Table S1 The sequence of protein used in phylogenetic trees.

Protein name	Gene ID	Protein sequence
SlPL1	Solyc01g010740	MAFISGNSILLVLFIWLASLVPHLHARIAEFDPYLEKQALEALNSSLE AYTNNPEEITNAFNKEVGNALLKYKSLRRHLKEKDKCMATNPIDRC WRCDKNWAENRMDLEECARGFGHKTTGGKNGKYYVVTDESDDNV QEPKPGTLRHAVIQEEPLWIIFEKSMVIKLRQELMITSDKTIDGRGVA VHIAYGAGLMIQFVHNVIIHNIRIQNIISTNGGMIRDSINHIGLRTVSDG DGISIFGSNHIWIDHCTLSECTDGLIDAIMASTAITISNCKFNYHNDVM LLGATDAFPQDAIMQVTVAFNRFGEGLIQRMPRCRWGFFHVVNNDY THWQMYAIGGSAHPTIISQGNRFKASDNPNTKQVTKRDYATESEWK KWQWVSEGDSFLNGAYFVESGPQDKKKTALTKNHKIKFKPGSHAG RLTRFAGVLKCKPGIPC
SlPL2	Solyc02g067450	MTKSLFIIFFVLGAIIPAFNAHIGDFDEVWRRRAEEAIKFTHETYESEP ANITLAFNQKTRHTVKELSTVVSKNETIRRALGTKKYDGPCTVTNPI DKCWRCDPNWADNRKKLVECSMGFGYKTTGGRDGEFYVVTDPSD DYTTPKPGTLRHAVIQKEPLWIIFEKNMKIKLHQELIMQGDKTIDGRG ATVHITGGASIMIQYTKNVIIHGLHIHDIVEGSGGMVRDAVDHIGLRT KSDGDGAAVAADNSTRRHLAKKYKGPCMATNLIDKCWRCDPQWA DNREKYADCAMGFGSKATGGKGGRVYVVSDNSDSDVENPAPGTLR HAVIQTEPLWIIFERHMHIKLQRELLMQGHKTIDGRGFNIHIEKGAGL KMQGVSNVIISNLHVHNIVITPGGMIRDSAEHVGIRSEDEGDGISLFSA TDIWIDHVSMSRATDGLIDAVKGSTGITISNCHFTDHDKVMLFGAND NHVEDKKMQITLAYNHFGKRLDQRMPRVRFGFFHIVNNDYTHWMR YAIGGNNGATIISQGNRFIAQASPLIKEVTHREKVEESEWKNWTWLSI DDDMQNGAFFKTSGDQDALSKLQDLNLIPAEPSYKVGIITKFAGSLA CTAGRPC
SlPL3	Solyc02g080910	MASLALVLALLFLCISTLQAEYYAPSKNYYAPSTTKKTMNVIDSCWR AKSNWAKNRYALADCAVGYGKAAIGGKNGAIYVVTNPSDDPVNPK PGTLRYGVIQSKPLWIIFNKDMVITLKNELMINSYKTIDGRGAKVEIA YGPCITIQRVSHVIIHGISIHDCKPGKRGIVRDSPVHAGHRNGADGDGI DIFQSTHVWIDHCYLARCTDGLIDVIHASTGVTISNNYFTQHDKVML FGHNDNNKEDKIMKVTVAFNYFGPGLIERMPRVRLGYAHVANNRY EKWLMYAIGGSANPTIFSEGNYFLASKSTQVTKRESKNGWQNWKW RSSKDKFLNGAYFIPSGYGTTNPYYSKAQSFPVADGSMVPSLTADAG PLRCTSYKSSKSSDKDETKSLHDFFPSYDPQPHKNGLLNVIDSCWRW KGDWSSNRKALADCAIGFGSSTIGGKYGDIYIVNDSSDDPINPKPGTL RYGAIQSEPLWIIFKRDMVLTLENELMVNSYKTIDGRGAKVEISNGP CITLDYVTNVIIHGISIHDCKPGKKGMVRSSPEHVGERSGSDGDAISV FTSSNVWIDHCYLARATDGLLDVIHASTAVTISNNYFTEHDKVMLLG HNDEYTADRNMKVTVVYNHFGRELVQRMPRVRHGYAHVANNYY DQWLMYAIGGSADPTIFSEGNYFIAPDKAYNKEVTKRETEEKGWKS WKWRSSNDMFMNGAYFLPSGYGSIAPKYTRGQSFIVAHGAFTPSLT SNAGPLQCVVNEPC

SlPL4	Solyc02g087670	MGGTKLVYLSLLLFSTFLVINGHIGEFDEVWRRRAQEADEWAIKAY KPDPINVTLAFAKETGQALKEIKEAKLAVNGTRRELKGGGKKYDGP CSVTNPIDRCWRCQPDWADNRKRLADCAMGFAKGTTGGKAGEIYV VTDSSDDTSDPKPGTLRYGVIQKEPLWIIFAKSMTIRLHQELIVQSDK TIDGRGVNVHIANGAGFMLQYVKNVIIHGLRIHDIVVGSGGMIRDAM DHVGQRTQSDGDGISIFGSSNIWVDHVSMWSCYDGLVDAIEGSTAV TISNSHFTDHNEVMLFGASDSSSIDQRMQITVAYNHFGKRLIQRMPR CRWGFIHVVNNDYTHWNMYAIGGSQHPTIISQGNRFIAPPDMFKKE VTKRDYSPESVWKQWSWRSQGDLFMNGAFFVESGDPDWTQKHIQL FDGVVSASGDQVTWITRFSGALNCKPGEAC
SlPL5	Solyc02g093580	MSTLFFTFSLLLLAPLLVISSIQDPELVVQDVHRSINASLTRRNLGYLS CGSGNPIDDCWRCNPNWEKNRQRLADCAIGFGKNAIGGKNGRIYVV TDSGNDDPVNPKPGTLRHAVIQDEPLWIIFKRDMVIQLKQELVMNSY KTIDGRGASVHISGGPCITIHHTSNIIIHGINIHDCKQSGNGNIRDSPNH SGWWDVSDGDGISIFGGKNIWVDHCSLSNCHDGLIDAIHGSTAITISN NYFTHHDKVMLLGHSDSFTQDKGMQVTVAFNHFGEGLVQRMPRCR HGYFHVVNNDYTHWEMYAIGGSAAPTINSQGNRFLAPNEKYRKEV TKHEDAPESQWRSWNWRSEGDLMLNGAYFRQTGAGASSSSTYARA SSLSARPSSLVGSITTNAGPVNCKKGSRC
SlPL6	Solyc03g058890	MGGPKIKYSFLFLCITFATIIPSLMAHIGHYDEVWRRRAEEAKEYARK IYEPHPENVTLAFNQKLRDTMKELKKVKGTHNNSTRRGLGTKKYTG PCMVTNPIDKCWRCDPNWADNRKKLADCAMGFGSKAIGGKDGEFY VVTDNSDDYNDPKPGTLRHAVIQKEPLWIIFKRGMNIRLHQEMIMQS DKTIDARGVNVHITKGAGITLQYIKNVIIHGLHIHDIVEGNGGMVRD AVDHIGIRTKSDGDGISIFGASNIWIDHVSMQRCYDGLIDAVEGSTGI TISNGHFTDHNEVMLFGASDSSSIDQVMQITLAFNHFGKRLIQRMPR CRWGYIHVVNNDYTHWNMYAIGGSMHPTIITQGNRFIAPPDIFKKQV TKREYNPESVWMQWTWRSEGNLFMNGAYFTESGDPEWSSKHKDL YDGISAAPAEDVTWMTRFAGVLGCKPGKPC
SlPL7	Solyc03g058910	MEYSYRTKINVLFIVLILFVFAALGTAINAPRRKLTKKYRGPCMAVN SIDKCWRCDPFWAEDRQKMADCALGFGINAMGGKYGPYYIVTDNS DDDVVDPKPGTLRFGVIQKGPLWITFARSMRIRLTRELIVSSNKTIDG RGKYVHIANGAGIKIQSASNVIISNLRIHNIVPTAGGLLRESDDHLGLR GADEGDAISIFNSHDIWIDHISMSRATDGLIDAVAGSTNITISNCHFTD HEKVMLFGANDHAEEDRGMKITLAYNHFGKRLDQRMPRCRFGFFH LVNNDYTHWERYAIGGSSGATIISQGNRFIAEDKLLVKEVTYREKST SSVEEWMKWTWITDGDDFENGATFTPSGDQNLLSKIDHLNLIQPEPS SKVGLLTKFSGALSCKIRRPC
SlPL8	Solyc03g071570	MSSQSLFYRAKMPPATPILLFIYLILSFFSPLIDSQLNLTLPNQHPYPES VVHQLHRRVNESRLLFQTIVRDSKCHSTGNPIDDCWQCDPNWAKDR QRLADCSIGFGQSAMGGKGGQIYVVRDSSDRDTVNPIPGTLRHAVV QEEPLWIVFAADMVIKLKHELIINNYKTIDGRGANVHITGNGCITLQY VSHVIIHNVHIYNCVPSGNTNIRSSPTHVGWRGKSDGDGISIFGSHNI WIDHCALSHCTDGLIDAIMGSTAITISNNYFSHHDDVMLLGHDDKYL

