEEAKTLVLSTVSLLSTNTSAEFYSRVGVIAASDIFEVIYALDMNATDNLDSVKQHNIDSIDIEAAFTAATQLFGTGSDQPSYRPKAKQIVLFLTHSSPTAANCAMGGVMYVCESAPCSCSGYCGPMWRMTQGTGHWRACEAFKISTGGDFSFVTFCSGQLPPLPAYDGCGDAFAWNKETEKCYKIGTPSTDFTRAHCTDANAELASIHSSQENTFVRQLAFSSGATNGVFLGGSTDENQTEFAWADGSIWDYDNTYPGYPKAGNGGCLVMDSFSSSGRWINSECSSKLPRKSASRVLIWTMESRRHHELIITSAGYPYNASIACDYILSVDAGKYVEVTIEDLQANSCCDNLLLTDAKIGGALVAKLSGQIPPSQPKTFVSASNFMRVSWQPNGGVNVKGFRMSYRAVDTRDTPTTSTTSTTANPTTEKITTDTTTITTTMSSTSTVKPTSTVVSPTTRGTSFIGTSAIIVPTLLIICLF

>Ppa|PPA38321

MQFPIVTFLPSSLIISTMWRLLLFSALFVTVSSDCPDDFDIVHDGKCAGMVPKRSCNWADPLCMAGACNSTDLRAFNLKPVIIHSVEEQTYWTEQAISNKKGIFLGLVCNNLTNLWGWSDGSFIDYKPYNNFDKDLGSCTLPPARNCAGYCGPIWWIEKDTGRWTAAAVSADCPNDFDIVHDGKCAGKVPRGRCNWADPSCMAQSCNSTDLRAFNLKPVIIHSEEEQKYWTEQATSNKNGIFLGLICNNLTNLWGWSDGSFIDYKPYNNFDKKDTGRWTAERSDHGSYDVFCIGQLPPLPSHDFCDDGFVSDKMKDQCYKIGSPATDFTRAQMACDDANADLAPIHSTQENSFVRQLAFNSGATNGIFLGGATDENQTEFTWTDGTAWDYDNTYAGYPKEGNGECLLMDTFSSSGKWINADCSSKLPYITSPGYPYDASTACDYILSVDTGKYVEVTIEELQANSCCDQLLLTDAKFGGALVAKLSGQIITGQPKTFISASNFMRVSWQPNGGVNVKRFKMSYRAVDTRELTTTTTTTTTTLKPTAQPEKKTHPTSSSSTAVKSTSTTIEELQANSCCDQLLLTDAKFGGALVAKLSGQIITGQPKTFISASNFMRVSWQPNGGVNVKRFKMSYRAVDARELTTTTTTTTTTLKPTAQPEKKTHPTSSSSTAVKSTSTTVLPTTTSGTSFVGSALMVMPLLTTCLF

>Ppa|PPA38859

MLIIDYISGMKTLVSIALLLSTIQEVSSYVFSCEEIKSKLINSPRIENTLFACVFLEEGLDVNTPYLNNIFIQDQQDKTSYSLSSIAASPSHCIRGSGPWQVVSDKPGDLRCDLEISLLFTSDEKTEYVLAIDDDTVHRTGNGRVTFVSPRSGMKITINNIDADLTVYTGAGKGPSEFMYELKTWSVWDIPRYFASFDNVLTFDTQAKDVIYYVTAEYRNGSFHPSLVSNLGVGEKAVILTSGKSDNLMNKHPDENYVRYNLWEAATANVHGNLAFDPNFGGSVNFTVRGDFMNEEQSFTDATIDWKFYASYFEVKYLTSVKPEDVWDNEDTFVIEIEMSELPTDITPIPGIRTTPQQEEITTQEEGMTTMKPSTRPPSTLAPTIIPVAAVDNYCNCAITDGWFDNDWDPANIWVDVIIILDTSKSMGASLEEAKSVITSFVGIMSTDVTVEFYSRIGVIAVSDTVEVIYNLNMTSSDDLDNIQQHKIDKIDVGAAFQAALKMFADGTKMTSYRENARQIIYYLTNSAPGANMNGVDDFKTGGGIIIVNDYILEGEVADPGLQKLASDNFFFTDLSENYINSLGVFCEANCFCSPDLHPFNDDDNSPRTQANRGCFHPVNNGIPQQKARETCQKEGAALVSIHDAQKEFFVNGVVSIFGPKKKFWLGYQNDGTQWIWDDKSTDPYTDWDKANNQPNTNGGKNMCAYAQQGTGFNTPWTAANCGMGGVVYVCESAPCSAGNKKC

>Ppa|PPA38981

MIYFQGGVVLLLLGSLHSVNSEIEKSPVPLCGIEWSCITTDTCMGGLSSMDLTTFSTQLITGDCKMIMKIRAYSAKKYRVSLESRDPNVNKLVVNKENTVLFSCEEGLQPKYKGAHQKSINHTEKPKLLMCEFIAEEKDEQTIVRSDEQTNIAIFANDVQVAKGKEFDLYSKIKRDSYCNPEKIAYDPAIERLIIGLTDLSCLPPYYIETRLKDNAGKLEPKHIKTTSIDCVKTGDTYEYVIMRENNKMEFTETLGRCAARSCTLCDWTPEVEGIDFTIFEESDGCKKLKCKTGKLNGDSMGVATCKMTGDKSAWDLNGKTIEKDDKVTCDTKLECRSPVPFSCPNDETAILDSKNVAISCDYNTGNWTYYQEGTVVTNPDPAKLSCLSKESKGSNDTGSQTKSASGTTIGVIVGGILILIALIAGIAIYLNRRRNAQNNNIGKTTKSQEPFSIQPTSKSKKSKKEPNICMGVDMSTVPTPSVPPVSPEPYKRPPPPQQVMLNAADIPSNATTGTDGIKRKKVTPDGGTNKGGDTTGAETGPFNIDETAINKKGFRRVCLTIVSIRHLFTCHVDRSMLLLFLLALIGTVNAVCPTGYQQINGGDCFKLYTTTQNYDNAEAECVKDGAHLASVHSLNEQNALMAIMGMTTPLIGMKCMDAVAAHCTWADGSIVDFSKFPGGAPLLAYGNCVHLASTDTNWYSWNCAAVITGFLCRVPLNAPPVAECTNGYVAYNGGCAALKTTSRVQSDAEASCALEGGHLASIHTEADNTFYAQLGTNAGLTNNIYVGLAWNTAANNYKWTDDSTYNFKKFANQFPNTVFGECVYSPNFPVSIPAGQTCEWVLATAVGTKVSMQFPIFNTDAGTTLSLYNGLDDTTPTNRLSGNAINPLTAYESTTNVMKMIFTPSAAPTGTGFQANFIPTGGVIPDPQPTFDPITQCPQQQYTADTYVYSPNWPEPYPPMSDCLYYIHSRDGKKMSIEFGYVDTEQCCDIVVVYDAPDNKDESKIIAYISGQSAVTPKTYYSTGTTLTLQFFSDSNNQGEGWIATVRNL

>Ppa|PPA39269

MLFLLIFLVIDIASSDCPTNFELFGSRCYFVSSENKNYHDASSFCRSLKSHLPSITNDEEQDSLIQIRSSNVFFLGLEFDFNNGYKMCSNMDARTRFKLSDTGLWEIIWDSADIQLVCATDEDGGNIDGDDFCCWWLLYYVLPIGSSIFGCLFLSLCCIALRRRAREQHETMMEYAQKNTQLESEIQRNAEWVNERKEYLEKFNELKKDEWEVERRFVDVDWSVELGNGAFGKVYKGTLPAEKLPSKSLESVIQVSELKKNDEKIAVKMLHESADRSTVLAFLDEIELMKNIGYHERLVNLLACVTESEPRMLIVELCIKGDLLRYMTQRREYMLSHRMDEVTDYNLVITHKHQFIFAVQIASGLLREFLSHRGFVHRDIAARNILVNRNDSVKIGDFGLCRKIVEDDGMYLSRGGRMPIKWMAPEALKDYEASSASDVWSFGVLLFEIVTLGGSPYAGWNIAEILLRLERGERMERPDECTDQMHEIMQSCWKFNPRERPDFTELRMKLGKALEKVTDDNYYLQLDGRKEYYLVSNERKEKMSRFFILLTVSAILFTSAFAAENNSSDPVLTRVRRQCGCFGQVFPPFFEFSLLWFDLFQLLRDDPRFLSIHSLVFSHLNRLIPLLLIFPPPSLSLLLTMSIYLGMTAAAAAGYYAITTKMSQISPLVDPRSQTTVLPDGSRVAANICGSPKAEYLYEDARTVYEAFARGRKMSGDRPMLGMRGGTADAPTDYSWITYNEFWKNGHWLAAGLMSLGLKQSTETIIGIFSKNRPEWIITELGTFANGMVNSPLYETLGLIETIYVCKLTTMPLVIVDSPSKAQLLLKHKTDLPDLKHIVVIDAKDLKSIESIATPLKVSIHSFSSLIEKGKTMKDFKPKFPQPDDLATICFTSGTTSMPKGVMLTHKNIISDTTTLLNVSTMRMIDNDDVMMSFLPLAHMFERVMEITLFSSGGAIGYFRGDIKGLADDIKTLRPTVFPVVPRVLNKIYDKIWAEASKSTVKSMLLSSAVAFKELEMKRFVVRNDSLVDTVVFKKIRDSLGGRVRLMVTGSAPLSTTVLTFMRAALGCVLVEGYGQTECVAGATLTIAGDSNPGHVGIPVPAIQIKLEDIPDMDYKADKNGGEVCIKGATVFTGYYKNAEETGKALDGEGWLHTGDIGRWTTEGTLKIVDRKKHIFKLSQGEYVAPEKVENVYVTSKFVGQVFVHGDSLKTCVIAIVVPDAEVNFTICHSNVRYAQVLLPHAKSIGMKGTLEELCKDAKIKKMIMDDMIAEGKKAKLNSIEQVKDIFLSHELFTIENDLLTPTMKSKRPNIKKRYTKELADLYSRLE

>Ppa|PPA39287

MYLRTWIFIVQSIIVVPPLILYILELKILLITRGNEFSSPFYTLFIACGITDIIGVILCQFFYALPMASDIGDAYISSLPVWFFTAANGLLFYLPIVEDFLNIAVALNRLFSPAIYIKLPVGRDDPPVNLLYPLTLVTFPGLFFFLNTSSPYAGYVVQSLPWILIFKCLLHPILLFLTNSSIRKRITCVNQSLNSSSEIAFVLLILPLLTLSDGICDDFDVYEGLLHTICLKVYRNEKNFYDAHTFCQSQKGNIAPLTISWYISFNNFVRRTSVANNITELIHIGFMHNRTDFYFQDDKYDEVYAWTDGTKRDYEHWNLNGYPSHLIANCTAMQTGTIEGRWINVPCENELPFVCKRKPSNQ

>Ppa|PPA39558

MLRLLSVLAAVLSLAVASKCPPFYDLKDGGKCIRALNLWVKGSLDTLLPQMNDQCGKDKATLPIIKSAQDQKMFNDIVASYPDIKDKSVFLVLGMVCNPSTHRLEWADHSAINYIQPPGNVNLNFDCVADAKHVVSRTWFNDWFVVDDDATLYTYTFLCEASPSDEDIDECGDYDVMSASKDWDKPCIKIFTDALSWRDAEAKCERDGGSLSTINSDEENSYIRRSANGLGVVGGVHIGAHESPVGSGKWSWIDGNGPIDKSVYSNFVNPFPISGRWSCGGMYTDSTAAPWIDVDCDSAKLPFVCRKQRK

>Ppa|PPA39562

MRALLFLPAIVAVTTALTCPSQYQLIYGRCIRLLELSKKFVLDDKLPDYKAQCAKDGAHLPVIKNDQENQNFNDIVLSLSGNLEESYYICMDLVCSKATRKLEWADGSPVSYSRKNSVNFNFDCMSSPKTAISRELFDDWSLVSTTQLENYWTILCDYEEPITTPKPTTTTPKPTTTTPKPTTTTPKPTTTTPKPTTTTPKPTTTTPKPTTTTPKPTTTTPKPTTTTPKLTTTKLTLPPSTTTAPKPTDKPTEQCGHYSTIVNPADNKSCFKVYTDSLSWSEAQNRCSSDFGALVTINSAEENKFFWRSAVTANLLNGIHIGAHQSPDLPSTWTWIDGEVPFGGKSYDNFVGSFPIPGLGACAAMMTDSTYDQWINEDCNYDPLPFICRRIDYTNLPKSCPVDAPAAGQDIFPPGFPSSDMPCSYLLSVEANMLVELEVITLVAEQNMDFLEIHEGPVGSTLLANLTGTILSPVKFTTAKSNVLRVNWKPNGSGEGRGYRVSLLSTVAEMRALLFLAITVATAPTLPCPSQYELIEGRCIRVLELFTSFIIDDKLPGYRSECAKYGGHFPVIKNDKENQDFADILYSLNGNQWENFFLVMDLVCNNTTRRLEWADGSPVTYSRKNSVDFNFDCVTTQQTAISREIGLDDWFLVSTTELYYYYTVLCEHDSAATTTKPTTTTVKTTTPTTTTSKTTPTGQCGDYSVYTDPISWNNASQKCASEFASLITINSADENKYLWRAALSNNILEGMHIGAHESPADSSVWTWSDGEIPFNGKTYDNFMSIFPIPGGGECSSMMTGTSAAYWINEHCDENDQPFMCRRADFSALPKSCPTDVPKAGDDIYSPGIPNSDIPCGYMLFVAANKLVELEVITLVADDNKDFLELLEGTSGPHLLANLTGKILAPTKFTTTKSNVLRMNWAPGGSGSGRGFRCSNAVVMRALLFVALFGINSCLSCPQNYDLVESGECIRKLFYGSDYLDHLLPDSRAKCVKDGARLPIIKNDKENEIFNRLVNAQSIGTYLVLDLTCNYTSRRLEWIDGTVVNYIPWKSNINLNFDCYTSSQTIITRPVVNNRTSWNQAQRKCSSDFASLITINSDEENKFFVRAAVSNNILEGMHIGTHISESTSVSLDSNVWIWTDSEMPLDGNTYNNFISGSEHNNNNKTLDTNLVFPIPGGGECTSMLTGSSEAYWINENCDQNMQAYMCRRADFSTLSKICPTDAPMAGEDFYPPGFPNSNIPCAYMLFVAANKRVELEVITLVADINKDFLEILEGTSGAHLLANLTGTILTPAKFMTVTSNVLRVNWAPGGSGSGRGFRAITSNFPVFEAANQRVEMRVIVLCLAVIFTTVWAGCPAQYQLLENRCIRPLHLWANDTIIDLQPQSQRDCGKDGASLPIIKSDEDNEAFIRITNSFDDIKGWNNYLMLGLVCNGWTQQLQWQDGSAVDYSPGLSLNFDCTKNTAVSRTKFHDWKLVSVEDTWSYTVLNYVTASKRSLFTVEEDTDKIHSAAIIGSISAQSCPPNYKLSEGRCVRALYLEVQQVLNNVLPQARTECAKDGATLPIIRSDEDYTVFNNIVNSFGLKGKNPYLVLDMVCNAATRKLQWVDGSTITYTPKGSSDISFDCVNVHNTTVSMTDANYWTNIQTDSSRMDTILCVTIDQEEQCGGYTLMDDAKIPKPCYKVYSEPLPWNAAQKQCDADYGSLITINNADENKFFWRTAVTNNFIEGMHIGAHQSSADPSVWTWVDGEVPFGGKTYDNFISSFPIPGAGACASMLTESAPALWINEDCANNKQPFICRREEAVVRIFIDVRIDPVSFYLTLYNLHNPSRFSDHQEELSRFFIVNADSSVRQRWRVVIEKSQIISVTEKKDVMNRAKSQPAIADKLSSNQNMRALLLLAALAGSVTSTLVCPPRYFYIEGRCIRPYTLYIADYLELIMKYGQEACAEDGANLPIIRSDEENDWYNRIALTFLQPKGMRIYLVLGIVCDEETQMTRWVDGSPIEYYGPAGSKYPAYYNCSESTTMPTSMVPENHWERLLKSDLFYFTSLCVIEEKAEPTEEVTEEPGNRCGDYERMDDGMDEETPCYKVFTEPLSWENAQRKCASDFGSLVAINTADENAFFWNVAASYNFTGGMHIGAHQSPDDSSKWTWIDGEMPITSKTYNNFIRSFPIAGSGRCASMATESVAAVWVNVDCDGVEQSFICQRGDFSKIPSSCPNAAPKSGVEIYSPSFPKSDISCEYFLTVDADKLVEIEIISLISERNSDYLELFEGSAGKTVVANLTGSLLKPTKFTTSKFNVLRVNWKPSGSADGRGFKIRYTEVGKVDAGGATTLEHFDTTTTMSATSYGIHSLVLTALIWFALSFYCFHNNNSDMSSEILLHRRQIIREYAQAACDEDGAHLPIIKSDEDNDLLNRIALAFIEPPGPENHWELLWNGDFMHFTSLCVIEKNVEEPTEAVATEEPDRNRQGFEYWLNKLRPFPLLQSLLSVRKLSKDEIYRCGDYEMAAEGMDEETPCITFLVFLKRRCQVFTEPQSWVNAQKKCAADFGSLVAINTAEENVFFWNIAAAHNFSGGMHIGAHQSPVDSSKWTWIDGEIPITSKTYNNFIRSFPISGSGNCASMATESIAAVWVNVDCDLVKQPFVCQREDFSKIPSSCPNAAPRAGVEIISIISERNNDYLEVLEGTAGVNIIANLTGTLLKPTKFMTSSSNVLRVNWKPSGSSDEGRGFKIRYTAVAKVDVSGATTTEPFEHFDTTTKTAMSKGIFTLIVAILHSFFASAAAITEQACPPDYLFFEEKCIRPFTIMADDYLVDLLPIVRDKCALDGAHLPMIKSHEENESYNRLTDLLTAPKGKMVRLVLDLVCDDNNELLTWSDGTDVEYKPLGSDNMSYNCSNSPSTVISAPLDHRWERVALNDKWLYTSLCVYDSQEQTTTEQPSTTEETTIDPAFEKCGYYDLMENTANGDQYCLKVHSEPLSWEDAQKKCSEDSGSLLTINSIEENNFFWSTAVSNNIHGGMHIGARQYQTNPSKWMWTNGEMPISCRAYNNFIESFPIPGVGECASMATESSLALWVNQDCNEAKLPFICQKGDFAAARNVCPKQVPSAGEAFYSPGYPDSDISCEYFLFVEANKRVEIEIQSLTADVYNDYLEILEGSSGSNILANLTGTIHAPTRFKTAKSNVLRVNWISNGEGIGRGFKIRYSEVGQEASITTARPITTTSSVASHGICGLIVALLFCLPK

>Ppa|PPA39563

MWRLLFLVTILQLAHCQSTCPKGYDLVRDGECRGHAKTATITLDLGSSIAVDTCAGVQPSSKPVIIHDDEHQDYWKAFAPENTSEGFLILGIVCDKKSGRYMWADGTRIDYKPSLVGWNPGGRGSPVSADFYCTYQIAPSPPGADGCDNFADDEDDGVCYQVSPATENWQDAHMTCKKLGAELASIHNQQENNFIRRLAVSKGAVNGVFLGASVQQDGSFAWIDGSKMDYENYYPGFPKKNFGDCIGMDSSTSAGQWMNVDCNSQLPVACIRQQGSTEGPVCTGDDYAEGTIITSPGFPNTASTECDWFLTVEPDKKVQMEIILLEANSCCDTLILYDGYLGGSVIEKLSGSIQNQTYTTKTSNIMRVSWQPNGGVNVRGLAVNHLSCCVIFIQGTSTLN

>Ppa|PPA39565

MRALLFLPAIVAVTTALTCPSQYQLIYGRCIRLLELSKKFVLDDKLPDYKAQCAKDGAHLPVIKNDQENQNFNDIVLSLSGNLEESYYICMDLVCSKATRKLEWADGSPVSYSRKNSVNFNFDCMSSPKTAISRELFDDWSLVSTTQLENYWTILFDYEEPITTPKPTT

>Ppa|PPA40555

FIIASLFRSLHSRSTDHFERLSCFIRVINSFQCSPAMRILSAALLAALTCAVYGSFRGEFEPIYNTWNPSEDAILVDDFAHLTQIFHPQEHEEEIVRRKRNVDETARFAAAAPISKECNRPGYTGQYCEFPICESFNPVSDPDQFLRDEGYVIDLTDLGNCTRVHKIIVDETMYDIHIEVQSLENVSPQLTVMDSNGLIGTPDRIVQEPDRYIAVYSVLSPGAYSVQPTATSIDSRCILTTTAQTTLTISGGFQTDERDRSDFPNENAGAHQFNSILLTLHGGRAPASLKTVSVVGPDNYVLRPRVLDKRYGCQYEFYFDSLFCYERGSYALIVDGVDFYGNLFRRVAPFQCVYQPGPTTSSIAPSTPQPNNPTSCANGGVLLESEGKTSCICQDHWTGYDCSKAVCVNSGTLIAGKCFCSVGFEGVHCEQVKCEPHSNHGFGVDRPTLVFVIRARVQQKEILQQVQEAIDEVIANLQFDPKYLSRFHLVLFNDHEVFRSKSYESIQKFDSDLFSYGVNSRDSDGDCNDNVMEALATAFTDASLTQGSTVYVITDAMADDETKYAESILQMNSYWRAAINFIYIQPAPEMECTGDLSDPGFRAFDDIANRFGGLAWNIQDRTKVKYVLYGHMNSILYKSQLMLTVDRDECNKGLGKVIQLEQNTETIVFVSRGRDFHLEMTAPDGTKVKPRMIVQEGIFTVTQWSSPLPGTYMIKTTSDTPSASCNLRAYQSSFHTLSPDPQTETYWAITTDADTDAMMYQPLAGTDNHPVGTTIYAWFNDKFKVFHIEDFGDDVDHSFAFLNMYAVRNGIETEVAILARNRMIKLLQVYASNGLYRGGCAFQFYFPSFRCRPNENLHYEFNLRNDYGFYIQRAGVMTCFNYIPTPAAPTDCRNGGVKYNNETCLCQSHYEGEHCENLICENGGTMVFGSCQCPSGWTGAFCEYPQCPTSGPIPSYGYHADMAFLVEVSEKGIEQINQMMNTLPDIIRDVGSQHTDWIDRLVLIGYNSDGVVGMVDTPMTNPKKFFDTLFEWSNSNPGFETCHVQIWNALDTLLNDRKDGDKKRVLPDRSIVNIITATMPYKKDDVAPLITSTSEELLERKAITNVFVYKNWNAAAVGDIQCGGKESDFDCLNQIARRGDGVMYFLGNGDLARAIRMIPTLFSSSIVYKFHSDDCSTAAQRVVYFPVDAYTQTITAVVSGEGATVSLMKKEGYYYTTFPDDGRVSILEDPRNVVIEFRNPCENDWAPISQSCAYYDYALSKTFQEASDLCESMGGFMVDDLNGDKTYWIGSVLNNKRGWLGLIFLNGQWMWQQDNGNYMPVPPNTAQWTGRETPDGTTGTCAYFYMNIWYPSTCDENYSVICQKHMFNRNNQPSNLDDDDISPGKYYFLVQTSSGAANKGCDVEVRVQSDLNVEYGFVDDLRKDKPHPIANVDSNNNLIVSTVSLGKAQTQSSVLQYVQLRSDDSSSTLLEAATNSLRAGCSFNYFSQPLNCGLTDGKDFSVVMIGEDDTGNTFQRYSTSLCSKWYVCQNGGVYSNGQCLCADYFTGESETNARGRCVRTEVASHPMELALAHSDSLDQLASSCDAYSGATFSNEGKAIVLVIELSENTADAIDKMSTYIGPTIQLMNERHNEWIEKFMVQTFTLDGTDGELRSFNSAYEMETYIIQLVDKARPLPGACQMPIWKALDNLFDSPLAQYLPGSEVLIIAAGVPMDADLAAIHATMEKFDIQTPVVDYLHIETTTCPIDDWSKDLRDFANFLSSTSGVVFRTSHSLIGMAFSALLPSRCAPQRLSYSDPLNCKNNDIFVQVSCSFPSDN

>Ppa|PPA41436

MAIPLRSLFLILVGLHSAAAYTYSCNALKNLPLSQHFDPSLIQACVILQEGYSDYDVLENVFLFDGAVATSFATIARAPGGCLTLLLSFDPLYVIHPRKGVLEYTIKGINTFVVPQTGMKLLKQGCNGSGHINVSTGAGINLYENRYPYHSWTCDTMPDTLVFFDTVITIEIVGDAVYTVKTSSDLATPIPTSTGDSIFVYTSGKSNDQQNMMGYDHRAKFELDDNPDLYDVKVNMDLTFDNMNSMVGFHSFDYTYEYYHGTSKDEFRTDYFEILYQPVGLKPEQIATSGDVVVVELKISGDAPAKTTGGTRTTGRAPTATTAKRTVQTTQKPVPTTTVPRTTPTASTAATAQSTAKTAAPATTTSKPKPVGQDSYCNCAVDKFGFPDGWNFNEIWLDIVVILDTSEAMGENGLLEAGAMIESFISDGVNDFLVTDPTAQFYTRVGVISMSDKAEVLYDLNMTKADSIQGKASIKKGVKEINIVDAFDAALNMFTGGYKDEPNRVGTRPVIYYMTSSNPGSNLLPLNQFKASQGIIIVDNFLEEGQVELPRLKELASDGYYYANSDYLEGLQAFCKANCFCQGNKDTLGGFDPAVAASGGCYHPSPSGVPFNKAKSTCVNEGGIIATVHDDDKGRYLQQLMAKVSTKSSFYWIGYEKSSDGSFQWEDESNNPYTNWDVDEPSTADVAKCTYVDSTSLAWGAGNCQLGFPYVCQYTPCSVGNKLMRSLFLLLLGLYNIDAYTYSCNELKYHVLGLGPFDATLINACVIPQEGYSDYDVLEKVFLDDGKVKKSFADIARSPGSCVSRPYDESVQWRLSGSLSCAKEVALILTYSPVAVLVPHKEATGYVISGSRAFVVPQTGMRLLKQSCTGTGHVNVSTGAGVNYHENHVYYHSWDCATMAETLVTFDTVITIDTDGSAVYTVAASSDLDTAIPTCPGDSMFIFTSGLSNDQQNMMGYDHRAKFKLEQGPGLNDVTVSLNLNFDNMDSMVGFHSADYTYEYHHGKHTDEYQTNYFEVLYQPSTLKPDQIGMSKDYVVVEVTIAGGASTATTATPAKTTQRPISTTAVPQTTTRRASTAAAKTIAPFGFPDGWNFNDIWLDIVVILDTSEAMGENGLLEAGTLIESFTSDGVDEFLVTDPTAQFYTRVGVISIAFDAALNMFTGGYKDEPNRVGTRPVIYYMTSSNPGSNLLPLDQFKASQGIIIVDNFLEEGQVELPRLKDLASDGYYFANSDYMEGLQAFCKANCFCHGNKDTLGGSDPAIEASGGCYHPTPSGVPFNKAKSTCMNEGGIMATVHDDNKGRYLQQLMVKVSTKSSFYWIGYERSSDGVFQWEDQSTNPYTNWDVDEPSTADVAKCAYVDSTSPNLAWGAGNCQIGFPYVCQYTPCSIREQESTLRSDDLRQVLPMAILERSLLLLLLGLHSTAANTYSCNELDYHAFGTPFDASLINACVVPQEGFADLAVLENVFLDDGKTRTSFAKIALSPGGCVSRVYDENVKWQLTGILTCAQEIALTMSFGPQTIIHLRKEVVEYSISGTRTLVVPQTGMKLMKKSCIGIGNVNVSTGAGVNENENRYPYHSWTCAAMPETLVFFDTVITIETDGDVVYTVEASSDLNTPIPSSAGDSIFIFTSGLSNDQQNMRGYNHRAKFQMLDESQHYVTVDMNLIFDNMDSMVGFKAYDFLYEYYHGRSTDKYLTDYFEVLYQPVGLKADQIGTSKDNVVIELHVATDAFTAAATRSTAKTVVPITATSNPTPVGQDPYCNCAVDKFGFPDGWNFDDIWLDIVFILDTSEAMSESKLQEAGTLIESFISDGVDDYLVTDPTKQFYARVGVLYDLNMTKADSIRGKATIKKGLKEINIVDAFDAAMNMFTSGYNKQPSRIGTRPVIYYMTPIRALSLLCNFLEKGQVELPLLKELASDGYYFANTDSMEGLQAFCKANCFCDNYNKEPLGGSDPAIVASGGCYHAVPSGVHFNNAKETCMIEGGFIATVHDDEKGRYLQQLMAKESSKSSFYWIGYQKSSDGVFEWEDKSTNPYTNWDIDEPSKAVVAKCAYVDATSPNLAWGAGNCQLGFPYVCQYAPCSIYRGLNGGLYLVYVSIGVAFCLIAIHTLRGLLKEKSFSSVSLFKQQRYLAIYTLASTASHTIFALTQFLWAYSFIVSDWELLTFVRNTGPFIYDLTTFTDPIVLFALSKQFFDATFAETLTYACVVAQESIVSFPTLFSQLCDLTAKLNNGTITHVFITRELRSATPNTSHGGQTGQRRRHRADARVLCGEDVVVCAVADVRRPGFGH

>Ppa|PPA41601

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>Ppa|PPA41686

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>Ppa|PPA41737

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>Ppa|PPA41745

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>Ppa|PPA41784

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>Ppa|PPA42695

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>Ppa|PPA42904

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>Ppa|PPA43102

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>Ppa|PPA43371

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>Ppa|PPA43391

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>Ppa|PPA44465

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>Ppa|PPA45693

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>Ppa|PPA46827

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>Sca|L596\_007052

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>Sca|L596\_008210.2

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>Sca|L596\_009840

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>Sca|L596\_010017

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>Sca|L596\_010190

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>Sca|L596\_010198

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>Sca|L596\_010319

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>Sca|L596\_010491

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>Sca|L596\_010509

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>Sca|L596\_010510

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>Sca|L596\_010511

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>Sca|L596\_010512

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>Sca|L596\_010515

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>Sca|L596\_010521

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>Sca|L596\_010522

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>Sca|L596\_010524

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>Sca|L596\_010526.3

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>Sca|L596\_010527

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>Sca|L596\_010595

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>Sca|L596\_010596

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>Sca|L596\_010609

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>Sca|L596\_010888

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>Sca|L596\_011877

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>Sca|L596\_011894

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>Sca|L596\_011895

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>Sca|L596\_012795

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>Sca|L596\_013844

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>Sca|L596\_014117

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>Sca|L596\_014167

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>Sca|L596\_015285

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>Sca|L596\_015286

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>Sca|L596\_015289.1

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>Sca|L596\_015289.2

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>Sca|L596\_015290

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>Sca|L596\_015291

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>Sca|L596\_015292.2

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>Sca|L596\_015295

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>Sca|L596\_015296

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>Sca|L596\_015300

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>Sca|L596\_015301

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>Sca|L596\_015302

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>Sca|L596\_015303

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>Sca|L596\_016111

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>Sca|L596\_016112

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>Sca|L596\_016113

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>Sca|L596\_016442

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>Sca|L596\_016446

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>Sca|L596\_016827

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>Sca|L596\_016891

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>Sca|L596\_016895

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>Sca|L596\_016897

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>Sca|L596\_016903

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>Sca|L596\_016910

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>Sca|L596\_016912

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>Sca|L596\_016913

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>Sca|L596\_016914

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>Sca|L596\_016915

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>Sca|L596\_016987

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>Sca|L596\_017901

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>Sca|L596\_019082

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>Sca|L596\_019168

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>Sca|L596\_019755

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>Sca|L596\_019884.1

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>Sca|L596\_021100

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>Sca|L596\_021209

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>Sca|L596\_022888

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>Sca|L596\_023329.1

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>Sca|L596\_023712

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>Sca|L596\_023713.1

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>Sca|L596\_023939

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>Sca|L596\_024101

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>Sca|L596\_024183

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>Sca|L596\_021507.1

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>Sca|L596\_022433

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>Sca|L596\_022717

MTTILILILLLATFAASHERVCPPGAVTSQDRFKCFFIVPVSTIFGYALRTCQNMNYRFASIDNDVDNDRVSETAYAMFRNMPGKHKSFWIGGVTASTKLCTGTMEITLTTRTGIQETFLIHISVFWWIAGLGIGVLWTALNERLMFVKRILKGFTTPPICPTCPSCTSSPQTCPPPTECTPCPSTVPLTSTLMTTSHPSTISTVSCTVTRSTETTRQPCSTTVSPASTSQSTSQPANSTQPASTSTQIPTTTIPPGWKQFNNSLYYFNPNATSWGAAEKWCQTQNAHLTSILSKKEDDFIGTICFGVCWIGAHSQGRKPAFKWSDSSRMSFTHWQVGQPKTYKGSFNCAWYQFNGWFAYSCAQSYPFVCKKPYNH

>Sca|L596\_022722

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>Sca|L596\_022723

MFWQGLLFLVFLATLDVSTAENWETPTFKYYFHTESKETWDKAEQICEDMGGFLVIISNALEDKYVLNKCGNTCWLGGRIKKGTDEQSRRNEKLFKWIDNSSMEYTNWKKDEPINNGRKYECMRMDKNGWSTSKCDRKYHFACKKLA

>Sca|L596\_022724

MLHLRFQVCTVYEDKVTGHRYRWYNVHNEYEIAFVCKKSGEKPKTEWWYKLMGQFLKMPWLRQACGLFAFSMVSVFASQIPQNQQISFLTWKRYGNFLYHFSKIWSNWHAAEEYCVARGAHLVSIQSSKEQHFVADNCSITCWIGGKSQKKNKVFNWVDSTKMAYTAWTDGHPWNEKPISTCIQTVKSEGGKWIETKCHRFSQFVCKKAV

>Sca|L596\_022726

MTWRHVVVALMSVSVFAASQAQQVHKQPQVKGAASQRMASVQTQELPVVTWKKTGNSLYYFSNDKKTWQDAEDFCVAHEAHLASIHNSQENEFVKKNINSETYWIGGKAQENGVFTWVDSTKMKFTSWFVETKRHSFSTFRCVSTHRKGKILLNNFQVDTLGTKWFIAKCNQEQRFVCKKSVQLGASHVKDLPTQRKASVKMPQIQRTEAMVWNKHGSSLYFFSKNKKTWKSAEEFCVAHGSHLTSIHNARENDFLNKNCGSCWIGGESKQKDVVFTWVDSSKMSYTNWFNGSPWKLGETNNCIGISGGKWLPTNCFSEAGFACKKTAQAQSSYKMIITPN

>Sca|L596\_022727.1

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>Sca|L596\_022728

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>Sca|L596\_022729

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>Sca|L596\_022730

MHLLFCLTLILLTHLTHASASPAPFIWVPFGDHFYVHVSLSTFKDEAEEWCAEQSGQLTSIMSKEENNFIGSICIGQCMTGGFSPFHNQTYVWEDYTPMVYTKWKEDMPENSNNRYCVVFTRKGWVSYQCMKPLPFICKKPLGV

>Sca|L596\_022731

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>Sca|L596\_022734

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>Sca|L596\_022735

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>Sca|L596\_024667

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>Sca|L596\_024903

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>Sca|L596\_025307

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>Sca|L596\_025308.1

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>Sca|L596\_025446

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>Sca|L596\_026181

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>Sca|L596\_026184.2

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>Sca|L596\_026242

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>Sca|L596\_026243

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>Sca|L596\_026494

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>Sca|L596\_027130

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>Sca|L596\_027679

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>Sca|L596\_028092

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>Sca|L596\_028397

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>Sca|L596\_028413

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>Sca|L596\_028935

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>Sca|L596\_029687

MDRRRRFLILLLFLLGSALGQLGKPSSCPQGTMTSYHRNKCFRVVPIAVSFEHAEITCHNFQSRLATVYNKYDNQIINNAASLITQNMFLKTKEFWLGGRDDIADNEGTWEWINAEENSRMNYTNWAKNEPSKNGLNCLQIHAHSGKWKAGNCYKPYPYVCESDLAMNTTKAPTTCPRKLKTTSEIQ

>Sca|L596\_029688.2

MTTASTLPSTASSTSKVPKSTTTSEKVTTTSTLPSTASSTSKVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTALCHQLLAPPRSPENNHNFGEVPKTTTTSEKVTTTSTLPSTASSTSKVPKTTTTSEKVTTTSTLPSTASSTSKVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPEIYYDFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPENYHNFGEGDYHEHSAINASSTSEVPKTTTTSEKVTTTALCHQLLAPPRKSRKLPQLRRSPENYYNFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTLAPPRKSRKLPQLRRSPENYTTSEKVTTTSTLPSTSSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTQLRRSPENYYNFGEGDYHEHSAINASSTSEVPKTTTLRRSPENYTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTALCHQQLAPPRKSRNYYNFGEEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTLAPPRKSRKLHDFGEEGDYHEHSAINASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTLAPPRKSRKLPQLRRSPENYYTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTLAPPRKSRKLPQLRRSPENYHNFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTLRRSSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLHNFGEAPPRKSRKLHTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTLRRSSTSEVPKTTTNFGEGDYHEHSAINASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTRLRRSPENYTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTHFGEAPPRKSRNYHTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLLRLRRSPENYHNFGEGDYHSTLPSTASSTSEVPKLHTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTQLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKTTQLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTNFGEEGDYHEHSAINASSTSEVPKTTTTRSEKVTTTALCHQQLAPPRKSRKLHTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLLRLRRSPENYTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLPQLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKLHLGSPENYYDFGEGDYHEHSAINASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTQLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTRLRRSPENYTTSEKVTTTSTLPSTASSTSEVPKLLRLRRSPENYTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPENYHNFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTLAPPRKSRKLPQLRRSPENYHNFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTLAPPRKSRKLPQLRRSPENYHNFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTHFGEEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTDTLPSTASSTSEVPKLHTSEKSRNYHNFGEGDYHSTLPSTASSTSEVPKLHTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTALCHQLLAPPRKSRKLHNFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTALCHQQLAPPRKSRKLPQLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLPQLRRSPENYTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLHTSEKSRNLLHFGEGDYHSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKLLRLRRSPETTTTSEKVTTTALCHQLLAPPRKSRKLPQLRRSPENYYDFGEGDYHSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKLLRLRRSPENYYDFGEGDYHEHSAINASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKSRNYYDFGEGDYHEHSAINASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTALCHQQLAPPRKSRNYYDFGEVPKSTTTSEKVTTTALCHQQLAPPRKSRNYYDFGEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPETTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTALCHQQLAPPRKSRNYYDFGEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKLHLGSPEIYYDFGEGDYHKHSAINASSTSEVPKTTTTSEKVTTTALCHQQLAPPRKSRNYYDFGEGDYHSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTALCHQQLAPPRKSRKLLRLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTALCHQLLAPPRKSRKLPQLRRSPEIYYDFGEGDYHSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTALCHQLLAPPRKSRKLPQLRRSPETTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKLHLGSPEIYYDFGEGDYHSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTSTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTRKSRNLLRLRRSSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKSTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSEKVTTTSTLPSTASSTSEVPKTTTTSKEHTTTSTLPSVTATLKSTTSVTVRPTNPPPPGWERWDENYYHYNKTPMPFLGAERYCAKEGGHLVSIHSQAEQAFLVKLVTKKHVNIPPTGIRAWTGGFAQVFTLDFAWTDGTPWNFQNWFSGYPQGDGFAVSVCVRMTIMSPTNTKWLTMDCGYYGPVICKKPIYSRMTSSLFERMKKKSQNPFSDAQT

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MLVRFRSKLIFRIESMIDNAAQFIEDVTHQHMNWINHYTIVSFTDKGYFPTCDSDDPNDFINGLKLLKTLTQQSGTSCNNLDILPMMYNAMQERYFTEGGLLFVFLNGVWKTELATYGDVLEISQVSKNPISFFQFSPTAPCGLQSSDNTLKLMQSLAIQTGGEYVQVQQKDAGSVLLSIASLYSSQLIYEAHQDDCSKALVNFYFPTESQTQSISVTFAGSLNGPPTYVKPSGDGKGALNNINVWNNYGISRQDLIIKACENDDWDSNGKQCYLTSTVPLTWIEAQQVCHQNKAVLTSILSKDTQDYLDSVDAHTDYWIGLNDKVKDGDWRWDTLGEYPAKLSGWTNWAPKQPSNSDTERCVFQQGSSSRKWVAADCGQKKPFVCVKHAYDFNYQPHDVTKVHLPRGMWKASVQTFNGPCAIQVRAQSGIRLYTVYTTDVHDDYGMPELADGKKVKNYIAAKVTGLESANPQMPLGNLDFAQMFYNDNMQMVLAEPFKRRSKCAYDYISHDFPCPAASFQITVSGIDSIGFPFQRIIPAMCFPRNTAKQCDNGGVWDKTRAECVCVPGFFGDKCEFAICAPHGNIGAGLSDCICDVGWTGSHCELPMCPGNQTETEDPFLQDTRKSFMVIMDGCNSGVQGDVISKFPDIINAVIAKASDLQDAWFTSFIGIVFRTTASKVPVSPIIKASNVSMFIKRMQDELNINKDTCEMTTDRQMMLALTDIMNEPTVALTPRSQAFLITNGVAGDYAQARPAMDAIAVSHTAVSIISTVGKTMPLASLSDPKIASMTSVAHDSGGAFYQIPDEPTLKKLLTADIGTLFESYHLSSLARKECSGLQEYVQVGGDTKMLVFDIFAQKTPVIHLYDPLNNKVDVTQVVSTATNSFFTVKNEKLPPGLWRVGIDNSDKNMGYCEVNIRGHSEEEIFLAFTQDTGNDNGYTSNIVNYFPQHGFDNAVIAATSFGTMTYAQILTNDERRLLWAAPMIKRSNCAYDYISKCNRVLIALVLTTSQTQNRQLIPAVTPHEFLQRSSNLMIDVPLSAVGFLLPYREKRERRFPLH

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MKTTVLLLMGLAATSLAACPPDSKTDFLGAEQLCKIFGGNLASIGNAADNAIIENGAKEYFRGEQVGEFWVGGDKAEDFKTWKWTDKSGFVYTNWYSGELDIFEHNCVSVERSSGKWIPNPCCDLKPYVCEVPNTSTGTTLPPPTCPPIPTCPPIPTCPVVTCPPPVTCPPTVTCPPKPTCPACPSAEPCPTTKPPLSTTPPPTEPPTLSHYEASSYTHSYHKASSDRASNAFSHHQGSHASSHNDSSQAHESPESQV

>Sca|L596\_030158

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MRTTSLLAFVAVLAPLAWAQLCPNNAVSSADNSKCFQFLALKSNFLAAEQTCRALGGHLASVYNAADVDIVNRGAQQFFKGPGRELYWVGGTNMNTNFEIWQWTDGEPFRYRNWAKPEDNNPLLFNKNCVAVERSNGTWVPDQCCLLKPFVCEAPVIVPPTCPRKFKFKKPNKLRILSLGDFV

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>Cel|clec-51

MQLQTGTAKWQTTNCTAQLPFICSYSSSVTPTCPSVTIPSHCPSGYTWYDETDFCYKNTVRFTSFNDARSSCQADGGDLASIHSANENQFLVDLSKAGITNKDKSHSDDVFIGLVYQNSKWQWTDGSAVNFLNWGDGEPNNMDKEWWTSLVADPHEDKNTENTRWNNVAQIDMRAFICKKAPLH

>Cel|clec-52

MFRSLLLVFCFSAPLISAQCGPGALYQQSSSRCLTLFRAAVDFQTAESICATLNGHLVSVHNAIDNTFVSGQAQKFIDGGAWLGAQASAPDVTNPLNWYWTDGTDFNYQNYKVGQPTQTGSTACMQLETGTSKWQTANCTTKLPFICSASASAMPTFPAVTIPSHCPSGYTWFELTDFCYKNTVQYTNFNDARSACQADGGDLASIHSLAENTFLVGFSKAGCTNKDKDWTGDVFIGLVFQNSKWQWTDGSVVDYVNWGDGEPNNMNKEWWTSLVADPHQGKYSEASRWNNVPQDDQRAFLCKIAPLH

>Cel|clec-225

MNSLRKANFFWAFSVIGVFLAESACPVGFDLVNLKCIAITSHLLSQHKAETTCKDMNAHLIFIQTAIDNTAVLNYASNITSPMWIGATCKVSEEPTKCMWDDGSYLSYSNFLPGYPVTNIGTCVYLDSPNQPLKGRWISATCDLAEYHAICEVNK

>Cel|clec-41

MWFHSTLLLAILVAVSADTCPAGFTALSTSKKCVKLITDVAKHSDATANCSSYGGHLISVQNAIDNNAYLQLAAVSVTPYWLGIKCSLSGNPASCQWDDQSGNAGGYNGFAPGYPLVEVGNCVYVPTSGSFAGKWLSGDCNTMSLNFICETAPTSPITDTCSFQYNGNCYYPSLSALPKQDAQFSCQQACGNLVSIHSIEENNYVQSLFTTNAPTYIRIGAVANNQNSNSWIDGTSWNYDNIGYSNINLGMCWSMALSNDIVSTGKWISSYCDTSLPFVCKRKVGTQCGTTSGPTQTPGQCTSPMFMDNSGRFYSPSWPYSYIGEQNPCNYILDTPVGSLVQIRFPVMNLDSQASISIYSRIEDTTPLVVLQGNSASNQWYTSTTNTMKVVFRPCIANCPNDGVNYRWEADFKPSTDVTQPPVTVTPNPNNPSGCNSTILVAPGSISTPNYPNYYPNFLLCMYHLSTTGGYRINLDFGAIDTEQCCDIIEVHDGPLLGSPKLGIVSGTWPAHAKTYQSSSNSMLVTFSTDSSGQGSGFSANFWAL

>Cel|clec-117

MLKALLPLLLWISTGSTAPAGVATYLRSNGIVAFHKLYHLKMNFPRAKKHCEQNGAHLAGITSREEAQKLIDLANEAGESNEQYWLGGQRKGECYGMRNYDKDHGLNATCSLSNVVQWLDNVAETIDPDWWKIPGPSHIPFNMPQQCLSFVHGDRDWTTPNDPGFLDDIGCDVPRKFFCTELHEW

>Cel|clec-2

MLFYFLLSLLQLTSASLPSVCTDGFTLVNGKCLMMFKDESNHDDAESFCRLFRGTLFDVKNAIDNRAVASFIGSQVETVWMGLFCFNNNLCLWDDNSGSTAAYDNFSGGYPEVTIGSCVYYATQGTLAGKWISADCTDRRSFVCETPTTHEDSCYYNYNNYCYTFHRDLYSFTTAQTICEEECGNLVSIHSANENRYVMTIASHTTQANVLIGGMWPMDHVNTWVDGTMWDYSNIDSGYDPTNHCIAMANNATSEYNLGQWFGVDCKDYYSFVCKRPAGVPCSTDQPKVTVTPVPSNESFCNSTVLMTPGIITSPNYPQNYDNNVYCSYKLSTLGSYNILLEFTSFSTEENVDLVTVYDGESTNGLKIGTYSGSREPFHLISKGNNFFLAFSTDSRNVFKGFSASFVAYST

