Supplementary Materials:

Table S1. Sequence identification of 24 PDI proteins from Pyrus betulaefolia (unit %)

protein	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X
PbPDI1-1(A)	100	**96**	43	47	35	32	20	27	32	36	16	16	34	40	22	23	29	21	21	19	15	26	30	32
PbPDI1-2(B)		100	42	43	35	35	22	26	32	35	16	16	34	39	20	25	29	21	22	20	14	23	23	27
PbPDI2-1(C)			100	**96**	37	37	27	26	23	23	11	13	30	35	26	21	31	9	21	16	14	31	32	23
PbPDI2-2(D)				100	36	37	26	24	23	21	11	13	29	31	25	24	30	10	10	20	21	31	32	24
PbPDI3-1(E)					100	**81**	22	29	32	29	15	12	36	32	27	30	30	24	29	31	24	11	10	10
PbPDI3-2(F)						100	25	29	30	30	15	15	29	30	27	26	23	24	28	27	24	10	11	9
PbPDI4-1(G)							100	**86**	39	38	19	20	21	17	29	29	23	23	23	22	27	19	19	17
PbPDI4-2(H)								100	44	44	20	20	31	26	25	24	32	22	18	29	26	14	17	8
PbPDI5-1(I)									100	**99**	16	16	31	30	29	27	16	21	19	28	24	16	16	16
PbPDI5-2(J)										100	16	16	30	31	29	27	22	20	20	27	24	16	16	16
PbPDI6-1(K)											100	**97**	16	15	13	13	12	21	19	15	21	12	12	12
PbPDI6-2(L)												100	15	15	15	15	13	20	20	18	9	11	11	11
PbPDI7-1(M)													100	**94**	22	22	31	27	26	25	19	7	7	8
PbPDI7-2(N)														100	26	21	31	28	28	25	18	8	8	8
PbPDI8-1(O)															100	**98**	21	23	24	30	19	13	13	14
PbPDI8-2(P)																100	22	24	25	30	22	13	13	16
PbPDI9-1(Q)																	100	21	21	25	18	7	9	8
PbPDI10-1(R)																		100	**93**	51	39	9	10	19
PbPDI10-2(S)																			100	50	38	9	9	7
PbPDI10-3(T)																				100	78	10	12	12
PbPDI10-4(U)																					100	10	13	13
PbPDI11-1(V)																						100	**97**	**83**
PbPDI11-2(W)																							100	**83**
PbPDI11-3(X)																								100

Table S2. Quantitative specific primers of PDI gene family in *Pyrus betulaefolia*

Primer Name	Sequence(5' to 3')
PbPDI1-1-F	CAAGACTACTGACGATGCAACTAC
PbPDI1-1-R	GATGAATCACCACGAGGAAGG
PbPDI1-2-F	CGTCCTCACTCTCGACAGCTC
PbPDI1-2-R	CCTCTTCATTGGCATCAACC
PbPDI2-1-F	CACGGAGGAGAACGAGCTGTC
PbPDI2-1-R	CACCAGAGAGTTGAGGTAGCCC
PbPDI2-2-F	GAGCTGTCGCAGGAGTACGGC
PbPDI2-2-R	CAGCAGTCAATATGCGTTCCGC
PbPDI3-1F	CTGTTTGTCAATGGCACCTCC
PbPDI3-1R	CGAACTGGATGGCACTGTCAG
PbPDI3-2F	AGACAGGTTCTTAGAGCGCC
PbPDI3-2R	AGCGCCTTATCGAGTTTCCC
PbPDI4-1-F	GAAGGAGGTCGGTCAAGATC
PbPDI4-1-R	CATTGAATTGTGGGATAGCCGG
PbPDI4-2-F	GTCGAGTTCTACGCTCCCTG
PbPDI4-2-R	GCAGTACGGGCACCTTCATAC
PbPDI5-1-F	GAGAGAGAGAGAATGAGAGAGAATC
PbPDI5-1-R	GGTGTAAGAGCCTGACAATGTCC
PbPDI5-2-F	CTGATTCGCACAACAAATCTCAG
PbPDI5-2-R	GTTAGAGCCTGACAATGCCCG
PbPDI6-1-F	CGCTGACACCTTCTCCGAC
PbPDI6-1-R	CTCGTACTACAATCAACCTCCC
PbPDI6-2-F	CCTGACAACCCATACCCAAG
PbPDI6-2-R	GCGACTTCTTCACCATCATAG
PbPDI7-1-F	GATGAGGATGAAGAGAAGGC
PbPDI7-1-R	GAACTGTGAGACTTGAGATGCC
PbPDI7-2-F	CTTGGACCTGGTCTTGGTTG
PbPDI7-2-R	CCATTGTATTCCATCGGAACAC
PbPDI8-1-F	CTCCGGCAAGATCAAGTCTG
PbPDI8-1-R	CAGATGTAGAGGTGCTGACGG
PbPDI8-2-F	CGTGAGTGATGTGTTGGGAAC
PbPDI8-2-R	CCAGAATACTCATCTCCATCCC
PbPDI9-1-F	CTGACAGGCAGGGAGACCAA
PbPDI9-1-R	CAGAAGAACCCATAACCCACAG
PbPDI10-1-F	CCGTTACAGCCTTCAATCTC
PbPDI10-1-R	GAGGGAACATGAAGCTGAGC

PbPDI10-2-F	GGTACAGCCTTCAATCTCAATG
PbPDI10-2-R	GAGGGAACATGAAGCTGAGC
PbPDI10-3-F	GTCAACGGCGCTTCCAGATC
PbPDI10-3-R	CTTGGCCTGATGGCTGATTC
PbPDI10-4-F	GCTTGCAGATCCGTTGAATC
PbPDI10-4-R	GATGGCTGATTCTTCAAATGC
PbPDI11-1-F	TTGAGGTGGAGGACTATGCTC
PbPDI11-1-R	CAGCCTCCCAGTATCCAAGC
PbPDI11-2-F	AGAGGTGGAGGACTATGCGC
PbPDI11-2-R	GCCGTAGTGCTTCTCTACTGTG
PbPDI11-3-F	GGGAGTGCTAATGTCCCAG
PbPDI11-3-R	CCCATCAGCTCTGAACTTACC