		PDSGMQVTIAFNHFGEGLVQRMPRIRRGYVHVVNNDFTHWQMYAI GGSANPTINSQGNRYTAPDDPNLKEVTKREDTDNGQWDEWNWRTD GDTMVNGAFFVPSGQGLSNQYTKAYSVDPKSALLINQLTANAGVLG GPRDNSISILPQVGGGTSEGSGRGHDQSNSGSVDLFGMIFSGTGASAA APPTTTPILFSFFILLTLYIITITTQLSKPFLHLL
SlPL	Solyc03g111690	MGTSSVFLLFLLSFLLLLPSLLASSNPQQVVDEVHRSINGSRRNLGYL SCGTGNPIDDCWRCDPNWEKNRQRLADCAIGFGKNAIGGRDGKIYV VTDSGDDNAVTPKPGTLRHAVIQTEPLWIIFARDMVIQLKEELIMNSF KTIDGRGASVHIAGGPCITIQYVTNIIIHGIHIHDCKQGGNAMVRSSPS HYGWRTVSDGDGVSIFGGSHVWVDHCSLSNCKDGLIDAIMGSTAITI SNNYMTHHDKVMLLGHSDTYTQDKNMQVTIAFNHFGEGLVQRMP RCRHGYFHVVNNDYTHWEMYAIGGSADPTINSQGNRFLAPDIRFSK EVTKHEDAPESEWKNWNWRTDGDLMLNGAFFTRSGVRTGSSSYAK ASSLSARPSSLVANLVSSSGALNCKKGSRC
SlPL9	Solyc03g113150	MGLPKRNLFLFFVLVVLVVSIEAHIKEFDEVWKKRAQQAKKAARHA YNPNPKIVADHLNYQVDKAVRGSKSRRRDLQRYSGKCMATNPIDQC WRCDPNWARNRMKLTDCVLGFGRKTTGGKGGKIYVVMDNSDNEL VNPKPGTLRHAVIQPEPLWIIFAKNMVIKLNQELIMTSNKTIDARGRQ VHIAHGGGLMLQFIHNVIISNLHIHDTKAGAGGLIRDSVSHYGYRSKS DGDGISIFGSTNVWIDHISMSNCQDGLIDAVEGSTAITISNCHFTKHN DVMLFGASDTASGDSVMQITLAFNHFGHGLTQRMPRVRWGFVHVV NNDYTHWLMYAIGGSMHPTILSQGNRFIAPPNPNAKEVTKRDYAPE NVWKNWVWKSQGDLMMNGAFFVESGDPKHAFLKGPDMITSKPGS SVSSLTQFSGSLKCIEGRPC
SlPL10	Solyc04g010230	MAALPYADVDSSLKALAGRAEGFGRFAIGGLNGPVYSVTTLADDGP GSLRDGCRKKEPLWIVFEVSGTIPLTSYLRVSSHKTIDGRGQRIILTGK GLQLKDCEHIIVCNLEFEGGRGHDVDGIQIKPNSRHIWIDRCSLRDYD DGLIDITRQSTDITISRCYFAQHDKTMLIGADPSHVGDRCIRVTIHHCF FDGTRQRQPRVRFGKVHLYNNYTRNWGIYAICASVESQIYSQCNIYE ASQKKKAFEYYTEKAADKEEARSGLIRSEGDMFLNGAQGSLLTGIG GECVFHPSEFYPVWTLEPASDSLKGILHICTGWQSVSLPQEECARQL KPAR
SlPL11	Solyc05g007080	MASISFNNSVIFLFSLFCFSSIIPKLYANIADFDPYLEKRAEEALQSSLA AYNENPEGVTQIFNKEVGETLLNGTRRHLKEKDKEDKNDKDDKEG DEKSVDGCKAYNPIDKCWRCDKNWANNRKALADCARGFGHGTTG GKDGRFYVVTDPSDNNVEEPVPGTLRHAVIQEEPLWIIFEKSMIIRLK QELMINSNKTIDGRGVSVHVAYGGGLTLQFVHNVIVHNIRVHHILSK NGGMIRDSVKHIGLRTVSDGDAISLFGANRIWIDHCTLTKGADGLLD AIMASTAITISNCKFNHHNDVMLLGANDAFPQDKIMQVTVAFNRFG KGCIQRMPRCRWGFFHVVNNDYAKWEMYAIGGTANPTIISQGNRFK AADNPNTKEVTNRNGAPEALWRNWQWRSEGDLFKNGAFFRESGPE IKSTPFTEHTTIQFEPAKFVGRLTRKAGVIQCKIGKAC

SlPL12	Solyc05g014000	MGMPLSFLLLLTLLSPIFTFSSHVPDPEVIVQQVNEKINASRRNLGYLSCGTGNPIDDCWRCDPNWEKNRQRLADCAIGFGKQAIGGKDGKIYVVTDTSDDPVNPKPGTLRYGAIQDEPLWIIFSRDMVIKLKEELMLNSFKTIDGRGASVHIAGGPCITIQYVTNIIIHGLNIHDCKQGGNAYVRDSPQHYGWRTISDGDGVSIFGGSHVWVDHCSLSNCNDGLIDAIRGSTAITISNNYMTHHNKVMLLGHSDSFTRDKNMQVTIAFNHFGEGLVQRMPRCRHGYFHVVNNDYTHWEMYAIGGSASPTINSQGNRFLAPNDIFNKEVTKHEDAAESEWKNWNWRSEGDLMLNGAFFIRSGAGASSSYAKASSLSARPSTLVNSITMNAGALGCKKGKRC
SlPL13	Solyc05g055510	MISLTFILSFFFFLILSFSSLITSTFNNQTLSHQHPFPESVVQQVNRRINESISRRQISDTTVINYQCLTGNPIDDCWRCDPNWVDNRQQLADCAIGFGHGAVGGKGGRYYLVSDPSDYDTVNPTPGTLRHAVIQDEPLWITFAGDMIIRLKHELMINNYKTIDGRGANVHVTGGGCITLQYVTNVIIHNIHVYNCIPSGNSNIRQSTTQVGWRGMSDGDGISIYSSRNIWIDHCALSHCTDGLIDAIMGSTAITISNSYFTHHDKVMLLGHDDRYVPDVGMQVTIAFNHFGEGLVQRMPRCRRGYIHVVNNDFTEWQMYAIGGSANPTINSQGNRFTAPEDPNAKEVTKRVDVDERDWTEWNWRTEGDEMVNGAYFVPSGDGISNQYALASSMEPKSAFLIEQLTMNAGVIGVPRDTTVAMSFGGRTRTTIAANRSSSVRPSRSKDGDGGFLEKVFGSVASAGSSTSSPSSSTITILFSLLILYIITNNIGLL
SlPL14	Solyc06g071020	MVTLINRSSFFVILCTLFFSIEANIGEFDEVWRTRATQANKNAKESYNPNPEKVAANFNKHVHRSEEGSNSTRRDLHKYNGPCVATNPIDRCWRCDPHWAKNRQKLADCVLGFGHHTTGGKGGKIYEVTDPGDTDMVNPKQGTLRHAVIQPGPLWIIFAHHMVIKLNQELIMTGDKTIDARGQQVHITGGASLMLQYINNVIIHGLHIHDIKAGNGGLIRDSINHYGFRTKSDGDGISIYGSTNIWIDHVSMSNCDDGLIDAVQASTAITISNCHFTHHNDVMLFGASDSFKQDEILQITLAFNHFGQGLIQRMPRVRWGFVHAVNNDYTHWLMYAVGGSQQPTILSQGNRFIAPPNPNAKEVTKREYSPESVWKNWVWRSQGDLMMNGAFFVESGDPNHKFTTGPDMIHPRAGSDAGRLTRFSGSLNCIEGKPC
SlPL15	Solyc06g071840	MATSSISLIFLLSFLLLIPSLLASSPLQNHQYVVDQVDRSINVSRRNLGYLSCGTGNPIDDCWRCDPNWEKNRQRLANCAIGFGKNAIGGRDGKIYVVTNSGNDDPVNPKPGTLRYGVIQDEPLWIIFASDMVIQLKEELIMNSFKTIDGRGANVHIAGGPCITIQYVSNVIIHGIHIHDCKQGGNAMVRSTPQHYGWRTISDGDGVSIFGGSDIWIDHCSLSNCVDGLIDAIMGSTSITXSNNYMTNHDKVMLLGHSDSHVQDKNMQVTIAFNHFGEGLVQRIPRCRHGYFHVVNNDYTHWEMYAIGGSANPTINSQGNRFLASDIRFSKEVTKHENAPESEWKNWNWRSDGDLMLNGAFFVKSGAGASSNYAKASSLSAKSSSLISSLVSGAGALSCWKGSRC
SlPL16	Solyc06g083580	MAAALRLSCLCFLQLLIVIVLFINSSADNSIEQAEQFQSLSNSTMTNRLSGNDELRHEHAEDDPEAIASMVDMSIRNSTERRKLGYFSCRTGNPIDDCWRCDRNWQRNRRRLADCSIGFGRNAIGGRDGRFYVVTDSGDDDPVNPRPGTLRHAVIQDEPLWIVFKRDMHITLKQELIMNSFKTIDARGVNVHIANGACITIQFVTNIIIHGLHIHDCKPTGNALVRSSPSHYGWRTM