>Cel|clec-223

MPKLLVLFILSLYISPVESNFYKNYNKQYKPIYNYPPPPNVYYPPDYIYEDYSPEDDYYQGPPGPPGLEGPPGPNGPPGPDGPPGPPGPPAEKSTSTTTVSPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTESTAAPSTSTETPTTKTTIGSTSTISQSCIETECDDGWIKTLRGNNPQKTLCMKLFSHDTSSYDDASMYCYDSHQAFLTGPDSNDEYDKIMEQALNISDQVSDSQSMILIGLKRTTECTTDSGEQDQNSICRRPKGFIWQDGLGETSNTLINQHFNDDPGVETSPDHVRACTGIIIVKGATNNKNVYSLDCSNGEKSSGEKSKMVVCGKLGKCPATTPSTISTTSGASSSTASVSSTILSSTATTMVTSTPTTEKSSTTTTSTPTSEATSTTTAMITTTSGTTENPTTTDCPTKVCRYGFHPTIRNGKVWCIRVFFHFVLNYQDGSDYCWNYFHSTLSGPADENEYNVLLDQTKTDPSLVQSLTKYTKVFMVLGAQRTPACLYESSSAQCEKPSGYQWLDNVTDTTYAFTKFNEDQPDTSPEQPEGCVGVLVYTDPTKRDKELVWSLSCNDAQSAHQVVLKLVVCGHEGVCPEESTIPPPSTQSTTTMKSTTTATTSMSTTKKVCAKSDLKCANGWTSFNRTSTNPFCFKVISSYNQSYEQSEALCAASGGYLSGVENITEYQFAVELAKAAVDYSTSFNEKILVTIALKRKVICLQTDSTESCITFKAYEFVDDKTKYVAILQHYSLWADNQPVIISDQPHGCVGIMVTQSTSTSGDSKLFSTRCETGTQTYGMSNAAYCARVPDVCPP

>Cel|clec-222

MIYRIVFFVVLFPALMECYRSHHSDDIVYYPDSYESEIRYIPGPPGKPGPPGRAGNYGQPGSQGPIGPPGSSSCNYECPPGYYSTSRNNAGIEHAWCIKMRSTAKTFNSNLFVNLDIECKKEGDVLTGFQNYTEFKAVYDKFKSSLSSVINVNKMPMILIGARRKDECTKIRQPECTSINGNQWTDGVTNGKNFFESPGFFAQQQPSPGSGTKMCFGIWTATKKLYSYKCTESDTNKPAKLIMCGKPAPCVF

>Cel|clec-10

MQAIAALLLIWLANVAISSNTPVCKNGFTLINNKCLRLFYEEVIHRDAELSCRNYGATLVTVKNAQDNQDVATIAGSAKLIWLGLSCFEDSFGKCFWDDASGSANSYNSFSGGYPNVQVGQCVYYSTQGVLAGKWISEDCERYRMPYICELPTTYQDSCSYNYNGYCYTFSSTAVPFVTAQKICELSCGNLVSIHSPNELQYIVNFAPFVDDGYFIGATWKNNYSLSWLDDSPWDYDRIDPSFSVKVGYCFTIYTGVGSKITGSWYSVDNWEIPNQYICKIPAGVPCSPAPPVTPTPNLSNCNGPRMMYSGVFTSPNYPNNYDNNEDCTYLISTLGPYGIFLFIAPFSTEHKYDVVTIYDGPTTSHKVLAHLSGEIGISMMTSSGNSLLVTFKSDKTNTFSGFSARFYSTRLIND

>Cel|clec-147

MLRGTFILLISSLLAVEAFIRPSYYGGGGGYDEDCDCDTSSTVVVPTSTPTTTTEGPTTTLKLTTICLEGWTKYPRTPSASNNNQDAYCLKFISSNTTITINNASQICQQAGGHLTAFENEIERQAIMAEAGDHITKTIKSTIGAIALAGDRIKQCSTKNSTIIENPPCNDKTKVFTLPLTAQTNPEYLWTTWAQGEPSANWWEYDIEDCLQMFINPSNNTGASGRINDFYCNRLVAPNEPDNIRYMMYGALCGRDVEMEAAG

>Cel|clec-89

MTLFHFISFFLTSLFSTTVGLSIPPTTFPNCPKSWHHDEPGRTCYHLARRRMRLTEAHSYCQKMIADGSAHVLRVECGGENDFISGLVKGHSEKVWIDARARFDIVDGAAGLFGPGFVYRWPNGKIVRYSNWANGNGLEEVGSSNSNKCINIKSDGHWMNANCSSTAAVICEKKLHRPYSKHCPKHWVYNKETQACYRTISKTNMTILEADNKCFDYGFEHRQDAMLTSIESESENQFVMNLAKEKDANFEFIYLGGYGRSRNGNKWHWMDGSEFNYMNWDRGMPFGRRALAVLVMNKRGKWINHYADKILSQYNAVAVCKFKS

>Cel|clec-48

MIRLTLLLFGLLGAATAQNCNTGGIYNSQFNRCYQYFTAPAQFSFAEQQCNLLGGHLASVQNGQENALLQSNAANSFKKSNYSDYWIGANDLETSGTWKWTDPSVTFDYSNWQLGEPQSGSDCAIQDKGDGTWSAIGCTSYRPYLCVTPVIMTATCPPITTPIPTTCPTPAPCPIKQCVPSCDQGWTYFSPTDFCYRVYHGEKFNDAEASCVLLGGHLASIHSLAENTFVNNIASCGIKEGKYEHLAWIGMHKVGQDWVWTDGTPSDYFNWAPKQPDNPKKEFCVQTAPDLSHDKWYENWNNLECNEVMRAYICKKASIHN

>Cel|clec-135

MKRWILCSVLLCFCIVNVKAVFNIDNDESCESEEQEKQKVKCPKHYKGYFRAPTATNNMTKMWCLRVVTVNVSVSEAAAQEACNREGSVLSTFACYDEQKHIVRHASKYFRRNNITQGAIWLDGVRIEKCRTLNVTQQIAAPCNDKTKVFDITDPRTDPKYAWTQWYRTAPSWAYWPLRAEEYSTYCDMAVPPYSFEKELSTNYGYVCGRPPVLSFY

>Cel|clec-124

MLRILVLAATFAVLVSAIDFGGSSSESCEDDGHGHGHGNGNGNGGANRGCDAGWKRFNRPAGGWCMRSFGGILSRDSAEAQCQTLGATLSGFQSFAEAQWVSTSAVSVIKRPSGYLWIGARPSGYLWIGARSPLPSSGLMPSRREPPVSTGTISNLTTRILINHAPLSWPPTHQSTSRAISSSRR

>Cel|clec-266

MSRIFKLVLLVAAVGFVSTRFAQVKLFNWSYKDFGTNAFTDISLDQRQHYHDFPTGTCPDGWVRFSDSCYWIEQHKQSFAEAEKRCYEKNATLFVVNSQDEWDAVREHFPQTGYTWIGLVRFTHFEKSQDAPIWQTEGAVNPTRLNWLIRPYKPVSNGWSALANCAAHFSAAINWDASAYTYFQPCSFKFYSICERNGTILDFLNRKFDFQD

>Cel|clec-185

MPDMVFRIILVVSCFTSFSCKPKVKIQHDHIEEFLENKTLSDVIELNQHVQRARYLERLENEKGKLSDEGQQNLVLADGAVLPCDATWHQYSGTGCCYRTTDEKSEWYGGTELCRALHPQAQLASFHSQGESEFVCKKYSSIHAWTGLSQTETPGVWTYTDGTPDWHWFFAQSSTMTTEKSCVEMMDGVLVLLFSWSAKKGQTQPYSCTESIASICKYCPQETTSTSTSTSTTTTTIPITSTVTTTVTTTSEPPTTVTSTTSTTESTSTVTTTIPTTTTTTTVSTTVPTTKTTTETETSIKPTETTVIITTPSTTTVTTTVPTTTVTSTSSETTTTTRTTVTSTPATTPSIAASTKAPTTQKSTPTTTITTSTVKTTVPGTCTPTCPTPTVSFNDRCYKMCRGLVKFEDSCTWCNGTMVTVSSKEENSFVSRVFGSNDETTRQIWIGNTESSGYLNWSPGQPTKPNDGLDYCISMDLSAGSTRGKYKYLACQSTVINSLCVMNP

>Cel|clec-231

MHWRLTVLFFASAQLSEGCLPMVPPEEPVTPVPVCPAGWFQFQRATGLWCYIFATPGAGWTTPQAACQANYGANLNGFESAAERTQFIQDMLASNLAPYTFVHIGAMRQCAPCTVNDPFVWLNGVSNDNTFANDYDSLYDLTGDCLSMDLGNNGQYNDITCDAETAYSCGKPAA

>Cel|clec-230

MYTIIIIFAFFCMFSVEGCIPMTPPEEPVVVPVPVCPAGWFSFQRATGLWCYIIAKPPAAGWTSPQQYCQDNQMGSFVNGFESAAERTQFLQDALAANLAPSQFLHIGAIRSCAAPPCATTDPYVWQNGVSNDNNFANDYIQLYDGSGQCLSMDLAKNGEYNDITCDALTAYSCGKYAA

>Cel|clec-199

MNRFFCLTVLFSYLYRFTFSANDNAKIDNLVARQYLFSNFVANNREALKKSDGSDERWLFKFMNENSIIPPTSNSKSGSLADSGQAGLVLADAIGTAKCASGWTRWTGNGCCYKEMASPMLSWYASEDWCYSQKAGAHLASVHSRAEAEWLNYQYKLWWSKMDDWIGLRRNCDNTAWAWTDGTPVDFLWWQPNYPIYGGIEDSCTAMWDSTVLRGMYDFYPGQMDDGRSCTGSVAWALCKYDPNTSIISPKWVKADCTTTSTTTTSTTTTTTPTTTTMPTTTTTTPTTTTTTPTTTTTTPTTTTTTPTTTTETTTTPTTETTTTPTTTTPTTTTTTPTTTTTETTTTPTTTTTETTTTPTTTTTTPTTTTTETTTTTPTTTTTTPTTTTTTPTTTTTTPTTTTTTPTTTTTAPTTTTTTPTTTTTTPTTTTTVPTTTTTTPTTTTTTTTTPTTTTTTPTTTTTPATTTSETTTTTPTTTTQTTTKPTTTTTTPTTTPTTTTTPTTTTTTAKTTKSTTTTTKTTKTTSTPTTTTTTPKTPFDTSKCTVMCSTGWVYYNNLCYAKLQGPGRLNDFNKECISYGGKIAEIPDAQVNDVLRKSFGTNINDEEAWVISSGYNNVASGYTAAADSCIAMTLSQKISGSVAQRGTWRPYACSLAKNFGICQKPI

>Cel|clec-202

MSVFAFSFCAVVIMPNLLAMSDEETRGRQAMVANFVKDNQKTIRNGKGDKWMSNFLKTQNLTFHRSLSSPSAMSDSSSQNLVVLADVGTAACASGWTRYDLTGMCYQQSKKTMNWYQGEDYCWNLRPGAHSASVHSQEEAKWLNSLYRDKKNGGQMDSWIGLRRDCDNVTYIWTDGSPTDCLWWQPDYPKSEFAEFSCVTIWETDWLYDNPAYIPGQYDDMKECSDDGSNVICKYDPNTLNIGAKYEWKKCGLVPETTKPTTTTPTTTTTTTIPSTTSSTTSTSTTTSVVTTTTVTSTTEPTTSTSTPTTTTTMQTTTPSTTSTPTTTSTTTTTSASTTTISTTKPPTTQIDIEKCTSNCPVGWIYFGGLCYSKIQGPGRFVDFNSECTRLGGKLGEVSGADGNEALRLALTSNNGNKILDEAWIQHIGSYNNVASGYVGTAGSCYTMILSKNNGGSFAKSGTWRPYDCTTTVKEF

>Cel|clec-245

MLFLILIPVVNSCIPTQQVETTTSTTTTTTTTTSTTTTTPIPCPTGWEEFERPSGTWCIKMYAALGDRANAISACAAEEAVLSGVQNQAELDYMITAFNAVDTIMAMDTTFWIGGERTSACLTSGLTATCTALTSFEWTDGSTTGTDGWIWRSGEPNNAGGLEICATVEITYVSLADQRCDRADFNGYACGKSPM

>Cel|clec-182

MTFENFQNIYEKTIDLSSIKTCWMFDGTIHEAEKDYPDRGYTCTVKIPGWVADEKEAKDYCNSKLPFYITGHRPGGASTRCTFLVTVACEPDYWQILGKCYKVYDGKFTYKEAEDTCSKQSVGPELSPKVANFFARNMHLFLMEIENIRKAWVSVPNLEDYYENGKGHAAVYVQDAAYRHDERVGSIMMFDQNSEHQVICEYTPPMTMAEMYYLAHRYSEIYPIHVYKHGAIIPTQSYYTITQLQGKEMYNTQELKDACKGVGNILNVESFPITAIEQEFEDVKPYLKDHQFSLVDAYKNDGCSSGDYLTEGKQVYLGGTAKTGHCDAHSCIVKF

>Cel|clec-5

MRELLVLLSLFVFSAFGAQPLVCTNGFTLINNKCLRLFSTPLGHTAAESKCTEYGATLVTVKNAIDNRAISTIAASSVSLLWIGLYCFDNDVTKCLWDDSTGSAEMYNSFASGFPLVDIGKCVYYSTQGSLAGKWLNGNCESDPRAFVCELPATHADNCTYNYNGHCFTLHTERNTFVQAQAICEQECGNLASIHSSNENRYLSSIMSSIMNLSNSSVYIGASWPSSSVFNWLDGSNSDYTNIDQSFGHGGNCALLSNYQPSVVPMGYWFSFPCTAAVPFICKRSAGIKCSGTPPPVTVTPVPSNPSFCNSTLLIAPGVITSPNYPSNYDNNQFCSYHLSTLGSYRVLLHFSAFATEVNFDLVVVYNGESASSSQIGRYSGSLDPFSVVSTGNNMFVTFKTDGSGVAQGFSARFTSFTL

>Cel|clec-6

MIKHLVVLSLFALSAFGAKPLVCTNGFTLINNKCLRLFSTPLGHSASKSKCMEYGATLVTVKNAIENNSVSKIAASSSSSLWIGLYCFDSDVTKCMWDDSTGSAEMYNSFASGFPHVDIGKCVYHFTQGFLGGKWLNGDCDTETRAFVCELTETLEDSCEYNYNGHCYSFHQPATFAQAQVICEQECGNLASIHSSNENRYLSSIISSLSNKNYYIGASWPSTSVLTWLDGSTSDYNNISPSSAHEGNCALLSSQEQWLSSPCTSSQPFVCKRSVGSQCFSTPPLVTITPTPPNPSSCNSTLLMAPGKITSPNFPSNYGNNQFCSYHLSTLGSYRVALYFLTFTTEFFFDFVVVYDGDSASSPKMGNYSGSKNPFALTSTGNNMFVTFKSDHSNTFQGFDARFQSSV

>Cel|clec-3

MLFAFIALIIIQLTNASLPPICVDGYTLVNGKCLRLFHEETYHTRAEQTCRIFEGTLFDVKNAIDNRAIASFIGSQVETVWMGLFCFNNNLCLWDDNSGSTAAYDNFSPGNPKVTTGSCVYFETSSGRWLSAPCTEPRSYVCETPSTHEDPCYYNYNNYCYTFSHNQSSFTTAQAICEEECGNLVSIHSANENRYLMNIASHRASDNVLIGGMWPMDHMNTWVDGTMWDYSNIDSVYNPKNRCIAMANNGTSEYNLGQWFGVDCEGLSSFFCKRPAGVPCSTDQPKVTVTPVPSNESFCNSTVLMTPGIITSPNYPQNYDNNVYCSYKLSTLGSYNILLEFTSFSTEENVDLVTVYDGESTNGLKIGTYSGSREPFHLISKGNNFFVTFATDSRNVFKGFSATFVAYST

>Cel|clec-179

MMWWISLLCFIPTNNALNTMIIHHGALMTCIDTEFAQKETWKDCVTSCAQNDTCVIAQANLTTPNECQLCSIQNLMHIQKRFRGNMIIALKTVSLDPITESMCTPFELGTINGHFNNTSNLTQYEYSTQLSEDGNVLNFSYSAMKSCPPQWEHFDRARGSWCIKVIRQDGTHVEASKACNEYNAALTGLETENETYHIWKTAYSLVERYPSQPKITERIWIDGVRKVTCQEKLTFNTKEGCVSFDGFDFEDKFLLEKQGYTWEQHNPDRLGPDSGPHQDCLALWITANNRTIDDEMCSKVLDDAPVKGFACGKEAG

>Cel|clec-115

MNTQLYLFVLGILTKLAFSNQTPQKMILIHGAPMIYFNFTEKTATWETCITTCYSSPGCIVAGFEDGICKLFEIGSISTIKRLDANSGKQVAVKIISNLTSCASTAAGNSLQSLIEPDQPYNITISLDTWTIRQPPKCPENFQIFERPLGSWCIGVITQQKATQPEGTRYCREVYNGVLSGFDNNTEKEFVVKSTKGTVASGNGYQGDAYWVNGERKSSCMWKNQTGPDCEGVKAFTITDPLISTISYNWGDYEPSGMIDNQGTSNCIVFRVGRTVGRGTDDAP

>Cel|clec-114

MVLIFGQPVVSPNYSNRTATISFCSGYCFSMDTCVAVYVEKGSKNCQVFSLGQLKRLRERESSTELKIAVKMEFTANTCSKTATANTMKNSVATDTSYLEYTMTVNSESQWIFTTTITLNCPVGYRLFKRPKGFWCIGVTSVNQCITQVDSVAKCKASEPSAILSGLQSMEETNYVYGIGQPLLKKDSGYYRYGYWVNGERKSSCMPPAKKSASCNSTNEFSYTDPLLSAYAGYQFAPPDQPDGLTTQDQFAKCLNLLIGNTVLVGIDDNGCNMSTAGLVPTNICYKGYVCGVKPTSLNSTF

>Cel|clec-197

MIRQLLILALCFVALQAMGVPMGNGDCGAEFKCPPNFHKSNRVNGVWCIKVYPGNMTWWEAERECRCTIKGGHLSGIESNSEKRYVEEQTLSILDDKNIKNGAVWLGAYRRKECPSGKVSSDSICHDEKTFQFTDQHTCKTLIFQDWAANQPTNNAGDDCAVLLASTEASGSNSEASGKAAVKNCLHVQGTTPILSSVGFVCGVKAAQEGGNYGGYGGGDFMVIGAAKPKH

>Cel|clec-198

MVVSMRWLLSVFTFLCMKYSEASNPRAIILQNFMDSNKEAVKNLKDDNVLSKALVKTFGLNSSSSSSLSDESSSNLVLMDSTTPCDSGWTKSTVNGMCYKIATADTTWYAAEDWCYSQRYGSHLTSVHSEAEAQWIAATYVSTGWFPYMDNWLGLRRSCDNSTYIWTDGTPVDYLWWQPGYPGSGDPEKSCVTIWVTSLLKLNPGYVQGQFDDIWDCGTNLATPTCRYDPTSTAPHIKYDTSYTCASTTTVSTTSTVTTTKPTTTTTTPTTTTTTPTTTTTTPTTTPTTTTTTPTTTTTESTTTETTSTTTPTTTTTAPTTTTTASTTTFKTTTITTTTQTTTPTTTATTTKPTTTTPTTTRTPVDCSAKCDPFWVSYSDGCYAKIQGTATFETAKLGCQSVGGEMAVITDAAMNEAIRLAFSTNIDSSVSNQAWIGTSSYSNWAPGKPDKAQGVAYSSYCNVIALSVVNKGKDFGFSRGVWTDYPCSLKQEFAICKRI

>Cel|clec-214

MWTLYVFLICFYSISCLTDLDILNVALENNILVFPSNISEASGMTLFHGRIETKSECRKVNATINSTLCTVICGKLEACQVALWTSAMFCDICEYGSVTMVVQEKTNDNVVALKRNSSSTILREPIDKCPAPSITLSQCEEGWKLFLRYNAYYCLKVINGDQFQNITQSEGVQLCLNNNSNISGLESDRERLYVFAMTIWNSLNKSKQEKWGWGVWIDGMRNKPCNMQKNETCNLMEGFNFTDATLYHKDGYIWNEGEPNGYNGNQNCVYMSLPTDSGDSRNGTLDDAGCEEHTYFLKKLVLCGKKATQIVTEAIER

>Cel|clec-215

MQRMRMLRVTLSLLCVVQCLGDMTNMNIWLPTNILNSLPNISTPSQMTFFRGSMQNISECLTMKVNSTACTVICGKFQTCQVAFWIPNNTCYLCEYGSVSLVSRIRTSKNYVALKRSSPNPFIREPLGTCPTPNLRLKTCAKGWKFALRYNASYCLKIIYDELATGALQDFIQAKAEQLCININSTLSGLESEAERIYVVVIEDQAVAIRNERSIDSRWGVWIDGKHQSSCPTTATGCDLTKNFSFRDTTLHFKAGYKWATGEPNGAGRKFCCAYVYITPNVQYHGMVDDTMCYDLTIYLKKLALCGKLAT

>Cel|clec-213

MFMIQYLFILTFPISSSSQLIILNIAISNSILTAQMNTSEQANMTLFSGFVSHNKSECLKLEVNTSSTICAVICGRLDSCQVAYWISQNLCYLCEFGSVKMITQKTVSSYVALKITAAYLPLGQPIQTCLTPNISLRPCETGWELFRRPAAFWCLKLVNKPINKTLDTFDQKTAVGLCNEHNSKISGAETIAELTYIIDKAFSQKNNVSKSEQWGVWFDGTRKTKCGPSELTQCNSLKGFKFNDKTLVSKSGYLFSEGEPNNKNGTQKCIVLRIGNVSTAHNHGTLDDVLTISRRKIFKETSSMRKISQVDEKQTELITNLAKTWWFIYLFIMVFKQKINVYIRYVTYR

>Cel|clec-11

MRTVAALLFLFTCLESFESSSATPVCTNGFTLINNKCLKLLNTPVNHKAAEISCSSFGATLVTVKNDHDNQAIATIVGSSTPLVWLGLYCFSSNSSQCLWDDESGSARSYNNFSSGFPLVALGQCVYYSTQGALTGKWLSAECESQRMAFVCELPTTFADNCLHNYNGYCYTFSSSPQTFIGAQSTCAQTCGNLASVHSPNENRYITTFAPQDYYYIGAIWKTDYSLRWMDGSAWDYNNIDPIYPNRYNYCLHMSTITTSGSGFWYGDDCSLSRKYVCKREAGVPCTTVPPPVTVRPSSTNPSNCNAGLLMSPGVFTSPNYPQNYFNNENCTYQLSTLGSYRITLKFSNFRTESNYDFVSVYDGPTTSSPSLGRYSGNIGSFYVSSSENNMLVTFTSDAGVVFQGFTARFYSVVHRS

>Cel|clec-86

MLRVLFFTLVALLCFVSPNCLPGDTPFEIYCFSYNRVHGTFNDSDAHCLKTVGGSLVSIHSMIENNWIQKLAVDNLDADYDLFWIGGSDEGHTNDWRWTDGSVLNFTNPGPGQPLEDRHCGAMQLSTGRWFSDLCTVKHQFLCQYPNGAYPTGGSYTCPPCPSCSK

>Cel|clec-177

MLLFWGYPASSIKFCEPQSTIIHFDSCINLCLKETYCMLAFGNDSSCTLCDIYAVSKITQSNYTSNIQTAIKIDSQLQCPKNMTTNQYTYTTGSNNYKLTFSDPSWTITYEKSCVNSTFRMFPRPTGPFCLDVLWSVGNRVKSSTYCKDLGEGLDLAGMQTKKEFDYVLKTAKTKSYYNTNYKYSTVWLSGIMRSACQTSPVPSGCDGIKAFSGFSYQDNFDVYKFAPGYPKIPSSASPRSMQLLISQSESAFEGMIGDALSDYICDGQSPPVICVFYMRRSCCMKIQTIQKKSIHS

>Cel|clec-176

MRAAFEKDNENNVLIFLHFYFDETSALSMFFSFCFFIISIILELNASVNMLLFWGYPASDTKFCEPQLKTSTFNSCIDLCLSETYCMLAFGNDSSCTLCDIYAVNKITQSNSITNIKTAIKVDSQFQCPKNMTINQYNYTNGFNNYKAKYSAPTWTISYDKNCLNTDFRMFPRPVGAFYLAVLPSVGNKIKSTSFCKNLSSSLDIAGMQSKKEFDYVLKTAKFITGYTPDYQYTTVWLSGTMRSACQTSPIPSGCDGLNAFSGFPYQDNFDVYQFAPGYPYIAKTSAPRSLQLLYAQTESELEGKVSDAYSEYVCDGQNPAVICVFSFTCGGLAK

>Cel|clec-17

MQLRFALLLLIICFKACLNSPLICTNGFTLLNKKCLKLFDTKVNHTSAESSCNSFGATLVTVKNVNDEQAIATVVAASSARLIWLGLYCFDSDPAKCLWDDNSGSAQSYDNFSIDFPLVDAGHCVYLSTLGALAGKWISEDCESKLMSYICELPTTHADDCTYNYNGYCYTFSSTAEPFIIAQTKCAETYGDLVSIHSSNENRYIETFAAQDYYLIGAVWKLDNSLYWLDKSKWDYNNTDPENSYRGDYCVAMSTVISSPIPSGFWFSTNCTRPAKYICKRPAGVQSTTASPVTVAPSPANPSNCNAGLLMSPGVITSPNYPENYFNNENCTYQLSTLGAYKIALRFASFSTEANDVVTVYDGLTTDSPCLRRCSGTQRPFALTSSGNTMLVTFTSDSKGISSGFYARFSSIVYRR

>Cel|clec-45

MSFPFSIFLLAFLLAPVAAIPCPTGFTRLVTTGQCLKMIVAPLSYSDASAKCKSLGAKVLTIQNAIQNNAVLSFATASATGNDKDYWLGLQCTTASSSSCNWADGSKFSFDGFAEGQPNNSLGTCVFVGNRGQTAGQWFSAECGLVKTNVICEVN

>Cel|clec-184

MFVWLIFSHFVIHTFCNTNDHIEDFLRNKTAEDIIGLRQQYHRAIYKKKKEESALADASQPNLVLADGAVLPCEAGWHQFPDTGCCYRVSDAESEWHGGTAICKALNPDAEMASFHSQAESIFVANKYSTIHAWTGLSQTEIPNTWTYTDGTPDWHWFPALAAAPSDADSSCVEMMDGLLGLIFALSLQKGQTNAYSCDESIQIICKYCPRETTSTTTVTPTTTKAATIKTSTTTVTPTTVTTTKAPTTTKTSTSTTTPKFTTTTIQTTKKITTSPTSTTASIPITCTSNCPVPAVNFKGLCYKMCRGLVKFEDSCTWCNGTMATISSGEENDFVSRVFGSNDETTRQIWIGNTESSGYLNWSQGQPTKPNDGLDYCISMDLSAGSTRGKYKYLPCQSTVINSLCVMNP

>Cel|clec-227

MICAVLTALLFAANIQVVTADVNHCPSGWTFSTNTSYCYIQSAQYLSYSEASNYCQSIGGTQVFIFTLRELTWLTDFTSSSFAQPWLATTRNITTDKWYNSDGTTPAATYWTSGEPGVNGDCATFKGAGASGLKATQCYSIQPALCRQMPALCPSQTSYGGQYTGSGTITSPGYPNQYYNNLDCVYTILSPNNTYITMQFSPYMVEEYFDWIDLFDGPNTTYPFLGTTDDWWSLRFNFESSSNAVSFIFHTDSIVTDKGWLLTWSAKTKTPPISQSGQNGSFTSPNYPNNYDPYTEQIYYVNAPTGFQVNLTIPDFVTEANYDVLEIYNTSTVISSGLVANLSGSAVAPYSWLSPSNYVTMRFRSDGVVQKQGFSIVWFIQ

>Cel|clec-57

MILLPIFLLFSIIGLSAASECPSGWIFNPSTTECYYFSTKLYTFDESVQFCSSIGGKSVSIDTYAERDALVAMTNTTMLQPWLGSRRNTTNNQFYNIDHSYFYSFMWTKNEPSVNGDCVTFKGATPFGLQVTQCYQFQPAFCKQTPALCNGGVFGGSDKWTGTIQSPGYPVQYYNNLNCNYLIISPNNTFITILFSPFLVEEWYDLVDVFDGNSTNYVDHIGQVSSYNLARGFESSTNMMTVRFKTNYDITDKGWLATWKAKKDMPVISQSGSNGTMVSPNYPLTYDSYDEQVYQISVAWGMQVNLTIDVFRTENKYDYLNIYNSTTQSNSTLVTTLSGQSVAPFNYISPRSYMSMKFVSDGSLQYTGWHAFWSIC

>Cel|clec-56

MIIAVLTGLLFASVFQGTYADTNHCPLGWTFSTNTSYCYTKSAQYFSFSEAANYCQSIGGTQVFIISSTELSWLTDFTSSSLAQPWVATTRNTTNNKWYNTDGSSPYSFFWTTGEPSLNGDCATFKGTGKAGLKAVPCYSIQPAVCKQMPALCPTQTSYGGLYTRSGTITSPGYPTQYYNNLNCLYSIKSPNNTYITMEFSPYLVQSYFDYINVYDGPNSTSTYLGTTDDGWDDYWWDSRRDFESSNNSISFVFRTDSSVTNKGWQLTWSAKPNTPPIKQSGQSGNFTSPNYPLNYDPYSEQLYYITAPTGFQINVTIPDFATEKTYDVLEIYNASYASNYRLVANLSGTAVAPWSWVSPTNYVTMKFKSDSAFQMKGFSIVWFIQ

>Cel|clec-54

MLATLLTSFLFFVSTFSDVTADNSLCPSGWSFSNETSYCYIVSDRYMPFSETSSYCQSLGGTQVFISLSYEFTFMKTFTQGLFAQPWLSITRDPTDNKWYNPDGTTPFISWWSTGEPSLNGDCATFKSTDPQGMKATPCWSIQPAMCKQMPAICPDPKKIYGGQYTRSGNITSPGYPVQYYNNLDCLYTITSPNKTYITLTFNPYLVEGYVDYVLIYDGPDTTYPSLGSTSSALKLEYESTNNSVTLKFHTDRSITNKGWLLKWNAKSNTPPVIQSGNGGNFTSPNYPNDYDSYTEQMFYLTVADGFQVNVTIDDFLTENRFDVLEVYDNYTIPGVNMIANLTGDSIAPWNWLSQSSHVTMRFRTDGSVQKRGFHGYWTIQ

>Cel|clec-55

MLAAVLTSILVFGSSVRNVSGDKSLCPDGWLLSNETSYCYLTSDRYMTFAEADGYCQSLGGSQAFMMNSYEFTFMKSYTQGMFAQPWLGVTRNLTNNKWYNNDGTTPYSSWWIAGEPSLNGDCVSFKSTDKQGIRATQCWSIQPVICKQMPALCPDPNKKYGGLHTRTGNITSPGYPVQYYNNLDCFYSITSPNNTYITLQLDPYLVENAIDYLTIYDGPNATYKSLGKATSSSKLTFESTSNSVSLVFHTDKTVTKKGWLLNWNAKAYTPNVNQSGNGGNFTSPNYPNDYDSYTEQMYYFSVADGFQVNVTIDDFLTENRFDVLEVYDNYTIPGVNMIANLTGDSIAPWNWLSQSSHVTMRFRTDGTNQKRGFHGYWTIQ

>Cel|clec-151

MRLKIFMALSLLCYTNAQVDRDWSFQQMCEFWGGEQTYRARSGYKSIEGDKCTFKFPKASNNKESAQRYCEETVPYHINNPKASEYKTTCEAEATLICKSGWVQMFGRCYKITKTMMTRDKAEEHCKNQQDQTSTIAFMHREALPFRWNDYFTRVSRIWMDASEVVTNDLIHDVEGGNVLLAFDGYKYNLPNVAIARVSKNETAMVLCEYTPSMTKAESNYLLRRYGEIYYPPLVTSESAYMRTTSSRIRNEEDPLADHNYCTELMKPVFRGGEAQSALPTQEFVKKLTETGAAEIIRTSSVSMNANKGERTIVDCVSHVDPYHRVHVKGDKNEETSITLNKTIWRQQEPHETCDAATWSSAAVLSRDSNRGLEAMSDARYAPLYCENILEYFSYSKCPEGFSEFPRVTSGQRWCHKYVHGAPLPYDDAEKKCAEMGAHLSGFTTQEEFKFLNELVNKEYPNKNDIEVWLGAQRKMSCPDAGKNFNGGFSTNEFDNCARSRVFEWRNGVAKNPPDFIGSGYDNWAELDEPNHLSDKERCVVMMHGKITKYWGYSSKYHDRRDMQINDIFCDWHFEYFCGLEVPVITVKKSS

>Cel|clec-153

MRIKIFMIICLLHKTNAQLARDWSFQEMCNFWGGEKTYHARKDGFKSLEGDKCTFNFPKASNNQESAQQYCEDNVPYHINNAEASEYKTTCEAEATLICKSGWVQMFGRCYKITKTMMTRDKAEEHCKNQQDHTSTIAFMHREALPFRWNDYFTRVSRIWMDASKVITNDLIYDIEDGNVLLAFDGYKYNLPNVAIARVPKDETAMVLCEYTPPMTKSESNYLLRRYGEIYYPPLVTSESVYMSTTSSRIRDETDQFADNKYCTNVMRPIFRGLAARSAFPTKEFVDKLEKEAAIIRSATVSQSANQKGREESECVVNQKPIHQVFASGQGGKTLNVKIDQALWRKGEPKETCDAASWSSAIVLSRDGEKGLETMSDARYAPIYCEAILDKYEYGPCPAGFLQYDRTELGIRWCHKLYSELETTYDDAEKECLSLGAHVSGFSDLKEKDFMHDMIMASPIKNKTFNRVWIGAQRRPECNTLGVEGKTGGFDTDDSKPCARSRVFYWLHGVALNPPDFIEHWADPNEPNFLGDKEKCVVVMTGSEWTHWKFGINKKINDVSCGRRYPFFCGKEAPIVKVTK

>Cel|clec-7

MHLLIFVLFYFFNSYSVTSSKVPVCTNEFTLINNKCLKLFTTPANHSAAEKTCRKYGATLVTVKNENDNHAISTFAGTSASLLWIGLYCFGNDPSKCLWDDSTGSADVYDNFASGFPLVDIGKCVYYSVQGALTGKWLTENCDLSSKAFMCELPTTFSDSCIYNYNGYCYDYYAEASFVVAQNTCEQFCGDLATIHTANENRYILTVAQHYPSSTIVRIGATWPASNVYQWVDGLPWEYKNIDLTGPRGGDCMVMSTRPPSPVAAGYWFGASCTDERNFICKRPAGLQCVGTPPSVTISPIQDNPSFCNSTNLLAPGVVTSPNFPRNYNNNAFCTYQLSTLGSYNILLRFAPFSLGTSDYVIVYDGESASSPVIGNYSGTLVPFSLISSSNNLLVVFNGNTGGQGFSARYTSYAPLI

>Cel|clec-250

MQLLLLILSMLVIRSFCDMKMVKLYGKVNESAISSTLNVETAEECITRCYYNSNCILVRIFQTSCEVFNFQKAIISVAMSNNTDSGYLVLKTTASITECPDSYKKLTFAITSGYTWTWKTDGDEYSFVGCRDGWKRFEREIDGTVVCMKSYYRTRVNNDYAKQLCVGEGAKLTGVASAEECQWIREAVNGMSPPWNNYGVWIDGRRNCTDEPCNVIYWTDGFTTTFDALVSTNAQIPSTKFKGGWEDCLTIVPGSGQGSTINDLSCGNTQLILGFVCGYQLEDL

>Cel|clec-254

MIFLSSFFYFSVFLLPFTSCDVKMIKIFGKVTETTEPQAFNTVKDCIDECFEDSDCLLAFFNSVCSHYYVSDQSITVVETDRSEGSYVAFKTELPDATCPASYKEIKFSVTSTNGEIYSWKKTDNGWIYKNCNDGWTRYPKSDGTILCVKIKLEKVTQQVAKERCIEESAVLARVETSEECEWKHGFVENRSAKLVETVVLNSMGTDTDIFWINGRATGDINLDDCINQYDHYSQFISYETSAGNCVALFDSMYPFSLSDLPCDWEIGYMCEYVLQ

>Cel|clec-252

MRLLLIFFYFSTFLFPLSTSDLKMIKIFGYTDILQLQNFENVQSCIDGCFEQPNCLAVHFKSVCSHYFVNNYSVTVVESDRSEEHYVAIKTELPEATCPASYKDIKYSVTSDSGDIYSWKKTDNGWSYRQCNFGWKRFQKTDTLVMCVKVMVDQVTQQVAKEKCIERGAVLARIETPEECKWKQDIVANKYFEKGIWIDGRAASGTRIESCDDKFPELVSYETSAGDCLYTAAFRHSGYFYDII

>Cel|clec-251

MIFLSSFFYFSVFLLPFTSCDVKMIKIFGKVTETTEPQAFDAVKDCIDECFEDSECLLAFFNSACFHYYVSDQSITVVETDRSEGSYVAFKTELPDATCPASYKDIKYSVTSDSGDIYSWKKTDAGWSYSQCREGWERFQKTEQVVWCVKVMVEQVTQQVAKDKCIEQGAVLAESGTFEECEWKQDTVATGDNMKNRQKRQALCVDSCLPLTQETEGQYGLTPSTNFYISYSTENGCMMAVITCVGGGATSFEYSIVSKKHVYIEYDSKELNVFKVQLSCYEYGWAAFTYTENAVQNNMISCDVDFQIPTTSTIATTTEASPSTSTESTSTPREPSCYHCYYKL

>Cel|clec-101

MKSLLILFLLGSCSANIPERECGRDLSNLWLDVVAVVDDSKGVTQGGLYNIIGTLNSVLQLSKIGTRKDNPRTTRLGLVSYNYNETIEATLNDYQFLDTNKMMDQLKISSNIGSYLVTGLSGAEQLFKQDKEHSREHYRKVVIVFASTYKDDGANDPKPVAARFLSSGGIIITVAYSQSHDTQLLEKLGGIATKEFNFTNDDPGLIEKIQDSLLKANCFCPNSWHQYQPKGTCIQPVTLPASWSIAQASCHHKGNNGHLVNEYSREKHDFVMAILKTYKEFQPTYKYHIGLNGNCSLWKWDQASGEEQVQLQGWQIWAPDFPRCSPMLEMLEGVTYVTDGWINVPSNFYANYVCETSTCDTDNYCARANDFLLNRV

>Cel|clec-42

MTTVIISSNCAMWSHSVLLLAALASVLADTCPDGFTILSTNKCVKLVTEASKHSDATAYCTSLGGNLISVHSVIDNNAYQKLAAVSVTPYWLGIKCAQSGSPKSCLWDDQSGDAGKYNGFAPGFPLLEIGSCVYVPTNSSSAGKWLSGDCDAMILNFICETTPITNTCTFQYNGNCYYPSQSALSEQDAQSACQQECGNLVSIHSDEENNFVQSLFTTNSPTYIRIGAKHSNNQNSNYWIDGSSWDYDNIGYSNPNLGMCWSMALTNDTIPAGKWISSHCDTSLPFVCKRTVGTQCGATPGPTPAQCTSPMFLHNSGSFYSPNWPNSYLGDQYPCTYILDTPIGSLVQIQFPILNLDSQASISLYNHVEDSTPFLVLEANSASDQWYTSTTNTMRVVFQLCISHCLNDGANYNWKAEFKPSTAVTTQPPITVTPNPNNPSGCNSNIMAPGYISSPNYPNYYPSNALCRYHLSTTVGNRIKLDFGAIDTDQCCDYIYVQDGAFTGSPFIANISGTYPAHMKTFQSTSNLMLVTFKSSIYDNKDYTGFSANFCTIQI

>Cel|clec-246

MIFLFLIPVVNSCIPTQQVETTTTTTTSTTTTTPIPCPTGWEEFERPSGTWCIKTFAIVGSWQDGQNGCATHGAVLSGVQNQAELDFMCDSAVEGAFWVGGQRTAACPGPGLTATCTALTSFEWTDGSTTGTDGWIWRPIEPNNAASCPVINAWTYNLADQVCTRSDFDGYVCGKSPM

>Cel|clec-109

MKPLHLLLLIIWVTITLGNFRNENPRKVIKIIKHVGSSSSYSSSSSEERSKRRHKNSRLTHSSRSRPTRTCPRDWITFERPQGRWCMKAFYGNMFQPEAEAKCNAVGARLSGLQNANERMTISYVLRGLIYQHGGGRYTAWLGGKRRARCPTGTSCARLDSIEWTDGHTTGTAGFSTGPRELDGYYLPQYGGVQQCLHMIVTPYSNTELGFADFVHESVDDEFCQATWVKAYVCGKLPS

>Cel|clec-110

MHLATPVVFLLLFATITIAIEFDGGKGGGRRRLDFSDSSLSSSSEEHRHRPPHRPRPPRPSRPTTPRGECDDGWLRFERDHEIWITNAMLTQPTAETLCQTMGATLTGYQNDNERVTTANEALKKLVAAGQSTIAATNVPACRYQSCGPYNTFTWTDGHTNGTAGFSKWGVGQPDNRNYGGPTICLQQFIMTPNWVGLRGDLEEWRAAFTNGDLDRYGCLDAPGLPQTKMYACGKVGVSRRSRG

>Cel|clec-221

MVHSFSVLLVLGTLFYYSQAQNAAQEVKTQVPKCNLWQGKCPPGWKTFIRPPGVRICLKIINQNATYLEAQNICRKQYNSRIHGIENKEEHNWVKMKSRLVIKQGASFMWVGARRKSWCYKTEAQLKTDDKCKSGLNSFEWDDQLTDGSYLFTQWDKTISAPEGIMSNNAPEDCVVMNVHEGDAPIDDKDCSLPQAGVLCGMTA

>Cel|clec-212

MCEEQVAHFAPTMCMFLLSILFVLFKASYCTVPQMIIIQGRIDENSESACVPFYVEDKEFNSCVASCGNSETCVAIKYKRECNHCHKAVLIPDCKGMKMAYKNTGENILCPNVEMYLEYAPEKNVSDYDSMVQTEAVLQNDFAQEISSTITTDPSTTTRQKQCPDKRFTIFDENWCFLIVFNSVINSEEKAKILCNNSNAQLSGPETDEELVAIMNSTIDYITSEHQGNDFALWVDGIISWPVKFNVIHVLKTFGSYITSSDPHLVKKSGYHFLNEDAYSLMKLPDLGNNRFCLQLTNGRAELGTISIVNCSFPISNKLAQVGVVCGTKAT

>Cel|clec-233

MPFYYIFYYQPPVSYKKQEFLRRKVRKMRVAILFLLFATSTLAIFIDGGGRGGGGGGGYYSHSSSSSSSSSEEHGHHRPPHRPHRPPHRPHRPPRPPPRPECDEGWLRFERPNGVWCINVVHSGVTNGYFSQPQAQAACSASGATLTGFQNDNERMTVASEALKKLTAAGGQIAGLWLGATNTPNCKVASCEPYATYTWTDGDTTGNGGFKWGRDEPDNLNWPGPTICIQQFIMQPNWVVGPNDYAVWKNYFTNGDLDKYQCGAQAYPFTRMYVCGKRGVSR

>Cel|clec-1

MVLALITLVVSAFLIPEVLADPCGDSNWRYFPQTNSCYKLIDENLPWTIAEFKCLFQGAHHVSIDSPEENQFVHELSRWSEIWTGAAFFGKDQHYVNSDGSRYGNFENWKDGRKPPMNRARRCIKMDGNGEWFQSCCKKKTFTICEKKAAYSASSYSGSNNSVNGFRFMRHRS

>Cel|clec-156

MQLLKSILLVGLIIGIAKAILFDDSDSSDESHESYSGGGRSHHHNHRPPSLRPPRPPRPPSPSRPQRPPPSRPQRPPPPRQPRCEAGWTLVQRQNGGWCIRIFQGITNQPQSEAICNQNGARLSAVESQREREIVRDLGTKYMTTTSNWKQGSLRLGMQRANVQSAFLPTDQNARGVDGIRWTPNEPRPGESRWGYYNCVLMWMKLPGAGAVEQRQHGEMFAKVCHQTWTGAFRASFVVNVLYNLQKLYKNKYFFNICK

>Cel|clec-157

MRSMKVFISIGVVLSVVNCIFFDHGDSSDGSYSDSSGEGRGHHHKHGPRPPRPNRPPRPPPATPPPTTPAPSCPGGWSLIHRRRGPWCIQVFNGAAGLEGSNNACRAQGAVLSSVENAQERETIARLGLEKMLPTGWKYGTIRVGLRKNSQGAPWYNTDGSTDANNLEGVLWSPAEPRNGNWGGVQLNCATMWLWGGIFEGGRIHGQFFTNICLANNPNDRYRGYVCGKPA

>Cel|clec-196

MSTVLGKLLILSVCLVGIFGNRIFGVKTCPKGWLQFEDNCYIRQPDFSSFRESVKNCEKRGAKLFHFDDSFEFEAVRNLFPDYYFTWMQAEVEEELEWLYEPYEEKMNGKNSAAKCIAFYSSPTKSYNYFYPCTSHFHSICEKSLQSFRQWMD

>Cel|clec-216

MSSNLFILLLLGGCFYNFFYTRRTHVHDEESSSDEDDYDNFFKEENSEETHLRRFSDTGPVNFNVFEDVPDATNKSIAEYEKIEPDEICMLQYGKCPQGNWRMFRRQNETVCLKVMNGCHYGTPLRKNAAEKYCREEADGRLMAISSHEEREWLHTLGIIFHNDAPLLIAGHRNRECKLNPNQNQELCSNRTTKYLEADGTNNYTYLYSFDNWLEAADDDCVGYRQTDISVKSLLISSKLCDPIPGVIPIQIYSWLCGVTVMK

>Cel|clec-217

MSGKLFIILLLGACFVTIVDSSRRPRNDVPDEPSCEDEDDNDNNYDSQGRPRRVGASRPTIRKVHIDDWDVVEDEDDESYNRYENTNQEGICILERKKCPQGDWKMFKRQNESVCLRVMGTPNKIDPPTAARLCRKEANGRLMTIDNQQEREWIKSTALGGSSYHWLIVAGYRSRNCQMKPHDCKDKETAFTKVNGTSDNKFLYTRWFPIVHNRITYSVLDNCLNYFTLQPLSADMLIQDFTCHDWYNIFLCGVTVM

>Cel|clec-234

MFTAFPIIPLLLSTVELINACIPTQQIETTAAPTTITTTTSLAPITTTSTARTTAPTTTTSLATTSAATSTTTTTTTTTVPTTTTTAIPCPTGWDGFERPSGPWCLRVYISPGNRAHAFSGCSAKGGSLSGVQNQAEIDYMASSYISLNGGAGFLWVGAQRTSPCLSSNLDASCTTLNSFEWTDGGKTTGTDGFIWQSGQPDNGGAALDEACCLLSSAAVLSDEQCLRADPTGYVCGQPGL

