

Table S4 The protein backbones of newly identified BrAGPs.

Gene name	BRAD locus ^a	Domains	Protein backbones
<i>BrAGP46</i>	<i>Bra008765</i>	-	<u>MAARSSLIRFAFVCIVLAVLVMTAESHNGVNH</u> GPAKSP <u>SSHDPKAH</u> APAP <u>SAATFSAYPO</u> <u>LIATALVGALS FVF</u>
<i>BrAGP47</i>	<i>Bra023457</i>	-	<u>MAARSSLVRFAFVCIVLAVLVMTAESHAGHHH</u> GPAMAPGMAP <u>MPHHH</u> TPAPAP <u>SGATFS</u> <u>AYPQLIATALVGALS FVF</u>
<i>BrFLA35</i>	<i>Bra007193</i>	FAS	MRRLLIKKNPVFFLFLITSSLTILIFSLRLPD SP PIIFTGKL RADLSDELGFFGNMIIEML PEDLVFTAFVPSEKAFDRDLGMTKPNNTRKSKSLEDEENTYAVVSRI LGFAVVPYRVEAG DVGKDETASYESLSGFTLKIWRKSGGLVVNGVETEKMGLKRGKIMVHIMDGVIMD SDF AQSVASTD TP QDEE EPKP
<i>BrFLA34</i>	<i>Bra018207</i>	FAS	MSPPP AGINLTQILING HNFNVALSLLVASGVITEL ENDDHGAGITVFVPTDSAFSDLPENQ NLQSLPADKKAIVLKFHVLNSYYTLGSLESITNPVNPTLATELMGAGSYTLNISRVNGSIV TINSGLV LALVTQTAFDQNPVS VFGVSKVLLPKELFPKSGQPVS TP ATT TPP RQVSL SP EG SDDQPSRLV APP GEVVSSSTVKRTRVFFYLCWCIAFWCAFLV
<i>BrFLA36</i>	<i>Bra023589</i>	FAS	<u>MRAIQTYVTLFFILVIITTTSTGAQK</u> SP HHGNNHDL SIAIEEMEKANYFSFVMLINMLHST NPRLLANI TFLMPRDKPLSRSNIIQQDSISDFLLRHSIPSPLLFEHLNLIPNGSIVPSSLPHYT LKITNGGRLNYFLNNVKIISRNICSLGSIKCHGIDGILPSP SAIND DS PRDNHT SP FISCPSSH NNSEHD SP HDNSEHD SP LNNSSNHSSRPDDHTHTHV APSP TS SP TLVPKSDSSTIREGDT

			<u>SGFVLLGLLSCVMGIAMAM</u>
<i>BrENODL7</i>	<i>Bra003532</i>	plastocyanin-like (PCNL) domain	MVVVASEGPRVFKVGDEFEWRVPLQNDTSVYSRWANTNRFHIGDSLSFVYDKDSVMEV DKWGFYHCNGSDPITAFDNGNSTFYLDRLPGLFYFISGSNAHCTSGQRLIVEVMHIHHHH NHHDVSLPPSMSPLSASSPSESAFDSHDPASSAAASSLLASFFPPFAALLVALFSCQP
<i>BrENODL19</i>	<i>Bra010371</i>	PCNL	MGLVKSFDAYLMIVMLTGLVFALGLSNGYKFYVGGKDGWVLTTPSEDYSHWSHRNRFO VNDTLYFKYPKGKDSVLEVSEEEYNTCNTTHPITSLSDGDSLFVLSRSGPFFVSGNSEN LKGQKLAVNVMSTAHHSRSPRQPSPPSPPTLSPIAWSPPAPSPGVVLSDSEALAPAPEPAK ARNSASLVGPGMVSLGLVLVVFIRSMV
<i>BrENODL35</i>	<i>Bra026261</i>	PCNL	MGLIKRFDAYLMTVMLMSLGFAGFSNGYKFYVGGRDGWVLTTPSEDYSHWSYRSRFQV NDTLYFKYPKGKDSVLEVSEEEFNICNTTHPITSLTDGDSLYVLSRSGPFFVSGNSEN KGQKLPVKVMSAAHHSHSPRQPSPPSPSPPTLSPSHQALSPPAPSPRVVLSESEALAPAPG PAKAHNSAGLVSPRAVSLGLVLVVIISFVL
<i>BrENODL40</i>	<i>Bra030730</i>	PCNL	MSLMVLSLSADAYKNYTVGESKGWFDIQRPSVNYQKWADSKSFSLGDFLIFNTDSNHS VVQTYDYKTYKSCDYNNEEDNSTREWSAAKPSATSPVPVSVKVPLVKEGSNYFFSGNY DGEQCKFGQHFMINVTHGQGLPSPDEDDETAPGPGQSSQSGDDDEVAPDTIVPANFDHP KDIESDDDDSLVKGRKNSSCIAKYNLVLCLVFMGLASFF
<i>BrENODL48</i>	<i>Bra036574</i>	PCNL	MRVTHAMYRSCNNNSNPSTFTTGNDSVTLTNHGHFFFCGVPGHCMAGQKLDLNVIHPI SSTPLSDPPISSSSSPPSTTTIPAAGVPGPSPSHAASLPAAAAVVYLLVSLIFANSAS
<i>BrENODL52</i>	<i>Bra041119</i>	PCNL	MGSNHSSGSGSSPWSGWGPNNNGQNTGSGGSGSGWGWGPKNNTNNSGSGSSGSGWGWG

			<p>WGS HSKGY NATYN AP RK FIVGG DKE W TYGF NYSDWASKTAPFFLNDILVFKYNPPAPFT HSVYLFSNPLSYEK CDVKKKGKMIASPKQGAGNGFELVLTKMKPYYIS CG EHDGAH CSN GT MKFTVMPILARW</p>
<i>BrUCL4</i>	<i>Bra005941</i>	PCNL	<p>MEKTSKKLFIFNLCINFGILVTRRCNATTYFVGDTSG WD ISSDLESWPLGKRFSVGDVLM FQYSSSH SV YEVAKDNFQSC NT TDPIRTFTNGNTTVALSKPGDRFFV CG NRLH CF AGMRL QVNVQGN GP SPAPVG AP RA AP AGILQPSSKKNNPATGVASSAAHIGGRGLRGSMNYFVY LMVFTFPLILYFINN</p>
<i>BrUCL7</i>	<i>Bra009259</i>	PCNL	<p>MGKTSTILFLFYLCIIFGISVITRCNATTYFVGDTSG WD ISSDLESWTLGKRFSVGDVLMF QYSSTH SV YEVAKDNFQSC NS TDPIRTFTNGNTTVALSKPGDRFFL CG NRLH CF AGMRL QVNVEGN GP SPSPVG AP GA AP VGILQPSSKKNNPPTGVATSS AP HVGGCGGRVSIIVTFVY LMVFGFPLLWTHILVTTKIRVYSIQCMHTYMYWFDYVKLWFGLV</p>
<i>BrSCL2</i>	<i>Bra007734</i>	PCNL	<p>MAMG MF GESLASSSLHKFH NV KQVSRRDFLSC NATSALATYNSGSDTVALKNPGHYFF LC GFPGH C QAGQKLHVLVVATSTA SP SL SP DL SP APSPSIGS SP SPAQATASDDSAQNGALS <u>VSLSTAMSGVVVFVVAFNLY</u></p>
- (divided into unknown PCNL-contai ning protein	Bra018282	insufficiently long PCNL	<p><u>MALIKNKSLFASFMI</u> FVALFVGTVHNVGDTKG WT MMGV DYEAWASSRTFQVRDSLIF EN NKDYHDDKTSV PASL GP AA AP VPRQVR SP SL SP LPDSTVNN GP RYQKKPSRVPHSA <u>ASNSSVWIGSYILISLPFFILE</u></p>

subfamily)			
<i>BrENODL53</i> (divided into BrENODL subfamily)	<i>Bra025873</i>	PCNL	<u>MVSSQQRLSFSSSKLVFFFCILSLFSRPSLS</u> ASFLVDGVS V WKTPVVHVGD S VIFR H KYGN DLYIFRTKDAFN V CDFTQATLLTKSNST S FTWYPSRPGSY F SFTNNTSLPK T QLSQKLT VQVLLAAASWPSQPP T PAI A PGPVSEGGDVSS S P S YPWPL G PREGSAL S PGPSPSEITSVT VPGKDGVPFINSNPAVPLPTGEVDST S INPLPTSTNSAHQVM M TVTVKLVLC C VAMFLLL
<i>BrXYLP1</i>	<i>Bra024265</i>	non-specific lipid transfer protein 2 (nsLTP2) domain	MATSFSAA T PFVFILL L SISSVT V HGASH H HTAAPAPAVD C STLIINMAD C LDFVMAGGTS AKPKSS C CAGLKT V LKADA E CEAFKNSAAFGITLNM T KAATLPTA C KLHAPSISN C G LSM T PTM A PG L APGGAVAA G P G AAGTTL A PTPSQ G NDGSS L IPISFTT L FSALFFVL F LSR <u>V</u>
<i>BrXYLP2</i>	<i>Bra031935</i>	nsLTP2	MATSFSTLTPFLFILL L SISSVLEA A HHHTAAPAPAVD C SMLILNMAD C LSFVSAGGTEAKP ASS C CNGLKT V LKTDA E CEGFKSSASLGVT L NMTKAATLPA A CKLHAPSMAA C GLS A A PTM A PG L APGGGAVAA G P D LSFL A PNPSPGNHGSSLLPFSFTTILSTMFFVL F LSRV
<i>BrXYLP3</i>	<i>Bra013135</i>	nsLTP2	MAPRTMETSILMIFTV V ALMSGERAIAVD C SSLILNMAD C LSFVTNGSTVEKPEGTCCSG LKT V VRS G PE C CEGFKNSASLGVTLDLAKAASLPSA C KVAAPPSAR C GLAVSASPPAS S P EISPTAGAG A PSSSSEANAAT P VPVPAGSSDASLVSVSFAFALFIALISS F Y
<i>BrXYLP4</i>	<i>Bra037870</i>	nsLTP2	MKQSLLSILIFLLSSSFAPIHARNKSQ P AN S PSSVA A PAPGPSNSD C SSVIYDMMD C LSYITP GSNDTKPTKV C CGGILSVLQYNPT C VGLESSKTMGFAVN N TRARAMPTT C KLPIVAT HCPMLDEV T PAAS T PVSQSAG T PM T SPSSVA S TS S PSLAES P VMT A PS P SSSGTNHLSAS

			<u>TLTLVVIKVSFVAYISFFFSN</u>
<i>BrXYLP5</i>	<i>Bra000652</i>	nsLTP2	MSPSPVATPAPGPSNSDCSSVIYGMMDCLSYITPGSNDTIPTKVCCGGILSVLQYNPKCVC VGLASSKDMGIEINSTRAHSMPTTCKLPAAAPHCAIPGASAPGASTPVSPSAGTPMTSPSS DESPTSPSSDESPSSSLAESPGMTAPSPSSSGTNQLSVSTLTFLAIIVSSITYILGFSN
<i>BrXYLP6</i>	<i>Bra028639</i>	nsLTP2	MALFSAALPLL LL FLFVSSLSVNGNTAQSVESAMIMTLTKCLPFVTIGSQVEKPETACCS VIKTVLDTKAECLCEGLKSSAAAGINLNLTKAGTLPDACLKAPPMPACALFAKPPASAP APVPAARPLNGSGPGSNSAPAPSPSHSNHGSSISVLSLAISGALVIMFTRI
<i>BrXYLP7</i>	Bra037988	nsLTP2	MEQSTRSLIITIVITSMVLVGFGSSDLDQDREECTNQLVVLSPCLTYVGGNAKAPTKDCCG GFGQVITQSQKCVGILVKDKDDPNLGLKFNASLAAHLPTACHITAPNITKQISLLHLSPNS TLAREFESLGRLEASANSAPPLQNVKDGAGGGKAESVKSDGGKKKKSWLAVELLIFALF SHLLLVISSFTSSSFI
<i>BrXYLP8</i>	<i>Bra004824</i>	nsLTP2	MESWRISLVAIAIALLMATLVSAGEDKAKDKEECTEQLVGMATCLPYVQGQAKTPTPDC CSGLKQVLKSDKKCLCVIIQDRNDPDLGLQINVSALALPSVCHAVADVTKCPALLHMD PKSQEAQVFYQLANGLNKTGPASASTISAPAPTSVSPTAGSEDGNNSGRATSLPSKNHAQ <u>SFRKPWLVLVAAHLFIISFTITL</u>
<i>BrXYLP9</i>	Bra036905	nsLTP2	MSTVSAQSTCTNVLISMAPCLGYITGNSSSPSQCCSQLAHVLRSSGECLEVLKGGGPR LGINFNKTQALALPKACNVQTPPVSLCNDSSVKSPGSPNTSEHGNGSKTVPGHRSTSR GSSIKVSFSLAVLSAVSYIINYSRY
<i>BrXYLP10</i>	Bra021454	nsLTP2	MGYTSIYAITFVALVGALLGVSKAQPSGSCVSTLTTLSPCLGYITGNSTTPSQTCCSQLDS

			VIKSSPQCICSAVNSPIPNIGLNINRTQALQLPNACNIQAPPLSQCNVATGPTTFLGALSPVE SPADKNPGVALTPTSSPGARSGVVVGARGGSKTIPSTGAGSSSGSVDRVPPHLFIFICEFY FKEENDLSDLVSCVLRVGIKCCKGCQTNAKRKLLSVSGVSAVEYNAEQGLLRVSGDNP AKLLRKLAKWDKNAELVSLPGEVSAPAPRTTPQLYQTKRMGKRTPKCFLLRFCGTKEKV EPYGVAGDENGSA ^{TP} FINTV ^{APP} MVYPPPPQPT ^{TP} GFAT ^{TP} IPYPPPCFGANQPPYTYTSGGMY Q ^{SPPP} TFQLRKTQFPQMVNYPHH
<i>BrXYLP11</i>	<i>Bra040833</i>	nsLTP2	<u>MKMGMGLMLLTVM</u> <u>AVMSSTRVLAQSTCT</u> <u>SALISMSPCLNYITGNTTTPSQQCCSQLG</u> <u>NVVRSSPDCLCQVLNNGGSQLGINVNQTQALALPRACNVQTPPVSR</u> <u>CNNGGGSTADSP</u> AD ^{SP} NSS ^{GP} GNGSKTVPVGEGE ^{GP} <u>SSDGSSIKFSYPLLAFLSVASYMAIFLKY</u>
<i>BrXYLP12</i>	<i>Bra023817</i>	nsLTP2	<u>MKMGRVLVLLTVFMAVMSSTRVSAQSSCT</u> <u>TALISMSPCLNYITGNTTSPSQQCCSQLGNV</u> <u>VRSSPDCLCQALNNGGSQLGINVNQTQALALPRACNVQTPPVSG</u> <u>CNNGGGSTADSP</u> <u>TDS</u> ^P NSS ^{GP} GNGSKTVPVGE ^{GP} GDG ^S FS ^D <u>GSSIEISYRLLTFLSVASYIAIFLKY</u>
<i>BrXYLP13</i>	<i>Bra001874</i>	nsLTP2	<u>MKTGMGLMFLTIFMAVMSSTRVSAQSSCT</u> <u>SVLISMAPCLNYITGNTTSPSQQCCSQLSSV</u> <u>VQSSPDCLCQALNNGGRSQLGLNINQTQALALPRACNVQTPPISR</u> <u>CNNGGGSNADSP</u> <u>ADSP</u> KSS ^{GP} GNGSKTVPVGE ^{GP} GDG ^S SS ^D <u>GSSIKFSYPLLAFLIAASYMAVFLKY</u>
<i>BrXYLP14</i>	<i>Bra018473</i>	nsLTP2	<u>MAQTTTVIFILATLLVPATVVSQTTPSPVPAPSPTINEAMNCAAGLTVCLPAFAQGGTPSK</u> <u>ECC</u> <u>TAVKTQQSCLCGFIKAPVLVVPFNITAFSALISKSCGINTNLNLCSE</u> <u>T</u> <u>PAQA</u> <u>PLPHMTA</u> ^A ^Y PPSG ^{AP} KTDKDAASKPAETGLVGIVLIMISALFY
<i>BrXYLP15</i>	<i>Bra025919</i>	nsLTP2	<u>MEVVRF</u> <u>AVAVFVLFVSSSKA</u> <u>EPTPAMGGGGGGGGDAHSMPCIQKLMPCQPYLHSVTP</u> <u>PPPASCCLPMKEIVEKDATCLCSVFNNVDM</u> <u>LKSLNLTKENALVLPKACGAKADISLCKSS</u>

			NGTTTPSTGTTTTPPASSTGSGSTGASSSTDKPTNSAPAINFAGASFASAFMALATIFF
<i>BrXYLP16</i>	<i>Bra016563</i>	nsLTP2	MEILKFAVIFVLCSISSNAATTPPSGGAGDAHSMPCIQKLMPQPYLRSVTPPPASCCM PLKEIVETDVNCLCSVFNNVDMLKSLNLTKENALVLPKACGANADVSQCKASTGTTTPS TSPGTTKTPPASPAESGSTGGSASSTAKPSDSAPAINFSGISFAAAFVALATIFF
<i>BrXYLP17</i>	<i>Bra031024</i>	nsLTP2	MEIVRFTVAVFFVLYSVSSSNAATAPPSGGGGGGGDAQAMPQIQKLMPQPFLLHSVIPPPP PSCCLPLKAIVANDATCLCSVFNNVDMLKSLNLTKDNALDLPKACGANPDISLCKASPA GGTTTNSTSPATPKTPPVSSSTGSGSTGASSSTTSPSTSSAPAINFAGLSFASTIVALATTF
<i>BrXYLP18</i>	<i>Bra031023</i>	nsLTP2	MKIVRFTVAVFFVLYSVSSSNAAVAPPSGGGGGGGDARALPCIQKLKSCOPYLHSVIPPLP ASCCLSMKEMVANDAPCLCSVFNNVDMLKSLNLTRDNALDIPKACDAEPDISLCKASPA DGP TTNSTSSTPSTSSAPAINFAGLSFASTIVALATTF
<i>BrXYLP19</i>	<i>Bra031022</i>	nsLTP2	MEIVRFAVAVFFVLYSVSSSNAAIAPPSGGGGGGGDAQEMPQIQKLMPQPFLLHSVIPPP PPSCCLPMKAIVANDATCLCSVFNNVDMLKSLNLTKDNALDLPKACGANPDISLCKASP AGGTTTNSTSPATPKTPPVSSSTGDFHCGTTGASASSTSTPTSSAPAINFAGLSFASTIVALAA TFF
<i>BrXYLP20</i>	<i>Bra015955</i>	nsLTP2	MASSILFITLLISLSSISLQLVFAQVPGTTTATCSSMLLSLAPCGPFVQGFVQLPAQPCCDGL NQIYSQQPTCLCLFLNNTSTLSPAFFINQTLALQLPPLCNVPANASSCSSPGGEAPSDSSSV APPPSSSTSSPVSPSAKNNSSVAGTPVAQLAPRPTSLMGLGYDLRSSGSKSKIQLIILALAVI LPGTLFI
<i>BrXYLP21</i>	<i>Bra032857</i>	nsLTP2	MKDLHFHIFLVTMTVIASISAATPTAPAAGGALSDECNQDFQKVTLCLDFATGKAPTPSK

