

SbGlyII-2.1 -MGTSVQVTVPLSGAYGEGPLCYLLAVDGRFLLD CGWTDLCOTSQ LPLAKVAPTVDVALL SHPDMMHGALPYAMKHLGLSAPVYATEPVFRLGLLTM YDHFLSRWQVSDFDLFTLDDVDAAFONVVRKYSONYLLNDKGE--GIVIP
SbGLVII-2.2 -MGTSVQVTVPLSGAYGEGPLCYLLAVDGRFLLD CGWTDLCOTSQ LPLAKVAPTVDVALL SHPDMMHGALPYAMKHLGLSAPVYATEPVFRLGLLTM YDHFLSRWQVSDFDLFTLDDVDAAFONVVRKYSONYLLNDKGE--GIVIP
SbGlyII-3 -----MKIIPVPCLEDNAYAILVDDEST--KKAAY
OsGlyII-2 -----MKIIPVACLEDNAYAILVDDEST--KSAAY
SbGlyII-4 -----MRMLSKACSI VASSLPRCSSAAPTMRGQPSLLPSVRKQWPKGP-----LLYGIGITLVMPLRLTLGVGRVFGAGRFLCHMTSVSSSLQIELVPCLRDNAYAILHVDVT--GTVG
OsGlyII-3 -----MRMLSKACSLVASSLPRCSSAAPTIRGQPSLLPSVRKEWLKGP-----LLYGIGITLVMPLRLTLGVGRMFGAGRFLCHMTSVSSSLQIELVPCLRDNAYAILHVDVT--GTVG
SbGlyII-5 -----MVLPLR--LIPRLASAARLTP--SASCAP--RLVLRRAP-----LLP--VALAMASAYSAGSGAD-----RRLLFROLFEKESSTYTYLLADVADPKPAVI
OsGlyII-1 -----MVALLRSCRRLIPHL SACAAAASSSSSCAPRARIRSGLR-----LLP--VVLAMAG--YSSGSAAGG-----RRLLFROLFEKESSTYTYLLADVADPKPAVI
SbGlyII-1 MASSAAAPSGAPPAGKRPAASSGREGDQMWITPLGAGSEVGRSCVHMTFKGRITLFDGCIHPAYSGMAALPYFDEIDPSTIDVLLITHFHLDHAASLPYFLEKTTTFKGRVFMTHATKAIYRLLSDYVKKVKSVEEDMLYDENDIARSMEL
SbGlyII-6 -----MALLMSLGAAYSYFSTATAPPRERR-----CILSFRAAASPAAALDRRRRQNVAGDFFVDQRCIDQTCRWMAAPQVFKRVDGKAAVAAP

SbGlyII-2.1 HVAGH-----LLGGTVWKITKDGEDVVAVDFNHRRKERHLNGTVLGSFVRPAVLITDAYNALHNOGYRKKQDQDFIDSLIIVLATGGSVLLPVDTAGRVLELLLLLDITYWDERRLQYPIYFLTINVTSTVDYVKSLE
SbGLVII-2.2 HVAGH-----LLGGTVWKITKDGEDVVAVDFNHRRKERHLNGTVLGSFVRPAVLITDAYNALHNOGYRKKQDQDFIDSLIIVLATGGSVLLPVDTAGRVLELLLLLDITYWDERRLQYPIYFLTINVTSTVDYVKSLE
SbGlyII-3 -----PEKVIKAAGEVGAAYDVCVLTTHHHWD--HAGGNEK-----MKLVQPGIKIFG
OsGlyII-2 -----PEKVLAAAAEFGVRIDVCVLTTHHHWD--HAGGNEK-----MAQSVPGIKVYG
SbGlyII-4 -----AMPIINALEKRNQHLTYYLNTHHHYD--HTGGNLE-----LKAKY--GAKVIG
OsGlyII-3 -----ATPIINALEKRNQHLTYYLNTHHHYD--HTGGNLE-----LKAKY--GAKVIG
SbGlyII-5 -----TVDRDLNLIKELGLKLVYAMNTHVHAD--HVTGTGL-----IKTKLPGVKSVI
OsGlyII-1 -----TVDRDLNLIKELGLKLVYAMNTHVHAD--HVTGTGL-----IKTKLPGVKSVI
SbGlyII-1 EVIDFHQTLEVHGIRFWCYTAGHVLGAAMFMVDIAGVRLTYGDYREEDRHLRAELPQFSPDICIESTYG--VQHQHPRIVREKRFEVIHNTVSGGRVLIPI
SbGlyII-6 SGEF-----RTKALQALLSCPSSIHTEKPPKDLIQVQNMFLP-----IDKLLPGVYLCG

