**Tracing the evolution of plant glyoxalase III enzymes for structural and functional divergence**

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>CrGlyIII1

MASAGVAPLEKTVLVPIGNGTEEMEAVIIIDVLRRAGAKVTVASVEDSPQVVCSRSVRLVADTLIGDCASNTYDLIALPGGMPGAERLRDCGELEALVRAQRDSGRLYAAICATPYVFLQAKGLLDGKVATAHPAFSDGLKDQSRAMDRVVVDGNLTTSRGPGTAFEFALSLVKQMYGEDKAKMVGGPMVMFQYFV\*

>CrGlyIII2

MLVPARRSAFTSTSGLVEFTHSYTVFKNAGCSVTVASPKGGLGPADSQGFAFYANDPDSKPLVAKRPDGSSYVPLTENTTAAGSITNAQLANFDILFFVGGTGSMWDFANDANLHRIIRVMWESGKVVSAVCHGPMALVHAKLSDNSSLVAGRAMTGFSNAEEEWLGSSNNVCGLCYPGNEATGCSAGLSPANCSGPHMPTEYAKQGSFLLEDGLKASGAIYMSTQQDWARFYFRPHVVR

HGRLVTGQNPGAGRETAEAAYDTHRLLRMTKKKNCPIWSQFADTFCSPVQQTAADPPVKCKTNGYIPKC\*

>EcsGlyIII1

MIGREKYAGALGLLLGLTGFLCYLLLSPPTGSGRSLAWVPGGPAEAAMAAAAPAGAKHVLVPVADGSEEIESVTIIDTLVRAGALVTVASVGPEVEVTCSRGVKIKADCKIAECEARDWDAVVCPGGMPGAVSLKENETLEAILRKQNSEGRIVGAICAAPAVVLASHGLLEGKQATCYPASVFQSKIPQLVSEKVVVDQNLITSQGPATSMAFALQLVGSLFGQEKSDEVAKGLLFN\*

>PhtGlyIII1

MPKVVILVTAAPDLNGHKTGLWLEECAAPYYIFKDKGYEVVLASPSAGPVPIDQVSVSDDFFTDDSKKFLHDAEAVGALSHSVELGSIDMSTVDCIYLAGGHGACVDFINNPSVTKAVQAIYAANKTVASVCHGVIALADCHQLDGTPLVKGRKVTGFSNSEEEAVELTEVVPYLLESKLKEQGCEYEKGENWSSKVCVDGNLITGQNPQSSAEVARTIVEILG\*

>ThpGlyIII1

MSKRVLVPIADDSEEIETTCITDTLVRFGAEVVVASVKPGGELVCKMSRGVKMVADISIDEAVGQEWDLVALPGGMPGAEHLRDSATLISILEKQKASGKLYGAICASPAVVLATKGLIGEGATCFPADGLRSKMASPVDEDVVVQGNVVTSKGPGTALKFGVKLGELLYGEERAKEVAGGLLI\*

>TgGlyIII1

MGEERPVCLGVLALQGAFFDHIKSFKRLNLGTRLRLTLVKKPADLEEIDALVIPGGESTAMRIIAGEEMMSALQAFVHEKKKPVWGTCAGCILLSNTVCTLETSSSPSASEIRETPSDDGYGDFIGGAAVRTCRNFFGRQVDSFEAPLRAVGRLKLAADGMHAICIRAPAIVDVSPEVEVLAYIDLPGRHTSVIAAAAHGPLLLTIFHPELTNDTRLHAFFLDNFVFPALGRASSAKATKREVEASGARNSEPSVSFPSGERRVSERAQAAQDAKSPQLGIRSS\*

>NgGlyIII1

MTKQILLLAGDFVEDYEVMVPFQALQMIGYDVHTVCPEKEGGDSCPTAIHDFEGDQTYTEKPGHEFELNHDFDAVDPTEYDALVVPGGRAPEYLRTYDDVLEIVQHFFEAEKPVASLCHGLQILAAADVLEGRTCTAYPALEADVIAAGAEWEDDVTRDENLVTAQAWPDHPEWLAEFLEVLGTDIDHAEPAAADD\*

>NgGlyIII2

MSETTAEIVLFDGFDELDAIGPYEVFENGAELGVALETRLVTLEGDTDEDGLVTASHGLCVEPERTLGEPDLLVVPGGGWTTEGGVRAVVEDGSIPAAVDECYTAGATVASVCTGGMILSEAGLLEGRPAATHHVAVDDLAETDANVVDERVVDDGDVLTAGGVTSGIDLALWLLEREFGEDVADAVSERMVHERRGEVFG\*

>NgGlyIII3

MTKALFVVSEEGYWGAECIEPLETLSDAGVEVTVATPSGGPPEIDEQSIDPGEVGEETAEHIQTVHENDERLTDPIPTAQADADDYDAVVFPGGHGTEWDVNQDSDARRLLRDAVAGDDGTALVVCHAVGLLAFARDSHGAFVVNGRDVTGFPNAWETDIVDENDCMPSGRKLPYWVEDEVKVAGGNWDAELESETSVTVDGDLLTARGPESSTAAADRLLDELDELDG\*

>VdGlyIII1

MAKAKILIIAGDAVEALELFYPYYRLKEEGWDVDVAAPSKKDLRTVVHDFEPGWETYSEKPGYLFKWVTKTLSEVRPEEYDGLVIPGGRMPEYVRVVALEDIKRIVRHFFETGKPVAAICHAPQILAAAGVIKGRRMTSYIAVRPEVENNGGIWVDQEVVVDGNLVTSRAWPDNPAWMREFIKLVKARIGSV\*

>VdGlyIII2

MKALVIVADMSYEGEYSMAVQALRQLGMEVNSGLISKNANVNFDIDLTDKLGEDVLGGYDVVIFIGGYWAYYAVTGKEMPGRVKPMVNREAFEKLLTQSVSGGKKTILPLATPAYAAKLGLLRGKRATVYPTTDLIGILRGNGVDYVNEDFVIDGNVITLKRITVEFLTKALNK\*

>MbMGlyIII1

MAIAYLMVFDGLSDWEPGLVVAEINKSNDYQVKTVGFNQDIVITMGGVSIVPDCTFKEIKYNDAAILILPGGKMWENDPVMDILPVVKKFIDLKIPVAAICGPTVFLAHHGFVENVKHTSNGREYLKSLIGEYEGSNLYVNQPSVSDKRIITANGIASVEFARDILDELDIYDKETLKSWYDFFKPPWLED\*

>MbMGlyIII2

MKVYIYILNTLADWEIGYLTAELNSGRYLDKTRPPVELITIGNTTEPIKTMGGITITPDENIDNIKFEEDDLLILPGADTWTEEENKKIIDIVSRIIDEKVIIAAVCGATIALANKGILNNRKHTSNDIEVLKMFCPEYTGENFYLNQPAVTDDNLITASGIAPLEFSYEVLKRTNLMKTETLEAWYQLYKTKEPKYFHALMESIEGA\*

>NoGlyIII1

MTNALFVVSEEGYWGEECVEPLETLSDAGVEITVATPSGGPPKLDETSADPDEVGEETAEHVREVHESDERLNDPIPVARADGETYDAVVFPGGHGTEWDVNQDSDARRLLREAVEGEDGKALVVCHAVGMLGFARDSQGAFIVNGREVTGFPNEWEEEIVDENDVMPDGRKLPYWVADEVEVAGGEFEPELDQDTSVTVDGDLLTARGPESSSAAADRLLEELDL\*

>NoGlyIII2

MSEQILLLAGDFVEDYEVMVPYQALQAVGHDVHAVCPEKEAGDQCPTAIHDFEGDQTYTEKPGHNFELTHDFDAVEPSDYDALVVPGGRAPEYLRTYDEVLETVRHFFEDEKPVASLCHGLQILAAADVLEGRTCTAYPALEVDMRQAGAEWADDVVRDGNLVTAQAWPDHPEWLAAFLDLLGTDLEQPAEAAED\*

>NoGlyIII3

MTADNSSDEREPETTGGEREPRTDGSGTDPGSTGTSDDAGGEIDENSKHEQLEEVRENSDGEHLTTDHGVKVSDTDNSLKAGERGPTIMEDFHFREKMTQFDHESIPERVVHARGTGAHGYFQPYEDPDLGEYDDISELTKASLFQDPDKKTPVFTRFSTVVGSRGSSDTVRDVRGFATKFYTEDGNWDLVGNNMPPFFIQDAMEFPDLVHAIKPEPDDGIPQASAAHDTFWDFASLKPEITHMIMWVLSGRALPRAYRMMQGFGVHTFRLVNDDGESVFVKFHWTPKLGTHQLVWDETTKLWGKSSDFNRKGLYDVIEEGYDPEWELGVQIFDEEQAAEFDFDVLDPTKIVPETEVPVRPIGKMVLNETPDNFFAEVEQVAFHPGNVVPGIDFSNDPLLQGRLFSYQDTQLNRFGGANWDEIPINRPIAERHNNQRAGFMRQEINEGKVSYKPNSIGDDDPQEAPAEEGGYEHYAEKVDGQKIRNRSDSFENHFTQARLFWNSMSEPEKQNIVDAAHFELGKVERVEIRERMVYDLFNNVDHEFAKRVAEGIGVEPPEEPGDEMPTHDREDPSLSMENRTPDTIETRKIAMLIDDGFDDEHVSKLRSALEEEGARVKIISKVLGEKSGVDGETVEPDKHHVAAASVSFDAVVIPGGDESVDAMRGQGDPKHFVAEAFKHYKPIAAVGEGTELFEAVDLPDTEIADEGDLVSDAGVVTCRSDDLESFAEAFVDAIAQHRHWDRDPEEVPA\*

>NpGlyIII1

MTDALFVVSEEGYWGEECVEPLETLSDAGVEVTVATPSGSPPVIDERSLDPDEVGEETAEHVREVHETDERLNDPIPVAQADAEGYDAVVFPGGHGTAWDINQDKHARQLLRDAVEGNGKALVVCHAVGILGFARDSHGAFIVNGRDVTGFPNAWEEGIVDEQDRMPDGRKLPYWTEDEVKAAGGNWDAELDADTSVTVDGDLITARGPGSSSAAADTLLEELDVELEA\*

>NpGlyIII2

MADIAAEIVLFDGFDELDAVGPYEVLRNGARAGASLETRLVSLAETDLVRASHDLRLEPDGTLGEPDLLLVPGGGWTTEGGVRAAVEDGALPEAVRERYDDGATIASVCTGAMVLSAAGILEGRPAATHPVAVDDLAATAATVVDERVVDDGDVVTAGGVTSGIDLALWLLEREFGVEIAEAVAAEMAHERRGDVFESS\*

>NpGlyIII3

MTEHRILLLAGDFVEDYEVMVPFQALEMIGHEVHAVCPEKEAGDTCPTAIHDFEGDQTYTEKPGHQFELTHDFDAVEPSEYDALVVPGGRAPEYLRTYDEVLEITRHFFAEDKPVAALCHGLQILAAADVLEGRTCTGYPALEADVRGAGAEWTGEVTRDGNLVTGQAWPDHPEWLAEFLEVLGTDVDHAEPAAADD\*

>MmGlyIII1

MEASIFLADGVEECEALLVVDLCRRAGIEIQTVAVNDRSGEAARTIHSSHKVSIICDTHLDDYQTAGEKILVVPGGLPGVNNLKANQKLSEILKAQGASAGRLAAVCAGPTVLGNLGLLDGKRATVFPGFDDGLGAAKYEDVPTVVDGQVITGRALGAGIEFALQIVTALRDKETAAKVAKQIVYPAIG\*

>AgGlyIII1

MPTPPQLATDKKAAVLLAAGCEEVEALAVVDALFRAGIRADLVSVSQSLEVVSSHGVRIIADALIADVELADYDLLYLPGGMPGTLHLKACPAVPLEILRRADVGEPIAAICAAPSILAELGVLDRRRATANPAFMEAIAQGGATAEEKPVVVDGAITTSRGAGTAFDLGLELVRQMLGDGAADAVRAGIVHSR\*

>ApGlyIII1

MTDDVKLLMLAGDYVEDYEIMVPYQALLMVGYKVDVICPGKKAGDKVLTAIHDFEGAQTYSEKPGHAFVLNADFDAIDTDEYLGLIIPGGRAPEYLRLNARVLEIVKAFADRPIAAICHGAQLLAAAGIIKGREVSAYPACRPDVELAGGTYADIPVTEAVTDGELVTAPAWPAHPAWLAQFLKVLGANVSI\*

>RCGlyIII1

MSLLKKSQAATYGHDKGNDGMNVMSKSPAAKRSLVFFLVPHFTMLPFAAAVETLRIANRMLGYSAYTWRLCSADGEKVYSSSGIGIEVNSSLADERRNLSGENRPNMVLVCSGIYVEEFNNKSVNAWLRETYNRGIAVGSLCTGAHVLAQAGLLNGKRCAIHWENLPGFAEAFPQAEVYADLYEVDSNLYTCAGGTASLDMMLNLIGQDFGENLVNRVCEQQLTDRVRNPHDRQRLPLRARLGVQNAKVLSIIEVMENNLSEPLSLVEIADDAGLSRRQIERLFRQEMGRSPARYYLEIRLDRARHLLVQSSMPVVEVAVACGFVSASHFSKCYREVYNRSPQQERAERKLNMNTSRTGVVV\*

>RCGlyIII2

MKLQVLALDPVFDTGLSTMLDVFSMANALSAMLSLEVPTFDVSVIGVRKKVKTAHGLAVPISGSFDPKAGGWLVVPAIACQMPDVLVPALDRPEIRDAGAVLREAKVAGMNIAAACVGTFVLAESGLLDGEKSTTSWWLAPLFRQRYPSVQLEDGRMLVKSGSLVTAGAALGHMDMALWLVRQVSPELAGLVARYLIVDNRPSQSAYVITDHLSHADPLVQRFERWARGRLSEGFSLDDAADVVGASKRTLARRMQQVLGKTPLSYFQDLRVERAVHLLKTSDKSPDEIAALVGYADGVTLRALLRQKTGRGVREVRAGG\*

>HYGlyIII1

MAKVAVLLAPGFEEVEAIAPIDILRRGGVEVLIVGVKDKVIPSARNVKIEVDVTIDELKDVDNLDMIIIPGGMIGVENLKKSEEVKNLINQMNAKKKYVSAICAGPLVLKNAGVVENKHITSHPSVKLEFNEHLYKEESVVEDENIISSRGPATAMVFGFRLLEKLTSKEKAKEVAKAMLFDY\*