			<p>KCCDAIEDIKEKDPKCLCYVIQQAKTGGQALKDLGVQEAKLIQLPTACQLRNASISNCPK LLGISPSSDAAVFTSNATTITTEAPAGKSPATPATSSEKGGSSASIRDGHAVVALAITLITVSE <u>VSTLL</u></p>
<i>BrXYLP22</i>	<i>Bra010912</i>	nsLTP2	<p>MKGLYFHLFLVTMTVVASISAATPAAPSGGGSLLDECSKDIQTVSLCLDFASGKAPNPSK KCCDAIEDIKEKDPKCLCFVIQQAQSGGQTLKDLGVQEAKLIQLPTSQQLHNASISNCPK LLGISPSSAAAIFTSNATSTTTTAAPGGTSPATPATSSEKGGSSASIKDGHAVMLLAVALMSI <u>SFLSTLPWMGLA</u></p>
<i>BrXYLP23</i>	<i>Bra021455</i>	nsLTP2	<p>MSSLILGGKGQQIISTPCTSSMISTFTPCLNFITGSSGGSVTPTAGCCDSLKSLTSTGMNCA CLILTANVPLPTGFINRTLSLALPRACKMTGVPVQCAAGTPLPAPGPVPFLLAPPPPMSA FSPGSSKAAATAPGLAPDAPLDGPMGPTATPGIRPVVQPLQPTSLAQYSTSPFLPLLFFLFT LLTLLNL</p>
<i>BrXYLP24</i>	<i>Bra023816</i>	nsLTP2	<p>MSKISGITIVLVALIAVLAFPVRSQQPPLSQCTPSMMTTVGPCMSILTNSSTNGTSPSSDCC NSLKSLLTTGGMGCLCLIVTGSVFPNIPINRTTAVSLPRACNMPRVPLQCKANIAPAAAPGP ASTFGPAMSPGPATPLVPEPTTAAAQTPQSVTTRPFTTPTADGAAPTADNGGSTSRPSLTPSS <u>AYALSPSLLFFGISLVALKFY</u></p>
<i>BrXYLP25</i>	<i>Bra001875</i>	nsLTP2	<p>MSKIPVITIAVALLAVLALPVRSSQQPPLSQCTPSMMTTVGPCMSILTNSSTNGTSPSSDCCN SLRSLTTGGMGCLCLIVTGSVFPNIPINRTTAVSLPRACNMPRVPLQCNANIAPAAAPGA GTFGPAMSPSPATPIVPEPTTAAAQTPQSDTTRPFTTPVDGAAPPTSDDGGNTRPSVTPSSS <u>YALSPSLLFLVVSLVALKFY</u></p>

<i>BrXYLP26</i>	<i>Bra015426</i>	nsLTP2	MDPRFCLISALIFLSLLSNSPILILAQISTPCSPTMLSSVTGCMMSFLTGGGSSPTSDCCEALK SLTGTGLDCLCLIVTASVPINIPINRTLAISLPACGMPGVVPVKCKASAAPLPAPGPVSLGP TTPPTETQSPQGSASF GPTT SPASSIIPDDQNIPASDKGENPTASTPSASSPSSSHSIKLPLLLL <u>TFFAFQIISLLLS</u>
<i>BrXYLP27</i>	<i>Bra032462</i>	nsLTP2	MDPKSFLISALIFSLSNSPVLMSLAQINTPCSPTMLSSVTGCMMSFLTGGATSTTSDCCRAL KTLTGTSMDCLCMIVTANVPLDLPINRTLAISLPACGVPVQCKASSALLYSPGPASV GPT TSPPTETQNPEGSASF GPTAT SPTSSMDPDGMPDGKAHIFNT
<i>BrXYLP28</i>	<i>Bra039713</i>	nsLTP2	MAATIVFILMLAITSSTAVAETQGPSSSPAPTSEELVMFSPCIPYVSAPPNNISKTPDALC CSVFSTSVHSAAGKCLCYLLRQPMILGFPLDRSRLLSLSQICTEFQSSDESFE SLCSPSVSP ELPPLQSIQFT SP FDYGDRDSA SP QSLGLPPETAKDPPISDQF SP DIDNV SP QLIINGSPMIS <u>NLLFLTTIIMTLATCILTRI</u>
<i>BrXYLP29</i>	<i>Bra025907</i>	nsLTP2	MASSSVFITVLISLVPVFLQPGLAQGQSPPASCSALLLALAPCGPFVQGFVQFPAQPCCSSL SQIYSQQPTCLCLFLNNNSTLSSAFFINQTLALKLPQLCSIPANSSVCSGASTASPPSTNST GSQVSMGAKNNSVAAATPVAQVAPKPSNMMGLGDGLRSSGPTFKIQVTIFVIAAILAGTL <u>FLV</u>
<i>BrXYLP30</i>	<i>Bra040823</i>	nsLTP2	MKQSLILSILILLSSSFAQIHARNKSHPANPPSPVATPAPGPSNSDCSSVIFDMMDCLSYLTP GSNDTTPTKVCCGGILSVLQYNPKCVQIGLASSKDMGIALNNTRALAMPTICKLPAAAPH CAILDASRPSASTPGMSSVSPSAVTPMTQSSAQSPTFSPSLPESPGITAPSPSSSGTNHLSV <u>SKFTFVAVVVSITYISAFSN</u>

<i>BrXYLP31</i>	<i>Bra021349</i>	nsLTP2	MTNVAVIAAILITVLLSASVSEQMAPSPSSGSPSGAPDCMTNLLNMTDCLSYVQVGNNGG AANPDKACCP ELAGLVDSSPQCLCYLLGGDMAAQYG IKIDKAKALKLPGVCGVVTPDP SLCSLFGIAVG AP EAMGKEEA SPAFAP SSGAE SP EGLGS GP SASRTSDAPNTPYSLFLSVIII <u>PLAFAFHLYS</u>
<i>BrXYLP32</i>	<i>Bra014833</i>	nsLTP2	MKQSLISILILLSSSFAPIHARNKPQPAK SPSP VAAL AP GPSNSDC SSIYDMMDCLSYLTP GSNDTKPTKVCCGGILSVLQYNPKCICVGLESSKTMGFAVNNT RARAMPTTCKLTIVAPH CAILDEAT PA ASIAV TP SAG TPMT SPSSGG SPTSAP SLAE SPVMTAP SPSRSGTNHLSVSTL <u>TLVSVIVSSVTYISFLF</u>
<i>BrXYLP33</i>	<i>Bra037069</i>	nsLTP2	MAATSNNAVVLIVILA ITFSSSSAVTETQAPSPPALTC TEELVMFSPCLPYVSAPPNNISDAP DPLCCSAFSTSVNSGAGNCLCYLLRQPMILGFPLDRSRLLSLQIC DLSSDES FESIC SPS E SP ELPPLQSIQFT AP FVYGDKASAS SP SFAISREAAGIS PT SDQPS P ETDSLSS TP ESIINGSP <u>KITSFCFLSTIIMTLPTFDLFLAL</u>
<i>BrCAGP1</i>	<i>Bra030067</i>	nsLTP2	MKGLHFHLFLVTMTVVVSVSAATPAAPAAGGALADECSQDFQKVTLCLDFATGKAPNP SKKCCDAIEDTKERDPKCLCYVIQQAKTGGQALKDLGAKKINSFNQLLASSTTLASPT VQEMHVVDYGF EFLGI SPSSP DAAVFTSNATSTT TPAAPAGKSPATPT TSMGTGGSPSIRD <u>GHATVALAFALIMTVSEFVSILPRMGLA</u>
<i>BrCAGP2</i>	<i>Bra039574</i>	nsLTP2	MKHLVVLNSVLLLLSCDAAVFM SPSE SP VFS PSSEPSNND STVVYGMFDCLSFLT VGST DLSPTKTCC EGIKIVLEYNSSCL CIALESSRAIGFDLINNRALAMPSTCNIPIDPHFV SP SKP PTTTLSSGSSTSITTT SPSVS SP ASSHSSAAKPGSS PT THQ SP P TLAAQSP AMF APSP SEYGME NMSLSKLFIIIMMISSFVYLLA

<i>BrCAGP3</i>	<i>Bra021876</i>	Pollen proteins Ole e I like (POeI-like) domain	<u>MGFIGKSVLLTLIALCCFTSSVFSTIAQVPPVKLI</u> ITPL TL PPTK API IKVPTFPPAK API IKVPT LPPAK API KPPV VLPPV SPP KFNRTLVA VRGVVFCKACKYAGVNNLQGA KPVKGAVVRL LCKNKKNATSEATTDKNGYFLLYAPKTVSNYAIRNCRAYLVKSPDAKCSKVSKLHGGYL GSFLKPVVKPEN <u>NATIIFNKLKYSLEFNVGPFAFEPVCPK</u>
<i>BrCAGP4</i>	<i>Bra032889</i>	POeI-like	<u>MGFLGKSILSSLLAIWFFTSCAFTEEVNHVNQ</u> TPSS APAPSP YHHGHHHPHPPHHHPHPPH HPPAK AP VKPPV SPP SKPPVKPPVYPPTK SP VKPPTKPPVKPPV SPP AKPPVKPPVYPPTK AP VKPPVKPPVKPPV SPP AKPPIKPPV SPP AKPPVKPPVYPPTK AP VKPPTK AP AKPPV SPP AKPPV SPP AKPPVKPPVYP PKFNRSLIA VQGTVFCKSCQYASFDSLIGAKPVEGAVVRLLC KSKKNIVAETKTDKNGYFLLLGPKTVTNYGFRGCRVYLVKSKDYKCNKVSKLFGGDVG AVLKPEKRKGK <u>SAVVINQLIYGIFENVGPFAFDPVCPK</u>
<i>BrCAGP5</i>	<i>Bra030083</i>	POeI-like	<u>MGFLGKSVLVSLIALWCFTSSAFTEEVNHVTQ</u> TPSS APAPAP YHHGHHHPHPPHPPHHPHPPH HPPAK AP VKPPV SPP AKPPVKPPVYP PAK AP VKPPTKPPVKPPV SPP AKPPVKPPVYPPTK AP VKPPVKPPVKPPV SPP AKPPVKPPVYPPTK AP TKPPTKPPVKPPV SPP AKPPVKPPVYP PKFNRSLV VQGTVFCKSCKYASYDSL TGAKPVEGAKVRLVCKSKKNIVAETETDKNGY FLLAPKTVTNFGFRGC RAYLVKSKDYKCNKVSKLFGGDVG AVLKPVK TP GKSSV VINK <u>LTYGVENVGPFADPVPCK</u>
<i>BrCAGP6</i>	<i>Bra003506</i>	POeI-like	<u>MAVTRAALAICFLLSLATIADYY</u> SPS TPP VY TPP AYKPTHPPP VYTRPVHKPTLPPP VYT TP AHKPTLPPP VY TPP TYKPTLPPP VY TPP TYKPKPTLPPP VYKPTL SPP VYTKPTIPPP VY TPP VYKPTL SPP VYTKPTLPPP VY TPP AYKPTLPPP VY TPP VYKPTL SPP VYKPTL SPP VYK KYTSYSHT TP YVPKPTY TPP TKPYVPEILKV VDGIILCKNGYETYP IQGAKAKIVCSEPGS YGQSKKDVVIYS DP TD SKGYFHVSLTSIKDLLHCRVKLYTSPVET CNNPTNVNKGLTG VP

<i>BrCAGP10</i>	Bra033328	glycosyl hydrolase domain (GH)	<u>MLVSSYTRNHILFFIALILTLTSLTESRYHHHKEKHKHNSHNHHSSKPEPPSSSISQPP</u> <u>TPPP</u> <u>GPND</u> <u>SPSP</u> <u>SLPP</u> <u>SP</u> SDEPEEDNNGFYNVKRFKFGAVGDGVTDDEAFKTAWDSS <u>CSNQNDT</u> <u>VSVLFVPYGYTFMIHSTIFTGPCHSYQILQVDGTIITPDGPESWPSNISKRQWLVFYRVNG</u> <u>MALKGAGVIDGRGQKWWDLPCPKPHRSVNKSAIFAGPCDSPIALRFFMSSNLTVEGLMIK</u> <u>NSPQFNFRFDGCQGVHVESLHITAPPLSPNTDGIHIENSNSVTIYNSVISNGDDCVSIGSGS</u> <u>YDVDIRNLTCGPGGHGISIGSLGNHNSHACVSNITVRDSIIKYS DN G VRIKTWQGGSGSV</u> <u>SGVTFNNIHVESVRNPIIIDQYYCMTKDCSNKTS AV F VSDIAYQGIGTYDIRSPPMHFGC</u> <u>SDAIPCTNLTLSGIELLPAKGDIV</u> <u>LDPFCWNAYGLAEELSIPPVWCPMSDPPTALPGALVD</u> <u>KCG</u> <u>SP</u>
<i>BrCAGP11</i>	Bra032600	GH	<u>MLISSYTRNQILCFIALIITLSSLTESRYHHHKEKHKHNSHNHHSSKPEPPSSSISQPP</u> <u>TPPP</u> <u>GPDD</u> <u>SPSP</u> <u>SLPP</u> <u>SP</u> SDDPEEDDNGVYDVRKFGAVGDGVADDTEAFKTAWDSS <u>CSNGNDT</u> <u>VSVLLVPYGYTFMIQSTIFTGPCHSYQLFQVDGTIVTPDGPESWPSNISKRQWLVFYRVN</u> <u>GMALKGAGVIDGRGQKWWDLPCPKHRTVNISAIVAGPCDSPIALRFFMSSNLTVEGLQI</u> <u>KNSPQFHFRFDGCQGVHVESLHITAPPLSPNTDGIHIENSNSVTIYNSVISNGDDCVSIGSG</u> <u>SYDVDIRNLTCGPGGHGISIGSLGNHNSHACVSNITVRDSVIKYSDNGVRIKTWQGGFGS</u> <u>VSGVTFNNIHVESVRNPIIIDQYYCMTKDCANKTS AV F VSDITYQGIGTYDIRSPPMHFG</u> <u>CSDAVPCTNLTLSGIELLPEKGEIVV</u> <u>DPFCWNAYGIVEELSIPPVWCLMSDPPTALQGALV</u> <u>DKCGSP</u>
<i>BrCAGP12</i>	Bra011100	GH and X8	<u>MSERLKLILWICLSILAFLDFGGAASK</u> <u>IGICYGRNADNLPTPNKVSELIQHNLNIKFVRIYDA</u> <u>NIDVLKAFANTGIELMIGVPNADLLAFAQFQSNVDTWLHNNILPYPPTTKITSISVGLEVT</u> <u>EAPDNATGLLLPAMRNIHTALKKSGLDKKIKISSSHSLAVLSRSFPSPSATFSKKHLPFLKP</u>

			<p>MLEFLVENESPFMIDLYPYAYRDSSEKLD AIYFALTAMNFKTVKVMVTESGWPSRGSP KETAATPDNALAYNTNLIRHVVGDPGTPAKPGEEIDVYLFSLFNENRKP GIESERNWGMF YANGTSVYALDF TGESSVPVSPSNSSTTSPGPSSSPGNSTVIIIGGGGGGARKKWCVASSQAS VTELQTALDWACGPGSVDCSAVQPDQPCFEPDTVL SHASYAFNTYYQQSGANSSDCSFG GVSV EVDKDPSYGNCLYMIAPSTDGMNRTMAGNITGNITAI DSPMA SPSSSDGYRQMV VSVAVSVLLPLFVVSLSLW</p>
<i>BrCAGP13</i>	Bra010330	GH and X8	<p>MSLFKTVAELGAASNIGICYGRNADNLPSNPKVSELIQH LNIKFVRIYDYNIDVLKAFANT NIELMIGVPNADLLAFAQFQSNVDTWLRNNILPYYPTTKITSISVGLEVTEAPDNATGLVL PAMQNIHTALKKAGLDKKIKISSSHSLAILSRSFPPSSATFSKKHSAFLKPMLEFLVENDSP FMIDLYPYAYRDSA EK VQLEYALFESSSQVVDPATGLLYSNMFDAQLDAVYFALTAMN FKSVKVMVTESGWPSK GSPKETAATPDNALAYNTNLIRHVIGDPGTPAKPGEEIDVYLFS LFNENRKP GMESERNWGMFYANGTSVYALDF TGESAVP GPVSPSNSSTTGVSPSPGDNGN STVTIGGGGGGAKKWCVASSQASVTELQSALDWACGPGNVDCSAVQPNQPCFEPDTVL SHASYAFNTYYQQSGGSSLDCSFGGVSV EVDKDPSYGNCLYMIAPSTDGMNRTMAGNI TGNITAI DSPLASPSTSNEGIRQMVVSVAVSALLPCFVVSLSLLW</p>
<i>BrCAGP14</i>	<i>Bra000732</i>	GH and carbohydrate binding domain (CBM49)	<p>MHPCKVLI SWDVKYAGVQTLVAKILMQGKAGEHTAVFERYQEKA EQFMCSMLGKSTK NIQKTPGGLIFRQRWNNMQFVTSASFLAAVYS DYLSSSKRNL RCSQGNVSPS QL LDFS KS QVDYILGDNPRGTSYMGYGHNYPRQVHHRGSSIVSYKVDQKFVTCRGGYATWYSRK ASDPNVLTGALVGGPDAYDNFADNRDNYEQTEPTTYNNAPLLGV LARLIS GP TGFDQRL PGV SPTSP VIIKP APIPKRKPT TPPAPAS SPSPITISQKMTSSWINEGKVYYRYSTKL TNRS KRLK NLKISITKLYGPIWGVTKTGNSYGFPSWMKSLPAGKSMEFVYIHS AAPANVLVSN</p>

			YSLE
<i>BrCAGP15</i>	<i>Bra001454</i>	GH and STAS domain	<u>MKTYLLLLLIFSLLLSYSSG</u> QQCGRQAQGALCPNGLCCSEYGWCGTTEAYCGRGCQSQ C <u>TP</u> <u>TPP</u> <u>TPT</u> <u>TPP</u> <u>SP</u> <u>TPP</u> <u>RP</u> <u>TPP</u> <u>GP</u> SGDLSG <u>IISRDQFYKMLKHMNDNACPARGFFTYDAFI</u> <u>TAAKFFPSFGNTGDLATRKKEIAAFFGQTSHETTGGWTDAPDGANTWGYCFKDEIGKSN</u> <u>PYCDSNNLEWPCAPGQFY YGRGPMMLSWN YNYGQCGRDLGLDLLRRPAIASSDPVIAF</u> <u>ETAIWFWMTPQAPKPSCHDVITDQWQPSAADISAGRLPGYGVITNIINGGLECAGRNV</u> <u>QVEDRISFYTRYCGMFGVDPGTV</u> <u>LGRLPGTTVYRNMKQ</u> <u>YPEAYTYNGIVIVRVDAPIYF</u> <u>ANISYIKDSCH</u> <u>IHRLKRRGSLERTLAVSNPNKEVLLTLARSGIVELIGKEWYFVRVHDAVQ</u> VCLHYVESKNQ <u>TP</u> TNVEESSSSSLWRRCNANKNSSHTEVEPD SKLV LKEPLL FNDK
<i>BrCAGP16</i>	Bra038726	GH	<u>MKSLLLLLLNFLFLLSFSSA</u> EQCGRQAGGALCPNNLCCSEYGWCGSTEAYCALPGCQSQ C <u>TPS</u> <u>GPPPPGPPPP</u> DPTGGLTD <u>IITRSQFDDMLKHRNDAACPARGFYTYDAFITAAKYFPS</u> <u>FCNNGDTVARKKELSAFFGQTSHETTGGWPTAPDGPYAWGYCFKEEVSPSSDYCQPSGQ</u> <u>WPCVPGKRY YGRGPMQLSWN YNYGQCGAAIGEDLLNNPD LVSN DPVISLKA AIWFWM</u> <u>TPQSPKPSCHAVINGQWQPSADIAAGRVPGYGVTTNIINGGLECGHGPDTRVYDRIGFY</u> <u>QRYCGIFGVNTGDNLDC</u> YNQRSFASFKSFLDAAM
<i>BrCAGP17</i>	Bra034754	GH	<u>MKTCLLLFLIFSLLLSFSSA</u> EQCGRQAGGALCPNGLCCSEFGWCGNTEPYCKQPGCQSQ CGG <u>TPP</u> <u>GP</u> TGDLSG <u>IISRSQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPGF GTTGDT</u> <u>ATRKKEIAAFFGQTSHETTGGWATAPDGPYSWGYCFKQE QNPSSNYCSPSAEWPCASGK</u> <u>SY YGRGPMQLSWN YNYGQCGRAIGSDLLNNPD LVSN DPVIAFKAAIWFWMTPQSPKPS</u> <u>CHAVIVGQWQPSDADRAAGRVPGYGVITNIINGGLECGRGQDATRVADRIGFYQRYCNI</u>