SbGlyII-2.1 WMRDQIAKSFESHRAAFLLKKVMLIINKEELEKLGDA PKVVLASMASLEVGFSDHIFVEMANEARNLVLFTEKGQFGLTAR--MLQVDP PPKAVKVTMSKRIPLVGD ELKAYEEEOER-----IKKEKALKASLVKEEELKASLG---S
SbGLVII-2.2 WMRDQIAKSFESHRAAFLLKKVMLIINKEELEKLGDA PKVVLASMASLEVGFSDHIFVEMANEARNLVLFTEKGQFGLTAR--MLQVDP PPKAVKVTMSKRIPLVGD ELKAYEEEOER-----IKKEKALKASLVKEEELKASLG---S
SbGlyII-3 -----GSLDN--VKGCTDQVENGTLSLKGDI EILCLHTPCHTKGHSYVYTSKEGEDP--AVFTGDTLFIAGCG--KFFEGTAEQMYQSLIVTLGSLPKSTRVYCGHEYT-----VKNLKFILTVEPEHEKTKQKLE---W
OsGlyII-2 -----GSLDN--VKGCTDQVENGTLSLKGDI EILCLHTPCHTKGHSYVYTSKEGEDP--AVFTGDTLFIAGCG--KFFEGTAEQMYQSLIVTLGSLPKSTRVYCGHEYT-----VKNLKFILTVEPEHEKTKQKLE---W
SbGlyII-4 -----SEKDKDRIPGIDITLKEGDTWMFAG--HQVLVMEIPGHTSGHVCYHFPGSG-----AIFTGDTLFLSLCG--KLFEGTPQOMYSSLOKII--ALPDDTKVYCGHEYT-----LSNSKFALSVEPGNKALQEYAA---H
OsGlyII-3 -----SAKDRDRIPGIDITLKEGDTWMFAG--HQVLVMEIPGHTSGHVCYHFPGSG-----AIFTGDTLFLSLCG--KLFEGTPQOMYSSLOKII--ALPDDTKVYCGHEYT-----LSNSKFALSVEPGNKALQEYAA---H
SbGlyII-5 -----SKASG--AKADHFVDHGDKIHFGN--LFLFVRATPGHTSGCVTVYTGADAGOPSPRMAFTGDALLIRACGRTD FGGGSSDLYQSVHSQIFTLPKDITLLYPANDYK-----GFTVSTVEEEVAYNARLT KDKE---T
OsGlyII-1 -----AKVSK--AKADHFIEHGDKIYFGN--LFLFVRATPGHTAGCVTVYTGEGDDOPSPRMAFTGDALLIRACGRTD FGGGSSDLYQSVHSQIFTLPKDITLLYPANDYK-----GFTVSTVEEEVAYNARLT KDKE---T
SbGlyII-1 -----AFALGRAQELLILDEYWSKHPLEHKPIIYASPLAKRCMAVYQTVINSMNERIRNQFAQSHPFHFHIESLSHSDIFHDVGPSSVYMASPGGLQSLSRQLFDKWCIDKKKNACVIPGVYVVGTLAKTIIEPREVTLANGLT
SbGlyII-6 -----YNSEDSYGATSYLVIHPOGNLILDSRPRYSKLANNIEKLGGARYMELTHIDDVADHRKWAELQKCERIIHMGDVEEATADVVEWKLEGNRPWNIGTDFFEFIHTPGHTP-----GSVCLYYKPPKPLFTGDHVAKS---