		ADGDAISIFGSSHIWVDHNSLSNCADGLVDAIMGSTAITISNNYFTHH NEVILLGHSDTYVRDKVMQVTIAFNHFGEGLIQRMPRCRHGYFHVV NNDYTHWEMYAIGGSAAPTINSQGNRYLAPVNPFAKEVTKRVEPWE GSWRQWNWRSVGDLLLNGAYFTASGRAAPGSYARASSLAAKSSSL VGMITSNAGALS
SlPL17	Solyc09g005850	MGNHHGRFSHSKHHHHHHNQQGPPFFVPTQQTQNTQMGIALPYAN VDSNLRGLAGQAEGFGGSSIGGRDGHVYQVLNLNDDGPGSLRDGCR KKEPLWIVFEVSGTIELRSHLSVSSFKTIDGRGQKIKLTGKGLRLKEC EHVIICNLEFEGGRGHDVDGIQIKPKSRHIWIDRCSLSDYDDGLIDITK ESTDITVSRCHFSKHDKTMLIGGDSSNCGDRCMRVTIHHCFFDGTRQ RHPRVRFAKVHLYNNYTRNWGIYAVCASVESQIYSQCNIYEAGQKK VAFKYLTEKAADKEEACTGSIKSEDDLFVCGTQAGLLSTCSENNVFN PSEFYQTWTVERPSDDLKHYLQHCTGWQCIPRPN
SlPL18	Solyc09g008380	MFQISYIVVFLILTSFFPLGFGIFLNVTTLPGQHPDPESVALEVNRKVN ASLSIFQSRRKMLSYTQSSCQTGNPIDDCWRCDHSWQLNRQRLADC AIGFGQYALGGKGGRYYVVTSSSDPDPVDPPPGTLRYGVIQEEPLWI VFSASMEIKLSEELIFNSHKTLDGRGVNVHITGGGCITLQYISNVIIHNI HVHHCYESGDTNVRSSPTHFGYRGKSDGDGISIFGSRDIWIDHCSLSN CKDGLIDVVMGSTGITISNNHFSHHNEVMLLGHNDDYLPDSGMQVT ISFNHFGKKLIQRMPRCRRGYIHVVNNDFTRWEMYAIGGSGNPTINS QGNRYIAPFDPFAKEVTKRVDTDEGKWRNWNWRSEGDVMANGAY FVASGEEVEIKYEKAYSVEPKSADFIDQITLNAGVLIHRGSNSGKWT ATTNNDTESAGDDGGGEDLVAISGDSDDDYGGDEESRSSTIYSNFSL LFNLLMALLALL
SlPL19	Solyc09g061890	MAIYWRSCLSLSALLILVLLVINVNPSHSAEEAEQFQSLKNLTMTNSL SEENVPNHEHAVDDPEKVVSMVDMSIKNSTERRKLGFFSCGTGNPID DCWRCDRNWQRNRKRLADCAIGFGRNAIGGRDGKYYVVTDPNDD DPVNPRPGTLRHAVIQDRPLWIVFKRDMVITLKQELIMNSFKTIDGR GVNVHIANGACITVQFVTNIIIHGINIHDCKPTGNAMVRSSPSHFGWR TIADGDGISIFGSSHIWVDHNSLANCADGLIDAIMGSTAITISNNYFTH HNEVMLLGHSDSYVRDKIMQVTIAYNHFGEGLIQRMPRCRHGYFHV VNNDYTHWEMYAIGGSASPTINSQGNRYLAPANPFAKQVTHRVEQS DVWKHWNWRSEGDLMLNGAFFTPSGHGAAASYARASSLAAKASSL VGTLTSNAGALTCRRGYQC
SlPL20	Solyc09g091430	MAMASKKWLSFSFSFLLILLLLVGVYAAGVQQSNDGSDTRTVEKEQ LLSSENSTMAVSLEDVEEKLSKHAVDDPEEVVAMVAQSIRNSTERR KLGYFSCGTGNPIDDCWRCDPNWQKNRKRLADCGIGFGRNAIGGRD GRYYVVTDNRDDDPVNPRPGTIRHAVIQEEPLWIVFSRDMVIQLKQE LIMNSFKTIDARGYNVHIANGACLTIQFVTNIIIHGLHIHDCKPTGNA MVRSSTTHFGWRTMADGDAISIFGSSHVWVDHNSLSHCADGLVDA VMGSTAITISNNHFAHHNEVMLLGHSDSYTKDKQMQVTIAYNHFGE GLIQRMPRCRHGYFHVVNNDYTHWEMYAIGGSANPTINSQGNRYL APANRFAKEVTKRVDTAAGQWKGWNWRSSGDLMLNGAYFTPSGA GASASYARASSLGAKSSSMVGAITSSAGPLACRRSRTC

SlPL21	Solyc11g008140	MFSLICILLFCLLVSFFPQIIASFNLTLPHQHPYPEVVVQEVQRKVNESISRRQLWNTTMNAITTQCETGNPIDDCWRCDPNWSKNRQRLADCAIGFGQNAIGGKNGKYYVVSDSSDLDTVNPTQGTLRHAVIQEEPLWIIFSGDMFIKLKHELIVNSYKTIDGRGAKVHITGNGCITLQYISNVIIHNIHIYNCLPSGNTDIRSTPTHVGHRGRSDGDGISIFSSRNIWIDHCALSHCTDGLIDAIMGSTGITISNSYFSHHDEVMLLGHDDSYSPDAGMQVTIAFNHFGVGLVQRMPRCRRGYIHVVNNDFTEWQMYAIGGSANPTINSQGNRYTAPVDANAKEVTKRVETDEGEWSGWNWRTDGDIMVNGAFFVPSGEGLSNQYAKASSVEPKSAAIIDQLTLNAGVFGATSESVDQIEDSVNSLKAKEYTLSISIFLVYFLFSSV
AtPLL1	AT3G09540	MGNLHGIHRSHHGGSNFPGEAPNSPFPPPYTAAPAPAPAPSSPSDHHMTVGPYCHVDSSLRSLAGKAEGFGRAAVGGLNGPICHVTSLADEGPGSLREACKRPEPLWIVFDVSGTINLSSFVNVSSHTTVDGRGQKVKITGKGLRLKECENVIICNLEFEGGVGPDADAIQIKPKSHNIWIDRCSLKNYYDGLIDITRESTDITVSRCHFMNHNKTMLIGADTSHVTDRCIRVTIHHCFFDGTRQRHPRVRFAKVHLFNNYTRHWAIYAVGAGVESQIHSQCNIYEAGEKKTVFKYITEKAADKEKPGAGFVRSEGDLLLNGAKSCLSQGGERYVFSPIQHYSEWTVESPTDILKNYLKHSTGWQNLPLPLDRPPTTA
AtPLL2	AT3G55140	MTSLPYADADCSLRALAGRAEGFGRFAVGGLHGDLYVVTSLADDGPGTLREGGRRKEPLWIVFAVSGTINLNSYLSVSSYKTIDGRGQRIKLTGKGIRLKECEHIIICNLEFEGGRGHDVDGIQIKPKSRHIWIDRCSLRDYDDGLIDITRQSTDITVSRCYFAQHDKTMLIGADPSHVEDRCIRVTIHHCFFDGTRQRQPRLRFGKVHLYNNYTRNWGIYAVCASVEAQVFSQCNIYEAGVKKKTFEYYSEKAADKEEARTGLVRSENDLFLNGAQPSLMTGASEECVFHPSEHYPTWTVEPPSETLKQIMQICTGWQSLSRPSDHGVPK
AtPLL3	AT5G09280	MTGNIGKGVTQYKVTDPSDDPLNPKPGTLRYGATLVKGKKWITFKRNMKIKLHKPLLISSFTALDGRGASVHISGPACLIVYRATDVIIHGLKIHDCKAHPPSSVMGPDSKIIQLGHMDGDAIRLVTAKKVWIDHNTLYDCEDGLLDVTLGSTDVTVSNNWFRNQDKVMLLGHDDGYVKDKDMRVTVVFNHFGPNCNQRMPRVRHGYAHVANNYYQGWTQYAIGGSMSPRVKSESNYFVAPKSGSKEVLEKHGPITAQIKGSQSQTLNRLKYSLLQPERYTAPETPSVSTTTLNMTF
AtPLL4	AT4G22080	MTLFTVSCLLVVLFLCHSLVHAENNGYYGYTPTVANYLPEKPQNIMNPVDSCWRLKSDWAANRKDLADCVVGFGSSTLGGKKGNLYVVTNPYDNAQNPQPGSLRYGVIQAKPLWITFAKDMVITLENELMVNSYKTIDGRGAKVEIAYGPCITIQDVTNVIVHGISIHDCKPGKYGMVRSSPTHVGHRKGSDGDAIAIFGSSNIWIDHCYLASCTDGLIDVIHASTGITISNNYFTQHDKVMLLGHNDDFVQDVKMKVTVAFNHFGPGLVERMPRVRRGYAHVANNRYDKWIMYAIGGSADPTIFSEGNYFIASDKSNSKEVTKREVKGGWNNWRWRTSKDVFKNGAYFVPSGYGSISLPYSSAQRFTVAPGNLVPSLTADAGPLNCNRNGPCY