			LGVNPGGNLDCYNQRSFASVNFFLDAAI
BrCAGP18	Bra033641	GH	MEPSVYRLFLLFFLCLYGLHQTKSQPFIGVNYGQTADNLPPPSATAKLLQSTSIQKVRLYG SDPAIIKALANTGIEIVIGTGDVPGLASDPSFARSWVETNVVPYYPASKITLIDVGNEATTF GDRNFMLQLLPAMKNVQSALEAASLGGKIKVSTVHTMSILSQSDPPSAGVFAADHADIL KGLLEFNRETGSPFAVNPYPFFAYQSDPRPETLAFCLFQPNPGRVDANSKIKYMNMFDAQ VDAVYSALSSFGFKDVEIVVAETGWPYKGDPEVGTTIENAKAYNKNLIAHLKSMAGTP LMPGKVIETYLFALYDENLKP GKGSERAFGLFKPDLTMTYDI GLTKTTNQTSMA PQSPTP RLPPAAAPTSQTLPAAPPQMILPSPTSPSDKNSGQTDVHNSTPR
BrCAGP19	Bra027699	GH and CBM49	MEIKFASVAALLLLLSFPVAFSGHDYGGQALSKSLLFFEAQRSGVLPRNQRTWRSHSGLT DGKSSGVNLVGGYYDAGDNVKFGLPMAFTVTMMAWSVIEYGNQLAANGELGHSIDAI KWGTDYFIKAHPEPNVLYGEVGDGNTDHYCWQRPEEMTTDRKAYRIDPSNPGSDLAGE TAAAMAAASIVFRRSNPAYSRLLLTHAYQLFDFADKYRGKYDSSITVARKYYGSVSGYN DELLWAAAWLYQASNNQFYLDYLGRNGDSMGGTGWSMTEFGWDVKYAGVQTLVAKF LMQGKAGRHTAVFQKFQKADFFMCSSLGKGSRNQKTPGGLIFRQRWNNMQFVTSAS FLTTVYSDYLTSSRSNLRCSAGNVAPSQLLSFAKSQVDYILGDNPRATSYMVGYGNNFPQ RVHHRGSSIVSYKVDRSFVTCRGGYATWFSRKGSDPNLLTGAIVGGPDAYDNFADRRDN YKQTEPATYNNAPLLGVLARLSSGHSYGYSQLLPVVPAPVVVRRPMPPIRKPRVTSPVRASG PVAIVQKMTGSWVSKGRTYRYSTTVINKSPRALKSLNLSIKNLYGPIWGLSRSGNSFGL PSWMQSLQSGKSLEFVYIHSTSEANVAVSSYTLA
BrCAGP20	Bra027735	GH and	MKNFASVAALLLLLCFPVAFSGHDYGGQALSKSLLFFEAQRSGVLPRNQRTWRSHSGLT DGKSSGVNLVGGYYDAGDNVKFGLPMAFTVTMMAWSVIEYGNQLAANGELGHSIDAI

		CBM49	<p>KWGTDYFIKAHPEPNVLYGEVGDGNTDHYCWQRPEEMTTDRKAYRIDPSNPGSDLAGE TAAAMAAASIVFRRSNPAYSRLLLTHAYQLFDFADKYRGKYDSSITVARKYYGVSVSGYN DELLWAAAWLYQASNNQFYLDYLGRNGDSMGGTGWSMTEFGWDVKYAGVQTLVAKF LMQGKGGRHTAVFQKFQKADFFMCSLLGKGSRNQKTPGGLIFRQRWNNMQFVTSAS FLTTVYSDYLTSSRSNLRCSAGNVAPSQLLSFAKSQVDYILGDNPRATSYMVGYGNNFPQ RVHHRGSSIVSYKVDRSFVTCRGGYATWFSRKGSDPNLLTGAIVGGPDAYDNFADRRDN YEQTEPATYNNAPLLGVLARLSSGHSGYSQLLPAVPAPVVRPMPPIRKPRVTSPVRASG PVAIVQKMSGSWVSKGRTYRYSTTVINKSPRALKSLNLSIKNLYGPIWGLSRSGNSFGL PSWMHSLQSGKSLEFVYIHSTTPANVAVSSYTLA</p>
<i>BrCAGP21</i>	<i>Bra018152</i>	Plant invertase/pecti n methylesterase inhibitor (PMEI) domain and Pectinesterase	<p>MLRGNGIFHICLLASFLLLPFSSAVHDGDFSGGANAPSSWDHNIAPSQETAPSPPTTSP TTSPSPGPAAAPSPINNDISISGDMTWWCNKTPHAETCNYYFQRSPHNNINRPPRFRSEFL RLLVQVALDQAVITHAQTVKFGPSCNTNNQRKAAWSDCVKLFENTVAQLNLTCLKLNPA ASSDVKCSNFDAQTLWLSTAQTNIETCRSGSEDLKVSDFVMPAISNKNLSDLIGNCLAVNG VLMKQHNHTTANHKEYFPSWVSRHERLLVSASLAKSRPHLVVSQDRSGHFERSIQSAIN FAGRRRIKSRFIIYVKKGVYRENIEVGNDNHNIMLVGDGARKTIITSGRSVKNGYTTYNS ATAGFGGQRFVAKDMTFINTAGPLRGQAVSVRSSDLSVFYRVGIHGFQDTLYIHSQRQF FRECYSISGTIDFIFGNAAVVFQNCMILVRRPLRGQANVITAQGRGDPFQNTGITHSSRIIA ASDLRPVIGAYKTYLGRPWQAYSRTIMKTYIDNSISPLGWSPWLGRSNFALNTVFYGE YKNFGPGSSSTRWRVRWKGFHAITSAAVASRFTVGS LIAGGSWLPSTGVPFKTGL</p>
<i>BrCAGP22</i>	<i>Bra033792</i>	PMEI and Pectinesterase	<p>MVRGIFHICLLASFLLLPQFSSTVNYRGFTVGANVPSPWDHNIPPPPETTPFA SPTTSPPTT SAQSPGPAAASSPINNSSISGDMTWWCNKTPHAKTCTYYFQKSPDRNISRPPRFRSEFLR</p>

			<p>MLVHVALDQAVIAHAQTVKLGQSCTNNQQKGAWSDCVTLFENTVTQLNQTFNGLNPG ASSDVKCSDFDAQTWLSTAQTNIQTCRSGAEDLKVSNFVMPAISNKNLSDLIGNCLAVN GVLMKQHNHKTANHKEYFPSWVSRHERLLVSASLAKSRPHLVVAQDRSGHFRSIQAAI NFAGRRIKSRFVIYVKKGVYRENIEVGNDNHNIMLVGDGERKTIITSARSVKGGYTTYN SATAGFGGQRFVAKDMTFINTAGPLRGQAVSVRSSSDLVSFYRVGIHGFQDTLFIHSQRQF FRECYSISGTIDFIFGNAAVVFQNCMILVRRPLHGQANVITAQGRGDPFQNTGITHSSRIVA ASDLRPVIRAYKTYLGRPWWQAYSRTIMKTYIDNSISPLGWSPWLRGSNFALNTVFYGEY KNFGPGSSSTRWRVRWKGFAITNAAVASRFTVGS LIAGGSWLPSTGVPFKTGL</p>
<i>BrCAGP23</i>	<i>Bra034140</i>	PMEI and Pectinesterase	<p>MKTLHFSSSLLFLSVLFLSCAFLISPQAPSPSPSELSSQPPSLPPSQSPSLPPSQPPSLPPSKPP SLPPSQSTSDACKSTPYPKLCRTILSAVKSSPSDPYSYGKFTIKQCLKQASRLSKVINGYV RRVRSKPGSMTAEIGAVADCGELAELSVSYLETVAEELKMADMMTAALVEHVNSLLSG VVTNQQTCLDGLVEAKSGFAAAIGSPMGNLTRLYSVSLGLVSHALNRNLKRFKASKGKI LGGRNSTYREPLETLIKVLRKTCNDKDCRKAARKLGELGVTSGGSILVSQAVIVGPYKS DNFTTITDAIAAAPNNARPEDGYFVIYAREGVYEEYIVVPINKKNLLLMGDGINKTIITGN HNVVDGWTTYNCSFAVTGERFMAVDVTFRNTAGPEKHQAVALRNNAEGSTFYRCSFE GYQDTLYVHSLRQFYRECDIYGTIDFIFGNAAAIFQNCNIYARKPMAKQKNAITAHGRTE PNQNTGISIINCTIKAAPDLAADPTSTMTFLGRPWKPYSTRVFMQSYISDIVQPVGWLEW NGTTGLDTIYYGEYDNFGPGAKTDRRVQWLGYNLLDMAQAMNFTVYNFTLGDWTWLP QTDIPFYGGLVRKE</p>
<i>BrCAGP24</i>	<i>Bra040283</i>	PMEI	<p>MESNKTFWIIILIVTVSTFLTPMVESKSVPLRDSYVARSLLSVSPPSESPSSSPAPGPEVENT IAVPASSPTEIDIDSPSPSPGAPADSISPTNAPTTSPPSPSPEAPANAPATDSPSPSPEVDMDSP</p>

			<p>SPSSEAPVDSTSPANPPTMDIISPSPSPEAPEDSASPANPPTMDIDSPSPSPETPEEIPGAPS GKTLISSATTLLKQTLLSPEIKTICGKTDNPELCESSISPLLTAAIKPDASSVLVLAIQASINA TKAVMPTVNKVAAADCQELYDDAVSNLEDAINAVNESDIATVNSNLSAAMTDYGTCDN GFEESGEPNPLADVADKLHKMVSNCCLAISTLIK</p>
<i>BrCAGP25</i>	<i>Bra024570</i>	PMEI	<p>MKKPSLHQPIFFLATLLPLILTVHSQPSPSPSPSPSPSPSPSDDSDFIQRSCNTTLYPDVCV SSLSNFSTYVHNDPALLARAAISVTLNALELGKYLSNVSTLLEIHEDGGHHPTAAAVFH DCFENLKDAVDEMRRSMKQMRDLVTTGSLESFRFQMSNVQTWLSAALTNEETCTDEFK DVQDEPRKDEV CARVDGVKKLTSNALALVNRCVDNAIH</p>
<i>BrCAGP26</i>	<i>Bra033660</i>	Xylanase inhibitor N-terminal (TAXi-N) and TAXi C-terminal (TAXi-C)	<p>MDRASLLALLLLLLLIIFDLTAADKIPDLAAESGMIFPLSYSSLPPRVEDLRLRRRILHQSQQ LPNAHMKLYDDLLANGY YTTRLLIGTPPQEFALIVDTGSTVTYVPCSTCKHCGKHQDPK FQPELSTTYEAVKCNPDNCDDDGKLCIYERRYAEMSSSSGILSEDLISFGNESQLSPQRA VFGCENVETGDLFSQRADGIMGLGRGKLSIVDQLVDKGVIEDSFSLCYGGMEVGGGAM VLGKI SPPAGMVFARSDPFR SPY YNIDLKQMHVAGKSLKLNPKVFNGKHGTVLDSGTTY AYFPKEAFNAIKDAVIKEIPSLKRIHGPDPNYDDICFSGAGRDVAEIHNFPEIAMEFGNHQ KLILSPENYLFRHTKVRGAYCLGIFPDRDSTTLLGGIVVRNTLVTYDRENDKLGLFKTNC SDLWRRLASPPDSPAPT SPVTQNKSLNNI SPSR SPSPAPSKAPTVDLPGVFRIGVITFQVVIS VNNASMKPNFSEIADFIAHELEIQSSQASLNMHFPLVRLLSITTSGNEYRLKWGIYPPQSS EYISNNTALNIMSLLKENKLRLPGQFGSYKLEWKAQKRKQSWLEKHLVGVVGVMI SLLVTSVIVKLALVWRRRQQEEATYEPVSAAVKEQELQPLSSSETSNA</p>
<i>BrCAGP27</i>	<i>Bra036814</i>	TAXi-N and	<p>MLQFGFCVMSLGCASVSGSFSFQIHHRFSDQVKTVLGSGLPEMGTLEYETLVHRDRG RRLTSNNNQTTVSFAQGNSTQEISFLHYANVTVGTPAQWFLVALDTGSDLFWLPCNCKSS</p>

		TAXi-C	<p> CIRSMETDQGERIKLNIYDPTISTSSSKVPCNSTLCALRNRCVSPLSDCPYRIRYLSPGSRSTGVLVDDVIHMRTEEGEPRDARITFGCSESQVGLFEKTAVNGIMGLAIANIAVPNMLAKAGVASNSFSMCFGLKGKGTISFGDKGSSDQLETPLSGTLSPPFYDVTITEFKVGSVTVETETAIFDSGTAVTWLIEPYTAVTTNYHLQVADRRLPARVKSPFEFCYIITSATDEEKIPSISFEMQGGATYNVFSPLVFDTSDDGGQVYCLAVLKEVTAGFNIIGQNFMTNYRIVHDRERMILGWKESDCNDKNGFTGPTASANPPSLPPTPSPRARSPSTRLNPLAASSLLILCFFSFICL </p>
<i>BrCAGP28</i>	Bra036815	TAXi-N and TAXi-C	<p> MAIGRHVFVLLSALVLSWGLERCEATGKFSFEVHHMFSDAVKQNLGFDNLVPEEGSLEYFKVLAQRDLFRGRGLASNNEDSLTAEGNLTVFVSFLGSLHYANVSVGTPATWFLVALDTGSDLFWLPCNCGVTCISDLKDAGFPQSVPLNLYSPNTSSTSSSIRCSDDRCFESSRCSSPSSVCPYQVSESTTTTSTGTLLQDVFHLVTEVDLKPVEANVTLGCGQRQTGLFQNFQAVNGVLGLGVKDYSVPSLLAKAKLAANSFSICFGRVIGVVGRISFGDKGYTDQSETPFISVEPSTAYGVNVTGLSVGKKAVGFSMFAQFDTGSSYTHLREPAYSFTKAFNSRALDIRTPSDPQFPFEFCYNLSPNATNITFPIDMTFEGGSVMSIKNPFVTIKTEGGGRMYCLSIVKIEDLSPNIIGQNL MAGYRIVFDRERMVLGWKRSNCFEDES LTSAPPAEFGDTPPPPSESEGPSPESEAPSPPTESNPLLRSPPPPPLVFTTTPPSDSTE SPGSSGVANVSPLGSLLLLSLLAFL </p>
<i>BrCAGP29</i>	<i>Bra012857</i>	TAXi-C	<p> MAVARHVFVFLSVLVVVS WGLERCEATGKFSFEVHHMFSDAVKQTLGLDNLVPEKGSM EYFKVLAHRDQLIRGRGLASNNEKPSVTFMRENLTIGVDVLGSLHYANVSVGTPATWFF VALDTGSDLFWLPCNCGTTCIRDLKDIGLPQNQTGLFGEGIALNGLLGLGLEDYSPSVL AKANITANSFSMCIGNVIDVIGRISFGDKGYTDQQETPLVPVGPSPTYAVDVTEVSVGGE ALGIKLLALVDTGTSFTHLLEAEYDLVTKTFDDQVKDKRRPIDPKIPFEFCYDLSPNSTTI YFPKIIMTFGGGSQMILRNPLFSVFNEDGTAMYCLGILKSVNFKLNIFGQNFLSGYRIVFD </p>

			RERMVLGWKRSNCYEDESLEATPPPPPEIEAPSPRLSAPLPSPPPPPLVSIATPPPFDPRSSTG NGSGGAASLSPLSSQLLLLLSLLAFLSFT
<i>BrCAGP30</i>	Bra013345	Leucine rich repeat (LRR)	MKLPLPLLLLLLLSPTTSAAPSLSPTPSPTIAPVPRTSPTPPRTSSSSSPLDPKQLKAESLN IPTLRNPCDHPSSSSKPPTTVVTCDTGSPFRLVTSLSFTNCSSDLSSSTALKALSPSLPSLS FHNCPSLSPPPHLPSDLHSFSAVSSFPRLSGLSLARLVNLTDTVSSVPVSTSGLFVILGNM HDIVSLTISHANLSGNIPKSFHSNLTFIDLSDNLIKGIPTSITLLSNLKALNLSSNSISGEIP SIGDLISLKNLSLSSNKLSGPIPDSSISIPDLTHLDLSGNQLNGTVPRFISKMKSLKYLNLAN NAFHGVLPFNASFLKKLEVFKVGGNSDLCYNHTVLSSKMKLGIAPCDKHGLPLSPPPRK EDSSSDDDYSEDDSSEKKKEEHGPNKAVLGVAIGLSSLVFLIIFMILLAKWCG
<i>BrCAGP31</i>	Bra020993	LRR	MKPLSPSLPLLLLLLLSSTTFAAPSLSPTPSPTIAPIPRTSPRTSSSPLDPKPLKAESLNIPTA KNPCDHRPTSKPPSTVVTCDAAGSPFRLVTSLSFTNCSSDLSSSAALRALSPSLASLSFLNC PSLSPPPRLPTSLRSFTATSSFLRRRKGLSGVYLARLVNLTDLTVSSVPVSTSGLFVILGNM DKIVSLTVSHANLSGNIPKSLHSNLTFIDLSDNLIKGS IPTSITQLSNLKSLNLSSNSISGEIP DSIGDLISLKNMSLSSNKLSGPIPDSSISLPDLTHLDLSGNQLNGTVPRFITKMKSLKHLNL ANNFRGVLPFNASFLKKLEVFKVGGNSDLCYNRTVLSSKMKLGIACDKHGLPLSPPP QKEDSSSDYDYGSEDETSVKKKEESRGPNKVVLGVSIGLASLVFLIIFLILCAKWCG
<i>BrCAGP32</i>	Bra026260	LRR	MALSITFHALTSLLLFHVSLVSTATHTPHHHTSHSSNHLQKAYRALQAWKKVIYSDPKNL TGDWIGPSVCSYTGIFCAPSPSDQNTLVVAGIDLNHGDIAGFLPEPIGLLSDLALIHLSNR FCGILPRLSQLSLLYELDLNNRFVGPFPDVVLSLPSLKYLDLRYNEFEGPLPPKLFNSNPL DAIFVNNNRLTSLIPRDFGTGTASVVVFANND FSGCLPPTIAHFA DTLEELLINSSLSGCL PPEVG YLYKLRVLDMSYNSLVGPVPYSLAGLGHELLNLDHNMFTGAVPLGVCVLP SLQ

			NLTVSDNYFSEEEGTCRNLTSGIVFDDSNCLPDKPHQRSHKVCEDVLDHPVDCYDHE CSAVAPQASPFAGPSLAPASAPAYT
<i>BrCAGP33</i>	<i>Bra039561</i>	Formin Homology 2 domain (FH2)	<u>MGRLRTAFLAVSLVFLVCVSE</u> EIISRRGANRGEAHGGDDVAEQTWIHCERKELKDKNRDC LIYIPPRVAAANDTYQKLSVLTGWFSNWF ^{GP} LLDSTTSYPTRKLIGKQKRKKKKKKRKKFR VS ^{AP} NFAL ^{GPAP} GF ^{APGPSRF} ^{APGPAPTTP} QSYDLV ^{APSS} ^{SPSY} ^{SPAE} ^{AP} DESSFG ^{GP} TKK RAKSIV ^{AP} SQSV ^{GP} PPPPPEKKNDILMDLIIAVASTAVLTFFLVALLFLCCFRRNNRKNV ^{GP} RN ^{GP} RDE ^{GP} LLHLSDL ^{SAGSNEN} ^{SP} KVAATSRRFFTATSKKRSFLSRVSLKRNHHDFP AEASSSSGLPLPPGRSSG ^{AP} LP ^{PPV} ^{APPP} ^Q ^{APPP} ^{PP} PK ^{PPPP} ^{AP} KLVR ^{PPP} ^{AP} PKRQGR SSSGDGSDVDS ^{ETGAPKTKLKPF} ^{FWDKMANPDQ} ^{KMVWHEISAGSFQFNEQEMESLFGY} ^{NDVNKNKNGQRGESSRDSPVQYIQIIDPRKAQNL} ^{SILLRALNVTIEEVDAIKEGNELPV} ^{ELLQTLLKMAPTSEEELKRLYSGLHLLGPAERFLKILVDIPFAFKRIESLIFMISLQEEVS} ^{GIKESLATLEVACKKLKNSRLFIKLL} ^{EAVLKTGNRMNVGTFRGDAQAFKLDTLLKLSDV} ^{KGTDGKTLLHFVLEIIRSEGVRALRLQRSSKS} ^{FSSVKTD} ^{DDTNTDTSPQ} ^{VERYRSTGL} ^{QVVSGLTTELEDVKRAAI} ^{DADGLASTLMNLSGSLTNAREFLKTMDEESDFE} ^{KALTGFIE} ^{RADGDIKWLKEEEE} ^{RIMVLVKSSADYFHGKS} ^{AKNEGLRLFAIVRDFLIML} ^{EKVCREVKE} TTMMTSSKNHSSKKETKMIPESNQPDNIRRHLFPAIAERRADSSDDSDSD
<i>BrCAGP34</i>	<i>Bra037491</i>	FH2	<u>MQTFCFSFLLLLSCAPS</u> PLSYASSALNLGRRHLSDDAGSALL ^{TP} ^{SP} ^T ^{SPPFFPLESS} ^{AP} LP PPP ^{SPP} ^{TFAAFPTTFPANISALVLP} ^{SP} KPHST ^{SP} AILVPAISAVLVVA ^{AVLGVALFLYGRWK} GQNRHFKDTNTTLGGSSSSSHTSEERHVITNNFSVSAS ^{SP} TSEVLYLGGE ^{EEEPDRVVT} SF VKPPE ^{SP} EIRPLPPLPRSFQPSYAEIH ^{SERNEEE} ^{EEEEEEFF} ^{SP} LASLASSANS ^{SP} SRSGF EQSSCSSSSSGWV ^{SP} ARSFMTL ^{SP} VQQQRSF ^{SRLSDVSLEQSLQSL} ^{SP} ERLVRN ^{NNGH}