>PdGlyIII1

MNLLLKNKTNMAKVYEFLANGFEEVEALAPVDILRRGGVEVKTVSITGSHLVESSHGVPVKADLLIEELSNADDADLLLIPGGMPGAKNLKDDSRVGKALLRQSDSGRRIGAICAGPMVLGALGLLKGRRATCYPGFDKFLTGAEYTNELCTVDGNITTGKGPAASFLYGLRLLEQLTSPEKADEIKKGMLINELAGLH\*

>RsGlyIII1

MAKKILMLVGDYVEDYEVMVPFQALQMVGHTVHAVCPDKQAGESIATAVHDFEGAQTYSEKPGHRFTVNASFADVDPAAYDALVVPGGRAPEYLRLDPRVLDIVRHFSGAGKPIAAICHGAQLLSGAGVLKDRACSAYPACGPEVTAAGGTYQDIPVDQAHTDGNLVTAPAWPAHPAWLAQFLEVLGTRVLH\*

>CaGlyIII1

MNALIILHPGFEEIEAITPIDLLSRADVHVTQVSIGPDKSVTGRSGITVSTSQLLGDCEDQDYDLVILPGGPGIQQIRHHPQLCRRLQQQAAADRWIACICAAPLLLKDAGLADGLQLCCHPSAEPDFTVTSSEAVVIDGKIITSRGAGTAHEFGLSLISALKGKALADQIAKSICWPH\*

>VbGlyIII1

MPATTPTALVIVFDGIEEIEALTPVDILRRAEIKVTVASVNGLPTVTGRNQITFAADTSITRVAEDSFDLVILPGGPGVLELLENQAVSHILVAQDKAQKELAAICAAPKVLANHGILNSRKATSHSSVRDALPRPSDDPVVIDSHITTSQGLGTAVDFSLTLVKKLKGEALAQKIAESIHHSSRIF\*

>PbGlyIII1

MSSVLVPLFEGFEEIEAVTIIDVLRRANIEVITASLDQLTVMGAHAIAIIADTTLDRVEPSKFDAIVLAGGAGTFRLREDPRIAAILKAQAKVNKLFAAICAAPTVLSDAGLLKGKRATSFPAVKEQLEVGEYLTDAVVVDGNAITSRGAGTAMVFALKLVEVLQDEAIANKLAQDMLV\*

>SPGlyIII1

MKQALLPLMQGFEEIEAVTIIDILRRGDVQVVTAGLESVIVDGGHGITIMADSLLEHVINQEFDLIVLAGGAGTFRLQADPRIIPMLQKHAGLGKLTAAICAAPLVLSASGLLTEKRATSYPAVKDQLVVGEYLNDLVVVDGNIITSRGAGTATEFALQLLELLQGKAIAEEVAGKIVFIKKTA\*

>CabGlyIII1

MSKALVVLAPGFEEIEAITIIDLLRRADIQVTVAGLQPNAITGSHHITVVPDTDIQHVKHETFDMLILPGGQPGTNNLKSSETLLGWIKERFIQGKKLAAICAAPTVFHAAGITKNLKITSYPSEKKVFTDSQYLEEAVVKDGAIITSRGVGTAIPFALRLIEELKDRQTAQQVAERILFEGRW\*

>DaGlyIII1

MGKVIVVLADGFEEIEAVSVIDILRRADVEVCAAGVKDGNVKGAHGLIVKPDSTLEDIDEDDYDMIVLPGGAVGAENIGKSKDADDILRKFKKDDKYIAAICAAPKILADKGLLNGCMATSYPSFKDAVAKDSDYQEAIVVVDENIITSRGPATAAEFAFTLVELLVEEDTAEKLREGMLFTDDDCE\*

>DalGlyIII1

MTAISIDNNDNIDIIVAMKLHLLVCDGVFDLGLAALTDTVGLANAMSGSLPQAPAPIEITLVGVRRRIRTAQGLTVPVVTARGVPEPDVVLVPAFGEKMPDTLSARLTRPDVPDAVAVLQQWSTAGAHLGAACSGSFLLAESGLLDGHRATTSWWLGPMFRQRYPNVTLDESRMIVNSTHFTTAGTALAHVDLALRIIRGRSPALAALVARYLLVEARSSQAEFVIPDHLAHADPMVERFECWARSRLAKGFSLAEAASAAGTSERTLARRLQSVLGKTPLSYFQDLRVEHAVHLLRTGNASVDQVAAQVGYSDGVTLRALLRRKLGRGVRELRRGG\*

>CjGlyIII1

MSKKVLIPLAQGFEEAEFIGIADVLKRARELNPDLEVVIASLNSELLVKGANSINIKADCSIEDVDIENLDAIALAGGFEGMMNLKNSNVILNIIKQLHSKNKIVAAICASPIVLNEAGVLEGEFACYPSCEVGLNGNRVNKAVVVNKNVITSAGPATAILFGLELAKKLCGDEIYQKLYEGMLLPLTK\*

>CjGlyIII2

MSKKVLIPLAQGFEEAEFIGIADVLKRARELNPDLEVVIASLNSELLVKGANDISIKADCSIEDVDIENLDAIALAGGFEGMMNLKNSNVILNIIKQLHSKNKIVAAICASPIVLNEAGVLEGEFACYPSCEVGLNGNRVNKAVVVNKNVITSAGPATAILFGLELAKKLCGDEIYQKLYEGMLLPLTK\*

>HbGlyIII1

MKRVLVPLAQGFEEAEFIGIVDVLRRAGVEVLVAGLESSGNIKGANGIEIKAELALSSIDINSLDGIALAGGFEGMQNLSNNAKILEIIQRLHKDKKIVAAICASPIVLNKAGVLSSEFTCYPGCEEGINAKRLNEAVVIRDNVITSAGPATAILFGLAITKALMGEDVYKGLYEGLQVPLTRA\*

>FsGlyIII1

MQILVLLADGFEETEFVVPVDLWRRAGFKVTVASVSGADVVDGLHGIKVQADVALSKLEPTDFDAVFLPGGGVGVQNLKASAAVENTVCSLNDDNKWVLAICAAPTVLSKARILVDRKATCYPGCETDLVCREFSEERVVVDGNIVTSRGPGTAEEFALKCIAVMGGAELSQKIQSQIVAR\*

>GhGlyIII1

MTKKVALFVENGSEELELIAPLDILRRANIQVDLISANNEEYITSSHDVKIIVDKKINDIDNILDYDAIVIPGGMPGSTLLRDNDKIIKFYQEMYNAGKLVAAICAAPIVLSKAGILEDKEVTSYPGFDKEINCKTYDKEKAVIADKNVITAQGPAVAILFGYEIVNYLLQDDTAQNISDGMLVPVLKNNL\*

>BcGlyIII1

MKKILLLLADGFEAVEASVFTDVLGWNKWEGDGSTEVVTVGLRNKLTCTWNFTVIPEKTVDDIQLDEFDALAIPGGFEEAGFYRDAYSREFLHVIQHFYAKQKPIASICVASLTLGKSGILVGKKATTYSHPTSKRKEQLKNFGAIVQNDLIVQDGNIITSSNPGTAFDVAFLLLEKLTSKKNAEHVKDLMGF\*

>BcGlyIII2

MKKILLLLADGFEAVEASVFTDVLGWNKWEGDGSTEVITVGLRDKLTCTWNFTIIPEKTVDNIQLDEFDALAIPGGFEEAGFYRDAYSKEFLHVIQHFHVKQKPIASICVASLALGKSGILIGKKATTYSHPTSERKEQLKNFGAKVQNDLIVQDGNIITSSNPGTAFDVAFLLLEKLTSKQNAKHVKDLMGF\*

>CsGlyIII1

MNKKIFVMLANGFELIEAMSPVDVLRRAGLNVVTVSTMENTLEVESAQKVKVVADINISDINVGEGVMVVIPGGFPGYVNLRSDSRVVEIVKEYLNSNDKFVGAICGGPTTLGINGLIGDYKFTCHTSVKEEMASEKYEHKDVVVDRNLITSPGAGKSVEFGLALASVFVDEATITKVKKGMELI\*

>CsGlyIII2

MKKKVLFIIPPERFNEEELIKPKNILVNKGIDVVISSTVTGEITGDYEGTVISSAIFSNLNPSDFDIISVIGGSGTIDYLWENPSLINYLKEAYNKNIIISGICAGAVAIAETNLLTNRTATCYPIDIMINKLIKHNVNYLEKNVVVHSDIVTSNGPDGAEDFGLALLNLYL\*

>LwGlyIII1

MKEKKVAVFLTNGFEEIEAITPIDLLQRAGINVDTVSITSDNLVESARKVKIMTDKVIGKIDFLEYDMLVMPGGPGTENYFKSQLFLDNVLKFSKNIENKKVAAICAAPTVLASLGILKGKNAVCFPACEDDLLKGKAILKKDRAVVDGNIITSRSAGTAMDFSLAIISELLGKEVAGKIAKEIVL\*

>EcGlyIII1 (Hsp31)

MTVQTSKNPQVDIAEDNAFFPSEYSLSQYTSPVSDLDGVDYPKPYRGKHKILVIAADERYLPTDNGKLFSTGNHPIETLLPLYHLHAAGFEFEVATISGLMTKFEYWAMPHKDEKVMPFFEQHKSLFRNPKKLADVVASLNADSEYAAIFVPGGHGALIGLPESQDVAAALQWAIKNDRFVISLCHGPAAFLALRHGDNPLNGYSICAFPDAADKQTPEIGYMPGHLTWYFGEELKKMGMNIINDDITGRVHKDRKLLTGDSPFAANALGKLAAQEMLAAYAG\*

>EcGlyIII2 (YajL)

MSASALVCLAPGSEETEAVTTIDLLVRGGIKVTTASVASDGNLAITCSRGVKLLADAPLVEVADGEYDVIVLPGGIKGAECFRDSTLLVETVKQFHRSGRIVAAICAAPATVLVPHDIFPIGNMTGFPTLKDKIPAEQWLDKRVVWDARVKLLTSQGPGTAIDFGLKIIDLLVGREKAHEVASQLVMAAGIYNYYE\*

>EcGlyIII3 (YhbO)

MSKKIAVLITDEFEDSEFTSPADEFRKAGHEVITIEKQAGKTVKGKKGEASVTIDKSIDEVTPAEFDALLLPGGHSPDYLRGDNRFVTFTRDFVNSGKPVFAICHGPQLLISADVIRGRKLTAVKPIIIDVKNAGAEFYDQEVVVDKDQLVTSRTPDDLPAFNREALRLLGA\*

>EcGlyIII4 (elbB)

MKKIGVILSGCGVYDGSEIHEAVLTLLAISRSGAQAVCFAPDKQQVDVINHLTGEAMTETRNVLIEAARITRGEIRPLAQADAAELDALIVPGGFGAAKNLSNFASLGSECTVDRELKALAQAMHQAGKPLGFMCIAPAMLPKIFDFPLRLTIGTDIDTAEVLEEMGAEHVPCPVDDIVVDEDNKIVTTPAYMLAQNIAEAASGIDKLVSRVLVLAE\*

>PGGlyIII1

MSKQVSTPLRRVSILAIDRVFASTLMQAKDFFHLASLRYGKQLGHGLTPAFETRLVSPDGKPVNSFSDVMMPVDGGLENADVIILPAFWDDFETLCGRYPQILPWLREQHARGAVLCGEATGVFWLAEAGLLNGKEATTYWRFFNAFAERFPKVYLNQDKHLTDADNLYCAGGTTSACDLYIYLIERFCGANVAQAVARDILYEVQRSYSPGRIGFGGQKLHQDVIILQIQHWLEEHFADKFRFEDVAREHGMSIRNFMRRFQTATGDKPLHYLQRLRIETAKGLLSGSRKSIKTISYEVGYDDASFFARLFRQHTELSPNQYRQQFQQAA\*

>PGGlyIII2

MGQTLIERRQFSGGMKGKNLRYLNEQSADSRLTRTGFLLLEHFSLPAFTQALDTIITANLLRAGLFSSRTFGLGEGEVISDLGLVIRPDARIGAASLGDLDLLVVCGGYRTELKASEELSNLLRAAAERGVSLAGLWNGAWFLGRAGLLDGYRCAIHPEHRPALTEIAKATQVSSEPYVIDRDRLTASSPSGAFHMALDWIKSLHGKALVEGIEDILAFEESRYRRIKPDENLCVSAPLREVVKLMDANLEEPLELEQLAVYAGRSRRQLERLFKEQLGTTPQRYYLELRITEARRLLQHTELSQMEVLVACGFVSPSHFSKCYSAFFGYRPSREKRLVK\*

>PGGlyIII3

MTLQIGFLLFPQVQQLDLTGPYDVLASLPDVQVHLIWKDLVPVTASTGLLLKPTTTFDDCPNLDVICVPGGAGVGPLMEDEQTLGFIKRQAAQARYVTSVCTGSLVLGAAGLLQGKRATTHWAYHELLPKLGAIAVQDRVVRDGNLFTGGGITAGIDFALVLAAELVGAEAAQLIQLQLEYAPAPPFNSGSPDTAPSAIVDEARLRAAASLKLRTEITERAAAKLNLH\*

>PGGlyIII4

MKTVAMVLFPDFLLLDMAGPMEVFSVANRYLKAEDHYQLITLGTERGMLRASNGVQVQTDSHIDDPAQAFDLLLVPGGPGAYNEKHPALLAWLQRSVGQAGCYGSICTGAFVLGHAGLLDGYRVTTHWNYTERLIKAFPEARVETDQIYTEDRNLITSGGVTAGIDLALAVVARDHGKRVAQDVAKVLLVVMKRQGGQAQFSPLMAAVAPQETAITRVQNHVLEHLDEAFTVERMAGLANMSTRHFARLFARDVNMTPMEFLQNARIDCARNLLETTELPLKTVAYKSGFGSVRHMRFLFAEKLGLTPAQYREQFS\*

>PGGlyIII5

MNKNVAIVVFPGVQALDVSGPMDVFAEANRFLPPEDHYRLEVIGLERGAMACSNGLNLSAHRHFSEAPDAYDLLLVAGGPQLPFMDFGKPFDTWLREACARARRFGSICNGAFMLARAGLLEGRTVTTHWNDAEALAQLCPSTQVEADRLYVEDGALYTSAGVTAGIDLSLYLLARDHGAEVALSVAKRLVVFTQRSGGQSQFSPFLTPHAEPTSAVAMVQLYVLANLTGDLTIADLANAANMSARNFSRVFAREARVTPAEFVESARVDAARVLLESTTAPLKTVAYQCGFRDAQHMRSVFNRRLGVTPQQFRLNFALML\*