Table S3. List of the PDI protein sequences used for phylogenetic analysis

Name	Accession	Sequence
PbPDI1-1	GWHPAAYT052317	MASSSRVSLCFFFLLAVFSTAIRAEEAESKEYVLPLDSSNFADTVGKHDFIVVEFYAPWCG HCKKLAPEYEKAASILSKNDPPVILAKVDANEEANKGLASDYEVKGFPTIKILRNGGKTIQ EYKGPREAEGIVEYLKKQSGPPSVEIKTTDDAITLVGDKKIVVVGVFKEFSGEAYNNFSAL AEKLRSDYEFGHTLDAKLLPHGDSSVSGPVVRLFKPFDELFVDIEDFHVDALEKFVEDASV PLVTEFNNDQTNHPFVIKFFNSPNEKAMLFLNFSDESSDAFKSTYREVAEKYKKEGISFLIG DLEASQGAFQYFGLKEDQVPLIIIQTPGGQKFLKPNLQPDHITSWVKEYKDGKVSPFKKSE PIPEQNNEPVKVVVADSIQDYIKSEKNVLLEFYAPWCGHCKKLAPILDEVAASYEKDSDV VIAKFDATANDVPSDFDVKYYPTLYFKTASGKVLSYDEEDRTKEAIIAFIEKNRDKIEKQA ESEKQESGKDEL
PbPDI1-2	GWHPAAYT023135	MASSSRVSLCFFLLLAVFATAIRAEEAESKEYVLTLDSSNFDDTVSKHDFIVVEFYAPWCG HCKKLAPEFEKAASILSKNDPPVILAKVDANEEANKGLASDYEVKGFPTIKILRNGGKTIQ EYKGPREAEGIVEYLKKQSGPASAEIKTTDEATTLVGDKKIVIVGVFKEFSGEVYNNFSAL AEKLRSDYEFGHTLDAKLLPRGDSSVSGPVVRLFKPFDELFVDFEDFHVDALEKFVEEASL PVITEFNNDPTNHPFVVKFFNNPNEKAMLFLNFSGESSDAFKSTYREVAEKYKKEGISFLIG DLEASQGAFQYFGLKEDQVPLIIIQTPDGQKFLKPNLQPDHITSWVMEYKDGKVSPYKKSE PIPEPNNEPVKVVVADNIQEYIKSGKNVLLEFYAPWCGHCKKLAPILDEVAVSYEKDSDV VIAKFDATANDVPSDFDVKYYPTLYFKTASGKVLSYDEEDRTKEAIAAFIEKNRDKIEKQV EAEKQESGKDEL

PbPDI2-1	GWHPAAYT007464	MASRLVLAFALSALLFFSHSVLCKDSHPTDDDDEDLSFLEEPTDHGDAAPHYPDSDHYDE DNLDDLENYSDFDEGGDHEDSYKQPEVDEKDVVVLKAANFSDAVEKNRFMMVEFYAP WCGHCQALNPEYAAAATELKGEDVVLAKVDATEENELSQEYGVEGFPTIFFFIDGVHKPY TGQRTKEGIVTWIKKKIGPGIQNVTTLEGAERILTAESKVVLGYLNSLVGPESDELAAASR LEDEVTFYQTVDPKVAKLFHLDAEVKRPALVLLKKEAEKLSYFDGKFDKSAIAEFVFANK LPLVITFTRDNAPQIFESTIKKQLLLFATSKDSEKSLPEFQKAAQLFKGKLIFVYVETDNEDI GKPVSDYFGVTSEAPTVLGYTGNDDGRKFVLDGEVTLANLKTFGEDFIEDKLKPFYKSDPI PETNDGDVKIVVGNNFDDIVLDESKDVLLEIYAPWCGHCQSLEPTYNKLAKHLRGIDSIVI AKMDGTTNEHPRGKADGFPTLLFFPAGNKSFDPIPVDCDRTVVAFYKFLKKNASIPFKLQ KPASTPKSEGSAATESQGSSSRRRRFEG
PbPDI2-2	GWHPAAYT035228	MASRLVLAFALSALLFFSHSVFCKESHPIDDDDEDLSFLEEPTDHGDDAPHYPDPDHYDED NYDDLENYSDFDEGGDHEDSYKEPEVDEKDVAVLKAANFSDVVEKNRFVMVEFYAPWC GHCQALKPEYAAAATELKGEDVILAKVDATEENELSQEYGIEGFPTIFFFIDGVHKPYAGQ RTKEGIVTWIKKKIGPGIQNVTTLEDAERILTAESKVVLGYLNSLVGPESDELAAASRLEDE VSFYQTVDPKVAKLFHLDAEVKRPALVLLKKEAEKLSYFDGKFDKTAIVEFVFANKLPLV ITFTRDNAPQIFESTIKKQLLLFASSKDSEKVLPDFQKAAQLFKGKLIFVYVETDNEDIGKP VSDYFGVTSEAPTVLGYTGNDDGRKFFLDGEVTLANLKAFGEDFIEDKLKPFYKSDPIPES NDGDVKIVVGNNFDEIVLDESKDVLLEIYAPWCGHCQSLEPTYNKLAKHLRGIDSIVIAK MDGTTNEHPRAKADGFPTLLFFPAGNKSFDPITVDSDRTVVAFYKFLKKNASIPFKIQKPA STPKSEGSAATESKGSGSAEDSKDEL
PbPDI3-1	GWHPAAYT055473	MSRSKPTSRFIIFVLTLILTLPLHFPTPIKSSEPQNLTADETEDGELEELLALDQQVKQEEDQ DGAPTTRSLEAELLSNAQRIVLELNHDNTKRVIENNEFVLVLMYAPWCSRSAELMPLFAE AATALKELGSPLLMAKIDAERHTKAASSLEIKGFPTLLLFVNGTSQAYTGGFSAKEIVIWA RKKTGEPVIRINSSDIFVVVLFEKFEGPEHKEFVKAATADNAIQFVEASNIEVANILFPNMK PTKGTFRADEILQFLDHNKFPLVNRLTEANSAKVYSSPIQIQVHVFADADDFKKLLEPLQD VARQFKSKILFIYIDITDGNLAKPYLTVFGLEESNSTVRSSKYLLESDPTQSNLEEFCSGLLQ GTVSPHFKSQLIPDNKNETVLSVVGKTLDDLVLNSHKNVVLEPSPHSKSSSSAQ
PbPDI3-2	GWHPAAYT029967	MSRPKPTSRFILFTLTLLLLLHFPTPIKSSEPQNPAADETEDGELEELLALDEQVEQEEDQD GGPATRSSEAELLSKAQRIVLELNHDNTKRVIENNEYVLVLGYAPWCARSAELMPQFAEA ATALKELGSPLLMAKLDAERHAKTASSLEIKGFPTLLLFVNGTSQAYTGGFSAQAEFLKKS DIFVFGLFENFEGPEHKEFVKAAAADSAIQFVEVSNIEVANVLFPNVKPTNVFLGIVKSEPE RYTAYEGTFRVDEILQFLDYNKFPLVNRLTEANSAKVYSSPIQLQVHVFADADDFKKLLE PLQDVARQFKSKILFIYIDITDENLAKPYLTVYGLEESNSAVVTAFDIRGNSKYLLESNPTPS NLEEFCSGLLHGTVSPHFKSQPIPHNKNVTVQSIVGKTFDDLVLNSHKNVVLENKKVNEL YHACIL
PbPDI4-1	GWHPAAYT012267	MVSSKTLFAFGALALLLASSVYADDVVVLTEDNFEKEVGQDRAALVEFYAPWLIVMSTR AVCGKYGVSGYPTIQWFPKGSLEPKKYEGGRTAEALAEFVNKEGGTNVKLAVAPSHVVV LTQDNFNEVVLDETKDVLVEFYAPWCGHCKSLAPTYEKVASAFNLEDGVVIANLDADKY KDLAEKYGVSGFPTLKFFPKNNKEGEEYGDGRDLDDFVKFINEKSGTSRDGKGQLTSKAG ILENLDELVKEFVKSSNDEKKAIFSKIEEEVGKLEGSAARYGKIYLKAAKNSLEKGPDYAK NEIQRLGRILEKSVNPTKADEFTLKKNILYTFTSSS