			VSSSLRMFSFFNQNLSPRISASTSPDRGGFVRTPPLSSLYSSVSNSPDGLFRKFINSSPPIW NDFSARNVKS VLLSSES VSSRRDFVINIGGQAGAVAAPPPTRPPPLVPPSQSFVVQNDVKKP SFS DKVNQGSCQNTAWDCLKANSFKLNKEIVETLFISNSSSPNLNQRGGLTYDLPTQNEVS YQNIATRLQLLNLTTKDVSNALLEGDSGALGAELLDCLSRAPSKEEERKL RNASDDSVI IKLTPAERFLKELLQVPFVFKRVDALLSVANFYPEVEYLRRSFGVVQAACEELRNKNTFS RLLEAILKTGNKMSVGTNSHAFKFDTLKLAEVKGLDGRSSVLHFAVQEMIKSEGSVKA LDRIRNLSSEMETVKKSADIEYGVLTNGVLKLYQGIRSIKELLILSEESGCSGDQWMKFE TKMGRFLETAGEEIVRIKAQESSTLSALEEVTELFHGGSFKEEGHTLRVFM AVRDFLSTL DEV CNDMGERFSA
BrCAGP35	Bra039436	FH2	MVYFRQIFLMIIVVAISLQCCSISADERYRTHIGKLVGEDGGEKKKLT VLEKFRALLDLIKP STPRRRNLAA SPWPAPSPSPFPNGGPVE SPAY SPAPQRPPIPHLRRLPQORTHPPRQHEIQR RKHEKGGVFVPLVVSTACGIGFVVCVVVVLCLCSRVRKKNGKTL SFKRKQRKSQKVSIN PTLDFLYLNSVGVDLERQSSVLVKETENDDELREEEVKRSVETEILLDS DNAGSYSTKEI VSVQEKTEHSVSASEDDEESFHSVGGGSQYSNPRLSNASSSSVSGIGSSSQRF SERELDIP ECSGISHPPPPPPPPPPQLLQFSNRGLLHTLSSPETAKPQTFSSQLSAKVSASSSKPLPPPPP PPPLPPSLQQQPQVMNKTPPPPLSLDFTQRTPLGKD GAPLPKLKPLHWDKVRATPDRTM VWDKIRTSSFEFDEEMIESLFGYTMQTSTKNEEGKCKTPSPGKHLLEPKRLQNFTILLKA LNATADQICSALGKGEGLC LQQLALVKMVPTKEEELKLC SYKGAVDELGSAEKFLRAL VGVPFAFQRAEAMLYRETFEDEVHLRNSFSMLEEACKELKSSRLFLKLL EAVLKTGNR MNVGTIRGGAKAFKLDALLKLSDVKGTDGKTTLHFVVQEISRSEGIRVSDSIMGRIMN QRPKNKNTAEKEEDYRRMGLDLVSGLNTEL RNVKKTATIDLEGLVSSVSNLRDGLEQL RCLASSEENRAFVSSMSSFLRYGEKSLEELREDEKRIMERVGEIAEYFHGDVRGDDKNPL

			RIFVIVRDFLGMLDQVCRELRCVRVPNSPSPLAPFR
<i>BrCAGP36</i>	Bra001148	FH2	<p> <u>MVYFRQILLMIIVLVISLQCCNVFADTKELGEWTALMVANGERYRTQIGKLAGEDGGEK</u> KKFPVLEKFRALLDLIKPSTLRRRSLATSASLAPWSAPSPSPFPNGGPAESPAYSPAPQRPPIP PHLRRPLPHRTHHPSRQHELTRRKHENRGAFIHVVVSAACGIGFVVCVVGAFFLYARRR KKNGKTPPFQSSTRKVSINPSHSLGDDLEKQSSVSVKEVRETEKDVDNDNKGVLLEDVK TSAETEILSDSDNASSFSTKEIVSVHENDEEQQTVDVSVPVVSNGCDSSDDNESFHSVG GGSSVGSSQRFSEIREILPPPPPPPPPPPLPGLHTLSLTKTTTLSSQLTAKVCASSSDSTLPS PPPLRPPPPPPPPSQQPQATNKTPPPLSLDFSQRRPLGKNGAPLPKLKPLHWDKVRATPN RTMVWDRLRASSFEFDEEMIESLFGYTMQSSTKNEEGKCKTPSPGKHLLEPKRLQNFTIL LKALNANADQICSALGKGLRLQQLEALVKMVPSKEEELKLCSYKGEVDELGSAEKFLR AVVGVPFAFQRAEAMLYRETFEDEVVHLRNSFSMLEEACKELKSSRLFLKLLEAVLKTG NRMNVGTIRGGAKAFKLDALLKLSDVKGTDGKTTLHFVVQEISRSEGIRVSDSIMGRI MNQRTNENRTAEIEDHRRMGLDLVSGLNTELNVKKTATIDMEGLVSSVSNLRDGLG GLKCLASEKLKGDEENRAFVSSMSSFLRYGERSLEELREDEKRVMMGRVGEIAEYFHGDV RGDEKNPLRIFVIVRDFLGMLDLVCRELCVRVPNSPSPLAPFR </p>
<i>BrCAGP37</i>	Bra037087	FH2	<p> <u>MGRLTKAFLAIFLVVLVCVSVEIIARDGANRLRSSVSEEAHGVDMAEKTKIRCRKELKDE</u> NKDCLVYISREAAANGYVKLSVLTGYGHWFGPLLDSTPRRKLISKKKKFTVSAPNFALG PAPRLTPGPAPSTSPSQSSHSPDESNSAPVKRKPSVVAPSPSVVLSPAKKYDILMQLIIV ASTAVLTFFLVLTLLFLCCFRNRSPRDGPRDEGQFLHLVDLSPGSNETSPAAANPSRRFFS ASSKKKSFLSRMSLKRSGHDQFSTAQASTSSGHPPPLKLPPGRTAAPPPPPPPAAPAPPP QPPPPPKSKPPPPPKLVRPPAPPKGAAGKRQGHHSDDASDVDS ETGAPKTKLKPPFFW </p>

			DKMANPDQKMVWHEISAGSFQFNEEAMESLFGYNDGNKNKSGQRGESSRDSHVQYIQI IDPRKAQNLSILLRALNVTTEEVEAIKEGNELPVELLQTLLKMAPTTEEELKLRLYSGD VNLLGPAERFLKILVDIPFAFKRIESLLFMISLQEEVSGIKESLSTLEVACKKLRSRLFLKL LEAVLKTGNRMNVGTFRGDAQAFKLDTLLKLSDVKGTDGKTLLNFVVLEIIRSEGVRA LRLQSKSFSSVRTEEDTNNNNTDSSPQSVERYRSTGLQVVSGLTTELEDVKRAAVIDADG LAATLTNLSDSLTAAREFLKSMEEEESDFEKALAGFIERADADIKWLKEEEEERIMALVKSS ADYFHGKSAKNEGLRLFAIVRDFLIMLEKVCRHVKETTTSATKTRTHSGKKETQVTMQE DSHQPSTDNIQQRLFPAIAERRDDSSDDSDDE
<i>BrCAGP38</i>	<i>Bra004786</i>	FH2	MSRIPSLRLRFATILFLFSSSSSSADQRLHSRHLHQPFFPIPTAAPPYQPPPPSSEPPSPSPRS HHHHKNHPETPPPHEKHPFSSASNPPPPPPPPSPPHNTFFPSSDPSSPTSHPPPSPSPHR APVPTFPANISSLVFPTHNKPHNSNPVAKLLAITIAVVSAAILLSLLAVATIFLRRRRRRAS PAKSTKTDARHLFNAAPSDVPLKHKQPPKYTSSNTSSEFLYLGLTVNSGLVDQQKSPGSV AGVLELPPAQGSSSSTPSYSQYQKLGSPELRPLPLPKLPVYTPNYRSTELLNPKGQDFDG DDNENDEFYSPRGSPVRKQSPRVKNSGSPGTSLKPPKSSLSPRLSLNSSNGSVSKKPVPT RPPPPPPQIHVLPVTNSVSEEKDETFKPKLKPLHWDKVRASSRVTVWDQIKSNSFQVN EEMIETLFRANDPTSRTKESVTTDVVQSTSHQFLDPRKSHNIAILLRALNVTADDEVCEAL VEGNSDALGSELLQCLLKMAPTKEEEDKKELKEDDDDESSPSKTGPAERFLRALLNIPL AFKRINAMLYIVNFESETEYLKRSFHTLEAACGELRNTRMFLKLLLEAVLKTGNRMNIGT NRGDAHAFKLDTLLKLVDIKGADGKTLLHFVVQEIHKSEGARVSTTPTQSPVGVNMAE QSAFQDDLELKKLGLQVVSTLSSQLTNVKKAAAMDSTLSDEAAELSKGITKVKEVIME LKQETGVERFLDSMNSFLNKAKEITEVQSHGDSVMKMOVKEVTEYFHGNSESHPSRIFT VVRDFLTVDQVCKEVGRVNERTVYGSVPRASVSNQVVTPLFPVANNDNNSEKSHSGSL

			GNQEDEDLF
<i>BrCAGP39</i>	<i>Bra000328</i>	FH2	<p> <u>MSKIPFLLRFAVIVFFIFSSYSSGDQRLNSRHLLHQPFYPIVTA</u>APPPLSSKPPSPSPDKQPPP PPPPPPLSSNPPSPSPDKPHHHKKHPAAAPPPQDKHLFSSVTPPPPPAPHSNPFFPSNAVHP SPPPPPPASIPTFPANISSLFFPPHNSSKPHTNNHHVAKLVSITVSVVSSSVLLSLLVVLILYL RRTRRRRRLPAYNTKSTRSDSLQLFNASPSDGARKHKQPHKHTSSNTSSDFLYLGLTVNS RSEGFAPQKSPVSRNVAGVLELPPVPASSSSSSSYSRNQRPSPELRPLPPLPKLPAFSPTY LSPEHLFPKRQDFDGDDEFFSPRGSSGRKQSPPRVVEDSGVVQSVNDSNSCSPTSFNDS PATSLKPTSLSPLSLHSETSSNGSVLKKTGPARPPPPPPPPPPPPQFSEVPAATSPSPPSDPKK KEETLKPKLKALHWDKVRASSSRVMVWDQIKSNSFQVNEEMIETLFRANDPSSRARDV GNAGVVQSANQENQFLDPRKSHNIEILLRALNVTADDEVCEALVEGNADMLGPELLECLL KMAPTKEEEDKLKELKDDDESTTSKIGPAEKFLRALLNIPLAFKRIDAMLYIVNFDSETE YLKRSFHTLEIACGELKNTRMFLKLLEAVLKTGNRMNIGTNRGDAHAFKLDTLLKLVDI KGADGKTLLHFVVQEIIKSEGARVSSPTPIQSPIGDDDIAEQSAFQDEIELKKLGLQVVSG LSSQLINVKKAAMDSTLSKEIAEISSGITKVKEVIMELKQETGVERFLESMNSFLDKGE KVITEIQSHGINVMKMVKEVTEYFHGNLESHPFRIFTVVRDFTILDQVCKEVGRVNERT VYGSRPSPSNQTVTPLFPVNVINHAELSHDDDSFQVITIG </p>
<i>BrCAGP40</i>	<i>Bra029012</i>	FH2	<p> <u>MILGGGMCNQNWARLVLLLVL</u>LSGFFLVIALAESSEKDETfISQFMAPSTEQANEQMVET LWAHRCWQDPDCVKEAVTVFNLCFPGSKDNNLELFGFTPSHLKQTLLMCIQKQGELNG HNLNYLKLLPSILDNAPRRNLASTPSPSPPKRSSRRPPPAASKKSVSEKLTSPAPAAKG KEDHQKTIIIAVTTAVSTFLLAACFLCCTKVCCKGSGGRINDERPLLSLSSNEYSLGSS NNYGGSGKGHQSFNNGNSDNFVTLERMSMDGMFNNINNSHGIPPLKAPPGRKSSKIS </p>

			<p> WKPPSGKVEPLPPEPPKFLKVSSSKKSSSAPSPSPPPPPMPSSAGPPRPPPPAPPPGSGGPKP PPPPGPKGPRPPPPMSLGKKAPPASPGPASSGDDDA PKTKLKPFWDKVQANPEQSMVW NDIRSGSFQFNEEMIESLFGYAAADKNKNDKKGGSGQAALPQFIQILEPKKGQNLSILLR ALNATTEEVCDALLEGNELPVEFIQTLLKMAPTPEEELKLRLYSGEIAQLGTAERFLKAV VDIPFAFKRLEALLFMCTLHEEMAFVKESFQTLEVACQELRGSRLFLKLLEAVLKTGNR MNDGTFRGAAQAFKLDTLKLADVKGTDGKTTLHFVVQEIRTEGRRRAARTIRESQSF SSVKTEDLMAEETSEEMEENYRGLGLQKVSGLSSELEHVKKSANVDADSLTGTVLKMG HALAKAREFVNSEMKSSDEESGFREALEDFIQNAEGSVVEILEEEKRIMALVKATGDYFH GKAGKDEGLRLFVIVRDFLIILDKSCKEVREAKGKQVKMARKQGSTASSVASEIPRAPSL DPREKLFPAITERRVDQSSSDSD </p>
<i>BrCAGP41</i>	<i>Bra019092</i>	Glycerophosphoryl diester phosphodiesterase domain (GDPD)	<p> <u>MRGLLLLCGVVLIQLLAAQTDA</u>QGSKSKWQTLTGFSRVIARGGFSGLFPDSSIDAYNFA MLTSVEDVVLWCDLQLTKDGAGICFPGLTMSNASNIEAAYPNRTNTYLVNGVSTQGWFT IDFSLKDLNKNVNLIRGILSRSERFDGNGYSILTVQDVNTELKPQGLWLVNQHEAFYAQHN LSMTTFLTTASKTVIIDFISPEVNFFKKIAGRFRILVPKSYVLPLDDKQYLLPSTSLVQD AHKAGLEV FVSGFANDVDIAHDYSYDPVSEYLSFVDNGNFSVDGVLSDFPISASASVEC FSHMGRNATKQVDFLVISKNGASGDYPGCTDLAYAKAIKDGAVIDCSVQMSSDGT PFC SSSIDLGKTTMVAQTPLRNRSTNVPEISSLGGIYTFSLTWPEIQTLTPAISNPYRTYNMFRN PNERNAGKLVSLSDFLNLAKNSTSLSGVLISVENAAYLRENQGLDVVKAVLDTLTETGY TNITTKKVMIQSTNSSVLLDFKKQSR YETVYKVEETIRDILDSAIEDIKRFASAVVIVKSSV FPDSEGFVTGQTNVVERLQKSQLPVYVELFQNEFVSQPYDFFSDANVEINSYVTGAGVN GTVTEFPFTAARYRRNRCLGSKETPPYMAPVQPGG LLQVNVHASLP AEAPNPVFTDAD </p>

			VTEPPLPPVTAKAPTSTTPGTPSKPSTNAPAPSGQTRLTSLLLSVFPMASLLLL
BrCAGP42	Bra026409	GDPD	MRGLRASSLLLCGVVLIQLLAVQIDAQRPKTQWKTLSGFSPRVIARGGFSGLFPDSSLDA YNFAMQTSVLDVAVLWCDLQLTKDGAGICFPDLTMSNASNVESVYPKGQSTYPVNGVPT PGWFTIDLSLRALTNVSLIRGILSRSDKFDGNGYTISTVQTVNKEMKPQGFWLNVQHDA FYAQHNLSMSNFLVSVTKTVIVDFISSPEVNFFRKIAGRFGREGPSFVFRFLEKEQFEPTTN RTYGSILSNLTFVKTFASGILVPKSYVLPLDDKQYLLPSTSLVQDAHKAGLEVFSVSGFAND VDIAHDYSFDPVSEYLSFMDNGNFSVDGVLSDFPITASASVECFSHVARNATKQVDFLVI SKNGASGDYPGCTNLAYEKAINDGADVIDCSVQMSSDGKPCSSSIDLGNTTMVAQSPL RNRSTSVPEISSVNGIYTFTLTWPEIQTLTPAISNPYSRRFNMFRNPNERNSGKLLSLSEFL NLAKNSTTSLGVLISVENAAYLREKQGLDVVKAVLDALTETGYSNRRTTKVMIQSTNSS VLVDFKKQSQYETVYKVEETIRDILDSAIEDIKTFASAVVIGKSSVFPVVDGFTVGTQTNV ERLQKSQLPVYVELFQNEFVSQPFDFSDATVEINSYVTGPGINGTITEFPFTAARYRRNR CLASKETLSYMAFVQPGGLLEVVSPPGSLPPAEAPNPVFTDADVTEPPLPPVTAKAPTPTP GTPSTTAPAPSGQTQLTSLLLSVFAMVLASLLLM
BrCAGP43	Bra002904	GDPD	MLGSRASKFLLSALILIHLLPTQLLAQRSKSPWQTLTGSAPLIARGGFSGLLPDSSVDAYS IVSQTSVSGAVLWCDVQLTKDGVGICFPDVKMMNASSIQDAYPKRKNSYLVNGVPTQD WFTIDFTLKDLSVFLIRGILSRSDAFDNNQYAISTVQDIAMELKPKSFWLNVQHDAFYA QHNLSISKFMLSPLKTVTINYLSPEVTFLRSIGGRFGKAGPKFVFRFLEKDDVEVSTNQT YGTLLGNLTFIKTFASGVLVPKSYIWPLEDQYLSPHTSFVQDAHKAGLEVYASGFANDFD MAYNYSFDPLAEYLSFMDNGDFSVDGFLSDFPLTASSAVDCFSHLGSNASTQVDFLVISK NGASGDYPGCTDLAYSKAIDGADIIDCSVQMSLDGIPFCLNSVDLGESTNIVQSPFRNR