>PGGlyIII6

MPDSPGLVAILAYDGLCTFEFGIAVEIFGLPRPEFDFPWYEHRIVAVDQGPMRAMGGIHVLADGGLELLAQARTIIIPGWRDRAAPVPPALIDALRQAHAQGARLLSICSGVFVLAASGLLDGHGATTHWRYTEELARRFPTIAVDPDVLYVDSGQLITSAGSAAGIDACLHLLARDFGTQVANSVARRLVMSPQRTGGQAQFIPMPVSATPRNDLSRVMQWARERLHQPLEVRDLASEAAMSERTFLRRFTEASGQSPKAWLQHERLARARELLESSVYNTEQIAQRCGYRSVESFRVAFRSVVGVPPSVYRERFGRGVKAIS\*

>PGGlyIII7

MSSVSLQTLTWPKSEPRDVVFIAYPRMSLLDLSGAQTVFWAASKALAERGQHGYQLHTASLEGGLINTIEGLAVDTRALRQLDMASLDTLVVPGAPDICQTLDDHAELTTWLRHESQAARRVVSVCSGAFLLAQAGLLDGRRAATHWAMCDTLRERFAAVEVDADAIFIQQGAVWTSAGVTAGIDLALALVEADCGREVALQVARELVVYLKRPGGQAQYSTLLQSQMQGSPQFDSLHLWLMEHSSDPKLTVERLAEQAKMSLRNFTRVYKQSTGHTPSRAIELFRLEAARRLLESSAHNIDQVARLSGFGDEERLRACFQRHLSISPRDYRSRFSREG\*

>PGGlyIII8

MTSFNSGAQPQNRAPQSIGFLLLDNFTLISLASAVEPLRMANQLSGRELYRWSTLTVDGGQVWASDGLQITPDASMHKAPPLDTVIVCGGIGIQRTVTREHVSWLQSQARQSKRLGAVCTGSWALACAGLLDGFDCSVHWECLAAMQEAFPRVAMSTRLFTLDRNRFTSSGGTAPLDMMLHLISRDHGRELSAAISEMFVYERIRNEQDHQRVPLKHMLGTNQPKLQEIVALMEANLEEPIDLDELAVYVAVSRRQLERLFQKYLHCSPSRYYLKLRLIRARQLLKQTPMSIIEVASVCGFVSTPHFSKCYREYFGIPPRDERVGSNTTQQVAMLPLPQAIVMSPLSGPMSALSQARNESTFASVRL\*

>PGGlyIII9

MTFRALITLAEGIDDLQSVTLIDVLRRAGVEVVAASIEGRRMLTCARGTRLTADGMLIDVPAQTFDLIVLPGGVVGAQHLAAHQPLQQLLKDQASAGRLFAAIAESPAIALQAFGVLRQRRMTCLPSASHQLLGCTFVDQSVVVDGNGITAQGSGGALVFALTLVEQLGGKALRAKVAGEMLV\*

>PGGlyIII10

MSQDFYFLLMPGFSAIGFISAIEPLRVANRFRGELYRWHVLSADGGAVLASNGMSVNADAALEPLKKGATLLVVAGFEPLKFATPTLEHWLRRLDNEGVTLGAIDTGSFVLAEAGLLDGHRLTLHWEAIDAFKESYPQLSVTQELFEIDRRRITSAGGTASIDLMLDLIAQVHGPQLAIQVSEQFVLGRIRPRKDHQRMEVATRYGISNKKLVQVIGEMEQHSEPPLTTLQLAESIKVTRRQLERLFRLHLNDTPSNFYLRLRLEKARQLLRQTDMSVLEVSIACGFESPSYFTRSYRARFARCPREDRRTAQA\*

>PGGlyIII11

MPKTIHVLAFANVQILDVTGPLQVFASANDIARQRGLPVPYAPSVIAREGGAVMSSAGLAVLAEPLPRQASDTLIIAGGWGIYLAAEDVPLVDWVREHAAKCRRVASVCTGAFLLAASGWLDGRRVVTHWTRCEQLAQQHPKLQVEANPIFINDGPVWTSAGVTAGIDLALAMVEEDLGRDIALDVARHLVVFLKRPGGQSQFSVTLALQNQGNRFDELHAWIAENLTCDLGVPTLAEQAGMSERSFVRHYRADTGQTPARAIELIRVETARRLLSDTGLPVKRIAANCGFGSEETLRRSFLRAIGVTPQAYRERFSVSAGADPVMP\*

>TpGlyIII1

MSVRVYLFVAHGFEEVETITPLDYLRRAGIALTLVGVGAEQVVSTRGLRVSCDCSLEALCASPGIADAACAADAVLLPGGLENCHTLAACAAVRDFVMRVHLRGGLVAALCAAPARVLSAWNLLGSRRYTCYPGMEPAVFSAHDDGVGKRTEEEKSRALRKPERARVVRDGNLLTACAAGAAEEFSFAVIEALCGVEVAQSVRAQVVAR\*

>TpGlyIII2

MSVRVYLFVAHGFEEVETITPLDYLRRAGIALTLVGVGAEQVVSTRGLRVSCDCSLEALCASPGIADAACAADAVLLPGGLENCHTLAACAAVRDFVMRVHLRGGLVAALCAAPARVLSAWNLLGSRRYTCYPGMEPAVFSAHDDGVGKRTEEEESRALRKPERARVVRDGNLLTACAAGAAEEFSFAVIEALCGVEVAQSVRAQVVAR\*

>SthGlyIII1

MARVAVCLADGFEDVEAVTPIDLLRRAGVEVVVAGVTGKEVTGSRGVRIVTDALLSDLSPEDFDGMVLPGGMPGSSNLAASDAVRAWLSHCMKAGKTIGAICAAPAVVLGKAGLLEGRRFTCYPGMEKEVEGGTWEPSPVVKDGNLITSRGVGTAGLFGLELVRAFAGEEAYQKVGKATLIL\*

>SchGlyIII1

MKFALFLAPGFEEGEAIITTDVLRRGQIKVDLVSITDQLEVTSSHQVVIKADQLVTEVKYEDYDGFILPGGKIGVDNLAKNSQIKEWLLKANHDEKTIAAVCAAPQILGHLGILDNREATSYPGCTEGMENSIYNDEMAAITDGHIITGASVGSTMNFALAIADRVLGPEKVFALQNELVIRD\*

>MsGlyIII1

MNLLVIVDNNFQDVELTTVVSILKRSQQFNKIAFYNPCSRKATGQFEIVKFNNLETSVNLKDYQAVFVPGGKACFSFKDNKEIIKKIRHFFDKDKWVFAICDAPNALRYNNLIKEQNYTSFPSAWSKELRSNSNYQNKGVVVFEKLITAKSSYYSQHLAFEIIRTLFGEKEYKLSKKLAKG\*

>DdGlyIII1

MTKKILLLLCKGFEVMEFTPFVDVMGWAREDDNNEDKADIQVVTCGLYNKMVTSTFGVKVQVDVLLGEVVKSLDEFDALAIPGGFENYSFYEEAYSEDVSQLIRDFDSKGKHIASVCVAALALGKSGILKGRNATTYRNSLREHSVRQQQLRDFGANVIADQSIVIDKNVITSYNPQTAPYVAFELLSRLSDENKAKKVKTLMGF\*

>DdGlyIII2

MAIQVAMIIFDGFEEIECVTTLDLLRRANIRVDLISIDNDKKSIKGSHYIELVTEYKFQDFIETLSNYNGIIIPGGPGIVQQLTNQKLIDAIKRFGLLYSNEINNNNNNNNNNNNNNNNNNNNNNNIENNNNRFLAAICAAPQIFGKCGLLKGRKVTHFPGCNQFMQDSIELLDQTIVVDGNIITASSAGVTIPFALKIVEFLKGIDASNLLYSQINPIQVKSS\*

>TcGlyIII1

MTKKVLVPAADGTEEIELTCITDILRRAEIQVTVASVMESQNLILSRGLKITTDSLLKDESAAAYDGVFLPGGLPGADHLGKNAHLKKILEEMRSQGKWYGAICASPVSALAPMGMLEGVKTVTCYPAMKEKIPSHVHWSTDPVVRCGKCLTSKGPGTAIAFGLAIVAALLTKDCALRLAKELLVDETPFVEKALSNF\*

>TcGlyIII2

MEVKTRWILRHYRMCVCVRLCFFFSIIYHHPPILLFQCVFICFFSFFLLLLLHGIPPQHMEWKIIILIIILQHYNIQKQQTKRKTMTKKVLVPAADGTEEIELTCITDILRRAEIQVTVASVMESQNLILSRGLKITTDSLLKDESAAAYDGVFLPGGLPGADHLGKNAHLKKILEEMRSQGKWYGAICASPVLALAPMGMLEGVKTVTCYPAMKEKIPSHVHWSTDPVVRYGKCLTSKGPGTAIAFGLAIVAALLTKDCALRLAKELLVDETPFVEKALSNF\*

>TcGlyIII3

MTKKVLVPAADGTEEIELTCITDILRRAEIQVTVASVMESQNLILSRGLKITTDSLLKDESAAAYDGVFLPGGLPGADHLGKNAHLKQILEEMRSQGKWYGAICASPVSALAPMGMLEGVKTVTCYPAMKEKIPSHVHWSTDPVVRCGKCLTSKGPGTAIAFGLAIVAALLTKDRALRLAKELLVDETPFVEKALSNF\*

>PfGlyIII1

MSGKKTALVAVASGSEDVEYITVVDVLRRAGVHVTTASVEKSEQVCLQSKNVVLADTTISKVRNNIYDVLVIPGGMKGSNTISECSEFIDMLKEQKANNRLYAAICAAPETVLDRHSLIDDVEAVAYPSFERNFKHIGKGRVCVSKNCITSVGPGSAVEFGLKIVEHLLGRQVALSLASGFLLHPAVTF\*

>PteGlyIII1

MQNQNKQVLVPVGDGCEEIETVAIIDILRRANIDVTFASIKPVEDEKAPVIVGRSGISFICDTYLTEAVLKQQFDLIALPGGLSNAQSLGTHQPLLDRLRQQQEEGKWIAAICASPQLVLDKNGFMINSTGTCHPAHVQDYKGQFSEDRVHVSNKFITSRSPGTAIEFALALVELLVDQHTAVQMAKSLLVKR\*

>EhGlyIII1

MKALVVIANGSEELEAVTIIDILARAKIQVTTATINSNLETACSRGVKIMADKFLSECNEQYDVIAIPGGLPGADNLAGSQLLIQKIKEQLAANRFVAAICASPAIVLEGNGIIEGRKCTAYPSFQPKLANQSAVHQRVVVDNHLITSQAPGSAIEFSLEIIRQLKGEEAMREVEKPLVLSFKY\*

>LdGlyIII1

MNVLVVAADHSEDIELISIIDVLSRAGIKVTLASVMESKSITLAHGVNVMCDALIGEVSAVEYDAVLLPGGMPGAVHLGNNEALKKILQNARVGKKLYGGICAAPAVALAPMGLLEGVDTVTCYPGFEDKLPSSVKYSTNAVVKSENCLTSRGPGTAIYFALAVVSILKSPDLAERLAKAMLVDHSNEMNDVRAIK\*

>SjGlyIII1

MVKVCLFVTGGSDEIETASCYGVFTRAKTPIDTVYVCEENKERLVNMLCGIRLYADRSLSEFQSAEDFMKEYDVVIIPGGWGGSLERSIPGTKMVQEIVRGMYKKPGKWVAMICAGSMGVMTSGLDPKTLELTSHACVIDVLRNAGYNWVDEPVVVSNNLITAQGPGTSMLFALKIAEQVLDKETYQQVYASLEMPQRN\*

>SjGlyIII2

MVKVCLFVADGSDEIEFSAPYGIFTRANTPIDTVYVGDNKDRLVNMSRGIQLYAKRSLSEFQSTEEFVKEYDVAIIPGGWQGSLTLSGNKKVQEIVKEMYNKPGKWVAMICAGSLTAKTSGLGVKTLTSHPCITKDLQEAGYEWKNESVVVTDNLITSQGPGTAMLFALKIAEQVLDKDTYQKVYDSLEMP\*

>AnGlyIII1

MTDSSTPSPLRIGVLLFPGFQALDVFGPLDVLNVLSWSPTTTPPVTLSLLSTTLSPISTLPPNFPHALSQSILPTATLSSSPPLDVLIIPGGWGTRAPLPEYTEYIRTVYPTLKYLLTVCTGGKLAARAGVLDGKRATTNKNDWEGVVRDAPGVQWVKEARWVVDRSDVGGDGKGTEVWSSAGVSAGVDLMFAWVESIWGEEVAAGVERVLEFRRWREGDVDPFVRD\*

>CgGlyIII1

MSRNGDREGGKKPLNFGIVVFPAFQALDVFGPLDALNLLSRSYEMNLSVIAETLDPVSTKQIPGAQQQPGAIPATGPAVPAANSDFGQTILPTHTFQTAPPLDVLIVPGGQGTRYAGIRASIDFIKERFPQLQYLITVCTGAGVAARAGVLDGKRATTNKLSWEQTIALRPEVNWVHKARWVEDGNVWTSSGISAGIDVTFAWISAVYGKDLAKNIADRMEYTPVEDSSWDPFADRWGSKKA\*

>CgGlyIII2

MKFTISIIAASLTAVVAGNPVQARVDTINGTNCTTALPVNYGALIFNGLDMIDIWGPLDVLQLNAHAYNMNVHLIAPTMDPIIAGVVNASDPTLNKFGSNFWPVIQPTATFADDLDLDVLIVPGGPGVRAAGLEPIVEYIKEMYPKVKYLITICTGASLAARAGVLDGKRATTNKRAWAQMTAFGPKVNWVAPARYVIDGNIWSSSGVTSSLDLTYAFVAEVYGQNQSTLIANTMEHTPLAADDDVFTDIWSVPHTNN\*

>CgGlyIII3

MTLAQDESSVQACIPRPTTTTPASPPPTSLPRTFGMIISRAFEMLDVFGPLDALGMLARIHQLNLYLIAETMDPVTVEPVSAAMNAKNSSFFPKILPTHTFATAPTDIEVLMIPGGLWTRSPNLNSTIAYVRATYPKLRYLVSICTGASIAARAGVLDGRRATTNKASWASTIAYGPNVTWVPKARWVVDGNVWTSSGISAGIDATLAFIQDVYGRENATYIADLMEYEWHEDSGWDPYAEKFNVTGS\*

>CgGlyIII4

MATKLGDKKSLRIGVMLEAVQLSDIMGIDLFGNISLEYYDKVKAFDPGFAPFEGLAPEIKFYFISSTLEPAEMTPGLKFVPNITYDDCPRDLDLVLIGGPLPSHRPPQADRFMKEAFVKTRVWMTTCIGSPWLASAGVLKGKKATVNREFLAFARQVHPDTEWLDQRWVVEEKEYDGEGKGELWTAGGAGAGLSMIIEYLNQNFDPAYVKKIALQGIGMEEIETNQFYKTIYGSGSVKP\*