PbPDI4-2	GWHPAAYT039863	MASSKTLIAFGALALLFASSAFADDVVVLTEDNFEKEVGQDRAALVEFYAPWCGHCKKL APEYEKLGSSFKKAKSILIAKVDCDEHKGVCGKFGVSGYPTIQWFPKGSLEPKKYEGART AEALAEFVNKEGGTNVKIAADPSHVVVLTQDNFNEVVLDETKDVLVEFYAPWCGHCKSL APTYEKVASAFKLEDSVVIANLDADKYKDLAEKYGVSGYPTLKFFPKNKKEGEEYGGGR DLEDFVAFINEKSGTSRDAKGQLTSKAGIVENLDELVKEFVKSSNDEKKAIFSKIEEEVGK LEGSAARYGTIYLKAAKKSLEKGADYAKNEIQRLERILEKSVNPTKADEFTLKKNILYTFA SSS
PbPDI5-1	GWHPAAYT028894	MRENQFRAVSIIFLFFFVVSVCDALYGPSSPVLQLTPSNFKSKVLDSNRVVLVEFFAPWCG HCQALTPIWEKAATVLKGVAAVAALDADAHKSLAQEYGIRGFPTIKVFVPGKPPVDYQG ARDVKPIAEFALQQIKALLKDRLSGKTTGGSSEKSEPSASVELNSQNFNELVLKSKDLWIV EFFAPWCGHCKKLAPEWKKAAKNLQGKVKLGHVDCDAEKSLMSKFNVQGFPTILVFGA DKDSPLPYEGARSASAIESFALEQLETNVAPPEVTELSGPDVMEEKCGSAAICFVAFLPDIL DSKAEGRNKYIQQLLSVAEKFKRSPYSFVWAAAGKQPDLENRVGVGGYGYPALVALNA KKGAYAPLKSAFEVDQITEFVKEAGRGGKGNLPLEGTPNIVKIEPWDGKDGEIIEEDEFSL DELMGEDTTNKEEL
PbPDI5-2	GWHPAAYT054427	MRENQFRAVPIIFFLFFFVFNVCDALYGPSSPVLQLTPSNFKSKVLESNRVVLVEFFAPWCG HCQALTPIWEKAATVLKGVATVAALDADAHKSLAQEYGIRGFPTIKVFVPGKPPVDYQG ARDVKPVAEFALQQIKALLKDRLSGKTTGGSSEKSEPSASVELNSQNFNELVLKSKELWIV EFFAPWCGHCKKLAPEWKKAAKNLQGKVKLGHVDCDAEKSLMSKFNVQGFPTILVFGA DKESPLPYEGARSASAIESFALEQLETNVAPPEVTELTGPDAMEEKCGSAAICFVAFLPDIL DSKAEGRNKYIQQLLSVAEKFKRSPYSYVWAAAGKQPDLENRVGVGGYGYPALVALNA KKGAYAPLKSAFEVDQITEFVREAGRGGKGNLPLEGTPSIVKIEPWDGKDGQILEEDEFSL EELMGEDTTNKDEL
PbPDI6-1	GWHPAAYT007378	MKAGSASLVFISVLLFLLPILTTYTEAEVITLTADTFSDKVKEKDTAWFVKFCVPWCKHCK NLGTLWEDLGKTMEGEEEIEVGEVDCSTSKPVCSKVDIHSYPTFKVFYDGEEVAKYQGPR DVDSLKNFVLDEAEKAATKAQLDSDKEL
PbPDI6-2	GWHPAAYT035173	MKTHLASLVLISVLLFLLPILTTHTQAEVITLTADTFSDKVKERDTAWFVKFCVPWCKHCK NMGTLWEDLGKTVEGEDEIEVGEVDCSTSKPVCSKVDIHSYPTFKVFYDGEEVAKYQGP RDVDSLKNFVLEEAEKAATKAQLDNDKEL
PbPDI7-1	GWHPAAYT024090	MSTMRMRVRALCCWLLLILLTALDWPAVAASSSWTVDGTVLELDDSNFDSAISALDLVL VDFYAPWCGHCKRLSPQLDAAAPLLAGLKHPVAIAKLNADKFTSVARKYEIDAYPTLKLF MHGVPLEYNGPRKAESLVRYLKKFAAPDVSILESDSAISEFVEAAGTYFPIYIGFGLDESLIS KLAIKYKKKAWFSVAKDFSEDVMVLYDFDKVPALASLHPTYDERNIFYGPFEEDFLEDFI QQSLFPLAMPINYETLKSLSDDERKIVLTIVKDEDEEKAKKLIKILKSAASANRDFVFGYVG IKQWEDFADTFGATKKTKLPKMVVWDRMEEYFTVNGSESIDEEDQASQVSQFLQGYKEG RIIKKRIGGPSFGSVMSSFFGMRTVYIMVFLVIVTMLIRSISKEDDEPPVVRTADQIDPATSS STEAESREHRSGEKED
PbPDI7-2	GWHPAAYT053038	MGRMIGMRVRPLWCWALLILLAALDSPAVAAVSSWAVDGTVLELDDSNFDSAISALDLV LVDFYAPWCGHCKRLSPQLDAAAPLLAGLKHPVAIAKLNADKFTSLARKYEIDAFPTLKL FMHGVPMEYNGPRKAESLVRYLKKFAAPDVSILESDSAISEFVQAAGTYFPIYIGFELNESL VSKLAIKYKKKAWFAVAKDFSEDVMVLYDFDKVPALASLHPTYDERNIFYGPFEEEFLED FIRQSLFPLAMPINYETLKSLSDDERKIVLTIVEDEDEEKSKKLINILKSAASANRDFVFGYV GIKQWEDFADTFGVNKKTKLPKMVVWDRMEEYITVNGSESIDEEDQASQVSQFIQGYKE GRIIKERIGGPSFASFMTSFIGIGTVYIIVFVVIVMMLIRSINKEDDESPVARTGDQVDRATSS TVEAESKEHRSGEKED