			SATVPEIAPLGGLYSFSLTWSEIQTLRPAITNPYNRDFNLFRNPKERSSGKLVSLSDFLNLA KSSTSLAGVLISVENAAYLREKQGLDVVKAVLDTLTKAGYSNATTTTKKVMIQSTNSSV LVDFKKQSRYETVYQVEETIRDILDSAIQDIKKFADAVVVRKNSVFPVSESFTTGQTNLVE RLQRFQLPVYVELFRNEFVSQPWDFLSDATVEINSHVTGAGINGTITEFPLTAARYKRNK CLTRKDLPPYMSPVQPAGLLSIMSPTSLPPAEAPNPVFTDADVTEPPLPPVIAKAPTSSPGP LSTDEKAPNGQTRVTLSSLSSAFAMVLASLLLL
BrCAGP44	Bra028979	GDPD	MITSYMQDNPSMFVSRASKFLLSVLVLIQLLPTQLLAQRSKSPWQTLTGEAPLVIARGGF SGLFPDSSFNAYSFVASTSAPDAVLWCDVQLTKDGVGICFPYVTMYNDSNVQEAYPKKK NSYLLNGVPTQDWFTVDFTSRDLNTVFLTRGVLSRSNAFDNTQNVISTVQEVASEFKPA GFWLNVQHDAFYTQHNLSMSSFLTVSKTVIIDYLSPEVSFFRNIGGRFGKTGPKFVFR FLDKDDVEVSTNQTYGSLMKNLTFIKTFASGVLVPKSYIWPVKDQYLLPHTSFVRDAHT AGLQVYGSGFANDFDIAYNYSYDPLTEYLSFMDNGDFSVDGFLSDFPLTASSAIDCFSHL GSNASTQVDFLVISKNGANGDYPGSTDLAYTKAIKDGAIDIIDCAVQMSSDGIPFCLNSTN LGESMNIVQTPFRNRSTTVPEFNLAGLYSFNLAWSEIQTLTPAISNPYSRNFHMFNRNPRE RSSGKLVSLSEFLNLANNSSSLVGVLINVEHAAYLREKQGLDVVKAVLDTLKESGYSNAT KRVMIQSSNSSVLVDIKKQSRYETVYQVEETIRDIQDSAIQDIKKFADAVVGRFSLYPISA SFITGQTNLVERLQKFKLPVYVETERNEFVSQAYDFLSDATVEINTHVTGAGVSGTITEFP LTAARYKRNRVCARKDTPVYMIPVRPAGLLEIVSPTFLPPAEAPNPVITDADVTEPPLPPV TAKAPTTSPGPLPTDKKAPNGQTRVTL SVFLSAFDVVLASLLLL
BrCAGP45	Bra035244	GDPD	MPTSTVLLCCVVLIIQLFAGQTDARSSSPWQTLSGDAPLVIARGGFSGLFPDSSLNAYSFAV QTSVPGSALWCDVQLTKDGAGICFPDLKLNNASTVEYVYPNRQKSYPVNGVSTQGWFT

			<p> IDFSLRDLNDVSLIRGILSRTEKFDGIYPILTVEDVTTQIKPESFWLNVQHDAFFEQQNLISM SKFLISASRIVSINYISSPEVNFFTKISGRFGRNGPLVFVFQFLRKEDIEPTTNQTYGSILSNLT FVKTFASGILVPKSYILPLDDKQYLVPPPKSLVQDAHKAGLQVYVSGFANDIDIAHDYSS DPVSEYLSFVDNGNFSVDGVLSDFPITASSSIDCFSHLGQNAIKQVNFLVISKNGASGDYP GCTDLAYDKAIKDGADVIDCSVQMSSDGVPFCRSIDLSNSTMISQTPFAQRSTLVPEISS SGGIYTFSLTWAEIRNLTPAIGNPYRSYTMFRNPNKKNNGSKLILLSEFLNLANNSTLLSGV LISVENAVYLREKQGLDVVKAVLDTLTETGYGNGTTKTKVMIQSTNSSVLVEFKKQSKY EAVYKVDEKISDISDAIEDIKKFANAVVIGKESVFSLLDSFITRQTNVVEKLQKSKLPVY VELFQNEFVSQPYDFFSDPTVEINSYILGAGINGTITEFPFTAARYKRNRC LGTQETLPPY MAPFKPGSLLQAVNAIPPAQAPNPVFTDDDVT EPLPPVTAKSPTS SPGTSFTNAQAPRPS GQTRLTSLRFSVFASLLLLWISSPLCS </p>
BrCAGP46	Bra004101	GDPD	<p> MGASRVLLCCVVLIIQLFAGQADAQRSSSPWQTLSGDAPLVIARGGFSGLFPDSSFNAYDF AKQTSVAGAALWCDVQLTKDGAGICFPDLKLNNASTVEDVYPNRQKTYSVNGVSTQG WFTIDFSLRDLISNVKLNRGILSRSEKFNGIYAIMTVEDVTTQIKPESFWLNVQYDAFYAQ HNLSMSSFLISASTTVSIDYISSPEVNFFKKIAGRFGRNGPSFVFQFLGKEDFEPTTNRTYG SILSNLTFVKTFASGILVPKSYILPLNDKQYLLLPPASLVLDAHKAGLQVYVSGFVNDNDI AHDYSSDPVSEYLSFVDNGNFSVDGVLSDFPITASASIVDFLVISKNGASGDYPGCTDMA YDKAIKDGADVIDCSVQMSSDGKPFCAHSIDLSNITNIAQTPFTKRSTHVPEISSNDGMY TFSLTWSEIQTLKPAISNPYRVYNMFRNPNNEKNSGKFILLSDFLNLAKTSTSLSGVLISVEK AVYLREKQGLDVVKAVLDTLTETGYSNGSTTKTKVMIQSTNSSVLVDFKKQSSKYETVY KVEEKIGDISDAIEDIKKFANAVVIGKETVFPLFDDGFIIRQTNVVEKLHKSKLPVYVEVF QNEFVSQPFDFSDPTVEINSYVSGAGIDGTITEFPFTAARYKRNRC LGTKESLAPPYMSPP </p>

			VRPGFFLNLVNAIPPAQAPNPVFTDDDVTPLPPVTAKSPTSSPGTSFTNAQAPRPSGQTRLTSLRLSVFASLLLL
<i>BrCAGP47</i>	Bra034037	GDPD	<p> MRASTVLLSSVLIQLFAAQIDAKSSRSPWQTLSGDAPLVIARGGFSGLFDPDSSSVAYKFA KQTSVADLFPNRQNFYPVNGVTSQGWFTIDFSLRDLKNASLIRGIFSRSEKFDGNGYSILT VQDVSMQIKPESFWLNIQHDAFYAQHNLSISSFLISASRTVSDYISSPKLNFFSKVKGRF WRNEPSFVFQFLGKEEFETTKRTYGSILSNLTYVKTFASGILVPKSYILPLDDKQYLLPPT SLVQDAHKAGLKLYVSGFANDVDIAYNYSFDPVSEYLSFVNNGYFSVDGVLSDFPITAST SIDCFSHIGRNARKQMDFLVITKNGASGDYPGCTDLAYEKAIQDGADVIDCSVKMSSDG KPFCSSSIDLTQSTMVIQSPFRNRSTIIPDISSDPGIYTFNLTWPEIQSLTPAIMNPYRSYNMF RNPNEKNSGRIISLSEFLHLANKSTSIYGVLSVEYVVYLREKQGLDVVKAVLDTLTETGY SNGTSTTKVMIQSTHSSVLVDFKKKSKYETVYKVEETIRDISDSAIEDIKKFANAVVIGKS SVFPDVGSFVTGQTNVVERLRKSKLPVYVELFQNEFVSQPYDFCSDATVEINTYITGAGI NGTITEFPLTASRYKRNQCLGRKETPSYMSPIKPGILLSLANPRSLPPAEAPYPVFTEDDVT ESPPQPPGTEKSPSSSTNAQTHRPSGQTRLTSLRLSVFASLLLL </p>
<i>BrCAGP48</i>	<i>Bra034311</i>	Protein kinase (Pkinase) and LRR	<p> MAATSLVLTCFFSIFLLTHRNVNSESLEKQALLTFLQQIPHENRLQWNESDSACNWVGVE CSSDRTSVHSLRLPGTGLVGQIPSGSLGKLSQLRVLSLRNRLSGQIPPDFSNLTHLRSLYL QNNEFSGEFPASVTQLTGLVRLDISSNNLTGPIPFVSVNNLTQLTGLFLGNNRFSGNLPSITV DLTDFNVSVNNLNGSIPTSLSKFPAASFAGNVNLCGGPLKPKCSFFVSPSPSPSPDAPLSG KKSKLSTAAIIAIAVAGAVVGLLVLALLFLCLRKRRRGKEGGTKAAETTATTRSVPSVPP AGGASSSKEVTGTSSGMGGETERNKLVFTEGGVFSFDLEDLLRASA EVLGKGSVGTSYK AVLEEGTTVVVKRLKDVAASKKEFESQMEVVVGKIKHPNVFPLRAYYSKDEKLLVDFD </p>

			MPNGSL SALLHGSRGSGRTPLDWDNRMRIAITAARGLAHLHVS AKLVHGNIKASNILLH PNQDTCVSDYGLNQLFSNSSPPNRLAGYHAPEVLETRKVTFKSDVYSFGVLLLELLTGK SPNQASLGEEGIDLPRWVLSV VREEWTAEVFDVELMRYHNIEEEMVQLLQIAMACVST VPDQRPVMQEVL RMIEDVNRSETTDEGLRQSSDDPSKGSEGQTPPGESRTPPRSVTP
<i>BrCAGP49</i>	Bra012045	Pkinase and LRR	MG AISLVLS CFVSILLTDRVSSESPEEKQALLAFLQQT PHENRLQWNASDSACTWVGVE CNSDRSSIYSLRLPGTGLVGQIPSGTLGKLTQLRVLSLRSNRLSGQIPPDFKNLTHLRSLYL QHNELSGEFPASITQLTGLVRLDISSNNLTGSIPFAVNNLTLLTGLFLGNNRFSGNLPSITVG LTDFNVS VNNLNGSIPSSLSKFPAASFAGNVNLCGGPLRPCKSFFISPSPSDDAPSPSRLS GKKSKLSTAAIIAISVASALIGLLLLALVFFLCLRKRRRGGSRTKQTKPAETTTTRNVPPEGI PPAGGASSSKDDL RASA EVLGKGSVGTSYKAVLEEGTTVVVKRLKDVAASKKEFESQ MEVVGKTKHPNVVPLRAYYYSKDEKLLVFD FMPSGSLSALLHGSRGSGRTPLDWDNR MRIAITAARGLAHLHVS AKLVHGNIKASNILLQPNQDTCVSDYGLNQLFSNSTPPNRLAG YHAPEVLETRKVTFKSDVYSFGVLLLELLTGKSPNQASLGEEGIDLPRWVLSV VREEWT AEVFDVELMRYHNIEEEMVQLLQIAMACVSTVPDQRPVMQEVL RMIEDVNRSETTDDG LRQSSDDPSKGSEGQTPPGESRTPPRSVTP
<i>BrCAGP50</i>	<i>Bra019320</i>	Pkinase and Gnk2-homolog ous (GNK2) domain	MSSCTSFIVLVLF SLLASYRAYAQNP HYTYHSCSNTTTYTRNSTYSTNLKTLSSLSSPDA SYSTGFQ NATVGRDPDRVTGLFLCRGDVSPEVCRSCVAYS VNETLSRCPNEKEVVLYYE ECMLRYSHRNILSTLVYEGGFFMFNGNISSNQEDRFEDLVSTTMNQAADKAANS SRKFY TIKANWTALQSLYGLVQCTPDLTRYDCLRLHQSIDGIPLNRIGGR LFWPSCNARYELYLF FNENDTRTPLEQHAPPPQPSP LPPPPASTSPVSSLTRTGKHHENSKVLIVAIVVGIVVAVLI FIAGYCF LAKRTKKTSDNAPAFYGDDITTIESLQLDYVIIQAATNNYSENNKIGEGGFGEV

			YKGTfangvevavkrlskssrqdtefknevavvaklqhrnlvrllgfsleqkerilvy eyvpnkslDYFLFDPAKHGQLNWTLRYKIIegITRGILYLHQDSRLTIIHRDLKASNILLDR NMNPKVADFGMARIFGMDQTQDNTSKIVGTYGYMSPEYALHGQFSMKSDVYSFGVLV LEISGMKNNSFYeidGAHDLVTYAWKLWGNGTALNLVDPIIIDNCHNSEVVRciHIGLLC VQEDPVDRPTFSTIFVMLTSDTVTLVPVRQPGFFVQSRPERDPLDSDQSTTTKSDPTSVD ASITDIYSR
<i>BrCAGP51</i>	Bra019323	Pkinase and GNK2	<u>MSSRASFI</u> FLFLYSFLT <u>SFRATAEIP</u> IFVHHYCRNTTRYTANSIYFTNLKTLWSSLSTNA SYSTGFQ ¹ NATAGQARDMITGLFLCRGDVSLEVCRDCVSYSVKDIVRKCPNQREATIYYD QCMLRYSDRNIFSNVTLDDGFIMYNDHYDIPSAEQARFENLVLTMTMIELAFEANSSRHF CTRETKWNDYQDLYVLVQCTPDLTRQDCFRCLDRSINELYFSTIGERYLYPSCNSRYEFY KFYNETLLPPPPLA ² AP ³ TPPVSS ⁴ APRPRDDITTIDSLQLDYRTIQAATNDYSENNKIGRGGFG EVYKGTFLNGTEVAVKRLSKSSGQGETEFKNEVVVAKLQHRNLVKLMGFSLEREERIL VYEYVPNKSLDYFLFDPTKKGKLCWTRRYKIIEGVARGMLYLHQDSRLTIIHRDLKASNI LLDADMNPKIADFGMARIFGMDQTQENTNRIVGTYGYMSPEYAMHGQFSMKSDVYSF GVLVLEIMTGRKNSSFYERDGAHNLVTYAWRLWTNKTELDLVDPVIVYNCQKSEVVRci HVGLLCVQEDPVERPTFSTILQMLTSNNVIL ⁵ PVPQQPGFVIQARPKRDLPSDQSTMTKC ATRSVGDasVTDLYPR
<i>BrCAGP52</i>	Bra019322	Pkinase and GNK2	<u>MCSWASLI</u> FLFIFSFLT <u>SFKASAQDPI</u> YVYHICPNTTTYTRNSTYSTNLRTLLSSLSSSNSSY STGFQTAISGQGTDSVTGLFLCRGDVSPEVCRRCVAFVNDTSTRCPNQREVVLYYDVC TVRYSNRNILSTLSTDGGVVLWNTQNITSNQKDQFRDLVLSTMNQAANEAAADSRRKFD ARKANWTASQSLYGLVQCTPDLTRQDCLSLQQSINQLPTDKIGGRFIMHSCGSRYELYA

			<p>FYNESAITTPPLPPQPPVSTPPVSAAPPAGKGGSSSVLVVAIVVPIIVVLLLIACYCFLAKR AKKTYGTASAFDGGDDITTAESLQLDYRSIQATATNGFSESNKIGQGGFGEVYKGTLSDGTE VAVKRLSKSSGQGDAEFKNEVILVAKLQHRNLVRLLGFCLEGEERVLVYEVVPNESLDYF IFDLAKQTQLDWSRRYKIIGGIARGILYLHQDSRLTIIHRDLKASNVLLDSDMNPKIADFG MARIFGMNQTEENTSRIVGTYGYMSPEYAMHGQYSMKSDVYSFGVLVLEIISGKKNSSF YQTDGAHDLVSYAWRLWSNGTPLDLVDPIVDNCQRNEVVRCVHIGLLCVQEDPVERPP FSTIVLMLSSNTVTLPVPRQPGLFFQSRLGKDPLDSDKFTTTKSLLSVDDASITDVYPR</p>
<i>BrCAGP53</i>	Bra019321	GNK2	<p>MLRYSYRNILSTAIYNEGGVIRLNNNVSSNQEDRFQVLVSTTMNQAADKAANSSRKFYT IKANWTALETLYGLVQCTPDLSRYDCLRCLHQSIDGMPLNKIGGTLIWPCSNARYELYLF FNETGTGTPPEQQAPPLQRLPPPPASTSPASSLPRPGKHWNFKMVIVAIVVAIVVAVLLS IAGYCFLAKRTKKTSDNAPAFYGNDITTIESLQLDYRIIQAATNNYSENNKIGQGGFGEVY KCLGNQVFFVQSRSGRDPLDSDQSTTTKSDPTSVDDASITDIYSR</p>
<i>BrCAGP54</i>	Bra019319	Pkinase and GNK2	<p>MEPVIQSLEAEPVIQVTLSDFDNAWEALMRRVIAEATSSSSGSNTMYYGADRQQLGTSR SIYGFVQCSKDISPSKCEQCLRKNVDDYRSCCSGRQRGITERPSCFMRWDLDPFFGLFED NIAPAPTTPPEKGDRKIPIGVVVGITGVLTFFVISMLLSLGVALCIRRKAHQENGNESEQEFK NEVLLVAKLQHRNLVRLLGFSVEGAERILVYEFVPNKSLNYFLFDPVKRSQLDWRKRYN IITGIMLYLHQDSRLTVVHRDLKASNILLDVDMNPKIADFGFLARNFRMNQTEANTGRVV GTVGYMPPEYVANGQFSMKSDVYSFGVLILEIIGGKKNSSFHKIDGSLRNLVTYVWRLW NNESLLELVDPAVGENDYDKHEVTRCIHIGLLCVQENPADRPTMSTIFQMLTNTSITLHVQPQ PPGFFFRDGA SPLAEGLTIGQSSIMSFACSVDDASITSVNPR</p>

<i>BrCAGP55</i>	<i>Bra011048</i>	Pkinase and GNK2	<p> <u>MASTLLLASFAVFLTLTLTPSPSTSTEVSRL</u><u>LDVLGWVCNNGSVDPQEAYRRSYQINIDKT</u> <u>RDDMRKLKFGTHEDGVPPQKMYFLSQCVSDLSPDECSCWSRATDLLFNCFPSPGGRFY</u> <u>LDGCFVRADNYSFYREPVTRQDSKICGGDESSSSREFKGLVKEVTKSIVDTAPYSQGFSV</u> <u>VARKSVHGLTAYGLGICRQTLDEELCQLCLADGALSATSCSPATEAFVMNAGCYLRYSN</u> <u>YTFYNERELLSMSLTKEHVLRLVISMVCVLAIASGFWCGKCIYLGASSKKKLKEKESKS</u> <u>VSNNSNLMCFKYSTLEKATNNF</u><u>NESCKLGVGGYGEVFKGTLSDGREIAIKRLHISGNKT</u> <u>REEIHNEIDVISRCQHKNLVRIGCCFTNMNSFIIYEFLANSSLDHILFNPEKKKELEWKKR</u> <u>RAIILGTAEGLEYLHEACKIIHRDIKASNILLDLKYKPKISDFGLAKFYPEGGKDIPSSSPSP</u> <u>SPSPIAGTLGYMAPEYISKGILSNKIDAYSFGVLVLEITSGFRNNKFRSDNSLETTLVTQVW</u> <u>KCYASDKMEEMIDKDMEEETDKTEVKRVMQIGLLCTQESPQLRPTMSKLVGDSIAIAVIR</u> QNRNRLPACSLCNSSRNRI<u>TPSP</u>TVSLHLLCRNPLGEIETV<u>SP</u>HLEIETISLHLLSEHRPKR GTCSSSVV </p>
<i>BrCAGP56</i>	<i>Bra032175</i>	Pkinase and LRR	<p> <u>MKTELVSPILFFFSFSCLLLVSSGL</u><u>NSDGVLLMSFKYSVLLDPLSLLQSWSYDHDNPCSW</u> <u>RGVLCN</u>NDFRVVTLSLPNSKLAGSIPSDLGFLQ<u>NLQSLDLSNNSLNGSLP</u>VEFFAAGELR FLDLSNNLFSGEIPATVGDMHNLQTLNLSDNILAGKLPANLASLESLTEVSLKNNYFSGEL PGGWRSVQFLDISSNLINGSLPPDFSGDSLRYLNVSYNQISGEVPPDVGDGFPRNATVDFS FNNLTGSIPD<u>SP</u>VFLNQKSISFSGNPGLCG<u>AP</u>TRNPCPISS<u>SP</u>AAVT<u>TP</u>ST<u>TP</u>ALAAIPKTFGS NPESDSV<u>GP</u>ENNKSNNRRTGLRPGVIIGIIVGDIAGIGILALVFFYVYRYKKKNNMQKNTHS LEANEVKDTTSL<u>SP</u>SSSTTTSSS<u>SP</u>EQSNRFVKWSCLRKSQETDETEEEDEEEHHQ<u>GP</u>GE TKKGTLVTIDGGEKELEVETLLKASVYILGATGSSIMYKTVLEDGTVLAVRRLGENGMS <u>QQRFRKDLEAHVRAIGKLVHPNLVRLRGFYWGTDEKLVYDFVPNGSLVNARYRKGS</u> <u>SPCHLPWETRLKIAKGLARGLAYLHEKKHVHGLKPSNILLGQDMEPKIGDFGLERLLA</u> </p>