>CgGlyIII5

MSFDLSKPNRKIHAGVILTKGITEMLDVAPFEFFHCFQWSGDKETAAAMNLPENTMDDGLKFELHWVTEDGKPAKLASNAQILPTDSFESCPPLDIALMGAHDFKYKTSPAEIDFIRKTFEQCSAFLTICGGMVPLLEAGILAGKTSTCPRMMFDLMKKTVPVVNWVDKRWARDGKLWTSSTLLNGTDLIRAFATETWGERTGMIEFFLDAGHYPDRDVDFKDFKGQNYQMKQLPA\*

>ScGlyIII1 (YDR533C-Hsp31)

MAPKKVLLALTSYNDVFYGDGAKTGVFVVEALHPFNTFRKEGFEVDFVSETGKFGWDEHSLAKDFLNGQDETDFKNKDSDFNKTLAKIKTPKEVNADDYQIFFASAGHGTLFDYPKAKDLQDIASEIYANGGVVAAVCHGPAIFDGLTDKKTGRPLIEGKSITGFTDVGETILGVDSILKAKNLATVEDVAKKYGAKYLAPVGPWDDYSITDGRLVTGVNPASAHSTAVRSIDALKN\*

>FgGlyIII1

MSPPTKYAVALFPGFQALDVFGPLDVLNFTSKRQHMEVSLLHASLDPVSTFVEGGPACIGQSVVPTHTYETAPDDIEVLLVPGGFGARDPENVMRVRQFVKERYPKLKYLLTVCTGSAIVAQTGILDGREATSNKRSFDWVLTQGANVKWARNARWVVDGNIWTSSGISAGIDMTYAFIAEQYGQDIADDTAKGSEYVRNTDPNADPFAV\*

>CvGlyIII1

MAGANVRVLVPIGTGSEEMEAVITIDVLRRAGAEVTVASVEDDLTVVCSRQVRLVADKSIKDCAGDWDLIALPGGMPGAERLRDSAALTELVAKQKAANKLHAAICATPAVAFEPQGVLAGKKATAHPAFSAKLTNQAAVEQRVVVDGKLVTSRGPGTAFEFALALVKMLYGEEKMREVAGPMVMADGYDKAL\*

>GaGlyIII1

LLYGKEKADEVAGPLVMRSNHGAEYNFKELNPVKWTVASSPQILVPIANGTEEMEAVIIVDVLRRAKANVVVASVEGSLEISASRKVKLVADVLLDEALNNPYDIIVLPGGLGGAQAFANSDELVDSLKKQRESGRFYGAICASPALVLEHHGLLKGKKATAFPAMCSKLSDTSEVENRVIVDGNLVTSRGPGTTMEFALAITEKFLGREKADELAEAMLFVH\*

>SmGlyIII1

MAVRALVTPGLVRAVAFSSGRGSLGLSADRPKRRRSCSSSCVKIIAMASPKKVLVPVADGTEEMEAVIVIDVLRRGGAHVTVASVGQEPKVTASRGVKLVADAIVSECGDEKYDLVVLPGGMPGAEHLRDSKALEDITRGQAQEQRAYAAICAAPAVALESWGLLNGLKATCYPSFVSKLSDPSSAESRVVKDGLVVTSRGPGTAMEFALTLVEQLYGKEKTQEVSKGLILLEGKPTKLEFNQTAWAAKVPSKPQVLVPIANGSEEMEAVIIIDVLRRAGMGVVVASVEETLQIVASRKVKIEADNLIGEVSSAHFDAIFLPGGMPGAEHLRDSKELQSILARQAKDSRVYGAICASPAVVLEANKILAGKKATAFPAFQSKLSDQSAVEARVVIDGLVATSQGPGTAMEFALAIVDKFSGKDSAVKTAEAMLFSY\*

>EtGlyIII1

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVIICPDASLEDAKKEGPYDVVVLPGGNLGAQNLSESAAVKEILKEQEKRKGLIAAICAGPTALLAHEIGFGSKVTTHPLAKDKMMNGNHYSYSENRVEKDGLILTSRGPGTSFEFALAIVEALNGKEVADQVKAPLVLKD\*

>EtGlyIII2

METVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVIICPDASLEDAKKESAAVKEILKEQEKRKGLIAAICAGPTALLAHEIGFGSKVTTHPLAKDKMMNGNHYSYSENRVEKDGLILTSRGPGTSFEFALAIVEALNGKEVADQVKAPLVLKD\*

>TchGlyIII1

MRRAGIKVIVAHLAGKDPVQCSRDVVICPDTSLEDAKKEGPYDVVVLPGVVKEILEEQEKRKGLIATICAGPAGLLAHKIGFGSKATTHPLAKDKMMNGSHYSYSENRVEKNGLILTSHGPGTSFEFALALVEAMNGKEVANPGKAPLVLKD\*

>TchGlyIII2

MVVLPRDNLGAQNLSESAAMKEILKEQEKRKGLIAAICAGPTALLAHEIDFGSKVKTHPLAKDKTMNGSHYSYSENRVEKDGLILTRHGPGTSFEFALAIVEALSGKEVAD\*

>TchGlyIII3

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLEDAKKESAAVKEILKEQEKRKGLIAAICAVCTAHAHELPKYGVKVGLRNDAAACCTGLLLGRRLLNRFGVDKIYEGQVEVTRDEYNVESIDGQPGAFTCYLDAGLARTTTGNKVFGALKGAKQVSEYIKNSVPDVMEEMYKKAHTAIRENPVYEKKPKKEVKKKKWNCPKMSLAQKKDRIFLLTLFVGPTALLAHEIGFGSKVTTHPLAKDKMMNGSHYTYSENRVEKDGLILTSRGPGTSFEFALAIVEALSGKEVADQVKAPLVLKD\*

>TchGlyIII4

MASKRALVILAKGAEEMETVIPVDIMRRAGIKVTVVGLAGKDPVQGSRDVVICPDASLKDAKREGPYDVVVLPGGNLGAQNLSESAAMKEILKEQEKQKGLIAAICAGSTALLAHEIGFGSKVTTHPLAKDKTMNGSHYTYPENRVEKDGLILTSRRPGISFEFALAIVEALSGKEVADQLHPFHVIRINKMLSCAGTDRLQTGMRGACGKPQGMVARVHIGQVIMSIRTKLQNKEHVIEALRRAKFKFPG\*

>TchGlyIII5

MASKRALVILAKGAEEMETVIPVDIVRRAGIKVTVVGLAGKDPVQGSRDVVICPDASLKDAKREGPYDVVVLPGGNLGAQNLSESAAMKEILKEQEKQKGLIAAICAGPTTLLAHEIGFGSKVTTHPLAKDKMMNGSHYTYSENRVEKDALLNLRQPWGGYLDELFG\*

>TchGlyIII6

MASKRALVILAKGAEETEMVIPVDVMRRAGIKVTVASLTGKDPVQCSRHIVICPDASLEDAKKEGPYDMVVLTGGYLGAHNLFNSAAMKEILKEQEKQKSLIAAIYAGPTALLTHEIGFGSKVTKHPLAKDKMMNGNQYSYSENHV\*

>HsGlyIII1

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVVICPDASLEDAKKEGPYDVVVLPGGNLGAQNLSESAAVKEILKEQENRKGLIAAICAGPTALLAHEIGFGSKVTTHPLAKDKMMNGGHYTYSENRVEKDGLILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD\*

>CeGlyIII1

MAAQKSALILLPPEDAEEIEVIVTGDVLVRGGLQVLYAGSSTEPVKCAKGARIVPDVALKDVKNKTFDIIIIPGGPGCSKLAECPVIGELLKTQVKSGGLIGAICAGPTVLLAHGIVAERVTCHYTVKDKMTEGGYKYLDDNVVISDRVITSKGPGTAFEFALKIVETLEGPEKTNSLLKPLCLAK\*

>CeGlyIII2

MAQKSALIILAAEGAEEMEVIITGDVLARGEIRVVYAGLDGAEPVKCARGAHIVPDVKLEDVETEKFDIVILPGGQPGSNTLAESLLVRDVLKSQVESGGLIGAICAAPIALLSHGVKAELVTSHPSVKEKLEKGGYKYSEDRVVVSGKIITSRGPGTAFEFALKIVELLEGKDKATSLIAPMLLKL\*

>XlGlyIII1

MASKRALVILAKGAEETETVIPADVMRRAGIKVTIAGLNGKDPVQCSRDVMLCPDTSLEEARTQGPYDVVVLPGGNLGAQNLSESPVVKEVLKEQEAKKGLIAAICAGPTALTVHGVGIGKSITTHPLAKDKIVNPDQYKYSEERVVKDENFITSRGPGTSFEFALEIVCTLLGKEVAEQVKTPLLLKH\*

>XlGlyIII2

MAGKRALVILAKGAEEMETVIPTDVMRRAGIKVTVAGLSGKDPVQCSRDVMLCPDTSLEEARTQGPYDVVVLPGGNLGAQNLSESPVVKEVLKEQEAKKGLIAAICAGPTALTVHGVGIGKTITTHPLAKDKIVNPDQYKYSEERVVKDENFITSRGPGTSFEFALEIVCTLLGKEVAEQVKTPLVLKD\*

>XlGlyIII3

MAGKRALVILAKGAEEMETVIPTDVMRRAGIKVTVAGLSGKDPVQCSRDVMLCPDTSLEEARTQGPYDVVVLPGGNLGAQNLSESPVVKEVLKEQEAKKGLIAAICAGPTALTVHGVGIGKTITTHPLAKDKIVNPDQYKYSEERVVKDENFITSRGPGTSFEFALEIVCTLLGKEVAEQVKTPLLLKD\*

>DmGlyIII1

MVFFGFPQISRHFSKFTKMSKSALVILAPGAEEMEFIIAADVLRRAGIKVTVAGLNGGEAVKCSRDVQILPDTSLAQVASDKFDVVVLPGGLGGSNAMGESSLVGDLLRSQESGGGLIAAICAAPTVLAKHGVASGKSLTSYPSMKPQLVNNYSYVDDKTVVKDGNLITSRGPGTAYEFALKIAEELAGKEKVQEVAKGLLVAYN\*

>HvGlyIII1

MSGKTALLLLAEGAEEMESVITIDVLRRAKIEVTVAGLDEHLVKCSRNVRIQPDDILENIKDKMYDAVIIPGGLGGAKKLSESTVVKNILEKHFKHEKLIAAICAGPTVLDAHNVGKGKKVTSYPSLKDKMKDYTYVAEKVVTDGNLVTSQGPGTSFNFSLEIVKILVGSDIAEEVSTGMLL\*

>AsGlyIII1

MIGDSVFTCLFQVTVAGLLGAGPVKCARRTTITPDVALADVKDRKYDVVVLPGGQPGSNSFAASDEVGGVLKNQQEAGRIVAAICAAPIALKSHGIAPGTLVTSHPSVHQKLVDGGYKYSEDRVVAVGNVVTSRGPGTAFEFALKLVELLVGEEKVKEISAPMILKL\*

>MmuGlyIII1

MASKRALVILAKGAEEMETVIPVDVMRRAGIKVTVAGLAGKDPVQCSRDVMICPDTSLEDAKTQGPYDVVVLPGGNLGAQNLSESPMVKEILKEQESRKGLIAAICAGPTALLAHEVGFGCKVTTHPLAKDKMMNGSHYSYSESRVEKDGLILTSRGPGTSFEFALAIVEALVGKDMANQVKAPLVLKD\*

>AtGlyIII1

MASSSLCHRYFNKITVTPFFNTKKLHHYSPRRISLRVNRRSFSISATMSSSTKKVLIPVAHGTEPFEAVVMIDVLRRGGADVTVASVENQVGVDACHGIKMVADTLLSDITDSVFDLIMLPGGLPGGETLKNCKPLEKMVKKQDTDGRLNAAICCAPALAFGTWGLLEGKKATCYPVFMEKLAACATAVESRVEIDGKIVTSRGPGTTMEFSVTLVEQLLGKEKAVEVSGPLVMRPNPGDEYTITELNQVSWSFEGTPQILVPIADGSEEMEAVAIIDVLKRAKANVVVAALGNSLEVVASRKVKLVADVLLDEAEKNSYDLIVLPGGLGGAEAFASSEKLVNMLKKQAESNKPYGAICASPALVFEPHGLLKGKKATAFPAMCSKLTDQSHIEHRVLVDGNLITSRGPGTSLEFALAIVEKFYGREKGLQLSKATLV\*

>AtGlyIII2

MASAVQKSALLLCGDYMEAYETIVPLYVLQSFGVSVHCVSPNRNAGDRCVMSAHDFLGLELTLNANFDDVTPENYDVIIIPGGRFTELLSADEKCVDLVARFAESKKLIFTSCHSQVMLMAAGILAGGVKCTAFESIKPLIELSGGEWWQQPGIQSMFEITDCVKDGNFMSTVGWPTLGHGIKLLLESLGGKVCSLEKKQASVLFLIGDYVEDYGINVPFRALQALGCKVDAVTPNKKKGEVCATAVYDLEDGRQIPAEKRGHNFFVTASWDDICVDDYDCVVVPGGRSPELLVMNEKAVALVKSFAEKDKVFAAIGQGKLLLAATGVLKGKRCASGKGMKVMVKVAGGEAVMEKGCVTDGKVVTAASATDLPAFLFDLSTALGLTVMF\*

>AtGlyIII3

MANSRTVLILCGDYMEDYEVMVPFQALQAFGITVHTVCPGKKAGDSCPTAVHDFCGHQTYFESRGHNFTLNATFDEVDLSKYDGLVIPGGRAPEYLALTASVVELVKEFSRSGKPIASICHGQLILAAADTVNGRKCTAYATVGPSLVAAGAKWVEPITPDVCVVDGSLITAATYEGHPEFIQLFVKALGGKITGANKRILFLCGDYMEDYEVKVPFQSLQALGCQVDAVCPEKKAGDRCPTAIHDFEGDQTYSEKPGHTFALTTNFDDLVSSSYDALVIPGGRAPEYLALNEHVLNIVKEFMNSEKPVASICHGQQILAAAGVLKGRKCTAYPAVKLNVVLGGGTWLEPDPIDRCFTDGNLVTGAAWPGHPEFVSQLMALLGIQVSF\*