>Cel|clec-263

MRKLYFLFCFTVLLAAQKGPSYKFGVIDGEPIDLINSTSVQVKDFDECVEKCEEDLNCILAYQKSDSEPCQLFPWNTISGVKGNESGGVGQVAFRVYTDQPACELNLPRLLNGKKYPIHENNTREYLWTIDTSEEGWKISYIRTTLDDNLRCGNWSFFRPYVDGCDANCSVTMVQDYAKPGPETVKPRDAQISNWDECMHMCYEEEECQIAYLDSDAKKCVWYSSDDGLTFMNKSSADSGKRLVIKMKVDETTCLFTTPQLLDSFKFGTQSTEPSTTEISTTEGTPKQSCKDTNARFIPAVEGCYKMVRVIPKDLVLSSDITNNEAQEQCLEIGGDGLMTVATNDTLNYFLKGDYLEDIKMTPRFHVGIIKKDDTWTWRLPQLKIDQSPIPWSLNTRKVADTEKCGYVQLPSDPLGFRPCVEPVDCDDPMYMNGYICHFPKIADSPDQPTATTTEMSVPKQSCKDADARFIPGVQRCYKMVFTKDKTDPTINAFTSHEEAAGNCTSIGGNGLMTVATNDSMKLFKTGILEKWHDFWWVGLIKKDSNWTWMLPELVTDNTPIPWARDQKFNEGDDCGYVQLVPDRMQIKDEVQPFSCKVPRPLKGYICHFVQ

>Cel|clec-264

MRFLLFFQFILQLTHSKTPCAPSWLHIAHLDSCFLSAPQPAEFSEALEYCTQSNASLVIINSEEEASIVREFFARENPSFFNWIGMRWNARAADFQWIDGKSKNYTYFLPDEPGVSGECIAWVLDDNLDGWQAISCYYSQFFMCQRPAEGIITTWHRDEEGTIVSPNWPNSYENLEYDTHIIKSEPGTRILMYFEEVDTEHNCDIITVTDDYGISGRTLFRLSGSHRNHSVISNRNHVMINFKSDEDNIGKGFVMRYKILRPLPVKVFSSNSFGTVTSNNYPNSPDSFLIQYYLIQCPIAHHVALKLKAMQLDKSDRVKIFNGNDETAGKLKIFRQFSPSSVDLIKTTQNSMFISYDTGEQFNASNHWAFEYNCIPDGNLGDEIII

>Cel|clec-102

MHPLTFLTLLLIPIFNCQVVKLIEIYGTVVDGISYGATCDDKNSCLSYCYYGSTCILVYCPSEGKCTVFDYIRRPKSLKVEKSSKDERNIVYFKTISTSENCEKSYKDVKISVPSEANGSYSWEVTSDIWSFQGCRDGWKRFDRTDGVSVCMKGVLKNTNRVEGSDECLRLGAQLIGVASYEESLWMFDFIGSVKNQQNIYFWVDGQRNNSEIDGFEWSDGFTTGKAALGIDIAMLDGMAGGENCLTIRYSPQNVEKPLNDVSCTHNGGSGVSCGYRIF

>Cel|clec-62

MLIGLLLLFLLSVTYGQVPPTDRNCGHDLANLWLDVVVVVDNSAPMTQEGLTEVAAQIVTVFGAGTRIGTNYIDKRTTRVGLVTYNTEATIQADLNRFQSPDDLFSTVFQILPNDLSTSEDVFLAKGIGAAEQLLAAGRKNNTRKNYKQMVIVYASAYNDEGEEDPRPIAERLKASGVSIATVAFDQTGDEEMIKLIGEIATPGFNFTNEDENLVKEIQTAMIQTNCYCSNLWTQYRETFEDPHSSKFGVCLRPVALTAGWTPAKFACQNMIQTGYMVTEYDQKKHDYVFKLVRNDTSFPEPYVYHIGLSYVNGGYAWQQPVGHALVPFQLNDSLWNPGFPTQSSTTTAVLNQQSSSAFRVGWQNVNQYTVSERYVCEVAACDTSTYCE

>Cel|clec-63

MFKLVSLALTLVALASAQDSTTSWQTGATQGPTPSTPPPTPGGSNVDRECGGDLTNLWLDVVVVVDNSKGMTNEGITEIAANIVTVFGNGTRIGNQYSDPRSTRLGLVTYNGRSTIVADLNLLQSIDDLYQSVFSTLNQVSNSDDSFLAKGIGAAENVLQSGRTNGVRSNYKRLVVVYASAYKGEGELDPIPVADRLKSSGVVVSTVAFDQDGDEALLAGLTNIASPNYAFTSKDLNLVGELQGAALQTNCFCPNLWTQYKSNFDDENSYKYGVCIRPATISSSWTAAKFACQNLAKNGFLAAEYDGQKHNFLFRVAQNNTAFQAPYIYHIGLSYVNGGWNWQQPAGYPLKPMSGYSKWNPSYPKSFTSNIGVVEQQFSSDLTVGWQNINAYSVAEYYMCEVASCDTDKYC

>Cel|clec-64

MLLNLLAIFTAFATTQASTDRNCGSNWNNLWLDIVIVVDNSKGMTNEGITEVAANIATTFASGPRIGTDYSDPRSTRLSILTYNSEATVVADLNQFQSADDVYQTLFSFLNEVSDSDDSFLAKGLGMAESVLYNGRMNGVRENYNRLVVVYASAYREDGEDPLNIAKRLRSSGVAIATVAFDPDGDGLLLSKLSKIASPNMSFKSRDPNLVGKIQAAALQTNCFCPRTWIQYRPSYDDEKSYKFGICIRAETITASWASAKIACQNSIKYGYLVTEFDDRKHDFLFRIALNNAEFTEPYAYHTGLSYVNGAWRWQQPEGHPLILQNGSYSHWNPTYPNTPFTNTVVVNHQHNSNLDVGWQNINGYRENENYMCEVASCDTDKYCD

>Cel|clec-65

MWKVLVLLCLAASPTLSVSDRRCGTNANKLWLDVVFVIDNCKIGSMNLVYQTISSLFSKQLQIGTGYDDPRSTRVGFITYNWNATDVADFYKLQSWADLNSQIQRLQYTPQSSSPASRMDTGLNAAIGMIDATAGFRDNYKKIVIVFTSVHGSYKSNQPRDVSKILKSRGIPVVTVNTGSSSDTQAYLKQIASDNMSFAIADGNVTQEILKAMTDTNCFCEQGWVQYNYPWNNLQNRYGTCLYTDTTDYSSRDGAKSKCRQYSPKSYLVNELDQQKRDFNFNLVNSDSTKPVNAFYNGLLNLNGNWYWDQPNDRSPIPLDPNSGAPPTRNACVADMKYSDGTTAWTPVSCANNFRFICEQVACDTDNYCDGV

>Cel|clec-66

MEIANKRAWREYISYEIIRLQMHQILTLFLLALAASPSQAVTDRSCGSDLSRLWLDIVFVVDNSKNMNLYNVYNTISNLFNPFVQIGTGYDDPRSTRVGFITYNWNATDVADFYKLQSYSDLSSQIQALSVTPLSRADETYIDTGLQAAINMINATGGLRDNYKKVVVLFTSKYNYYHTYPEDLTDYLKSTGVTIITVNTGGDSYTTQSLRDKIASKGMAFAMSDGNTTAELQKAVLAINCFCRPGWMQYHYPLKSDNIYSNYGVCLYRPDSAMTKFAAQSYCHSLTTNGYLVSELDQQKRAFNWDYLNSKGITINAFYNGLTNYNGTWWWDQPSGQPLWPLNPNSGAPPQRSGCVVDMKYSDGSISWTPISCTSFFRFLCESVACDTDNYCEF

>Cel|clec-139

MRSVFLILIVALCGVVEASNATEKEVVCPKGFKLYERKPTQRNKFTKNWCMKVIENEDVYDRPIARSVCLDYDAVITNVENQEELDDINALIRKNNKRVAVDGVFNPKCRGFSDWRMRKFGGLCAKEKELFILEDDHTDPAFILTKWSGEPPTSSDKYQEKGDSTEIFTIAECLSLHNLQAIKNTGNLKDFLCGEEPDKQVGEVPFFGVLCGCAPV

>Cel|clec-136

MFVFFLLFLTAVFAKDPQCPEGFSHVKRVPTARNNHTKDWCLGVFQFKNMGNRDRARSFCSYVNASLTIPENEHEIQVFSEIARAHGIEAPYAVDGQISPKCNGRINKVEIILRHRFNSTEEKGDCNIKNNLFLFDDVNSDTTFMLSHYKRRLPAAYMVHQADNGPIFRFAADCIVLKSGIVKANGTETRKNWGSLEFCVGKNAVQAYTDDEKPYGNDVEAVLCGRHPL

>Cel|clec-137

MLKAFYEVQYKMLVLFLLFLAVPEFSAKDPRCPGNFTYFKRTPTAKNNFTKGWCLGIFNETDLGNRDRARSVCIYYNASLSIPENSHELEVISKTASLRNISVPIALDGQLSPRCKFAIYKGQVKGAKRFNQTSEEGICNIKYELFIYDDINTDTSFIRTKLGVSAGSNVRSVQADDDIEYRSTADCTVLEKGSYHYSNGTLKDGHTNLMDCMGQLAGSKRLPEKNVTAVLCGRLPF

>Cel|clec-138

MLVLFLLFLVVPAVSAKDPRCPKNFTFVKRTLTFKNNFTKGWCLGIFNGTDVGNRDRARSVCLYHNASLSNPENSHELEIVSDVIRARNISLPIALDGQLSPRCKALIFRGEQSQQYFDQRTEEGDCNINNHLFVYDDINTDTLFIRSKLGTSAGTNGGYSSQEDGVKFRFTRDCNALTDAYYYFSNGTHFYAVDGRTELLGCFGEKDKQNKHEYSSVLCGRFPL

>Cel|clec-207

MLVVFLFLLLSTTYGIDFSDSSESCEDGGRGGHNHGRPPRPPGNGGGGRVCDAGWKFFSRPSGGWCIRVFAGRLGRDSANQACATQGGVLSGMQNVEEINYIVSQSLSVISPARSGGVWVGARRRPACISSGITATCTKTNSFYWTDNSATGINGMLFTNGEPNNGGVKLDQDCALLTVASTPVVFNKFRTGQMDDVPCTWQDPTPTADKANKGYVCGKKARR

>Cel|clec-208

MLVVFLFVLLSTTYGIDFSDSSESCEDGGRGGHNHGRPPRPPGNGGGGRVCDAGWKFFSRPSGGWCIRVFAGRLGRDSANQVCATHGGVLSGMQNVEEINYIVSQSVRLISPEVSGGVWVGARRRPACISSGITATCTKTNSFYWTDISATGINGMLFTDGEPNNGAAALDQDCALLTVASTPLVMNAFRTGQMDDVPCTWQDPRPSSDKANKGYVCGKKARR

>Cel|clec-232

MNKILIFFFLLTIVSLAASHRHKHGKVKKIVKVMTVGGKPMNDFGGSRRGGFRRRGGDTHVHHHHHHHQPKASSSSSSSSSESREEPIVGAEKPVHTTLSAPLPTPKPLPPACEKEWLSFKRKSELWCVLVGNQGADNHAFSQAEAEKICKKHGATLTGVISSEERDKIADEALHQLGEMKMEVGAVWLGATTTPDCTVKSCGEEDTFKWTDGHTTGVAGFKWGEHEPDNQDYGSDKACIQQIVMSPTYAKDSTNHKFAEFFEHGDFDKHSCKGGESPKTRLYACGKKAV

>Cel|clec-19

MLQFLAFLLVFPFLASAAKEPICTHGFTLVKNRCLKLFHEPLSHKNAERVCSNFGATLVTIRNSTENLDVIALSNKERNVWIGLFCLKTDLSSCLWDDSLGSAEKYSGFESEGLNSEKGRCVTVNTTSGYWSSTHCEKKANMFVCELPTTFEDTCQHNYNGFCYIPHSPKSFIGAFTTCEKECGELASINSANENRYLNTLASIFSPNENVFIGAVWQSFHAPRSDWNYEKMDPLHERVDACVVVSGERSKVWGYWYTADCDSKHKFFCKRSAGLKCNGDFETVTVAPWISYTCNSSLILTPASVSSPRSQAGGTERSYCEYQVFTTGSNSILMTFLNFDMHPSDDELTVYDGDSANSSLIGTFSGKYGNGLSLASSGNKMFVTFRSNGTNSNWSGFVARFTEFYYASPMNKLI

>Cel|clec-170

MILQLFLPLVLASFAHSACLDSRDKEIKGLCFTFVSQQLTFNDARNWCHYQNPVTSSYLAYVPDQYTSSFLASDARTAFETNSGSFWIGLSRNSSSSPFAWDNGSPVTYTNFGTQLGQNYLAQSVVNTKWNAFGENDKNLFVCSYSPVAPPTFSPPSISTTQQIPITFAPPLVSTTQKITPVISTTQRMPVTEENSCKPTENGTILFAFSNDYGAQTVKKAWDGYPFKVTPCSGYAIARFDVRVEESIVYFTDFGDAQSYVYSHLPDSKLGFRDKKAGSDALQMVEKFYNSNKIPICGSIVLILLKRYPNDWDISKTVSLVRQHHGIVHALCSADPSGGTQSKAIHSLTSKTNGLYNIGKGRDFHNLIDWFPMYSYKHPIYCANPVLSGQKIIELPPMNVPFSTYYEVYVTVQDHIPISSFVSMDLIMKNDNYSGGNFQVYSKDVSGILASHSNHFSPVTYSMQLQYEYKNWAEEDTQVRVYSDRLPPYWLPYCD

>Cel|clec-165

MFLQLFSLVLCVSYACSTCLDSGDIDIKGLCFKFVAQQMTFNDARNWCHYQNPVISSYLAYVPDQYTSNFLASYARTAFRSANGIFWIGLSRNNISSWVWDNGNPVTYTNFGTQLGQNYVAESSANSKWSTFGENDKNFFVCSYDPAAPPTFRPPIVTTTQVPITEDTSCKPIGSLTYLFAFSNDLDPQVVKDSWNNFHVGGIAIARFDVRDEEDIVYFTDFKNATAYLLDHLPNSKLGFGDTMTGSSSLRTIEKFYNSKEIPVCGAVCMVFSKR

>Cel|clec-169

MLLQLFLLVFFASYAKSECMVNSDKEFEGSCFTFYSQQLNFTDARNWCHNKNPAGPSYLAYVPDQITANFLATRASHEYGLGFGRFWIGLSRNSSTSPYAWDNGKPVTYTNFGTTELDQNYIFEDMGTSRWGSYKNSSLTWFVCSYAATPAPTISPEDNSCKPGKKVTLLFAYSNDFDSATVRSTWYQGFLTFTDDYAGYAIVRFDVNTGQEGIAYFTDLDNATSYVFSHLPDSNLRFGDNTTGSDSLEIIEKFYNNNSKQYSVCGSRCVILEKRYSNRLDISKTVSTVRKHYGMVHAFSSVDPSGGTQSKAIYNLTSKTNGVCNFGKDSKFADFTEEYQFFSAPYPMYCANPVVSGQNTAVLPSMNVNTECFLYWTLVTVQDHGPPDSFQSFDLKWSNEKSGGDDWYISSKSLFGVHGDQSYYFDLGSYSMQLQYNYTSAVEQTIQVRVYMNSAPKDWLPYCD

>Cel|clec-167

MTKKSFFIKLIIFISQMCLLFILLVFLFYTDKVCFDNDDKEIKGLCYKFVSQQMTFTDARNWCHYQNPVTSSYLAYVPDQHTNSFLASHARSVFGTTDGSFWIGLSRNSSSDSFTWDNGSPVAFTNFVTQLDQDYIVEDIVNTKWNSFRESDKNFFVCSYNPAAPPTFAPPTISTTQEVPVTQNNSCKPKRDQATLLFAYSNDLDPQVVKNTWDMLFHDRTYSRFAIARFDVRNQEAIAYFLFFEFAKSYLYSHLPDSSLGFGDNTTGSDSFKTIEKFYNNQEAPVCGSVCLILEKRYPNDEDISKTVSLVRYYHGIVYAVSSINPSGGTQSKAIYNLTSRTNGICNFGTENYAGKLIDRVPMSSLSYVIYCANPVVSGQNIIELPPMTVPFEDVYWITLVVQDHGPSDFFVSSNLSWSNDKEGGDDLPANSTSPDILFLGSWYNFSPAVYSMKLGYSYSNNNKEALQVRVFRANQFRPNADWLPYCD

>Cel|clec-166

MLLQLLLPIALVAYASGACFDNDKEVKGACFKFVNQQLTFNDARNWCHYQNPVTSSYLAYVPDQYTSSFVAAYARTAFGTNYGNFWIGLSRNSSSSPFAWDNGSPVAYTNFDTQFGQNYIAEKIVNSKWTAFGEKDKNFFVCSYNPTFSPAIISTTQEPTTEGNSCQPVDRMTLLFAYSNDLDPQAVNNSWNWAGINLYSTFSGFAFARFDVRDEEDIAYFTDFESATSYLHSHLPDSSLGFGDNNTGSDSLVTIEKFYNSKEIPVCGAISMILSKRYPDDWNLPRTVSLVREHHGIVHAVSSVDPSGGTPSNALYNLTSKTNGMSNFGTDDGFPRLVGLISFNYGPQPIYCANPEVSGQNTIELPAIDILSSESYWVSVLTQDHGPLDAFQSFNLTWSSSEYGGNTLNSSSTQGLYGLVGLNWFPFNAETYSMKLQYNYINNINEVIQVRLYGVRAQRDWLPYCD

>Cel|clec-168

MFLQLILFLLSASHADSDCIDIEDKEIGGLCYKFVNLSMEFYDARKWCHYQSPVPSYLAYVPDLSTSNFLATYARAAFETNRFWIGLSRFDYFDPYLWDNGRPVTYTNFGTGTGNFVAEHTLNGKWYLYGNGAKNVFVCSYDPAAPPTFPPPFILTTRQSTITSANSCQPGGPISFLFAYSNDLDPQVVKDSWDLSNIDDYSGYSVYAIAKFDVLEEEDIVYFLDKKLATTYVHSHLSNSSLGFNGTTTGSDSLRIIEKFFNNKDVTVCGSVCLILEKRYPNDEDISKTVSLVRYYHGIVYAVSSINPSGGTQSKAIYNLTSRTNGICNFGTDYYAGKLVTSVPMFYPPYPIYCANVLVSGQNITELPSMYVPQSIMYYTVFASVEDHGPLDNFQSFDFSWFNSDEPRYIQHLQSNSTVMDGVTSSGVYYIAPEIYTMKVQYNYTNKMEQAMQVRVYTYDGENSADWIPYCD

>Cel|clec-191

MRLLVFFLKIAFLIKLAMPIEKMLLFYGKIVKFNKEAISITVTDLDSCVQNCFEESTFILAFWNSSGYCNLFGFSSFDEIREIESDEGDVGQYLAVKADLPNNTCPAFPFETDIKRPGNQTWKSGNGWTTRLCKAGWTLFSRPDSIFVCLKFFELKLGTNRTVALQTCVDNGAIMTGLATRSEVYWLTEFIVAPLQTGQWDGIWLNGMRDCSSNTNKTCQNFVWSDGYTIDTELLKPGFLWDPGYVNNQQDCLAVISSISDLKLNMVNCTSYDVAIGVACGYQFK

>Cel|clec-148

MFLSFIILSTFLPSVVFSASFPSFFNESAYETSGHKPEIYQLEYSGGCISGYTWFSYTNFCYKSTARAANFNDAHNACRSEGSELASIHSLTENQFLVQLSAAGNRVNSKTNYVMIGLIFENREWSWTDGSSVNYLNWAAGEPNNMKHELWTALVSDVNPKKGQMYTHWNNVNMDRQRAYICKRAPLN

>Cel|clec-78

MLEKYGRCRKRRLLKEVVLILLVAAVQPVLSSSKSTPEAQLTDVELTCPDDWIRHGTKCYLPFNIHQSWPFAMTTCQRYGSTLAKIQTGSENQFIASLLSKPGKPTEGKEYWIGLTVEVLDDDELYLWSDGTPTSRYVGFWRQDQPNFLNGSCALGKVERKDLEWRLDTCNLLRRFVCERPACVQGSYFCSSGSCISESKKCNGHNDCDDGSDEQNCPSAFQPNCRTYEKGESGQLSSTNYPNSYDPNLNCRHVLEGPINSRIELTIEHFETEPDFDILTVLDGGPAENSTTVIKRLSGSMETVQTITSATNMMIVQFRTDAQSNARGWQLKWRAVPFTCGGHFTAQAYIQSFVSPGYPKTFANGAECVWTVESTPGQVVSLIFDDFSLRAEDSLIVYNGATPSATVLASFSGNLTTKKYITSSTNIVYIYMMTRTTSSSRGFSISYKRGCDLSMTDPHGEIISPGYLATEYPNDVTCTFTIEIENLKADRSLSIIPNRFDVADDDSVRIFENLVKGKALHESDGFTAKSKPEKQIDSEANRLQMVFKSSASRQAMGFNFSYSIDCPAFPTVPMVTLSTKQRSVNTKVTVECPIGFEFASGEGVSKTVECLIGGTWSQSQISTCQPIYCGAVPQIANGFVDSATNVSFGGQVKYSCHKGFFFASGKDVETVYCGELGKWGIPPACKAATCQPLAQFSNGDRRLEFGDGTGYGSVFRFDCHSGYRREGVESSLCKSDGTWSSKQPNCTKVACTHLPEVANAKIEVPDRFLFGDVARVVCNSGFTIDGPEEIRCLANQTVSSTPKCIDIDECSSGVSQCQSLGTQCVNLPGSYMCQCLDGYQPQLMCLESNPIDARSSSKWCVDSKNVGKDRKYPTKVVKFAIPMIVEQIKFANVRNGKITKISIKYSETDKTRTKKLIIDNESILDVDEDNIATLPMAIEVQVLEIEVVGLEGSPCLEVETLGCQRTSCADINECLKDNGHCDHLCINTQGSYKCDCRNGYDIFTENGQSGVNVSTGETGNNMNDFIRFNKSCVPRQCSHIGSPENGQLLSTAERFEYPMIVQFQCAFGYQMMGPDYIQCLADGTWNGTEPFCLSATCQGIEASSKSDGLTVTPNNSTISFGQNVTISCSFPNRPGKLSSPLSNYRQCIFDPQDDGRDYWLSGPAPECSFIECPAPPTMPGAVYNGDVTDRKMGSTLEFTCRQPYTVVGRSSAGDQNIKCSPDATWDLGDLRCEGPVCVDPGYPYDGQVDLESVEEGAIAKFSCKRPGFVPFPSDTLQCTLGASCVLSEDVGIVSGFVPDGAFADNSDSTNLGYEPHHARMGSSGWCGAKEDFIFLSVDLQRIYTLTTLRIAGVAGSGHLKGHVTKFQLFYKTENQHTHKPYPVEFESPAGNHNAMHHFDLKFPLRARYILFGVTEYEGNPCMKFDLMGCVAPASPSHELDSHLQIGWNGSVPQCVDMEPPKFENCPESEIFAKVDENGQLKAVEFEEPAASDNSGKIAYTQIEPLGMRTGLMITEDMDVTYTAFDSAGNTAVCVLKIRIPDTQPPVMKCPDSYTIPVGNSTKHVIFDMTTVDMVLHDTSNVSDVTFTPSEATLKIGEFEEVTAQAEDENGNRNSCKFQVAYAPEACSPASLASSNQIVKNCVHEEGAVVCSVYCAQGYRFVDPDQITQNFVCKDGRWSPRNNAPACVPIPKDPAGFHVNVGISYPVSSPVPNHCLKGYAELAAKEFDNLDKVLSSRCSSSVEVHVKLLKLDFSNQNGVLTGNYTIQVLPTEQQSVFYDLCGLTLRTIFDLNIPGANQPIQALLSLSGEAIASQTAGCPSITAKASSVVQGFACATGEVLRQEAKDRLPECMACPSGSVNINNTCMLCPRGSYQDESGETSCKPCPDGTYTLDEGSQSVGSCLAICGFGMYSSTGLIPCQLCPRHTFSGAAPIGGFRECEACPSGAYTAKLGASSASECKQACKTGTYSNSGLEPCSACPINFYQPTVGQQSCIECSNTTATQTTGESLESSCFPIDCSAKMCENNAECSVFMHRAQCHCKPGYVGDRCEMLEDVCSTQPCYNGGKCEQVGTTYKCTCPKMFNGARCQFESDECNGVKCPNGGVCHDLPGVKSTTCLCRTGFAGPQCEEITDICSTNNPCRNGARCIGEKLGRFKCQCVPGWEGPNCDKNIDDCADSPCALNATCVDLINDYKCECPTGFSGKRCHIKENLCASSPCVHGLCIDKLYSRQCLCQPGWTGENCDQNIDECAASPCQNDAKCIDEINGYMCECADGYEGVHCQHLVDHCAKQPCHNNATCTNMGATYHCDCTLGFDGVHCEMNIDECAENQCDKLGTESCRDAVNDFKCVCKPGYTGPRCDVKQDQCADSPCLNDAQCVDMGGAYKCVCKSGWTGPKCEQDNGSCAAKPCRNNGFCVSLVADYFCVCPPGVSGKNCESAPNRCIGQPCHNGGECGDFGSHLECACPASFTGKGCEFKNTGCKTCENGGKCAEAAGGLQKCECSPGFTGERCETNIDECSTAHCPSGATCVDQVNTHICVCPFNLTGVHCDKMINTNYDLQFLDPFRPTSASLYAPFRIESSALSVGLWVKFEKPHQHAAFFSLHRFDNSSQEYVRVSSNLVRLTLFPGLAAVEVPLSSSQHLNNGKWNHLLITWQSKTGAYSVIWNSLRTYSNNGYATGKQLDVMTGITLGSTALPSFVGSIARVGVWNRVIDFEEELPLMVQHCQRSEEIYKGLLVRFEGFTKIIGRVERTHKSTCGVEEKSAMQKSQSQILIEDCPSDMVISSMDRETNVTWPEPTFLSSNSKIEKIEKNLKQGQMFTWGEYDVLYTATDNATNQAQCNFKIRVGKENCVDAADPVNGVQSCESWGPQLKYKACSVECRDGFEFPRSPAVFYTCAADGKWKPNKSPSTMFRYPQCTKHVPATKVVIVRIIYGSSPACTESSKEAFTQKVQQTIDAIDSKWKMCSLTDANGCVGTQVRVECGGSKLPEEGRRRRRNPESVLASSFGVEIEIPVKRRMLVDPSSGLETTIRDALHNEILSGVLNFEKVLPNGRPDVGSLKIKEEYLCQAGQVVVRDLCVPCAPGTYHSAATGECELCPIGEYQPLTARTECFKCAPGQITASEGAISEGECKDNCPPGHQYDSLTSDCVTCGYGYYQPSAGAFECIPCGIGKTTLSEFATSEDECRDECPDGEQLSASGVCQPCQIGTYRSRGENKKCVACPPGTTTEATMSTRREQCNTPKCKPGQFLVKETKNCQFCPRGTFQNEEQESTCKLCAPDHTTAAPGATAESQCFSTNQCATGEYNCSWHANCIDLPDENDVPSYECRCKPGYRGNGTHCTDACNDFCLNDGICKKNNIGNVECICKDHFSGDRCELRFQASNNKLWIATVIVGVVVIGIIIVIIVFMISFRFNHVQDTNEKSSTLADLSPTANNILYGTPPVCEPPRAFGYYYEDDDVYETKSREMIGSGSERRPTTSTVTSMGGAMSRAIEQHKYEQRMRQAQQHMYQPGGGNDEE

>Cel|clec-79

MTTKVVSVWLGFIVSAFFTTSWGLLLNSDEGFEKACKQSGGDYTQRAGNDSNTGDICLMKFSVVTSDEQDARDFCELNAPWRLREARRETQDSIPVVICDVEATYTCNAGWIQMYGYCFKMSEMHDVYTHEEAEKYCKEQAGPSFHGEIASIHQRYILTPWKNYFRTIKQFWVQAPETWNEYVVKTNKVDGDYLALAFFGDHFEFSVPVNSLIKINGNVKLQALCQYKPAITPAEINYMGRRYSEIYYPTVPVKDGIIVRSASSYTRSSNQLDVCKKVLKPYMYTKESHFFPDPDSMEQLAKLEPETYSLMRSPLVSEIDQSYRNRHNCQTPGAHYEVVLGGKKTANFVVEHDKIKGKPTCDNMMSASISHFKGQAPEFHPMVDSQSLPIWCKLGKVVKYKFDVPPGWLDFRRLNGQVVLHWLSEEKLKFTDAAKACEAKGAHLAGINSLKEAEQLGNHVVGAKLNNEQFWLGAQRKTECLENNDWKAPCTRGKIFEWNNNVATDFREEWWKKNNNNHSPNPSGTGQRCLSFAFGDLYWSEKGDKGFLDDIECHNELRYFCSKMATFTECEENCD

>Cel|clec-119

MLLAFFIALLIPRAHSTTLTFSQFQELHSKTADMTSMKVCWMLGGDILPVDANIPEKGHKCTATVDRWSSNAKDAKEACASRIPYHIDSAQYGTKTQCTFLINLACAEDHWQIHGKCYRLHNGKYTWAQAKAICQTGVGDDVKSQVAIFYSEALSIYLNDMENIGAAWVNVPNLNDYFTNPNNDHGGVYIQGAAYKYDTRQGSIMMFKAESKHQVICEYTPPTTMAEMFHLAKVYAQIYPIGVYSHGAVFPTSSYVRITQTDIIAYNGKFTDKYGNEVEKFDASGLEKKCASIGNILNVKSYPVSGHADDFNAMKSLLKGHQCYLTSSYKNDGFKKTDYRAKSGNNSLEGGIFEGASSDEYCNAHSLSMSTTERLPTMAATGACALCAMHQIHYEYGPCPDKPDWIDEVYRFERPSRVFCHYINNHEVETRADAVVRCESFGASLSGVDSDPEFQGLAQKLSPKYPPGNTVDITPHSRTVYFGDANKGAIRIDDHYWLGGISPCETDCSGGPTGVREASWDAGVAVNTTFLNNYNHDGHPWNLLPVTQYVSFRNDFNAFHIHPLDHYYTKNGSIVHYEKMFFVCGKSAHLTQSTTIKSALQQTST

>Cel|clec-113

MMVTFGEPGVYSSYSNPLPSTDTWEDCLEYCLGLSTCVAVYNNNCQMFEIGQISTATSTSETKIAFKFLADNATCPIQEPTSLQGHYFTNTTYQPYTVSYSAPTWTFANSTQLECPTNYALFVRDLGPWCMKVIQHYACCNKTIAATMCNSYGAQLSGLDSTAEYDFMLAGSWPIFKNVTTNKIGSTQYYATGVWVDGARTLACMGNTTYPCNTTQAFSFTDPTLSSPPGGYLWLPGRPDGGDAPADGIVLNLYTTELYGMEDTPSSEPVSGVYCWMGYLCGAVPT

>Cel|clec-31

MKLSVQHDWKLGPSSLIDESTSLVSKNPQPLSTRPPLSKKWSQFLKHHWLAVLIGVISEILILSGAVLLTYYLANNSTSVTGNTASSDIDSSTALSFTGTRSAPANISSCTFGFTYINGKCWRLFTDPQTRENADSACMSYGGSTLVSIKNEQENNAILNFVPNSAVENLWTGLHCKANTTCNWDLESRSTDTNLVYTNFASGLSSNECVYFITAGSEAGKWKSDSCNQTMSFICELPSTIHDDNCDNIYNNHCYLRYDLSYTVAEAQTFCKTKCANLVSINSANENRYVQSIYNDTNGYIQLGAMLLSSDDIYWLDGSLPVYNNIKRTLNGNCLFMSVSKHRRGFWYTVECTQRSWFLCKRPAGIVC

>Cel|clec-22

MSTSHLLEPLECDEQPDIQTRFERFQHVVSNYWKNILIGLLFQIVYLTIVVFLTYFLARENICEADSTSTSTKRLPIYSAFPTSAPGDYSCADGFTYVNHKCWKFVTGPQRRADADKACFNLDGSTLFSIRNEQENQAALEFVKDQKVDNLWTGLMYYADDPFSCTWDVNSGTTEAYHNFAEDHPNNEYGDCIYYMTTGTQAGNWANGSCTETMSFVCELPATVYDKNCKYNYENYCYTPYNQLETSRDAKNFCASSGSNLTSIHSANENRFLVSILPSYSIIVLGGFAFSKNVVLWLDGTPTIFINAILINRGNCLFLSSQNGHWFGYDCLTEKAHFVCKQRISGQ

>Cel|clec-24

MFNKFLKRFTAHFSISTICVICITLFTGVTPHLNELIFLSILPIPPVIKMMLGKLNRFLQLHWMVILLGIIFEILFTIGVVRLTYFLTKQASVESNKITSSAIQTSTVSTFSGISTKSHTSPTPRLLSTSSTLASGNRTCTDGFTHINNKCWKLVTGPKSRADADKTCYDLGGSTLFSIRNDQENQALMEFVKDQKVENLWAGLICDRHGPAWCTWDLQSGTTAVYNNFADGWPSNEDKICNYFMTNGTQAGKWASASCTETMSFVCELPATIYDNTCEYNYDNYCYTPYFELKLSSEAQTFCASSGSNLVSIHSANENRFVYNIIPPGTETSIGGVAYSDDSLLWYDGTPPLFTNMIQLENGNCLFLYNDYVHWFGNNCLTTKCHFVCKRRISEK

>Cel|clec-28

MSDIDEIQELQEPSQPKTQPYSEKFKLFMTNHWKNILIGGLAEIIIIVFAFMLTFILAKQPACETGIVTTSIFHTSTLPSTLTYASSSYSTKPDKSSIATSTTLKPKTLPVTTTSNSLSTHTKLDTTSISATFATMPTPVSGNLTCASGFTYVGNKCWKLVTVQKNRADADQACFSLGGSTLFSIRNDQDNQAVLEFLKDQHVENLWTGLNCVGINPFTCTWDVKSGTTSAYNNFADGYPNNMAGGCIYYKTTGTQAGQWSSGSCNEIMSFVCELPATIYDSTCKYNYNNYCYTPYDQLQISSDAQSICASSGSNLATIHSANENRFFMGIFPSFSMIALGGVALSGDKVIWYDGTPSTYTNIRTLTRGNCILLSNDVGRWDGYKCMIDRAKFICKRRIIGK

>Cel|clec-33

MSASHLVPEKWIQFLRLHWLIILIGVITEIVIITGVVLLTYFTTHHAACAADKITSSDFQRSNVFSLTSDSTNSEALSSSTTNIPMTTFSTNEASSSTKLLSTSSTAEISSTTRTVSRSIKPETSTASTTIRPLTTTTTPAPSNNVGCTFGFNYINGKCWRLVTSLQTRDNADFDCMREGGSTLFSIRNEQENNATLDFVSNSGVAYIWTGLICNANTSSSCTWDLKSGSAANYDNFAKGFPNKTIGDCVYFIANGTEAGHWKSSACNQTMSYVCELPPTIHDDNCDNNYNNNCYVRYDKSSTIADAQEFCKTKHGGNLVSINSANENRYVQTLYYVSGYIPLGAVVPNYNVIYWMDGSPATYNNILYYTNGTCLFLNFSWGGSGDFWETVECTDKSWFLCKWPIGIDYAQ

>Cel|clec-32

MSESYVFEELDCDEPTNEQTRFKRLQHVVSGQWKNILIGLLSQTLYATFLVLLTYFLTKGRVYETEIVTSSTFPALPSTSSKADSTSASTTTLLTPAPSNINTCVFGFTYINGKCWRLFTDPQTRENADSVCMSYGGSTLFSIRNEQENNAIFDFVSNSSVDYFWTGLICKGNTISSCIWDKESGSADGYDNFSDDYPDVAIGECVYFITTGSEAGKWKSGSCNPTMSFICELPPTIQDNNCENNYNNHCYLRYDLSYTVAQSQKFCRSICGNLVSITSANENRYVQSIYIGGGYITLGAVVPNVNIIYWMDGSPATYNNIQHYTNGTCLFLNLAWDSTDHWYTVDCAEESWFLCKRSTGANYIC

>Cel|clec-240

MAMTGISPSVFCPPWSMFTAYLILSLHFFTGTLISACIPTQQVETTFVPVTTTTSSLIPLTTTSTAIPSIVTTTTTTTTTTTTTMPTTTTTAIPCPTDWEEFVRPSGTWCIRVFMGIGDQPTAAGLCGGEGAVLTSIQSQEELDFMRSSYNTVVGTLGFFWIGGQRTGACISSGLTATCTALNSFSWTDGSATGTAGFVWNTGQPDNGGAMLNEPCVTVNYLGVLSDDACDRYDGFGYACGKEPM

>Cel|clec-241

MSLVFIIYFFLFFTISLMNACIPTQQVETTSAAPTTMTAIVTTTSTVSPTTTTTITTTTTTPIPCPTDWLGFARPSGPWCIRVFVASGDQPTADSLCSSEGAVLSSIQSQEELDYMANSFIALNGASSAFWIGAERTAACMSSGLTATCTRLNSFSWTDGSATGTAGFVWNGIEPNNGAGMTESCVVENYMALLSDQQCTRVFPGYACGKAS

>Cel|clec-68

MFFNFLIFSVIAGLSNAACLDSNDQEIQGFCFKFVAQQMTYSDARNWCRYKNPAGSSYLAYVPNKDTSNYLAFYARSAFGTSAEYFWIGLSRNESSGSLSWDNGLPVVYTNLGSYLGQNYFSEKISNTKWDTLGDNSTNYFVCSYASTSDQATSTEPPTNNCQPGGQQTILFAYSNDLDPSVVTDTLINSYLSSQPVTFAVSRFDLRQPEDIGYFNTYNEAASYVSTHRPDSTKRLGDNSTGSDVLDVINKFYNNTQLSPCESVVMVLSKRYPNTTDISNIVSKVRKYHGIVNFLASNTPSGGTQTRVLFDLASKTNGIYSIESDSNFSHFIEWMPLRERYPIYAVNARVLGQGSQALPSMSVPVYAEYLLMIALQNHMPVSNVQSVSLSWYNQFSVDSSSFDMQPLGWAYVDSNSDGTREHLGTVVYNMTIDYVYNDIDVETMQVRFYSPYATDFWQPYSD

>Cel|clec-67

MLLKLFLLAAFAGLAYAACPDSNDKEIRGFCFKFVVQKMAYNDARNWCHYQNPVGPSYLAVVGNKETNNNLAVYARSAFGASAEYFWIGLSRNGSSGALTWDNGFPVIYTNFGSHVGNNYFTEKISNSKWDTPGDSEKNYFVCSYDPTVQPVTPKATTPTTTTAANVNCPLGGQQTVLFAYSNDLVPSVVLNTFSSSYLNSQPVTIAISRFDTRQPQSMMYFNDYNQAYSYLSTNLPDSTLGFGDSTAGSNVLDVINNFYSSPSACGSVVMVLAKRYPNTTDISNTVAKVRQYHGIVNFLASNTPSGGTQSRVLFDLASKTNGIYSIDDDSTFSHFIGWMPLRERYPIYAVNPKVSGQGSQTLSPMSVPRYAQYLMMVTVQSHVPVSNVQSATLGWHNQSSSYSGIFGMQPAGWEYINSNDDGTRENIDANVFNMTIDYVYTNTDVETMQIRFYSPYATTYWLPYSD

>Cel|clec-18

MKCNNCILLLTFLCSFVDAKSSLICTDGFTLINNKCLKLFSTPSNHQEAEKSCSRFGATLVTVKNANDSQAISTITKSSAPLVWLGLYCFDNYPSRCLWDDGTGSAHMFSNFSNGFPLVQLGNCVYYSTRGVLAEKWLNSDCAGNRMAYICELPPTFKDNCTHNYNGFCYTISQYAKVPLKAQESCQKEGGNLVSIHSENENRYINTIAPVVDYFIGATWNFYNILKWIDGTDMQYTNIDLLNSNRVDYCTAMATKSGGAHSTGSWYSADCSITKQYICKRRAGVQCSMTSTTAIPFPEIPSNCNVGIQMAPGVINSRNLSGSVNCTYQLATLGPYKIALKFTFFDTGNDYVTIYDGPSTESPILGRYSGNMYEFTRTSSGSTMVVTFKSDGFGNQSGFNAGFSSIVY

>Cel|clec-90

MDDSTIRRRPPVNFSMSLRLIIIIVIMLSASQVPVSATRKPVMCLQCGGEKYEGSVRLSRDECCKATPIMCLQGQVCLRALVYSPYGNFFLSGCHPEEDHLSGCDFHSLPHNSSVHRCVCKDGECQNDFPGDCPINGITDITKPTITSTTSPPSSTPPSLISRNRTRSNNSSPRNRHHHNHSMTSSHVFTLSTFISTWVVAITVL

>Cel|clec-206

MLLQLFLSLFLASYAKSACFDGRDKEIKGLCFTFVPQQMTFNDARNWCHHQNPVTSSFLAYVPDQYTSNFLAYDARTAFETKNGNFWIGLSRNRSSSPFVWDNGRPVTYTNLGTQLGQNNLAQSVVNTKWNAFGENDKNFFVCSYDPAAPPTFSPPVITSTREPRTEDSFCKRTDRVTLLFAFSNDFNSQTVRQSWDRKTLNLAQYSGYAIARFDVRVAESIAYFTDYRSATAYLHSHLPDPRLGFGDKTTGSDSLQVIEKFYNNNDIPTCGSIILILSKRHPNNADISKTVSLVRQHHGIIHAVCSVAPSGGTQSKAMYNLTSKTNGVCNIGEDGDFDELMDYIPIYDAPYPIYCANPVLSGQNITELPQMNIPFSNEYWVALTIQDHAPIDSIRSLHFFITKTNDKYSIIDWQVYPASFNGILTGNGFTLSPVTYSMELQYDYTNEAEEATQFRVYSISPPQDWLPYCD

>Cel|clec-229

MIQRIYYLFLVFLNVNACIPMVPPEEPTTTTTTATTTTTAPPPVCPDGWFSFQRANGLWCYIIARPPAAGWTSPQQYCQDNQMGSFLNGFETAAERTQFLNDVMTVNLAPYNFVHIGAMRVCAAPPCAVTDPYEWLNGVSTNNALANDFMPLYDGSGDCVSMELPQGGRYNDITCDALTAYSCGKYAS

>Cel|clec-228

MIHPNSIYCLFWIISHVSACIPMVPPETTTTTTTTTTTTTTTLPPVCPDGWFSFQRTNGLWCYIIATPPADGFGAGGAQQYCQDNQQGSFLNGFETAAERTQFISDLNTVDIAPYNFVLIGAKRVCAVEPCATTDPYEWQNGVSTNNALAGDFMPFYDGTGDCQSMEKDMGGRYNDITCDATTAYSCGKYAA

>Cel|clec-13

MHTISALLIFTVCLASCVTSSPICTNGFTLINNKCLKLFSTPVNHTTAEKSCGSFGATLVQAKNNIDNQAIATIAGSGSSTLIWLGLYCFESDPSQCFWDDETGSAHTYNNFSSGFPIVELGQCVYYSTQGVLTGKWLSENCESQRISYICELPTTIADSCKYNYNGYCYTFSTADAPFSTAQGICAQSCGNLASIHSSNEARYLTTFAPEGYYYIGAVWHHDSSLIWLDRSAWDYSDIDPIFPRVDYCLKMSAFNGYPTGMWYSNNCVDNNKYVCKRPAGVQCPAVPPTTVAPSSSYCNAGRLMNNAVITSPNYPENYFNNANCTYTLSTLGSYKIILVFYDFRLEAGRDFVTVYDGETTSSPVLAARLSGTIKGGFSYTSTGNNMLVTFTSDASIVGPGFTARFTSVIYRP

>Cel|clec-142

MNIRNLIFLSVLTHFTAAFLCTEDWELLNVKSGPVCWALLDVPNFDSKFSLASKVCESAGADVATIHNWAERSVFTDLTNRVTEPTLTCYKSSQFSIEGQFKTIDYEKPPEYLRILNEKGKIRLSKGIKRGDRISINFAFKARTNLNGVNELTGEIRIGKNSSHYSINIKCTLQNSSPTKLCELSHPNFKRRHAVQFLKEGMENHLTVKYFGRVNLDFHGNRINLWDTEFILPTEYSYVGMDEISIENFIVNRVEHSNNCQGMDEYEFDRQSISVGTLPSILLKDENIPVPRRTLNTSTYVIPEYRLDYYDFEGSNSFLYDIRLSQDPSIAGNVAIVFWNKKLKQIILKLTLTSKRIKIEAPNEHGLLVEKLRKLDINTKICRGRSLDFRFKTISKSSSMDFFTTVSGLEKEMNEAKLELLNINFDEIRFFSDNGNFYEVKMNPLEEVVMTTCNYRKIKYIDSSETIPFLDTCYRKRRILCQKRAENAVDKTILNEPKEKSVWKEKIIEIIQTTPETKKIEKKVEKKKERKIKEEVKEVQKEKNQITDFGEF

>Cel|clec-149

MTASLILLPVLLNILYQPAGSSLPTFSPGNKHLCEGFGFNWAAEIRCLRDIINDCEEGTQEKSRGGRSLQRSEFPTDNTPQADYGNPYSYPRPYSRTYHRNSISPIRPPVPMPIPQISQGCNCNHDIEALEAKFDKKLYEVKMHAQYETEKGVGDLRKQFETDLREYERITTKDIVEIKRHLDYLQAPRITNNDLEYFFIQREESWYTASEKCIGYGAHLASIHSRLELGFVQRLVPVNQTAWIGVNDIQKENVFRNSDGTPVDFYKWGKKQPDNQEHNENCVEVDHSGQWTDKLCIITRPFVCKKKI

>Cel|clec-172

MISQLILASSLISLAHTACLLDSDRQFGNSCYIFVNQRMDFDSAENSCRRQPQIWANLAKIDNVIESNYLARTAATIFGMEHGSFWIGVYRPTVYDPFKTMDGRYCQYTHFKNANPSMDYAAESVTDGYWSTFSKETRMPFVCYYPASEAYASTMSSDWLENLRKTKEEK

>Cel|clec-116

MCPQKKFYVLATPLHSQRTQIMVLMHGEVLTHGGGLSDFTKKPVNWSTCVTNCHSKVNCIVAGFEYETCTHIELGRVFTIKRLNAYSEKMVAVKGTWTIQELKCSEGFRMFHRHKGSWCIKVVTRPGTSQAEGANFCYTQHNGVLSSFDSEEEKNFVLNETMRFVEKYQIHAGYQGDAYWMNGERKNSCMHQYQEGSDCDGIKAFNITDPLISEVFENWADNQPSGMRDNKGAGGCIVFRVGTKEGRSTDDVPCDWGNFPLGTFQYLIKGFICGTRPG