			<p>GDTSYNRASGSSRIFSSKRSASASTREFGTPSPSPSSVGPVSPYCAPESLRNLKPNPKWD VFGFGVILLELLTGKIVSVDEVGIGNGLTVDDGNRALIMADV AIRSELEGKEDLLLGLFKL GYSCASQVPQKRPTMKDALVVFERFPMSSSAKSPSYRYGHY</p>
<i>BrCAGP57</i>	<i>Bra019878</i>	Pkinase and LRR	<p>MIFTSRQVFFVLSVLALTTMPFSAGVTNLRDVSAINNLYITLGA^{PS}SLHRWLAFGGDPCGE KWQGVVCDSSNITEISIRGMKVGGSLSDTLADFSSIQVMDFSDNHISGTIPQALPS^{TIRNL} SLSSNRFTGNIPFTLSFTELSELSLGNNVLSGEIPDYFQQLTKLTKLDLSANILEGRLPPSM GDLAALKILKDGT^{TP}FNTSII^{TPPPP}AADPPPATHH^{APPL}LPRVPPVSNVPP^{APFAP}LLPPPPPLV W^{SPP}SDNVGGDPWNSGSGQPTLQI^{SPP}SGSGSGKFWSTQRIILVVSSVAIIVLVSGLCVTL WRCCRGKKYNRYGADARKDLQRPYFNKPPSQP^{TP}TLGKVSREPMVKPYDGYGGGDRK YGYPMPPPRPEESRRAIPPASYYNKDVQKPLQQPPRRFQSNDDSAASKRAAHFPPGLNSS SSATVFTVASLQQYTNGFS^{EELIIGEGSLGNVYRAVFPHGKYLA}VKKLSNTINKTQSDGEF LNLVSNVLKLKRGNILEFLGYCNEYGQRLVYEYCPNGSLQDALHLDRKLHKKLTWNV RINIALGASKALQFLHEVCQPPVHQNFKSSKVLLDEKLSVRVADSGLAYMLPPRPTSQV AGYAAPEVEYGSYTCQSDVYSLGVVMLELLTGRRPFDRTRPRGHQTLAQWAIPRLHDID ALTRMVDPSLHGAYPKKSLSRFADIISRLQMEPGFRPPVSEIVQDLQHMI</p>
<i>BrCAGP58</i>	<i>Bra002639</i>	Pkinase	<p>MESPMRFNLRTAFSIIFLTFLPLNLKSQEVFDPSQDHS LIQSEASWNRRSLVE^{TPPLPGK}^{GP} AVGA^{SPPSP}DQAFEGSTKPPP^{APETQ}^{TPP}GGDGT^{TP}SPPSSSVRTAQ^{TPNPPSEPPPQLL}^{SPPP} RTKKTHNISMIVGIVGVFTVSVALIIFFLIHTRKIPKWTNSGQLQNALITGNHTLFNVP RMQLSELRAAC^{EDFSNIIGSFSDGTIYKGTLSTGAEIAVVSIAAGSRANWSTD}METQLLQ KIRKLSKVDHKNFLNVIGYCHENEPFHRMLVFEYAPNGTLSEHLHSQHTEHLDWPTRLRI FMGIAYCLEMHMNLNPPILHTNLDSSCIYLTEDNAAKVSDFSVLNFISSKESSSSKNLLE</p>

			HSTLDPQTNVLNFGALVFEIITGRLPDPDSLFLEPKPARDLVDPTLKTFFQEDVAERLLGVV RQCMNPYSAQRPTMRKVVKLREII ^{SP} GIEADAALPRL ^{SP} RWWSEMEIITTDGN
<i>BrCAGP59</i>	<i>Bra029710</i>	Pkinase	MEAVGRISPHGNVAPLRAYYFSKDEKLLVYDYYQGGNFSMLLHGNNEGGRGALDWEQ RLKICLGAAGIAHIHSSSGAKLLHGNIKSPNVLLTQDLNACVSDYGIAPLMSSHHTLLPS RSLGYRAPEAIETRKHTQKSDVYSFGVLLLEMLTGKAAGKTTGHEEVVDLPKWVQSVV REEWTGEVFDVELIKQQHNVEEEMVQMLQVAMACVSKHPDSRPSMEEVVMNMMEEV RPSNGSGAGSGNRAS ^{SP} EMIRSSD ^{SP} V
<i>BrCAGP60</i>	<i>Bra040054</i>	Pkinase and LRR N-terminal domain	MPLLKVIPPLSLSIYSIQRSASNATSQD ^{SP} MNPPQRSADI ^{SP} DSDKQALLEFASLVPHARKLN WNTTNPICTSWTGITCSKNNSRVLTALRLPGSGLY ^{GP} LDPKTFEKLDALRIISLRNNLQGN IPLTILSLPFIRSLYFHDNNFSGTIPPTL ^{SP} RLVNLDLSNNSLSGNIPASLRSLTQLTDLNLQ NSLT ^{GP} IPDLPPNLKYLNLFSNNLNGSVPSLKSFPASSFQGNLLCG ^{SP} LT ^{SP} CPDNTT ^{SP} APA KKVLSTAAIVGIAVGGSVLLFILLAVITLCCA ^{SP} KRDDNGQDSTST ^{SP} AKAKTIRSDNKAEFF GSGVQEPEKNKLVEFEGSSYNFDLEDLL ^{SP} RASAEVLGKGSYGTTYKAILEEGTTVVVKRL REVAAGKREFEQKMEAVGRISPHVNVAPLRAYYFSKDEKLLVFDYYQGGNFSLLLHGN EGGRAALDWETRLKICLGAAGGISHIHSASGAKLLHGNIKSPNVLLTQDLNACVSDYSIA PLMSSHHTLLPSRSLGYRAPEAIETRKHTKSDVYSFGVLLLEMLTGKAAGKTAGHEELV DLPKWVQSVVREEWTGEVFDVELIKQQHNVEEEMVQTLQIAMACVSRHPDSRPSMEE VVMNMMEEIRASTGS ^{GP} GSANRAS ^{SP} EMIRSSD ^{SP} V
<i>BrCAGP61</i>	<i>Bra013336</i>	Pkinase and LRR	MGCGFHYSYVFFLIITLQAPLSFSV ^{NS} QEYTLLKFRERVNSDPHGTLANWNISDLCSWS GVTCVDGNVQILDLSGCSLGGTL ^{AP} EFNQELRLSLILSKNHFFGEIPKEYESFS ^{SP} KLEFLDL RDNDLTGTIPPELTNLSLKHLLSGNKFQSDMSIKILRMKLLH ^{SP} FAVLGCANRKLGHCS

			<p> RNHIIRVKKIEAFVFRIKATSRRLKAFPSKFDKRRELLEETSNLAAEPAPQAPSPSPETIT EASPRSSGSFPAVTNAKKRIPPLVPPPPSPDENTSSDSSKNQPQDNKQSKGSKHVWLYVVI AVASFLGLLIIVAVIFLCRKRAVKSIGPWKTGLSGQLQKAFVTGVPKLNRAELETACEDFS NIETFDGYTVYKGTLSGVEIAVASTAVCESKEWTRAMEMAYRRTIDALSRINHKNFVN LIGYCEEDEPFNRMMVFEYAPNGTLFEHLHDKEMEHLDWASARMRIIMGTAYCLQHMHE MNPPMAHSDFNSSEIYLTDDYAAKVSEIPFNLEARLNPKKHVSGDLEQASLLLPPEPETN VHSFGLLMLEIISGKLSFSDEYGSIEQWASKHLENDLDEMVDPSLKTFFKEEELEVICYVI RECLKPDQRHRPSMKDVAEQLKQVINITPEKATPRSSPLWWAELEILSSEAT </p>
<i>BrCAGP62</i>	<i>Bra011747</i>	Pkinase and LRR	<p> MKMQLITAFFFFFLLCFVLGSSGLSPDGLLLMNFKSSVLVDPLSLLQTNWYNHETPCSW RGVSCNNDISKVINLSLPNSHLLGSIHSDLGSLRSLQSLDLSNNSFNGLPVSLFNGTELRS LDLSGNMISGEVPASIGDLHSLQTLNLSDNALAGKLPANLVTLRNLTAVSLRSNYFSGEIP GGWRDVQFLDLSSNLINGSLPPDFGGASLRYLNVSFNQISGEIPPEIGANFPINATVDLSFN NLTGSIPDSPVFLNQKSIFFSGNPGLCGDPCPISSSPSTISDADSPTSTPAIAAIPNTISSNPVT NPTTQQTNRTPRTGLRPVVITGIVIGDIAGIGILAVIFLYIYRRKKNIANNNDKQREETD TITLSPSSSSSSSPDESRRFTKWSCLRKDPETTPSDEESGYNADQSRSDSEGLTVTDGEK EMEIETLLKASAYILGARGSSIMYKAVLEDGTVYAVRRLGETGLTQRRFKDFESNIRAIGK LVHPNLVRLRGFYWGIDEKLVYDFVPNGSLVNPRYRKGGGASSPYHLPWETRLKIARGI ARGLAYLHEKKHVHGNLKPSSVLLGHDTEPRIGDLGLERLLTGETSYSRAGGSSRIFGSK RSRGSSLDFFSIGPTPSPSPSSLGPLSPYCAPESFRSLKPSPKWDVFGFGMILLELLTGKVL AEEVGLGIGLTVEDGHHALRMVDVTIRGELLGKEDFLLGCLKLGYNCASPIPQKRPTMK ESLAVLERFTPSSDVVKSPSFHYMNH </p>

<i>BrCAGP63</i>	Bra036670	Pkinase	<p>MSCFSCFSSKNLENEGSSLPAPYRQTGSPNNQRERTREVVANNAPSQSNNIEAQGFSFRE LATATNNFKLENLIGEGGFGRVYKGKLNKTGQVVAVKQLDRNGLQGQKEFLVEVLMLS LLHHSNLVNLIGYCADGDQRLLVYEYMPGSGVEDHLLDLEPDQKPLDWNRSRIKIALGAA KGLEYLHDKANPPVIYRDLKSSNLLLDQDFDTKLSDFGGLAKLGPTGDTLHVSSRVMGTY GYCAPEYQRTGHLTVKSDVYSFGVVLELITGRRVIDTMRPSHEINLVTWAQPIFRDPTRF PQLADPLLRRGEFPEKSLNQAVAVAAMCLNEEPMVRPLISDVVTALSFLGASSDFSADSS HLQQNPSEIYHDAVQWDSSPR</p>
<i>BrCAGP64</i>	<i>Bra011439</i>	Pkinase and LRR N-terminal domain	<p>MERRLMKIARFFWLVLVFDLVLRTSGNAEGDALSALKNSLSDPNKVLQSWDATLVTPCT WFHVTCNSNSVTRVDLGNANLSGQLVTQLGQLPNLQYFFANTNLTPLPASPPPISTPP SPAGSNRITGAIAGGVAAGAALLFAVPAIALALWRRKKPQDHFFDVP AEEDPEVHLGQLK RFSRELQVASDNFSNRNILGRGGFWKVYKGRLADGTLVAVKRLKEERTQGGELQFQTE VEMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLDRPESQPPLDWPKRQRI ALGSARGLAYLHDHCDPKIIHRDVKAANILLDEDFAVVGDFGLAKLMDYKDTHVTTA VRGTIGHIAPEYLSGKSSEKTDVFGYGVMLLELITGQRAFDLARLANDDDVMLLDWV KGLLKEKKLEALVDVDLQGNIDEVEQLIQVALLCTQSSPMERPCKMSEVVRMLEGDG VAERWEEWQKEEMFRQDFSQYNQNPNTAWLIGDSTSHIENDYPSGPR</p>
<i>BrCAGP65</i>	<i>Bra037006</i>	Pkinase	<p>MVFCYWWFRRLNNNSLSGEIPRSLTAVSSLQVLDLSNNPLTGDIPVNGSFSLSFTPISFANT KLTPLPASPPPLSPTTPSPAGSNRITGAIAGGVAAGAALLFAVPAIALALWRRKKPQEHFF DVPAEEDPEVHLGQLKRFSRELQVASDNFSNKNILGRGGFCKVYKGRLADGTLVAVKR LKEERTQGGELQFQTEVEMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRE RPESQPPLDWPKRQRIALGSARGLAYLHDHCDPKIIHRDVKAANILLDEDFAVVGDFGL</p>

			AKLMDYKDTHVTTAVRGITIGHIAPEYLSTGKSSEKTDVFGYGVMLLELITGQRAFDLAR LANDDDVMLLDWVKGLLKEKKLEALVDVDLQGNIDEVEKLIQVALLCTQSSPMERP KMSEVVRMLEGDGLAERWEEWQKEEMFRQDFNYQNYNQPNNTSWLIGDSTSHIENEYP SGPR
<i>BrCAGP66</i>	<i>Bra034562</i>	Pkinase and LRR N-terminal domain	MRGMMKPSFLWLLLVDLVLRVAGNAEGDALSALKNSLADPNKVLQSWDATLVTPCT WFHVTCNSDNSVTRVDLGNANLSGQLVMQLGQLPNLQYLELYSNNITGTIPETLGNLTE LVSLDLYLNNLSGPIPKSLGRLQKLRFFFANTNLTPLPASPPPISTPPSPGGSNRITGAIAG GVAAGAALLFAVPAIALALWRRKTPQDHFFDVPAAEDPEVHLGQLKRFSRELQVASDN FSNRNILGRGGFGKVKYKGRADSTLVAIKRLKEERTQGGELQFQTEVEMISMAVHRNLL RLRGFCMTPTERLLVYPYMANGSVASCLRDRPESQPALDWPKRQGIALGSARGLAYLHD HCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGITIGHIAPEYLST GKSSEKTDVFGYGVMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEKKLEALVD VDLQGNIDEVEKLIQVALLCTQSSPMERP KMSEVVRMLEGDGLAERWEEWQKEEMFRQDFNYQNYNQPNNTSWLIGDSTSHIENDYPSGPR
<i>BrCAGP67</i>	<i>Bra022410</i>	Pkinase	MVLHKQALLLTFISVLGFHQLPSPTEAECPLDLTSSNFTLVASVCSTNADRAKCCRYMNA FVAVSVSRYANHTADLGVAPELTSICITTISRTELYGIPTNATLFCGLGTKILVSYDCEGLT TVTQMLQSPKFGDVSRNCELPFRCKSCLNSGITYIRSLVDRGNINIKMSTCRDATYAALAS RVDSSSALELASCFNVSELTTPEFPLSPEASPVVADSPSGNDDLVLSPRRSHHGYHL TVVPAIGIAVTVFSVMMLAVLIVLIQRKKRELDDDDSEGKDHNPCTKLPKVMMIHEGSSL AFRKFSYREIRKATKEFSSVIGSGGFGTVHRGEFSNGLVAAVKRMKRSSEQADDEFCEIE LLARLHHRHLVALKGFCCKNERFLVYEYMANGLTDHLHSTKPPLSWATRMKIAIDV

			<p>ANALEYLHLYCDPPLCHRDIKSSNILLDDNFVAKLADFGLAHASRDGVSCEFINTDIRG TPGYVDPEYVVTQELTEKSDVYSYGVVLEIITGRRVDEGRNRVEMSQPLLVSERSRVD LVDPRIKDCIDGEQLETVVAVVRWCTEKEGVARPSIKQVLRLLCESCDPLHMEAMAVEE HKGRSLRGGGDSGLASSSTTSRSHCSRSFLLLETGSPPNGLSF</p>
<i>BrCAGP68</i>	<i>Bra031115</i>	Pkinase	<p>MRNFAMHLLLFLLLHSPVCFARLFPFPFSRSKSHQMRFFHPLYPSLAPAPSPALAPKPNII PTPRHNKGGHYHHHRLVTSASPSSSHDCQQACVEPLTSSPLGSPCGCVFPMKVQLLLSV APFSIFPVTSELEIEVAAGTYLEQSQVKIMGASADTENQGKTVDINLVPLGEKFDSTTAT LIYQRFRRHKKVPLNESVFGDYEVTTHISYPGIPSSSPNDDIVDGAPTSTRGLPLTANFANRS QGIDFRTIAIIVLSGFVLALVLAGAIFVMQWNKVGMPTAVGPALASSMKKTPGAGFMF SSSVRSSGSDSLMSCMAMCALSVKTFTLSELEKATDKFSAKRVLGEGGFGRVYQGSMED GAEVAVKLLTRDNQNRDREFIAEVEMLSRLHHRNLVKLIGICIEGRTRCLIELVHNGSVE SHLHEGTLWDARLKIALGAARGLAYLHEDSNPRVIHRDFKASNVLLEDDFTPKVSDFG LAREATEGSQHISTRVMGTFGYVAPEYAMTGHLVKSQVYSYGVVLELLTGRRPVDMS QPSGEENLVTWARPLLANREGLEQLVDPTLAGTYDFDDMAKVAAIASMCVHLEVSHRP FMGEVVQALKLIYNDADETCGGDYCSKKESSVPDSADFKGDLAPSDSSWWNLTPRLRY GQASTFITMDYSSGPHHEEMENRPHSASSIPREGGLFLENRSGLRPVRSRRNYFRSRGSM SEHGSPSSSRHLWSGNGDWF</p>
<i>BrCAGP69</i>	Bra036461	Pkinase	<p>MRNYAMLVLLLLLLHSLASFPVCFARLFPMSFPFTRSKSHQMRFFHPLYPPASSPAFSPN PSHIPTRHSAHHHQHRRWHLRPNVTAAPPPSNDCQQTCVEPLTSTPFGSPCGCVFPMKV QLLLSVAPFSIFPVTSELEIEVAAGTYLEQSQVKIMGASADSENQGKTVDNFNLVPLGEKF DNTTATLIYQRFRRHKKVPLNESVFGDYEVTTHISYPGIPSSSPYGDIVEGVPTASTDGLPVT</p>

			<p> ANVANKSQGIGFRTIAIIVLSGFVLTLLLAGAIFIVRKWNKVGKSSTAV^{GP}GLPPSMNKRL GARSMFSSSARSSGSDSLMSSMATCALS VKTFTLSELHKATDK^{FSAKRVLGEGGFGRVY} ^{HGSMEDGTEIAVKPLTRDNQNRDREFIAEVERLSRLHHRNLVKLIGICIEGRTRCLIELV} ^{HNGSVESHLHEGTLWDARLKIALGAARGLAYLHEDSNPRVIHRDFKASNVLLEDDFTP} ^{KVSDFGLAREATEGSEHISTRVMGTFGYVAPEYAMTGHLLVKSDVYSYGVVLELLAGR} ^{KPVDMSQPSGEENLVTWARPLLANREGLEQLVDPRLAGTYDFDDMAKVAAIASMCVHQ} ^{EVSHRPFMGEVVQALKLIYNDADETCGDYCSQKESSVPESAGDLAFSDSSWWNL}^{TP}RRLR YGQASTFITMDYSS^{GP}PEEMENRPHSVSSIPREGGLYLPNRS^{GP}LRPVRTRRNFFRLRGSM SEHG^{GP}SSSRHLWSGNGDWF </p>
<i>BrCAGP70</i>	Bra036687	Pkinase	<p> ^{MRNFAMMLLLLLLVHSLASFPLCFAARLFPMSLPFTRSKSHQIHFFHPRSNPSL}^{APAPSP}AL LPNQRHRGHHHHRRWHLRRNVTA^{SP}SSHDCQQTCEPL^{TPTPFG}^{SP}CGCVFPMKVQLL LSV^{AP}ISIFPVISELEIEVAAGTYLEQSQVKIMGASADSENQGKTVDINLVPLGDKFDKTT ATLIYQFRHKKVPLNESVFGDYEVTHISYPG^{TPS}^{SP}YGDIVEGVPSASAGGLPVTAIFAN KSQGIGFRTIAIIVLSGFVLALVLAGAMFIVRKWNEVGRSSTAV^{GP}ALPPSVNKRLGGGS MFSSSARSSGSESLMSSMATCALS VKTFTLTELEKATDK^{FSAKRVLGEGGFGRVYQGNM} ^{EDGTEIAVKLLTRDNQNRDREFIAEVEMLSRLHHRNLVKLIGICIEGRTRCLVYELVHNGS} ^{IESHLHEGTLWDARLKIALGAARGLAYLHEDSNPRVIHRDFKASNVLLEDDFTP}^{KVSD} ^{FGLAREATEGSQHVSTRVMGTFGYVAPEYAMTGHLLVKSDVYSYGVVLELLTGRKPV} ^{DMSQPSGEENLVTWARPLLANREGLEQLVDPTLAGTYDFDDMAKVAAIASMCVHQEVS} ^{HRPFMGEVVQALKLIYNDADETCGGDYCSQKESSVPDPADFKGDL}^{AP}SDSSWWNL^{TPR} LRYGQGSSFITMDYSS^{GP}LEEMENRPHSASSIPRGGMFLPNRS^{GP}LRPVRSRRDFFRLRGS </p>