PbPDI8-1	GWHPAAYT008875	MISSGKIKSVDFYRKIPRDLTEASLSGAGLSIVAALAMMFLFGMELNNYLTVSTSTSVIVD KSSDGDFLRIEFNISFPALSCEFASLDVSDVLGTNRLNITKTIRKFSIGTDLRPTGTEFHSGPV LHNIKHGDGDEFSGDGSISLTAQNFEKITHQHPILVVNFYAPWCYWSNRLKPSWEKAAKII RERYDPEIDGRILMAKVDCTEEGDLCKRNHIQGYPSIRIFRKGSDVRDDHGHHEHESYYG DRDTDSLVKTMETLVAPIPVESEKLALEGKSNNGGENAKRPAPLTGGCRIEGYVRVKKVP GNLVISAHSGAHSFDASQMNMSHVISHFSFGRMIAPKVMSDVKRLVPYLGVSHDRLNGRS FINHRDLGANVTIEHYLQIVKSEVITGRSHKLIEEYEYTAHSSLAQSLQIPVAKFHFELSPM QVLITENPKSFSHFITNVCAIIGGVFTVAGIMDSILHNTIRMMRKVELGKNF
PbPDI8-2	GWHPAAYT036573	MISTGKIKSVDFYRKIPRDLTEASLSGAGLSIIAALAMMFLFGMELNNYLTVSTSTSVIVDK SSDGDFLRIEFNVSFPALSCEFASVDVSDVLGTNRLNITKTIRKFSIGTDLRPTGSEFRSGPV LHNIKHGDGDEYSGDGSISLTAQNFEKFTHQHPILIVNFYAPWCYWSNRLKPSWEKAAKII RERYDPEIDGRILMAKVDCTEEVDLCRRNHIQGYPSIRIFRKGSDVRDENGHHEHESYYGD RDTDSLVKTMEALVAPIPVESEKLSLEDKSDNRGENAKRPAPLTGGCRIEGYVRVKKVPG NLVISAHSGAHSFDASQMNMSHVISHFSFGRMIAPKVMSDVKRLVPYLGGSHDRLNGRSF INHQDLGANVTIEHYLQIVKSEVITGRSHKLIEEYEYTAHSSLVQSLQVPVAKFHFELSPMQ VLITENQKSFSHFITNVCAIIGGVFTVAGIMDSILHNTIRMMRKVELGKNF
PbPDI9-1	GWHPAAYT013244	MSPALRLLILSLFSLTSALSPASASSAAGSRSILRAVNDDNADVRDFAVDLNASSFDAVLS DTPATFAVVEFFAHWCPACRNYKPHYEKVARLFNGPDAVHPGMVLMTRVDCASKVNTK LCDKFSVGHYPMLFWGPPSKFVSAGWEPNQAKSVIRVIDDGRTADRLLSWINKQLGSSFS LDDQKFENEHISSNASDPEQIARAVYDVEEATSTAFEIILEHKMIKSKTRASLVKFLQLLVA HHPSRRCRKGSAEVLVNFDDLYPLDILAADRLGDQDVQAALQKFQICGKDVPRGYWMFC RGSKNDTRGFSCGLWVLLHSLSVRIEDGESNFVFTTICDFVHNFFVCEECRQHFYDMCSSV SSPFNKSRDLVLWLWSAHNKVNERLIKEESSLGTADPKFPKMIWPPRQLCPSCYLSSSQKN KEIDWHKDEVFKILTSYYGKTLVSLYKDKGIVGNDKISGALEDLVASTNALVVPLGAALA IAVASCAFGALACYWRSQQKSRKPRRSWS
PbPDI10-1	GWHPAAYT009923	MDKSVILLYIAALAASFRLVSSSALCPHESDFFRYSLQSQCPISISPHPPLKVDGNFLDRALA SQQRTDYTAVLFYASWCPLSRTMYPTFEKLSFMFPQVEHLAIEQSSALPSVFSRYGIHSFPS ILLVNQTSMVRYHGPKNLSSLAQFYQKTTGLEPVQYFDGDHTVSLNIREKSIIRSMSNMSL REISRREPFLAFATLFLCLRVLLYIFPKVLTRLQAFWVLYVPHFNLGIFGETSQIMGRILHM VDVRRIWTKLRLCKTRNFHEGAKNARVWASSLTSVSLGKSSSARSSTN
PbPDI10-2	GWHPAAYT016488	MDKSVIFLCIAALATSLRLVSSSSVLCPHDSDFFRYSLQSQCPIWISPHPPLKVDGNFLDRA LASQQRTDYTAVLFYASWCPFSRTMYPTFEKLSFMFPQVEHLAIEQSSALPSVFSRYGIHSF PSILIVNQTSRVRYHGPKSLSSLAQFYQKTTGLKPVQYFDGDQIVSLNIREKSLIQSMGNMS LREISRREPYLAFAILFLCLRVLLYIFPKVLTRLHAFWVLYVPHFNLGIFGEASQSMGCILP MVDVRRIWTKLRLCKTRNFHEGAKNARVWASSLTSVSLGKSSSARSSSLSS
PbPDI10-3	GWHPAAYT023589	MGIRVWESGIVILVLWVRLISAAEPTSCPAESAADAIFGFRYSNCPVNGASRSVESMGVIV GDEVSLQRALNMVHKNTHDYVAVLFYASWCPFSRMFKPTFSILASLYPSIPHFAFEESAIR PSILSKYGVHGFPTLFILNSTTRIRYQGARTPGSLIAFYSHVTGIKTVSLDQLSLEKIGYPLN HEKHDSTEQESCPFSWARSPENLLRQETYLALASAFVLLRLLYSFYPALLSFVQSAWRQHI QNMRLGSLLEHPLAFLKRAVQLFNSLKEPCKRSNLQEGAMNARVWASKSLATVSIGDAS TSRGYSSD