AtPLL5	AT4G22090	MTHFTVSCLLVALFLCQSLVHAAYNGYYGYSPAAAPYPAEEPQNIMNPVDSCWRLKSDWDVNREDLADCAVGFGSSTLGGKKGNIYVVTNPYDNAQNPHPGSLRYGVIQAKPLWITFAKDMVITLANELMVNSYKTIDGRGAKVEIAYGPCITIQDVTNVIVHGISIHDCKPGKSGKVRSSPTHVGHRKGSDGDAITIFGSSNVWIDHCYLASCTDGLIDVIHASTAITISNNYFTQHDKVMLLGHNDNFVKDVKMKVTVAFNHFGPGLVERMPRVRRGYAHVANNRYDKWIMYAIGGSADPTIFSEGNYFIASDKSYSKEVTKREVKGGWNNWRWRTSNDVFKNGAFFVPSGYGSIPLPYSSAQRFTVAPGNLVPSLTADAGPLNCNRNGPCY
AtPLL6	AT1G11920	MASLFLTIISLLFAAFSSSVVEAAYSNGYTIPKLLPNPIDSCWRRNPYWASNRRALADCAVGFGKSAVGGKYGSIYVVTNPSDDPENPRPGTLRYAVIQSKPLWITFARDMVIVLRNELIMNSYKTIDGRGAKVEIAYGPCITIQHVSHVIIHGISIHDCKPGKSGRVRSSPTHVGSRKGSDGDAIAIFDSSHIWIDHCFFSRCQDGLIDVLHASTAVTISNNYFTQHDKVMLLGHNDNNVEDKIMRVTIAFNHFGPGLIERMPRVRRGYAHVANNRYEKWQMYAIGGSADPTIFSEGNYFVASDDPSKKQVTKRIDSGYDWKRWKWRTSKDVFKNGAYFVPSGYGTVTPLYGRAERFPVSHGSLVPLLTSSAGPLHCYSGRIC
AtPLL7	AT1G30350	MASLVVIVSLLLAAFASPLLETAHSYNVTAPRVSLNPIDACWRRNPKWATNRQALAHCAVGYGKAAIGGKNGPIYVVTNPSDNPTRPSPGTLRYAVSQPKPLWITFARDMVIVLKSQLMINSYKTIDGRGAKVEIANGPCLRIRQVKHVIIHGISIHDCKADPNGMDGDGIRVFQSTHVWIDHCFLSRCHDGLIDVIVSSTAVTISNNYFTQHDKVMLLGHDDSYMGDKDMRVTIAFNTFGPGLIERMPRVRRGYAHVANNRYEKWQMYAIGGSANPIIFSEGNYFVAPEKRSSKQVTKRMMAGPDSKRWKWGTSRDVFMNGAFFGPPGVIVRPLYKGGEGFRVAHGSLVPSLTSSAGPLRCYVGRIC
AtPLL8	AT1G14420	MAAAFLNLGGYVFVFFSSFLAIVAPQVRGNVAVFDSYWTQRQSDALKQTIGSYDPHPLNVTNHFNYHVNIAVDASESRNDTRRELTQVRSGRKTHKSSGKCLAYNPIDNCWRCDRNWANNRKKLADCVLGFGRRTTGGKDGPIYVVKDASDNDLINPKPGTLRHAVTRDGPLWIIFARSMIIKLQQELMITSDKTIDGRGARVYIMEGAGLTLQFVNNVIIHNIYVKHIVPGNGGLIRDSEAHIGLRTKSDGDGISLFGATNIWIDHVSMTRCADGMIDAIDGSTAVTISNSHFTDHQEVMLFGARDEHVIDKKMQITVAFNHFGKRLEQRMPRCRYGTIHVVNNDYTHWEMYAIGGNMNPTIISQGNRFIAPPNEEAKQITKREYTPYGEWKSWNWQSEGDYFLNGAYFVQSGKANAWSSKPKTPLPNKFTIRPKPGTMVRKLTMDAGVLGCKLGEAC
AtPLL9	AT2G02720	MVNLGSYVFVFVALSLTVVVPSVQAHIAEYDEYWTQRQTNALRETLESYDPNPENVTDHFNYHAALAMETTGIVNETRRDLRQVGRGKKTTRRGGRFESLNAIDKCWRGDKNWDKNRKKLADCVLGFGRKTTGGKNGPIYVVTDPSDNDLLKPKPGTIRHAVTRDRPLWIIFARSMIIKLQQELIITNDKTIDGRGAKIYITGGAGLTLQFVRNVIIHNIHIKQIKRGAGGLIIDSEQHFGLRTVSDGDGINIFGATNVWIDHVSMTDCSDGMIDAIMGSTAITISNSHFTDHDEVMLFGGTNKDVIDKKMQITVAFNHFGKRLKQRMPRVRFGLVHVVNNDYTHWEMYAIGGNMNPTIISQGNRFIAPPIEDSKQ

		VTKREYTPYPEWKSWNWQSEKDYFLNGAYFVQSGKANAWSATPK NPIPRKFAIRPQPGTKVRRLTKDAGTLGCKPGKSC
AtPLL10	AT3G01270	METARLFKLVCVICIASLIPTIRANVADETDEYWVNKANEARKHTLM AYHPDPYEIVDHFHERHYDNSTDVEGTEEEKAVASEEEDVIEMISSPT NSTRRSLTGRGKGKGKGKWSKLTGPCTASNPIDKCWRCQPDWARR RKKLVHCVRGFGYRTTGGKRGRIYVVTSPRDDDMVNPRPGTLRHA VIQKEPLWIVFKHDMSIRLSQELMITSDKTIDARGANVHIAYGAGITM QYVHNIIIHGLHVHHIVKSSGGLIRDSINHFGHRGEADGDGISIFGATN IWLDHISMSKCQDGLIDAIMGSTAITISNSHFTHHNDVMLLGAQNNN MDDKKMQVTVAYNHFGKGLVQRMPRVRWGFVHVVNNDYTHWEL YAIGGSQGPTILSHGNRFIAPPHKQHYREVTKRDYASESEWKNWNW RSEKDVFMNNAYFRQSGNPHFKCSHSRQQMIKPKNGMAVSKLTKY AGALDCRVGKAC
AtPLL11	AT5G15110	MEMVRLSKLMFTFCIAVLIPTIRGNISELDEYWSQRADEAREFTLQA YHSDPYEIVDHFHERHYDNSTDVTTPEEDGDAKPEEEEKEFIEMLGS STNSTRRSLRGKGKGKWSKLKGPCTASNPIDKCWRCRSDWAKRRK KLTRCVRGFGHRTTGGKRGRIYVVTSNLDEDMVNPKPGTLRHAVIQ KEPLWIIFKNDMSIRLNQELLINSHKTIDARGANVHVAHGAGITMQF VKNVVIHGLHIHHHISESSGGMIRDSVDHFGMRTRADGDGLSIYGSSNI WLDHISMSKCQDGLIDAIVGSTGITISNSHFTHHNDVMLLGAQNTNE ADKHMQVTVAYNHFGKGLVQRMPRIRWGFVHVVNNDYTHWELY AIGGSQGPTILSHGNRFIAPPHKPHYREVTKRDYASEDEWKHWNWR SDKDVFMNGAYFRQSGNPQYKCAHTRQQMIKPKNGLAVSKLTKYA GALDCRVGRRC
AtPLL12	AT5G04310	MVAHERRIHNLQKPTCICIIWFCLLVSLSHHGRASSTSASIFNLSLPHQ HPFPEHVVLNVQRKLNDSLSRRQLLTYQQDDGTTASSPIPSCITGNPI DDCWRCDPNWSANRQRLADCSIGFGQGTLGGKGGQFYLVTDSSDN DAANPIPGTLRHAVIQPEPLWIIFSSDMGIKLKHELIIGSYKTIDGRGT NIQITGHGCLTIQQVSHVIIHNVHIHHCKPSGNTLVASSPTHVGFRGVS DGDGISVSASHHIWVDHCSLGYCADGLIDVILASTAVTISNNYFSHH DEVMLLGHDDRYTADKGMQVTIAFNHFGEGLVQRMPRCRHGYIHV VNNDFTAWEMYAIGGSASPTINSQGNRYTAPIDPNAKEVTKRVDSN EKHWSGWNWRTEGDVMVNGAFFVPSGDGVSPAYARATSVQPKAA AIIDQLTVNAGVFGDPSGRNGQGGSFPGITNGGGTITRGYSKSGPAG GGSGSDSDDGLFTLIFGNNSGAVALRPGQVWSILLIIILYWYIPHHTRS
AtPLL13	AT3G54920	MLLQNFSNTIFLLCLFFTLLSATKPLNLTLPHQHPSPDSVALHVIRSVN ESLARRQLSSPSSSSSSSSSSSSSCRTGNPIDDCWRCSDADWSTNRQR LADCSIGFGHGTLGGKNGKIYVVTDSSDNNPTNPTPGTLRYGVIQEE PLWIVFSSNMLIRLKQELIINSYKTLDGRGSAVHITGNGCLTLQYVQH IIIHNLHIYDCKPSAGFEKRGRSDGDGISIFGSQKIWVDHCSMSHCTD GLIDAVMGSTAITISNNYFTHHDEVMLLGHDDNYAPDTGMQVTIAF NHFGQGLVQRMPRCRRGYIHVVNNDFTEWKMYAIGGSGNPTINSQG NRYSAPSDPSAKEVTKRVDSKDDGEWSNWNWRTEGDLMENGAFFV