			MSEHGGPSSSRHLWSGNGD
<i>BrCAGP71</i>	<i>Bra035635</i>	Pkinase	<p> MEILMFLVRIYLVSSVLVAASSSGLDLLSPSSSPPPLLPETSKGFGEVPISSESHKPGNAPP PKASLPSSPPLADVAAPPSYSSGTKAPNREPIVSVSPAPGPVSSPVSDIPPFPSVALPQPPTP SIVPPRNASNKKPVAPVASPPTISVDISPPVIPKLPHSRSPDSTSTAPSPPKFNGHSHHTSSS PPLNHLHHQEPKKIKDSPPPPCKMSNRPISSSMHPISIAPSPSPTQGLLPPLLKLFPTTHRQ NLIAKLSFISPKAFPLRSSSKPRKLPLQALPPPPNSDCSSTVCLDPYTNTPPGSPCGCVW PIQVELRLTMPLYDFFPMVSEFAREISAGVFMKQSQVRIMGANAATEQPKTILLIDLVLPL GDKFDNMTAMLTYQRFYRKKVYIDATTFGQYEVVYVRYPGLPVSPSGGMTVIDHEPFS RNNNNNGMVKKPFGVDVPKKMRRKEINGGSIIVVLSAAAFIGLCFVVVWFLAFRRGR ARRRLSTRASLPSTKPPGSVRSLTGSRFSSTLSFESSIAPLTLSAKTFTASEIVKATSNFAE SRVLGEGGFVKVYEGLFDDGTKVAVKVLKRDDQQGGREFLADEVMLSRLLHRLNVLNLI GICIEDNRNSLVYELIPNGSVESHLHGVDKESLPLDWEARLKIALGAARGLAYLHEDSNP RVIHRDFKSSNILLEQDFTPQVSDFGFLARNALDDEDNRHISTRVMGTFGYVAPEYAMTG HLLVKSDVYSYGVVLELLTGRKPVDMSQPPGQENLVSWTRSFLTREGLEAIIDQSLGQ PEIPFDSIAKVAAIASMCVQPEVSHRPFMGEVVQALKLV^CNECDEAKELNSVTSLTHDDL GDDNGAESSCGGEGSRRMVRYPLLPSYDSEPGTERGLSVSEMFTGSGRLERVSNSGPLA SGGGKRFWQKMRRLSTGSLSEHGSSSLMVRSGSR </p>
<i>BrCAGP72</i>	<i>Bra002786</i>	Pkinase	<p> MEILMFLRLICLVSSVLVAA^SPASGLDLLPPLSSPSP^LPEASKGFQ^APITSQPSLPPLPN VAAPPSIS^IIGDVADPPPADSAGSK^APAGEPIVSVPN^APATIPVKDLPGKSPPVASPPRD APKEPPFSGRVSPGPVS^SPVSDIPPLPSVALPPPIPSVPPNNASNSHKPI^APVASPPTDISPP VHPVIPKLPS^SPVPTS^SPTRK^SPIHPVFPIES^AAAG^SPDHPPSDNGGENK^SPAPSNEAAK </p>

			<p>PLPIFPHKASPPSVAPLAPKFNHSHHTSPSTTPPPDTTPSNVHRTSSSAPPPPSYHRHHQE RTKITNSPASSPPPPPTHLSPPKKPKRNGSVSPLSPHHARSPPVPSLISPVHPPVSSSMHRIS IAPSPSTQVPLRSSSRPSKSRKFPLGPPLPAPPPPPNSDCTSTVCLEPYTNTPPGSPCGC VWPIQVELRLSMALYDFFPMVSEFAREISAGVFMKQSQVRIMGANAASEQPKSIVLIDL VPLGDKFDNMTAMLTQYRFWSKKVQIFGQYDVIYVRYPGPLASPPVSGMTVIDQGPYPG GDNNGRAMKPLGVDVPKKMRKKQLTGETVAVIVLSAAAFIGLCFVIVWFLVFRRRRDQ RVSKRAPLARPSLPSLTKPSGSARSLTGSRLSSTLSFASSIAPFTLSAKTFTASEIVKATNNE AESRVLGEGGFGKVYEGLFDDGTKVAVKVLKRDDQGGREFLAEVEMLSRLHHRNLV NLIGICIEDNRSLVYELIPNGSVESHLHGVDKEASPLDWEARLKIALGAARGLAYLHED SSPRVIHRDFKSSNILLEHDFTPKVSDFGLARNALDDEDNRHISTRVMGTFGYVAPEYAM TGHLLVKSDVYSYGVVLELLTGRKPVDMTQPPGQENLVSWTRSLTSREGLEAIIDQSL GQPEIPFDSIAKVAAIASMCVQPEVSHRPFMGEVVQALKLVCNECDEAKELNSVTSLTQD ENRAESSCGGEGSGRMARYPLLPSYDSEPDTERGLSVSEMFTGSGRLERQSNSGPLASG RGKSFQKMRRLSTGSLSEHGASLMLRSGSR</p>
<i>BrCAGP73</i>	<i>Bra021861</i>	LysM	<p><u>MAARTLHALSTSPLFLLLLFAASSPTKA</u>QQPYVNNHQDCENRDFDNITNGFTCNGPS CRSYLTFWSLPPYNTPNSIATLLNASAAEIQTLNLTSLTTVIPTRRLVVIPTTCSCSGGGG FYQHNATYRLSGERQETYFSIANDTYQALSTCQAMMSQNPYGERNLTAGLNLVPLRCA CPTANQTAAGFRYLLTYLVAQGDSVSAIAEMFRSSTPAVSSGNELTSDNIFYFTPLLVLPLRT EPTRIVITPPSPTPPVATPPQSPVDPGSSSSSHKWIYIGVGIGAGLLLLISILSLYFCYYKR RSKTSSLIEQNKLTDSSTKQSLPTTSSRSPLAVYKDTTSGDQTETDKSKPEFGSWLMLGG RAERNKENNALPGKWAAFKVPQKPIVRAAASSFEVVFVDEKECTDERVQKKKKSETISS</p>

			SNVLPLNDGREIKK
<i>BrCAGP74</i>	<i>Bra008320</i>	LysM	<u>MKNPEKPILLFLILASTLASTATSKSTIEPCSTSSTCNSFLGYTLYTDLKVTELASLFQADP</u> VSILLSNSISTSYPDVENHVLPSHLFLKIPITCSCVDGIRKSTSTRYKTRTSDTLDSIAGSVY GGLVSPEQIQVANPDIESLDVGTSLVIPLPCACFNGTDESLPAVYLSYVVVRGVDTMGGIAR RFSTTVADLTNVNAMGAPDINPGDILAVPLLACGSNFPKYATDYGLIIPNGSYALTADHCV QCSCALGSRSMYCEPASLEVSCSSMQCRNSKFMLGNITSQETSAGCKLTCTYNGFANG TILTTLSRSLQPRCPGPPQLAPLIAPPDTPKELMFAPSPSPSPAPASDGVVSEGPSTVAA APRGPTVASSSSIPGYPANGPAGSISIASCLTSYHSLVVVSFISFASYSSVILV
<i>BrCAGP75</i>	<i>Bra017956</i>	LysM	<u>MRNPENHILFLILASSLLFFTATSKSTIEPCSSNDTCNSLLGYTLYTDLKVSEVASLFQVDPI</u> SVLLANAIDISYPDVENHILPSKLFLKIPLTCSCVDGIRKSLSTRYKTRPSDTLGSIAHSVY GGLVSAEQIQEANSVSDPSVLDVGTSLVVPLPCACFNGTDNSLPAVYLSYVVVRGVDTLA GIARRYSTTVTDLNMNVNAMGAPDVSSGDILAVPLSACASNFPKYASDFGLIVPNGSYALA AGHCVQCSCALGSRSLYCEPASLAVSCSSMQCRGNSLMLGNITVQQSSAGCNVTSCDYN GFDNGTILTMLSRSLQPRCPGPQQFAPLLAPPDTLPKDIMYAPAPSPDFDGP GSVASSPRSS IIPPGGSFPGNPANGPAGSISMATASSVSHFFVIFLISISSFSFVFSS
<i>BrCAGP76</i>	<i>Bra016402</i>	LysM	<u>MKTPDKPIFYFLFLILASSSLFFTATTAKSTIEPCSSNDTCNSLLGYTLYTDLKVSEVASLFQ</u> VDPI SILLANAIDISFPDVENHILPSHLFLKIPLTCSCVDGIRKSVSTRYKTRPSDTLASIAGS VYGGLVSAEQIQEANSVTDPSVLDVGTSLLVPLPCACFNGTDNSLPAVYLSYVVKGVDT LAGIARRYETTVDLMNVNAMGAPDVSSGDILAVPLSACASNFPKYASDYGLIVPNGSY ALAAGHCVQCSCALGSRSLYCEPASLAVSCSSMQCTNSNLMLGNITVQQSSAGCNVTTC DYNGFANGTILTMLTRSLQPRCPGPQQFAPLLAPPDTPKDLMYAPAPSPDYDGP GSIAA

			<u>SPGSSVIPPGGGSLPGNPANGPAGSISTAATVYSESYFFIMFLISISFVFSC</u>
<i>BrCAGP77</i>	Bra002362	La domain	MMAETEGSLADDREVIGGFETKSPWKTTASPVETVDAPVMGAHSWPALADAQQPRPK NLPTAAPPSKVIPTSIPAPAAQGVAGQGKSKGGGKGNPAHKNLSGRHSKPGPKSNQSGPPP PPPPYVMHGVYPYHPSPFPPMVPPPHATGPDFPYAPYPPYPVPGAPVAESGNEKKAQASPL PPVLPAPQGDHPGQPWQDQGRFGPRNMPHGAAAPRNFVRPPFMGQAPGFMVGP GSGFP GPVYYLPVPPPGAIRGYPLRYAPYPVNQADSSGNFLEYFSALSPSLLVNWVAPHLAMLT CVFLPFFSDENLQNDKYLISLMDKQEGWVPIKIIADFKRVKMMTMDVEFIVYALGYSSS VEVQGEKIRRRDEWAKWVPASKRSDSEEKVGDNNDGDSPESTTSRDNSEKQSNDSKPTA CSSEGAQPSRTDANGSDILKSSSSEQRNMDLSTDFSNTFLLDEEIDLEHKSPRRSGLSVC KRIEDEDDDIAVDDHDHDIQKLVIVTQNSGRSDGTGISGTKAKNIPKELASTINDGLYYFE QELKKNRPGRKKNNSHLDSRDGKVKGGGLNIKLGENSAANGGEEHSIRRKQNKGTHK NQMAHVRRFFSGNTRNHGAVSESPSSSIGFFFGSTPPDSHGHRLSKLSSSPQYSLSGSSPP VGSLPKSFPHFQHPSHQLLEENGFKQEKYLYRKRCNLNERKKLGCGCSEEMNHLRYFW SYFLRETFVPSMYEDFQKFALEDAAGNYYYGLECLFRFYSGLEKQFDEDLYKDFEQLT LDFYHKGNLYGLEKYWAFHHYRGQKEPIKKHPELEKLLKEEYRSLDDFRAKDSATSQK ENKSH
<i>BrCAGP78</i>	Bra020153	La	MAETERSLADDREMIGHVTGSETKSPWKTAPIEPADAPVMGAHSWPALADAQQPRPKN PPPPPPAAAAKSIPTSIPNHSQAVVTGHAASKAGGKANPAHKNNPPGRYSKPGSKSNQSG PTPPAAAAYPMHAVPYHPPFPFPPMSYPTGPDFPYPLYPPYPIPGAPAAESGSEKPVQASPLP PPPPQGEPRQHQRGFGPRNMPHGAPAGGPRNFVRPPYMGQGP GFMVGP GP GFGP VYYL PGPPPGAIRGYPPRFGPYPGNQGPQALSP EQLDLDRHVTFRILIPFFSDENLQNDQYLISL

			<p> MDEQGWVPIKIIADFKRVKMMTMDVEFIVYALRFSTSVQGDKIRKRDEWSKWVPAS KKSASEEKIGDNDKDSSSVTSKDNFKNSLKPTAFSSEGAQSSRTKSDNRKSLSDQQRKM DVLSSDFSNTFLLDEEMDLEHKSPRKSGLSMSKRIDDEDEDIAVDDHDIQKLVIVTQNSG RSDGTGISGTKAKNIPKELASTINDGLYYFEQELKKNRSGRRKNISHLDNRDGKVKAGG GLNTKLGENSAANGGSEEHSIRRKQSKGAHKHHTAHARRFFSGNMRNHGASLSSHTSE SPPSSSIGFFFGSTPPDNPGQRLSKLSSSPQCSLSGSPPVGS LPKSFPPFQHPSHQ LLEDNG FKQEKYLKYRKRC LNDRK LGGSGCSEEMNHLYRFWSYFLRET FVPSMYEDFQKFALED AAGNYNYGLECLFRFYSGLEKQFEEDLYKD FEQLTDFYHKGNLYGLEKYWAFHHYR GQKEPTIRKHPDLEKLLKEEYRSIADFRAKDPITSHKENKSH </p>
BrCAGP79	Bra011647	La	<p> MASAASSDSTSSSTSENQRSRPSPWSQIVRGESDPPTISSSAAAPSSPQHKAPIDPVPSAS TAPLAPVAGDVRSEESGAQGNAGKKPVWKRPSNGASSEVGGPVMGASSWPALSETTKA PSSKSSDSLKSLGDVASSSVVVTVTSQGNSNASAPAPKQGGRANPNPTPYNSRQRSFK RNNSASGSTANGTVSQGPVVETPSHNPSPRGQNQRNGSASQPHGGGSDNFSRDRSHRNQ NGNHHHHHQGHGRRNQEHGNQWNFSRSFNGRDGNNAHSQRGAPAFVRHQPPTMQSI PPQFMAAQPIQPFGGPVPFPPELASPYYPMPFIGPLSPGPVYYQVQDPPLNVKLQKQIQ YYFSEENLIRDTYLRGLMDDQGFVPLHVIAGFKKVAELTDSIQQIVEALQGSPFVEVQGD RIRKRYNWQHWLLPEDASLQFVNAVASGVRNLSIGQSSADPIGGPSSQLQPAGAENKAA SDGQQQFSVVNPVNNLNGSNGANR </p>
BrCAGP80	Bra010506	La	<p> MASAATNNSTSSPSLSPRHVSDYPRHVSESTRHVSSP TAAQSRQVSSPWTQIVRGESIPP PTIAAAATSKPPIEPIASAAPPAALLTVEAAAGEDKSEGNAGKKPAWSRPSNGASEIGPVM GASSWPALSEATKAPSNKPSSDSSIGDVPSSVSQGAASASVPAPKQAGRANPNPTPNHS </p>

			RQRSFKRNGASGSTANGTASQPSAQGSLVEGTSHNPSPRGQNQKNGFASQPHGGADNQ RDSHRNQNGNHHHQNHGGRRNQEHGNQNWNFHRSFNGRDGNASPRGAPAFVRYAP PPPPPPVQAIPPQFMAAQSFSPVPYPPELAPPFYPGMPFVAPLSPGPVFYHVQDPPLNIKL QNQIHYYFSEENLIKDTYLRDQMDDQGFAPLHVIAAGFRKVAELTDSIQEIVEALQGSFV EVQGDGIRKRHNWQLWLIPSPQSVDASRVGNLSIGQSSAEPIGGSGSQLQPPEAENKA VADGQPQSSGADPVSNRNGSGGANR
<i>BrCAGP81</i>	<i>Bra026880</i>	X8 domain	MRMFLGVLLLLALTSSSAIYCLCKDGIGDNGLQTSIDYACGTLADCNPIDKGACYQP NTIKNHCDWAVNSYFQKAAQVPGSCNFSGTATTSQTTPSNLVTGCIYPSSASSAGSPPSTT PPTGTTPTTNGTGGFTFPFGTPPAFGPTGTGGFTPSKAASSLVISSVFTLCFSSLAFLM
<i>BrCAGP82</i>	<i>Bra026878</i>	X8	MRMFLALFLLLALTSSNATYCLCKDGTEDNALQASIDYVCGKLDCNPIRDKGACYQPD TIKSHCDWAVNSYFQSQAQAPGSCVFTGTATTSQNPPSNLVTGCVYPSSPSSPGGCSPSTNG ASSLVISPAFAICLSTLAFLM
<i>BrCAGP83</i>	<i>Bra026879</i>	X8	MRMFLALFLLLALTSSNATYCLCKDGTEDNALQASIDYVCGKLDCNPILDKGACYQPN TIKSHCDWAVNSYFQNVAAQAPGSCDFSGTATTSQNPSPYLVTGCVYPSSASSPGSLPSTTP PPGTKQTNGTVTPTNGASVYQH
<i>BrCAGP84</i>	<i>Bra019700</i>	X8	MKVFLGLLLLLALTTPSSAIYCLCNDGIGEKELQTAIDYACGTLADCNPIQEKGPCYQPIT VKSHCDWAVNSYFQNAAQVSGSCNFSGTATTNLNPPSNLATGCIFPSSPSSAGTTPPTGPT PPTGPTPPTGPAPGAPATPVGPTPPTPTNGTNTFPGAPLAPSPPGTGGFTPSNGASSLLISS VLTLCFSSLAFL

<i>BrCAGP85</i>	Bra016724	X8	<u>MRVFLGLLLLLALTKSSSAI</u> <u>YCLCKDGVGEKELQTAIDYACGSLADCNPIHDNGPCYQPN</u> <u>NIKSHCDWAVNSYFQKASQVSGSCNFSGTAT</u> TNQNPSSLNLTGCIYPSSASTT <u>SPT</u> GTTLT NGT <u>TPAF</u> <u>GPT</u> GTGGFQGNASSLVISHVLTHCFSSLVFLWGS <u>SDVRLGFSHA</u>
<i>BrCAGP86</i>	Bra013621	Hydrophobic seed protein domain	<u>MAPHCSTKTIVFVLALISIFFLSETEA</u> QGR <u>SPP</u> RQPP <u>APRR</u> PPPPRRPPPPPLRPPPPPPFVCPP CVCPPPVFPPNIPPPEI <u>TP</u> LEIQPPGV <u>TPP</u> ETEP <u>TP</u> QPEIPPPEIQPPEI <u>TPPEI</u> <u>SPP</u> ETEPK <u>TPPP</u> EIT <u>TP</u> LEIQPPGV <u>TPP</u> ETEP <u>TP</u> LPEIPPPEIQPPEI <u>TPPEI</u> <u>SPP</u> ETEPK <u>TPPPEI</u> <u>TPS</u> QVPPPEI <u>TPPE</u> IQPPKIEPPEI <u>TPPE</u> <u>SPPPKI</u> <u>SPP</u> QIEPSEI <u>TPPEI</u> <u>TPPEI</u> <u>TPPEI</u> <u>TPPEI</u> PPPKI <u>SPP</u> QIEPPEIT <u>SPEI</u> P PPKI <u>SPPD</u> <u>TPPPSG</u> <u>TPPKQ</u> <u>SPLL</u> PPPNFQPPPPPLP <u>TCPRNAAQQRACANVRRYGNFLDFG</u> <u>RAQPCCSLIRDLSDREAAACLCGFVQPPGQRRSPPPRNIFVLCRACGRRVPRGFMCP</u>
<i>BrCAGP87</i>	Bra016093	Ring finger domain and PA domain	<u>MKMMMNRALVLLLLLLFHLTLSSLASAKVILIRNNITRSFDDIEAN</u> <u>FAP</u> SVKAAGEIGLL YVAEPLDACSDLTNKPEQSSNGT <u>SPF</u> VLIVRGGCSFEDKVRKAQRAGFKAAIHDNEDRG <u>ILIAMAGNSGGIKIHAVFVTKETGDAL</u> KEFAGLSDTKVWLLPSFENSAWSIMAVSFISLLA MSAVLATCFFVRRHRIRRRTSRSSRVREFHGMSRRLVKAMP SLIFSSVHEDNTTAF <u>TCAIC</u> <u>LEDYSVGDKLRLLPCRHKFHAVCVDSWLT SWRTFCPVCK</u> RDARTANGEPPASE <u>TP</u> LLSS AASSFRSSALSSFRSSAMLI <u>GP</u> SMGSLPTSISF <u>SP</u> AHASSSYIRQSFRSSLRR <u>SPP</u> ISVSRSS MDLRQQGA <u>SPSP</u> SQRSYMA <u>SP</u> HSFNYPAM <u>SP</u> LNSRYM <u>SP</u> YRP <u>SP</u> SNA <u>SP</u> GMIGSSSNHPL NPLRYSESAGTF <u>SP</u> YASANSLPDC
<i>BrCAGP88</i>	Bra036147	COBRA	<u>MGFLLPILLGVFLFTATPPSLSQFPPEIDPP</u> <u>APAPI</u> <u>SP</u> SEL CNGIFLSYTFILGRQIPPNDTTD QPYRFESVLTVLNNGREELKEWRVFGVGFQHHEILTSASDAIIVNGTDLP <u>AP</u> VGNGTIFAGY PVSDLKTAIQTAGDLKQMTATIELVGTQFMV <u>APP</u> AIPLPSNISLVNDGWSCPEPTAT <u>TP</u> LSKR QITTCIRDPTFEVNTTTITDKFLPRQPGDLTIMYDVIRAYDQN <u>YLA</u> EVTMENHNPLGRL