PbPDI10-4	GWHPAAYT052662	MGIRVWESGIVILVLWVRLVCAAEPASCPTESVANTIFGFRYSNCPVDGACRSVESMGVIV GDEVSLQRALNMVHKNTHDYVAVLFYASWCPFSRMFKPTFSILASLYPSIPHFAFEESAIR PSVLSKYGVHGFPTLFILNSTMRIRYQGARTPGSLIAFYSHVTGFKTVSLDQLSLEKIGYPL NHEKHDSTEQESCPFSWARSPENLLRQETYLALASAFVLLRLLYFFLPALLSFAQSAWRRH IQGHDIGELVGAPFGFSKAGSAVV
PbPDI11-1	GWHPAAYT005858	MALAVTSSSSASISGRTFTPSSEPKAPQLGSIRVFDRSYGQIQCHAVTFSERRSSVKPVNAQ PKRSESIVPSAATVVAPEVVEEVEVEDYAQLARELENASPLEIMDKALEKFGNDIAIAFSG AEDVALIEYAHLGRPYRVFSLDTGRLNPETYQLFDTVEKHYGIRIEYMFPDAVEVQALVR TKGLFSFYEDGHQECCRVRKVRPLRRALKGLRAWITGQRKDQSPGTRSEIPVVQVDPVFE GLDGGAGSLVKWNPVANVEGDIWNFLRAMNVPVNSLHSKGYISIGCEPCTRSVLPGQHE REGRWWWEDAKAKECGLHKGNIKQEGGGENGKAAQSNGAATETDIFTSQNLVTLSRTGI ENLAKLEDRKEPWIVVLYAPWCQFCQAMEASYVELADKLAGSGVKVGKFRADGEQKEF AQKELQLGSFPTILFFPKHSSQPIKYPTEKRDVNSLLAFVNALR
PbPDI11-2	GWHPAAYT044219	MALAVTSSSSASISGRTFTPSSEPKAPQLGSVRVFDRSYGQIQRQAVTFSQRRSSVRPVNAQ PKRSESIVPSAATTAAPEVVEKVEVEDYAQLAKELENASPLEIMDKALEKFGNDIAIAFSG AEDVALIEYAHTGRPYRVFSLDTGRLNPETYQFFDTVEKHYGIRIEYMFPDAVEVQALVR TKGLFSFYEDGHQECCRVRKVRPLRRALKGLRAWITGQRKDQSPGTRSEIPVVQVDPVFE GLDGGAGSLVKWNPVANVADIWNFLRAMNVPVNSLHSQGYISIGCEPCTRSVLPGQHER EGRWWWEDAKAKECGLHKGNIKQEGGQNGMAAQSNDAATETDIFTSQNLVTLTRTGIE NLAKLEDRKEPWIVVLYAPWCPFCQAMEASFVELADKLAGSSVKVGKFRADGEQKEFA QKELQLTSFPTILFFPKHSSQPIKYPTEKRDVDSLMAFVNALR
PbPDI11-3	GWHPAAYT036474	MAFVATSPSTQSLLHASLSSHEPKAQWTSSVNPSDQFSFASTAVASFQGPSLAKPLSAESK RSKSVVPLAAKMASPGIHVLRKLAKELENASPLQIMKKALDKFGNDIAIAFSGAEDVALIE YAKLTGRPFRVSLDTGRLNPETYQFFDTVEKHYGIHIEYMFPDAVEVQALVRGKGLFSFY EDGHQECCRVRKVRPLRRALKGLRAWITGQRKDQSPGTRAEIPVVQVDPSFEGIDGGIGS LVKWNPVANVEGHDIWNFLQMNVPVNPLHSQGYISIGCEPCTRPVLPGQHEREGRWWW EDAKAKECGLHNGNIKEKEALHLNGNGNGISTTNGSANVPDIFNSKNLVSLSRTGIENLAR LENRSEPWLVVLYAPWCRFCQAMEGSYIELAEILAGTGVKVGKFRADGEQKKYAQQELK LGSFPTILFFPKHSSKPVKYPSENRDVASLLAFVNALR
ATPDI1-1	AT1G21750	MAMRGFTLFSILVLSLCASSIRSEETETKEFVLTLDHTNFTDTINKHDFIVVEFYAPWCGHC KQLAPEYEKAASALSSNVPPVVLAKIDASEETNREFATQYEVQGFPTIKIFRNGGKAVQEY NGPREAEGIVTYLKKQSGPASAEIKSADDASEVVSDKKVVVVGIFPKLSGSEFDSFMAIAE KLRSELDFAHTSDAKLLPRGESSVTGPVVRLFKPFDEQFVDSKDFDGEALEKFVKESSIPLI TVFDKDPNNHPYVIKFFESTNTKAMLFINFTGEGAESLKSKYREVATSNKGQGLSFLLGDA ENSQGAFQYFGLEESQVPLIIIQTADDKKYLKTNVEVDQIESWVKDFKDGKIAPHKKSQPI PAENNEPVKVVVSDSLDDIVLNSGKNVLLEFYAPWCGHCQKLAPILDEVAVSYQSDSSVV IAKLDATANDFPKDTFDVKGFPTIYFKSASGNVVVYEGDRTKEDFISFVDKNKDTVGEPK KEEETTEEVKDEL*

ATPDI1-2	AT1G77510	MAFKGFACFSILLLLSLFVSSIRSEETKEFVLTLDHSNFTETISKHDFIVVEFYAPWCGHCQK LAPEYEKAASELSSHNPPLALAKIDASEEANKEFANEYKIQGFPTLKILRNGGKSVQDYNG PREAEGIVTYLKKQSGPASVEIKSADSATEVVGEKNVVAVGVFPKLSGDEFDSFMALAEK LRADYDFAHTLDAKFLPRGESVEGPAVRLFKPFDELFVDSKDFNGEALEKFVKESSIPLVT VFDSDPNNHPYVAKFFESPATKAMMFVNFTGATAEALKSKYREVATSNKDQSLAFLVGD AESSQGAFQYFGLEESQVPLIIIQTPDNKKYLKVNVEVDQIESWFKDFQDGKVAVHKKSQ PIPAENNEPVKVVVAESLDDIVFKSGKNVLIEFYAPWCGHCQKLAPILDEVALSFQNDPSVI IAKLDATANDIPSDTFDVKGFPTIYFRSASGNVVVYEGDRTKEDFINFVEKNSEKKPTSHG EESTKSEEPKKTEETAAKDEL*
ATPDI2-1	AT3G54960	MASSSTSISLLLFVSFILLLVNSRAENASSGSDLDEELAFLAAEESKEQSHGGGSYHEEEHD HQHRDFENYDDLEQGGGEFHHGDHGYEEEPLPPVDEKDVAVLTKDNFTEFVGNNSFAM VEFYAPWCGACQALTPEYAAAATELKGLAALAKIDATEEGDLAQKYEIQGFPTVFLFVD GEMRKTYEGERTKDGIVTWLKKKASPSIHNITTKEEAERVLSAEPKLVFGFLNSLVGSESE ELAAASRLEDDLSFYQTASPDIAKLFEIETQVKRPALVLLKKEEEKLARFDGNFTKTAIAEF VSANKVPLVINFTREGASLIFESSVKNQLILFAKANESEKHLPTLREVAKSFKGKFVFVYV QMDNEDYGEAVSGFFGVTGAAPKVLVYTGNEDMRKFILDGELTVNNIKTLAEDFLADKL KPFYKSDPLPENNDGDVKVIVGNNFDEIVLDESKDVLLEIYAPWCGHCQSFEPIYNKLGKY LKGIDSLVVAKMDGTSNEHPRAKADGFPTILFFPGGNKSFDPIAVDVDRTVVELYKFLKK HASIPFKLEKPATPEPVISTMKSDEKIEGDSSKDEL*
ATPDI2-2	AT5G60640	MAFRVLLLFSLTALLIFSAVSPSFAASSSDDVDDEDLSFLEDLKEDDVPGADSLSSSTGFDE FEGGEEEDPDMYNDDDDEEGDFSDLGNPDSDPLPTPEIDEKDVVVIKERNFTDVIENNQY VLVEFYAPWCGHCQSLAPEYAAAATELKEDGVVLAKIDATEENELAQEYRVQGFPTLLFF VDGEHKPYTGGRTKETIVTWVKKKIGPGVYNLTTLDDAEKVLTSGNKVVLGYLNSLVGV EHDQLNAASKAEDDVNFYQTVNPDVAKMFHLDPESKRPALVLVKKEEEKISHFDGEFVK SALVSFVSANKLALVSVFTRETAPEIFESAIKKQLLLFVTKNESEKVLTEFQEAAKSFKGKL IFVSVDLDNEDYGKPVAEYFGVSGNGPKLIGYTGNEDPKKYFFDGEIQSDKIKIFGEDFLN DKLKPFYKSDPIPEKNDEDVKIVVGDNFDEIVLDDSKDVLLEVYAPWCGHCQALEPMYN KLAKHLRSIDSLVITKMDGTTNEHPKAKAEGFPTILFFPAGNKTSEPITVDTDRTVVAFYKF LRKHATIPFKLEKPASTESPKTAESTPKVETTETKESPDSTTKSSQSDSKDEL*
ATPDI3-1	AT1G52260	MSLIPKPISKVSTFTFILLILLSFTIIIAYSSPDSNVESNEPGFDSDLDQLLAVDEQLQEDRPEQ QSEAETVSKAQRIVLELNGDYTKRVIDGNEFVMVLGYAPWCARSAELMPRFAEAATALK EIGSSVLMAKIDGDRYSKIASELEIKGFPTLLLFVNGTSLTYNGGSSAEDIVIWVQKKTGAP IITLNTVDEAPRFLDKYHTFVLGLFEKFEGSEHNEFVKAAKSDDEIQFIETRDSDVAKLLFP DLKSNNVFIGLVKPEAERYTVYDGSYKMEKILEFLGSNKFPLFTKLTETNTVWVYSSPVK LQVMLFSKADDFQKLAQPLEDIARKFKSKLMFIYVDITNENLAMPFLILFGIEAGNKTVVA AFDNNLNSKYLLESDPSPNSIEEFCSGLAHGTVSRYYRSEPVPDNENASIVTVVGKTFDGL VLNSRENVLLEVHTPWCVNCEALSKQIEKLAKHFKGFENLVFARIDASANEHTKLQVDD KYPIILLYKSGEKEKPLKLSTKLSAKDIAVFINEELLKPKNGSAKDEL*