>Cel|clec-88

MQFIFFGTLFSGLLLVCAVTNDIEDASGETPGIVSQITEEQPHQRQKLYNWDYKDLGTIAFEDIPFPTLQPSQTIDQSENCPEGWIRYSDSCYWVETELLGFAKAERKCSEKQSTLFVANSIDEWEAIRGHSKDSFSSWIGLVRFSHYERSEQLPRWQTEGAVNPSKMCVYFASVLFQRKKFRNWLIKPYSPLVNGWSQLANCAASYKSPASLETASYTYFYPCTYLFYSICERNSTIANSLH

>Cel|clec-265

MSQNLIFVISLIASVFYCTNALTCPTGTKIYNAKCYAALGMDMTRDNALAYCRKTYGPYARLTTPLTYAENNFVTEQVQLHANWHTWLEYVADGTYIVGDDGKPPIYTNFAVGEPFSVNVGYCITIGMNGYWYAQPCPDSHSVLCEFDLVPPTPKPVLTTTVKPSGFPSCVQKYLNFVPCQSGWEYYPPTCACFKIISNTTYYNAMNTCRSMGGTLASVHNAGEAAFINRLGVQANSYWVSTATARDNIIIGLTYNSDRGYFQWDDSTVFDYAQGFAPAEPADYTSQGQIILNNPMGYATYMRMGNCAYQTCRYAACKRYVY

>Cel|clec-258

MFPKLLFLAILIPSSLTDCPDIDGQTREIKGICYKFVTSLMKYEDARDWCHHHNPAGPSWLAYVPDQETSNFLAVYAGSIFGEGFKHFWIGLNRDPISKTLSWDTGLSVSYTNFGSNVAQNYFSENITNTKWNTLGDDEVHNFVCSYRPSTVPATVTRQPQARRLAAMKN

>Cel|clec-190

MIKASLVFFAFLALASGRRHHYDYYDCEPERGPRGREGREGPRGAQGAPGPNGTGFFWPGTCEQSDCPDGWISVNRKINNDVEKKWCINMFWNQATNDLYKTSEKVCNSYGGVMTGFKDKGEFISVFALLKNRFPNIKPVSQVMIGARRLETCASISNFGNCTITKGTKWTDLVMSIDSFFNELQQSARFSPLKKCIVANPTNLKLYVANCNVLESDYPQDLFMCGRFAPCKK

>Cel|clec-189

MKVAFKVKTAEGSCPDIEGSPVTGDASTTTFFAKIQNYTITFIGTFEKFSMSRCEEGWAFFKRESVNWCFTSVTKTDVTYSAAEASCVQFGATLSGLESQLEANAVVSILQTSRSQKQLQSIYMRIDGQRTEECQETPTTENCMSIDGLTRHDKGVKNFDAYQFMTDSSAGATDGKNCMVSVCDGVNDGKIEFAECEISTSYSISYMLCGCRIDNVSMQFIVPTLK

>Cel|clec-150

MLREHIFSASLLFLISVSVGSAATCHGEEKLDPSGKFCYVVHTGAASFHDAEKACYDYGGYHLASVPSMIDNNFLYNLSSNSNVWANYFWIGLTDMTADGSWEWIDGLDLVFMNWASSSTAGYCGAMRAADARWQAQDCTKPYPFFCYGPALGAPTNPPNTPKTTQKPVRNQENMIKFMADAESVGDPNVDPNALSFYNKEREFIRAVTDYLFANPTSDGNTCLYYMSPAFYGFTQYEQQFDTSPAWSHYQFDNLLESNVWDQGKTDHDYNITDAITGAQKFRWVPSMNNIGYTTLVFLTARRDFSGIPSLFQPFPKFDEVVVISLNGSQMPGIPAGVKNVAVSNDFSSTDIQNVINVLKCH

>Cel|clec-43

MKIFIICLLHIYATFSVSQITSRAPYNTQTPSYSGCPDGFIVLNGYTCIQVSTTKKLFMDALSDCQSFPGGNLVSIHNSIDNKALAFSVTSSDPKWIGLICTETSSPCNWTDYSSDTSSYSNFVAGNPNLDVGNYVYMLVSGSSAGRWVSADQYTQLKYICEVPFHVTSTSGTPTRAPTPTPNGSVPCPEGFWSYKDNTCLKLFNTPMLYQDASYVCGNFSKGSNMVSVLEAQDDFTLKLISGLNNLTRPIWLGLSCQYPSASSCSWTDGSGTTSNYNNFAPGNPNTDVGTRAYMLTSGNSAGKWISSDGDYSYYSFFCEVPRADSCEHTYNGFCYSVNTNLLDEPDARQVCQRVSGDLVSIHSQAENLFLQSLVNSTGVAEYRIGAATDGVGKYWVDGSTFDYSNFGYFNPNLGKCSSLAMSGSVIPKGQWLSTNCNNKIPFICKHPQNLPTPTPTALGQCNGTQFLTGNGSFYSPGYPDQASGYPTPCTYIITESQGSIAQLQFEVLHLFWGQNMQLFSGIDETQPFAIVDIYSNKIYNSTTNVLKVVFHCITSNYATYSWAANYGTNIS

>Cel|clec-44

MFSGGSLVSIHNSIDNRALVQSSISYDPKWIGLICSDANKPCNWTDHSSDTSNYNNFDAGNPNLYAGNYTLMAQSGSAAGKWVSADDFSQFRYISTTAAISTRAPATTPEAPGRCPAGSSSLNDITCVKLFDTPMIFQGANLVCRNISGGGNLVSIHSAEDNTALLNLAALNNKTKTIWLGLTCQSPSPSSCEWTDGSGTTSNYNNFTSGYPKPVRGPRGYMWALGSDIGKWFSSDEDYSTHSFFCEVPKSSNVSAAETPLILIFHFCYSVNTYLLSEPDAREFCLSLSEDLVSIHSQAENDFIQSLISNTVIDEFRTGAATDGVGKYWVDGSFFDYSNFGYFGTNLGKCSSLSMSGSVVSKGQWLSNDCSNKIPFICKHPKHFSTPAPYVSGQCNETQFLSGKGTFYSPNYSYGFSGYPNPCTYLITEPPGTIAQLRFAELHLPLGRTIVLYSGIDETKPLAIVTENTFEVYSSTTNVLRVVFNCPLTTIDNYIWAVNYGTDLS

>Cel|clec-175

MRLLLVFFLVVGYVLGQNSNQPITSNGTPLDFGLKKACEDVGGIFKQRENANAIIGDICTITFRVLTETDDDANEFCRLYAPWRLRSAIRNEDGGIPQTICEVEATMACDDGWIQMFGYCFRHPYKNKIFTQAEAIKVCSNLDGHTGEIAFLHHRYIVGVWKNYFRGIDQIWVNGSETWNQYVQSTGAVDGDALALALTGHTVVFSVFPNSLIRIDPIIRLGILCQYKPERTLAEIAYLGRRYSEIYHQSIFLEDGVLIRSASHYTRSKTNAEICQKTLRPFFVDDVEPFIPNDDIMSALSDQYTEPWAISNSGAHFTMDVSKRKSSDVCLKSTHKYSVAYPDPKMPPFVLPVETSVGCDNMNSVAIVHSEIDTEFRPMSDSQSVPVWCKFGRKMNYFVDLPKGYTHYERANGMHVGHKVVSMILPFDKAMKYCQDDGGAQLGGFNDKAEFEAIDKLISKKVHHWIGNRRRPDCPGFYFHSDPNHQCGHNKIHEWLNNVATEDIPIELWGFKQPDHAWKPQGRQECGSIAYGMPGSNGEPKLDDGSCEVKMPFICTAKGVLKATTASRL

>Cel|clec-226

MNLCFIIAFFVFATTMLHLLLLIIMHSKVFCNSYSMIVTYGRPTNFSSSIPNSAPTWNDCVVQCYISNTCVLAYSPASPIKCQLFNVNRVFVVEKLQASDDQFVAFKTVKSEVTGTCEDGRTSFTRPTTNWCIKVFVDPNALYTASNAISSCSNVNSVLSGLETLEERNLIATTAVSALGPGYSQFAALWVDGTRKDQCVADGWESNPDCTGANMNQFSYTDMYLTNYAGYLWDPNQPDKQAAGPWQNCIQMWIRIESADPNFPYATYQNGNVDDAICDGTNSSAYALRGFACGKLPYVPLGA

>Cel|clec-53

MLRPLILALCLVVHLISAQCGPGSIYQQSNSRCLTLFRAAVNFQTAESICATLSGHLVSIHNAIDNAFVSSQAQKYMDGGAWIGAQASAPDVTNPLNWYWTDGSNFDYQNYKVGQPTPPGSTACMQLETGTAKWQTANCTNKLPFICSAAATVVPTCPTITIPSHCPSGYTWFETTDFCYKTTVQFTNFNDARSACQADGGDLASIHSIAENAFLVGLSKAGITNKDKDWNDDVWIGLVYQNSKWQWTDGSVVNYVNWGDGEPNNMNKEWWTALVADPHEGKNSEGTRWNNVPQDDQRAFLCKIAPLH

>Cel|clec-140

MHFSFIFLVLVYLTFAFGDSLICNNGFTVVNSNKCLKLFSSAVKHRTAEANCASYGGTLVNIRNSIDNRAVTQFVGNIGLSFWIGVYCLESNNPSSCYFDDDLGTDTAFNNFAKGFPNTDIGGCVYSATSGSLAGQWISSECDNVEMAYVCEIPMTRADSCAHNYNGYCYIMSHENSTSPILSFNDAYKSCQDNCANLVSIHSRRELSYIQGIYSPFNISSVTIGGLSTAPMAPYWSDLSH

>Cel|clec-15

MHTISALLIFTVCLASCVTSSPICTNGFTLINNKCLKLFSTPVNHTTAEKSCGSFGATLVQAKNNIDNQAIATIAGSGSSTLIWLGLYCFESDPSQCFWDDETGSAHTYNNFSSGFPIVELGQCVYYSTQGVLTGKWLSENCESQRISYICELPTTIADSCKYNYNGYCYTFSTADAPFSTAQGICAQSCGNLASIHSSNEARYLTTFAPEGYYYIGAVWHHDSSLIWLDRSAWDYSDIDPIFPRVDYCLKMSAFNGYPTGMWYSNNCVDNNKYVCKRPAGVQCPAVPPTTVAPSSSYCNAGRLMNNAVITSPNYPENYFNNANCTYTLSTLGSYKIILVFYDFRLEAGRDFVTVYDGETTSSPVLAARLSGTIKGGFSYTSTGNNMLVTFTSDASIVGPGFTARFTSVIYRP

>Cel|clec-21

MQHSLILLLVFIFLASASKDPICTHGYKLVKNRCLKLFSEPSNYENAQRQCYQHGGPLVTIRSKEENLDVLALAGKGHNLWIGLYCFTVLDQNGSLSNCIWDDSLGTAEQYHAFESFAGSGSRETPCVTVNTTTGYWISTKYENGMYPFVCEMPTTIEDDCQNNYNGYCYIPHSEAKSFENAQKSCEEECGNLVSIHSANENLYLNILAYNFLPGEYIYIGGMVQDFGFSRWTDGSRWSYEKFDRILKRKNGECVVVAGDWEDVIPIDQWVTTPCNRIRQYFCKRPAGEKCLGGRPKEIGPLVSYTCNSTLLQTPGIIVSPQSQERQYCEYQMHTPGFYSILLTFTTFDLDPKSDELKVYDGDSEQNRLIGTFKGNNEISVTSSGSAMFVTYRSNGTGSGKGFEAKFQNYHYPNPLKKSNQ

>Cel|clec-20

MLQLLAFLLALPFLASASKEPICTHGFTLVGNKCLKLFHEPLSHKNAERVCSTFGATLVTIKSSDEHIDVTTLSGKDKNVWLGLYCINNYRSNCLWDDSNISTDQRNGFQSRPNVTQGNCVTVNTTSEHWSSTDCSKESNLFVCELPTTFEDNCQHNYNGSCYIPHVASSFIRAQRTCEEECGSLVSIHSANENRYFNILASTFAQNEQVFIGGMWTLSGRPSWIDGSRWDHDKIDSLRKREGACLVVSGEKSNERQPWGLWYTGNCDYDRKFFCKRPAGEKCNPDRPEDPTPPVLYTCNTTILVTQGLIIAPPITEAGLEHGFCYYHIYTVGSSSIMLTFTQLDMHPNYHELNAYDGDSENSRLISTIHNYNSPTLTSSGNAMFVTFRSNGTSTNWFGFHARFTEFYFASPMNKLL

>Cel|clec-47

MGIITYLIFVLAIFIFPIASISCPSGFTLLVSTSRCAKFISGELNYDGATLSCNSSGGKLISIHNAIDNRVMMQFANSSITNDNYNYWLGLKCSETGNPNACAWADSTKFSYSGFAKAYPNTGYGNCVFVETAGNSAGQWFSATCNAIRTNAICEIAVNS

>Cel|clec-178

MILLLLYLLIPTINTVVIPSPLKSSYQSIAGQRAINLDVNVRLLTVLALQQSGWQLYEDHWYKMFETDVMWIPAENVCRSMGGHLVSIKDESENLFVHKLRKKNNIWIGLNKLNDTFHVYKWSDGSEADYLNWASSQPNEPDVDCAYMAFHQEQRGTWFDYGCREMLPQFFVCKLPMP

>Cel|clec-40

MLSGLRKVFRFSRATAVDAPENYSIPSVSAEETEPDETPNERTIVDAYDPPKSEFEPGDRQRHFGILHYTVNNRFKKMMLIGIINVFLILAFFLFMFFFVVQPNVHGGETAVTTLSPTTSSEKVPICTNNFVLIDEKCLQLNTTLYSKPTAEATCNRLGATLLTIQSSEENQKIQSFLSIHQISQIWLGLICNGKSVTSCQWDNGSNVTYYDFAPGFPNVDTGICVSYNITHNSIGQWESLVCYKQLPFVCELPTTTSDNCTNNYKNHCYIQVDQSATIPDAQRICQAQCSNLPSVHSVTENLYLTSIYKFSDTSIILGGIASTPKSIWWFDGSPVNFLNFKTSQRTVASSCIVLHVGDGGDWDTVDCSTTVSTFLCKRATGVSCK

>Cel|clec-25

MPKSSVCEDQEFDKPHEQKHVERLQRVVSDHWKNILIGGLSEIIIVSFAVLLTYFLARQPTCETEIALSSTLPTSTLPITTIGPKSSQIPISSTLSTAAPDKNYCTGNFTYVNHKCWKLVTGPQSRAEADQACFILGGSTLFSIRNEQDNLAVLEFVKEKSVENLWTGLVCVGHDPFSCTWDVKSGTTAAYSNFAKDNPNGDCIYYMTTGTQAGQWASGSCDEAMSFVCELPATIYDETCVFNYDNYCYIPYDQINTSKQGQSICELSGSNLASIRSGNENRFLMSTVSVFSIFAIGGFAFSDDLILWYDGTPMGRLHRNHALSVHWTVFQTPLPPLKRLMKTQVPLVD

>Cel|clec-36

MPNLPPVLGKLNQFLHLHWKIILIVVTFELVIIIGTAYFTYVLSSHAACETDKFTSSAIQTSTVSTFKETTTTSDISATTRPVTTSSTQAPPNNLTCSVGFLLINGKCWQLLTWGDYRSNVDYDCWGKGGSTLLTIRNQQENDALVNFVSDIYYENFWLGLVCKGNTTSSCIWDKFSGTAEGYDNFAPGHPNVTIGECVTINTRGSRVGQWESCSCNVYMYFVCELPPTINDNNCYNNYNNHCYLRYDKDKAYSIADAQKFCKTKCANVVSINSANENRYVQSIYYIKDGYITLGAAVLDRDDIYWLDGSTSTYNNIRNYNNGTCAEMLLSWDTGYWTTTECSSNGWFLCKRPAGIECLN

>Cel|clec-183

MRLLPVTLLLGAVIFVSTKSTCRTRTKPPSTVPMNEVTEAVTTKKASNVTVKPTTCEASWTRVERSIGGWCLKVYNGFVHQDQASQACIRIGAELSGSESSAERAVIARLGKERMLAASDYKFGTIRVGIARPTTTRAWALTDGNNDGGQQGIQWSKGEPQLGPTSGYSHNCALMWIWASTGTSPYEHGKYFHKFVHLLGRTCTEDLFVESVLLDF

>Cel|clec-38

MAIFYDDPLERLNQPIKTKSYRKKQVVQRVHVFIFDNWKLILLGILNLIFLIIAIVFAILFFVGSADCAQLPDYTTSPASQLTTSAISSRTSEVQTNAITTTQGTPSNKTSTTTPSTSKVICASGFTLVGTKCGKLVSSNQPRTEADSICKGYGGSTLFSVRNEQETRDMLDFVKDSNIDFLWTGLVCNQTARTSCIWDVKSGTTADYNNFADGFPNVVYGYCIYFIVTGNSAGQWGSEQCSQLMNFVCELPTTIRDPDCKYNYNKNCYIRFDITLTIPQAQRFCNEKGADLVSIHSANENRFILTIYDIHGQILLGGLAPAVDFIVWLDGSPTTYSNLLYFYDTRSCVLMTVARGGPYDGDWYTMNCNVQEFFLCKRAIDF

>Cel|clec-39

MTSFYDNSSSSSKPVPLKTSRAQKIQILIFDNWKLILYGAISTLILVLAIMFSTLFFALPAANCDENSEPTKYYTTNAEITTTITTTNQKTTSTASSHLTTISSSATQIYSESSSSSTSQSTFTQSPPEISTTTIAPSDFSCQHGFTLVNNKCWKLVTSNQARPDADKICNGYGGATLFSIKSEQDNRAMIHFVKGQDIDFLWSGLLCSAGEPISCIWDIENGSTANYSNFADGFPNIVYGNCVYFITSGDEAGQWGNEQCGQVMNFVCELPATFQGKDGCKNNYEKSCYLRFDLNLTVPQAQNFCLEKCANLVSIHSANEVRFIMTIYDFIGEILIGALAPAQDFIYWLDGTPANYNNLKFFYNSTCVHMTVAPGMQNVGKWFTRFCTETGKFLCKRSIKNSCT

>Cel|clec-34

MPGCLPSVFEKWSQFLKFHRRIILIGGASEIIIITVAVIVTYCLTKQPACEIYTGTSSPAFQTSTVSSFTESLSNSDTSPASTTTEPLPTSSTPGKIPPNNITCAVGFTYINHKCWRLFTDLQTRENADGACMRYGGSTLFSIRNEQENNAMLGFMLNAGVDNLWTGLICVGKTTFSCTWDMESGTTSVYNSFASESPDNTYGNCVYFIITGTQAGQWKSGLCNMTMSFVCELPPTVHDKNCINNYNNHCYLRYDDSDTVVEAQRFCNTKCANLVSIHSANENRFIQTIYYVDGYIALGAVAPIIDYIVWMDGSPQLYNNIQDNSNGTCVFMRILWGGAGYWYTIDCVKRSWFLCKRPAGIVC

>Cel|clec-29

MPTFYEEHSENAQPEDQTLLQKLHLFVYDRWKSLLIGGISQICIITSVVLLTYFLARQPTCEAVFATSSTSTLQTMTTSDSLSSHTKPDTTIISTRTLPISSTMPTHASDNVTCAVGFTYVNKKCWKLITGPQRRADADEACMNLGGSTLFSIRSDIENRALVDFVKDKRIENLWTGLICVGKNSFSCTWDVNSGTAAVYNNFAEGYPNNVYGDCIHYMTTGTQAGQWASGSCNETMSFVCELPATIYDDTCDYNYDRYCYTPHYFIKHSSEAQQFCAGLCSNSVSIHSGNENRFVLTLYLYTNSSILIGGIAPSYDFVLWYDGTQTTYNNIDSIANGNCLYLNDLNTRGNWFGLNCLTSRSWFICKRRIGENC

>Cel|clec-173

MIRIKYLIALSSIISLANCRGCLDADDKEIGGICFKFVNQKMTYENARDWCHYKNPVTQSYLALVQNQFTANFVASYGHNAFGSSDATFWIGLSRDRNWNPFVFDNGVTLGQGWSNFDNQNSLNFVAERVSNAKWTTFNDSTTMPFVCSYDPTEPPVFSPPTPSRAPTTTPSTTTTTPGPTTTCKFV

>Cel|clec-103

MCAKMIIPLVFLIGFAAAGNFGSSSSESCEDGNGGGRPRPGNGGGRPPGNGNGNGNGGGRPTNGGCDAGWRRFNRPNGGWCVRVFGARMTQADAQIQCQSYGATLSSLQNMEEALQINNMALSVIKANTGSVWIGAKRTTACLKQWLWTNGCGRQNSFAWTDGSATGVAGFVWDNLQPDNDELKQPCAVMLAARAAVTWGGKFWQPAMLDDNNCMFDLEGKHPRSVYGYVCGKNSRA

>Cel|clec-144

MSRMIFLFLIPVVTSCIPTQQIETTTTTTTTTTTTMTTTTTTEMPCPTDWEKFERPSGPWCVKLFVGLYLQGNRNEASARCAAEGAVLSGVQNQAELNAMTRQFTKLRYGYFWVGAMRKTSCLMSQLTATCTALNSFEWTDGSTTGTDGFIWKTGDPNNYLYNLYDEPCVAVDVNLMKDIA

>Cel|clec-12

MQAIAALLFLSIYLENFLTSSRSIHCTDGFTLINSKCLKLFPSLVSHTVAESSCNSYGATLVTVKNVKDDEAIAAIAGSSTPLIWLGLYCFDSDPAQCLWDDVSGSASNYNNFSAGFPLVVLGQCVYYSTQGALAGKWLSEECESQHVAYICELPITYTDNCDFNYNGYCYTFSSTTNSINTFISAQGTCAQDCGYLASIHSPLEIRYINTFAPHAYFYIGAIWKNDGSLYWLDNSPWDYNNIDPVQTNRVDYCLTMSTTNFGSSPAGFWFSTNCNNPGYYICKRQAGVQCSAAPPATVTPSPANPSNCNAGRLMSDGIITSPNFPQNYFNNANCAYQISTLGSMRIALTFTFFNTQPYDLVTIYDGETSSSPVLGKYGGNQSSLTFTSSRNNMLVTFITDGKDTSNGFSARFSSIVYGNI

>Cel|clec-219

MQRKLFIIVFLAVLTESMIRPISSRNYEGCECETSVKPCEEEPTPPGNEEETTSIPPITSPSTTQSTTSLPSTTSPYICNVQGYQFRVKRKNGFWWCMFASVPVYRPGEMSLSYSNAQLACASDDGWPAIITSIESDEELDVMYALIDSVTAPHLLVRPITGFWVNVTQYPNQTYYWSDGSASEQMVPQPEVIAPGGKALYTFDPVARGRGIVRIMEPTFASKNVSIPIPNVTVCGFQGIRYN

>Cel|clec-218

MRFFPVATILFLAFCAVRCAEPNTEKECQCILNNIWLDVYLLIDNSAKMGSVGLLEVASNVNSVFGFTQIRVGSNYPDKRGARVSVLTYSDSPTVHANLSDFKSTDELTSMIYALKPSTSYDSNLQSSLKLVKNMMNYKDINAPRNNTQTVIIIYAGDYVDYDEPTIAQFGDQLKADGVKIITVADISNTDHQHVSKLKWLKELASEGNGFNINDDYVSEEVQKALCSANCFCPRKYHHFITSNNETTHKYGTCVQFSIEQLSWTKAKFFCQNLHKQGYLATEYTDEKHLFNEKYFEALSSQPKPFKYHIGLHYVNGGYFWEQAIGIPLIPVSTPLYPLDNVPSTTQQCVRNIGTLDSEDLKWDNENCFNDVSPLMCEVPACDTENYCP

>Cel|clec-49

MTRLTLLLFGLLGAATAQTCNTGGIYNEQFNRCYQYFTAPAQFSFAEQQCNLLGGHLASVQNGQENALLQSNAANSFKRSNYSDYWIGATDLETSGTWKWTDPSVTFDYSNWQLGEPQSGSDCAIQDKGDGTWSAIGCTSYRPYVCVTPVIMTATCPPITTPIPTTCPTPAPCPIKQCVPSCDQGWTYFSPTDFCYRVYHGEKFNDAEASCVLLGGHLASIHSLTENTFVNNIASCGIKEGKYEHLAWIGMRKVGQDWVWTDGTPSDYFNWAPKQPDNPKKELCVQTAPDLSHDKWYENWNNLECNEVMRAYICKKASIHN

>Cel|clec-50

MARLLLLTLALFGATAAQTCNTGGIYNAHFNRCYQYFTAPAQFEFAEEQCNLLGGHLASVQNGQENALLQSNAANSFKRSNYSDYWIGANDLETSGTWKWTDPSVTFDYSNWQLGEPQSGSDCAIQDKGDGTWSAIGCTSYRPYVCVTPVIMTATCPPITTPIPTTCPTPAPCPVKTCVPSCDQGWTYFAPTDFCYRVYHNAKWEDAEAACVLLGAHLTSVHSETENTFVANLASCGIKEGNPKDLAWIGMHKVGQDWVWTDGTPSNYINWAPKQPDNPGKENCVETAPDLSHDKWYENWNNEACSTEMRAYICKKGSIHA

>Cel|clec-118

MIFLFFIPVVTSCIPTQQIETTTTPTTTTTTTMTTTTTTEMPCPTDWEKFERPSGPWCVKLFVGLYLQGNRNEASARCATEGAVLSGVQNKAELNAMISQFTRLGNGYFWVGAMRKTSCLMSQLTATCTALNSFEWTDGSTTGTDGFIWKAGDPNNYQYNLYDEPCVAADVNLMEDIACTRTDVTGYACGKPL

>Cel|clec-126

MLQKYSIIVLCCSAVLARVPVAKNCPTGWTWFLRSRGGWCMKVFTEALNQPSAEAKCKAAEAVLAGIQNKEEVAWMSKELTGTMWIGTKRTPPCMNSGVTKQCSQITSYYWTDGSTVGVQGFYWNSGEPNNQGGQGCAKLITSSSVLDDVACTTELTNGYVCGKIATF

>Cel|clec-125

MTLFSPYLSIFFLLTLEFSPIFCMFRPRSSGGNCLDVQAHFYVSEEYDGYTNDVENAYYWRLPGSRNRGNGPCVDLTTYYSVEEDYDGKSDDDGSKYWMVEDLEQTLKLRSDAQEDQKMKLQVEKSSRSSKDQSLDLGDSKTGIALVGVKLQADGSQGSKDQNLVGKIQKDQASQKDQKLNLQANESSRNSKDQSSDSSGSKSGNAKVIMELQADGTYRLKDQKLTAKIQKDQNSDSKTIEDIFNREFEADGLKDQNSKSKDSNTDEASLNVKLQGSQASKDQKASSGAFKSLLSQSSDLTASSSNLTAQLTSTNLGGSGSELSQKLNDLKSNSDSSDQVHLASHQHTRNELSQKTDLSVTTDEKNQKTGFSQNHLINSSLAVSELNNNGKLSGTEVQETVEINQRKDLGNLRDQSSKNLKLEGSEALRSSVDLKKRSLEDQKLSSKDLKTGVAGAQSSSSSDRKDQSSSSTDLNTDASQLELNQNQKRVLIGSDVPLTGEACSKKEQGNCEAGWKSFLRPSGEWCMKIFYENSITQPSAENRCQAQGATLSGLQNQIESFYITYTVSSHIYPESGSIWIGLKRREECKNVGRTQNCTSDNSFEWTDKSTTGLDGIDWDGGQPDNARRYSQQCATLTASHQRSVIGYHVGRLDDVGCEFDYIKTNRKQRDIKAFVCGKKA

>Cel|clec-134

MRIFLNTVHLFALCAAAAIATEESTTPKPASWKFGTIAGEPDDYTNSTAVQVNNFKECIAKCSAIFDCIIASQKSKSEPCNLFLWNSVTKVKRAESGGEGQTAFRVFTEQPRCKLSMDELLNGKKYQIYKNDTEHYIWTINKTEDGWAMEYSKTILNNIIHCNDPDAYKYPGVRGCYKIVLPFKEDKKWESGMLSYPEAVGNCTLLGGDGLMTIPSSDFASQIKQNQNSTQSSTVYFIGLTRPDDSSNDNWVWTLPDLKIDSSPLPPWSFPPSLNVEAIWAENCALVSIEADPTKSLLHATLCQQWNRMSGYICHFAQ

>Cel|clec-133

MKSALVLLVCFGSVLATVPVATKCPDTWKWFKRSRGGWCMKVFAAIGTQADAEAKCKAEGAVVAGVQNTEEIKWMSATLQSLQTNPVGTLWVGAKRTKPCISSGLTKQCSAITSFYWSDQSAVGVQGFFWRAGEPNNALGGQGCAQVYSTTNDMDDVGCGSTNQGYICGKVATF

>Cel|clec-132

MLSKTAPLLLLLLASCVALCSADCTVAYKSILNAQLTESLANGCEPGWKFFNRPSGGWCMKVINEYKGAKAEAEKECKAVGSTLSGIQNKAEASYIQSALLAQLPASVNSGSLWVGIQRVKKCLAQKLSATCSARTAFQYTDGSVTGTDGFVFQKGQPDNMYGKQNCAIFLASRTPTIVSGSFFAGTLDDTGCEGRIKNENPRVMRGYICGKKAAK

>Cel|clec-130

MFCKTALLLLICLGSTFADCPAAWKTILNSQYKESEDNGCEPGWKFFNRPSGGWCMRVFAGFNAKKADAEKSCQAVGSTLSGIQNKNEALYIQTALLAQIPQSSGSVWIGIQRTQKCLKQKLTAACSALTAFEYTDKSVTGTDGFVFQKYQPDNSQLNQNCALLLASKTPTILNDQYFAATLDDTNCDGMLEGDAARVLRGYICGKKADK

>Cel|clec-129

MLGKTALLISVCLALSAADCPAAWKAILNSQAEESEDNGCEAGWKFFNRPSGGWCMRVFEGFNAAKTDAEKSCKSVGSTLSGIQNRNEALYIQTALLAQIARSSGSVWVGMQRTQKCLKQPKSDTCSALTAFEYTDGSVTGTDGFIFQGNQPDNKELNQDCAVLLASKAASVSTNGQFYAATLDDIMCDEQVDDNGPRVMRGYICGKKAAK

>Cel|clec-127

MLSLKFYLIFTLLAVGMSGQITTLLADTSDEDCEIDEEQTCAQACQATTTLSSTTASTVTPTPILTTVTTTSTTTTVTTTPIPTTVTSTHIPTTVTTTSIPTTVPSTQLPTTVTTTPIPTTTTRKTTTTTLRPTKPRPMTKPRVKVCPYGWATFNRPSGKWCIKVFIGHHAAQADAEEACRSIGTTLTGLQNKQEALFIQKSLLSLIPQQSGSVWLGLQRTARCMGQPLTATCSRTTAFEWTDNSATGTDGFLFQTGQPDNGRLNQNCALFLASIDPFIDARGRYYAATFEDVNCVATFVTGNMNRKTRGFACGMRPT

>Cel|clec-128

MSASRCYIFLVLLVMGVHSQTTPLSMANCLLDGDAEFCAACLDMASTTVSTTTVTTTTTPAAVTTTAAPPVVVTTAAPPPVVVTTAPPVVVVTTPAPVVVPTPAVVVGCLPGWRFTNRPSGGWCMRVFTGIHDAKIEAERACAAKGGTLTGLQNRDDALFIQRSLLALIPQNSASVWVGIQRTAACTRQQITAACTRTTSFEWTDGSATGTDGFVFQPGQPDNILLNQNCALLLASRTPTITARGTYYAATLEDVNCVATFIPANIARQTRGYACGRHNRCEPGWRFFNRPSGGWCIRVFTGFHAAKADAEAACQAVGATLSGLQNPQEAAYIQSSLLGQIPQRSASVWVGIQRTAACMNQPPSAACSRTTAFRWTDNSATGTAGFVFQPGQPDNIRLNQNCALLLASETPTITARGTYYAATLEDVNCVANFIPENEARRTRGFACGKRG

>Cel|clec-27

MSKSYEFEELECDEPTQQTRFEKIQNVASDHWKDILIGVLSQIMYLSFVVLLTYFLARQHLCETELFTSSTLPTIPITSSRSRPDSTSTSTTRSVTSTIPTPSVGNYTCTDGFTYINNKCWKLVTSSQSRADADQACYNLGGSTLFSIRSDQENQAVLDFVKNENVDNLWTGLICDDHGQFLCTWDVDSGDISAYNNFAKTYPNNVTGGCIYYMTTGSQAGQWTNGACNKALSFVCELPATIHDETCKYNYNNYCYITNDQLKISSDAQQICTSSGSNLVSIHSANENRFLTTIYSPPVLVGGVAFSSNLILWYDGTPSTFNNIKSITNGNCLFINDTHGGWYGFDCFTGSGDFICKQKIREM

>Cel|clec-35

MMFEKLHRFLQLHWKIILFGVIFEILITIGAVRLTYILSKPFCETDTITSSAIQTSTVSSFATTSTGSDTSSNSTTTRPLSTSTEPAPPFTLDCTIGFTHINGKCWFLIPIRRTREDADAVCMGYGGSTLFSIRNEQENTAALDYLSNAGVNYVWTGLICAGNTSSSCTWDMKSGSAADYDNFANGEKVIGFPNETNTSCVYFITSGPDAGQWKSGSCNQTMGFMCELPPTIHDGSCDYNYNNQCYLRYNTPHNIPDAQEICKTRCANLVSISSANENRFIRSLFTTQGYVLLGAAVIYYDDIYWLDGSPAVYNYIERYQHGACLLLNVNWVYITDGAWYTERCTTPGKFLCKRPAGTVC

>Cel|clec-37

MPTLPPVLGKLNHFLQLHWRIILIVVIFELSVIIGTAHFTYVLSNHAACETDIITKTTIRTSTVTSFTKTSTISETPSTTSLVSISSTHAPSNNLSCHIGFELIGGKCLQLLTGVGTRANGNHNCWLHGGSKLFSIRNEQENSAILDFASKNNIGNIWTGLLCHGHTISTCIWDIVSGSAESYDNFASGYPNVSTASCGYFITTGKEAGQWKTGLCNQQNSILCELPPTIYDKNCEKNFNNHCYTRFDDAYTVAEAHEFCKPMCAEVVSINSGDESRYVQSIYNVKEHIILGVAVLNDNNIYWLDGSSTVFINIGNNDNGTCAIMDVSFGMGYWTTIECSQKAWILCKRPAGIEC

>Cel|clec-239

MICVCLFVLISVARSCIPTQQIETTSAPITTTTTTTTTTTTSTTTTTPIPCPTGWEQFERPSGTWCIKVFIGLGDKANAVSMCAAQGAVVSGIQDQTEREFIVSSYVSLNGNTVGVWLGAQRTAACWSSPLTATCSKTTSFEWTDGSATGSDAFIWNVATEPNNGSLNEHCLLMNWQGFMSDQFCTIPDYTGWVCGKRPM

>Cel|clec-238

MICVCFFVLISAVNSCIPTQQVETTTTTTTTTTTTTTSTTTTTPIPCPTDWEQFERPSGTWCIRVFVGSGPRSNADSMCSVQGAVVSGIQNQEEIDFIVGSWISMYGSTGSMWVGAQRTAACWTLQGQTAACSKTTSFEWTDNSATGTDGYVWNSAVEPNNVGGMEQCLVLTWTGLMSDQTCARTDYVGYVCGKAPM

>Cel|clec-193

MKKLIQLIACFFLLIPAASVFIRDPSFSSSSEEGYGRGKHHHGGHHSPTPNPCEVGWYAFHRPQGVWCVKVVASKLTYLAAQTACINLGGALSGLQNDKERVWIGNKGMEIMLANGGTDSGTWLGAKCSSSGCTWTDGNTVGTQGMMFAPGEPNQLSYPPCLYIWAKIGDTLKRYPYGNGYIDDTRLTTAMMSYACGKPGLRNN

>Cel|clec-194

MLWIFLLYFIPAYNASVKMITHHRALMTCNSTEYSITETWRDCIELCAHNDSCVIAQTNLTVPKECQWCSIQNLMYIQKRFSANNNMIIALKTDTINEITESVCTPFEQGIVNGNFNNTSNLTQYKYSAQPSEDGNFLHFSYSAIKSCPSEWEPFDRIRGGWCIKVFRQGGSHDDAHRACKEYNAVLTRLETPKEMEYVWNTAYSVEAIFQKPSWEVYLETVWIDGVRKNECQVPNWKSIEGCDGLDGFEFEDKFISKKGGYTWSDKNPDRLDNVQDCLVLWINPNDKEVDDDACGSNAKIKGFACGKEAG

>Cel|clec-195

MRLLVFFLKIVFFLKPAMPVEKMLIFYGTIDKFNVNPLINMDLNSCVRIVSDFSTVILASWNSSENCHLFGFDQILDQILEIKTNEGDMGQYLILKSDQPNSTCPAFPETDIRRPVNESWSKTENGWTTRLCKNGWMLFSRPDSIFVCMKFIQLERGATREVALQTCIDNGAIMTGLATRSEVDWLNKFVVAPLQTGEWDGIWINGMRDCSANTNKTCQNFVWSDGYTTDTELLLSGILWDPGYDTQQQDCLTVYNAYSDTKLNLVSCTEYNLAIGVACGYKFE

>Cel|clec-256

MWSWPVFACFLHFLVPEAACQVKMVLIYGSVTSDATGISTTFSTVEDCKNGCFGSESCIIAYFSLTTCVFYNYVNDGKTITVEENSNNAYVAIKTNISNIPNGTCPASYNDLKLSVTSAVGEKNSWTRASTGWKMVNCRTGWKRFERDDNGTVVCMKIFPLFNEGGQAAAMRRCQQDNVTLSGIASMEEAEWVRDYEITTPRQRVFIGGERDCPDTPCTTFKWTDGYTKSYEVFSNAELTQQMNEEGYNCLVIRIKVGTAAIMFSQNCAASGIPFVCGYKIDI

>Cel|clec-257

MRFWSLFFLSFYLILELLVPKAYCQTRMVLIYGSVTSSGTSTSTTFKTVEDCKNGCFEKEDCIMMYFMLEKCRFYSYATNGQSFSILAQSKSYVAIKTDASNIPNNTCPDTFTNIKFSYTSPATGDTYSFKKNSTGLSYTSCKTDWKRFERADGTFVCMNIVLSNGTTYTKAQERCQELGGTVTGVASVEESKFLQTKVPGPQPKGFWIGGGRNCPTVPCSSFRWVDGYTTSYDALVPSNAALTVSKNTDANSENYLTVFASNGTPLTINDINQDFTSLIVGFVCGYKIL

>Cel|clec-104

MRSILLLLLAASIASAIFAPGASGGFGGGGFGSRSSSSSSEEGRGHHGHGHGHHHGRPPRPRPPRPPVSREPECPSDWLSFDRPQGVWCVKVFYESLTQPIAESRCQAQGATLSGYQNANERMQVSYAARTLTNQNGGGLAEVWVGAYRKARCPNKPSCTPLDTFEWTDGHTTGTDGFHYPGTEPNGYVNEHGQQYCMEMHIHPSSDTEAARYGYHQGDLDDMLCVVPVRLYACGKVPEQV

>Cel|clec-106

MKLLLLLFLLGFTFAIFINGGRSRGGYKSYSSFSSSSSSEEDYHHGRPPHSPRPPRPQPVQPRPECESGWTSYNRPQGTSCIKVFYASTSQSTAESLCRSIGAALTGYQNSNERMQVSYAFRDIINQNGGGTAEVWVGGRRKAQCPNRNACAPLDTFEWIDGHTTGTDGFHWANTEPNANNGPYCLQMIIHPTSDTAGAKYGYHHGEMDGVNCGDGIGRAYACGKVPQ

>Cel|clec-209

MFRLVVALSILQLVAGQCAHYEDKLIGDLCYSFYTETRNFDGAERACSGNNQNLAVLHNTLQTNFLASIVRSQTGATKFWIGLSRATPSSRFQWDDGTTMYWSNFNMNHAKDNNYVAEHTTDGKWQTIGKHHELPFVCSYDPKNFTPIPSGSGSTPDFTNGPASGATDEPISDATGAYSTDLPFSDSPTGASDLPFFGSSGATDFPVSGGPSDSPIYPASGATDEPISDATGVASSDGPLAYSTDLPFSDSPTGASDMPFFGTSDYPVSGGPFGTPDFPVSDGPSGSSDYPVSAGF

>Cel|clec-123

MSLMFALFLGILCSQKELYAQQITGGLIVDSGLQKACAQAGGVFRPRTDAQSVTGDICEMSFSVVTSDEADATNFCELYAPWRLRSVRIEKDVAGFTRTVCVVEATFTCGAGWIQMFGHCFRRLDKFSRHNQTEAKNICANLDGHKGSIAYLHHRYIVGVWKNFFKGISQIWVDGSETWDQYIVKTGSVDGRALALAFTGDTFDFSVMPNSLISIDPNLKLEVLCQYKPDLTPAEVNYLGRRYSEIYYPGVHVSDGVLIRSASHYTRSKTNLEVCKKVLKSFYITEIEPFMPTQEVMELLTNNRPKSSHFTRSGGEYPFNLYRDLIRPKECFGGAHTYEIPYANGSSKPFELPLREIIECDNMNSVAITHFAKGAAFVPMSDSQTAPVWCKFGKRMNYKIIAPEGWTPYVRSNGEVVAHKIFMEAASYDQALHWCRNENAKLGGFNDRKEFEAIAALITVHQTNRYYRLGAHQRDECDGVSGYTGIEGGTCYRDRIFGWIDNVASENIDESLWGDDEPDGGRRRSALGCWGSNCVQNTLVFSHFVNSHTDGIPRITDSFHDDRLPYVCTMDVTMIPIL

>Cel|clec-122

MFTPTFSSIFLLVLLMAGALSQDTSTSTVTTTTVASTSSGSTTASTAAGGSTSTTAAGGSTASTAAGGSTSTTAAGGSTVSTAAGGSTASTAAGGSTASTAAGGSTATTAAGGSTATTAAGGSTASTAAGGSTATTAAGGSTASTAAGGSTASTAAGGSTASTAAGGSTATTAAGGSTATTAAGGSTASTAAGGSTATTAAGGSTASTAAGGSTASTAAGGSTATTAAGGSTATTAAGGSTASTAAGGSTASTAAGGSTATTAAGGSTATTAAGGSTASTAAGGSTATTAAGGSTASTAAGGSTASTAAGGSTATTAAGGSTATTAAGGSTASTAAGGSTASTAAGGSTATTAAGGSTASTGVTVASSPAPAAACEPGYKRFNRPSGPWCIKVFTGYFAAQIDAERACQAAGGALTGLQNQDEALYIQSSLLSQIKQPSASVWIGIKRKASCVGKPQDATCTRTQSFEWTDDSADGVNGMVFQKGQPDNGGKALNQDCALLLASRTPTIKAGGTYYAAQMEDVNCIATFHAANAARKTGGYACGQQPKTCQPGWKFFDRPTGGWCMKVFTGFHEYQADAEKACQAVGATLSSIQHKDEALHMQGM

>Cel|clec-121

MFSPTFKSFLLLCLLVVNSWAQDPTTTATSTTTVPSTSTVTTTTVASTSSGSTTASTAAGGSTSTTAAGGSTASTAAGGSTSTTAAGGSTASTAAGGPTGSTAAGGSTASTAAGGSTASTAAGGSTASTVAGATSVVPSSPAPPTQPPVNNGCELGWKFFNRPSGGWCIKVFPGYFALKEHAENACQANGAATLTGLQNKAEALFIQSSMLSEMSAPSGSVWIGIHRTPACNRKPLSAQCNKNTAFRWTDKSATGVDGFVFQRGQPDNGGRALNQNCALLLASSKPFIDAGGRYYAAQMEDVHCNATFVPGNMARKTSGYACGKPNKCQPGWKFFDRQSGGWCMKVFTGFHAAKVDAEAACKDVGATLSGLENKEEAIFIQNALLARISQASGSVWIGIQRKAECLGKGLTASGTPTTSFEWTDNSASGVGGMVFQAGQPDNGVTALNQNCALLLASSQPYIDARGRFYAATMEDVPCVANFVASNEARRTRGYVCGKPL

>Cel|clec-107

MWLSVLLSSLLFTAGTAASDAVCGNWGPNRPYSDSCDPKCNTTMVQVLAKPGPGTISKYSQNVTAATWIECMKICFADGKCATVYFLEATKQCTKYWMSALTFLNRTEESEGHRIAIKIPLSKRSCSLTTEQLLHNQYYMYYPYVFTFMKRIYIGIRTSPKYYAITSFKDDLETYMPYDLSCPKSQLTSWAERRATDNSSVCYSHIVAPGITQLEAKELCELQGMKLLIERYEGMIPMPDTQRLSQSVLLTTPFEPDFGFVGIEDVRTWFGLERDPVDRTWKWSETSFIYMGFSGNPPMTWAPGEPKEVNNCAYLQRNDATVAKWPGYAFFSAPCNSTDVGGFSCGSVTQSARGIPTWNSLVAEYGHNQTCCVPDAETRIQWRGVM

>Cel|clec-108

MIFLALFTILYAFASAEKCTGPQRPKCDAGWYTSYRPQGIWCLRVGGSLMYKEAATQCAQYGGVISGVQNDFERDLLVREAQRQLAGYKVPMSGMWLGAQRNGSGFYWTDGFTTGTAGFTYGPGQPDNMNIDARVPQTCLILITMAPSYTGVWTRFKNGELDDTWCNSPSDPPYRMYACGKRGPKDIQFV

>Cel|clec-8

MQLLFQSIFLILLFSHAQLSPVCSNGYTLVNNNKCLRLFKTPETHKTAELTCLKNGGATLANIKSSIDNRAITIFVGGASNSIWIGLFCTKSSAKECFWDDDSGSADQFQNFKSGFPLVEKGRCVYSSQVAFDRGQWSSGDCEKESRAFVCELPVTNEDQCQKNYNGYCYFDFAPLPFVSAQKICKENCGIIASILSPMENRYINANFYTYSALLIGATWSYNSSYTWFDGSSWSYHNIDHTARRGGVCLAMSTGTGSMVPTGSWYPVDCKASNSFLCKRPAGTSCPWVEPETPPTPVIPSMCNSSMIMAPGTISSPAYPGYYDNNMYCSYLLSTTGAYNILLKFTDFSTNLNLDYVTVYDGETTSSPMLGSFSGFNETPINLVSTGNTMLVTFRSGNSEDSNIRYGFSATFSKFVQML

>Cel|clec-4

MQFYSVLLLVSLLLLLTISEASYPPVCTSGFTLINGKCLRIFVDVSTHTAAEKTCKGYGATLVTVKNSIDNRAIADFTGNNANLFWMGLYCFDSDVSKCLWDDATGSAEVYDNFAAGFPHIALGNCVYYSVQGALAGMWLSSDCNDRRSFICELPASHADPCPYNYNGFCYTFHNTASTYTKGQKICEQECGNLASIHSANENRYIMTFGGRATKEDLLLGGMWPADDVYNWVDGSLWEYENFDPINVRDSVCVIMSNGDSRPIALGMWYSGECKNEYSVVCKRPAGIQCPPNPTIVPVTPMPAVQSFCNSSVMAPSEITSPHFPYNYYNSDFCSYQISTLGSYNVLLRFSTFDTEKVNDVVTVYDGDSTNDPVIGVYAGSFYPFTVISTGNKMLVTFKTDKSNTRQGFSGRITSYSTTESGERD