			DHWELSFDMREEFIQKMQGAYPTVVDATKCIFGPQSQIYTGLDFADVLTCCERRPIIVDL PPTKAEDPVLGKIPSCCRNGTILPRTMDPSKSASIFTMQVAKMPPDFNRSALSPQNWRIK GTLNPDYSCGPPVRVSPPLYPDPSGMPTNKTSEFASWQIVCNITHAKTETPKCCVSFSAFFN DSIIPCNTCACGCVSETRRTCSEATPSLLIPPDALLVPFENRTSLTVAWNALKHKTIPNPMP CGDNCGV SINWHIATDYRGGWTARITIFNWGEIDFPDWFLAVQMKKPAIRGFEEKAYSFN ASLLSIEGGVNNTIFMEGLPGLEYLVAERDELDPKKKLRVPGKQQSVIQFSKKLTPGINVP ERDGFPAKVIFNGEECLLPDVLPLPSGGRNGFDTMVLLCMMIFVVALVI
BrCAGP89	Bra010350	PsaE	MAMMSASSVFLLPANVTAPAGASSRNSVSFLPMRNAGSRLVVRAADEAAPEPAPEGA PATAAPAAAAATKPKPPPIGPKRGAKVKILRRESYWFKSVGSVVAVDQDPKTRYPVVVR FAKVNYANISTNNYALDEIEEVKA
BrCAGP90	Bra011057	PsaE	MAMMSASSAFVLTSNVTASAGVSSSRNSVSFLPMRNAGSRLVVRAAEDAAPETSSSEGA PATAVAPAAAAATKPKPPPIGPKRGSKVKILRRESYWFKNVGSVVAVDQDPKTRYPVVVR FAKVNYANISTNNYALDEIEELKA
BrCAGP91	Bra037792	Prolamin-like	MSPNTTSKRSLTFLTLSYLLSTVHIITVAEARNMQTMTVAAEHSGSGNLVDCWNAALEL KSCTDEIVKFFMSRNGTAEPGVTGGIDKDCCGAIGLIGKECWSVMFTSLGLTTMEGNML REYCDFEAEKLVFSPSPSPAPEALALSPVEITYPGLD
BrCAGP92	Bra001249	DOMON	MASINSSLLLVLAVACFISPAISQTCSTQNVSTSFDS CMDLPVLDSYLHYTYDAANSSLSV AFVATPPRSGDWVWVGINPTGTRMIGSQAFLAYSPRAGARPMVDTYNISSYNLTGRLTF DFWNVRAESMPGNLIVIASVKVPMGANSVNQVWQIGGNVTNGRPGVHPMTPANMAS TRVLRLTGSDAPSSAPGSAPGSAPGSVPGSAQGPTTPGASTTPGQAGGPENAGSMSTSVN

			<u>FGVNEFGILVMLATIFIF</u>
<i>BrCAGP93</i>	<i>Bra001259</i>	DOMON	<u>MKLCSVSFISSLIALQLLPLFTIVNGQQATDSCNSTLPLKDLAFDSRHHQCVEVWRVQNY</u> <u>ILRYARTVENTWSFILSAPDSSAYIGIGFSTTGQMVGSSAVVGWITSDSRSGSAKQYLLGG</u> <u>KSPGEVIPDQGDLKIINGSLKIESVSSRLYLSFQLRAELPRERLLYARGPAEFFPS</u> <u>SP</u> DFRLR <u>EHQFMTTTTINYNT</u> <u>GP</u> ATF <u>GP</u> SM <u>SP</u> GP <u>GS</u> <u>SPP</u> <u>SP</u> SSAYGLSPSLLFLFMGLVALKFY
<i>BrCAGP94</i>	<i>Bra006651</i>	Thioredoxin	<u>MTNLTHSLLFFSCSLSLIRVAIAGSRPAH</u> <u>GP</u> AYSNP <u>SAF</u> <u>SP</u> EAYDFFHPKSSLPDNNPPRNS HSLPFL <u>SPSPSP</u> SKASNVEADTQGSKVSSDERISESRREEGRGETVGIVIGISFTALLLMGIY FVIKKRLANLTRITVALKWRSASFSSAS <u>SP</u> SQLFSF <u>SP</u> SFAASSSDVDDDEDFSLEDLNDE <u>G</u> <u>P</u> GEPLT <u>SP</u> VSLSQTNSTEEKPEDPEAYDDVEYGD ^{FD} SDLGFTDLVRKIHIFRPNISLIGGRQR AVLRLKGD <u>GVGLAKVDATEENELTHQYSVQGVPTIILFFVDGEHKPYTGGR</u> TK
<i>BrCHAE1</i>	<i>Bra013339</i>	LRR	<u>MKTKKMAQIYALFVLHFTFLFSTGLSHSYSLASSNSDLS</u> <u>DK</u> EVHLIRQRQLLYRDDDFGD RGENVVVDPSLVFENPRLRSAYVALQAWKQAILSDPNNFTTNWIGSDVCSYTG ^{VY} C <u>APA</u> <u>P</u> DNPRIRTVAGIDLNHADIAGYLPQELGLL <u>TDLALFHVNSNRFCGTVPHRFNRLKLLFEL</u> <u>DLSNNRFAGIFPAVILQLPSLKFLDLRFNEFE</u> <u>GP</u> VPRELFSKDLD ^{AI} FINHNRF ^{RF} ELPDNL GD <u>SP</u> VSVIVVANNQFHGCIPTSLGDMKNLEEIIFMNNGFN ^S CLPSEIGRLKNVT ^{VF} DFSFN ELVGSLPASTGGMVSLEQLNVAHNRFSGKIPASICQLPRLENFNFSYNFFTGEPPVCIGLPG VDDRRNCIPARPAQR <u>SP</u> GQCAAFSLPPVNCASF ^G CGRSV <u>TPSP</u> RPPVVVP <u>SPPT</u> <u>TPSP</u> GG <u>SPPSP</u> SI <u>SP</u> AS <u>SPP</u> MMVPP <u>SP</u> IPAPV <u>SP</u> SSPPSI <u>GP</u> SPPSTPPSP <u>GP</u> SP <u>GP</u> VVPFPPP <u>SP</u> VYS PPSPPPSTGH <u>SPPSP</u> SPPTKF <u>SPPSP</u> PPSAGHPPPSPPPST <u>GP</u> SPPPSPSTGYSPPPPPSTGY <u>S</u> PPPPPPSTGY <u>SPPSP</u> PPPPSTGY <u>SPPSP</u> PPSAGHCPP <u>SP</u> APPTY <u>SP</u> SPPPPPPTYYPPQPPQPS QPPQF <u>SPPPT</u> YYYS <u>SPPPP</u> PHYWLPPPPHSPPPP <u>VY</u> HYPSPPPP <u>TP</u> VYSPPPPCIDHSPPPP

			PPPTVHYSPPPSPVYYNSPPPPPSVHYSPPPSSPPPPVIHHSPPPPPPGYEGLPPIPGVSYASPPPPPPYY
<i>BrCHAE2</i>	<i>Bra002969</i>	FH2	<p> <u>MGNQNRGGLLLWFILISGFLVISSLEVNL</u>DKDEPFLTPFVAPSTGMVNEPVVESSWAKSC WQSDSCVKEAVAVFNLCLPASRELFGFKHSHLKQTLLGCIQEQAKLNGHNLKYLKLLPY LLDTPRRNLASRPVSLSPSPSPSPPKRSRVPPTRSRSPSPSNSFFPPSRSPPPAKKTASSSAK RKEEHEKTIIIAVVSTAVSTFLLAALLFLCCTRVCVGKSGGGRKNDERPLLSLSSSDHSVSGSS INYGGSIKGGNQSFNIYSNQGKMSSFDGNSNSDTSDSLEERLSHEGMRTHGLPPLKPPPGR TSSAHLGKPPSGKVEPLPHEPPKFLKVSSNKGSHHTQPPVPPPPMPSSAGPPRPPPPAPPPG SGGPKPPPPPGPKGPPPPPGPKGPRPPPPMSLGPKAPRPSSGPAKSPSDDDGAPKTKLKPF FWDKVQANPEHSMVWNDIRSGSFQFNEEMIESLFGYAAADKNKNDKKGAAGQAAPQF VQILEPKKGQNL SILLRALNATTEEVCDALREGNELPVEFIQTLLKMAPTPEEELKLRLYC GEIAQLGTAERFLKAVVDIPFAFKRLEALLFMCTLYEEIAFVKESFQTLEVACQELRG SRL FLKLL EAVLKTGNRMNDGTFRGGAQAFKLD TLLKLADVKGTDGKT TLLQFVIQEIIRTE GRR AARTIRESQSFSSVKTEDLMAEEASEEMEDSYRNLGLQKVSGLSSELEHVKKSANI DADGLTGTVLKMGHALSKARDFVNSEMSSGEVSGFREALEDFIQNAEGSIVSILGEEKRI MALVKSTGDYFHGKAGKDEGLRLFVIVRDFLIILDKICKEVKGKPVKMARKQGSTASAS SETPRQAPSLDPKQKLFP AITERRMDQSSSDSD </p>
<i>BrCHAE3</i>	<i>Bra017734</i>	La	<p> MASSATSTNPNSSSSSAAQSRRPSPQVSSPWTLIVRGGDSVPTIAAAAAAPSPPQSKPPIEP IADASPPPAAGEEKPEGNAGKKPVWKRPSNGGAAASEVGPVMGASSWPALSVAANKSS SDSLKSLGDVAPSPPPVLVSQGIANASVPSSASKPAGRANPNPTPNNSRQRSFKRNGASGS SANGTASQPSVQGSLAESPSHNPSPRGQNQRNGFPSHTHGGSGADNVSQRDSYRNQNG </p>

			YHHQSHGGRRNQEHNQNWTFSSFNDRDGNASQSRGAPPAFVRHPPPPPLQTIPPQF MAAHPFASPLPFPELASQYYQRMFPVAPLSPGPVFYHVQDPPLNIKLQKQIHYYFSEEN LIKDTYLRRQMDDQGFVPLPIAGFNKVAELTESVQQIAEALQGSFVVEVQGERIRKRY WQHWLIPQDPSSPQSVGAVASRVGNLALGESSAGPNGGSSSQLQPAGAENKAVSDGQQQ SPGGVPGSNRNGSDGANR
<i>BrCHAE4</i>	Bra027650	GNK2	MVTFCNPSDNFTQTSSYQANRDLSSSLRDSSSLGTYSNATVGRSPNKVHGMFLCRGDT TAASCSDCVQTATVEIATNCSLNKAAVIYYEECMVRYANVSFFSVLEVRPSIVLYSLRSAP NSDTFNETLADKFNQLILNVSSSLVPYFVEDQERVTAEGSYEFESLVQCSPGLDRFNCT VCLRFALLRVSTCCGSPSSALIFTPKCLLRYQTSALSSPPPLSPSPPPPPSPALFSPPTLSQ PPPPPLVFTRPQDVPSLSGSFSNVIKGNKIFGRIVITMAALVFALVNL
<i>BrCHAE5</i>	Bra020846	Hydrophobic seed protein	MAPKGVNTNLVFLALISILFIGQTKAQGRPSPRLPPPPPLQRPSSPPPLLLVCPPCVCPILS PPPPNTPPPTPQTSPITPVAPPPQTPPSNLPPAFPPNNPSATTPPQTSTPPPQTPSVSPITPTI SPQLPPSNIPTPTTEEILPVRPSVPPSQTPPVHSPIFSPKSPSILPPQVPSVPLPITPSETPTSTIPP QTPLQSPPQTPPTTPPQTPLAPPPNTQPSSPPLNFQPPPPPPQTPPSPPNSQPPSVPLPITPP QTPPQSPPQTPPTTPPETPPVSPPNTPPLSPPLNLFHPPPPPPQTPPSPPNSQPPSVPLPITPP QTPPQSPPQTPPTTPPETPPVIPPNTPPLSPPLNLFQPPPPPPQTPPSPPNSQPPSAPTCPRNA SQLRACSNITRRFGNFDLDFGRAQPCCSLIRDLSDAEVAACLCGLVQPQSQRYSTPSRNIFI CRACGRPMPRGFMCP
<i>BrCHAE6</i>	Bra038210	Root cap	MDLAKHTTLQMLGFILLASLVLTMAPPGLTKPSHATCKIKKYKHHCYNLEHVCPKFCPD TCHVECASCKPICGPA SPGDDGGDTPPTPVPPVSPPPAPVPPVSPPPVTPTPSYPTPTDPL PPAPVSPPPAPVPPVSPPPPTPTPYVPSTPPVSPPPSPPTDVPSTPPSSPPPTPTPAVPS

			<p>TPSSPPPPSPTPAVLTPPHVTPTPTTPAVPSPPDVTPPTPTSPVSPDTPTAPLPPYSPPATPAPS</p> <p>VPSTPTTPSSPTTPGSTPTTPTPSVPTPSPSVPVPSAPNSPPYVPPSSPTPTTPSDGEAGAGV</p> <p>RRARCKKKGSPCYGVEYSCPSACPRSCEVDCVTCKPLCNCCKPGSVCQDPRFIGGDGLT</p> <p>FYFHGKKDSNFCLISDPNLHINAHFIGKRRPGMARDFTWVQSIAVLFGTHRIFYVGALKTA</p> <p>TWDDSVDRISASFDGNVISLPQLDGATWTSSPGVYPQVSVKRVNADTNNIEVEVEGLLKI</p> <p>TARVVSITMEDSRIHGYDVKEDDCLAHLDLGFKFQDLSDNVDGVLGQTYRPNYVSRVKI</p> <p><u>GVHMPVMGGDREFQTTGLFAPDCSAARF</u>IGNGGRNGGWSKMELPEM<u>SCASGVGGKGV</u></p> <p><u>VCKR</u></p>
<i>BrCHAE7</i>	Bra022423	Root cap	<p><u>MALATRVQILGCILLASLALTMA</u>TPPGIAKNPSHATCKIKKYKHCYNLEHVCPKFCPDS</p> <p>CHVECASCKPICGPPSPGSDDDDGEDDGGYTTPAPVPPVSPPPTPTPAVPSTTPPVSPPPP</p> <p>PPPTPTPAVPSPPPPVSPPPPPPTPTPAGASPTTPVSPPPPSPTPAVPSTPTSSSPPPPTPTPAVP</p> <p>TPTPTPSVPSPPGTPTAPVPPYSPPATPTPSIPSTPTSPGSTTPYVPPSSPTPTTPSDGEAGA</p> <p>GVRRARCKKKGSPCYGVEYSCPADCPRSCEVDCVTCKPLCNCCKPGSVCQDPRFIGGD</p> <p>GLTFYFHGKKDSNFCLISDSNLHINAHFIGKRRPGMARDFTWVQSIAILFGPHRLYVGAL</p> <p>KTSTWDDSVDRISASFDGHVISLPQLDGATWTSSSLGVYPQVSVKRVNADTNNLEVEVE</p> <p>GMLKITARVVPITVEDSRIHGYNVTEDDCLAHLDLGFKFQDLSDNVDGVLGQTYRSNYV</p> <p><u>SRVKIGVHMPVMGGDREFQTSGLFEPDCSAARF</u>TGNRGSNGGRSKMELPEM<u>SCASGVG</u></p> <p><u>GKGVVCKR</u></p>
<i>BrHAE1</i>	Bra030020	-	<p><u>MKSSIVLVAAAILCIVAFPTATVGKNLRFGLKPTQGWPHPSEASTNQMFMTSQKFNYGD</u></p> <p>SKVWRCTYSNGSAPAISISI SPTPTMPSPSTPTTPSPSPPTPKTSPPPPTPSPPPTSKKAPSP</p> <p>SPPPPPPTPSLPPPTTKVPSPPPPTLSPPPPTTKASSPPLPKPSLPPP TPKKTPSPPPPTPSLP</p>

			PPTPKKSPSPSPSSDDESSSPSQPSNPPQEHHHHHEFPLEHIGRCYRNMGQVGFRCGQMAI SFYTRLFKVSKYCCNLIVNMKNECDDVIWGYFYDPHFVPLVRCTCHVSF
<i>BrHAE2</i>	<i>Bra009880</i>	-	MVSLNLSFALVFILAILFTFAEANYSRKLLQTPNTYQPAYSPPSPTPVYSPPVNPPPTPTVT YPPPTPAYPPPVALPPPAPINSPPPPAPIIPPLKANPSPQAYRAFYRKSPPPPSGKPWWLL
<i>BrHAE3</i>	<i>Bra014023</i>	-	MKSLIILIVAHFCIIVSPTTTMGGWPKPSEVSNEEKLVTGQAQPHLYAGKFNFGDSKVV KCTYNNGSGVAISISYPSPQPPSQKPPTPSSPPTPKMAPPLPKPSPPRPSPKKSPPPPKPSSP PPTPKKSPPPPKPSPPPTPKKSPPPPKPSPPPTPKMSPPSPTPSPPRPSPKKSPNPSSLTPNE SPPPAKTSILIIHSPPPHPIPAQSPPKEPTTPSTQWPPYRNWNPLGL

^a Italics indicate a newly identified BrAGP that is highly similar to AGP-like amino acid sequences predicted in *Brassica rapa* by Ma et al. (2017). XXX, N-terminal signal peptides predicted by SignalP 5.0 Server; XXX, conserved domains predicted by HMMER; XXX, [Ala/Ser/Thr/Gly]-Pro; XXX, [Ala/Ser/Thr/Gly]-Pro-X(0,10)-[Ala/Ser/Thr/Gly]-Pro (two consecutive Pros are not separated by more than 11 amino acid residues); XXX, [A/S/T/G]-P₂₋₄; XXX, ≥ 2 SP₃₋₅; XXX, PPVK/T and KKPCPP; XXX, GPI-anchor addition signal predicted by the GPI-SOM or the BIG-PI Plant Predictor. The conserved residues (His, Cys, His and Gln/Met) involved in Cu binding and Cys residues involved in the disulfide linkage are marked with Grey and dark blue in the amino acid sequences of the plastocyanin-like (PCNL) domains of the BrPLAs, respectively. The eight conserved cysteine residues were marked with dark green in the non-specific lipid transfer protein 2 (nsLTP2) domains of the BrXYLPs.