ATPDI3-2	AT3G16110	MLTKPKPNSKFSILFTFLLLLSFLIFVARSSDVAVEAGSEEELDDLEQLLAVDEQLQEERPE QQSEAETVSKAQRIVVELNGDNTKRLIDGNEYVMVLGYAPWCARSAELMPRFAEAATDL KEIGSSVLMAKIDGERYSKVASQLEIKGFPTLLLFVNGTSQSYTGGFSSEEIVIWVQKKTGA STIKLDTVDEASGFLKKHHTFILGLFEKSEDSSGHDEFVKAASLDNEIQFVETSSIDVAKLL FPNLKTNNVFVGLVKTEAEKYTSYDGPCQAEKIVEFLNSNKFPLVTKLTESNTVRVYSSPV KLQVMVFSKTDDFESLAQPLEDIARKFKSKLMLIYIDISNENLAMPFLTLFGIEDAKKTVV AAFDNNLNSKYLLESDPSPSNIEEFCFGLAHGTVSAYYKSQPIPDNQNASVVAVVGRTFDE VVLRSSENVLLEVHTPWCINCEALSKQVEKLSQHFKGFENLVFARIDASANEHPKLTVDD YPTILLYKTGEKENPLKLSTKSSAKDMAVLINKELKWKDQSGKDEL*
ATPDI4-1	AT2G47470	MAKSQIWFGFALLALLLVSAVADDVVVLTDDSFEKEVGKDKGALVEFYAPWCGHCKKL APEYEKLGASFKKAKSVLIAKVDCDEQKSVCTKYGVSGYPTIQWFPKGSLEPQKYEGPRN AEALAEYVNKEGGTNVKLAAVPQNVVVLTPDNFDEIVLDQNKDVLVEFYAPWCGHCKS LAPTYEKVATVFKQEEGVVIANLDADAHKALGEKYGVSGFPTLKFFPKDNKAGHDYDGG RDLDDFVSFINEKSGTSRDSKGQLTSKAGIVESLDALVKELVAASEDEKKAVLSRIEEEAS TLKGSTTRYGKLYLKLAKSYIEKGSDYASKETERLGRVLGKSISPVKADELTLKRNILTTF VASS*
ATPDI5-1	AT1G04980	MERKMYKSTVFPICCLLFALFDRGNALYGSSSPVLQLTPSNFKSKVLNSNGVVLVEFFAP WCGHCQSLTPTWEKVASTLKGIATVAAIDADAHKSVSQDYGVRGFPTIKVFVPGKPPIDY QGARDAKSISQFAIKQIKALLKDRLDGKTSGTKNGGGSSEKKKSEPSASVELNSSNFDELV TESKELWIVEFFAPWCGHCKKLAPEWKKAANNLKGKVKLGHVNCDAEQSIKSRFKVQGF PTILVFGSDKSSPVPYEGARSASAIESFALEQLESNAGPAEVTELTGPDVMEDKCGSAAICF VSFLPDILDSKAEGRNKYLEMLLSVADKFKKDPYGFVWVAAGKQPDLEKRVGVGGYGY PAMVALNAKKGAYAPLKSGFEVKHLKDFVKEAAKGGKGNLPIDGTMEIVKTEAWDGKD GEVVDADEFSLEDLMGNDDEASTESKDDL*
ATPDI5-2	AT2G32920	MYKSPLTLLTLLTICFGFFDLSSALYGSSSPVVQLTASNFKSKVLNSNGVVLVEFFAPWCG HCKALTPTWEKVANILKGVATVAAIDADAHQSAAQDYGIKGFPTIKVFVPGKAPIDYQGA RDAKSIANFAYKQIKGLLSDRLEGKSKPTGGGSKEKKSEPSASVELNASNFDDLVIESNEL WIVEFFAPWCGHCKKLAPEWKRAAKNLQGKVKLGHVNCDVEQSIMSRFKVQGFPTILVF GPDKSSPYPYEGARSASAIESFASELVESSAGPVEVTELTGPDVMEKKCGSAAICFISFLPDI LDSKAEGRNKYLEMLLSVAEKFKKQPYSFMWVAAVTQMDLEKRVNVGGYGYPAMVA MNVKKGVYAPLKSAFELQHLLEFVKDAGTGGKGNVPMNGTPEIVKTKEWDGKDGELIE EDEFSLDELMGGDDAVGSKDEL*
ATPDI6-1	AT1G07960	MTLGARLVAPMIILLLFIPIELVKAEVITLTPETFSDKIKEKDTAWFVKFCVPWCKHCKKLG NLWEDLGKAMEGDDEIEVGEVDCGTSRAVCTKVEIHSYPTFMLFYNGEEVSKYKGKRDV ESLKAFVVEETEKAAEKAQLEDKEL*
ATPDI7-1	AT1G35620	MRSLKLLLCWISFLTLSISISASSDDQFTLDGTVLELTDSNFDSAISTFDCIFVDFYAPWCGH CKRLNPELDAAAPILAKLKQPIVIAKLNADKYSRLARKIEIDAFPTLMLYNHGVPMEYYGP RKADLLVRYLKKFVAPDVAVLESDSTVKEFVEDAGTFFPVFIGFGLNESIISGLGRKYKKK AWFAVSKEVSEDTMVSYDFDKAPALVANHPTYNEHSVFYGPFEDGFLEEFVKQSFLPLIL PINHDTLKLLKDDERKIVLTIVEDETHESLEKLYKALRAAAHANRDLVFGYVGVKQFEEF VDSFHVDKKTNLPKIVVWDGDEEYDQVTGIETITQEEDHLTQVSRFLEGYREGRTEKKKI NGPSFMGFINSMIGIRSVYILVFLVAVIMMLRSLGQVEEPTGVRTATAVRERVDQATTVPE DESSEHKPSDKKED*