		ASGEGMSSMYSKASSVDPKAASLVDQLTRNAGVFGGPRDDQGQSG NSYSPYGGDGGGGGSSGGSSGGGMDVMGGTTRGSSSSSGDDSNVF QMIFGSDAPSRPRLTLLFSLLMISVLSLSTLLL
AtPLL1 4	AT5G 55720	MSIVCTFFLFLLNTSFAFAFAIPKPPIVRRLSTTVTSNSTASSCSANGNP IDECWRCDENWKDNRKNLADCAVGFGRDSIGGRAGEFYTVTDSGD DNPLNPTPGTLRYAATQDQPLWIIFDRDMVIQLKQDLQVASYKTIDG RGNNVQIAYGPCLTLYKVSNIIINNLYIHDCVPVKRNALSSLGGYSDG DGISIFESRDIWIDHCTLEKCYDGLIDAVNGSTDITISNSYMLNHNEV MLLGHSDEYSGDRDMRVTIAFNYFGEGLVQRMPRCRHGYFHIVNNI YRDWKMYAIGGSANPTIFSQGNVFIASNNQFTKEVTKRESADGDEE WKEWNWKSEGDEMVNGAFFTPSGKEDSPSYAKFSSMVARPASLLK TTHPSVGVLSCEIDQAC
AtPLL1 5	AT5G 63180	MFRPNSLLIPSNLSTTKSQRNTMLNSSYLSFALIFFCCILFSALASSLPV SDPELVVEEVHRKINESISRRKLGFFSCGSGNPIDDCWRCDKDWEKN RKRLADCGIGFGKNAIGGRDGEIYVVTDPGNDDPVNPRPGTLRYAVI QDEPLWIIFKRDMTIQLKEELIMNSFKTLDGRGASVHISGGPCITIQYV TNIIIHGLHIHDCKQGGNTYVRDSPEHYGYRTVSDGDGVSIFGGSHV WVDHCSLSNCNDGLIDAIRGSTAITISNNYLTHHNKVMLLGHSDTYE QDKNMQVTIAFNHFGEGLVQRMPRCRHGYFHVVNNDYTHWEMYA IGGSANPTINSQGNRFLAPDDSSSKEVTKHEDAPEDEWRNWNWRSE GDLLLNGAFFTYSGAGPAKSSSYSKASSLAARPSSHVGEITIASGALS CKRGSHC
AtPLL1 6	AT1G 67750	MRMTLVHLSLSLFSCLLLVLSPTFIASTPVSEPELVVQEVNEKINASR RNLGVLSCGTGNPIDDCWRCDPKWEKNRQRLADCAIGFGKHAIGGR DGKIYVVTDSSDKDVVNPKPGTLRHAVIQDEPLWIIFARDMVIKLKE ELIMNSFKTIDGRGASVHIAGGACITVQYVTNIIIHGVNIHDCKRKGN AYVRDSPSHYGWRTASDGDAVSIFGGSHVWVDHCSLSNCADGLIDA IHGSTAITISNNYLSHHNKVMLLGHSDSYTRDKNMQVTIAFNHFGEG LVQRMPRCRHGYFHVVNNDYTHWQMYAIGGSAAPTINSQGNRFLA PNDHVFKEVTKYEDAPRSKWKKWNWRSEGDLFLNGAFFTPSGGGA SSSYAKASSLSARPSSLVASVTSNAGALFCRKGSRC
AtPLL1 7	AT3G 53190	MMLQRSCIVLFFSLFLLVPQMVFSMLNRTLLLIPHPDPELVAYQVQW KVNASITRRQALDTTDQAGSTPCITGNPIDDCWKCDPNWPNNRQGL ADCGIGFGQYALGGKGGQFYFVTDSSDDDAVNPKPGTLRYGVIQEE PLWIVFPSNMMIKLKQELIFNSYKTLDGRGANVHIVGGGCITLQYVS NIIIHNIHIHHCYQSGNTNVRSSPTHYGFRTKSDGDGISIFGSKDIWIDH CSLSRCKDGLIDAVMGSTGITISNNFFSHHNEVMLLGHSDHYEPDSG MQVTIAFNHFGEKLIQRMPRCRRGYIHVVNNDFTQWEMYAIGGSGN PTINSQGNRYTAPTNPFAKEVTKRVETPDGDWKGWNWRSEGDILVN GAFFVASGEGAEMRYEKAYSVEPKSASFITQITFHSGVLGVGGRNNN LGMWTTTGSEGTSGLDSYNDYTDEMSGAGSTNRLSFSVLVFLLSSIS YLVVFTSSTQMFML

AtPLL18	AT3G27400	MVSYSNNHFAYAFLLLLTIGNTLAFSSSLPDHVQDPNLVVDDVNRSV FNASRRSLAYLSCRTGNPIDDCWRCDPNWETNRQRLADCAIGFGKN AIGGRKGRIYVVTDPANDDPVNPRPGTLRYAVTQEEPLWIIFKRDMV IRLKKELIITSFKTIDGRGSSVHITDGPCLKIHYATNIIIHGINIHDCKPG SGGMIKDGPHHTGWWMQSDGDAVAIFGGKHVWIDHCSLSNCDDGL IDAIHGSTAITISNNHMTHHDKVMLLGHSDSYTQDKNMQVTIAFNHF GEGLVQRMPRCRHGYFHVVNNDYTHWEMYAIGGSASPTIYSQGNR FLAPNTRFNKEVTKHEDAPESKWRDWNWRSEGDMLLNGAYFRESG AEAPSTYARASSLSARPSSLVGSITTTAGTLSCRRGRRC
AtPLL19	AT4G24780	MKMQTKKLFITIVSFLLYAPLFLSSPVPDPESVVEEVHKSINASVAGR RKLGYLSCTTGNPIDDCWRCDPHWEQHRQRLADCAIGFGKNAIGGR DGRIYVVTDSGNDNPVSPKPGTLRHAVVQDEPLWIIFQRDMTIQLKE ELIMNSFKTIDGRGASVHISGGPCITIQYVTNIIIHGIHIHDCKQGGNA MVRSSPRHFGWRTISDGDGVSIFGGSHVWVDHCSFSNCEDGLIDAIM GSTAITLSNNHMTHHDKVMLLGHSDTYSRDKNMQVTIAFNHFGEGL VQRMPRCRHGYFHVVNNDYTHWEMYAIGGSANPTINSQGNRFLAP NIRFSKEVTKHEDAPESEWKRWNWRSSGDLLLNGAFFTPSGGAASSS YAKASSLGAKPSSLVGPLTSTSGALNCRKGSRC
AtPLL20	AT3G07010	MAVTKLILFASALLLTALFIGVNASRSNETWHEHAVENPDEVAAMV DMSIRNSTERRRLGYFSCATGNPIDDCWRCDRKWQLRRKRLADCSI GFGRNAIGGRDGRFYVVTDPGDDDPVNPIPGTLRHAVIQDEPLWIIFK RDMVITLKQELIMNSFKTIDGRGVNVHIANGACLTIQYVTNIIVHGIH VHDCKPTGNAMVRSSPSHYGFRSMADGDAISIFGSSHIWIDHNSLSN CADGLVDAVMSSTAITVSNNFFTHHNEVMLLGHSDSYTRDKVMQV TIAYNHFGEGLIQRMPRCRHGYFHVVNNDYTHWEMYAIGGSAGPTI NSQGNRFLAPVNPFAKEVTKREYTGESKWKHWNWRSEGDLFLNGA FFTRSGAGAGANYARASSLSAKSSSLVGTMTSYSGALNCRAGRRC
AtPLL21	AT5G48900	MAVTQILVVFASALLLSMFFTGVDSTRSNETWHEHAVENPEEVAAM VDMSIRNSTARRRLGYFSCSTGNPIDDCWRCDRRWQSRRKHLANCA IGFGRNAIGGRDGRYYVVSDPNDDNPVNPKPGTLRHAVIQEEPLWIV FKRDMVITLKEELIMNSFKTIDGRGVNVHIANGACITIQFVTNIIIHGIH IHDCRPTGNAMVRSSPSHYGWRTMADGDGISIFGSSHIWIDHNSLSN CADGLIDAVMASTAITISNNYFTHHNEVMLLGHSDTYTRDKVMQVT IAYNHFGEGLIQRMPRCRHGYFHVVNNDYTHWEMYAIGGSASPTIN SQGNRYLAPRNRFAKEVTKRDYAGQWQWRHWNWRSEGDLFLNGA FFTRSGSGLGASYARASSLAAKSSSLVGVITYNAGALNCRGGRRC
AtPLL22	AT3G24670	MVIFSRSFLALSTTLIILALCINSSTMAQETEDLNSHSSSNSSTANKLPN DDGAWNEHAVKNPEEVAAMVDMKIKNSTERRRLGFFSCATGNPID DCWRCDRNWHLRRKRLANCAIGFGRNAIGGRDGRYYVVTDPSDHD AVNPRPGTLRHAVIQDRPLWIVFKRDMVITLTQELIMNSFKTIDGRG VNVAIAGGACITIQYVTNIIIHGINVHDCRRTGNAMVRSSPSHYGWRT MADGDAISIFGSSHIWIDHNSLSNCADGLIDAIMGSTAITISNNYMTH HNEVMLMGHSDSYTRDKLMQVTIAYNHFGEGLIQRMPRCRHGYFH VVNNDYTHWVMYAIGGSANPTINSQGNRFLAPGNPFAKEVTKRVGS