>AtGlyIII4

MASFTKTVLIPIAHGTEPLEAVAMITVLRRGGADVTVASVETQVGVDACHGIKMVADTLLSDITDSVFDLIVLPGGLPGGETLKNCKSLENMVKKQDSDGRLNAAICCAPALALGTWGLLEGKKATGYPVFMEKLAATCATAVESRVQIDGRIVTSRGPGTTIEFSITLIEQLFGKEKADEVSSILLLRPNPGEEFTFTELNQTNWSFEDTPQILVPIAEESEEIEAIALVDILRRAKANVVIAAVGNSLEVEGSRKAKLVAEVLLDEVAEKSFDLIVLPGGLNGAQRFASCEKLVNMLRKQAEANKPYGGICASPAYVFEPNGLLKGKKATTHPVVSDKLSDKSHIEHRVVVDGNVITSRAPGTAMEFSLAIVEKFYGREKALQLGKATLV\*

>AtGlyIII5

MGSMAQKSVLMLCGEFMEAYETIVPLYVLQAFGVSVHCVSPGRKTGDKCVMAAHDLLGLEIYTELVVDHLTLNANFDGVIPDQYDAIIIPGGRFTELLSADEKCVSLVARFAELKKLIFTSCHSQLFLAAAGLLTGGMKCTAFESMKPFIELSGGAWWQQPGVQTLFEITDCVKDGSFMSTMGWPTLGHSLKVLLESLGSKISSSKENHQTSLLFLIGDCVEDYSINVPFKAFQALGCKVDAVTPTKKRGEKCATIVHDLEDGRQLPTEKFGHNFYVTVAWDDVSVDDYDCIVVPGGRSPELLVMNPKAVELVRKFVEKGKFVAAIGMGNWLLAATGALKKKRCASSYGTKVAVKVAGGEIVESERCVTDDKLVTAASTSDLPAFLYALSTALGLSVVF\*

>AtGlyIII6

MGSLGYSISMIASLSPTLMESRLISSMGCVSMTVAPSFSSVSVVSSSLGTTRRDRTLKLRSSMSPGMVTTLDSDVGVGSSATTKKVLVPIGYGTEEIEAVVLVDVLRRAGADVTVASVEQKLEVEGSSGTRLLADVLISKCADQVYDLVALPGGMPGAVRLRDCEILEKIMKRQAEDKRLYGAISMAPAITLLPWGLLTRKRTTGHPAFFGKLPTFWAVKTNIQISGELTTSRGPGTSFQFALSLAEQLFGETTAKSIEEFLLLRDGYQNPKNKEFNSIDWSLDHTPRVLIPVANGSEAVELVSIADVLRRAKVDVTVSSVERSLRITAFQGTKIITDKLIGEAAESSYDLIILPGGHTGSERLQKSKILKKLLREQHESGRIYGATNSSSTVLHKHGLLKEKRTTVYPSESDEPMNQQMIEGAEVVIDGNVITSLGLATVTKFSLAIVSKLFGHARARSVSEGLVHEYPRQ\*

>OsGlyIII1

MAAQASPPTKKVLVPIVAGTEPVEAAVPIDVLRRAGADVTVASADDGELVVEVMYGVRIVADALVAGGDCAAAHFDLIVLPGGVPGAANLGGCAALEAMVRRHAATGGLYAAICAAPPLALASWGMLNGLKATAHPLFVDKFPPEVAAVDASVVVDASAVTSRGPATSTEFALALVEQLYSKNKAEQIAKEMLVRYDAGYTIDEVNSVQWKCNGTPKVLVPVANGTEEMELITIIDVLRRADADVVVASAENAGVEIVARHGMRIVADTTLDEAAADDQTSSFDLIILPGGTPGAKTMSSNEKLVTLLKKQAAASKPYGAIGAATAHVLEPHGLLEGKKAADQDGGDECESRVVVDGNVITSGGTGTAMEFAVAAVEKLLGRDVAQRVAEGLLFA\*

>OsGlyIII2

MAMAAASASAMARRAASWPRLLLLSRAFAAAAAEPKRVLVPVADGTEPVEAAATADVLNRAGARVTVATADPAGDDRGLLVEAAFGVKLVADGRVADLEGEAFDLIALPGGMPGSANLRDCKVLEKMVKKQAEQGGLYAAICATPAVTLAHWGLLKGLKATCYPSFMEKFTAEIIPVNSRVVVDRNAVTSQGPATAIEYALALVEQLYGKEKSEEVAGPLYVRPQPGVDYVIDEFNSVEWKCSGTPQVLVPVANGSEEMEALNLIDILRRAGANVTVASVEDKLQVVTRRHKFNLIADIMVEEAAKREFDLIVMPGGLPGAQKLSSTKVLVDLLKKQAESNKPYGAICASPAYVLEPHGLLKGKKATSFPPMAHLLTDQSACDSRVVVDGNLITSKAPGSATEFALAIVEKLFGREKAVSIAKELIFM\*

>OsGlyIII3

MAPKKVLLLCGDYMEDYEAMVPFQALQAYGVSVDAACPGKKAGDSCRTAVHQGIGHQTYAESRGHNFALNASFDEVNINEYDGLVIPGGRAPEYLAMDEKVLDLVRKFSDAKKPIASVCHGQLILAAAGVVQNRKCTAYPAVKPVLVAAGAKWEEADTMDKCTVDGNLVTAVAYDAHPEFISLFVKALGGSVTGSNKRILFLCGDYMEDYEVMVPFQSLQALGCHVDAVCPDKGAGEKCPTAIHDFEGDQTYSEKPGHDFALTASFDNVDASSYDALVIPGGRAPEYLALNDKVISLVKGFMDKAKPVASICHGQQILSAAGVLQGRKCTAYPAVKLNVVLGGATWLEPNPIDRCFTDGNLVTGAAWPGHPEFISQLMALLGIKVSF\*

>OsGlyIII4

MLPSSRYLLAPAPLPAMVVRPPPPHPPSRGTSPLARPPLCRAMARAAPSLSAAASTAASSSTTPAKKKVLLPIAMGTEEMEAVILAGVLRRAGADVTLASVEDGLEVEASRGSHIVADKRIAACADQVFDLVALPGGMPGSVRLRDSVILQRITVRQAEEKRLYGAICAAPAVVLMPWGLHKRKKITCHPSFIEDLPTFRTVESNVQVSGELTTSRGPGTAFQFALSFVEQLFGPCKAEDMDNTLLTKVDDNLERSIEVNEIEWSSDHNPHVLIPIANGSEEMEIIMLTDVLRRANVNVVLASVEKSTSIVGSQRMRIVADKCISDASALEYDLIILPGGPAGAERLHKSSVLKKLLKEQKQTGRMYGGICSSPVILQKQGLLQDKTVTAHPSIVNQLTCEVIDRSKVVIDGNLITGMGLGTVIDFSLAIIKKFFGHGRAKGVANGMVFEYPKS\*

>OsGlyIII5

MATRPLAASTLLPPLRFCSPLKTPPPSPPPPHLRRLQTLTRALASSSSAMASPPAKKVLVPIASGTEPMEAVITVDVLRRAGADVSVASVDPGSAQVGGAWGVKLAADALLDDLADAEFDLISLPGGMPGSSNLRDCKLLENMVKKHAGKGKLYAAICAAPAVALGSWGLLNGLKATCYPSFMDKLPSEVNAVESRVQIDGNCVTSRGPGTAMEYSVVLVEQLYGKEKADEVAGPMVMRPQHGVEFSLKELNSTSWNVGETPQILVPIANGTEEMEATMIIDILRRAKANVVVASLEETLEIVASRKVKMVADVLLDDALKQQYDLILLPGGLGGAQAYAKSDKLIGLIKKQAEANKLYGAICASPAIALEPHGLLKGKKATSFPGMWNKLSDQSECKNRVVVDGNLITSQGPGTSMEFSLAIVEKLFGRERAVELAKTMVFM\*

>OsGlyIII6

MAPCKKVLMLCGDYMEDYEAAVPFYALAAFGVAVDCVAPGKKPPGDACLTAVHEFLGHDLYTELPGHRFAVTADFAAAAAADASRYDALVVPGGRFVERLSVDPLAVSLVAAFAGEGETATRRRPVVVTCHSQLLLAAAGAMRGVRCTAFFSMRRVVELAGGTWVEPDPLGLCVADGNVLSAIGWPAHGEIIRELLRAMGARVAGGRGQAVLFLCADYVDDYEANVPFRALAGVGCRVEAACPTKRKGEACVTAIYDATPAAASDERRGHNFAVTADWGDVDADRYACVVVPGGRAPELLATRGEAVALVREFAGKGKVVASIDQGHLLLAAVGLLDGRSCASGVATRVVAGLAGAASVRHGGAVADGKLVTAASWPDLAEFIAHIISLLGITVSF\*

>BrGlyIII1

MIASLSPTLTEPMLISSMGSISAIVTSPSLYSISLIHSPIKQRKAQSLRLRASSASLSIDVDVVTIPKKVLVPIGYGTEEIEAVVLVDVLRRAGADVTLASVEQKLEVEGSSGTKLLADVLISKCSEQVFDLVALPGGMPGAVRLRDCGALEKIMKRQAEEKRLYGAISMAPAITLLPWGLLTRKKTTGHPAFFGKLPTFWAVQTNIQISGELTTSRGPGTSFQFALSLANQLFGETTAKSVGELLLLRDGFQNPEIKEVNSIDWSLNHTPRVLMPVANGSEEVEVVTISDVLRRAKVDVTVASVERSLRITASQGTKIVTDKLIGEAAESAYDLILLPGGRAGSERLQKSKFLKKLLKEQQEAGRIYGATNSASTVLHKHGLLKEKRTAVYVSDTDGPASDQMIEGAEVVIDGNVITSLGLATVTNFSLAIVSKLFGHGRARSVSEGLVHEYRGNLKAS\*

>BrGlyIII2

MASSRKKVLIPIAHGTEPLEALAMITVLRRSGAYVTVASVENQVGVDACHGIKMVADTLLSDITNSTFDLIMLPGGLPGGETLKNCKPLENMVKKQETDGRLNAAICCAPALALGTWGLLEGKKATCYPVFMEKLAATCGTASESRVEIDGKIVTSRGPGTTIEFSLTLIEKLCGKQTAVDVSSILLPRPNPGEEFTFTELNQINWTFEDTPQILVPIAEGSDEIEAISVVDILRRAKANVVIASVSNSLEVVGSHKANLVADVLLDEVLEKSFDMIMLPGGLNGASRLSRSEKLVNMLKKQAEANKPYGGICASPAYVFEPHGLLKGKKATTHPVVSNRLSDQSHVDHRVVVDGNLITSRAPGTAMECALAIVEKFYGREKALQLAKATLV\*

>BrGlyIII3

MAPSTKTVLIPIAHGTEPLEAVAMITTLRRGGADVTVASVETQVGVDACHGIKMVADTLLSDITDSIFDLIVLPGGLPGGETLKNCKPLENMVKKQDTDGRLNAAICCAPALALGTWGLLQGKKATGYPVFMEKLASTCATAVESRVQIDGRIVTSRGPGTTIEFSITLVEQLCGKEKADEVSSILLVRPNPGEEYTFTELNKTEWLFEDTPQILVPIAEDSEETEAIALVDILRRAKANVVIAAIGNSLEVVGSCEAKLVADVLLDEVAEKSFDLIVLPGGNGAQRFASCEKLVNMLNKQAEANKPYGGICKSPVYVFEHNGLLKDKKATTHPRVSNELSDQSHIDHRVVVDGNVITSRAPGTAMEFSLAIVEKFYGREKALQLAKATLV\*

>BrGlyIII4

MGSSSVQKSALLLCGDYMEAYETLVPLYILQSFGVSVHCVSPNRNSGDRCVMAAHDFTGLELYTELVVDQLTLTASFDDVTPDNYDAIIIPGGRFTEILSADERCVDLVARFAELKKLIFTSCHSQVMLMAAGALAGGVKCTAFESMKTLIEFSGGEWWQQPGIQSMFEITDCVKDGNVVSTVGWPTLGHGVRVLLESLGGQVSSLKENQVSVLFLIGDYVEDYGINVPFRALQALGCKVDAVTPNKKKGEMCATLVYDLEEARQLPAEKRGHNFLVTACWDDVCVDDYDCVVVPGGRSPELLVMNPKAVALVKKFDEKDKVFAAIGQGKLLLAATGVLKGKRCASGKGMKVMVKVAGGEAVVSKGCVTDGKLVTAASASDLPAFLSGLSSALGVSVMF\*

>BrGlyIII5

MASSTKTVMIPIAHGTEPLEAVAMITVLRRGGADVTVASVEDKVGVDACHNIKMVADTILSDITDSIFDLIVLPGGLPGGETLKNCKPLENMVKKQDTDGRLNAAICCAPALALGTWGLLEGKTATGYPVFMEKLAATCATASESRVEIDGRIVTSRGPGTTIEFSITLIEQLFGKDKADEVSSGLLVRPNPGEEFTFTELNQTNWSFQDTPQILVPIAEDSEEIEAIALVDILRRAKANVVIAAVGNSLEVVGSRKAKLVADVLLDEVAEKSFDLIVLPGGLNGAPRLASCEKLVNMLKKQAEANKPYGGICASPVYVFEPHGLLKGKKATTHPCVSNKLSDQSHIEHRVVVDGNVITSRAPGTAMEFSLAIVEKFYGREKALQLAKATLV\*

>BrGlyIII6

MANSRTVLILCGDYMEDYEVMVPFQALQAFGVSVHTVCPGKKSGDSCPTAVHDFCGHQTYSESRGHNFTLNATFDEVDLTKYDGLVIPGGRAPEYLSMNASVVDLVKQFSSSGKPIASICHGQLILAAADTVNGRSCTAYATVGPALIAAGAKWVEPVTPDVCVVDATYEGHPEFIQLFVKAMGGKITGANKRILFLCGDYMEDYEVKVPFQSLQALGCQVDAVCPEKKAGDRCPTAIHDFEGDQTYSEKPGHTFGLTAAFDGVDSSSYDALVIPGGRAPEYLALNQHVLNVVKEFMNSGKPVASICHGQQILAAAGVLKGRKCTAYPAVKLNVVLGGGSWLEPDPIHRCFTDGNLVTGAAWPGHPEFVSQLMLLLGVQVSF\*

>BrGlyIII7

MASPTKKVLIPVAHGTEPFEAVVMIDVLRRGGADVTVASVENQVGVDACHGIKMVADTLLSDVTDSVFDLIMLPGGLPGGETLKNCKPLENMVKKQNSDGRVNAAICCAPALALGTWGLLEGKKATCYPVFMEKLGATCATAVESRVEIDGRIVTSRGPGTTMEFSVALVEQLFGKEKAAEVSAPLVMRPNPGDEYTTTELNQIKWSYENTPQILVPIADGSEEMEAVAIIDVLRRAKANVVVAALGNSLEVVASRKVKLVADVLLDEAEKNSYDLIVLPGGLGGAEAFATSDKLVNMLKKQAESNKPYGAICASPALVLEPHGLLKGKKATAYPAMCNKLSDQSHIEHRVLVDGNLITSRGPGTSLEFALAIVEKFYGREKGLQLAKATLV\*