ATPDI8-1	AT3G20560	MVSSTKLKSVDFYRKIPRDLTEASLSGAGLSIVAALFMMFLFGMELSSYLEVNTTTAVIVD KSSDGDFLRIDFNISFPALSCEFASVDVSDVLGTNRLNITKTVRKFPIDPHLRSTGAEFHSGL ALHNINHGEETKEEFPDGAIPLTSASFEALSHHFPILVVNFNAPWCYWSNRLKPSWEKAAN IIKQRYDPEADGRVLLGNVDCTEEPALCKRNHIQGYPSIRIFRKGSDLREDHGHHEHESYY GDRDTDSIVKMVEGLVAPIHPETHKVALDGKSNDTVKHLKKGPVTGGCRVEGYVRVKK VPGNLVISAHSGAHSFDSSQMNMSHVVSHFSFGRMISPRLLTDMKRLLPYLGLSHDRLDG KAFINQHEFGANVTIEHYLQTVKTEVITRRSGQEHSLIEEYEYTAHSSVAQTYYLPVAKFH FELSPMQILITENPKSFSHFITNLCAIIGGVFTVAGILDSIFHNTVRLVKKVELGKNI*
ATPDI8-2	AT4G27080	MVSTSKIKSVDFYSDPEVVGFASRVCALSLSFDLSDIELFRCYFLGFKMIVSHFDFGIVAKR VASKKIPRDLTEASLSGAGLSIIAALSMIFLFGMELNNYLAVSTSTSVIVDRSADGDFLRLD FNISFPSLSCEFASVDVSDVLGTNRLNVTKTIRKFSIDSNMRPTGSEFHAGEVLSLINHGDET GEEIVEDSVPLTGRNFDTFTHQFPILVVNFYAPWCYWCNLLKPSWEKAAKQIKERYDPEM DGRVILAKVDCTQEGDLCRRNHIQGYPSIRIFRKGSDLKDDNAHHDHESYYGDRDTESLV KMVVSLVEPIHLEPHNLALEDKSDNSSRTLKKAPSTGGCRVEGYMRVKKVPGNLMVSAR SGSHSFDSSQMNMSHVVNHLSFGRRIMPQKFSEFKRLSPYLGLSHDRLDGRSFINQRDLGP NVTIEHYLQIVKTEVVKSNGQALVEAYEYTAHSSVAHSYYLPVAKFHFELSPMQVLITEN SKSFSHFITNVCAIIGGVFTVAGILDSILHHSMTLMKKIELGKNF*
ATPDI8-3	AT1G50950	MVSTSKIKSVDFYRKIPRDLTEASLSGAGLSIVAALAMLFLFGMELSSYLAINTSTSVIVDK SSDGDFLNIDFNISFPALSCEFASVDVSDVFGTHRLNISKTIRKVPIDPHLRATAEEFHSTSD LHLINHGDEDHGDNSTYADIPLTGAAFEKFTHHFQILVVNFYAPWCYWSNRLKPSWVKA SQITRERYNPGTDDRVLLGSVDCTEEPTLCKSLPIFSNHIQGYPSIRIFRRGSGLREDHGNHE HESYYGDRDTDSLVKMVEELLKPIKKEDHKLALDGKSDNAASTFKKAPVSGGCRIEGYV RAKKVPGELVISAHSGAHSFDASQMNMSHIVTHLTFGTMVSERLWTDMKRLLPYLGQSY DRLNGKSFINERQLDANVTIEHYLQIIKTEVISRRSGQEHSLIEEYEYTAHSSVARSYHYPE AKFHFELSPMQVLISENPKSFSHFITNVCAIIGGVFTVAGILDSIFQNTVRMVKKIELGKNI*
ATPDI9-1	AT1G15020	MSLIHLFLLLGLLSLEAAASFSPGSRSILRDIGSNVADQKDNAIELNATNFDSVFQDSPAKY AVLEFFAHWCPACRNYKPHYEKVARLFNGADAVYPGVVLMTRVDCAIKMNVKLCDKFS INHYPMLFWAPPKRFVGGSWGPKQEKNEISVVNEWRTADLLLNWINKQIGSSYGLDDQK LGNLLSNISDQEQISQAIFDIEEATEEAFDIILAHKAIKSSETSASFIRFLQLLVAHHPSRRCRT GSAEILVNFDDICPSGECSYDQESGAKDSLRNFHICGKDVPRGYYRFCRGSKNETRGFSCG LWVLMHSLSVRIEDGESQFAFTAICDFINNFFMCDDCRRHFHDMCLSVKTPFKKARDIAL WLWSTHNKVNERLKKDEDSLGTGDPKFPKMIWPPKQLCPSCYLSSTEKNIDWDHDQVYK FLKKYYGQKLVSVYKKNGESVSKEEVIAAAEEMAVPTNALVVPVGAALAIALASCAFGA LACYWRTQQKNRKYNYNPHYLKRYNSNYMVMNTFSNTESEREKER*
ATPDI9-2	AT2G01270	MSLVHLLLFAGLVIAASSSSPGSRLILREISDQKDKAVELNTTNFDSVLKDTPAKYAVVEFF AHWCPACRNYKPHYEKVARLFNGPDAIHPGIVLMTRVDCAMKTNTKLCDKFSVSHYPM LFWGPPTKFVSGSWEPKKDKSEILVIDDGRTAERLLNWINKQIGSSYGLDDQKFKNEHAL SNLTDYNQISQAVYDVEEATAEAFDIILAHKAIKSSETSASFIRFIQLLAAHHLSRRCRKGA AEILVNYDDLCPSGNCSYEKSGGNDTLGNFPICGKDVPRGYYMFCRGSKNDTRGFSCGL WVLMHSLSVRIEDGESHFAFTTICDFVNNFFMCDECRLHFNDMCLSVKTPFKKARDFVL WVWSTHNKVNERLLKDEASLGTGDPKFPKIIWPPKELCPLCYLSSNQKSIEWDHEHVYKF LKNYYGPKLVSLYKEKSVSRSKEETVSATEDLTVATNALVVPIGAALAIAIASCAFGALAC YWRTQQKNRKPRRR*