		WQGEWKQWNWRSQGDLMLNGAYFTKSGAAAPASYARASSLGAKP ASVVSMLTYSSGALKCRIGMRC
AtPLL23	AT4G13210	MVVARTLFSISATLIIFLALFLHVNAVQETREPKHESSRNTSTVDNLS DGEWHEHAVKDPEEIAAMVDMSIRNSTYRRKLGFFSSCSTGNPIDDC WRCDKKWHRRRKRLADCAIGFGRNAVGGRDGRYYIVTDPSDHDPV TPKPGTLRYAVIQDEPLWIVFKRDMVITLSQELIMNSFKTIDGRGVNV HIAGGACLTVQYVTNIIIHGINIHDCKRTGNAMVRSSESHYGWRTMA DGDGISIFGSSHIWIDHNSLSSCADGLIDAIMGSTAITISNNYLTHHNE AILLGHTDSYTRDKMMQVTIAYNHFGEGLIQRMPRCRHGYFHVVNN DYTHWEMYAIGGSANPTINSQGNRFLAPGNRFAKEVTKRVGAGKGE WNNWNWRSQGDLMLNGAYFTSSGAGASANYARASSLAAKSSSLV GMLTSSSGALKCRIGTLC
AtPLL24	AT3G24230	MATSSLKLTSACFVLLFIFVGCVLTATNLRNNEISRSRKLKTEDSKSF NSSPMTTRLDGVVELNEHAVTDPDKVAHEVSNLIHMSEQNITARRK LGFFSCGNGNLIDDCWRCDRNWNKNRKHLADCGMGFGSKAFGGR NGSYYVVTDHSDDDVVNPKPGTLRHAVIQVEPLWIIFKRDMVIKLK QELIMNSFKTIDARGANVHIANGACITIQNITNVIVHGLHIHDCKRTG NVTVRSSPSQAGFRGTADGDAINIFGSSHIWIDHNSLSNCTDGLVDV VNGSTAITISNNHFTHHDEVMLLGHNDSYTRDKMMQVTVAYNHFG EGLIQRMPRCRHGYFHVVNNDYTHWKMYAIGGSANPTINSQGNRFA APKNHSAKEVTKRLDTKGNEWMEWNWRSEKDLLVNGAFFTPSGEG ASGDSQTLSLPAKPASMVDAITASAGALSCRRGKPCY
AtPLL25	AT4G13710	MASSSQKLISVCVAVLVVLALTAMIFRNSEISLSRKLKTEVIQSSNSST MAAIRKLKTEEFQSLNSSTMAATRLDGEPQQQQHAVADDPDMVAD EVAKLVQMSEQNRTARRKLGFFSCGTGNPIDDCWRCDRNWHKNRK RLADCGIGFGRNAIGGRDGRFYIVTDPTDEDVVNPKPGTLRHAVIQE EPLWIVFKRDMVIELKQELIMNSFKTIDARGSNVHIANGACITIQFITN VIIHGLHIHDCKPTGNAMVRSSPSHFGWRTMADGDAVSIFGSSHIWI DHNSLSHCADGLVDAVMGSTAITVSNNHFTHHNEVMLLGHSDSYT KDKLMQVTIAYNHFGEGLVQRMPRCRHGYFHVVNNDYTHWEMYA IGGSAEPTINSQGNRYAAPMDRFAKEVTKRVETDASEWKKWNWRS EGDLLLNGAFFRPSGAGASASYGRASSLAAKPSSMVDTITSTAGALG CRKGRPC
FaPLc	maker-Fvb2-4-augustus-gene-151.44-mRNA-1	MHFYMTPLLLLLALLVCVSASVENGKPVQSRFVEVVEEPrSSFNSSM ADrSNDHWNEHAVDNPEEIASLVDTSIRNSSTRRELGYFSCATGNPID DCWRCDPQWQRHRKRPANCGIGFGRNAVGGRDGKYYVVSDPGHD DPVNPRPGTLRHAVIQDRPLWIVFKRDMVITLKQELIMNSFKTIDAR GVNVHIAYGGCITIQFVTNVIIHGLHIHDCKPTGNAMVRSSPSHYGW RTMADGDGISIFGSSHIWVDHNSLSNCADGLIDAIMGSTAITISNNYF THHNEVMLLGHSDSYTRDRQMQVIAYNHFGEGLIQRMPRCRHGYF HVVNNDYTHWEMYAIGGSADPTINSQGNRYLAPNNRPAKEVTHRV QTTGRWRHWNWRSEGDLLLNGAYF

AtPLL26	AT1G04680	MAVLPTWLLAMMCLLFFVGAMENTTHDNISSLPRSDETEWNQHAVTNPDEVADEVLALTEMSVRNHTERRKLGYFTCGTGNPIDDCWRCDPNWHKNRKRLADCGIGFGRNAIGGRDGRFYVVTDPRDDNPVNPRPGTLRHAVIQDRPLWIVFKRDMVIQLKQELIVNSFKTIDGRGANVHIANGGCITIQFVTNVIVHGLHIHDCKPTGNAMVRSSETHFGWRTMADGDAISIFGSSHVWIDHNSLSHCADGLVDAVMGSTAITISNNHLTHHNEVMLLGHSDSYMRDKAMQVTIAYNHFGVGLIQRMPRCRHGYFHVVNNDYTHWEMYAIGGSANPTINSQGNRYAAPKNPFAKEVTKRVDTPASHWKGWNWRSEGDLLQNGAYFTSSGAAASGSYARASSLSAKSSSLVGHITSDAGALPCRRGRQCSS
VvPL2	VIT_201s0026g01670.1.v2.1	MAAVKSSSLLLLFFVLFAVIAPTIRAHIAEYDDYWKEREEEAKKAALEAFHPTPQEVNDHFNLHVEDELTGSNGTRRSLRVNKGPCKATNPIDRCWRCRPNWASQRKRLADCVLGFGRNTVGGKYGKYYFVTDPSDNDMVNPKKGTLRHAVIQPRPLWIVFARSMIIRLNQELIMTSDKTIDGRGVNVHIAYGAGITIQFVKNVIIHGLHIHDIVSGSGGLIRDSVNHFGYRSRSDGDGISIYGSSHVWIDHNSMSNCKDGLIDAIQGSTAITISNNHFTKHNEVMLFGASDSNSADEIMQITVAFNHFGRGLIQRMPRCRWGFFHVVNNDYTHWNMYAIGGSAHPTIISQGNRYTAPHLVDPKHDAKQVTKRDYAMESEWKKWTWRSEGDLMRNGAFFVPSGNPSKRMPYSRLDMIKAKPGTYVSRLTRFSGALTCRRGGPC
VvPL3	VIT_201s0026g01680.1.v2.1	MAAPKSNSLLLLFVVMFMVVVPTIRAHIAEYDDYWKAREKEAKTVAIDAFDPSPEDVNDDFNKNVEKSIFGKNGTRRNLKVNKGPCKATNPIDRCWRCRRNWAMDRRRLADCVLGFGRRTVGGKHGRLYIVTDPSDNDMLNPKPGTLRYAVIQPQPLWIVFGRSMIIKLKQELMVTSDKTIDGRGVNVHIAYGAGITIQFARNVIIHGLHIHDIVSRPGGLIRDSVHHFGLRTRSDGDGISIFGSSHVWIDHNSMSKCEDGLVDAIQGSTAITISNNHFTKHNETMLLGASDGYSGDIIMQVTVAFNHFGRGLIQRMPRCRWGFFHVVNNDYTHWNMYAVGGSAHPTIVSQGNRYVAAPLMDPKHDAKEVTKRDHATKAEWSKWTWRSEGDLMVNGAFFVQSGVPFKKKPFSRYDMIKAKPGKFVPRLTRYSGALTCWRTSPC
VvPL13	VIT_214s0108g00030.1.v2.1	MGAYKFSSLLLLSFFAFAVLAPSIRAHIGEFDEVWQKRAEEAQKAALEAYQPNPEEVTNQFNKNVRKSMQGTNTTRRNLRSNNGPCMATNPIDRCWRCKQDWAKNRKKLADCVLGFGRRTTGGKDGEFYVVTDASDNDMIDPKPGTLRHAVIQKEPLWIIFARDMIIRLKQELIMAGNKTIDGRGANVHIAYGCGITIQFVKNIIIHNLHIHDIVPAQGGMIRDSVDHYGLRTASDGDGVSIFGSSNVWVDHLSMSNCKDGLVDVIMASTAITISNCHFTNHNEVMLFGGSNNFQGDKIMQVTVAFNHYGRGLVQRMPRCRYGFVHVVNNDYTHWLMYAIGGSQNPTIISQGNRFIAPPNMACKEVNKKW
VvPL15	VIT_217s0000g05740.1.v2.1	MRLVILIPFLVIVPAVTANIGDFDEVWQTRAEEARKAALQAYNPHPEKVTDNFNKKVHKSFDSTNHTRRNLSKFSGLCMATNPIDRCWRCRSDWASNRMKLADCVLGFGQKTTGGKGGKIYVVTDPSDNDMVNPKPGTLRHAAIQEEPLWIIFAHSMAIRLNEELIMTSNKTIDARGANVHIANGAGLTLQFVHNIIIHGLHIHDIKVGNGGLIRDSASHYGFRTRSDGDGISIFGATNIWIDHISMSNCADGLIDAIMASTAITISNCHFTHHNEVMLFGAS