>BrGlyIII8

MGSMAQKSVLMLCGEFMEAYETIVPLYFLQAFGVSVHCVSPGRKTGDKCVMAAHDLLGLEIYSELVVDHLTLNANFHEVIPEQYDAIIIPGGRFTELLSTDEKCVSMVARFAELGKIILTSCHSQLLLAAAGILGRGMKCTAFESMKPLIELSGGSWWQQPGVQTLFDITDCVMDGKFISTLGWPTLGNTLRILLESIGSKITCCKETQPSLLFLIGDCVEDYSINVPFKAFQALGCKVDAVSPNKKKGDKCATIVHDLEEGRQLPTEKFSHNFYVTVAWEDVSVDDYDCIVVPGGRSPELLVMNDKAVGLIKKFVEKGKFVAAIGMGNWLLAATGALKKKRCASGYGTKVAVKVAGGQILESEQCVTDDKLVTAATTSDLPAFVHALSTALGLSVVF\*

>BrGlyIII9

MAFHCLNPITATPFSSTRLHRSTWRRTSRSFSVSATMASPAKRVLIPVAHGTEPFEAVAMIDVLRRGGADVTVASVENQVGVDACHGIKIVADALLSDVNDSVFDLIMLPGGLPGGETLKNCKPLENMVKKQDSEGRLNAAICCAPALALGTWGLLEGRRATCYPVFMEKLGATCGTAVESRVEVDGRIVTSRGPGTTMEFSVTLVEQLFGKEKAAEVSAPLVMRPNPGDEYTITELNQMNWSFDSTPQILVPIADGSEEMEAVAIIDFLRRAKANVVVAALGNSLEVVASRKVKLVADVLLDEAVKNSYDLIVLPGGLGGAEAFASSEKLVNMLKKQAESSKPYGAICASPALVFEPHGLLKGKKATAFPAMCNKLSDQSHIEHRVLVDGNLITSRGPGTSLEFALTIVEKFYGREKGLQLAKATLV\*

>BrGlyIII10

MVSLGVSLSMIASLSPPSTMVAPSLYSASFISSPVLVPIGFGTEEIEVVVLVDVLRRAGAEVTLVSVEQKLEVEGSSGTKLLADVLISKCSEQVFDLVPLPGGMSGAVRLNCVTLEKIMKRQAEDKRLYRAISMAPAITLFPWGLLTRKKTTGHPAFFGKLPTFWAVKTTFRSQGSLQLAVDQALCSEEVEVVTVADVLRRAKVDVTLIGEAAESSYDLIILPKLLKEEQEAERIYGATNSSSTVLHKHGLLKEKRTVVYLSDTDMPVDDQMIQGAEVDGNVITGLGLATVTYFSLSIGGKLFGHGRPRSVSQGLVHEYQWNLKAS\*

>PpGlyIII1

MAKCKAVLMIIGDYVEDYEVMVPFQALLAYGLKVDAVCPGKKAGETCATAIHDFLGHQTYSESKGHNFALTANFEDVDADSYDALVVPGGRAPEYLSLDENVLNLVKKFESAHKPIASICHGQLILAAAGVLKDKQCTAYPAVKPVVVAAGGIWKDPSPISACFTDGKLVTGAAWPGHPEFLKQTLAALSATVQGGDKKVLMLCGDYMEDYEAMVPFQAMQALGYQVDAVCPDKKSGDTCATAVHDFEGAQTYSEKPGHNFALTATFSEVKVQDYDALVVPGGRAPEYLSLNEKVLDLVREFDDAKKPIASICHGQQILAAAGVLKGKKCTAYPAVKSHVVLSGGQWLEPEPISKCFTDGHLVTGAAWPAHPEFVAQLMALLGTAVTF\*

>PpGlyIII2

MEGQVGAGKRILILATSHDKLGNTNQATGCWAEELTAPYYIFKDAGAHVDVASIKGGKIPMDEASFSEGFVTDHVKRYLEDEELKQRVEHSLSVKDVSGNYDALFVPGGHGIIYDGPVDQDFIALGNRFWAEGKIISSVCHGPAGLVGMTAPDGTSIFKGKKVCGFSNAEEEAVGKTNVVPFLLEDKLKELGGLYEAGPNWHPKAAADGQLVTGQNPGSSAKVAELVLEALSK\*

>PpGlyIII3

MEPMRVTRMLQVAIVIFPNITVLDFIGPYEPLNRLPNVNVVLVSHSKGIIRAEKSLIGFEATATFDEVQEPDIVIVPGGYGVNALIRDKPILDWIRKTHEKTLYTTSVCTGSLLLAAAGILNGLEATCHWRVLPELSKFGAKPTSSRIVESGKIITAAGVSAGIDMGLKLVALLSNDTTCKLIQLVIEYDPQPPFDCGSPAAAGPELVSMARAYAEKNYPDYFIF\*

>PpGlyIII4

MAAMAISVLPIVSGLLPCLVLRVIEGQSRRDICNLSSALCPVSESLQFERSQAWCRTKVKESSRRSRRVDARVVMAQANSAMEKSPAKKQVLVPVANGTEEMEAVIVIDVLRRAGAAVTVASVEEGKLVNASRGVNLLADCLISECEGVEYDLVVLPGGMPGAERFRDSQVLKRITVKQSQEKRMFAAICAAPVVALQSWGLLAGLNATCHPGFAVKLEDKSSVGGRVVRDGALTTSRAPGTAFEFALALIEQLYGPESVPAVADPMVLPSHDGIVSAALKFNDEDWTTSSIPRVLVPVANGSEEMEVVIIVDILRRAGAEVVVASVESETTIKASRNVQLVADTLVSEIVQTKFDLVVLPGGMPGATRLQESEELSKILNQQVESGRCYGAICAAPAVVLEANGLLNGKKATSHPAFSSILKDQSAVEGRVVIDGRLITSRGPGTAMEFTLNIVEKLFSRSKAQEVAEPMVFNYV\*

>PpGlyIII5

MDIHTMATKINPATELAPAENKKKVLVPVANGTEEMEAVIVINVLRRAGATVTVASVEEGMQIAASRGVNIVADCLISECEEQEYDLVALPGGMPGAERLRDSKALKSIAEKQVKAKRMIAAICAAPVVALQAWGLLKGLHATCHPSFTGKLEDKAAVESRIVRDSILTTSRAPGTAFEFALALVEQLYGPENLPTVSGPMVLPPDDGTDARALKFNDQEWSTSSTPQVLVPIVNGSEETEVVIIVDILRRAGAKVVVASVESEATIKAARNVQLVADTLISEVANTKFDLVVLPGGMPGADRLQKSKELMRILQEQAEEGRIYGAICAAPAVILESSGLLHGYCGELRSSGI\*

>PpGlyIII6

MMLEKAKLQKSGGKNMKLVIRADAPLMLQGLIEPLKRLGIWSDQKHAEGIAAGWRLQEQAQKWKAECPDAAWDEAQWAAEEAALLKIMAHCPPDRQTASWFLQRLLVPADMPLSVLELLTGWEIREKAQWRSDSISLHAILWLKEIGAKPMPQLYGTLLRIERGDDLAVLVMDEETTGETEIPTLWEHRDHSVEHVDEGMLIMQVNLDDSSPEWLAYVLEQCMRAGANDVHFLPVTMKKSRPGTLLQVMCYQSAAEAIKTILFSETTTFGIRTFPVACHRLARRFATAQTQWGEVQVKLGYHRGKRVQVAPEYAVCAQLAEAAQVPLKQMSKKVLIVTGDAVEALEVFYPYYRCLEEGFETVIAAPNVKTLHTVLHDFEAHSETYTEKPAYQLAAHASFAEINPEAFDALIIPGGRAPEHIRLNEHLKPIVAHFFEANKPVAAICHGAQVLTIVREYIAGKEMTAYQACRPDVEACGAIYQTETLHVDGNLVSGHAWPDLPGFMREFLKLLR\*

>PpGlyIII7

MRYLPALSVNDIVVDEYAALVIPGGSPHPLLQNQELIKVIRAFYDQEKLLAAICGGPSLLGAAGILQEIAYTASLEPTDLEYRDVMNWENKRSELLVIDKNVITATGSNYLHFAEEVLRKLGAVLPTEENPLQYFREPSLS\*

>PtGlyIII1

MANCKPRKKVLLLCGDYMEDYEAMVPFQALQAYGIAVDAVCPGKKAGDYCRTTVGDSGAYHGYQTYTEKPGHNFSLNATFDEVDFSKYDALVIPGGRAPEYLAMNESVLNCRKCTAYRALGPVLIDAGALWIEPKTMMDCVSDGNLITGVIYKAHPEYIQLVVKALGGKIAGSDKRILFLCGDFMEDYEVTVPLQSLQALGCHVDAVCPKKKAGDFCPTAVHDFEGDQTYTEKPGHNFILTASYEGLDASSYDALVIPGGRSPEYLALDETVIALVKKFMQSKKPVASICHGQQILAAAGVLKVVSNVFFHFHRITQVIIFFTLAILILVYVNHVAAGKKVHRIPCCEAERRLGRGNMARTGSNRSLLHRRKPGYRSCMARAPSVCVSADGLTWYPSVILAVLLQ\*

>PtGlyIII2

MANCKPQKKVLLLCGDYMEDYEAMVPFQALQAYGIAVDAVCPGKKAGDYCRTTVEDSGAYHGYQTYTEKPGHNFSLNATFDEVDFSKYDALVIPGGRAPEYLAINESVLNCARQFSDSGKLIAAICHGPLILAAAGLLKGRKCTAYHALGPVLIDAGALWIEPKTMMDCVSDGNLITGVIYKAHPEYIQLVVKALGGKIAGSDKRILFLCGDFMEDYEVTVPLQSLQALGCHVDAVCPKKKAGDFCPTAVHDFEGDQTYTEKPGHNFILTASYEGLDASSYDALVIPGGRSPEYLALDETVIALVKKFMQSKKPVASICHGQQILAAAGVLKGRKCTAYPAVKLNVVLGGATWLEPDPIDRCYTDENLVTGAAWPGHPQFVSQLMALLGIRVSF\*

>PtGlyIII3

MANCKPQKKVLLLCGDYMEDYEAMVPFQSLQAYGIAVDAVCPGKKAGDYCRTTVGDSGAYHGYQTYTEKPGHNFSLNATFDEVDFSKYDALVIPGGRAPEYLAINESVLNCARQFSDSGKLIAAICHGPLILAAAGLLKGRKCTAYHALRPVLIDAGAHWIEPKTMMDCVSDGNLITGVIYKAHPEYIQLVVKALGDKIAGSDKRILFLCGDFMEDYEVTVPLQSLQALGCHVDAVCPKKKAGDFCPTAVHDFEGDQTYTEKPGHNFILTASYEGLDASSYDALVIPGGRSPEYLALDETVIALVKKFMQSKKPVASICHGQQILAAAGVLKGRKCTAYPAVKLNVVLGGATWLEPDPIDRCYTDENLVTGAAWPGHPQFVSQLMALLGIRVSF\*

>PtGlyIII4

MESMLCLLSPSPTKLSPFKKLTSTCALKTTFSSLSFASMTSPPQPKTPSTKKLSSSKPTKTLSPKTPTTSTSVQETSTPFSPPLKKVLVPIGFGTEEMEAVIIVDVLRRAGAEVIVASVEPQLEVEAAGGTRLVADTSISKCANEVFDLVALPGGMPGSARLRDCEVLRQITSKQAEDKRLYGAICAAPAITLLPWGLLRRKQMTGHPAFMDKLPTFWAVASKIQVSGELTTSRGPGTSFEFALSLVDQLFGESVAKEVGQLLLMQADDDTQRKEEYNKVEWSFDHNPRVLLPIANGSEEIEIVAIVDILRRAKVDVVVASIEKSVQILASRGIKIVADKLIGDAAESVYDLIILPGGNAGAERLHKSKVLKKLLQEQYTAGRIYGAVCSSPAVLHRQGLLKDKRATAHPSVVTNLNNVSNGAKVVIDGKLITSKGLSTVTDFALAIVSKLFGHARTRCVAEGLVFDYPRS\*

>PtGlyIII5

MSILLRHVIPPPHSVLYSTSEKSKLNFPSFRNPRFSFSSIKATAATPMASTTKKVLVPIANGTEPIEAVITIDVLRRGGADVTVASIEKQIRVDATYDVKLVADSLLSECSDAVFDLITLPGGIPGATNFKNCQLLEKLVKKQVEDGKLYAAVCASPAVAFGSWGLLNGLKATCHPFFMDELKSSGAITVESRVHEEGNVVTSRGPGTTMEFAVALVEKLFGKEKADEVSGPLVMRSNHGDEYSIKELNPMQWTFDNVPQVLVPIANGTEEMEAIIIIDILRRAKVNVVVASVEDSLEILASRKVKLEADMLLDEAAKLSYDLIVLPGGLGGAQAFAKSEKLVNMLKKQRESNRPYGAMCASPALVLEPHGLLKGKKATAFPAM\*

>PtGlyIII6

MANCKPQKKVLLLCGDFMEDYEAMVPFQALEAYGIAVDAVCPGKKAGDCCRTVIQDSGAYHGYQTFTEKLGHNFSLNANFDEVDFSKYDGLLLPGGRAPEYLAINESVLDCVRKFSDSGKPIGSICHGHLILAAAGSVKGRKCTALHALGPVLIDAGAHWIEPKTRMDCVADGNIITGVIYRAHPEYIRLFVRALGGKVTGSDKRILFLCGDFMEDYEVTVPFQSLQALGCHVDAVSPKKKAGDICPTAVHDFEGDQTYSEKPGHNFILTASYEGLDASTYDALVIPGGRAPEYLALDETVIALVKEFMQSRKPVASICHGQQILAAAGVLKGRKCTAYPTVKLNVVLGGATWLEPDPIDRCYTDENLVTGAAWPGHPEFVSQLMALLGIQVSF\*