>Cel|clec-163

MTAMFLLNYILLGFALCTGSPIVSQLSSYVDRPCGKDPKHLWLDIVAVVDNSKEMTDDGVLSIAGELSSLFSHAEQLGIDPNQPRTTRIGLVTYNEEATVVADLNNITTADELSNTLFAALTWTSSVEHSYLQTGLKAADDLLAKQSFNTSRGHYQKLVIVYASEYRVSGTQDPLPLATRMKTYLTIATVAYRQDIVVGFNDALTKIASPGYNFTNFNGNNVVSELKTTMIQVNCYCPNEWFQMRSSSKYGVCIRPFATMATRTAARLSCRNQWNNAYMLNEFTQMKHDFVLQVIGNITTFTQPYYIGLSYSNGNWQWDQPNGQPLIPLEHWNNWSPGYPTASSTDTAVINVNTSWQNTNPSLSNMYICEVAACDSANYCAAENI

>Cel|clec-73

MTTKVVSVWLGFIVSAFFTTSWGLLLNSDEGFEKACKQSGGDYTQRAGNDSNTGDICLMTFQAVATDMDAARDFCNIKAPWRLREAKIDKSQDSIPVIICDVEATFTCNAGWIQMFGYCFKMSEVHDRYTREKAEQYCKDQAGPSFQGEIAGIHHRYILTPWRSYFTRLQQFWIRAPETWDEYVIKTDKVDGDNLALSFYDVHPDFSVPQNAMIKINGKVELQALCQYKPAITPAEINYMGRRYSEIYYPTVPVKDGIIVRSASSYTRSSNQSDVCKKVLKPYMYSKESQFFPDPDSMEQLAKLEPEAYSLMRSPLVSNSVERYRTNRYCQAPSNPHYEVVLGGKKTANFVVEENKIKGKPTCDNMMSVSISHFKGQAPEFHPMVDSQSLPIWCKLGKVVKYKYKVTPGWTDFRRLNGQVALHWLSKDKLTFADAAAACEAKGANLAGINSLKEAEQLGNHVVGANLNNEQFWLGAQRRTECLENNDWKPPCTRDKIFEWMNNVATDFRSEWWKKNNNLHSPNPSGTGQRCLSFAFGDLWWSYKGHTGFLDDIECHTELRYFCSKMAPFTECEENCD

>Cel|clec-174

MLVKYTLFATLFGLVSAVCPVGNDLEIKGLCFKFVAQKMTYDDAHNWCHFKNPVGFSYLAYVPDQVTSNYLAVFARTEFGPDAEKFWIGLHRNGSSGLLEWDNMRPVVHTNFGNNVTKNYFTENISDAKWETLDDNGKNYFVCSYDSRWATKPTPSTMKSTPTTPTTIKSTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTMKSTPTTPSTMKSSPTTPTTMKTSSITN

>Cel|clec-70

MLLLKFIFLSTLAGLASAVCPDSNDHEVQGFCFKFVAQQMTYTDARNWCHYKNPVGSSYLAYVPDQKTSNYLAFYARTAFGPAAQHFWIGLSKNGSSGSLTWDNGSPVGYTNLGSQNGNNLYFTESLANTKWNTLGDDKINYFVCSYNPATTPTTPSTTTTADKNCQPGGQQTVLFAYSNDLDPSVVTDTLKQSSLEYQPIYFAVSRFDLRQPEDIGYFTDYDNVTDYVDSHAPDSSLGFGDTKTGSNVLDVIDKFYDNTKLTPCGSIVMVLLKRYSNSNDISNIVAKVRKHHGSVNFIASNTPSGGTNSRVLFDLSSRTNGLYVIDRDSYFMQSIDMMPLIERYPIYAANPVVTGAGFKDLPLLEVPSFRKHLIMVAVQDRIPVTNVHHVTVQWENSFSEYSGKLDMHPETWNNPYTNANGKRANLDASGFAMTVEYVYNDSGDHPMQIRFYSPEATDFWLPYTD

>Cel|clec-71

MILKLCLLATLFGITNAACPDSSDQEIRGFCFKFVVQKMTYTDARNWCHYQNPVGPSYLAVVGNQETSNNLAFYARSAFGQSAESFWIGLSRNGSSGSLSWDNGFPVIYTNFGSKVGNNYFTEKISNSKWVTPGDNETNYFVCSYDPTVQPVTQKATTPGTTTTAANVNCQFGARQTVLFAYSNDFEPYIVQNTFSNSILYKQQVTFAIIRFDTRQPQSIMYFNDYNQALAYVRNHLPDYKLGFQESTTGSDVLDVINNFYNNSSACASVVMVLSKRYPNTPDISRTVAKVRQYHGIVNFLASNVPFGGSQSQVLFDLASQTNGLYGIEQDSLFSKRILYMPLRTRYPIYAVNAKVSGEGFQVLPPMSVPQFDDFLIMVSVQSHLPVSNVQYVNLKWYNPSFPYSDKFEMQPVYWDSNTNYNTLTIGLSQNVYNMTIDYIYTNTDVETMQIRLYSSYFTNYWLPYSN

>Cel|clec-72

MFLKLFLLATLLGIAIAACPDSNDKEIRGFCFKFVVQKMTYNDARNWCHYQNPVGPSYLAVVGNKETNNNLAVYARSAFGASAEYFWIGLSRNGSSGSLSWDNGFPVIYTNFGSHVGNNYFTEKISNTKWDTPGDNEKNYFVCSYDPTVQPVTPKATTPTTTTAANVNCQLGGQQTVLFAYSNDLAPSVVLNTFSNSYLNEQLVTIAISRFDTRQPQSIMYFSDYIQAYTYVSSHLPDSTLGFGDSTTGSNVLDVINNFYNDISSCGSVVMVLSKRYPNTMDISSTVAKVRQYHGMVNFLASNAPSGGTQSRVLFDLSSRTNGIYSIEEDATFLHFIGWMPLRERYPIYAVNVKVSGHGSQVLPPMSVPRDVTYLIMVSLQSHLPISNVQSAKLNWFNPPFPQGALSMQPSEWAYTNSNSGGNRRIIDPAVYNMTIDYIYTNTDVETMQIRFYSSFYTNSWIPYSN

>Cel|clec-74

MVLKLLILTKLVGLSSSACPSSKDQEIKGLCFTFMPYQLTYNASRNYCHHNNPVGFSNLAYVPDKETSNYLAVYAHSAFGSAAENFWIGLSRDPVSKSLSWDNGFPVTYTNFGSHVGKNYFSEKISNAKWDTLGDNDKSYFVCSYDPAVKSTTQSVTKTTTTPDSSNCQVGGPQTVLFAYSNDLNPFIVMDTLQRSSLDSQNVSFAISRFDLPQPEDIAYFTTYNQAMSYVSLHKPNVSLGFNDTTRGSNVLDVIDMFYNNTQTPCGSFVIVLSKRYPNTLDISNIVAKVRQRHGMVNFLASNTPSGGTQSRVLYDLSSQTNGVYAITRDTSFSSTIDYIPTRERYPIYAVTPRVSGEGSQILPPMTVLVHASYLLSLSIQSHVPTNNVKDVELYWRNPSSTNTGYFGMPVASWGFFDFNSDGTHANLAADVYNITINYDYTNSDVEVVQVRFYSSSPTNYWMPYSD

>Cel|clec-75

MLLKLLYLAILVGIVYAICPDSNDQEINKLCFKFVAQKMTYNDARNWCHHQNPVGPSYLAYVPKKDTSSYLAFYARSAFGVDAQQFWIGLFRNVSSGMLSWDNGLPVGYTNFGSHVGENYFYEKISNTKWDTLGDNDVNYFVCSYDPMVKPSTMMTSTMKSTTTTELVNPSCQHDDKKIVFFAYSNDLDPTVLLNALRDNYLYYSNVSFAVARFDALEPFTISYFSVYQQVVSYVSSHLPNSTLAFGDSTTGSNVLDVINYLEKNFLRKFEFSGKFCRRARWMPLEEKYPIYAVNARVSGNGSQVLPPMSVPRMDDFLMVITLQSHVPLSNFQSANLRWYNSQSSDSSSFPVYPPLGYTNSNTDGIRKILHALVYNMTIDYAYTNSNVETMQIRVFSQSATNYWLPYSD

>Cel|clec-76

MLLPKFLLLTAFLEFASAICADSNDQEIKGFCFKFVTQQLTFTDARTWCHLKNPVGPSYLAYVPSQDTSTYLAFYARSAFGADAEVFWIGLSRNASSGSLSWDNGLPVAYTNFGTNVGKNYFTESISNTKWDTLGDGDLNFFVCSYAPIVNSTTMTSITGTTKRMTTTTIEKLNCKPGDHQIILFAYSNDLAPSVVTDALYYSSLSSQSVTYAVSRFDLRQPEDIQYFSDYSLFSSYVSSHLPDYTLGFEEATTGSNVFEVINKFYDNTQATCGSNLIILSKRYPNTADVSNIVLKVRKSQGMVNFLASHAPSGGTVSQGLYDLCSLTNGIYSIGRDSSFSNMIESMPIRYRYAIYADNPKVSGQGSQTLASMSVPADGTYYLSMMLQNHTPVNTTQSVLLHWYSPYSRYSSTASVHGLSFETNNNGANSEILDAAIYNVTLDFVYFTSETMQIRFYGTSTDHWLPYAD

>Cel|clec-205

MNILLVYLSYLFICFILLFKRVDSVICTDYIQSSTAVSLEEINGKCLAVTKSAVSGSATSSCNSVGKGAGLGKFVKLSIDNQLENDFVADGLMDTTYQTAYIGLGQSEAGWGWMNGDSSTYSNWAQPPVTYPPTIGQTTVPFRSTLPPAEQRRSTAVVIGIDASIFSTNALTFAQVEFARSLSTYIGDRGPAEFALFAYGCTQVSPYIYQYPNFVSTFVDTDTMIRNLNETINHDCVRNNPLDFKSMFRDQSVYYNRYPTSYRPFKSQFLSMIYFSSSTDSDNIKAASSLYPIADSSVITINVGDNSIDISPLSIPVGKNGIRVKTADDILGLVPKVDSMIFGATVASPGGAAWKAFEEPSIDATTYTDCAYMNVSDKLWYSDGNCTSTKRQVLCQYVLPLPSTPEPTSNPSDPCFYDTTNFTYFSGLANTKCYRVSSDKKQFAEAENLCLSDHPLFLHTPKLTSIETKEEEEKVRTIVPPVSDGMFWFGLKRDPTNSSNWYFINGDTYDSSYQNWRSGYPRDADGCDCVALVINDNSWVNTDCNKQLYSICAFRYN

>Cel|clec-204

MNLLPCLLIFLLYKQVESDDCANYILNSNAVSLNKINGKCIAVPNTAFSGSAAASCSDTGNGVQFVKLSIDSKEENDFVANGLKAIPYKMAYIGLGHSVAGWEWMNGDSSIYRNWAHPPDAPTAEPTTEPSTLPPAEQRRSTAVVIGIDASLFSTNSLTFAQVEFARSLSAYIGARGPAEFAFFAYGCAQMSPYMNQYPNFVSTFVDTDTMIRNLNETINHDCVRTNPLDFRSMFRDQTVYYNRYTTSYRPFKSQFLSMIYFSSSTDSDNIKAASSLYPMADSSVITINIGDKSIDISPLSIPVGKNGIRVKTADDILGLVPKIDSMIFGTTAAAAGGASKEFKEPSIDATTYTDCAYMNVTDKLWYSDGECTTERQVLCQYVLPTPPTPNPTISWQDPCFYETTTFKYFESLHNAKCYRVSSEKKQFVDAENLCLSKHPLFLHTPKLTSIETKIEEDQVRTLIHTQPLVNEGMFWFGLKRDPSNSSNWYFINGDTYDSSYQNWRSGYPRDADGCDCVALVINDNSWVNTDCNKQLYSICAFQFNFTDTAF

>Cel|clec-145

MHPKCGIILLSLIFICITEIESRKVTQKPAAPPPPKNDKSWVRSKIDSAKEKYHAGKEKLKTKISDVKSKLRGPAPTPQPRPPAQNNLPKSQYGWNTQAPGPRAPAPAPTRPQYGVPAPRAPQPTIPALTTKKSVFERLKEKAKGKEKYVGKAVGWAKKDLGIGVEGPKKPSKILKFGKKAKTPKTQNPALVHSSGQIVGQVASGSHGLDRKVEYLKSRLDIMQSEIQGTWNTSESGTKYKIFEERMNWNDAQLHCEELGSHLAYLDSESKNTYATSLIDSQNISMVWFGLRTEVGLGSGSDTYSNFSNLDGCGVVDRNGTWSISSCAIELPYLCQAFRFNVLVEIP

>Cel|clec-146

MRSIFSVLLLAAVVQTQFNFHGMRSFFSTDEEFPTQLQNFEGRTETEIRTLKEKVARLEKLIDGLQSVLMKEWNTTESGSKYRLFEERKSWDNAERHCQGFGAHLAIIDNEAKNGFVTNLINSSETSDFAWIGMKTKTTTQTSTPFTNFDSESPIDGCAVMDAKGVWSIRSCIQLRPFVCQIIKNDVKI

>Cel|clec-203

MPSRSLPTTQTDPLLPRSSNRSRSTSSHHSCKTIVKILFIFIGILMISAPIAYGLTIMTGNYDDSKPYSFTYFITNVFNTFISIVPVSISSVASKQSPPTTKTEFPIPSSSNFSTETEFNSPIKRTETFNEEESNATNETFLSKEPISTFSTTITALPVSGERPISTIIVNHGENHENPPLAQVATCPDDWMTYERPQGRWCMKAFYGKMSQSDAEAECNAVGAKLSGLQNANERMNISYVLRDLVYKDGGGKYTAWLGGKRKASCPTGASCARLNSIEWTDGHTTGTDGFSTGTRELDGTYLQKFRGVQQCLHMIVTPYSDTELGFADFVHGSVDDEFCTATWVKAYVCGKLPS

>Cel|clec-247

MLFVILSLLLLSHTTQSCMRMVPPDDVSITTPVPTDDPDNPVTEPMVTDPTAPTAPTTEVPISSTATEPVTTAMPCPTDWMMFDRPSGAWCMKVFKTEKVLPGIAAERCEAEGGVLSGIQNQEELDYITNSYSAFGEPFDAIWIGAQRTTACLASVQTATCTKDNSFEWTDMSTTGIDGFLWSGADPNNGGPALNEHCVIAFVDGPRLADISCARDFDGYVCGTAAV

>Cel|clec-248

MNSIFYLLALVACVANFIFCQNIQDAASNIIGQATRAVGDAAGAAAAANVRLSNGHFASNFHIGHHSDHDNEDNGHIYQGGVANGAVEGGVINDGVLEGGVLNKGHHGTDYIVG

>Cel|clec-249

MNSIFYLLALVACVANFIFCQNIQDAASNIIGQATRAVGDAAGAAAAANVRLSNGHFASNFHIGHHSDHDNEDNGHIYQGGVANGAVEGGVINDGVLEGGVLNKGHHGTDYIVG

>Cel|clec-92

MELQIFLIFTLIGLVIAYTDYYGGGKGRPPPARPPPPPPPRGVKCPAGWTLWKRSQGNWCIRVFHGQYTNPQAEAQCHAKGATLTGLQTAAERNSLAKLGYNLIHQHKYGDAAIWLGARRKGSCPRAGICSPRDTFFWTDKHTRGTAGFVFSPGQPDGITDGYNGPWGVQSCVHQFVFPSGSTHPRWPGIPHGALDDQYCQEGKKNPFTKFYACGRKAT

>Cel|clec-100

MFLILFLVFITTSAIDFDDSSCDSSSEEHGGGRPARPGTCGQHWHTFKRPQGTWCVRVVTGDVDYYRGLAECAKYGAVLSGIQNNQEREWIANKAVSLNVAAGKTHSGVWLGAQRTSATAFRWTDGHTTGTEAMVFGPGQPDNDHGAGRGPQRCLQLMALTPSYWNIPGHLINLKSGQLDDIWCNVTLSPRVRMYLCGKKA

>Cel|clec-83

MTLHWFSIALPLLLTTSVHSQCASGDNSIGDLCYVVVNQQLSYQDAVGYCHGISTSLAVVHTTLQANFLASTIRTKTGTSDSLFWIGLSRASSSSRFTWDDGSVMYWSNFDLNFPKDNNIVAESVINGKWRTLAGQQKLVFACSYNPNNVNPASTTPTYSTDASSSTYAPYSTYATDSSTAGYGSSATPYSTDSTTNTYGPTDSSASPYPTDSSTSSYPTDSSTSPYSTGSTTSYIF

>Cel|clec-84

MKFLLYVAAIIGLASGACFDNGDKEIQGMCFKLVPQMLTYQDARDWCHYKNPVTSSNLAYVPNQFTANFLASYARSAFGSNDGYFWIGLSRTSSNSPFTWDNGQPLGYTNFGTQLGQNYIAESIVNTKWNAFGASDKNFFVCSYDPAAPPTFSPLPTRMPETTMMPMPTTTG

>Cel|clec-80

MKQFLLILLFFTSLAAAQQCWDSSDRLINGRCYKLVNQQLSYQDARSWCRYQNSVVSYLATVSDQITASFLASYAVTAFGSNEGSFWIGLSRSSSTYKWDDGTPLGWTNFNYQNSQDYVAESVTNAKWTAYNSETELKFVCSYYPLMPTTNLASSTDAPRTTEASTYWTSETLTSSST

>Cel|clec-80

MKNLILLTFSSFFAISHCQAQKCSDDSDNLINGRCYKLVTQQLTYSDARGFCHQADPGYTLATVLDKSTANVLSVLAHSVFNSSNGGQFWIGLSRNSTGSPWTWDDKSSFGWSNFGTQLGQNYVAQSSTNSKWGTFGSTDKNYFVCSYDPASVPTTAKPLSSVTCLIMYDTQSLGIDQNAINSYKAYFNFAHLVASKLNDKTMLTGYIDNYGYSAGLNDHQNYPTDDFFDLRGIPFPIDGTDDDIDLDLKDVDGSLAAASWTPPVTDQTCMIFISAAPEAEYGGTTIKSTYSSFGTVVGVLVGGATSIPGLSIDTNVIAAPALSDSDADAVVSKLLELLPTA

>Cel|clec-85

MFRLAFSLCVLQLVFGQCTRPDDKYIGDLCYSISAQLLKFTDAQSACYSQNQNLAVIHTSLQANFLASIVRTQTGSQKFWIGLSRASSSSRFQWDDGTTMYWSNFDMNFPKDNNYVAESTLNGKWQTLAGQKELPYVCSYDPKYFTAGPPGSTPNYGSTGYPVSYPVSGATEYPASSMTDSPASGATGYPASGATGYPVSGATGYPVSGATGYPASSMTDSPASGATDYPASGATGYPASGATGYPASSMTDSPASGATGYPASGATDYSASGAPVSAST

>Cel|clec-82

MRTVLIFLLPLVAAVSAQRCLDNGDNLISGICYKMVNLQLSYNDALDWCHYKNPVVQSNLATIPDPSTANFLASYARTAFGVDSGQFWIGLRRNSSGGIPWWWDDGSSLRWTNFGTQLSHDYVAQSIVNAKWNTFLGTEKNFFVCSYNPNFITTEYPTTTDDTSCQPESPVTLLFAYSNDLDPDVLESTWGATDFGEYPNFAAYATVRFDLRVAEDIAYHTTIESANTYITSHPPDPTLGFTSTSVGSDSLSIVENFYKNQQLSVCGSVVLLLSKRNPNETEISQIVSLVRRHHGLVHAIMSVNPSGGSQPKALYNLVSKTNGVAAFEQDSEFSDFILHLPMFLTPYPLYCANPKVSGTNSTELPPLSVSSEDSYYTIMVVQDHYPSDSFQSSQLKWWPSGQQPFGFSLTKSDLIGNDANTWITLEATSYNMTLDYSYATTVPQAIQIRIFSGSPLDYWLPYCD

>Cel|clec-164

MLLLIFFLPTVKALSGFSVIKLKVPYSYLVSRTPIFTSTSSTSFNLNDVIYKNCASKMCIAAFHDNSSKYQLLTDVQNSCTKAPNCLAFTESQYNIAIVFMNNTSNECSANTTELLTEKFKPKECPAKWFPWTRPNGQIWCHMISSVGRTYQEASDYCQGMGAEMNGFQTVEERNAFIGFLKAKPASSIISWVYIGAKRSCPTDTCAKTVQFQWQNGVSTNHSLANDNFYSPWWEGLGNCLGMLYYKEGMYDDTECVQKAAASCGMLAK

>Cel|clec-181

MLQVSIFLLFFVFPGCFGNLIFATSNEETCEDDSNNGGGKVKKPCEPGWLKFNRPSGVWCIKVFNGTHSQADAEKLCQKNYGATLSGVQNQREISYVTQQALGTMSQGSGSIWIGAKRTTLCKASRLSKYCNTLTSFQWTDGSASGLDGLIWNNNQPDNNYNRTDQCVVLLAARTPTVSDDLQWGANRLDDCCM

>Cel|clec-260

MGRPTRQKQSNIRNLANWKAAQAEARILAEEQQRGSTQNRRATLPAASPRQLNGRLTNGPRRSSTPRSSIATSSQAVKRKLRSLANIIYFSFLLAFFGNNKHDGAEAACQAQGAKLSGFQTTDESMRATHLLRAVINQASPGANTVAWLGGIRKASCPTVQSCTPANSYQWTDGHTTGTAGFTFGVNQPDILGGVQFCLTQNVHAKVDSGLTSAQWHFFNGNLDDVECYATLNTYLCGKVPN

>Cel|clec-243

MLLFFLIPVVNLCIPTQQVETTSTTTTTTTTTSTTTTTPSVYCCWRSHSCGQCCAAEGAVVSGVQNQAELQYMQDSYVSLYGSETGSFWVGAKRTAACLESQLTLTCNALNSLEWTDGSTTGTDGFLWRNGDPNNGGIYYPAYKDNCLAVDARVGLLADQPCGTAHYMGYGCGKTPM

>Cel|clec-242

MLLLFIFPVVNSCIPTQQVETTSTTTTTTTTTTSTTTTTPIPCPTGWAQSDERPSGPWCIKAFRDFGITQYDAQAACGAQGAVLSGIQNQVEMQMMAGLAMTGGHWLGARRTAACIGQLVTATCTRLNSFEWTDGSATGTDGFNWRLSDGEPNNLFLNVFIQYENSWFFFQYWYRQVILQNTLKLCCNILGSKNSTIGLSYYYINHFIF

>Cel|clec-9

MLLKSIPLFFLVHYSLAKTPICTNGFTLVNGRCLRYFPNARNHRAAENSCFSYDATLVTVKNSIDNRAVSTFVGNAASSIWMGLFCFNMDVTNCLWDDGNGTAQGYNNFMNGSPQIESGKCVYISLMGSSSGRWYSGNCDLDSRPFVCELPITFEDDCSNNYNGFCYSYNPPASFVRAQQNCENQCGSIVSILSPNENRYVGALFPRYESNDMIIGATWTTKDTYSWFDGSPWNFNQINPASPKKNCLAMVTSLNDASASGSWYPIVCYSAYGYLCKRPAGVQCPQYPPVTVTPAPSNPSGCNSTIMSFGTITSPNFPMNYNNITSCNYLLTTLGSYNVMLKFNKFYTDMKNDFVTLYDGDSTKSPVIAKYSGYYEWPFFNVSTGNSMLVTFRSNSTFGYYGFTAIASSYVHHD

>Cel|clec-111

MVVFYGQPVDYSQVSMKSYSLSTCIAYCYNMDTCVAVYTPDSSEVCIVFEFGQISTLQQLEASSGKVMGVKVGPTSTYSIDMASFRCYPPTPPTAQQLPMGIPWCISDTWTFTSGSSVSCQANFTMFVRPLGSWCIGIIPTTTCLTQQDSATQCKSLYGGVLSGLQTLAERDFVAATAQPWLGLQSNFTTYGVWINGARKTSCMETVKSVDCNGTNEFAYSDPLLTAYDGYTWAANQPSGVDYVPSSSNCLNLYFTETTILGIDDYMCNVASLRGELCYKGYACGIEPS

>Cel|clec-112

MLKFYLIMLILIFLETSIPYKMVLIYGTPEDVTMNPSPLTMDFDACVEYCYGLSACMMVSHAIGTQNCIAYEIGQVSTVRETDSGGSNKVAIKMNGTETAQCPLTAEENSMKFGAETANYTYREFDITVSNSLWTFTPVPACPKNFTMVTRPKGQWCIGVVPAKACITQKQGSSMCTKSYGNSILSGVENFEEYGLIQDLAQPHLTDLPSGAAGRSTVGFWINGDRKPICTGVNKTASCNGTNEFTFSDPTLSLNPTGYIWGVDQPSGTLAKDSLCVHYGFNSTTKQSIGVDDYSCTVSSTNGTCFIGYICGFRPS

>Cel|clec-210

MISKFLRLSLILAQVHISVSDICRYPHEKFIGSRCYAFVPKRHNFETAEIYCHGQGYSLATVDSAITSNFLASSAATEFGSNSGQFWIGLSRKTEFQLFYWDDGTNVAFTHFDAGFPNELNYVAENVKNGRWQTRDDQDELAFVCSYDPSLTTTTAPSTSLPTSTISTTKPTTTTSVRTTTQWNAVTSTTLQQSTKRTGCPDGFTYFAPTQKCYIVVVYGYDSDYPPVPIDAPFLTKENQRCQKYGTTIATIHSSSVNDFFTDLIKKSFNDSRFATIGLRNTDLKATGGKWQWFDGSSADFLKFGDSFPKTGDYIAQTSAQGFWVTYTHTAANEGVVCSVDF

>Cel|clec-171

MLVWGIPNTTNNTQVNTSLTWDGCLTACFYSPACVMAWQNDSTCYNYAFYYVDYVSRTTSANESVVAFKVNSPNGTCPTGAIPPTFDNQNATGHLYVNDYPPYFPYHSDYSIYATPTGWKISSRMNHSCIDMTDVIVRADNSMVCLMTFRTSTAGSFSYNRSLELCKSKGVDALFGAVYPEDFEQLAEIGERERNETANRNTYARIDGIRTKACQSTPRTPYCMSPKGFTFLSSVPTFEHYNWVTNSSAMATANDNCLVLVFNGNNAVKVDVKSCEGNFNPLPAQFFVCSRPAWEN

>Cel|clec-262

MHIHIMYLLFVILIPKMLSLQMIVTYGKPTNFTDATSFSESSWESCVEECYLQNTCVLAYSPTSPLNCQLYPVNRIFSVQKLYSTDLVAFKVTNSTATCPTGDNPPTFGNLTNYGSISTDLVDYTYSVSYGSDDTWSLSYNLTGRVCADGWSMFVRPTTNWCLQVFGSPSVSYTQADAIHNCTNIGTVLSGLETLDERDFVAAGALTLLGAGYPEFAAVWVSGMRKPECYSDGWENLAECAGTNMEQFTYTDTYMANYAGYTWDPNTPDRNSTGVWQNCIQMWIRIESVSPDFPYDTNPNGNSDDATCNVADSDDFSLRGFACGKLPEIPADA

>Cel|clec-261

MKSVTVFLLAGTTFAIYFDGKGSRHSSSSSEEHGGHGPRPGPGGPGRGGNCSPGWLRFERQSGVWCVFVGLAGINDNSFAQKDGQSACVALGATLTGFQNDKERMAVADEAGRKLGAAGGGIAGLWLGATTRAGCKAGACGPLNTFMWTDGVTTGTAGLKWATGEPDSVDYPGTAACIQQFIMLPNWVPGPYDLEGFRTGFTHGILYKFSCIAPVTPGTRMFACGKMAAG

>Cel|clec-95

MTKFILLALVGLAAAIDFDSSSSESCEDGNGHGHGHGNGNGNGNGNGNGNGGRANGGCETGWRHFRRPSGSWCVRVFGGRLNQGAAQSQCQSFGATLSGLRNLEEARTISNLALSVIGRSSGGIWLGARRTTACAKQHKTTSCSTTSSFRWTDSSASGTAGFVWNNVQPDNSDLNSQCAVLHAGSSAATVSNAVWQPAMMDDVTCSFDPAGRDPRSIYGYVCGKKPSRR

>Cel|clec-94

MVKLILLTVLVIGATNAMFFIPSKVSCDDKNGGGETNGGCGAGWRRLNRPSGGWCIRVFEGVLTQADAEAKCKSRGATLSGLKNAEEARIIADMALPVLNRDSGSVWIGARRTDACMTKSITSDCTATNSFTWTDGSTSGTAGFVWDSRQPDNDYKKQPCVILLSSKTPETPVSVKNRPWLPRMIDDVACSLDPAEGSARIVAGYVCGKKSSQ

>Cel|clec-93

MIKIILLAVLVIGAATAIGFSSSSSESCEGGRGGGNGGGRPPGGGANGGCGAGWRRLNRPSGGWCVRAFGGYLTQANAEIQCKSHGATLSGLQNMEEARIISNMALSVLNRASGSVWIGAKRTAACTRNGISSQCTATNSFYWTDNSASGIAGFVRAHQQPDNAHGKTQLWAILLSSRTSLRVKHVMWQPGMLDDVACVMNPSDPSPRAVSGYVCGKKSSRR

>Cel|clec-96

MLLLLAVSLLGTVTCQTCETGWSVQGLRASGFWCVKVFLGTYTQPQAQAQCEAVGATLSGIQSANDAQVFQSLGLAALGGQSGSFWIGARRRAACQTQRITADCTAQNSFEWTDDTVTGTDGFVWNDKQPDNSDLNSGCAVLLASGPPVQWGNGMWAGAKLDDHVCDFVDKTPANPRRIRGYICGKRSN

>Cel|clec-97

MAMSLLLALSLLGVATVTSQTCDTGWQLFSRPSGEWCVKAFAGAYTQPLAQAQCISAGAILSGVQGHNEAAAFSNLGLTSLGNQSGSFWIGAHRITTCMTQIITAQCTPTNSFSWTDNSATRTDGFVWETQQPDNSDFNSSCAVILAANVPVMAAQRWWSPSKLDDHVCGYVDEDVSNPRRVRGYICGKFAT

>Cel|clec-98

MTSLLVLLAIFIGAVASHGGDYHGRGNGGGNGRGGSNQSNRGCDSGWKRFNRPSGAWCIRIYRGTHSQADAENRCRQNVGATLSGVQNQVEINFITKSALDLISEASGSIWIGGRRTQACRNSALSTSCGSLNSFQWTDGSTTGTAGLVWNTNQPDNKDSRSQQCLVLLASRASSIQDKWTWYANRMDDVQCAASGGESAARALRAYAYMNFICNPFAILYFSTQLGFSIRSQTFHKCIHEHVSG

>Cel|clec-99

MSSLSFLLCFSLLIGTLVAIDFDSSSSESCEESHEHKHGGGHEGGNNGGGNNRGCDAGWTRFNRPSGGWCVRVFPGTYHQPLAESRCQSQGAVLTGVQNQEEAKKIASLLLPQISQQSGSIYIGLHRTPACSKSPISSSCNSMNSFHWTDGSTTGTDGLLWNNNQPDNAHAATQQCAVLLAAHTPTVVDKWTWQANRLDDVQCQVPAGSNVARTVRGYACGKKARS

>Cel|clec-58

MNTVFACLAIFVFGIYCSPVPQNAAAYTDPACPGNIKNLWLDVVVVVDRSMQMTDAQLWQVRQTLTQVFGSDIRIGTGYSDKRSTCVGFVTYNSNATVTAELDIAKSFPDIYNIIQGSLVDVASTNASSLGEGLLAAQRVLNSGRQRTNRYNVKQVILAFAADFQDEFSNLNAIELSRDLQSNGISIITVACTKDSYALPRINMCATPGYAFVDEMNTSKLVKQLTGALININCFCPEDWVQYTGSDKKKLGVCIKGFDFSGSAWGYDHAVQYCQNQVSRGHLANEFSKEKHDFINLYMMNTFNRGMHLDYSIGLRYLNSTWVWEEPKGQPKLPLNPDIYSTWAPGYPQKNSTGQVVGVKANGILTNWVGSATSEWLFVCQVQSSSTEHYTTYVEQQ

>Cel|clec-59

MSKNICLLFFLFHAYLSSSYTDRICGQDLSNLWLDVVAVVDNSAGMTKGGLTSVAANIASIFSKNTQIGTNPTSPKTTRLALVTYNVDATTAADLNKFQSIDDIYSGINSALATISSSEESYLARGLSQAEKVFQAGKHGFNRAHYQKVVIVYASTYKGSGDLNPVPVAQRLKTSGVTIITVAYDQNKDGDILVDLEKIATPYHNLSNENLNVIGEIQGFLLQANCFCPTSWIQYRALHDDVDSYRYGICILPVGLTAVWRAAQLSCRNRWRNSYLLNEYDNRKHNFVISSVKNFSGFHFPLSYHIGLNKVNGMWQWDQPQDWTQPQLQNYEIWNSGYPISDSSLTTVLNRQTTVDLEIGWQNVHQFAAASNYVCETAACDTNNYCSSGGDSISNH

>Cel|clec-60

MKLTFLIVLIGVYACSAQDSSTTPSPSYTDRRCGEDLGNLWLDVVAVVDNSIGMTNGGLTSIAANIASVVSSGTRIGTNPSEPRTTRLGLVTYNKAAAIQADLNQYQSLDDVYDNVFRALSSVSTSEESYLANGLARAEDVLEAGKQGYNRTHYQRVVIVYASAYKGSGALDPVPVAERLKTSGVTVITVAYDQDGDGALLADLAKIASPPYNFTNTEDNGQVIGEIQDALLQVNCFCRNSWIQYRVSYTDVHSYRYGVCILPVGFNAVWRAAKSSCMNRNAYLVTEFDSNKHDYVLTAVSNYTGFSVPLTYHNGLSMVKGVWVWDQPQGMPQPQLQSYAGWNPGYPISDSTLTGVLNQQSSVQLQSGWQNIKPLTTGANYVCETASCDTDNYCTEAGLAEISVKH

>Cel|clec-61

MAMKFLLTCFLLGITFCLGSPVSQSSNCQDGYMDRVCGEDETHLWLDIVAVVDNSKGMTDKGVVTVAGQIVSLFVDGQQLGIDPNQPRTTRIGIVTYNRDATVVADLNKITSIDQLADIVFGALHKASSIADSYLHAGLEAADDLLQRQSFATSRGHYKKLVIVYASEYSGTGTQDPLPLATRMKVDVAIATVAYGQDNVNGFLRQLSQIATPGYNFTNQNGIQLVPELRATMVQVNCYCPNQWFQMRQSYSDESSLKYGVCIHPVTLGATRTAAKLSCRNQWNNAYMINEYTQTKHDFTLQVIENITAFTQPYTYYIGLSYSNGNWQWEQPNGQPLAQLQTWSDWCPGYPTASSTDTAVVNVQSSSSSAKTCWQNTKSSLTNMYVCEVATCDSTNYCTAEKI

>Cel|clec-143

MSTLVIFLTLAVVGTLCSPVLQNSAAVYADRVCQGDIKNLWLDVVVVVDKSQLMTNAQLWQVRNTITQLFGSSRIGPTKYPADPRSTCVGVVTYDSDATTNAQLDGPHSFTDLYNVVQGSLNNVDSTNSSYLSKGLLAAEQALKNGRSRTYRFNFLKVVIVFAADYQGSGTSNDAFPIARRMKYDNTIIITVACTTNQAALDGLAQISSPQFSLVDEMNTSKLVKQLTTALLSINCFCPENWVQFTGNGTQYGVCLRGFTATGGSYGYQHAIDYCASEVKNAHLANEFSQAKHDFMQILMAISFPKYKPLEYYIGLRNLGNQWLWEQPQGQDMIPLNPLIYSKWAPGFPQANSTNQVISTQPLQEGSTDFFWAPPQTNDWLFICQVQASSTEYYTTYLEN

>Cel|clec-224

MKRFQVFIYFCAYILVVSSASAKLDLGSIKKQQTYPSGTGTTISTSVSTVEPCNVGCQNGWVPYGGNCYRKMVDVLTQESAEQECVELGAHLASFETTDEATSVKNLVLSSPLFSDDLLSFTSSSQETWIGLSKTNNGAWKWVNSSDVDFTNLPDGTTVNGASCVSMNISGIWQPKECTSTASSFICKRTAASQI

>Cel|clec-187

MHFLLLITSLFSSFLLVSSSIANCNYGDIEYDGYCYTFVNQRLLFPDAQTHCATLGGVLVRVRGDQDGRWLAAIAGTEFHATYGNFWIGLQLVDGQWEWEDASTSTYKNWAPGYPFSGYDYVGAQLSNAKWVTVRSSLMLPFICYYQKGHNRNQLTTPAPSQNPGGICTGAELLLEHRCYSFIPTLLPYAAAKQKCESIGKTLAIFDDQMQINFVTSVSVSKFSMNYGSFWVGLTKNTADNTFHWADGNVNSLKNWTPGYPFQHQTVVSQQVSNGKWKTSETDTLLPSVCSGYLQ

>Cel|clec-186

MLLFSAFLIFGFSIGFSEEASCRHPHERFIGTRCYAFVSKKHTYNTAKEYCDSHGYSLATVDNAITSNFLASSAATEFGSNNGQFWIGLSRKKDYELFNWDDGTIVSYTNFEAGFPNKQDFVAENVRNGRWQTLAEHKELEFVCSYDPTATTSAAPTTIPPTTTTTRAPTTTTVRKTTQTTATTMTTPKPTTTVSTTTTTTVPPTTTPKACPQGFVLFEPTQKCYIVLVYGNDSDYPDVPDDAPFLTRENQRCAKYGATVATIHSSDLNDLFRSLIYERFNDTRYATIGLRNIDMKTISGKWQWFDGTSPDYLNFGNMFPKTGDYIAQTSSQGFWVSYTHTAPNEGVVCSVDF

>Cel|Y55F3C\_5.1

MLLLIFFLPTVKALSGFSVIKLKVPYSYLVSRTPIFTSTSSTSFNLNDVIYKNCASKMCIAAFHDNSSKYQLLTDVQNSCTKAPNCLAFTESQYNIAIVFMNNTSNECSANTTELLTEKFKPKECPAKWFPWTRPNGQIWCHMISSVGRTYQEASDYCQGMGAEMNGFQTVEERNAFIGFLKAKPASSIISWVYIGAKRSCPTDTCAKTVQFQWQNGVSTNHSLANDNFYSPWWEGLGNCLGMLYYKEGMYDDTECVQKAAASCGMLAK

>Cel|F38A1\_10.1

MFLQLFSLVLCVSYACSTCLDSGDIDIKGLCFKFVAQQMTFNDARNWCHYQNPVISSYLAYVPDQYTSNFLASYARTAFRSANGIFWIGLSRNNISSWVWDNGNPVTYTNFGTQLGQNYVAESSANSKWSTFGENDKNFFVCSYDPAAPPTFRPPIVTTTQVPITEDTSCKPIGSLTYLFAFSNDLDPQVVKDSWNNFHVGGIAIARFDVRDEEDIVYFTDFKNATAYLLDHLPNSKLGFGDTMTGSSSLRTIEKFYNSKEIPVCGAVCMVFSKR

>Cel|F38A1\_5.1

MLLQLLLPIALVAYASGACFDNDKEVKGACFKFVNQQLTFNDARNWCHYQNPVTSSYLAYVPDQYTSSFVAAYARTAFGTNYGNFWIGLSRNSSSSPFAWDNGSPVAYTNFDTQFGQNYIAEKIVNSKWTAFGEKDKNFFVCSYNPTFSPAIISTTQEPTTEGNSCQPVDRMTLLFAYSNDLDPQAVNNSWNWAGINLYSTFSGFAFARFDVRDEEDIAYFTDFESATSYLHSHLPDSSLGFGDNNTGSDSLVTIEKFYNSKEIPVCGAISMILSKRYPDDWNLPRTVSLVREHHGIVHAVSSVDPSGGTPSNALYNLTSKTNGMSNFGTDDGFPRLVGLISFNYGPQPIYCANPEVSGQNTIELPAIDILSSESYWVSVLTQDHGPLDAFQSFNLTWSSSEYGGNTLNSSSTQGLYGLVGLNWFPFNAETYSMKLQYNYINNINEVIQVRLYGVRAQRDWLPYCD

>Cel|F38A1\_4.1

MTKKSFFIKLIIFISQMCLLFILLVFLFYTDKVCFDNDDKEIKGLCYKFVSQQMTFTDARNWCHYQNPVTSSYLAYVPDQHTNSFLASHARSVFGTTDGSFWIGLSRNSSSDSFTWDNGSPVAFTNFVTQLDQDYIVEDIVNTKWNSFRESDKNFFVCSYNPAAPPTFAPPTISTTQEVPVTQNNSCKPKRDQATLLFAYSNDLDPQVVKNTWDMLFHDRTYSRFAIARFDVRNQEAIAYFLFFEFAKSYLYSHLPDSSLGFGDNTTGSDSFKTIEKFYNNQEAPVCGSVCLILEKRYPNDEDISKTVSLVRYYHGIVYAVSSINPSGGTQSKAIYNLTSRTNGICNFGTENYAGKLIDRVPMSSLSYVIYCANPVVSGQNIIELPPMTVPFEDVYWITLVVQDHGPSDFFVSSNLSWSNDKEGGDDLPANSTSPDILFLGSWYNFSPAVYSMKLGYSYSNNNKEALQVRVFRANQFRPNADWLPYCD

>Cel|F38A1\_7.1

MFLQLILFLLSASHADSDCIDIEDKEIGGLCYKFVNLSMEFYDARKWCHYQSPVPSYLAYVPDLSTSNFLATYARAAFETNRFWIGLSRFDYFDPYLWDNGRPVTYTNFGTGTGNFVAEHTLNGKWYLYGNGAKNVFVCSYDPAAPPTFPPPFILTTRQSTITSANSCQPGGPISFLFAYSNDLDPQVVKDSWDLSNIDDYSGYSVYAIAKFDVLEEEDIVYFLDKKLATTYVHSHLSNSSLGFNGTTTGSDSLRIIEKFFNNKDVTVCGSVCLILEKRYPNDEDISKTVSLVRYYHGIVYAVSSINPSGGTQSKAIYNLTSRTNGICNFGTDYYAGKLVTSVPMFYPPYPIYCANVLVSGQNITELPSMYVPQSIMYYTVFASVEDHGPLDNFQSFDFSWFNSDEPRYIQHLQSNSTVMDGVTSSGVYYIAPEIYTMKVQYNYTNKMEQAMQVRVYTYDGENSADWIPYCD

>Cel|F38A1\_14.1

MLLQLFLLVFFASYAKSECMVNSDKEFEGSCFTFYSQQLNFTDARNWCHNKNPAGPSYLAYVPDQITANFLATRASHEYGLGFGRFWIGLSRNSSTSPYAWDNGKPVTYTNFGTTELDQNYIFEDMGTSRWGSYKNSSLTWFVCSYAATPAPTISPEDNSCKPGKKVTLLFAYSNDFDSATVRSTWYQGFLTFTDDYAGYAIVRFDVNTGQEGIAYFTDLDNATSYVFSHLPDSNLRFGDNTTGSDSLEIIEKFYNNNSKQYSVCGSRCVILEKRYSNRLDISKTVSTVRKHYGMVHAFSSVDPSGGTQSKAIYNLTSKTNGVCNFGKDSKFADFTEEYQFFSAPYPMYCANPVVSGQNTAVLPSMNVNTECFLYWTLVTVQDHGPPDSFQSFDLKWSNEKSGGDDWYISSKSLFGVHGDQSYYFDLGSYSMQLQYNYTSAVEQTIQVRVYMNSAPKDWLPYCD

>Cel|F38A1\_1.1

MILQLFLPLVLASFAHSACLDSRDKEIKGLCFTFVSQQLTFNDARNWCHYQNPVTSSYLAYVPDQYTSSFLASDARTAFETNSGSFWIGLSRNSSSSPFAWDNGSPVTYTNFGTQLGQNYLAQSVVNTKWNAFGENDKNLFVCSYSPVAPPTFSPPSISTTQQIPITFAPPLVSTTQKITPVISTTQRMPVTEENSCKPTENGTILFAFSNDYGAQTVKKAWDGYPFKVTPCSGYAIARFDVRVEESIVYFTDFGDAQSYVYSHLPDSKLGFRDKKAGSDALQMVEKFYNSNKIPICGSIVLILLKRYPNDWDISKTVSLVRQHHGIVHALCSADPSGGTQSKAIHSLTSKTNGLYNIGKGRDFHNLIDWFPMYSYKHPIYCANPVLSGQKIIELPPMNVPFSTYYEVYVTVQDHIPISSFVSMDLIMKNDNYSGGNFQVYSKDVSGILASHSNHFSPVTYSMQLQYEYKNWAEEDTQVRVYSDRLPPYWLPYCD

>Cel|Y54G2A\_37.1

MTYLKLFGIFILLQLANGQCRREEDDFIDGLCYSFPTGPLKFNDAQNACHSMNQHLAIVQSYVQVNFLSTLIRTRLGVSTGKFWIGLSRPSVKLGYQWDDGSQVVWSNFDPNKIQNNRFVAENLLNGKWQTMCGQVALPFACSYDPNEKFTTVAIETSTTTKPNHVTTSTIETSTTTKSKPSVTCLFMYDTQSSGISTSAISTYKTYFNFAIFIASKLNDKTMLTGYIDNFGYSTGLNDHENYPTDHYNNLNNIPFPIDGTDDNIDLDLKDVDGSLATASWTPPVADQTCMIFISAAPEAEYGGTTIKSTYTSFGTVVGVLVGGATSIPGLSIDTNVIAAPALSDSDADAVVSKLLELLL

>Cel|Y54G2A\_39.2

MKNLILLTFSSFFAISHCQAQKCSDDSDNLINGRCYKLVTQQLTYSDARGFCHQADPGYTLATVLDKSTANVLSVLAHSVFNSSNGGQFWIGLSRNSTGSPWTWDDKSSFGWSNFGTQLGQNYVAQSSTNSKWGTFGSTDKNYFVCSYDPASVPTTAKPLSSVTCLIMYDTQSLGIDQNAINSYKAYFNFAHLVASKLNDKTMLTGYIDNYGYSAGLNDHQNYPTDDFFDLRGIPFPIDGTDDDIDLDLKDVDGSLAAASWTPPVTDQTCMIFISAAPEAEYGGTTIKSTYSSFGTVVGVLVGGATSIPGLSIDTNVIAAPALSDSDADAVVSKLLELLPTA