SbGlyII-2.1 NAKASDPMVIDASSSRKSANAGSHFGGNTDILIDGFVPPSTSVAPMFPFFENTAEDWDFGEVINPDDYMMKQEEMDNTLMLGPGDGLDGKIDDSARLLLDSTPSKVISNEMTVQVKCSLVYMDFEGRSDGRSVKSVIAHVAPLKLVLVH
SbGLVII-2.2 NAKASDPMVIDASSSRKSANAGSHFGGNTDILIDGFVPPSTSVAPMFPFFENTAEDWDFGEVINPDDYMMKQEEMDNTLMLGPGDGLDGKIDDSARLLLDSTPSKVISNEMTVQVKCSLVYMDFEGRSDGRSVKSVIAHVAPLKLVLVH
SbGlyII-3 AEKQRQANQPTVPSTIGDEFEINTFMRVDPPEIQAQFGANSVPEA--LREVRKTKDNWKG
OsGlyII-2 AEKQREANQPTIPSTIGEEFETINTFMRVDPPEIQAQFGAKSPVEA--LREVRKTKDNWKS
SbGlyII-4 AAELRNKNIPTPVTTIGREKECNPFLRTSNPEIKSTLSIPDHFEDEDRVLEVVRRAKDNF
OsGlyII-3 AADLRKRNTPTVPTTIGREKOCNPFLRTSSPEIKNTLSIPDHFDARVLEVVRRAKDNF
SbGlyII-5 FKTIMSNLNLSPKMMDVAVPANLYCGIQDPPP--KI
OsGlyII-1 FKKIMDNLNLAYPKMIDVAVPANLLCGIQDPPPSKV
SbGlyII-1 APLHMSVHYISFAHADFPQTSNFDDELRRPNIILVHGEANEHSRLKQKLKTQFDGNTIVSGKNCQSVEMYFTCEKMAKTIIGRLAEKVPEGGESSGGLLVKKGFTYQIMAPEDLRVFTQLSTANITQRIAVPYSGSFEVIKYRLKQIYES
SbGlyII-6 --EESDDLNLFLMYSKQSVSLQLESIRKLLLEVFEFWLLPGHGVRIRYKDVQAKNAAMESL LAHYLS

SbGlyII-2.1 LVVHGSAAEATEHLKMHCTKNLDLHVHAPQIEETIDVTSDLCAKVKQLSEKLSMNIISKKLGEHEIAWVDAEYGKEDEKLILLPPSSTPPPHKPVLYGDLKLSDFKQFLENKGWQVEFAGGALRCGEYIMVRKIGDSSQKGSTSQQIVIE
SbGLVII-2.2 LVVHGSAAEATEHLKMHCTKNLDLHVHAPQIEETIDVTSDLCAKVKQLSEKLSMNIISKKLGEHEIAWVDAEYGKEDEKLILLPPSSTPPPHKPVLYGDLKLSDFKQFLENKGWQVEFAGGALRCGEYIMVRKIGDSSQKGSTSQQIVIE
SbGlyII-3 -----
OsGlyII-2 -----
SbGlyII-4 -----
OsGlyII-3 -----
SbGlyII-5 -----
OsGlyII-1 -----
SbGlyII-1 YEESVESATEESDVPALIVHERVTVRLDSESYVTLQWSSDPSIDMVSDSVVAMILNIIGREGPKVVPVEEAVKTEETEKVAQKVYALMTSLFGDVKVTAEGKFVISVDGNVAHLDGMSGDVKCENATLKERIKTAFRRIQSAVRPIPLS
SbGlyII-6 -----

SbGlyII-2.1 GCEDYYKIRELLYSQFYLL
SbGLVII-2.2 GCEDYYKIRELLYSQFYLL
SbGlyII-3 -----
OsGlyII-2 -----
SbGlyII-4 -----
OsGlyII-3 -----
SbGlyII-5 -----
OsGlyII-1 -----
SbGlyII-1 A-----
SbGlyII-6 -----

Figure S4