>StGlyIII1

MASATKKVLVPIAIGTEPIEAIVPIDILRRAGAEVIVASVENQLQIEVMYGIKIVADALISDCVDTEFDLISLPGGVPGAANLGNCKILESIVKKQAENGKLYAAICAAPAVALGSWGLLKGLKATCYPSYMEELSSHAIAVESRVQKDAKVVTSRGPATSIEYAVALVEELYGKEKANEVSGPLVMRPNHSEEFAFADLNSVNWTLTSKPRILVPIANGSEEMEATIIIDVLRRANAQVVVASLEDKLEIVASRKVKLVADVLLDEAAKQSYDLIVLPGGLGGAETFAKSEKLVDMLKKQRESSKPYGAMCASPALVLEPHGLLKGKKATAFPALCNKLSDPSEAENRVVVDGNLVTSRGPGTTMEFALAIADKFIGHKETLELAKEMIF\*

>StGlyIII2

MANQKRVLLLCGDYVEDYEVMVPFQALLAYGVAVDAVCPGKKSGDICRTAVHQLSGHQTYSESRGHNFALNATFDEIEASKYDGLFIPGGRAPEYLAMNESVLDLVKSFANAKKPIVAICHGQLILAAADVVSGRRCTAYPAVKPVLVAAGAHWEEPETLASCTIDGNLITGSTYEGNPEFIRLFVKALGGSIVGSGKRILFLCGDFMEDYEVKVPFQSLQALECHVDAVCPKKKAGEKCPTAVHDFEGDQTYSEKPGHDFTLNANFESVDVSSYDGLVIPGGRAPEYLALDDDVIKLVQEFMESKKPVASICHGQQILSAAGVLKGKKCTAYPAVKLNVILGGATWLEPEPIDRCFTDGNLVTGAAWPGHPEFISQFMALLGVHVKF\*

>StGlyIII3

MANQKRVLLLCGDYVEDYEVMVPFQALLAYGVAVDAVCPGKKSGDICRTAVHQLSGHQTYSESRGHNFALNATFDEIEASKYDGLFIPGGRAPEYLAMNESVLDLVKSFANAKKPIVAICHGQLILAAADVVSGRRCTAYPAVKPVLVAAGAHWEEPETLASCTIDGNLITGSTYEGNPEFIRLFVKALGGSIVGSGKRILFLCGDFMEDYEVKVPFQSLQALECHVDAVCPKKKAGEKCPTAVHDFEGDQTYSEKPGHDFTLNANFESVDVSSYDGLVIPGGRAPEYLALDDDVIKLVQEFMESKKPVASICHGQQILSAAGVLKVSISVNII\*

>StGlyIII4

MKSISPLFSVSTAKSPIFYFSPISQRLSSVKFAAPPKINSPDTKRPSSKSVKTLSAAPTIDPITTTAASASPKKVLVPIGFGTEEMEAVILADVLRRAGAEVTVASVEQQLEVEAYGGTRLVADTFISTCSTEIFDLVALPGGMPGSARLRDCEVLQKITSRQAEEKRLYGAICAAPAVTLLPWGLLKRKQTTCHPAFIDKISSFRVVKTNTRVSGELTTSRGPGTSFEFAICLVEQLFGEPVAREIGELLLMNPAGDDPKRQEFNEVGWSLDRTPQVLIPIANGSEEIEVVTLIDILRRAKVNVVVASVEKSAQVLASKGTKIVADKLINATSDSIFDLIILPGGAAGAERLHKSKILKKLLKEQESAGRIFGAICSSPAVLQKQGLIKDKKATAHPAVLDKLKDGVNDAQQKVLSISTPRARNASPETLRVPKYVKGATQIDGLHTYFTGNYKKGNFLVLDDLVADITSSRGDFPKISPNLQYRVPTRSLTGIREFTITRPGRIGNRDDQSNDASYGQIVLRLISVSSGHYIAPPAHKFLFFV\*

>StGlyIII5

MKSISPLFSVSTAKSPIFYFSPISQRLSSVKFAAPPKINSPDTKRPSSKSVKTLSAAPTIDPITTTAASASPKKVLVPIGFGTEEMEAVILADVLRRAGAEVTVASVEQQLEVEAYGGTRLVADTFISTCSTEIFDLVALPGGMPGSARLRDCEVLQKITSRQAEEKRLYGAICAAPAVTLLPWGLLKRKQTTCHPAFIDKISSFRVVKTNTRVSGELTTSRGPGTSFEFAICLVEQLFGEPVAREIGELLLMNPAGDDPKRQEFNEVGWSLDRTPQVLIPIANGSEEIEVVTLIDILRRAKVNVVVASVEKSAQVLASKGTKIVADKLINATSDSIFDLIILPGGAAGAERLHKSKILKKLLKEQESAGRIFGAICSSPAVLQKQGLIKDKKATAHPAVLDKLKDGVNDAQVVIDGKLITSQGLATAIQFALAIVSKLFGHARARSVAEGLVYQYPKS\*

>StGlyIII6

MPGSARLRDCEVLQKITSRQAEEKRLYGAICAAPAVTLLPWGLLKRKQVTIAFSL\*

>ZmGlyIII1

MAAAAASSVARRAASRGGQFIARAFASGVGGGGEKAKRVLVPVAAGTEPIEAATTADVLNRAGARVTVATADPPGDDGLLVQAAYGVKLVADGRVADLQGEPFDLIALPGGMPGSVGLRDCKALEKMVKTHAEDGGLYGAICAAPAVTLAYWGMLKGLKATCYPSFMEKFTAEVIPVDSRVVVDRNAITSQGPGTAVEFALALVEKLYGKEKMEEVAGPLYLRPQHGVEYTIEELNSVEWKCGSTPQVLVPVANGSEEIEAVNLIDVLRRAGANVIVASVEEKLQIVTRRHKFNLIADMMLDEAIKMQFDLIVMPGGLQGAQKFASTKQLVDLLKKQAESNKPYGAICASPAHVLEPHGLLKGKKATAFPPMSHLLTDQSACEHRVVVDGNLITSRAPGTATEFGLAIVEKLFGRDKAVSIAKELIFM\*

>ZmGlyIII2

MATRSLTSALPLSRTPRVPSHRPSLRRLQTLTRALTSSSPQAMASSPTPKKVLVPIANGTEPMEAVITIDVLRRAGADVAVASVEPGATSVAASWGIKLTADALLADLADDEFDLISLPGGMPGSSTFGECKVLEKMVKKHVEKGKLYAAICAAPAMTLGTWGLLNGLKATCYPSFIDKLPSEVHAVESRVQIDGKCMTSRGPGTAMEYSVILVEQLYGKEKAKEVAGPMVMRPQHGVEFSMKEVNSTSWNVGETPNILVPIANGTEEMEATMILDILRRAKANVVVASLEDKLEIVASRKVKMIADVLLDDALKEQYDLILLPGGLGGAEAYAKSDKLMDLIKKQAAANRLYGAICASPAIALEPHGLLKGKKVTSYPAMWNKLADQSECNNRVIVDGNLITSQGPGTSMEFSLAIVEKLFGRERALELAKSMVFI\*

>ZmGlyIII3

MAAKKVLMLCGDYMEDYEVMVPFQALQAYGVSVDAVCPSKKAGDICRTAVHQLTGHQTYSETKGHNFTLNASFDEITASEYDGLVIPGGRAPEYLAMDEKVLDLVRMFSGAKKPIASVCHGQLILAAARVVENRTCTAFPAVKPVLVAAGAKWEEPDTMAKCTVDGNLITAATYNSHPEFISLFVKALGGSVAGSDKRILFLCGDYMEDYEVMVPFQALQALGCHVDAVCPDKGAGETCPTAIHDFEGDQTYSEKPGHDFTLTASFGSVDASSYDALVVPGGRAPEYLALNDKVISLVKAFAESGKPIASICHGQQILSAAGVLKGKKCTAYPAVKLNVLLGGGTWLEPDPIHRCFTDGNLVTGAAWPGHPEFVSQLMALLGVKVSF\*

>ZmGlyIII4

MASPAAVKKVLVPIAAGSEPAEAFVPIAVLRRAGADVTVAAAGAGTGLRVHAMYGVTVVADASVADCADASYDLVVLPGGVPGADNLGGCAALEGIVRRHALGGGLCAAICAAPPLALARWGLLDGVKATAHPEFVDKFPAEVAGVDANVVVDGRVVTGRGPAAAMEFALALVDQLYGKGKVDEIAKPMMVRYEPGYAFEELNPVQWRCSGTPRVLIPVANGSEEMEVLVTVDVLRRAKADVVVASAEEVVVARHGTRIVADALLQDAAGQQFDLIVVPGGMPGVKTTLADKVELMALLKEHAAAGRAYGAIGAATAQVLEPHGLIGGSMKATTCASRADRPSECGSRVVVDGNLATSGSTGTAMEFALAVVEKLLGPEAAREVAEALLFV\*

>ZmGlyIII5

MAAAAASSVARRAASRGGQFIARAFASGVGGGGEKAKRVLVPVAAGTEPIEAATTADVLNRAGARVTVATADPPGDDGLLVQAAYGVKLVADGRVADLQGEPFDLIALPGGMPGSVGLRDCKALEKMVKTHAEDGGLYGAICAAPAVTLAYWGMLKGLKATCYPSFMEKFTAEVIPVDSRVVVDRNAITSQGPGTAVEFALALVEKLYGKEKMEEVAGPLYLRPQHGVEYTIEELNSVEWKCGSTPQVLVPVANGSEEIEAVNLIDVLRRAGANVIVASVEEKLQIVTRRHKFNLIADMMLDEAIKMQFDLIVMPGGLQGAQKFASTKQLVDLLKKQAESNKPYGAICASPAHVLEPHGLLKGKKATAFPPMSHLLTDQSACEHRVVVDGNLITSRAPGTATEFGLAIVEKLFGRDKAVSIAKELIFM\*

>ZmGlyIII6

MLSPWHPLLSPVAPPAMELRSPLNSHNCSLTSSIRPPPPRSLARAPPTLSATAAAVSSLSATSAAISSPSCPKKKVLVPIAMGTEEMEAVIIAGVLRRASADVTLASVEDGLEVEASCGSRIIADTHIASCADQVFDLVALPGGMPGSVRLRDSDILQRITVRQAEEKRLYGAICAAPAVVLVPWGLHRRKKITCHPSFIGDLPAFRAVESNVQVSGELTTSRGPGTTFQFALSFVEQLFGLRAAEDMDKILMAQTHDGLERSAEVNELEWSCGRNPDVLIPIANGCEELEIIILVDILRRAKINVVLASVEKYPAVLGSQRMKIVADKSIMSASDSIYDLIILPGGPAGAEQLHRSRILKKLLKQQMQAGRMYGGVCSALKVLQQEGLLEDKTVTAHHAVASELTCQVIDQPNVVIDGNLITGKGLGTVVDFALAIIRKFFGHGRAKAVANGIVFEYPKS\*

>ZmGlyIII7

MASPAAVKKVLVPIAAGSEPAEAFVPIAVLRRAGADVTVAAAGAGTGLRVHAMYGVTVVADASVADCADASYDLVVLPATAHPEFVDKFPAEVAGVDANVVVDGRVVTGRGPAAAMEFALALVDQLYGKGKVDEIAKPMMVRYEPGYAFEELNPVQWRCSGTPRVLIPVANGSEEMEVLVTVDVLRRAKADVVVASAEEVVVARHGTRIVADALLQDAAGQQFDLIVVPGGMPGVKTTLADKVELMALLKEHAAAGRAYGAIGAATAQVLEPHGLIGGSMKATTCASRADRPSECGSRVVVDGNLATSGSTGTAMEFALAVVEKLLGPEAAREVAEALLFV\*

>TaGlyIII1

MKGSANLGDCKQLEKMVRKHTQSGRLCAAIGAAPAMVLARWGVLKGFTATCHPALLGRLGDDDGVIAVDDRVVKDRNVVTSQGVGTAIEFALELVEQLYGELKAHEVAGPLYMRPQQGVKYSIQEYNQIQWKCTGTPRVLVPVANGSEEMEALNLIDVLRRAGARVTVASVEDTPRIVTRHYKLNLITDVMLEQAAEMEFDLIVMPGGLPGALKFTSSEKLVGMLKKQAESGRPYGAICASPAYVLEPHGLLKGKKATSFPPMAHLLTDQSACEYRVVVDGNLITSRAPGTATEFALAIVEKLFGEEKAVALAKELVFM\*

>TaGlyIII2

MAAKRVLLLCGDYMEDYEAMVPFQALQAYGVSVDAVCPGKKAGDACPTAVHKPIGHQTYAESKGHNFALNASFDEVDAAAYDGLVIPGGRAPEYLAMDEKVLALVRKFSDAKKAIASVCHGQLILAAAGVVRDRTCTAYPAVKPVLVAAGAKWVEADTMKKCVVDGNLVTAAAYDGHPEFISLFVKALGGSVAGADKRILFLCGDYMEDYEVMVPFQALQALGCHVDAVCPDKGAGDKCPTAIHDFEGDQTYSEKPGHDFALNASFDSVDASSYDALVIPGGRAPEYLALNEKVLSLAKGFMDKGKPVASICHGQQILAAAGVLEGRKCTAYPAVKLNVVLGGGTWLEPDPIHRCFTDGNLVTGAAWPAHPEFVAQLMALLGIKVSFT\*

>TaGlyIII3

MALSWHIAPAARSVPSKGEASRVHSVQACWLAWTLELGEIRSVSRARWGVSAAMAARRVLLLCGDYMEDYEAMVPFQALQAYGVSVHAACPGKKAGDACPTAVHKPVGHQTYAESKGHNFALNASFDEVDAAGYDGLVIPGGRAPEYLAMDEKVLDLVRKFSDAKKPIASVCHGQLILAAAGVVRDRTCTAYPAVKPVLVAAGAKWVEADTMKKCVVDGNLVTAAAYDGHPEFISLFVKALGGSVAGSDKKILFLCGDYMEDYEVMVPFQALQALGCHVDAVCPDKGPGDKCPTAIHDFEGDQTYSEKPGHDFPLNASFDGVDASSYDALVIPGGRAPEYLALNEKVLSLAKGFMDKGKPVASICHGQQILAAAGVLQGRKCTAYPAVKLNVVLGGGTWLEPDPIHRCFTDGNLVTGAAWPAHPEFVAQLMALLGIKVSFA\*

>TaGlyIII4

LLKGKKVTAFPPMAHLLTDQSLCENRVVIDGNLITSRAPGTATEFALAIVEKLFGREKAVSIAKEFVFM\*

>TaGlyIII5

MAAKRVLLLCGDYMEDYEAMVPFQSLQAYGVTVDAVCPGKKAGDACPTAVHKPIGHQTYAESKGHNFALNASFDEIDAAGYDGLVIPGGRAPEYLAMDEKVLALVRKFSDAKKPIASVCHGQLILAAAGVVRDRTCTAYPAVRPVLVAAGAKWVEADTMKKCVVDGNLVTAAAYDGHPEFISLFVKALGGSVAGADKRILFLCGDYMEDYEVMVPFQALQALGCHVDAVCPDKGPGDKCPTAIHDFEGDQTYSEKPGHDFALNASFDGVDASSYDALVIPGGRAPEYLALNEKVLSLAKGFMDKGKPVASICHGQQILAAAGVLQGRKCTAYPAVKLNVVLGGGTWLEPDPIHRCFTDGNLVTGAAWPAHPEFVAQLMALLGIKVSFA\*