>Cel|Y54G2A\_8.1

MRTVLIFLLPLVAAVSAQRCLDNGDNLISGICYKMVNLQLSYNDALDWCHYKNPVVQSNLATIPDPSTANFLASYARTAFGVDSGQFWIGLRRNSSGGIPWWWDDGSSLRWTNFGTQLSHDYVAQSIVNAKWNTFLGTEKNFFVCSYNPNFITTEYPTTTDDTSCQPESPVTLLFAYSNDLDPDVLESTWGATDFGEYPNFAAYATVRFDLRVAEDIAYHTTIESANTYITSHPPDPTLGFTSTSVGSDSLSIVENFYKNQQLSVCGSVVLLLSKRNPNETEISQIVSLVRRHHGLVHAIMSVNPSGGSQPKALYNLVSKTNGVAAFEQDSEFSDFILHLPMFLTPYPLYCANPKVSGTNSTELPPLSVSSEDSYYTIMVVQDHYPSDSFQSSQLKWWPSGQQPFGFSLTKSDLIGNDANTWITLEATSYNMTLDYSYATTVPQAIQIRIFSGSPLDYWLPYCD

>Cel|Y54G2A\_7.1

MKILPFVLIAIASAAKQCYDSEDRLISGMCYKLVNQQLSYDDALNWCHYSNPVAQSYLAMVADQTTASFLASYARTTFNINEGKFWIGLSRKSSTSPWSWDNGIPLQWTNFAAPLGQNYVAQSMVNTKWSTYTGTDKNFFACSYDPDGVLATTTQEVPTTTGAA

>Cel|Y54G2A\_14.1

MTLHWFSIALPLLLTTSVHSQCASGDNSIGDLCYVVVNQQLSYQDAVGYCHGISTSLAVVHTTLQANFLASTIRTKTGTSDSLFWIGLSRASSSSRFTWDDGSVMYWSNFDLNFPKDNNIVAESVINGKWRTLAGQQKLVFACSYNPNNVNPASTTPTYSTDASSSTYAPYSTYATDSSTAGYGSSATPYSTDSTTNTYGPTDSSASPYPTDSSTSSYPTDSSTSPYSTGSTTSYIF

>Cel|Y54G2A\_33.1

MKFLLYVAAIIGLASGACFDNGDKEIQGMCFKLVPQMLTYQDARDWCHYKNPVTSSNLAYVPNQFTANFLASYARSAFGSNDGYFWIGLSRTSSNSPFTWDNGQPLGYTNFGTQLGQNYIAESIVNTKWNAFGASDKNFFVCSYDPAAPPTFSPLPTRMPETTMMPMPTTTG

>Cel|Y54G2A\_6.1

MFRLAFSLCVLQLVFGQCTRPDDKYIGDLCYSISAQLLKFTDAQSACYSQNQNLAVIHTSLQANFLASIVRTQTGSQKFWIGLSRASSSSRFQWDDGTTMYWSNFDMNFPKDNNYVAESTLNGKWQTLAGQKELPYVCSYDPKYFTAGPPGSTPNYGSTGYPVSYPVSGATEYPASSMTDSPASGATGYPASGATGYPVSGATGYPVSGATGYPASSMTDSPASGATDYPASGATGYPASGATGYPASSMTDSPASGATGYPASGATDYSASGAPVSAST

>Cel|T26C12\_6.1

MIRIKYLIALSSIISLANCRGCLDADDKEIGGICFKFVNQKMTYENARDWCHYKNPVTQSYLALVQNQFTANFVASYGHNAFGSSDATFWIGLSRDRNWNPFVFDNGVTLGQGWSNFDNQNSLNFVAERVSNAKWTTFNDSTTMPFVCSYDPTEPPVFSPPTPSRAPTTTPSTTTTTPGPTTTCKFV

>Cel|F56D6\_2.1

MLLKLFLLAAFAGLAYAACPDSNDKEIRGFCFKFVVQKMAYNDARNWCHYQNPVGPSYLAVVGNKETNNNLAVYARSAFGASAEYFWIGLSRNGSSGALTWDNGFPVIYTNFGSHVGNNYFTEKISNSKWDTPGDSEKNYFVCSYDPTVQPVTPKATTPTTTTAANVNCPLGGQQTVLFAYSNDLVPSVVLNTFSSSYLNSQPVTIAISRFDTRQPQSMMYFNDYNQAYSYLSTNLPDSTLGFGDSTAGSNVLDVINNFYSSPSACGSVVMVLAKRYPNTTDISNTVAKVRQYHGIVNFLASNTPSGGTQSRVLFDLASKTNGIYSIDDDSTFSHFIGWMPLRERYPIYAVNPKVSGQGSQTLSPMSVPRYAQYLMMVTVQSHVPVSNVQSATLGWHNQSSSYSGIFGMQPAGWEYINSNDDGTRENIDANVFNMTIDYVYTNTDVETMQIRFYSPYATTYWLPYSD

>Cel|F56D6\_1.1

MFFNFLIFSVIAGLSNAACLDSNDQEIQGFCFKFVAQQMTYSDARNWCRYKNPAGSSYLAYVPNKDTSNYLAFYARSAFGTSAEYFWIGLSRNESSGSLSWDNGLPVVYTNLGSYLGQNYFSEKISNTKWDTLGDNSTNYFVCSYASTSDQATSTEPPTNNCQPGGQQTILFAYSNDLDPSVVTDTLINSYLSSQPVTFAVSRFDLRQPEDIGYFNTYNEAASYVSTHRPDSTKRLGDNSTGSDVLDVINKFYNNTQLSPCESVVMVLSKRYPNTTDISNIVSKVRKYHGIVNFLASNTPSGGTQTRVLFDLASKTNGIYSIESDSNFSHFIEWMPLRERYPIYAVNARVLGQGSQALPSMSVPVYAEYLLMIALQNHMPVSNVQSVSLSWYNQFSVDSSSFDMQPLGWAYVDSNSDGTREHLGTVVYNMTIDYVYNDIDVETMQVRFYSPYATDFWQPYSD

>Cel|Y46C8AL\_3.1

MLLLKFIFLSTLAGLASAVCPDSNDHEVQGFCFKFVAQQMTYTDARNWCHYKNPVGSSYLAYVPDQKTSNYLAFYARTAFGPAAQHFWIGLSKNGSSGSLTWDNGSPVGYTNLGSQNGNNLYFTESLANTKWNTLGDDKINYFVCSYNPATTPTTPSTTTTADKNCQPGGQQTVLFAYSNDLDPSVVTDTLKQSSLEYQPIYFAVSRFDLRQPEDIGYFTDYDNVTDYVDSHAPDSSLGFGDTKTGSNVLDVIDKFYDNTKLTPCGSIVMVLLKRYSNSNDISNIVAKVRKHHGSVNFIASNTPSGGTNSRVLFDLSSRTNGLYVIDRDSYFMQSIDMMPLIERYPIYAANPVVTGAGFKDLPLLEVPSFRKHLIMVAVQDRIPVTNVHHVTVQWENSFSEYSGKLDMHPETWNNPYTNANGKRANLDASGFAMTVEYVYNDSGDHPMQIRFYSPEATDFWLPYTD

>Cel|Y46C8AL\_4.1

MILKLCLLATLFGITNAACPDSSDQEIRGFCFKFVVQKMTYTDARNWCHYQNPVGPSYLAVVGNQETSNNLAFYARSAFGQSAESFWIGLSRNGSSGSLSWDNGFPVIYTNFGSKVGNNYFTEKISNSKWVTPGDNETNYFVCSYDPTVQPVTQKATTPGTTTTAANVNCQFGARQTVLFAYSNDFEPYIVQNTFSNSILYKQQVTFAIIRFDTRQPQSIMYFNDYNQALAYVRNHLPDYKLGFQESTTGSDVLDVINNFYNNSSACASVVMVLSKRYPNTPDISRTVAKVRQYHGIVNFLASNVPFGGSQSQVLFDLASQTNGLYGIEQDSLFSKRILYMPLRTRYPIYAVNAKVSGEGFQVLPPMSVPQFDDFLIMVSVQSHLPVSNVQYVNLKWYNPSFPYSDKFEMQPVYWDSNTNYNTLTIGLSQNVYNMTIDYIYTNTDVETMQIRLYSSYFTNYWLPYSN

>Cel|Y46C8AL\_2.1

MLVKYTLFATLFGLVSAVCPVGNDLEIKGLCFKFVAQKMTYDDAHNWCHFKNPVGFSYLAYVPDQVTSNYLAVFARTEFGPDAEKFWIGLHRNGSSGLLEWDNMRPVVHTNFGNNVTKNYFTENISDAKWETLDDNGKNYFVCSYDSRWATKPTPSTMKSTPTTPTTIKSTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTMKSTPTTPTTPTTMKSTPTTPTTMKSTPTTPSTMKSSPTTPTTMKTSSITN

>Cel|Y46C8AL\_5.1

MFLKLFLLATLLGIAIAACPDSNDKEIRGFCFKFVVQKMTYNDARNWCHYQNPVGPSYLAVVGNKETNNNLAVYARSAFGASAEYFWIGLSRNGSSGSLSWDNGFPVIYTNFGSHVGNNYFTEKISNTKWDTPGDNEKNYFVCSYDPTVQPVTPKATTPTTTTAANVNCQLGGQQTVLFAYSNDLAPSVVLNTFSNSYLNEQLVTIAISRFDTRQPQSIMYFSDYIQAYTYVSSHLPDSTLGFGDSTTGSNVLDVINNFYNDISSCGSVVMVLSKRYPNTMDISSTVAKVRQYHGMVNFLASNAPSGGTQSRVLFDLSSRTNGIYSIEEDATFLHFIGWMPLRERYPIYAVNVKVSGHGSQVLPPMSVPRDVTYLIMVSLQSHLPISNVQSAKLNWFNPPFPQGALSMQPSEWAYTNSNSGGNRRIIDPAVYNMTIDYIYTNTDVETMQIRFYSSFYTNSWIPYSN

>Cel|Y46C8AL\_1.1

MTTKVVSVWLGFIVSAFFTTSWGLLLNSDEGFEKACKQSGGDYTQRAGNDSNTGDICLMTFQAVATDMDAARDFCNIKAPWRLREAKIDKSQDSIPVIICDVEATFTCNAGWIQMFGYCFKMSEVHDRYTREKAEQYCKDQAGPSFQGEIAGIHHRYILTPWRSYFTRLQQFWIRAPETWDEYVIKTDKVDGDNLALSFYDVHPDFSVPQNAMIKINGKVELQALCQYKPAITPAEINYMGRRYSEIYYPTVPVKDGIIVRSASSYTRSSNQSDVCKKVLKPYMYSKESQFFPDPDSMEQLAKLEPEAYSLMRSPLVSNSVERYRTNRYCQAPSNPHYEVVLGGKKTANFVVEENKIKGKPTCDNMMSVSISHFKGQAPEFHPMVDSQSLPIWCKLGKVVKYKYKVTPGWTDFRRLNGQVALHWLSKDKLTFADAAAACEAKGANLAGINSLKEAEQLGNHVVGANLNNEQFWLGAQRRTECLENNDWKPPCTRDKIFEWMNNVATDFRSEWWKKNNNLHSPNPSGTGQRCLSFAFGDLWWSYKGHTGFLDDIECHTELRYFCSKMAPFTECEENCD

>Cel|Y46C8AL\_8.1

MVLKLLILTKLVGLSSSACPSSKDQEIKGLCFTFMPYQLTYNASRNYCHHNNPVGFSNLAYVPDKETSNYLAVYAHSAFGSAAENFWIGLSRDPVSKSLSWDNGFPVTYTNFGSHVGKNYFSEKISNAKWDTLGDNDKSYFVCSYDPAVKSTTQSVTKTTTTPDSSNCQVGGPQTVLFAYSNDLNPFIVMDTLQRSSLDSQNVSFAISRFDLPQPEDIAYFTTYNQAMSYVSLHKPNVSLGFNDTTRGSNVLDVIDMFYNNTQTPCGSFVIVLSKRYPNTLDISNIVAKVRQRHGMVNFLASNTPSGGTQSRVLYDLSSQTNGVYAITRDTSFSSTIDYIPTRERYPIYAVTPRVSGEGSQILPPMTVLVHASYLLSLSIQSHVPTNNVKDVELYWRNPSSTNTGYFGMPVASWGFFDFNSDGTHANLAADVYNITINYDYTNSDVEVVQVRFYSSSPTNYWMPYSD

>Cel|Y46C8AL\_9.1

MLLKLLYLAILVGIVYAICPDSNDQEINKLCFKFVAQKMTYNDARNWCHHQNPVGPSYLAYVPKKDTSSYLAFYARSAFGVDAQQFWIGLFRNVSSGMLSWDNGLPVGYTNFGSHVGENYFYEKISNTKWDTLGDNDVNYFVCSYDPMVKPSTMMTSTMKSTTTTELVNPSCQHDDKKIVFFAYSNDLDPTVLLNALRDNYLYYSNVSFAVARFDALEPFTISYFSVYQQVVSYVSSHLPNSTLAFGDSTTGSNVLDVINYLEKNFLRKFEFSGKFCRRARWMPLEEKYPIYAVNARVSGNGSQVLPPMSVPRMDDFLMVITLQSHVPLSNFQSANLRWYNSQSSDSSSFPVYPPLGYTNSNTDGIRKILHALVYNMTIDYAYTNSNVETMQIRVFSQSATNYWLPYSD

>Cel|Y46C8AM\_1.1

MYVKLFFLATLSVLSSAVCPDSNDQEIKGLCFKFVAQQVTFNDARDWCFNYNRAASSYLAYVPNQETSNFLAFYARSAFGADAENFWIGLTRDGSSGYYRWDNGSPVLYTNFGDNIGNTFFTESISNTKWYTLGDFDKNYFLCSYDPPGNSTTKSGITTH

>Cel|Y46C8AR\_1.1

MLLPKFLLLTAFLEFASAICADSNDQEIKGFCFKFVTQQLTFTDARTWCHLKNPVGPSYLAYVPSQDTSTYLAFYARSAFGADAEVFWIGLSRNASSGSLSWDNGLPVAYTNFGTNVGKNYFTESISNTKWDTLGDGDLNFFVCSYAPIVNSTTMTSITGTTKRMTTTTIEKLNCKPGDHQIILFAYSNDLAPSVVTDALYYSSLSSQSVTYAVSRFDLRQPEDIQYFSDYSLFSSYVSSHLPDYTLGFEEATTGSNVFEVINKFYDNTQATCGSNLIILSKRYPNTADVSNIVLKVRKSQGMVNFLASHAPSGGTVSQGLYDLCSLTNGIYSIGRDSSFSNMIESMPIRYRYAIYADNPKVSGQGSQTLASMSVPADGTYYLSMMLQNHTPVNTTQSVLLHWYSPYSRYSSTASVHGLSFETNNNGANSEILDAAIYNVTLDFVYFTSETMQIRFYGTSTDHWLPYAD

>Cel|F47C12\_4.1

MTTKVVSVWLGFIVSAFFTTSWGLLLNSDEGFEKACKQSGGDYTQRAGNDSNTGDICLMKFSVVTSDEQDARDFCELNAPWRLREARRETQDSIPVVICDVEATYTCNAGWIQMYGYCFKMSEMHDVYTHEEAEKYCKEQAGPSFHGEIASIHQRYILTPWKNYFRTIKQFWVQAPETWNEYVVKTNKVDGDYLALAFFGDHFEFSVPVNSLIKINGNVKLQALCQYKPAITPAEINYMGRRYSEIYYPTVPVKDGIIVRSASSYTRSSNQLDVCKKVLKPYMYTKESHFFPDPDSMEQLAKLEPETYSLMRSPLVSEIDQSYRNRHNCQTPGAHYEVVLGGKKTANFVVEHDKIKGKPTCDNMMSASISHFKGQAPEFHPMVDSQSLPIWCKLGKVVKYKFDVPPGWLDFRRLNGQVVLHWLSEEKLKFTDAAKACEAKGAHLAGINSLKEAEQLGNHVVGAKLNNEQFWLGAQRKTECLENNDWKAPCTRGKIFEWNNNVATDFREEWWKKNNNNHSPNPSGTGQRCLSFAFGDLYWSEKGDKGFLDDIECHNELRYFCSKMATFTECEENCD

>Cel|F47C12\_2.1

MLEKYGRCRKRRLLKEVVLILLVAAVQPVLSSSKSTPEAQLTDVELTCPDDWIRHGTKCYLPFNIHQSWPFAMTTCQRYGSTLAKIQTGSENQFIASLLSKPGKPTEGKEYWIGLTVEVLDDDELYLWSDGTPTSRYVGFWRQDQPNFLNGSCALGKVERKDLEWRLDTCNLLRRFVCERPACVQGSYFCSSGSCISESKKCNGHNDCDDGSDEQNCPSAFQPNCRTYEKGESGQLSSTNYPNSYDPNLNCRHVLEGPINSRIELTIEHFETEPDFDILTVLDGGPAENSTTVIKRLSGSMETVQTITSATNMMIVQFRTDAQSNARGWQLKWRAVPFTCGGHFTAQAYIQSFVSPGYPKTFANGAECVWTVESTPGQVVSLIFDDFSLRAEDSLIVYNGATPSATVLASFSGNLTTKKYITSSTNIVYIYMMTRTTSSSRGFSISYKRGCDLSMTDPHGEIISPGYLATEYPNDVTCTFTIEIENLKADRSLSIIPNRFDVADDDSVRIFENLVKGKALHESDGFTAKSKPEKQIDSEANRLQMVFKSSASRQAMGFNFSYSIDCPAFPTVPMVTLSTKQRSVNTKVTVECPIGFEFASGEGVSKTVECLIGGTWSQSQISTCQPIYCGAVPQIANGFVDSATNVSFGGQVKYSCHKGFFFASGKDVETVYCGELGKWGIPPACKAATCQPLAQFSNGDRRLEFGDGTGYGSVFRFDCHSGYRREGVESSLCKSDGTWSSKQPNCTKVACTHLPEVANAKIEVPDRFLFGDVARVVCNSGFTIDGPEEIRCLANQTVSSTPKCIDIDECSSGVSQCQSLGTQCVNLPGSYMCQCLDGYQPQLMCLESNPIDARSSSKWCVDSKNVGKDRKYPTKVVKFAIPMIVEQIKFANVRNGKITKISIKYSETDKTRTKKLIIDNESILDVDEDNIATLPMAIEVQVLEIEVVGLEGSPCLEVETLGCQRTSCADINECLKDNGHCDHLCINTQGSYKCDCRNGYDIFTENGQSGVNVSTGETGNNMNDFIRFNKSCVPRQCSHIGSPENGQLLSTAERFEYPMIVQFQCAFGYQMMGPDYIQCLADGTWNGTEPFCLSATCQGIEASSKSDGLTVTPNNSTISFGQNVTISCSFPNRPGKLSSPLSNYRQCIFDPQDDGRDYWLSGPAPECSFIECPAPPTMPGAVYNGDVTDRKMGSTLEFTCRQPYTVVGRSSAGDQNIKCSPDATWDLGDLRCEGPVCVDPGYPYDGQVDLESVEEGAIAKFSCKRPGFVPFPSDTLQCTLGASCVLSEDVGIVSGFVPDGAFADNSDSTNLGYEPHHARMGSSGWCGAKEDFIFLSVDLQRIYTLTTLRIAGVAGSGHLKGHVTKFQLFYKTENQHTHKPYPVEFESPAGNHNAMHHFDLKFPLRARYILFGVTEYEGNPCMKFDLMGCVAPASPSHELDSHLQIGWNGSVPQCVDMEPPKFENCPESEIFAKVDENGQLKAVEFEEPAASDNSGKIAYTQIEPLGMRTGLMITEDMDVTYTAFDSAGNTAVCVLKIRIPDTQPPVMKCPDSYTIPVGNSTKHVIFDMTTVDMVLHDTSNVSDVTFTPSEATLKIGEFEEVTAQAEDENGNRNSCKFQVAYAPEACSPASLASSNQIVKNCVHEEGAVVCSVYCAQGYRFVDPDQITQNFVCKDGRWSPRNNAPACVPIPKDPAGFHVNVGISYPVSSPVPNHCLKGYAELAAKEFDNLDKVLSSRCSSSVEVHVKLLKLDFSNQNGVLTGNYTIQVLPTEQQSVFYDLCGLTLRTIFDLNIPGANQPIQALLSLSGEAIASQTAGCPSITAKASSVVQGFACATGEVLRQEAKDRLPECMACPSGSVNINNTCMLCPRGSYQDESGETSCKPCPDGTYTLDEGSQSVGSCLAICGFGMYSSTGLIPCQLCPRHTFSGAAPIGGFRECEACPSGAYTAKLGASSASECKQACKTGTYSNSGLEPCSACPINFYQPTVGQQSCIECSNTTATQTTGESLESSCFPIDCSAKMCENNAECSVFMHRAQCHCKPGYVGDRCEMLEDVCSTQPCYNGGKCEQVGTTYKCTCPKMFNGARCQFESDECNGVKCPNGGVCHDLPGVKSTTCLCRTGFAGPQCEEITDICSTNNPCRNGARCIGEKLGRFKCQCVPGWEGPNCDKNIDDCADSPCALNATCVDLINDYKCECPTGFSGKRCHIKENLCASSPCVHGLCIDKLYSRQCLCQPGWTGENCDQNIDECAASPCQNDAKCIDEINGYMCECADGYEGVHCQHLVDHCAKQPCHNNATCTNMGATYHCDCTLGFDGVHCEMNIDECAENQCDKLGTESCRDAVNDFKCVCKPGYTGPRCDVKQDQCADSPCLNDAQCVDMGGAYKCVCKSGWTGPKCEQDNGSCAAKPCRNNGFCVSLVADYFCVCPPGVSGKNCESAPNRCIGQPCHNGGECGDFGSHLECACPASFTGKGCEFKNTGCKTCENGGKCAEAAGGLQKCECSPGFTGERCETNIDECSTAHCPSGATCVDQVNTHICVCPFNLTGVHCDKMINTNYDLQFLDPFRPTSASLYAPFRIESSALSVGLWVKFEKPHQHAAFFSLHRFDNSSQEYVRVSSNLVRLTLFPGLAAVEVPLSSSQHLNNGKWNHLLITWQSKTGAYSVIWNSLRTYSNNGYATGKQLDVMTGITLGSTALPSFVGSIARVGVWNRVIDFEEELPLMVQHCQRSEEIYKGLLVRFEGFTKIIGRVERTHKSTCGVEEKSAMQKSQSQILIEDCPSDMVISSMDRETNVTWPEPTFLSSNSKIEKIEKNLKQGQMFTWGEYDVLYTATDNATNQAQCNFKIRVGKENCVDAADPVNGVQSCESWGPQLKYKACSVECRDGFEFPRSPAVFYTCAADGKWKPNKSPSTMFRYPQCTKHVPATKVVIVRIIYGSSPACTESSKEAFTQKVQQTIDAIDSKWKMCSLTDANGCVGTQVRVECGGSKLPEEGRRRRRNPESVLASSFGVEIEIPVKRRMLVDPSSGLETTIRDALHNEILSGVLNFEKVLPNGRPDVGSLKIKEEYLCQAGQVVVRDLCVPCAPGTYHSAATGECELCPIGEYQPLTARTECFKCAPGQITASEGAISEGECKDNCPPGHQYDSLTSDCVTCGYGYYQPSAGAFECIPCGIGKTTLSEFATSEDECRDECPDGEQLSASGVCQPCQIGTYRSRGENKKCVACPPGTTTEATMSTRREQCNTPKCKPGQFLVKETKNCQFCPRGTFQNEEQESTCKLCAPDHTTAAPGATAESQCFSTNQCATGEYNCSWHANCIDLPDENDVPSYECRCKPGYRGNGTHCTDACNDFCLNDGICKKNNIGNVECICKDHFSGDRCELRFQASNNKLWIATVIVGVVVIGIIIVIIVFMISFRFNHVQDTNEKSSTLADLSPTANNILYGTPPVCEPPRAFGYYYEDDDVYETKSREMIGSGSERRPTTSTVTSMGGAMSRAIEQHKYEQRMRQAQQHMYQPGGGNDEE

>Cel|R08C7\_6.1

MRLLLVFFLVVGYVLGQNSNQPITSNGTPLDFGLKKACEDVGGIFKQRENANAIIGDICTITFRVLTETDDDANEFCRLYAPWRLRSAIRNEDGGIPQTICEVEATMACDDGWIQMFGYCFRHPYKNKIFTQAEAIKVCSNLDGHTGEIAFLHHRYIVGVWKNYFRGIDQIWVNGSETWNQYVQSTGAVDGDALALALTGHTVVFSVFPNSLIRIDPIIRLGILCQYKPERTLAEIAYLGRRYSEIYHQSIFLEDGVLIRSASHYTRSKTNAEICQKTLRPFFVDDVEPFIPNDDIMSALSDQYTEPWAISNSGAHFTMDVSKRKSSDVCLKSTHKYSVAYPDPKMPPFVLPVETSVGCDNMNSVAIVHSEIDTEFRPMSDSQSVPVWCKFGRKMNYFVDLPKGYTHYERANGMHVGHKVVSMILPFDKAMKYCQDDGGAQLGGFNDKAEFEAIDKLISKKVHHWIGNRRRPDCPGFYFHSDPNHQCGHNKIHEWLNNVATEDIPIELWGFKQPDHAWKPQGRQECGSIAYGMPGSNGEPKLDDGSCEVKMPFICTAKGVLKATTASRL

>Cel|T19E7\_1.1

MILLLLYLLIPTINTVVIPSPLKSSYQSIAGQRAINLDVNVRLLTVLALQQSGWQLYEDHWYKMFETDVMWIPAENVCRSMGGHLVSIKDESENLFVHKLRKKNNIWIGLNKLNDTFHVYKWSDGSEADYLNWASSQPNEPDVDCAYMAFHQEQRGTWFDYGCREMLPQFFVCKLPMP

>Cel|F32E10\_3.2

MRHLIFTGFVLTLTALEAVNVAKSTDNDIVLKVSTEKHSSRDSHHFSGEWLESPWGDLYQFRAGDQNWLTAREHCLSLNADLAAIRNVEQLDWILSHYAPLSSRFAQRLVQIGLYAPEGQTHEWKWLNGNEINKTLLWSSGEPYDHSMEGRERCGLLNVEKRVLDDVDCESTSPDHHAQRYICQRTSENHKQQQRSNNYIWQKIENLFSFFGIGGSPTPHNATIPNDYEDEVLKNETSATVKSTVKFSDSEEETSSEEEESVSKTLAALPKIEGSGESTALKELQEPEGSGQIVEKKAIETTGDLVSGVDEEKLDKMINKMEEMIKSIDDLTVPPAVLERTTVSTVVLKKEEIVKQEKTDEKKVEDKKETLANELNDNKISESIEGDFDQAQSKDMPKADIEPPKEEDCDEEGSGSGSGEEDEKDESSEKIELAPEKEDKIKEFLGVLRLFLDRAEHGDLRKLLDDQSGKTLLERMKNAVREANRREFEMLEKLENSKKSEEEKEELAKKDQMSTEEQKDLYKKISSAVMKAAKIHKIEEADKVQDEQAMEKFNIAKVKADSEEAESEGTVEVLKSAKEGKAEIKEKVGNDDYYGDYLDDNNVIKIQNREKKDAKEESSSDDKKSTDEKKKEIKKIEKTNKVNHDEPKKEEKKNEEQVKETKLESSTTVAKKEDVTTVASTTEEPKSDKDSEGSGSDIEESTVSSAKPAEAEENEAELEASGHEEVSTTTESTTVAVKEVPVDEIEKIAKLEAKQHTEDEKVTVETKQETAVTPAPTTSEKTSTTAAPSTKPAEETTTTTEAPSTTTKPVTVAVKKVSPEEMEKLVKKESTEKVTLLPPLPTFTFPTLAPFTFPTLPTLATTKPSPAPKVPTLEEILGNLNDQFKKLLSPPKPLPK

>Cel|B0218\_6.1

MFQPTIFVFSFLIPLVSAQCGPGAIYQASGSRCLNVFRTASSFQSAEEICATLSGHLVSIHNTIDNTFISSQAQKYFDGGVWLGAKTTAPDVTNPLNWYWTDGSNFDYQNYKVGQPSPQGDTACMQLQTGTAKWQTTNCTAQLPFICSYSSSVTPTCPSVTIPSHCPSGYTWYDETDFCYKNTVRFTSFNDARSSCQADGGDLASIHSANENQFLVDLSKAGITNKDKSHSDDVFIGLVYQNSKWQWTDGSAVNFLNWGDGEPNNMDKEWWTSLVADPHEDKNTENTRWNNVAQIDMRAFICKKAPLH

>Cel|B0218\_8.1

MFRSLLLVFCFSAPLISAQCGPGALYQQSSSRCLTLFRAAVDFQTAESICATLNGHLVSVHNAIDNTFVSGQAQKFIDGGAWLGAQASAPDVTNPLNWYWTDGTDFNYQNYKVGQPTQTGSTACMQLETGTSKWQTANCTTKLPFICSASASAMPTFPAVTIPSHCPSGYTWFELTDFCYKNTVQYTNFNDARSACQADGGDLASIHSLAENTFLVGFSKAGCTNKDKDWTGDVFIGLVFQNSKWQWTDGSVVDYVNWGDGEPNNMNKEWWTSLVADPHQGKYSEASRWNNVPQDDQRAFLCKIAPLH

>Cel|Y59H11AR\_5.1

MLQVSIFLLFFVFPGCFGNLIFATSNEETCEDDSNNGGGKVKKPCEPGWLKFNRPSGVWCIKVFNGTHSQADAEKLCQKNYGATLSGVQNQREISYVTQQALGTMSQGSGSIWIGAKRTTLCKASRLSKYCNTLTSFQWTDGSASGLDGLIWNNNQPDNNYNRTDQCVVLLAARTPTVSDDLQWGANRLDDCCM

>Cel|F08G5\_7.1

MFVWLIFSHFVIHTFCNTNDHIEDFLRNKTAEDIIGLRQQYHRAIYKKKKEESALADASQPNLVLADGAVLPCEAGWHQFPDTGCCYRVSDAESEWHGGTAICKALNPDAEMASFHSQAESIFVANKYSTIHAWTGLSQTEIPNTWTYTDGTPDWHWFPALAAAPSDADSSCVEMMDGLLGLIFALSLQKGQTNAYSCDESIQIICKYCPRETTSTTTVTPTTTKAATIKTSTTTVTPTTVTTTKAPTTTKTSTSTTTPKFTTTTIQTTKKITTSPTSTTASIPITCTSNCPVPAVNFKGLCYKMCRGLVKFEDSCTWCNGTMATISSGEENDFVSRVFGSNDETTRQIWIGNTESSGYLNWSQGQPTKPNDGLDYCISMDLSAGSTRGKYKYLPCQSTVINSLCVMNP

>Cel|C25G4\_1.1

MPDMVFRIILVVSCFTSFSCKPKVKIQHDHIEEFLENKTLSDVIELNQHVQRARYLERLENEKGKLSDEGQQNLVLADGAVLPCDATWHQYSGTGCCYRTTDEKSEWYGGTELCRALHPQAQLASFHSQGESEFVCKKYSSIHAWTGLSQTETPGVWTYTDGTPDWHWFFAQSSTMTTEKSCVEMMDGVLVLLFSWSAKKGQTQPYSCTESIASICKYCPQETTSTSTSTSTTTTTIPITSTVTTTVTTTSEPPTTVTSTTSTTESTSTVTTTIPTTTTTTTVSTTVPTTKTTTETETSIKPTETTVIITTPSTTTVTTTVPTTTVTSTSSETTTTTRTTVTSTPATTPSIAASTKAPTTQKSTPTTTITTSTVKTTVPGTCTPTCPTPTVSFNDRCYKMCRGLVKFEDSCTWCNGTMVTVSSKEENSFVSRVFGSNDETTRQIWIGNTESSGYLNWSPGQPTKPNDGLDYCISMDLSAGSTRGKYKYLACQSTVINSLCVMNP

>Cel|C25G4\_17.1

MLFPSLFLVFASAVLASDDLNPCNSSWHFFKKTGCCYKTSDDMGTWFDGTGMCAKMQVGARLASLRDEDESKFVAKSHKSGIDGIHAWTGLSQTQTANNWTFTDGSKPWSSFFTPYVFPNNHTSCVEIVDNWLVELFQNTGKTQPTFCYHYRKALCKYCPVPPEIPSEPTSTTLAPVVRAKRDLM

>Cel|ZK896\_7.1

MLLFSAFLIFGFSIGFSEEASCRHPHERFIGTRCYAFVSKKHTYNTAKEYCDSHGYSLATVDNAITSNFLASSAATEFGSNNGQFWIGLSRKKDYELFNWDDGTIVSYTNFEAGFPNKQDFVAENVRNGRWQTLAEHKELEFVCSYDPTATTSAAPTTIPPTTTTTRAPTTTTVRKTTQTTATTMTTPKPTTTVSTTTTTTVPPTTTPKACPQGFVLFEPTQKCYIVLVYGNDSDYPDVPDDAPFLTRENQRCAKYGATVATIHSSDLNDLFRSLIYERFNDTRYATIGLRNIDMKTISGKWQWFDGTSPDYLNFGNMFPKTGDYIAQTSSQGFWVSYTHTAPNEGVVCSVDF

>Cel|ZK896\_6.1

MHFLLLITSLFSSFLLVSSSIANCNYGDIEYDGYCYTFVNQRLLFPDAQTHCATLGGVLVRVRGDQDGRWLAAIAGTEFHATYGNFWIGLQLVDGQWEWEDASTSTYKNWAPGYPFSGYDYVGAQLSNAKWVTVRSSLMLPFICYYQKGHNRNQLTTPAPSQNPGGICTGAELLLEHRCYSFIPTLLPYAAAKQKCESIGKTLAIFDDQMQINFVTSVSVSKFSMNYGSFWVGLTKNTADNTFHWADGNVNSLKNWTPGYPFQHQTVVSQQVSNGKWKTSETDTLLPSVCSGYLQ

>Cel|Y116A8C\_21.1

MRLLVFFLKIVFFLKPAMPVEKMLIFYGTIDKFNVNPLINMDLNSCVRIVSDFSTVILASWNSSENCHLFGFDQILDQILEIKTNEGDMGQYLILKSDQPNSTCPAFPETDIRRPVNESWSKTENGWTTRLCKNGWMLFSRPDSIFVCMKFIQLERGATREVALQTCIDNGAIMTGLATRSEVDWLNKFVVAPLQTGEWDGIWINGMRDCSANTNKTCQNFVWSDGYTTDTELLLSGILWDPGYDTQQQDCLTVYNAYSDTKLNLVSCTEYNLAIGVACGYKFE

>Cel|F26D10\_12.1

MSTVLGKLLILSVCLVGIFGNRIFGVKTCPKGWLQFEDNCYIRQPDFSSFRESVKNCEKRGAKLFHFDDSFEFEAVRNLFPDYYFTWMQAEVEEELEWLYEPYEEKMNGKNSAAKCIAFYSSPTKSYNYFYPCTSHFHSICEKSLQSFRQWMD

>Cel|C49C3\_12.1

MIRQLLILALCFVALQAMGVPMGNGDCGAEFKCPPNFHKSNRVNGVWCIKVYPGNMTWWEAERECRCTIKGGHLSGIESNSEKRYVEEQTLSILDDKNIKNGAVWLGAYRRKECPSGKVSSDSICHDEKTFQFTDQHTCKTLIFQDWAANQPTNNAGDDCAVLLASTEASGSNSEASGKAAVKNCLHVQGTTPILSSVGFVCGVKAAQEGGNYGGYGGGDFMVIGAAKPKH

>Cel|C49C3\_13.1

MVVSMRWLLSVFTFLCMKYSEASNPRAIILQNFMDSNKEAVKNLKDDNVLSKALVKTFGLNSSSSSSLSDESSSNLVLMDSTTPCDSGWTKSTVNGMCYKIATADTTWYAAEDWCYSQRYGSHLTSVHSEAEAQWIAATYVSTGWFPYMDNWLGLRRSCDNSTYIWTDGTPVDYLWWQPGYPGSGDPEKSCVTIWVTSLLKLNPGYVQGQFDDIWDCGTNLATPTCRYDPTSTAPHIKYDTSYTCASTTTVSTTSTVTTTKPTTTTTTPTTTTTTPTTTTTTPTTTPTTTTTTPTTTTTESTTTETTSTTTPTTTTTAPTTTTTASTTTFKTTTITTTTQTTTPTTTATTTKPTTTTPTTTRTPVDCSAKCDPFWVSYSDGCYAKIQGTATFETAKLGCQSVGGEMAVITDAAMNEAIRLAFSTNIDSSVSNQAWIGTSSYSNWAPGKPDKAQGVAYSSYCNVIALSVVNKGKDFGFSRGVWTDYPCSLKQEFAICKRI

>Cel|C30H6\_1.3

MNRFFCLTVLFSYLYRFTFSANDNAKIDNLVARQYLFSNFVANNREALKKSDGSDERWLFKFMNENSIIPPTSNSKSGSLADSGQAGLVLADAIGTAKCASGWTRWTGNGCCYKEMASPMLSWYASEDWCYSQKAGAHLASVHSRAEAEWLNYQYKLWWSKMDDWIGLRRNCDNTAWAWTDGTPVDFLWWQPNYPIYGGIEDSCTAMWDSTVLRGMYDFYPGQMDDGRSCTGSVAWALCKYDPNTSIISPKWVKADCTTTSTTTTSTTTTTTPTTTTMPTTTTTTPTTTTTTPTTTTTTPTTTTTTPTTTTETTTTPTTETTTTPTTTTPTTTTTTPTTTTTETTTTPTTTTTETTTTPTTTTTTPTTTTTETTTTTPTTTTTTPTTTTTTPTTTTTTPTTTTTTPTTTTTAPTTTTTTPTTTTTTPTTTTTVPTTTTTTPTTTTTTTTTPTTTTTTPTTTTTPATTTSETTTTTPTTTTQTTTKPTTTTTTPTTTPTTTTTPTTTTTTAKTTKSTTTTTKTTKTTSTPTTTTTTPKTPFDTSKCTVMCSTGWVYYNNLCYAKLQGPGRLNDFNKECISYGGKIAEIPDAQVNDVLRKSFGTNINDEEAWVISSGYNNVASGYTAAADSCIAMTLSQKISGSVAQRGTWRPYACSLAKNFGICQKPI

>Cel|C30H6\_4.1

MSVFAFSFCAVVIMPNLLAMSDEETRGRQAMVANFVKDNQKTIRNGKGDKWMSNFLKTQNLTFHRSLSSPSAMSDSSSQNLVVLADVGTAACASGWTRYDLTGMCYQQSKKTMNWYQGEDYCWNLRPGAHSASVHSQEEAKWLNSLYRDKKNGGQMDSWIGLRRDCDNVTYIWTDGSPTDCLWWQPDYPKSEFAEFSCVTIWETDWLYDNPAYIPGQYDDMKECSDDGSNVICKYDPNTLNIGAKYEWKKCGLVPETTKPTTTTPTTTTTTTIPSTTSSTTSTSTTTSVVTTTTVTSTTEPTTSTSTPTTTTTMQTTTPSTTSTPTTTSTTTTTSASTTTISTTKPPTTQIDIEKCTSNCPVGWIYFGGLCYSKIQGPGRFVDFNSECTRLGGKLGEVSGADGNEALRLALTSNNGNKILDEAWIQHIGSYNNVASGYVGTAGSCYTMILSKNNGGSFAKSGTWRPYDCTTTVKEF

>Cel|F40G9\_10.1

MFLSFIILSTFLPSVVFSASFPSFFNESAYETSGHKPEIYQLEYSGGCISGYTWFSYTNFCYKSTARAANFNDAHNACRSEGSELASIHSLTENQFLVQLSAAGNRVNSKTNYVMIGLIFENREWSWTDGSSVNYLNWAAGEPNNMKHELWTALVSDVNPKKGQMYTHWNNVNMDRQRAYICKRAPLN

>Cel|K02F3\_5.1

MTASLILLPVLLNILYQPAGSSLPTFSPGNKHLCEGFGFNWAAEIRCLRDIINDCEEGTQEKSRGGRSLQRSEFPTDNTPQADYGNPYSYPRPYSRTYHRNSISPIRPPVPMPIPQISQGCNCNHDIEALEAKFDKKLYEVKMHAQYETEKGVGDLRKQFETDLREYERITTKDIVEIKRHLDYLQAPRITNNDLEYFFIQREESWYTASEKCIGYGAHLASIHSRLELGFVQRLVPVNQTAWIGVNDIQKENVFRNSDGTPVDFYKWGKKQPDNQEHNENCVEVDHSGQWTDKLCIITRPFVCKKKI

>Cel|R06B10\_3.1

MLREHIFSASLLFLISVSVGSAATCHGEEKLDPSGKFCYVVHTGAASFHDAEKACYDYGGYHLASVPSMIDNNFLYNLSSNSNVWANYFWIGLTDMTADGSWEWIDGLDLVFMNWASSSTAGYCGAMRAADARWQAQDCTKPYPFFCYGPALGAPTNPPNTPKTTQKPVRNQENMIKFMADAESVGDPNVDPNALSFYNKEREFIRAVTDYLFANPTSDGNTCLYYMSPAFYGFTQYEQQFDTSPAWSHYQFDNLLESNVWDQGKTDHDYNITDAITGAQKFRWVPSMNNIGYTTLVFLTARRDFSGIPSLFQPFPKFDEVVVISLNGSQMPGIPAGVKNVAVSNDFSSTDIQNVINVLKCH

>Cel|F10F2\_7.1

MRLKIFMALSLLCYTNAQVDRDWSFQQMCEFWGGEQTYRARSGYKSIEGDKCTFKFPKASNNKESAQRYCEETVPYHINNPKASEYKTTCEAEATLICKSGWVQMFGRCYKITKTMMTRDKAEEHCKNQQDQTSTIAFMHREALPFRWNDYFTRVSRIWMDASEVVTNDLIHDVEGGNVLLAFDGYKYNLPNVAIARVSKNETAMVLCEYTPSMTKAESNYLLRRYGEIYYPPLVTSESAYMRTTSSRIRNEEDPLADHNYCTELMKPVFRGGEAQSALPTQEFVKKLTETGAAEIIRTSSVSMNANKGERTIVDCVSHVDPYHRVHVKGDKNEETSITLNKTIWRQQEPHETCDAATWSSAAVLSRDSNRGLEAMSDARYAPLYCENILEYFSYSKCPEGFSEFPRVTSGQRWCHKYVHGAPLPYDDAEKKCAEMGAHLSGFTTQEEFKFLNELVNKEYPNKNDIEVWLGAQRKMSCPDAGKNFNGGFSTNEFDNCARSRVFEWRNGVAKNPPDFIGSGYDNWAELDEPNHLSDKERCVVMMHGKITKYWGYSSKYHDRRDMQINDIFCDWHFEYFCGLEVPVITVKKSS

>Cel|F10F2\_8.1

MRIKIFMIICLLHKTNAQLARDWSFQEMCNFWGGEKTYHARKDGFKSLEGDKCTFNFPKASNNQESAQQYCEDNVPYHINNAEASEYKTTCEAEATLICKSGWVQMFGRCYKITKTMMTRDKAEEHCKNQQDHTSTIAFMHREALPFRWNDYFTRVSRIWMDASKVITNDLIYDIEDGNVLLAFDGYKYNLPNVAIARVPKDETAMVLCEYTPPMTKSESNYLLRRYGEIYYPPLVTSESVYMSTTSSRIRDETDQFADNKYCTNVMRPIFRGLAARSAFPTKEFVDKLEKEAAIIRSATVSQSANQKGREESECVVNQKPIHQVFASGQGGKTLNVKIDQALWRKGEPKETCDAASWSSAIVLSRDGEKGLETMSDARYAPIYCEAILDKYEYGPCPAGFLQYDRTELGIRWCHKLYSELETTYDDAEKECLSLGAHVSGFSDLKEKDFMHDMIMASPIKNKTFNRVWIGAQRRPECNTLGVEGKTGGFDTDDSKPCARSRVFYWLHGVALNPPDFIEHWADPNEPNFLGDKEKCVVVMTGSEWTHWKFGINKKINDVSCGRRYPFFCGKEAPIVKVTK

>Cel|C35D10\_14.1

MRELLVLLSLFVFSAFGAQPLVCTNGFTLINNKCLRLFSTPLGHTAAESKCTEYGATLVTVKNAIDNRAISTIAASSVSLLWIGLYCFDNDVTKCLWDDSTGSAEMYNSFASGFPLVDIGKCVYYSTQGSLAGKWLNGNCESDPRAFVCELPATHADNCTYNYNGHCFTLHTERNTFVQAQAICEQECGNLASIHSSNENRYLSSIMSSIMNLSNSSVYIGASWPSSSVFNWLDGSNSDYTNIDQSFGHGGNCALLSNYQPSVVPMGYWFSFPCTAAVPFICKRSAGIKCSGTPPPVTVTPVPSNPSFCNSTLLIAPGVITSPNYPSNYDNNQFCSYHLSTLGSYRVLLHFSAFATEVNFDLVVVYNGESASSSQIGRYSGSLDPFSVVSTGNNMFVTFKTDGSGVAQGFSARFTSFTL

>Cel|C35D10\_15.1

MIKHLVVLSLFALSAFGAKPLVCTNGFTLINNKCLRLFSTPLGHSASKSKCMEYGATLVTVKNAIENNSVSKIAASSSSSLWIGLYCFDSDVTKCMWDDSTGSAEMYNSFASGFPHVDIGKCVYHFTQGFLGGKWLNGDCDTETRAFVCELTETLEDSCEYNYNGHCYSFHQPATFAQAQVICEQECGNLASIHSSNENRYLSSIISSLSNKNYYIGASWPSTSVLTWLDGSTSDYNNISPSSAHEGNCALLSSQEQWLSSPCTSSQPFVCKRSVGSQCFSTPPLVTITPTPPNPSSCNSTLLMAPGKITSPNFPSNYGNNQFCSYHLSTLGSYRVALYFLTFTTEFFFDFVVVYDGDSASSPKMGNYSGSKNPFALTSTGNNMFVTFKSDHSNTFQGFDARFQSSV

>Cel|F09G8\_8.1

MDLKSWILLSCTLLPLSVTSYECYVTPCTRDIIIVVDGSSSMQTSTYVSQEINMITKLTYSWTLDDAKVRLALVGAYLGNEFNGLDYFTDSSLIEKRLQSFRLAAMQYGLFSGDFNTTVRFLDERYVGPRATFGPRANVQKRIIIFSAHKGASDIASTKSKLQEFAQLGYAVTIVGIGVSEDVYKGTFYHKFVSVQWFELGVVAQSIIDTITEDGICFLDQGWTTPKQEICTTSTTTTRAPTTTTTVTTVKGVTGKPATTAKPVPPTHPPFPVGDYQDCSCTTQSLYIDIIFVIDVSEGMGQGGLMMVKAEINTLVGQMSLDPNIQKHVQVGLIKYSDKAEVVFKPSDYTNEDEFTEDLWSDPRLEDVDEKSDEVNLHLGLQQAAKMTASMRNGVRKVIVVYAASYNDEGNDDARQIAANIRETGYAIITVAFVEPESSNLVMKIGEIASPRMNFTSFRDDLLVEQMEDALCQVNCYCPNGWKQLVLENRKYGECFFPTKIDASWTASKFECPVLSKEHTGNGHLVYVNSELKNTFLNQFYMDNWYPENQENPNYDIGYYYDQATKKFIWVNGVTNNPYSNWATGHPDVKQGDCVMAKLLKDSKNDFRWNSVSCTSEYGRGLCQEAACDTDFYCAPSSN