		DGYSGDAIMQITITFNHFGQGLTQRMPRCRWGFFHVVNNDYTHWL MYAIGGSHHPTILSQGNRFIAPPDINCKEVTKRDYSPESVWKSWTWR SQGDLMMNGAFFVESGDPNFDFSNKYVIRAKPGAFVTRLTRFSGALS CREGMPC
VvPL5	VIT_205s0051g00590.1.v2.1	MKLFSDSLNLFSTCHPYLLLQLDPSRERAFDPMPMAGSKGWTSLCSL LLFFLFVAVMANDRNGGTEQLQSSNNSSMAARNEHAVDDPDAVAS MVDMSIRNSTERRKLGYFSCGTGNPIDDCWRCDHNWQKNRKRLAD CGIGFGRNAIGGRDGRFYVVTDPGDDDPVNPKPGTLRHAVIQDAPL WIVFKRDMVITLKQELIMNSFKTIDGRGVNVHIANGACITVQFVTNVI IHGLHIHDCKPTGNAMVRSSPSHFGWRTMADGDAISIFGSSHIWVDH NSLSSCADGLVDAVMGSTAITISNNHFAHHNEVMLLGHSDSYERDK QMQVTIAYNHFGEGLIQRMPRCRHGYFHVVNNDYTHWEMYAIGGS ASPTINSQGNRYLAPVNPFAKEVTKRVDTPSGQWKGWNWRSEGDL LLNGAYFTPSGAGASASYARASSLGAKSSSMVGSITSNAGALSCRRG SQC
VvPL6	VIT_207s0005g05520.1.v2.1	MAVSLRWFSLCSLLVLVLFLRVNADELQKLRVEEKPDQLQSLENST MAERLDKSEGWNERNEHAVENPEEVASMVDMSIRNSTERRNLGYFS CGTGNPIDDCWRCDPHWQLHRKRLADCGIGFGRNAIGGRDGRYYV VTDPGDYDAVNPRPGTLRHAVIQDKPLWIVFKRDMVIKLKQELIMN SFKTIDARGVNVHIANGACITIQFITNVIIHGLNIHDCKPTGNAMVRSS PSHYGWRTMADGDGISIFGSSHIWIDHNSLSNCADGLIDAVMGSTAI TISNNYFTHHNEVMLLGHSDSYTRDKQMQVTIAYNHFGEGLIQRMP RCRHGYFHVVNNDYTHWEMYAIGGSAEPTINSQGNRYLAPANPFAK EVTKRVITSNSVWKHWNWRSEGDLLLNGAYFTPSGAGAAASYARA SSLGAKSSSMVGTITSGAGALSCRRGRQC
VvPL17	VIT_219s0015g00510.1.v2.1	MSTLSLSFLVILLYVSTAYSARLLPLESEATTWSSRGGSLRTQLDEVS CRTGNPIDDCWRCDPDWETNRKMLADCGVGFGRNAIGGRDGELYV VTDSGNDDPANPIPGTLRHAVIQYVPLWIVFDHDMVINLKEELIMNS YKTIDGRGFNIQIANGACITIQNVSNIIIHGVYIHGCVPTGNAIVRDRP DHYGMRGMSDGDGISIFGGTDIWIDHCTLADCYDGLIDAVYGSKSIT ISNNYMLNHNEAMLMGHSDDFLADKNMQVTIAFNYFGEGLVQRMP RHGYFHIVNNVYTDWEMYAIGGSANPTINSQGNVFIARDDNSTKEV TKRESLLGYEEWKDWNWRSDGDLMLNGAYFRASGEEAPASYSKAS SMVARPASLLTYITASAGVLNCKIGYAC
VvPL12	VIT_214s0219g00230.1.v2.1	MATFAMSLLFLFSLLPPILGSSAPVQDPEVVVQEVHRSINASRRNLGY FSCGTGNPIDDCWRCDANWDKNRQRLADCAIGFGKDAMGGKNGRI YVVTDSEDDDPVNPRPGTLRHAVIQDEPLWIIFKRDMVIKLKQELVM NSFKTIDGRGASVHIAGGPCITIHYASNIIIHGLHIHDCKQGGNANIRN SPHHSGWWTVSDGDGVSIFGGRHIWVDHCSLSNCHDGLIDAIHGST AITISNNFMTHHDKVMLLGHSDSYTEDKNMQVTIAFNHFGEGLVQR MPRCRHGYFHVVNNDYTHWEMYAIGGSADPTINSQGNRFLAPNDR FKKAVTKHEDAPESEWRHWNWRSEGDLMLNGAFFLQSAAGASSSY ARASSLSARPSSLVGSITLGSGALGCRKGSRC