>TaGlyIII6

MMLDEAAKMEFDLIVMPGGLSGAQKFASTDKLVDLLKKQAGSGKAYGAICASPAHVLEPHGLLKGKKATAFPPMAHLLTDRSLCENRVVIDGNLITSRAPGTATEFALAIVEKLFGREKAVSVAKEFVFM\*

>TaGlyIII7

MPGSVNLRECKVLERMVKMHAEKGGLYGAICAAPAVTLAHWGMLKGLKATCYPSFMEKFTAEVIPVNSRVVVDRNVVTSQGPGTAIEFALALVEQLYDKEKMEEVAGPLYVHPQHGADYTIEELNSVEWKCSGTPQVMIVH\*

>TaGlyIII8

MLVRYECGYSMKEVNSVEWHCSGTPKVLLPLANGIEEMEAIILVDALRRAKADVVVASIEGGVEITARYGTRIVADVMLGEAADRAPFDLIIVPGGMPGAKTLGGCEQLVALLKKQAEANRPYGAIGAATAHVLEPHGLLKGRKATTCASMAGLLTDGSECENRVVVDGNVITSRSPGTAMEYAVAVVEKMLGRDEARRLAEGLLFLG\*

>TaGlyIII9

MLDEAADRAPFDLIIVPGGMPGAKTLGGCEQLVALLKKQAEANRPYGAIGAATAHVLEPHGLLKGKKATTCASMAGLLAD\*

>TaGlyIII10

MMLNEAAKMEFDLIVMPGGLSGAQKFANTDKLVDLLKKQAGSGKPYGAICASPAHVLEPHGLLKGKKVTAFPPMAHLLTDQSLCENRVVIDGNLITSRAPGTATEFALAIVEKLFGREKAVSIAKEFVFM\*

>TaGlyIII11

MPGSTNLRECKVLERMVKMHAEKGELYGAICAAPAVTLAHWGMLKGLKATCYPSFMEKFTAEVIPVNSRVVVDRNVVTSQGPGTAIEFALALVEQLYDKEKMEEVAGPLYVRPQHGAEYTIEELNSVEWKCSGTPQVLVPVANGSEEIEALNLIDVLR\*

>TaGlyIII12

MMLDEAAKMEFDLIVMPGGLSGAQKFASTDKLVDLLKKQAGSGKPYGAICASPAHVLEPHGLLKGKKATAFPPMAHLLTDQSLCENRVVIDGNLITSRAPGTATEFALAIVEKLFGREKAVSIAKEFVFM\*

>TaGlyIII13

MPGSTNLRECKVLEKMVKMHAEKGELYGAICAAPAVTLAHWGMLKGLKATCYPSFMEKFTAEVIPVNSRVVVDRNVVTSQGPGTAIEFALALVEQLYDKEKMEEVAGPL\*

>TaGlyIII14

KSRRSPPGRRAACLSGVSFALRPCPSGEPRAAASSPPLPSPSWLLPLLICRLLPRPADRRGGAPVTAFVQPDLDPDVWRSASAKVSWRARPRGRCGLYRFTCALRQKGCIFIGWILLVSELQIPMLSASKPLLSPSSLIAMPIRPPPHAPTHYAPPHRRTLPLRSIARAAPSSSTAATAVSLPPSPKKVLVPIAMGTEEMEAVILAGVLRRAGADVTLASVEDGLEIEASYGTRIIADKPIAACADQGGMPGSVRLRDNEILQRIMVRQAEEKRLYGAICAAPAVVLMPWGLHKGRKITCHPSFIGDLPTFRAVESNVQVSGELTTSRGPGTAFQFALSFVEQLFGPHAVEDVDSTLIDAALERSTEVNRVEWPFDHKPQVLIPIANGSEEMEIIMLVDILRRANINVVLASVDESTNVVGSQRMKIVADKCILGASDSKHDLIIIPGGPAGAERLHRSTTLKKLLKEQKQAGRMYGGISYSPLILQKQGLLEDKTVTAHPSIVDQLTCQVIDGSKVVIDGNLITGKGLGTVMDFSLAIVRKFFGHGRAKGVANGMVFDYPKSRNA\*

>TaGlyIII15

MRPQHGAEFSMKELNSTSWNVGENPQILVPIANGTEEMEAIMIIDILRRAKANVVVASLESTLEIVASRNVKMVADVQLDDALKQQYDLILLPGGLGGAQAYAKSDKLIGLIKKQAEANKLYGAICASPAIALEPHGLLKGKKATSYPAMWSKLVDQSECKNRVVVDGNLITSQGPGTSMEFSLAIVEKLFGRERAFELAKAMVFV\*

>TaGlyIII16

MPGSVRLRDNEILKRIMVRQAEEKRLYGAICAAPAVVLMPWGLHKGRKITCHPSFIGDLPTFRAVESNVQVSGELTTSRGPGTAFQFALSFVEQLFGPHAVEDVHSTLIDAGLERSTEVNRVEWPFDHKPQVLIPIANGSEEMEIIMLVDILRRANINVVLASVNESTNIVGSQRIKIVADKCILDASDSKYDLIIIPGGPAGAERLHRCTTLKKLLKEQRQASRMYGGICYSPLILQKQGLLQDKTVTAHPSIVNQLTCQVIDRSKVVIDGNLITGKGLGTVIFPGHCKKILWPWASERCGKWNGF\*

>TaGlyIII17

MLSVSKPILAPTSLTAMAIRLPPHAPTHYALPHRRTPPFRSIARAAPSPSTTSTAVSLPPSPKKVLVPIAMGTEEMEAVILAGVLRRAGADVTLASVEDGLEVEASYGTRIIADKSIAACADQEFDLVALPVTHLSYYYYYFYFRYVYKRSKSFLFSLLKNDKTGDKQFCWHQHRCAGILKFWPD\*

>TaGlyIII18

MPGSVRLRDNEILQRIMVRQAEEKRLYGAICAAPAVVLMPWGLHKGRKITCHPSFIGDLPTFRAVESNVQVSGELTTSRGPGTAFQFALSFVEQLFGPHAVEDVDSTLV\*

>TaGlyIII19

MLLYESGGMPGASTFGDCKILENIVKKHAEKGKLYAAVCAAPAVALGAWGLLNGLKATCHPSVMDKLPSEVQAVESRVQIDGNCVTSRGPGTTMEYSVVLVEQLYGKEKADEVAGPMVMRPQHGAEFSMKELNSTSWNAGENPQILVPIANGTEEMEAVMIIDILRRAKANVVVASLEGTLEIVASRNVKMVANVLLDDALKQQYDLILLPGGLGGAQAYAKSDKLIGFIKKQAEANKLYGAICASPAIALEPHGLLKGKKATSYPAMWSKLTDQSECKNRVVVDGNLITSQGPGTSMEFSLAIVEKLFGRERALELAKSMVFV\*

>TaGlyIII20

MPGSVRLRDNEILQRIMVRQAEEKRLYRAICAAPAVVLMPWGLHKGRKITCHPSFIGDLPTFRAVESNVQVSGELTTSRGPGTAFQFALSFVEQLFGPHAVEDVESTLIDAGLERSTEVNRVEWPFDHKPQVLIPIANGSEEMEIIMLVDILRRANINVVLASVDESTNIVGSQRMKIVSDKCILGASDSKYDLIIIPGGPEGAELLHRSTALKKLLKEQKQASRMYGGICYSPLILQKQGLLQ\*

>TaGlyIII21

MAPSKKVLMLCGDYMEDYEAAVPFYALAGLGVAVHCAAPGKAPGDPCLTAVHDFLGYELYTELPGHRFRVTADF\*

>TaGlyIII22

MLSTSKPLLAPTSLTVMAIRLPPHAPTHYAPPHWQTPPFRSITRVAPSPSTTATAVSLPPSPKKVLVPIAMGTEEMEAVILAGVLRRAGADVTLASVEDGLEVEASYGTRIIADKSIAACAHQVFDLVALPEGMPGSVRLRDNKILQRIMVRQAEEKRLYGAICAAPAVVLMPWGLHKGRKITCHPSFIGDLPTFRAVESNVQVSGELTTSRGPGTVFQFALSFVEQLFGPHSVEDVDSTLISQIDAGLERSTEVNRVEWPFDHKPQVLIPIANGSEEMEIIMLVDILRRANINVVLASVDKSTNIVGSQRMKIVADKCILGASDSKYDLIIIPGGPGGAERLHRSTTLKKLLKEQKQASRMYGGICYSPLILQKQGLLQDKTVTAHPSIVNQLTCQVIDRSKVVIDGNLITGKGLGTVMDFSLAIVRKFFGHGRAKGVANGMVFDYPKS\*

>TaGlyIII23

ALVGKFAAEGKVVASIDQGHLVLAASGLLKGKRCASGVPMRVISNLAGAAAVVPEGAVADGKLVTAASWPDLAEFIAHLVDLLGITVSF\*

>TaGlyIII24

MATRPPVFSTLTASFSPSPPHLLRRLQTLTRALASSSPQPMASSPPLKKVLVPIANGTEPMEAVITIDVLRRAGADVAVASVEPGAAQVAASWGVKLAADTLLADLAEADFDLISLPGGMPGASTFRDCKILENIVKKHAEKGKLYAAVCAAPAVALGAWGLLNGLKATCHPSVMDKLPSEVQAVESRVQIDGNCVTSRGPGTTMEYSVVLVEQLYGKEKADEVAGPMVMRPQHGAEFSMKELNSTSWNVGENPQILVPIANGTEEMEAVMIIDILRRAKANVVVASLEGTLEIVASRNVKMVADVLLDDALKQQYDLILLPGGLGGAQAYAKSDKLIGLIKKQAEASKLYGAICASPAIALEPHGLLKGKKATSYPAMWSKLADQSECENRVVVDGNMITSQGPGTSMEFSLAIVEKLFGRERAFELAKSMVFV\*

>TaGlyIII25

MGTEEMEAVILAGVLRRAGADVTLASVEDGLEIEASYGTRIIADKPIAACADQVFDLVAVPGGMPGSVRLRDSEILQRIMVRQAEEKRLYGAICAAPAVVLMPWGLHKGRKITCHPSFVGDLPTFRAVESNVQVSGELTTSRGPGTAFQFALSFVEQLFGLHAVEDVDSTLIDAALERSTEVNRVEWPFDHKPQVLIPIANGSEEMEIIMLVDILRRANINVVLASVDESTNVVGSQRMKIVADKCILGASDSKYDLIIIPGGPAGAERLHRSTTLKKLLKEQKQAGRMYGGISYSPLILQKQGLLEDKTVTAHPSIVSQLTCQVIDSSKVVIDGNLITGKGLGTVMDFSLAIVRKFFGHGRAKGVANGMVFDYPKSRNA\*

>SpGlyIII1

MVKVCLFVADGTDEIEFSAPWGIFKRAEIPIDSVYVGENKDRLVKMSRDVEMYANRSYKEIPSADDFAKQYDIAIIPGGGLGAKTLSTTPFVQQVVKEFYKKPNKWIGMICAGTLTAKTSGLPNKQITGHPSVRGQLEEGGYKYLDQPVVLEENLITSQGPGTAMLFGLKLLEQVASKDKYNAVYKSLSMP\*

>SpGLYIII2

MASEGKVLLVASSYYGPFYPDGMNTGVHFAELLIPYQVFREAGYEVQLTSETGKCKFDDHSIKKSALGEVERDAFDNKDNEFWYALKDIKPADKINYKEFCIMFIAGGHAAMFDLPHATNLQTLAQQIYASNGVLAAVCHGPVMLPFVDDTKSPEGRSVVYGKKVTAFNSTGELVMGVSSALRERNMQDLNSLFREAGAEFVDPPTPMSDFTQVDGRIVTGVNPMSAKSTAEAAIKVSQSLRKT\*

>SpGLYIII3

MSIAKGKNALLVASSYYGPFYPDGKNTGVHFSELLIPYNVFKKAGFNVQFVSENGSYKFDDHSIEESKLGDFERKVFNDKNDDFWTNLNNMKKASDIVGKDYQLLFVAGGHAAMFDLPKATNLQAVAREVFTNGGVLSAVCHGPVLLANVKNPQSVEGKTVVYHKHVTAFNKAGEEKMGVMDELKKRGMKSLNEIFAEAGATFIDPPNPNVNFTQIDGKIVTGVNPQSAKSTAEAAVSAL\*

>SpGLYIII4

MPAKTRNVLIACSDYYGPFYKDGENTGAFFLELLHPYLVFRDACFNVDIVTESGKIQFDDHSVAGPAIDKGSKGEEFLSYDDHIASGPELSKAEKYVLENKDDMFWRIVQNSKTADEVNPDKYDIFFVAGGHATLFDFPKATNLQKLGTSIYENGGVVAAVCHGPTLLPFMKRQTSDGSVSIVCGKDVTAFDRVAEDKSKLMEALKKYNLEVLDDMLNDAGANFIKSPNPFGDFVIADGRLVTGSNPASATSTAKTALRVL\*

>SpGLYIII5

MVLFMKTVQRPEHISLKSCIPFKSLQRQGIVFRLSVRMVMLADDHSISDSALSDSDKNAFKDKNNDFWKAIKNAKNASDINFSDYSIFFAAGGHGTLFDFPSATNLHKGAAKIYSMGGVIAAVCHGPVILPCIKDSTGFSIVKGKTVTAFNEIAEQQMNLMPTFEKYHFKTLNKLFQEAGSNFVDPQEPFDDFVKTDGKLVTGANPASAASTAKAALNSLNS\*

>SpGLYIII6

MDERHEAAGETSEKPKVLFLLNSYYGPFYDDGDNTGVNVVDLYEAFKVFEENGFDIVIASDTGDYGFDDKSFRDPAIVDETQSIFSNPDCSLMKKLKNIARLDRLNPSDYVIVYIPGGYGCSFDFPHAKVVQDFLYRFYETKGIICAVAQANIALAYTTNSDGQALCTNRRVTGCTWKDEVQNGVLNVMNRLNFYSFGHIAENIGAIFESPPVYVEDPFIVEDGQLFTGSNTNSAKGVAMEAVRAVLNYDG\*