>Cel|F58A4\_5.1

MYRRTTLWFLLLFQPILVFAQNRTELYECKIGTVNPLASTSLNACFKLYNTPKSFQAARRYCVSLGGQLADKINKDDSSLYSANADLEVANSTKFWVGASNLKCNIAWENGGEIEFNDMWAPESRYYGVAIDKMSIGGLWHTVPVGQKLPFVCTFQGKSNEAGPAPVHAMRAPAKKRVPKVEKPEEKDIDESLNAALSDKKEKKEVASDKKKESKKDEEDINESMNAALSDERKKSASLASSDKKESSKKDESSDEANLSASQVANAEMSASISASSANSSSDESSDEAYDSAEIEMRKKIGKTVIAMKSQEMASQSDDYDKYTEEDLLSAAASLIGGYILNAHWADSRTTNTSSFDSQTDEETLNMMMAIAEQIAMTMRSSKRRESSSSNTDSESASISESSQASEQAVMAAAMSAKSSKKSESSSKDESEDSASLNLEQKASAAASAALASKSKSDSSDQSKDQKSANVALAVVSENKHPTKKPEDPKSTKTTTEEPDIDESLNAALANQRSTTTKNSDLTTIITTVKPNALPIAIVAKQSEKDPACPAEWTQFNTNATAPALCFKRYEKPMNFEDARLFCVGKGGHLASIHNERQLLLLSALLHNNGPDALSDQTWIGLNRIHQKYYVYEDETAMDFTRWLPGAPNINDCTVFTGNELPNYPHKGTQYKFGDFPCEEVQKSVLCEVTLGKDKLKSQTTCQDGWSYYSHDGTAKNGKCYKRIDQSKKFSEAREVCKVENSYVASVQNEGEARFVSALVQTEKNYTVDEQTWIGYVKYDRDFGWEDGNKGLQFDPWTEKMPRQKKCTVFTGNEIHENCRSQFRFVSVDCNKTQRSVLCSKPPMKNGTPFVYKDTDNSSKKI

>Cel|C07A9\_1.1

MNIFTLLFIYFLSDTVAAYCYYGTEYKNATGCFQFFRTPLNFTNAVRFCRVNMKSTLVRPTSSIRNQQIRGAALKLGIEEYWIGASNVDNDWEWLDGSMLTYSNFDVGGGYPKKTESQIGAVSMSSLAGLWYTKLDAMFLPFVCEFPPSTVYDNGILYRSPKTQSLIFPSAGTKAALLMVDAVDQSRLYSKNEIGPLKTEAETGEKVYLKPINISTNGFPEFSGPPIVILNPYKRKIKVKPVMVSQTETEMSRSRKEKEETEDSINVKSLKEGGTARGNGSSVAEELNSNSKEKREREENETIRSKTIQISRG

>Cel|Y39A1B\_1.1

MTAMFLLNYILLGFALCTGSPIVSQLSSYVDRPCGKDPKHLWLDIVAVVDNSKEMTDDGVLSIAGELSSLFSHAEQLGIDPNQPRTTRIGLVTYNEEATVVADLNNITTADELSNTLFAALTWTSSVEHSYLQTGLKAADDLLAKQSFNTSRGHYQKLVIVYASEYRVSGTQDPLPLATRMKTYLTIATVAYRQDIVVGFNDALTKIASPGYNFTNFNGNNVVSELKTTMIQVNCYCPNEWFQMRSSSKYGVCIRPFATMATRTAARLSCRNQWNNAYMLNEFTQMKHDFVLQVIGNITTFTQPYYIGLSYSNGNWQWDQPNGQPLIPLEHWNNWSPGYPTASSTDTAVINVNTSWQNTNPSLSNMYICEVAACDSANYCAAENI

>Cel|ZK1193\_2.1

MLKFVITSILLLRVCSGVSIPNKSQHGELTKSLNSKLKQLVALNLSEPSQRVQPTFSSRPKLLDQTSPVTCYNKSIDILPHDGTAKFGDLVESDFSATCSDTFTFYVDNFIEEFFVIINTLDALNPRATVYNPIGGEVSTCKDITTDVTQTIHLICNGKNVHGTGAYTVQLSADLNKPCIFEVRAPTKLTVDGGFVEDVRDDDVQKVIFSTANQGIFRFPLENQAAFLAFKVESEEFPIHPDEVHLYVNGLFDQKMDLNLRYGCSTPHITQQSYNCTSQNLYHAKFRGYDSDGNRFQRIYDFSCDLSEITFTTPSVHVSTTPARFCENGGILYNETGCYCGEFFTGGNCEIPLCLNGGTTTPDNAGCICDVGYSGAHCEHISCLQQSDDNFDEAQSAIAFVIRSSSSMKAQLNEIAEAATNIVEYYELHYPIFFQKFILTVVSNNAITFSHEYDIGEDFANSIRSLVAPPTETECDDALLAGISKTLENSAFKKYPNSPVFVFSDGTANDDFTTAGFLMEQIVNTRAQILFMITESASGSCNVDVSTNIFESLRSLSQLSRGLLIQTSLMQLSDATFSVAQDLWQYDTILTNDLEDCRKAPMFQPFFVDQSIDFLTLRASGSNLSPILTLPNNTQLSPQLFYSNGDFYVWRTEKPPVGAYFLNINTNSSHNSFCQYRLMGRSTYRLYTSVTDNIGTDDTYHAPVYQTTSHLVARMDSLYLDDPLDTTLEAVVWFNDPQTSQRQVLYASSGAWRDQCEYEMYFGMFSCPQPYLPLYINIYTNDGYGQVVLRTATSYCSATIPNPVDSNCLNGGVYYNSTCQCPTHFSGDKCQQIICENGGNALFGTCQCPSGFSGQFCEVTRCFEYNSYGFWGFNHRSLTIMIHDSLTTRSTLRTLNDAAPRVINDILYQHPKWISNYQLIEFNSTTHTLIVDSESGQDLVTGIFNLYDQNRNHAGYSCLGLNFYSTLLEAISHDNVQWGGMIYVFLYGQPAQDLDSYEKILQRIEVNKIQINVVQSSLNPCGQDISLDGLISLTQFSGGSFITATTPNAGNVFNQVPTNYMSNLIYENIAQDCTDTTFYVPIDVGTQSFTTYVQGFLNTDVQYTSPTDSLSTVTNVFNDLGTNARIDHVARVCDDGWTADGIHCFKFSFEEKSWYAALADCHSEKSVLTGIFNQAEQDGLHYSSDGAQFWIGLSDVLNPGQWEWDTLNDKLNLTLQDTQYTNWMPGQPVLDAKKSCVVDSNKGDKSYRGWMTEDCTKKYYFVCQKHAYSADYSPSDPEINHLSRGIWKIRVRANGQCSISIRSQSTVQVATRFTTNIHDDVGKEEPNKNTDMNRLVIFTYGVENKNGAEYAHFYYDNFTMLQAQSLTYRDNCMFSFISTPFSCPNFYYQMLITGIDDSGYLYQRIVPAACIGGVNENSCANGGVYYKGTCICAPNFYGDACDYAYCQNGGYLSANLNKCTCPSNFGGQFCEMPICDRNQLDVPAIGDVHRTFIVVLDGSNNDIMKSVNDNIEKTINGVLTAIQSQDPAWFTNFVGVVFRDAESAKANPPIPSTSKVFTTTNSSEFASMLATEVKNNPYTAGQQKRDIFTGIVKAIVNQNVVLNSKVFVITAGNAEDTLDRPTVISALALSHSSVNFLFIGDTKPPGDAVTYDDPTVRSMFEAAHITGGAAYQLTSADDLQTTWLSVLASLHQSYYVVTHQLNNCSNYQDYIQLDANGTEAIIDIFAQTAPEIGIYDVDNKQVDSFSIVKSKTNTVRVFKQTGEQPGVWTIDVDYGMSNSGPCTLNIRTQSKLEVDLGFTQDVASDQGYHDGGAVLFPRGGDFENAIVADISEGGTLTYAQIFDLDETRIAWASPLIKRDGCAYPFISEYTFQCYRNQFVVALDGLDFEGHPFRRTFTVHCDGEIRPQPTPSAASPTLEFTTATTVKTCDPSTAMLDVIIAFDSSGSISDEMYYATVGAVNTIGNAISIGHDHSRILLGTYDAISHFSGDLNTLDTFEAYQNKLADLFSLGYTGINGNNIQSVMDYIVLQNNSAPFRPAPVRKFLMLLSSQGWDKGNVSEGKENGFSDPAPAARNLHKLGLETFAIGLGTSANMTQLNAIAKCSTQVNDQNELTSTISQIISLLCGSIPIC

>Cel|C43H6\_6.1

MRCTIWPLWLSRLLILYYLSVPVIVIAQNTTCSGTVVLNATKELQYLTTPNYELSYKYPPFLDCRFFIKAPDKTRVVVEIIDMEMEPRIFDECSDYVGFAEDVTEKNISKMLTLCETLTKRQYISSTNTLTIIFQSDELIEYRGARLSYQYHDITTCPPGWTELSDGKCVRHEIDQKTDWITAQNRCMEQQSNLITIETGAKTTELENLFKSVPTRFWTGDTDATTEGLLVGINDREAPNIPGRESGNSYTDNNDNNDCMTVHFGDNQPFRMDGCASFNAYICEMKKDGTTVLYPPPVQNIQDGSNSHNSAYALWLLLFLIGLLFLTIMAFLCFMCWKQKDARVHTETSGVQQNAFMSETTHRIDQQSRTSGNGQQIAPVASSSGGANRTSRNSPINVPIENNRPIKKFPMAPVPNRLPMAEEPSGGSEHVVETGILGANNDDDVESVSAAPRAQTRTLPPMPTREGTFQSINTRDGSTMRTRRNKELFERPVMHVLDNVSAISLDEFWSNKKP

>Cel|M02F4\_7.1

MSQNLIFVISLIASVFYCTNALTCPTGTKIYNAKCYAALGMDMTRDNALAYCRKTYGPYARLTTPLTYAENNFVTEQVQLHANWHTWLEYVADGTYIVGDDGKPPIYTNFAVGEPFSVNVGYCITIGMNGYWYAQPCPDSHSVLCEFDLVPPTPKPVLTTTVKPSGFPSCVQKYLNFVPCQSGWEYYPPTCACFKIISNTTYYNAMNTCRSMGGTLASVHNAGEAAFINRLGVQANSYWVSTATARDNIIIGLTYNSDRGYFQWDDSTVFDYAQGFAPAEPADYTSQGQIILNNPMGYATYMRMGNCAYQTCRYAACKRYVY

>Cel|F28B4\_3.1

MRSWVLIAALAVICLGAEPELSHKERIRKVLKSWNPANSNQLFHPVSEQKIQFDEQSDLFVDTHHISKRSIAEPHVFAGMATRGCNKPGYTGATCQYPLCSARNPYIPDNKDSDDISIDATNLANCSQTYVVVVDETMRNIKIEVETESPLNPTFYLQSESGDLIFPDTDRKTVTSYVATYETLAPGQYLLGPRADSGDEFCTMMMTAHTNIQVTGGFTSGDQPERSDYPTLKFAYFDTESAVVLHAQGLHFPGQIQAIGFTGAENHISRYIPMATRFNCTYPYILERYTCRKIGNNDIGHNLLQVEGMSDNGYVFRRILPYQCILPPVSTTTVPAPTTTAAPLTTCQNGGQVLKDSSGSPYCYCFGLYTGRDCSQMLCANGGFLPTPTSEHCECPEGFTGFHCQNIVCPGASGIDFNAENPTVTLVIRSRSQLSDVIQQATNSVSRIVDELSAEPGYLTNFIVVLFDNAKLLVNQRYDSWDAAMVDLLKAINSAPSDGGCDDVVFSAVASALSLYPTNKSPIYVITDANPNDSTEKQTIVHLESYWRAPVYFIYVQPAIGSGCNTSPDSAGYRDMVDMAAMSSGNTFYFNNRTTISNFFYVHMYNTLFRSQLALSGDYSHCANQNIYKSVAVDVTADQVVVVATGSNLKLQVTTPTGAHPDFFVAFNDGVNYIWTSNQIFAGQWFFNLVSDSPNSACTFKVYQKKYNLGGMSQYNPDYDIFWSFATTLTSAAGVLRQPVAGFDASPVFHVSNYPEFISMDRVHANLQIYAIRDGVQTEVYGSSGMYRDACEFHFYFPPFICNVPDEVLYFNFFARDNNDMALQRAGTMLCSAVHPTPPPQHQCQNGGVMNPTNTTCFCTPQFTGTYCQNIVCYNGGTVSGGQCVCPPGYAGESCEVPRCIETGPNPEFIRYGVDMVFAVEITQQSLASIVMLDNNFQEILRDVQMQDRGWIRNFVLVGFNSTWGGPIAQSPSNNLTAIIAALHNLATNVPSDNGCSVKLWDALNHAIFARDLVPGSFIEIFQTTPEYELDQRSLGLFYDMSRAMDISLYGFLTAKPTLLPAGFVCNATQVNYYVLFGMVTSSTGQTYILQALEISNAIRLIPIQFSNGQVTINGNNDCRHEDGLTTYFPVDAYTQTIQLTVFGYGTTIQVYNGNGVLAEALELFYDDYTGQSVYEIRQACDNGWESFGQYCVKFLTVNDDILSMPQARNFCASAGGYLADDLGDDKNNFYSSIAANTQFWIGLFKNSDGQFYWDRGQGINPDLLNQPITYWANGEPSNDPTRQCVYFDGRSGDKSKVWTTDTCATPRPFICQKHRYDSDHKPNTIGDADLPAGDWYVKIKTNPTNSNPPYCSLSVRVQSSLQIVSGFATKIGDDNPQIDPIQDFSSNRLITYVHSVDNENRVPIMTDAILWDFYNGTFYNGLKYQARFGCQYGWVSQDFPCPNSDNQNNEFGVLHVGEDEFGNTFQRLTFGHCSPATIVCGNGGIRQNGQCICTDYWTGSRCTVPICVNGGTKNSDEATCTCPDGYAGLNCQFEVCQPKVPQIFTDDTKTLLFVVETTRQNSDTVNQLIANLKNIVTSATNFAPFWFSYFGLVTFDTTGRTFEKYNYTTIDALITDLTAQSTAISTDGACSMPYLGVLAHLLEHDNVISIPNSEIFLVTAAGPSDLNKYGEAMNSLFNTEAHLHYIVSKSANCPTFEGVNNVQDMTWLGYGSSGNILFTDSSNIVSLMNSYLPSLYGASILQDPTGPANYSCTDGSLPWFVPVDSNTTFIYVTTSSEFGSLSVKDPLGQAHNVAPAYNVNSQKFYKIEVDRLGGIWTLQLVQPPGLCLAHIYSTGGARVYTKFSLPNPVGGKEDPLGAHQDGRFVQPVSGFDNVAVFHIAGKPMQRGQLQYVEIFDIGQVTVTNVLRSELYRREGCSYEYYSDLFTCSGDMIAVFIHGVDEYNQKFRRQQIVVCNGRNPTTGQPMTGTMVPVTGSMAPVTQATQQTQGPVTQQTQGPITQATQPPQTVQTQAPVTPTQNPQTGLQFDIVFLIDGSQAAQQNFDSFTKFIQTMMVSFDVGIAGAHVGLVVVAADLNDQAPPVANLNAITSQQMLISYLNGLKDGYTDFDDAGQVLTYNLQVVSSTDYMAATAGYRAGISNHVIVYITSTTSFFTDPTPSAKTIIAQKKYGIITVGYGGAVDTGKLQTISGGSACSFTATDFTTLNNQIKPIQQLITAASTNGGNYCKST

>Cel|F40F4\_6.2

MRNWVLIAALAVICLATEQELSHKDRIRAVLRSWSPASQKQFFEPVREQKYRTMEERVIFLDTHHISKRSIAEPHVLAGMATRGCNKPGYTGETCQYPLCSARNPYIPNNDGFDDIAIDAYNLANCSESYIVVVDETMRNIKIEVETASALNPTFYLQAENGDLIFPDESIQLPTMFTANYLHLPPGQYMLGPRADTSEQFCTMMMSSRSSIHVSGGFTSGDQAERSDYPNLKFTYFDTESVVAIHAQGLDFPGQIQAIGFTGAENHISRYIPMTTRFNCTYPYILERYTCRKTSNNDAGHNLIQVEGVTNSGYKFRRIVPYQCVLPPVTTTTPAVPTTPAAPITSCQNGGQLLTDSNGVAYCYCFGLYSGSTCSQMLCANGGFLPTPTSDRCQCPEGFSGFHCQNILCTDMSGFDFNAENPTLTLVIRSRSQLSAVIEQATESVQSIVDLLASEPGYLSKFIVVLFDNGKLLVNRQYDSWDAAMVDLTKAIHSAPSEGGCDDVVMSAVASALSLYPTNKSPIYVITDATPNDSAEKETVFHLESYWRAPIYFIYVQPSPADGCNSSPDNSAYRDMVDMAARSSGNTFYFSDRSTISTFFYRHMLNTLFRSQLVLSGDYSHCSSQNLYKSAAFDLSVDYVTIVATGTNLTLVVTSPTGQYPTFNTAFSDGVNYVWTYNSPVAGQWFFSIRSLEPEAACTFKVYQKKFNFGGQTQYSPDYDIFWSFASTLTSAAGVLRQPVLGFDSSPVFHVTNYPQFLSMDRVHANLQIYAIRDGVQTEVYGSSGMYRDACEFNFYFPPFTCRVPEEVLYFNFFARDNNDMALQRAGTMFCAAVHPTPPPDHQCQNGGVMNPSNTTCFCTPEFTGTYCQNIICYNGGTASGDHCVCPPGYAGESCEMARCIETGPNPEFIRYGVDMVFAVEITQNSIASLSMLNINFQEILRDVLMQNRGWIRNFVLVGFNSTWGGPIAESPADNLTAITTALRTLASSVPADTGCTVKLWDALNYAIFSRQMAPGSFVEIFQTTPEDDTDTRSLGLFYDMSRTMELVLYGFLTSNPRLQPEGFVCNATVENYYTLLGIVSGSTGTTYSLQANEISNAVRLIPLQFSNGQVTFNALDDCRHDDGLITYFPVDAYTQTIQIQTFGYGTTIQVYTGAGVMAEALELFYDDFTGQSVYEIRKACDEGWEPIGQYCIKFMATVENILPMPQAKAFCASAGGFLVDDLTDDKNGFLKSVAANTQFWTGLFKNNDGQFYWDRGTGINPDLLNQPITYWADGEPSDDPTRQCVYFNGRSGDANKVWTTDTCAEPRAFACQKHRYDADHRPNVIGDDDLPAGWWYAKVKSNPPSGYPNMCTMSVRVQSSLQIVTGFSTKIGNDFPLPDPIQDSTENRLISYVHSVDNENRVPILTDAILWDAYNGTFYNGLKYQVRFGCQFAWVTQDFPCPNGDSQANEFGVLHVGEDEFGNTFQRLTFGHCSRAQITCGNGGIRQNGQCVCTDYWTGSRCTVPICVNGGTRNPDEATCSCPDGYEGPNCQFEVCQPNVPQLFSNDRKSLLMVVETTRQNSDTVNQLIANLKNIVSAVTNNMPLWFTNFGLVTFDTTGRTFEKFDYTSIDDLITDLTTQSNAISTDGVCSMPYLGVLAHLLEHDDVIAMPNSEIFLVTPAGPSDLGNYVETMEVLFNTQAHLHYVVSKTANCATFDGVNNVRDMTWLGYGSSGNILFTDPANIVNLFNSYLPTLYGASVLQDPTGITNYTCSDGSLPWFVPVDINTTFIYVTTSAEFGSLSVKDPLGAAHSATPVYNVNDQKIYAIEVDRLGGIWTLQLVQPPGLCLAHVYSTGGAKVYTKFSMPNPIGGKPDPLGSHQDGRFVQPTAGFDNVAVFHLAGNPFHRGQLQYVEIFDIGANSITNILRSELYVRAGCSYEYYSDLFTCNGDMIAVYVHGVDEANQKFRRQEIVICNGRSPTTNQPATGTIGPITMPTQQTALTQGPVTQQTQVPGTQPTQGPVATTQNPYTSAQFDVVFMIDGSQSAQSSFDSLTKFVQTFMVSFNVGQSGARVGLIVVGGDITNPIPPAANLNSLSSQAMLNSNLAQLSGGYTDFEDAGQILNYTLQIVSSPDFMAANNGYRSGISNHVLIYLTTTTAFDTDPTPAAQTILAQKQYGIITIGYGGATDNNKLQTISGGSACSFTAPDFASLNNQIKTIQQLILNANANGGVYCINN

>Cel|C25B8\_4.2

MTKLNIPPVSLDSKSVLCLTVTIYQSSFEKFYVTKSYFRIFKLVLLVAAVGFVSTRFAQVKLFNWSYKDFGTNAFTDISLDQRQHYHDFPTGTCPDGWVRFSDSCYWIEQHKQSFAEAEKRCYEKNATLFVVNSQDEWDAVREHFPQTGYTWIGLVRFTHFEKSQDAPIWQTEGAVNPTRLNWLIRPYKPVSNGWSALANCAAHFSAAINWDASAYTYFQPCSFKFYSICERNGTILDFLNRKFDFQD

>Cel|C54D1\_2.1

MLRVLFFTLVALLCFVSPNCLPGDTPFEIYCFSYNRVHGTFNDSDAHCLKTVGGSLVSIHSMIENNWIQKLAVDNLDADYDLFWIGGSDEGHTNDWRWTDGSVLNFTNPGPGQPLEDRHCGAMQLSTGRWFSDLCTVKHQFLCQYPNGAYPTGGSYTCPPCPSCSK

>Cel|T25C12\_3.1

MRLLLALFLLVTAVAAAPNLDSVFHHLPNYYPELTNTDAFHIRAKRAIFAVLGIANQCENGWTGDGCKNPICTDPKPAPTSGQTSSIEIMFIQGSCGGPFYIPVDSTGNKPTQTIQIHVSAAGIPYVNMTDAKGVVFSPSYSVADDSYSLNVYADLPSGGYTLSIDNQGVPTSECIIEVNGDPSGLKAVDGFVYSPQSDDPPYGESAINGVPMYMAAHVDNSPAQVQSITIRQGNSLAPVYRAALTRRYQCGYEYYAGQWQCQLGNAYFYHIDGVDANGFNFRRTGRFSCMQLLTSPAPPTTTQAPVTTCFNNGTLLNVANQGQTCFCSELFNGKQCEKVNCMNAGFPDPDGNLCECAAGYHGTNCQDVTCPLNWEQYLTNYKTLVVIIRSTVSMNQNLNAISSAIYKELTSNDGNNYEVYKGFVIVKFANGAYTNTYYPAFDQNAFLAAINQASTAVGQCSDATFDAIGSIFNEVALYQKSPVYLFTDATASDVEKWQTVIEQNTRMKFPIYTHYFVQSNCAFDEMSQGFQAIEYASYYSGGLILRPSVDSLQQIFQYVIKATAYKMNSVLIDDLASCATPTRVFFVDTSTTELMILAVGQQLTVSVTDPNGNTNTLLKIVDSGTTQLYEISNPVVGEHLVTVVSNVQNTPCSYRVQARSEYDLFIGTSVGVNDDASDSEPVVGQSSHIVAQLTGLKGKVADPFRLFSEISITSNVNVDNKYQKPMYYSSGKYRDGCGFHMYFGAADFCDFMSQPFYATVYADDGKGFTIQRTTTGFCSGTPTTPYPPNSCQNGGVTDPTNNATCICPPGFYGQYCTNIQCVNGGTPRGGMCVCPVGTAGTFCEQYMCTTFNNNPDVSFDGQSIAFVVSTRSTMKVAVQKIADNVQAMTRDMQQASDKWINKWILIAVNSNTSYLLVNSARPADFVAGVTNLNGNFSNYAADETSCQIQIEQAMLGAVLLSERRSSVWVFADSDGPNDLSYVQLFDVSQQYQLSLNLVGVGSSICTTPENNGQFPYYLRSLSQTTLGDIYMTDKLDQIMLFIVSMYKSAVSHRYYVPDCTSATSYYMPVDGWTQSLTLAVTGTDLYSVEVTFPDGQKGQNSDYELVAINDPETKLNQYVAACSGSFWNHRQQNCFTFTADKLSWLDTWDMCHAQKAYLLHIDSQATNDYVASQIGSYRVWIGLAFNNGQWYWDVPDGNFAQPLTGYTNWAPNVDPTNPAYNHAVINSNGKWEPADPNDAANNFAACMKHRYGQGYYPGEGVNIVPGGLWKVTVQSNSGSCEIQARSQSDIQVFFGFVTDPRNDKPSTYANIQSNSNYLIAYPTGVLPYTPDTKPSMEGKLNYAVLSSNRTITNSLPLGNRACTYATISAPFSCPVTDGSLSDFSIKFTGIDQYGYAFERYSDALCTKAVINCANGGFLNNGVCVCRAGWVGTDCSTPVCQNGGIEKSGVCDCSSVPQFTGQFCQLAQCEPPYPTSFNDKDRTLVLMLETSYNMGSSIFQLKKNLKASLDSINNDPTTQGWFTNFVLYPFDSTSNKDSWYPPTISRNSDDIVTALKNISTMSCPGSAPCSSQCPRPIVSVLSSILDMNALAAPNSVIVVITRSSPEDYLQVGQISQKLQTKKAYINFVFPAIDSPCGEGWNSPNTDALFQIISYSQGNTFTMNAVDLSKNFLTQYVPTLYSSGGIAASNGNCQTDEIIFQVEHEMYEFSIDFYHPLMETIKVFDPSGDQLTLPDNIINSDSNYIGVFPVNETGATRAGTYRILLTGTGGNNCFATVRGRSNLELFLGFVDSSSDGHNGATNDATHYAPVNLENNTIVVHANGLGAGIVRYVQIVMPRFGLLHTTEMRKRDSACSYEWYATTPFSFDYDQYYVIIYGSSEFGSNWKRNFYVSTVGQRPPLPPPPATCDLNVVKQDTLFLIDSSLKDSNVTFRILQQFAVQAVQPFNYVSGLGQVAALRVADKAYGGFSYNAGENSFDRVSELIYNMQYIGIDGQNVTAGLQYALDYYDLPSQGYRTGSDVRHLLVYVTQTNPTDADPSELLRTIKRSGLYEVVVVALDMQPSDKLTNMVNPRCFYLAQDFHDLMNYGVNFVQGQSCLRWNFCNY

>Cel|T03F1\_10.1

MLRPLILALCLVVHLISAQCGPGSIYQQSNSRCLTLFRAAVNFQTAESICATLSGHLVSIHNAIDNAFVSSQAQKYMDGGAWIGAQASAPDVTNPLNWYWTDGSNFDYQNYKVGQPTPPGSTACMQLETGTAKWQTANCTNKLPFICSAAATVVPTCPTITIPSHCPSGYTWFETTDFCYKTTVQFTNFNDARSACQADGGDLASIHSIAENAFLVGLSKAGITNKDKDWNDDVWIGLVYQNSKWQWTDGSVVNYVNWGDGEPNNMNKEWWTALVADPHEGKNSEGTRWNNVPQDDQRAFLCKIAPLH

>Cel|C09D1\_2.1

MTLFHFISFFLTSLFSTTVGLSIPPTTFPNCPKSWHHDEPGRTCYHLARRRMRLTEAHSYCQKMIADGSAHVLRVECGGENDFISGLVKGHSEKVWIDARARFDIVDGAAGLFGPGFVYRWPNGKIVRYSNWANGNGLEEVGSSNSNKCINIKSDGHWMNANCSSTAAVICEKKLHRPYSKHCPKHWVYNKETQACYRTISKTNMTILEADNKCFDYGFEHRQDAMLTSIESESENQFVMNLAKEKDANFEFIYLGGYGRSRNGNKWHWMDGSEFNYMNWDRGMPFGRRALAVLVMNKRGKWINHYADKILSQYNAVAVCKFKS

>Cel|ZK858\_3.1

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>Cel|C25A1\_8.1

MRFCLLVAFILPGLFLVHAAPTSSTELPEASGEAPETSPLVQNDEQPHQRLTFYNWDYKDLGTTAFEDISFPARQPPAFVNQTEKCPDGWLRFADSCYWIEKELLGFAKAERNCFEKQSTLFVANSIEEWDAIRVQAKEAFFSWIGLVRFTHYEKLEQLPRWQTEGALNPTKINWLIKPYKPLFNGWSSLANCAASYKSPSSLESASYTYFYPCTYMLYSICERNSTIVNALQ

>Cel|ZK39\_3.1

MVKLILLTVLVIGATNAMFFIPSKVSCDDKNGGGETNGGCGAGWRRLNRPSGGWCIRVFEGVLTQADAEAKCKSRGATLSGLKNAEEARIIADMALPVLNRDSGSVWIGARRTDACMTKSITSDCTATNSFTWTDGSTSGTAGFVWDSRQPDNDYKKQPCVILLSSKTPETPVSVKNRPWLPRMIDDVACSLDPAEGSARIVAGYVCGKKSSQ

>Cel|ZK39\_2.1

MTKFILLALVGLAAAIDFDSSSSESCEDGNGHGHGHGNGNGNGNGNGNGNGGRANGGCETGWRHFRRPSGSWCVRVFGGRLNQGAAQSQCQSFGATLSGLRNLEEARTISNLALSVIGRSSGGIWLGARRTTACAKQHKTTSCSTTSSFRWTDSSASGTAGFVWNNVQPDNSDLNSQCAVLHAGSSAATVSNAVWQPAMMDDVTCSFDPAGRDPRSIYGYVCGKKPSRR

>Cel|ZK39\_5.1

MLLLLAVSLLGTVTCQTCETGWSVQGLRASGFWCVKVFLGTYTQPQAQAQCEAVGATLSGIQSANDAQVFQSLGLAALGGQSGSFWIGARRRAACQTQRITADCTAQNSFEWTDDTVTGTDGFVWNDKQPDNSDLNSGCAVLLASGPPVQWGNGMWAGAKLDDHVCDFVDKTPANPRRIRGYICGKRSN

>Cel|ZK39\_7.1

MTSLLVLLAIFIGAVASHGGDYHGRGNGGGNGRGGSNQSNRGCDSGWKRFNRPSGAWCIRIYRGTHSQADAENRCRQNVGATLSGVQNQVEINFITKSALDLISEASGSIWIGGRRTQACRNSALSTSCGSLNSFQWTDGSTTGTAGLVWNTNQPDNKDSRSQQCLVLLASRASSIQDKWTWYANRMDDVQCAASGGESAARALRAYAYMNFICNPFAILYFSTQLGFSIRSQTFHKCIHEHVSG

>Cel|ZK39\_8.1

MSSLSFLLCFSLLIGTLVAIDFDSSSSESCEESHEHKHGGGHEGGNNGGGNNRGCDAGWTRFNRPSGGWCVRVFPGTYHQPLAESRCQSQGAVLTGVQNQEEAKKIASLLLPQISQQSGSIYIGLHRTPACSKSPISSSCNSMNSFHWTDGSTTGTDGLLWNNNQPDNAHAATQQCAVLLAAHTPTVVDKWTWQANRLDDVQCQVPAGSNVARTVRGYACGKKARS

>Cel|Y53H1A\_3.1

MFLILFLVFITTSAIDFDDSSCDSSSEEHGGGRPARPGTCGQHWHTFKRPQGTWCVRVVTGDVDYYRGLAECAKYGAVLSGIQNNQEREWIANKAVSLNVAAGKTHSGVWLGAQRTSATAFRWTDGHTTGTEAMVFGPGQPDNDHGAGRGPQRCLQLMALTPSYWNIPGHLINLKSGQLDDIWCNVTLSPRVRMYLCGKKA

>Cel|F15D3\_2.1

MKSLLILFLLGSCSANIPERECGRDLSNLWLDVVAVVDDSKGVTQGGLYNIIGTLNSVLQLSKIGTRKDNPRTTRLGLVSYNYNETIEATLNDYQFLDTNKMMDQLKISSNIGSYLVTGLSGAEQLFKQDKEHSREHYRKVVIVFASTYKDDGANDPKPVAARFLSSGGIIITVAYSQSHDTQLLEKLGGIATKEFNFTNDDPGLIEKIQDSLLKANCFCPNSWHQYQPKGTCIQPVTLPASWSIAQASCHHKGNNGHLVNEYSREKHDFVMAILKTYKEFQPTYKYHIGLNGNCSLWKWDQASGEEQVQLQGWQIWAPDFPRCSPMLEMLEGVTYVTDGWINVPSNFYANYVCETSTCDTDNYCARANDFLLNRV

>Cel|F56H6\_8.1

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>Cel|E03H4\_10.1

MQLRFALLLLIICFKACLNSPLICTNGFTLLNKKCLKLFDTKVNHTSAESSCNSFGATLVTVKNVNDEQAIATVVAASSARLIWLGLYCFDSDPAKCLWDDNSGSAQSYDNFSIDFPLVDAGHCVYLSTLGALAGKWISEDCESKLMSYICELPTTHADDCTYNYNGYCYTFSSTAEPFIIAQTKCAETYGDLVSIHSSNENRYIETFAAQDYYLIGAVWKLDNSLYWLDKSKWDYNNTDPENSYRGDYCVAMSTVISSPIPSGFWFSTNCTRPAKYICKRPAGVQSTTASPVTVAPSPANPSNCNAGLLMSPGVITSPNYPENYFNNENCTYQLSTLGAYKIALRFASFSTEANDVVTVYDGLTTDSPCLRRCSGTQRPFALTSSGNTMLVTFTSDSKGISSGFYARFSSIVYRR

>Cel|C54C8\_7.1

MRTVAALLFLFTCLESFESSSATPVCTNGFTLINNKCLKLLNTPVNHKAAEISCSSFGATLVTVKNDHDNQAIATIVGSSTPLVWLGLYCFSSNSSQCLWDDESGSARSYNNFSSGFPLVALGQCVYYSTQGALTGKWLSAECESQRMAFVCELPTTFADNCLHNYNGYCYTFSSSPQTFIGAQSTCAQTCGNLASVHSPNENRYITTFAPQDYYYIGAIWKTDYSLRWMDGSAWDYNNIDPIYPNRYNYCLHMSTITTSGSGFWYGDDCSLSRKYVCKREAGVPCTTVPPPVTVRPSSTNPSNCNAGLLMSPGVFTSPNYPQNYFNNENCTYQLSTLGSYRITLKFSNFRTESNYDFVSVYDGPTTSSPSLGRYSGNIGSFYVSSSENNMLVTFTSDAGVVFQGFTARFYSVVHRS

>Cel|T27F6\_2.1

MQAIAALLFLSIYLENFLTSSRSIHCTDGFTLINSKCLKLFPSLVSHTVAESSCNSYGATLVTVKNVKDDEAIAAIAGSSTPLIWLGLYCFDSDPAQCLWDDVSGSASNYNNFSAGFPLVVLGQCVYYSTQGALAGKWLSEECESQHVAYICELPITYTDNCDFNYNGYCYTFSSTTNSINTFISAQGTCAQDCGYLASIHSPLEIRYINTFAPHAYFYIGAIWKNDGSLYWLDNSPWDYNNIDPVQTNRVDYCLTMSTTNFGSSPAGFWFSTNCNNPGYYICKRQAGVQCSAAPPATVTPSPANPSNCNAGRLMSDGIITSPNFPQNYFNNANCAYQISTLGSMRIALTFTFFNTQPYDLVTIYDGETSSSPVLGKYGGNQSSLTFTSSRNNMLVTFITDGKDTSNGFSARFSSIVYGNI

>Cel|T07D10\_4.1

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>Cel|H16D19\_1.1

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>Cel|T26E3\_1.1

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>Cel|ZK666\_3.1

MNTVFACLAIFVFGIYCSPVPQNAAAYTDPACPGNIKNLWLDVVVVVDRSMQMTDAQLWQVRQTLTQVFGSDIRIGTGYSDKRSTCVGFVTYNSNATVTAELDIAKSFPDIYNIIQGSLVDVASTNASSLGEGLLAAQRVLNSGRQRTNRYNVKQVILAFAADFQDEFSNLNAIELSRDLQSNGISIITVACTKDSYALPRINMCATPGYAFVDEMNTSKLVKQLTGALININCFCPEDWVQYTGSDKKKLGVCIKGFDFSGSAWGYDHAVQYCQNQVSRGHLANEFSKEKHDFINLYMMNTFNRGMHLDYSIGLRYLNSTWVWEEPKGQPKLPLNPDIYSTWAPGYPQKNSTGQVVGVKANGILTNWVGSATSEWLFVCQVQSSSTEHYTTYVEQQ

>Cel|ZK666\_7.1

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>Cel|ZK673\_9.1

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>Cel|Y46H3B\_2.1

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>Cel|Y46H3B\_1.1

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>Cel|F59A7\_1.1

MLLQLFLSLFLASYAKSACFDGRDKEIKGLCFTFVPQQMTFNDARNWCHHQNPVTSSFLAYVPDQYTSNFLAYDARTAFETKNGNFWIGLSRNRSSSPFVWDNGRPVTYTNLGTQLGQNNLAQSVVNTKWNAFGENDKNFFVCSYDPAAPPTFSPPVITSTREPRTEDSFCKRTDRVTLLFAFSNDFNSQTVRQSWDRKTLNLAQYSGYAIARFDVRVAESIAYFTDYRSATAYLHSHLPDPRLGFGDKTTGSDSLQVIEKFYNNNDIPTCGSIILILSKRHPNNADISKTVSLVRQHHGIIHAVCSVAPSGGTQSKAMYNLTSKTNGVCNIGEDGDFDELMDYIPIYDAPYPIYCANPVLSGQNITELPQMNIPFSNEYWVALTIQDHAPIDSIRSLHFFITKTNDKYSIIDWQVYPASFNGILTGNGFTLSPVTYSMELQYDYTNEAEEATQFRVYSISPPQDWLPYCD

>Cel|Y19D10A\_9.1

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>Cel|F56A4\_2.1

MFRLVVALSILQLVAGQCAHYEDKLIGDLCYSFYTETRNFDGAERACSGNNQNLAVLHNTLQTNFLASIVRSQTGATKFWIGLSRATPSSRFQWDDGTTMYWSNFNMNHAKDNNYVAEHTTDGKWQTIGKHHELPFVCSYDPKNFTPIPSGSGSTPDFTNGPASGATDEPISDATGAYSTDLPFSDSPTGASDLPFFGSSGATDFPVSGGPSDSPIYPASGATDEPISDATGVASSDGPLAYSTDLPFSDSPTGASDMPFFGTSDYPVSGGPFGTPDFPVSDGPSGSSDYPVSAGF

>Cel|Y73C8C\_2.1

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>Cel|R02F11\_12.1

MIFPLVLFFIGFAAAGNYGYSSSGNGGGRPRPGNGGGGGGVRPSNSGCDAGWRRFNRPSGGWCVKVFGARMNQADAQIQCQSHGATLSGLQNSEEAQQISNLALSVISANSGSVWIGTRRTAACMKQWLNTNGCTRTNAFYWTDGSATGIAGFVWDTLQPDNEKLSQSCAVLLASRSTVTWGGKFWQPAKMDDNNCLFDLEGKHPRSVYGYVCGKRSR

>Cel|F25B4\_9.1

MVLALITLVVSAFLIPEVLADPCGDSNWRYFPQTNSCYKLIDENLPWTIAEFKCLFQGAHHVSIDSPEENQFVHELSRWSEIWTGAAFFGKDQHYVNSDGSRYGNFENWKDGRKPPMNRARRCIKMDGNGEWFQSCCKKKTFTICEKKAAYSASSYSGSNNSVNGFRFMRHRS

>Cel|T15B7\_1.1

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>Cel|F10G2\_3.1

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>Cel|F07C4\_2.1

MSFPFSIFLLAFLLAPVAAIPCPTGFTRLVTTGQCLKMIVAPLSYSDASAKCKSLGAKVLTIQNAIQNNAVLSFATASATGNDKDYWLGLQCTTASSSSCNWADGSKFSFDGFAEGQPNNSLGTCVFVGNRGQTAGQWFSAECGLVKTNVICEVN

>Cel|F52E1\_2.1

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>Cel|ZK863\_9.1

MKRFQVFIYFCAYILVVSSASAKLDLGSIKKQQTYPSGTGTTISTSVSTVEPCNVGCQNGWVPYGGNCYRKMVDVLTQESAEQECVELGAHLASFETTDEATSVKNLVLSSPLFSDDLLSFTSSSQETWIGLSKTNNGAWKWVNSSDVDFTNLPDGTTVNGASCVSMNISGIWQPKECTSTASSFICKRTAASQI

>Cel|B0365\_5.1

MNSLRKANFFWAFSVIGVFLAESACPVGFDLVNLKCIAITSHLLSQHKAETTCKDMNAHLIFIQTAIDNTAVLNYASNITSPMWIGATCKVSEEPTKCMWDDGSYLSYSNFLPGYPVTNIGTCVYLDSPNQPLKGRWISATCDLAEYHAICEVNK

>Cel|B0365\_6.1

MWFHSTLLLAILVAVSADTCPAGFTALSTSKKCVKLITDVAKHSDATANCSSYGGHLISVQNAIDNNAYLQLAAVSVTPYWLGIKCSLSGNPASCQWDDQSGNAGGYNGFAPGYPLVEVGNCVYVPTSGSFAGKWLSGDCNTMSLNFICETAPTSPITDTCSFQYNGNCYYPSLSALPKQDAQFSCQQACGNLVSIHSIEENNYVQSLFTTNAPTYIRIGAVANNQNSNSWIDGTSWNYDNIGYSNINLGMCWSMALSNDIVSTGKWISSYCDTSLPFVCKRKVGTQCGTTSGPTQTPGQCTSPMFMDNSGRFYSPSWPYSYIGEQNPCNYILDTPVGSLVQIRFPVMNLDSQASISIYSRIEDTTPLVVLQGNSASNQWYTSTTNTMKVVFRPCIANCPNDGVNYRWEADFKPSTDVTQPPVTVTPNPNNPSGCNSTILVAPGSISTPNYPNYYPNFLLCMYHLSTTGGYRINLDFGAIDTEQCCDIIEVHDGPLLGSPKLGIVSGTWPAHAKTYQSSSNSMLVTFSTDSSGQGSGFSANFWAL

>Cel|F08H9\_6.1

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>Cel|F08H9\_5.1

MICAVLTALLFAANIQVVTADVNHCPSGWTFSTNTSYCYIQSAQYLSYSEASNYCQSIGGTQVFIFTLRELTWLTDFTSSSFAQPWLATTRNITTDKWYNSDGTTPAATYWTSGEPGVNGDCATFKGAGASGLKATQCYSIQPALCRQMPALCPSQTSYGGQYTGSGTITSPGYPNQYYNNLDCVYTILSPNNTYITMQFSPYMVEEYFDWIDLFDGPNTTYPFLGTTDDWWSLRFNFESSSNAVSFIFHTDSIVTDKGWLLTWSAKTKTPPISQSGQNGSFTSPNYPNNYDPYTEQIYYVNAPTGFQVNLTIPDFVTEANYDVLEIYNTSTVISSGLVANLSGSAVAPYSWLSPSNYVTMRFRSDGVVQKQGFSIVWFIQ

>Cel|F08H9\_7.1

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>Cel|F08H9\_8.1

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>Cel|F08H9\_9.1

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>Cel|T09F5\_9.1

MGIITYLIFVLAIFIFPIASISCPSGFTLLVSTSRCAKFISGELNYDGATLSCNSSGGKLISIHNAIDNRVMMQFANSSITNDNYNYWLGLKCSETGNPNACAWADSTKFSYSGFAKAYPNTGYGNCVFVETAGNSAGQWFSATCNAIRTNAICEIAVNS