VvPL1	VIT_201s0137g00240.1.v2.1	MKEVDPIIPALFLYNPTPFSQLSHYFFFSSLFFLFSRREKAMAIPLSVLLFLLPLLSPTFISSSPVQDPELVVEEVHKRINASRRNLGFLSCGTGNPIDDCWRCDPDWEKNRQGLADCSIGFGRHAIGGRDGEIYVVTDSGDYDPVNPKPGTLRYAVIQKEPLWIIFQRDMVIKLKEELIMNSFKTIDGRGASVHIAGGPCITIQYVTNIIIHGLNIHDCKQGGNANVRDSPDHYGWRTISDGDGVSIFGGSHVWVDHCSLSNCNDGLVDAIHGSTAITISNNYMTHHNKVMLLGHSDSYTQDKNMQVTIAFNHFGEGLVQRMPRCRHGYFHVVNNDYSHWEMYAIGGSAEPTINSQGNRFLAPDDRFSKEVTKHEDAPQSQWKNWNWRSEGDLLLNGAFFTASGAGASSSYAKASSLGARPSSLITTITNGAGALNCKKGKRC
VvPL16	VIT_217s0000g09810.1.v2.1	MASSSLSLFFLFSLLSPILIASSPVQDPELVIQEVHRSINESRRNLGYLSCGSGNPIDDCWRCNANWEKNRQSLADCAIGFGKNAIGGKNGKIYVVTDSSDDDVVNPKPGTLRYAVIQDEPLWIIFARDMVIKLKEELIMNSFKTIDGRGASVHIAGGPCITIQFVTNIIIHGLNIHDCKQGGNTNVRDSPSHYGFRTISDGDGVSIFGGSHIWVDHCSLSNCHDGLIDAIHGSTAITISNNYMTHHDKVMLLGHSDSYTQDKNMQVTIAFNHFGEGLVQRMPRCRHGYFHVVNNDYTHWEMYAIGGSADPTINSQGNRFLAPNDRFSKEVTKHEDAPESQWKNWNWRSEGDLMLNGAYFTPSGAGASSSYARASSLGARPSSLVASITGSAGALSCKKGSRC
VvPL4	VIT_201s0010g03340.1.v2.1	MDELVPKKRFEEGSVTTGKDSSIMRHENLVAHHVDSLHSLKKMHQDIVITPRLIMNNYKTIDGCRVNVHIAKGACITIHFDTTIIIHGLHIHDCKPIVNAMVRSPPSHFVVEGGQLVSKASKNRKQGRGIQATSLLCLTV
VvPL9	VIT_210s0116g01160.1.v2.1	MAYTALFLVLSCTLAYYASTLQAYSSLDYTPQTFTSYMPSSSKSSTKKVMNPIDSCWRRKANWASNRRALADCAVGFGKGAMGGKYGAMYVVTTPSDDPVNPKPGTLRYGVIQTKPLWIVFAKDMVITLKNELIMNSFKTIDGRGAKVEIAYGPCITIQGVSHVIIHGISIHDCKPGKSGLVRSTTMHVGHRLGSDGDAISIFTSSHVWIDHCYLASCTDGLIDVIHASTAITISNNYFSHHDKVMLFGHDDHFTADKVMSVTVAFNHFGTGLVQRMPRVRFGYAHLANNKYDEWEMYAIGGSANPTILSEGNHFTAPDNANTKEVTKREVKSGWKNWKWRSSKDKFVNGAYFVHLDGEAVPRFTLDPKHFLLLMVQWFLL
VvPL11	VIT_213s0019g04910.1.v2.1	MLPNTCILLLCLLCSLSPLIRATLNLNLTLPHQHPNPEVVVDEVQRRLNVSISRRQVLSVQENDGSSCLTGNPVDDCWRCDPNWQNNRQRLADCGIGFGLDAMGGKGGQFYVVTDSSDEDPINPAPGTLRHAVIQTQPLWITFSTNMLIKLKYELIVNSFKTIDGRGANVHITGRGCMTLQYVSNVIIHGVHVHHCVPSGNADIRSSPTHVGWRGKSDGDGISIFGSRKIWIDHCSLSYCRDGLIDAIMGSTGITISNNYFSHHDEVMLLGHDDKYSPDSGMQVTIAFNHFGEGLVQRMPRCRRGYIHVVNNDFTQWEMYAIGGSANPTINSQGNRYTAPGDINAKEVTKRVETDEEDWAEWNWRTEGDVMVNGAFFVPSGVGLSTQYAKASSVEPKSAALIQQLTMNAGALSGSRDDSMGVSYPGFSSGGTSSSISNNGGHGSSDDPDYFGMIFGSGSGSGAPPPPSVTIPMFFSLLIILILYVTINHGGVLLFL

VvPL18	VIT_200s0317g00150.1.v2.1	MASLPYADVDSNLRDLAGKAEGFGRLAVGGLHGPIYSVTTLADDGPGSLREGCRRQEPLWIVFEISGTINLSSYLSVSSYKTIDGRGQRIKFTGKGLRLKECEHIIICNLEFEGGRGHDVDGIQIKPNSRHIWIDRCSLHDYDDGLIDITRQSTDITVSRCYFSQHDKTMLIGADPSHIGDRCIRVTIHHCFFDGTRQRQPRVRFGKVHLYNNYTRNWSVYAVCASVESQIYSQNNIYEAGEKKVAFKYYTEMAADMEEAKSGLIRSEGDLFLSGAQSCLLTGIGEECIFHPSEYYPTWTIELASDSLKNVLQVCTGWQAIPRPAELMTSA
VvPL7	VIT_208s0040g02740.1.v2.1	MGGAHGRCSGTHRKHPTPAYTTFPDTTAPASAFGRDPSNTVRTNMSCLPYAHVDSNLRALAGQAEGFGRLAIGGLHGPLYHVTTLADDGPGSLRDGCRKKEPLWIVFEVSGIIHLSSYLNVSSYKTIDGRGQRIKLTGKGLRLKECEHVIICNLEFEGGRGPDVDGIQIKPNSKHIWIDRCSLRDFDDGLIDITRASTDITISRCHFSQHDKTMLIGADPSHTGDRCIRVTIHHCFFDGTRQRHPRVRYGKVHLYNNYTRNWGIYAVCASVESQIYSQCNIYEAGHKKVAFKYLTEKAADKEEERTGCLRSEGDLFINGTQAGLMTVASEMFHPREFYPTWTVEAPSDALKQVLHHCTGWQCVPRPADEAAIA
VvPL8	VIT_208s0007g04820.1.v2.1	MLDVDHSRRKPTQTHPSASAMLRRTCIVLISLLSSLSALATPMQNLTLLGQHPDPEAVVQEVQRRVNVSVSRRQTLEVSQSDQSSSCVTGNPIDDCWRCDPNWEADRQRLADCAIGFGQYALGGKGGQIYVVTDSSDHDAVTPRPGTLRYAVIQSDPLWIVFATNMLIKLSQELIFNSYKTLDGRGANVHIVGGGCITLQYISNVIIHNIHIHHCVQSGEANVRSSPTHYGWRTLSDGDGISIFGSRDIWIDHCSLSHCKDGLIDAVMGSTGITISNNFFSHHDEVMLLGHSDSYVPDSGMQVTIAFNHFGEQLVQRMPRCRRGYIHVVNNDFTRWEMYAIGGSGSPTINSQGNRYTAPSNRNAKEVTKRVDTDEKKWRDWNWRSEGDILVNGAFFIASGETVEVLYEKAYSVEPKSAALIDQLTTNAGVLGGSGNNLGTWRTERSGGGYGFGDDYSENMLSGSPSSFALSSTLLPPLFLLSSFLLLYL
VvPL10	VIT_213s0019g04900.1.v2.1	MLRNTHIVFICLLGCLCPVITATDLPHQHPNPEAVVLQVQRRLNASLARRGLLGVHENDQVSCLTGNPIDDCWRCDPNWEADRQHLAECGIGFGQQAVGGKGGQVYVVTDHSDSGNPGSLRYAVTKPEPLWIIFSSDMLIKLKRELIVNSYKTIDGRGANVQITGGGCIGLKYVTNVIIHNIQLHHCVPSESDGDGISIMGSRYIWIDHCSLSYCKDGLIDATLGSTAITLSNNYFSHHDKVMLLGRSDGDEMDDGMQVTVAFNRFGEALEQRMPRCRRGYFHVVNNDYTQWGIYAIGGSASPTINSQGNRYTAPPSTNAKEVTRRMDAKDGDWARWNWRTEGDIMVNGAYFVPSGDGLGAQFAMASSVEPKSAGFIDQLTMNAGALPPTSVVGSIPNGQVPNSIPNSQVPNGVPNDPVPNVGGTNGDNGGLGSYSGGAGANSGYAGGGAASGSNYGDGGGAAAAGANPGYAGGGAASGSNYGDGGGAAASGSNYGDWNFFGMTHGSGAPRLPPPSTTSVLSAPFVTLFLYFIINYGCCILPL
VvPL14	VIT_216s0039g00260.1.v2.1	MTNNIGTDLIRYEVTDPSDHPLNPKPGTLRFGATNIKGKVWITFKQSMRIKLEKPLLISSFTTIDGRGASIHIAGGACLLLHEVTNVIIHGIRIHHCRAQMPGQVLGPDSKMMELGHVDGDAIRLVASSQIWIDHNTLYECQDGLLDVTRGSTDITISNNWFRNHDKVMLLGHDDEYLQDKNMKVTVAFNHFGPNCYQRMPRVRHGYTHVVNNLYLGWEQYAIGGSMNPSVLSEANLFIAPESGTKEVTWRQDNNENGRSWNFQSVRDVFENGAHFSQ

		TGDSAKRPHYNHLQTFRVADAKAVRPITRSSGALRCRKRSRC
FvPLA	FvH4_4g05760.1	MAVSENKKWITACVSVLLLFCFVAAMSGRVSLDGTPILRNGGTEEL QSSSNSSMAPRVNENDDGGLNKHAVENPDEIAAMVDMSIRNSTERR KLGYFSCGTGNPIDDCWRCDPNWQKNRKRLADCGIGFGRNAIGGRD GRFYVVTDPNDDDPVNPRPGTLRHAVIQDEPLWIVFKRDMVIQLKQ ELIMNSFKTIDGRGVNVHIANGACITIQFVTNVIVHGLHIHDCKPTGN ALVRSSPSHFGWRTMADGDAISIFGSSHIWVDHNSLSNCADGLVDA VMGSTAITISNNHLTHHNEVMLLGHSDSYTRDKQMQVTIAYNHFGE GLIQRMPRCRHGYFHVVNNDYTHWEMYAIGGSADPTINSQGNRYA APTNPFAKEVTKRVETSQTQWRGWNWRSEGDLLLNGAFFTPSGAG ASAVYARASSLGAKSSAMVGTITAGAGALGCRRGRTC