>Cel|C06B8\_7.1

MILRSLLLIVIFHVTWCQIGQPGQAPGQVPLDPGYRQPLEPIKNVLQGAYGSNITLYYRNSPYRVMGDLTVEYGVTMDIETGTRIYFDTGVGLIVKGTLRAIGNEFAHIEMLPYQQQINYDSEMPNFRLVDGPTVRQGRLQVQFRDRWRSVCTMVTNWTSIDTGTACRSMGYSDGGFWKWFRRNNDTYPFVMPKPDCHGAAKNLWDCPAFSNPQKIRLSENLCQGEDDIGIYCWGPPTFTGWARHWKGIQILNSPFHYVNSDPDLVAVNRESDSRLEFVDILYAGYDGVNKNTTSALYIEGVPPIMNGLRIEHSARDGLQLLDANGPAIIANSTFSYNRGHGISVVNTTDARIFINNTKIQGNWGDGIWYKQQTGVNLIDYGMRERRSIGSGRLEEQKPRIDMCAEHRVDDNHFFPHLIAVNLKNRTYLDLAQPAICWMTVSLPPRLPYTYSIQWLHIRDRNPQTARTTLLVCDSNNVDENSCSTPRFRIPIRNEIFPQSISLKSSGKPLYLALEHVLDGDQAGYVQGDVHLLFNIHASVLDKAYYGLNVTNCIIEKNTGNGVFANDIRERTALTNVTLDENQGYAGFLVKDGAADIWLNETRILNNWGDGMNISYAGGSIMVNGTRIEKNRWRGAAIHYNQTLPFLPMYNEVIFKGRPSNNKFYLPTIISENEWGGLLVGNFCAYSNESNWHSKYRIPINSVYPKLVPKILISWVEFLKNQYHPSMEIFSCRDPDVIWNIVDVTGNRIDGNLGYGMRIAPAVNMHTVINSNQFLHNNDTTLYIRNAQWPELGDLPAEVTISKNVFKFNVAKYIISIGMNEDAPRQFLTFNQQNEIRANTVFDPFPSLPPRSTPYAALVVSSSNVKIHRNCFNNERSKYEIATELEQHAKWIDARENNWGFQEIPRFIDKFFDQFNRYSLASIDIEPYMAACNQRMPYITLLNGAFRQFKKQSEPFKLGGIIYENHDLLKGRYQVTEDLQVVPGAKLTIASGSVLEFQHGIGMLVQGDLIRNEYDQDEKVIFTSTPFTLERRSDIRLVDVDGNYEVTEGRLEVLVDDQWGTVCNRSWTPQLTILACNQLGLVADVQYFENWRIFPEPGDLPMIMDNIRCEENEVDITKCRHDGVERNCAAGCRSTEVVGLRCLEPRWAGVRYSLLANPPTVTGQTTMDNWRIEKGGLFNFRTSEFCAAFKVDWNYHTFHRLEIRNNFWDGIDVVYNDLVKKPAIRNSVIYNNRRNGFHIRSAGITVENVTINFNGQSGMRYNPSLSALEQNDIVSWLSLKEQPELEANNIFRIPDQQLDLIEVMESNLNQRKFLVAAETQDCPADPHQECVYNLMIRSVGYQYGLASKMAIQIVNAPSNVSDEDAIFTEVSTGKSWSARKDQVYFPVVSTENAMRMRYTRSFGKPKLVILVLFLDTQEYVDRFIHLYKSRVEDNQYGFSSVHYSNLTYSDGRLSNRWNNEKIWLQKVNFTRNSEAVMWLHSPQHAVVPGTPIAEITYHFDNCSVTDNSGPIIESHRDLYASANVFHWILWSNTFANNSRSGIAVALPDTYDLLAKQTHSFWLTENRFERNSEFKILLDGYYAFANISSNNFTLNTAPKQFGMVELRGMEKNLICERNRFFFNWGHWMIKLDATSQYLRQIDVPSYVQYNYIEKNRFINQRGDYVDMWPRSYALGVFGSQKVEVHFNRFFNELIDFELVSGAKYSDVFETMNTTHNWWGTGNEAVIAQRVFDFDDWNTFTRAEWTPFYVSNDLSINFWWNPWRDGQLANATYLEPGVHDLHGRVYEDKNLTLITERWYSFPYNYRPFRPYRITRDVTIMPGATLYIEQNVEVHVWPNVRILVLGNLVARGEYWQPIRFKPINVTEYMQYKGEIPTEYRKKRGIEWPEKSQRHAGYAHLAGPNGPFVIKGTSGNSKLSDHLERTKRHDCQWPENPNHPHESIHPDTPNGPYRLKGLKQERPKRASDRSKPDLVYRDFPTLHRDDPYYQRFTVSLTTNGSDYGRAGFIQIYNATTGEVVPSCDRQFTIRNAQVVCRELGLQTQNVYHWLTPRWDYNPHVRILKTYMEPRQCRGDEPSLDRCDLRLSGNDSQWMCMDSEHFNYVYCGSNRSLSRDYIGNWGGITFAQPNLEHAYGEKSGAKKEKSILQYVEIVGGGAGHKDSWQSAGLQVFHRSPILDHINVTNCSVHGIQVISPNDRITLANLNVTFNQGQGVNILTTFVQAPSSSQNAMRKPMSIPYYTQGMLDMCAARKRFEVENRIMLYYKYDSYPVDCVKVFTSRGRRVAFRIVQYQLYSSPTDLGRSDALRLYSSESFAPMALLADFRSDYQSVDPSVAVTSDEIAVHLRATAADGVYGFIAEVSALPSNAEQHTVGEIIIRGSRVDHNDRGAIEYSNLGEMSPNLVIESSSFAFNGIHLFGNISTSSQAVQLNLHNTVFFLFRANSIAHNRGGLYISATSSSPVVRLGALIKNCLFAYNSNSTALALSGNNYQVITLLNNIISHNFALYHDTIVAHDVAINMTRNTLFSNTGLHTLDIHANSKLSVDKNTFFYNNFYDNLALGHGQQYLEMYGYQPAKENNEFFNRPRRDLVKRQVLTQQGVSFDWWTHVDNETTRYRSTIIAGSSQEVFKFNTFNDPLNDYELTTGRQSPYEMGSIDAKENYWGYPGTVGVAAGKIRDHEDYPGLVKVDFTPVLESNTSLIEGDCPAGWFQAGHEEFKSCFLFVPSAVTFSRAVEYCEELDAFVPYLRINDILQSQLAQRIEKFSIDLRTDQERLKPYGMDDDIPVWISAVNIPNTQCGWLRSRSKKIEQANCNLLTAFICEKGTHPYSEPILWRPGIIIPIILAAVILFLLVILLICWCVKSRKRNDLLGERKENIRASMRLQKLHQEHEKREMKRGSDHTHTSGHASLNSGSTVSAYSGRAIHRPPAYQSDTLSTATSENTYSYAYTPHGGPTASYNTRPSRSVSTNPNGYSEITHPTVTQTTTTVPYRSTSSPNNHVRMRPYQPRSDTASNATLSYTTDSERTSTATDLSSSYTSDASESTVQSTVVNKRRSPQPPVSPIPRAPPLRNSNGFLASTNNFQPLPTDIPMRSDPELNHFVELHAAPRTGGSIRFKKPAMETSM

>Cel|Y70C5C\_2.1

MLLKSIPLFFLVHYSLAKTPICTNGFTLVNGRCLRYFPNARNHRAAENSCFSYDATLVTVKNSIDNRAVSTFVGNAASSIWMGLFCFNMDVTNCLWDDGNGTAQGYNNFMNGSPQIESGKCVYISLMGSSSGRWYSGNCDLDSRPFVCELPITFEDDCSNNYNGFCYSYNPPASFVRAQQNCENQCGSIVSILSPNENRYVGALFPRYESNDMIIGATWTTKDTYSWFDGSPWNFNQINPASPKKNCLAMVTSLNDASASGSWYPIVCYSAYGYLCKRPAGVQCPQYPPVTVTPAPSNPSGCNSTIMSFGTITSPNFPMNYNNITSCNYLLTTLGSYNVMLKFNKFYTDMKNDFVTLYDGDSTKSPVIAKYSGYYEWPFFNVSTGNSMLVTFRSNSTFGYYGFTAIASSYVHHD

>Cel|T25E12\_10.1

MAIFYDDPLERLNQPIKTKSYRKKQVVQRVHVFIFDNWKLILLGILNLIFLIIAIVFAILFFVGSADCAQLPDYTTSPASQLTTSAISSRTSEVQTNAITTTQGTPSNKTSTTTPSTSKVICASGFTLVGTKCGKLVSSNQPRTEADSICKGYGGSTLFSVRNEQETRDMLDFVKDSNIDFLWTGLVCNQTARTSCIWDVKSGTTADYNNFADGFPNVVYGYCIYFIVTGNSAGQWGSEQCSQLMNFVCELPTTIRDPDCKYNYNKNCYIRFDITLTIPQAQRFCNEKGADLVSIHSANENRFILTIYDIHGQILLGGLAPAVDFIVWLDGSPTTYSNLLYFYDTRSCVLMTVARGGPYDGDWYTMNCNVQEFFLCKRAIDF

>Cel|T25E12\_8.1

MPGCLPSVFEKWSQFLKFHRRIILIGGASEIIIITVAVIVTYCLTKQPACEIYTGTSSPAFQTSTVSSFTESLSNSDTSPASTTTEPLPTSSTPGKIPPNNITCAVGFTYINHKCWRLFTDLQTRENADGACMRYGGSTLFSIRNEQENNAMLGFMLNAGVDNLWTGLICVGKTTFSCTWDMESGTTSVYNSFASESPDNTYGNCVYFIITGTQAGQWKSGLCNMTMSFVCELPPTVHDKNCINNYNNHCYLRYDDSDTVVEAQRFCNTKCANLVSIHSANENRFIQTIYYVDGYIALGAVAPIIDYIVWMDGSPQLYNNIQDNSNGTCVFMRILWGGAGYWYTIDCVKRSWFLCKRPAGIVC

>Cel|T25E12\_9.1

MPTFYEEHSENAQPEDQTLLQKLHLFVYDRWKSLLIGGISQICIITSVVLLTYFLARQPTCEAVFATSSTSTLQTMTTSDSLSSHTKPDTTIISTRTLPISSTMPTHASDNVTCAVGFTYVNKKCWKLITGPQRRADADEACMNLGGSTLFSIRSDIENRALVDFVKDKRIENLWTGLICVGKNSFSCTWDVNSGTAAVYNNFAEGYPNNVYGDCIHYMTTGTQAGQWASGSCNETMSFVCELPATIYDDTCDYNYDRYCYTPHYFIKHSSEAQQFCAGLCSNSVSIHSGNENRFVLTLYLYTNSSILIGGIAPSYDFVLWYDGTQTTYNNIDSIANGNCLYLNDLNTRGNWFGLNCLTSRSWFICKRRIGENC

>Cel|T25E12\_7.1

MTSFYDNSSSSSKPVPLKTSRAQKIQILIFDNWKLILYGAISTLILVLAIMFSTLFFALPAANCDENSEPTKYYTTNAEITTTITTTNQKTTSTASSHLTTISSSATQIYSESSSSSTSQSTFTQSPPEISTTTIAPSDFSCQHGFTLVNNKCWKLVTSNQARPDADKICNGYGGATLFSIKSEQDNRAMIHFVKGQDIDFLWSGLLCSAGEPISCIWDIENGSTANYSNFADGFPNIVYGNCVYFITSGDEAGQWGNEQCGQVMNFVCELPATFQGKDGCKNNYEKSCYLRFDLNLTVPQAQNFCLEKCANLVSIHSANEVRFIMTIYDFIGEILIGALAPAQDFIYWLDGTPANYNNLKFFYNSTCVHMTVAPGMQNVGKWFTRFCTETGKFLCKRSIKNSCT

>Cel|T20B3\_13.1

MLSGLRKVFRFSRATAVDAPENYSIPSVSAEETEPDETPNERTIVDAYDPPKSEFEPGDRQRHFGILHYTVNNRFKKMMLIGIINVFLILAFFLFMFFFVVQPNVHGGETAVTTLSPTTSSEKVPICTNNFVLIDEKCLQLNTTLYSKPTAEATCNRLGATLLTIQSSEENQKIQSFLSIHQISQIWLGLICNGKSVTSCQWDNGSNVTYYDFAPGFPNVDTGICVSYNITHNSIGQWESLVCYKQLPFVCELPTTTSDNCTNNYKNHCYIQVDQSATIPDAQRICQAQCSNLPSVHSVTENLYLTSIYKFSDTSIILGGIASTPKSIWWFDGSPVNFLNFKTSQRTVASSCIVLHVGDGGDWDTVDCSTTVSTFLCKRATGVSCK

>Cel|T20B3\_15.1

MPKSSVCEDQEFDKPHEQKHVERLQRVVSDHWKNILIGGLSEIIIVSFAVLLTYFLARQPTCETEIALSSTLPTSTLPITTIGPKSSQIPISSTLSTAAPDKNYCTGNFTYVNHKCWKLVTGPQSRAEADQACFILGGSTLFSIRNEQDNLAVLEFVKEKSVENLWTGLVCVGHDPFSCTWDVKSGTTAAYSNFAKDNPNGDCIYYMTTGTQAGQWASGSCDEAMSFVCELPATIYDETCVFNYDNYCYIPYDQINTSKQGQSICELSGSNLASIRSGNENRFLMSTVSVFSIFAIGGFAFSDDLILWYDGTPMGRLHRNHALSVHWTVFQTPLPPLKRLMKTQVPLVD

>Cel|T20B3\_16.1

MPNLPPVLGKLNQFLHLHWKIILIVVTFELVIIIGTAYFTYVLSSHAACETDKFTSSAIQTSTVSTFKETTTTSDISATTRPVTTSSTQAPPNNLTCSVGFLLINGKCWQLLTWGDYRSNVDYDCWGKGGSTLLTIRNQQENDALVNFVSDIYYENFWLGLVCKGNTTSSCIWDKFSGTAEGYDNFAPGHPNVTIGECVTINTRGSRVGQWESCSCNVYMYFVCELPPTINDNNCYNNYNNHCYLRYDKDKAYSIADAQKFCKTKCANVVSINSANENRYVQSIYYIKDGYITLGAAVLDRDDIYWLDGSTSTYNNIRNYNNGTCAEMLLSWDTGYWTTTECSSNGWFLCKRPAGIECLN

>Cel|T20B3\_12.1

MSKSYVFGELEIEEPSNNQTRLEKLQLVASDHWKNILIGGLSEIIIVASVALLTYLLTRQPICETAVSTISTLATSTLPITTKSSTTHWSTSSTPISSTSPTSAPENYSCAAGFPYINHKCWKLVTGPQNRADADQACNNLGGSTLFSIRNDQDNQAVLEFVKDQQVKNLWTGLICDNNDPSLCTWDVQSGTTAAYNNFAKGYPSGVNEECIYYMTTGTQAGQWASGLCNETMSFVCELPTTIYDETCKYNYNTYCYTPYSLGKTASDAQSYCTSLGSNLVSIHSGNENRYVMTINFGRNKNILIGGVAFSNDVMLWYDGTESNFNNIYQIKDGNCLNMNNTNGGWYGGDCMASNNYFICKRRILEK

>Cel|Y102A5B\_3.1

MPTLPPVLGKLNHFLQLHWRIILIVVIFELSVIIGTAHFTYVLSNHAACETDIITKTTIRTSTVTSFTKTSTISETPSTTSLVSISSTHAPSNNLSCHIGFELIGGKCLQLLTGVGTRANGNHNCWLHGGSKLFSIRNEQENSAILDFASKNNIGNIWTGLLCHGHTISTCIWDIVSGSAESYDNFASGYPNVSTASCGYFITTGKEAGQWKTGLCNQQNSILCELPPTIYDKNCEKNFNNHCYTRFDDAYTVAEAHEFCKPMCAEVVSINSGDESRYVQSIYNVKEHIILGVAVLNDNNIYWLDGSSTVFINIGNNDNGTCAIMDVSFGMGYWTTIECSQKAWILCKRPAGIEC

>Cel|Y102A5B\_2.2

MMFEKLHRFLQLHWKIILFGVIFEILITIGAVRLTYILSKPFCETDTITSSAIQTSTVSSFATTSTGSDTSSNSTTTRPLSTSTEPAPPFTLDCTIGFTHINGKCWFLIPIRRTREDADAVCMGYGGSTLFSIRNEQENTAALDYLSNAGVNYVWTGLICAGNTSSSCTWDMKSGSAADYDNFANGEKVIGFPNETNTSCVYFITSGPDAGQWKSGSCNQTMGFMCELPPTIHDGSCDYNYNNQCYLRYNTPHNIPDAQEICKTRCANLVSISSANENRFIRSLFTTQGYVLLGAAVIYYDDIYWLDGSPAVYNYIERYQHGACLLLNVNWVYITDGAWYTERCTTPGKFLCKRPAGTVC

>Cel|Y102A5B\_1.1

MSKSYEFEELECDEPTQQTRFEKIQNVASDHWKDILIGVLSQIMYLSFVVLLTYFLARQHLCETELFTSSTLPTIPITSSRSRPDSTSTSTTRSVTSTIPTPSVGNYTCTDGFTYINNKCWKLVTSSQSRADADQACYNLGGSTLFSIRSDQENQAVLDFVKNENVDNLWTGLICDDHGQFLCTWDVDSGDISAYNNFAKTYPNNVTGGCIYYMTTGSQAGQWTNGACNKALSFVCELPATIHDETCKYNYNNYCYITNDQLKISSDAQQICTSSGSNLVSIHSANENRFLTTIYSPPVLVGGVAFSSNLILWYDGTPSTFNNIKSITNGNCLFINDTHGGWYGFDCFTGSGDFICKQKIREM

>Cel|F49A5\_2.1

MKLSVQHDWKLGPSSLIDESTSLVSKNPQPLSTRPPLSKKWSQFLKHHWLAVLIGVISEILILSGAVLLTYYLANNSTSVTGNTASSDIDSSTALSFTGTRSAPANISSCTFGFTYINGKCWRLFTDPQTRENADSACMSYGGSTLVSIKNEQENNAILNFVPNSAVENLWTGLHCKANTTCNWDLESRSTDTNLVYTNFASGLSSNECVYFITAGSEAGKWKSDSCNQTMSFICELPSTIHDDNCDNIYNNHCYLRYDLSYTVAEAQTFCKTKCANLVSINSANENRYVQSIYNDTNGYIQLGAMLLSSDDIYWLDGSLPVYNNIKRTLNGNCLFMSVSKHRRGFWYTVECTQRSWFLCKRPAGIVC

>Cel|F49A5\_3.1

MSTSHLLEPLECDEQPDIQTRFERFQHVVSNYWKNILIGLLFQIVYLTIVVFLTYFLARENICEADSTSTSTKRLPIYSAFPTSAPGDYSCADGFTYVNHKCWKFVTGPQRRADADKACFNLDGSTLFSIRNEQENQAALEFVKDQKVDNLWTGLMYYADDPFSCTWDVNSGTTEAYHNFAEDHPNNEYGDCIYYMTTGTQAGNWANGSCTETMSFVCELPATVYDKNCKYNYENYCYTPYNQLETSRDAKNFCASSGSNLTSIHSANENRFLVSILPSYSIIVLGGFAFSKNVVLWLDGTPTIFINAILINRGNCLFLSSQNGHWFGYDCLTEKAHFVCKQRISGQ

>Cel|F49A5\_9.1

MSESYVFEELDCDEPTNEQTRFKRLQHVVSGQWKNILIGLLSQTLYATFLVLLTYFLTKGRVYETEIVTSSTFPALPSTSSKADSTSASTTTLLTPAPSNINTCVFGFTYINGKCWRLFTDPQTRENADSVCMSYGGSTLFSIRNEQENNAIFDFVSNSSVDYFWTGLICKGNTISSCIWDKESGSADGYDNFSDDYPDVAIGECVYFITTGSEAGKWKSGSCNPTMSFICELPPTIQDNNCENNYNNHCYLRYDLSYTVAQSQKFCRSICGNLVSITSANENRYVQSIYIGGGYITLGAVVPNVNIIYWMDGSPATYNNIQHYTNGTCLFLNLAWDSTDHWYTVDCAEESWFLCKRSTGANYIC

>Cel|F49A5\_4.2

MFNKFLKRFTAHFSISTICVICITLFTGVTPHLNELIFLSILPIPPVIKMMLGKLNRFLQLHWMVILLGIIFEILFTIGVVRLTYFLTKQASVESNKITSSAIQTSTVSTFSGISTKSHTSPTPRLLSTSSTLASGNRTCTDGFTHINNKCWKLVTGPKSRADADKTCYDLGGSTLFSIRNDQENQALMEFVKDQKVENLWAGLICDRHGPAWCTWDLQSGTTAVYNNFADGWPSNEDKICNYFMTNGTQAGKWASASCTETMSFVCELPATIYDNTCEYNYDNYCYTPYFELKLSSEAQTFCASSGSNLVSIHSANENRFVYNIIPPGTETSIGGVAYSDDSLLWYDGTPPLFTNMIQLENGNCLFLYNDYVHWFGNNCLTTKCHFVCKRRISEK

>Cel|F49A5\_5.1

MSDIDEIQELQEPSQPKTQPYSEKFKLFMTNHWKNILIGGLAEIIIIVFAFMLTFILAKQPACETGIVTTSIFHTSTLPSTLTYASSSYSTKPDKSSIATSTTLKPKTLPVTTTSNSLSTHTKLDTTSISATFATMPTPVSGNLTCASGFTYVGNKCWKLVTVQKNRADADQACFSLGGSTLFSIRNDQDNQAVLEFLKDQHVENLWTGLNCVGINPFTCTWDVKSGTTSAYNNFADGYPNNMAGGCIYYKTTGTQAGQWSSGSCNEIMSFVCELPATIYDSTCKYNYNNYCYTPYDQLQISSDAQSICASSGSNLATIHSANENRFFMGIFPSFSMIALGGVALSGDKVIWYDGTPSTYTNIRTLTRGNCILLSNDVGRWDGYKCMIDRAKFICKRRIIGK

>Cel|F49A5\_7.1

MSASHLVPEKWIQFLRLHWLIILIGVITEIVIITGVVLLTYFTTHHAACAADKITSSDFQRSNVFSLTSDSTNSEALSSSTTNIPMTTFSTNEASSSTKLLSTSSTAEISSTTRTVSRSIKPETSTASTTIRPLTTTTTPAPSNNVGCTFGFNYINGKCWRLVTSLQTRDNADFDCMREGGSTLFSIRNEQENNATLDFVSNSGVAYIWTGLICNANTSSSCTWDLKSGSAANYDNFAKGFPNKTIGDCVYFIANGTEAGHWKSSACNQTMSYVCELPPTIHDDNCDNNYNNNCYVRYDKSSTIADAQEFCKTKHGGNLVSINSANENRYVQTLYYVSGYIPLGAVVPNYNVIYWMDGSPATYNNILYYTNGTCLFLNFSWGGSGDFWETVECTDKSWFLCKWPIGIDYAQ

>Cel|Y102A5C\_16.1

MICVCLFVLISVARSCIPTQQIETTSAPITTTTTTTTTTTTSTTTTTPIPCPTGWEQFERPSGTWCIKVFIGLGDKANAVSMCAAQGAVVSGIQDQTEREFIVSSYVSLNGNTVGVWLGAQRTAACWSSPLTATCSKTTSFEWTDGSATGSDAFIWNVATEPNNGSLNEHCLLMNWQGFMSDQFCTIPDYTGWVCGKRPM

>Cel|Y102A5C\_17.1

MGDCFGIVLSGKNPRKDRIKLRSSYMICVCFFVLISAVNSCIPTQQVETTTTTTTTTTTTTTSTTTTTPIPCPTDWEQFERPSGTWCIRVFVGSGPRSNADSMCSVQGAVVSGIQNQEEIDFIVGSWISMYGSTGSMWVGAQRTAACWTLQGQTAACSKTTSFEWTDNSATGTDGYVWNSAVEPNNVGGMEQCLVLTWTGLMSDQTCARTDYVGYVCGKAPM

>Cel|F49H6\_1.1

MAMTGISPSVFCPPWSMFTAYLILSLHFFTGTLISACIPTQQVETTFVPVTTTTSSLIPLTTTSTAIPSIVTTTTTTTTTTTTTMPTTTTTAIPCPTDWEEFVRPSGTWCIRVFMGIGDQPTAAGLCGGEGAVLTSIQSQEELDFMRSSYNTVVGTLGFFWIGGQRTGACISSGLTATCTALNSFSWTDGSATGTAGFVWNTGQPDNGGAMLNEPCVTVNYLGVLSDDACDRYDGFGYACGKEPM

>Cel|F49H6\_2.1

MSLVFIIYFFLFFTISLMNACIPTQQVETTSAAPTTMTAIVTTTSTVSPTTTTTITTTTTTPIPCPTDWLGFARPSGPWCIRVFVASGDQPTADSLCSSEGAVLSSIQSQEELDYMANSFIALNGASSAFWIGAERTAACMSSGLTATCTRLNSFSWTDGSATGTAGFVWNGIEPNNGAGMTESCVVENYMALLSDQQCTRVFPGYACGKAS

>Cel|C14A6\_1.1

MIRLTLLLFGLLGAATAQNCNTGGIYNSQFNRCYQYFTAPAQFSFAEQQCNLLGGHLASVQNGQENALLQSNAANSFKKSNYSDYWIGANDLETSGTWKWTDPSVTFDYSNWQLGEPQSGSDCAIQDKGDGTWSAIGCTSYRPYLCVTPVIMTATCPPITTPIPTTCPTPAPCPIKQCVPSCDQGWTYFSPTDFCYRVYHGEKFNDAEASCVLLGGHLASIHSLAENTFVNNIASCGIKEGKYEHLAWIGMHKVGQDWVWTDGTPSDYFNWAPKQPDNPKKEFCVQTAPDLSHDKWYENWNNLECNEVMRAYICKKASIHN

>Cel|C31G12\_2.1

MLFLILIPVVNSCIPTQQVETTTSTTTTTTTTTSTTTTTPIPCPTGWEEFERPSGTWCIKMYAALGDRANAISACAAEEAVLSGVQNQAELDYMITAFNAVDTIMAMDTTFWIGGERTSACLTSGLTATCTALTSFEWTDGSTTGTDGWIWRSGEPNNAGGLEICATVEITYVSLADQRCDRADFNGYACGKSPM

>Cel|F16H6\_2.1

MIFLFLIPVVNSCIPTQQVETTTTTTTSTTTTTPIPCPTGWEEFERPSGTWCIKTFAIVGSWQDGQNGCATHGAVLSGVQNQAELDFMCDSAVEGAFWVGGQRTAACPGPGLTATCTALTSFEWTDGSTTGTDGWIWRPIEPNNAASCPVINAWTYNLADQVCTRSDFDGYVCGKSPM

>Cel|F16H6\_1.1

MTTVIISSNCAMWSHSVLLLAALASVLADTCPDGFTILSTNKCVKLVTEASKHSDATAYCTSLGGNLISVHSVIDNNAYQKLAAVSVTPYWLGIKCAQSGSPKSCLWDDQSGDAGKYNGFAPGFPLLEIGSCVYVPTNSSSAGKWLSGDCDAMILNFICETTPITNTCTFQYNGNCYYPSQSALSEQDAQSACQQECGNLVSIHSDEENNFVQSLFTTNSPTYIRIGAKHSNNQNSNYWIDGSSWDYDNIGYSNPNLGMCWSMALTNDTIPAGKWISSHCDTSLPFVCKRTVGTQCGATPGPTPAQCTSPMFLHNSGSFYSPNWPNSYLGDQYPCTYILDTPIGSLVQIQFPILNLDSQASISLYNHVEDSTPFLVLEANSASDQWYTSTTNTMRVVFQLCISHCLNDGANYNWKAEFKPSTAVTTQPPITVTPNPNNPSGCNSNIMAPGYISSPNYPNYYPSNALCRYHLSTTVGNRIKLDFGAIDTDQCCDYIYVQDGAFTGSPFIANISGTYPAHMKTFQSTSNLMLVTFKSSIYDNKDYTGFSANFCTIQI

>Cel|Y51A2A\_1.1

MLFVILSLLLLSHTTQSCMRMVPPDDVSITTPVPTDDPDNPVTEPMVTDPTAPTAPTTEVPISSTATEPVTTAMPCPTDWMMFDRPSGAWCMKVFKTEKVLPGIAAERCEAEGGVLSGIQNQEELDYITNSYSAFGEPFDAIWIGAQRTTACLASVQTATCTKDNSFEWTDMSTTGIDGFLWSGADPNNGGPALNEHCVIAFVDGPRLADISCARDFDGYVCGTAAV

>Cel|Y17D7B\_8.1

MRFWSLFFLSFYLILELLVPKAYCQTRMVLIYGSVTSSGTSTSTTFKTVEDCKNGCFEKEDCIMMYFMLEKCRFYSYATNGQSFSILAQSKSYVAIKTDASNIPNNTCPDTFTNIKFSYTSPATGDTYSFKKNSTGLSYTSCKTDWKRFERADGTFVCMNIVLSNGTTYTKAQERCQELGGTVTGVASVEESKFLQTKVPGPQPKGFWIGGGRNCPTVPCSSFRWVDGYTTSYDALVPSNAALTVSKNTDANSENYLTVFASNGTPLTINDINQDFTSLIVGFVCGYKIL

>Cel|W04E12\_6.1

MTRLTLLLFGLLGAATAQTCNTGGIYNEQFNRCYQYFTAPAQFSFAEQQCNLLGGHLASVQNGQENALLQSNAANSFKRSNYSDYWIGATDLETSGTWKWTDPSVTFDYSNWQLGEPQSGSDCAIQDKGDGTWSAIGCTSYRPYVCVTPVIMTATCPPITTPIPTTCPTPAPCPIKQCVPSCDQGWTYFSPTDFCYRVYHGEKFNDAEASCVLLGGHLASIHSLTENTFVNNIASCGIKEGKYEHLAWIGMRKVGQDWVWTDGTPSDYFNWAPKQPDNPKKELCVQTAPDLSHDKWYENWNNLECNEVMRAYICKKASIHN

>Cel|W04E12\_8.1

MARLLLLTLALFGATAAQTCNTGGIYNAHFNRCYQYFTAPAQFEFAEEQCNLLGGHLASVQNGQENALLQSNAANSFKRSNYSDYWIGANDLETSGTWKWTDPSVTFDYSNWQLGEPQSGSDCAIQDKGDGTWSAIGCTSYRPYVCVTPVIMTATCPPITTPIPTTCPTPAPCPVKTCVPSCDQGWTYFAPTDFCYRVYHNAKWEDAEAACVLLGAHLTSVHSETENTFVANLASCGIKEGNPKDLAWIGMHKVGQDWVWTDGTPSNYINWAPKQPDNPGKENCVETAPDLSHDKWYENWNNEACSTEMRAYICKKGSIHA

>Cel|M162\_2.1

MFPKLLFLAILIPSSLTDCPDIDGQTREIKGICYKFVTSLMKYEDARDWCHHHNPAGPSWLAYVPDQETSNFLAVYAGSIFGEGFKHFWIGLNRDPISKTLSWDTGLSVSYTNFGSNVAQNYFSENITNTKWNTLGDDEVHNFVCSYRPSTVPATVTRQPQARRLAAMKN

>Cel|Y38H6C\_8.1

MLRLFIIVCLVCSVAPDCVPGDVGFGDSCYSFNRVHGKFKDANDLCVKMFGGSLVKITNIIDNNWMQKLAVNHLDADYNSFWIGASDAAHYTNWTWIDGSPMRFSNWGPGQPLEDRHCGTMLISTGKWFSQVCDERIQFLCQYPNGAYSPTCPPCLEI

>Cel|F31D4\_4.1

MRFLLFFQFILQLTHSKTPCAPSWLHIAHLDSCFLSAPQPAEFSEALEYCTQSNASLVIINSEEEASIVREFFARENPSFFNWIGMRWNARAADFQWIDGKSKNYTYFLPDEPGVSGECIAWVLDDNLDGWQAISCYYSQFFMCQRPAEGIITTWHRDEEGTIVSPNWPNSYENLEYDTHIIKSEPGTRILMYFEEVDTEHNCDIITVTDDYGISGRTLFRLSGSHRNHSVISNRNHVMINFKSDEDNIGKGFVMRYKILRPLPVKVFSSNSFGTVTSNNYPNSPDSFLIQYYLIQCPIAHHVALKLKAMQLDKSDRVKIFNGNDETAGKLKIFRQFSPSSVDLIKTTQNSMFISYDTGEQFNASNHWAFEYNCIPDGNLGDEIII

>Cel|B0432\_12.1

MLKALLPLLLWISTGSTAPAGVATYLRSNGIVAFHKLYHLKMNFPRAKKHCEQNGAHLAGITSREEAQKLIDLANEAGESNEQYWLGGQRKGECYGMRNYDKDHGLNATCSLSNVVQWLDNVAETIDPDWWKIPGPSHIPFNMPQQCLSFVHGDRDWTTPNDPGFLDDIGCDVPRKFFCTELHEW

>Cel|C03H5\_1.1

MQAIAALLLIWLANVAISSNTPVCKNGFTLINNKCLRLFYEEVIHRDAELSCRNYGATLVTVKNAQDNQDVATIAGSAKLIWLGLSCFEDSFGKCFWDDASGSANSYNSFSGGYPNVQVGQCVYYSTQGVLAGKWISEDCERYRMPYICELPTTYQDSCSYNYNGYCYTFSSTAVPFVTAQKICELSCGNLVSIHSPNELQYIVNFAPFVDDGYFIGATWKNNYSLSWLDDSPWDYDRIDPSFSVKVGYCFTIYTGVGSKITGSWYSVDNWEIPNQYICKIPAGVPCSPAPPVTPTPNLSNCNGPRMMYSGVFTSPNYPNNYDNNEDCTYLISTLGPYGIFLFIAPFSTEHKYDVVTIYDGPTTSHKVLAHLSGEIGISMMTSSGNSLLVTFKSDKTNTFSGFSARFYSTRLIND

>Cel|R07C3\_12.1

MFSGGSLVSIHNSIDNRALVQSSISYDPKWIGLICSDANKPCNWTDHSSDTSNYNNFDAGNPNLYAGNYTLMAQSGSAAGKWVSADDFSQFRYISTTAAISTRAPATTPEAPGRCPAGSSSLNDITCVKLFDTPMIFQGANLVCRNISGGGNLVSIHSAEDNTALLNLAALNNKTKTIWLGLTCQSPSPSSCEWTDGSGTTSNYNNFTSGYPKPVRGPRGYMWALGSDIGKWFSSDEDYSTHSFFCEVPKSSNVSAAETPLILIFHFCYSVNTYLLSEPDAREFCLSLSEDLVSIHSQAENDFIQSLISNTVIDEFRTGAATDGVGKYWVDGSFFDYSNFGYFGTNLGKCSSLSMSGSVVSKGQWLSNDCSNKIPFICKHPKHFSTPAPYVSGQCNETQFLSGKGTFYSPNYSYGFSGYPNPCTYLITEPPGTIAQLRFAELHLPLGRTIVLYSGIDETKPLAIVTENTFEVYSSTTNVLRVVFNCPLTTIDNYIWAVNYGTDLS

>Cel|R07C3\_1.1

MKIFIICLLHIYATFSVSQITSRAPYNTQTPSYSGCPDGFIVLNGYTCIQVSTTKKLFMDALSDCQSFPGGNLVSIHNSIDNKALAFSVTSSDPKWIGLICTETSSPCNWTDYSSDTSSYSNFVAGNPNLDVGNYVYMLVSGSSAGRWVSADQYTQLKYICEVPFHVTSTSGTPTRAPTPTPNGSVPCPEGFWSYKDNTCLKLFNTPMLYQDASYVCGNFSKGSNMVSVLEAQDDFTLKLISGLNNLTRPIWLGLSCQYPSASSCSWTDGSGTTSNYNNFAPGNPNTDVGTRAYMLTSGNSAGKWISSDGDYSYYSFFCEVPRADSCEHTYNGFCYSVNTNLLDEPDARQVCQRVSGDLVSIHSQAENLFLQSLVNSTGVAEYRIGAATDGVGKYWVDGSTFDYSNFGYFNPNLGKCSSLAMSGSVIPKGQWLSTNCNNKIPFICKHPQNLPTPTPTALGQCNGTQFLTGNGSFYSPGYPDQASGYPTPCTYIITESQGSIAQLQFEVLHLFWGQNMQLFSGIDETQPFAIVDIYSNKIYNSTTNVLKVVFHCITSNYATYSWAANYGTNIS

>Cel|T07H3\_10.1

MRTPGFYSKLLIFTTFDLDSKSDEVKVYDGDSEQNRLIGIFKGNNSNEISVASSGSAMLVTFRSNGTGSGKGFEARFEKYLYPSPLKKINSMTYIIVNHSLILLFVFIFLASASKEPICTHGYKLVKNRCLKLFSEPSNYKNAQRQCVQNGGTLVTIRSEEENLHVIALAGKEQNLWIGLHCKILGK

>Cel|T07H3\_4.1

MQHSLILLLVFIFLASASKDPICTHGYKLVKNRCLKLFSEPSNYENAQRQCYQHGGPLVTIRSKEENLDVLALAGKGHNLWIGLYCFTVLDQNGSLSNCIWDDSLGTAEQYHAFESFAGSGSRETPCVTVNTTTGYWISTKYENGMYPFVCEMPTTIEDDCQNNYNGYCYIPHSEAKSFENAQKSCEEECGNLVSIHSANENLYLNILAYNFLPGEYIYIGGMVQDFGFSRWTDGSRWSYEKFDRILKRKNGECVVVAGDWEDVIPIDQWVTTPCNRIRQYFCKRPAGEKCLGGRPKEIGPLVSYTCNSTLLQTPGIIVSPQSQERQYCEYQMHTPGFYSILLTFTTFDLDPKSDELKVYDGDSEQNRLIGTFKGNNEISVTSSGSAMFVTYRSNGTGSGKGFEAKFQNYHYPNPLKKSNQ

>Cel|T07H3\_5.1

MLQLLAFLLALPFLASASKEPICTHGFTLVGNKCLKLFHEPLSHKNAERVCSTFGATLVTIKSSDEHIDVTTLSGKDKNVWLGLYCINNYRSNCLWDDSNISTDQRNGFQSRPNVTQGNCVTVNTTSEHWSSTDCSKESNLFVCELPTTFEDNCQHNYNGSCYIPHVASSFIRAQRTCEEECGSLVSIHSANENRYFNILASTFAQNEQVFIGGMWTLSGRPSWIDGSRWDHDKIDSLRKREGACLVVSGEKSNERQPWGLWYTGNCDYDRKFFCKRPAGEKCNPDRPEDPTPPVLYTCNTTILVTQGLIIAPPITEAGLEHGFCYYHIYTVGSSSIMLTFTQLDMHPNYHELNAYDGDSENSRLISTIHNYNSPTLTSSGNAMFVTFRSNGTSTNWFGFHARFTEFYFASPMNKLL

>Cel|F36H5\_6.1

MLQFLAFLLVFPFLASAAKEPICTHGFTLVKNRCLKLFHEPLSHKNAERVCSNFGATLVTIRNSTENLDVIALSNKERNVWIGLFCLKTDLSSCLWDDSLGSAEKYSGFESEGLNSEKGRCVTVNTTSGYWSSTHCEKKANMFVCELPTTFEDTCQHNYNGFCYIPHSPKSFIGAFTTCEKECGELASINSANENRYLNTLASIFSPNENVFIGAVWQSFHAPRSDWNYEKMDPLHERVDACVVVSGERSKVWGYWYTADCDSKHKFFCKRSAGLKCNGDFETVTVAPWISYTCNSSLILTPASVSSPRSQAGGTERSYCEYQVFTTGSNSILMTFLNFDMHPSDDELTVYDGDSANSSLIGTFSGKYGNGLSLASSGNKMFVTFRSNGTNSNWSGFVARFTEFYYASPMNKLI

>Cel|C41H7\_7.1

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>Cel|B0454\_7.1

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>Cel|Y25C1A\_3.1

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>Cel|W09G10\_6.1

MTLFSPYLSIFFLLTLEFSPIFCMFRPRSSGGNCLDVQAHFYVSEEYDGYTNDVENAYYWRLPGSRNRGNGPCVDLTTYYSVEEDYDGKSDDDGSKYWMVEDLEQTLKLRSDAQEDQKMKLQVEKSSRSSKDQSLDLGDSKTGIALVGVKLQADGSQGSKDQNLVGKIQKDQASQKDQKLNLQANESSRNSKDQSSDSSGSKSGNAKVIMELQADGTYRLKDQKLTAKIQKDQNSDSKTIEDIFNREFEADGLKDQNSKSKDSNTDEASLNVKLQGSQASKDQKASSGAFKSLLSQSSDLTASSSNLTAQLTSTNLGGSGSELSQKLNDLKSNSDSSDQVHLASHQHTRNELSQKTDLSVTTDEKNQKTGFSQNHLINSSLAVSELNNNGKLSGTEVQETVEINQRKDLGNLRDQSSKNLKLEGSEALRSSVDLKKRSLEDQKLSSKDLKTGVAGAQSSSSSDRKDQSSSSTDLNTDASQLELNQNQKRVLIGSDVPLTGEACSKKEQGNCEAGWKSFLRPSGEWCMKIFYENSITQPSAENRCQAQGATLSGLQNQIESFYITYTVSSHIYPESGSIWIGLKRREECKNVGRTQNCTSDNSFEWTDKSTTGLDGIDWDGGQPDNARRYSQQCATLTASHQRSVIGYHVGRLDDVGCEFDYIKTNRKQRDIKAFVCGKKA

>Cel|W09G10\_5.1

MLQKYSIIVLCCSAVLARVPVAKNCPTGWTWFLRSRGGWCMKVFTEALNQPSAEAKCKAAEAVLAGIQNKEEVAWMSKELTGTMWIGTKRTPPCMNSGVTKQCSQITSYYWTDGSTVGVQGFYWNSGEPNNQGGQGCAKLITSSSVLDDVACTTELTNGYVCGKIATF

>Cel|W10G11\_12.1

MKSALVLLVCFGSVLATVPVATKCPDTWKWFKRSRGGWCMKVFAAIGTQADAEAKCKAEGAVVAGVQNTEEIKWMSATLQSLQTNPVGTLWVGAKRTKPCISSGLTKQCSAITSFYWSDQSAVGVQGFFWRAGEPNNALGGQGCAQVYSTTNDMDDVGCGSTNQGYICGKVATF

>Cel|W10G11\_14.1

MFCKTALLLLICLGSTFADCPAAWKTILNSQYKESEDNGCEPGWKFFNRPSGGWCMRVFAGFNAKKADAEKSCQAVGSTLSGIQNKNEALYIQTALLAQIPQSSGSVWIGIQRTQKCLKQKLTAACSALTAFEYTDKSVTGTDGFVFQKYQPDNSQLNQNCALLLASKTPTILNDQYFAATLDDTNCDGMLEGDAARVLRGYICGKKADK

>Cel|W10G11\_15.1

MLGKTALLISVCLALSAADCPAAWKAILNSQAEESEDNGCEAGWKFFNRPSGGWCMRVFEGFNAAKTDAEKSCKSVGSTLSGIQNRNEALYIQTALLAQIARSSGSVWVGMQRTQKCLKQPKSDTCSALTAFEYTDGSVTGTDGFIFQGNQPDNKELNQDCAVLLASKAASVSTNGQFYAATLDDIMCDEQVDDNGPRVMRGYICGKKAAK

>Cel|W10G11\_5.1

MLSLKFYLIFTLLAVGMSGQITTLLADTSDEDCEIDEEQTCAQACQATTTLSSTTASTVTPTPILTTVTTTSTTTTVTTTPIPTTVTSTHIPTTVTTTSIPTTVPSTQLPTTVTTTPIPTTTTRKTTTTTLRPTKPRPMTKPRVKVCPYGWATFNRPSGKWCIKVFIGHHAAQADAEEACRSIGTTLTGLQNKQEALFIQKSLLSLIPQQSGSVWLGLQRTARCMGQPLTATCSRTTAFEWTDNSATGTDGFLFQTGQPDNGRLNQNCALFLASIDPFIDARGRYYAATFEDVNCVATFVTGNMNRKTRGFACGMRPT

>Cel|W10G11\_6.1

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>Cel|T05A7\_2.1

MHFSFIFLVLVYLTFAFGDSLICNNGFTVVNSNKCLKLFSSAVKHRTAEANCASYGGTLVNIRNSIDNRAVTQFVGNIGLSFWIGVYCLESNNPSSCYFDDDLGTDTAFNNFAKGFPNTDIGGCVYSATSGSLAGQWISSECDNVEMAYVCEIPMTRADSCAHNYNGYCYIMSHENSTSPILSFNDAYKSCQDNCANLVSIHSRRELSYIQGIYSPFNISSVTIGGLSTAPMAPYWSDLSH

>Cel|K10B2\_3.2

MQFIFFGTLFSGLLLVCAVTNDIEDASGETPGIVSQITEEQPHQRQKLYNWDYKDLGTIAFEDIPFPTLQPSQTIDQSENCPEGWIRYSDSCYWVETELLGFAKAERKCSEKQSTLFVANSIDEWEAIRGHSKDSFSSWIGLVRFSHYERSEQLPRWQTEGAVNPSKMCVYFASVLFQRKKFRNWLIKPYSPLVNGWSQLANCAASYKSPASLETASYTYFYPCTYLFYSICERNSTIANSLH

>Cel|Y38E10A\_4.1

MQLLFQSIFLILLFSHAQLSPVCSNGYTLVNNNKCLRLFKTPETHKTAELTCLKNGGATLANIKSSIDNRAITIFVGGASNSIWIGLFCTKSSAKECFWDDDSGSADQFQNFKSGFPLVEKGRCVYSSQVAFDRGQWSSGDCEKESRAFVCELPVTNEDQCQKNYNGYCYFDFAPLPFVSAQKICKENCGIIASILSPMENRYINANFYTYSALLIGATWSYNSSYTWFDGSSWSYHNIDHTARRGGVCLAMSTGTGSMVPTGSWYPVDCKASNSFLCKRPAGTSCPWVEPETPPTPVIPSMCNSSMIMAPGTISSPAYPGYYDNNMYCSYLLSTTGAYNILLKFTDFSTNLNLDYVTVYDGETTSSPMLGSFSGFNETPINLVSTGNTMLVTFRSGNSEDSNIRYGFSATFSKFVQML

>Cel|Y38E10A\_5.1

MQFYSVLLLVSLLLLLTISEASYPPVCTSGFTLINGKCLRIFVDVSTHTAAEKTCKGYGATLVTVKNSIDNRAIADFTGNNANLFWMGLYCFDSDVSKCLWDDATGSAEVYDNFAAGFPHIALGNCVYYSVQGALAGMWLSSDCNDRRSFICELPASHADPCPYNYNGFCYTFHNTASTYTKGQKICEQECGNLASIHSANENRYIMTFGGRATKEDLLLGGMWPADDVYNWVDGSLWEYENFDPINVRDSVCVIMSNGDSRPIALGMWYSGECKNEYSVVCKRPAGIQCPPNPTIVPVTPMPAVQSFCNSSVMAPSEITSPHFPYNYYNSDFCSYQISTLGSYNVLLRFSTFDTEKVNDVVTVYDGDSTNDPVIGVYAGSFYPFTVISTGNKMLVTFKTDKSNTRQGFSGRITSYSTTESGERD

>Cel|F35C5\_6.1

MFKLVSLALTLVALASAQDSTTSWQTGATQGPTPSTPPPTPGGSNVDRECGGDLTNLWLDVVVVVDNSKGMTNEGITEIAANIVTVFGNGTRIGNQYSDPRSTRLGLVTYNGRSTIVADLNLLQSIDDLYQSVFSTLNQVSNSDDSFLAKGIGAAENVLQSGRTNGVRSNYKRLVVVYASAYKGEGELDPIPVADRLKSSGVVVSTVAFDQDGDEALLAGLTNIASPNYAFTSKDLNLVGELQGAALQTNCFCPNLWTQYKSNFDDENSYKYGVCIRPATISSSWTAAKFACQNLAKNGFLAAEYDGQKHNFLFRVAQNNTAFQAPYIYHIGLSYVNGGWNWQQPAGYPLKPMSGYSKWNPSYPKSFTSNIGVVEQQFSSDLTVGWQNINAYSVAEYYMCEVASCDTDKYC

>Cel|F35C5\_8.1

MWKVLVLLCLAASPTLSVSDRRCGTNANKLWLDVVFVIDNCKIGSMNLVYQTISSLFSKQLQIGTGYDDPRSTRVGFITYNWNATDVADFYKLQSWADLNSQIQRLQYTPQSSSPASRMDTGLNAAIGMIDATAGFRDNYKKIVIVFTSVHGSYKSNQPRDVSKILKSRGIPVVTVNTGSSSDTQAYLKQIASDNMSFAIADGNVTQEILKAMTDTNCFCEQGWVQYNYPWNNLQNRYGTCLYTDTTDYSSRDGAKSKCRQYSPKSYLVNELDQQKRDFNFNLVNSDSTKPVNAFYNGLLNLNGNWYWDQPNDRSPIPLDPNSGAPPTRNACVADMKYSDGTTAWTPVSCANNFRFICEQVACDTDNYCDGV

>Cel|Y48E1B\_16.1

MHPKCGIILLSLIFICITEIESRKVTQKPAAPPPPKNDKSWVRSKIDSAKEKYHAGKEKLKTKISDVKSKLRGPAPTPQPRPPAQNNLPKSQYGWNTQAPGPRAPAPAPTRPQYGVPAPRAPQPTIPALTTKKSVFERLKEKAKGKEKYVGKAVGWAKKDLGIGVEGPKKPSKILKFGKKAKTPKTQNPALVHSSGQIVGQVASGSHGLDRKVEYLKSRLDIMQSEIQGTWNTSESGTKYKIFEERMNWNDAQLHCEELGSHLAYLDSESKNTYATSLIDSQNISMVWFGLRTEVGLGSGSDTYSNFSNLDGCGVVDRNGTWSISSCAIELPYLCQAFRFNVLVEIP

>Cel|Y48E1B\_9.1

MRSIFSVLLLAAVVQTQFNFHGMRSFFSTDEEFPTQLQNFEGRTETEIRTLKEKVARLEKLIDGLQSVLMKEWNTTESGSKYRLFEERKSWDNAERHCQGFGAHLAIIDNEAKNGFVTNLINSSETSDFAWIGMKTKTTTQTSTPFTNFDSESPIDGCAVMDAKGVWSIRSCIQLRPFVCQIIKNDVKI