ATPDI10-1	AT3G03860	MDSRVSILFVCAIAVSCFTSGSASSPVDFSVCNYEFELFRFDLEAKCPPSLYPTPPIEVDGDS LDRLMASQHGNAYMSVLFYASWCPFSRAVRPKFDMLSSMFPQIQHLAVEHSQALPSVFS RYGIHSLPSILMVNQTLNARYHGRKDLISLIEFYEEATGLQPVQYVAEGEPTGLNAGDGNL ITWLRKGTSIREIFKQDPFLVLSLLFICLQMAILVFPIAESRMRALWASYVANLNLGRFGEIS QLFNRGIHMVDVRRLWLKLSLVKTRNFHERAKNAQAWASSLASVSLGQTSSDQS*
ATPDI10-2	AT1G34780	MEKEILLLLLVIMFLTVADVDAVRVPFCATKSAKDSIFGLRDQTCSVSGVESDERPRFVAV TEGDERWLQIALDMIHKNKCDYVALLFYASWCPFSRSFRPSFDVISSLYSSIPHFAIKESSIK PSTLSKYGVHGFPTLLLLNSTMRARYRGTRMLDSLVAFYSDVTGIETLDKTSLERSVSVPH LGNENNTEPENCPFTWARSPENMLRQETYLALAIVFVLLRLLHLIYPTLVVFMKFTWRRIA QNMRLESLLEHTVGFLSRAVQLCMHRRSNLQGGAMNARAWASKSLATVSIGDSSSSNRR SSSSQ*
ATPDI11-1	AT4G21990	MALAINVSSSSSSAISSSSFPSSDLKVTKIGSLRLLNRTNVSAASLSLSGKRSSVKALNVQSI TKESIVASEVTEKLDVVEVEDFEELAKRLENASPLEIMDKALEKFGNDIAIAFSGAEDVALI EYAHLTGRPYRVFSLDTGRLNPETYRLFDTVEKHYGIRIEYMFPDAVEVQALVRNKGLFS FYEDGHQECCRIRKVRPLRRALKGLRAWITGQRKDQSPGTRSEIPVVQVDPVFEGLDGGV GSLVKWNPVANVEGNDVWNFLRTMDVPVNTLHAAGYVSIGCEPCTRAVLPGQHEREGR WWWEDAKAKECGLHKGNIKENTNGNATANVNGTASVADIFNSENVVNLSRQGIENLMK LENRKEAWIVVLYAPWCPFCQAMEASFDELADKLGGSGVKVAKFRADGDQKDFAKKEL QLGSFPTILVFPKNSSRPIKYPSEKRDVDSLTSFLNLVR*
ATODI11-2	AT1G62180	MALAVTSSSTAISGSSFSRSGASSESKALQICSIRLSDRTHLSQRRYSMKPLNAESHSRSES WVTRASTLIAPEVEEKGGEVEDFEQLAKKLEDASPLEIMDKALERFGDQIAIAFSGAEDVA LIEYARLTGKPFRVFSLDTGRLNPETYRLFDAVEKQYGIRIEYMFPDAVEVQALVRNKGLF SFYEDGHQECCRVRKVRPLRRALKGLKAWITGQRKDQSPGTRSEIPIVQVDPVFEGLDGG VGSLVKWNPLANVEGADVWNFLRTMDVPVNALHAQGYVSIGCEPCTRPVLPGQHEREG RWWWEDAKAKECGLHKGNIKEEDGAADSKPAAVQEIFESNNVVALSKGGVENLLKLEN RKEAWLVVLYAPWCPFCQAMEASYIELAEKLAGKGVKVAKFRADGEQKEFAKQELQLG SFPTILLFPKRAPRAIKYPSEHRDVDSLMSFVNLLR*
ATPDI11-3	AT4G04610	MAMSVNVSSSSSSGIINSRFGVSLEPKVSQIGSLRLLDRVHVAPVSLNLSGKRSSSVKPLNA EPKTKDSMIPLAATMVAEIAEEVEVVEIEDFEELAKKLENASPLEIMDKALEKYGNDIAIAF SGAEDVALIEYAHLTGRPFRVFSLDTGRLNPETYRFFDAVEKHYGIRIEYMFPDSVEVQGL VRSKGLFSFYEDGHQECCRVRKVRPLRRALKGLKAWITGQRKDQSPGTRSEIPVVQVDPV FEGLDGGVGSLVKWNPVANVEGNDVWNFLRTMDVPVNTLHAAGYISIGCEPCTKAVLP GQHEREGRWWWEDAKAKECGLHKGNVKENSDDAKVNGESKSAVADIFKSENLVTLSR QGIENLMKLENRKEPWIVVLYAPWCPFCQAMEASYDELADKLAGSGIKVAKFRADGDQ KEFAKQELQLGSFPTILVFPKNSSRPIKYPSEKRDVESLTSFLNLVR*
BrPDI1-1	Bra016405	MAMRGYALFSILALSLLASSVRSEETATETTKEFVLTLDHTNFTDTVNKHDFIVVEFYAPW CGHCKQLAPEYEKAASELSSHVPPVVLAKIDASEETNREFATQYEVQGFPTIKIFRNGGKA VQEYNGPREADGIVTYLKKQSGPASFEIKAAEDASEFDKKVIVVGVFPKLSGSEFDSFLAT AEKLRSDYDFAHTSDAKLLPRGESVTGPVVRLFKPFDELFVDSKDFDGEALEKFVKESSIP LITVFDKDPNNHPYVIKFFDSSNTKAMLFINFTGEGAESLKSKYREVATSYKGQGLSFLLG DAENSQGAFQYFGLEESQVPLIIIQTVDDKKYLKTNIEIDQIESWVKDFKDGKVAPHKKSQ PIPTENNEPVKVVVAESLDEMVFNSGKNVLLEFYAPWCGHCQKLVPILDEVAVSYQSDPS VVIAKLDATANDFPNDTFDVKGFPTIYLRSASGNIVLYDGDRTKEDIISFIDKNKDTAGEPK KEETTTEAVKDEL

BrPDI1-2	Bra012293	MAAMRRGYALFSILALSLLASSVRSETKEFVLTLDHSNFTDTINKHDFIVVEFYAPWCGHC KQLAPEYEKAASELSSNVPAVVLAKIDASEETNKEFATKYEVQGFPTIKIFRNGGKAVQEY KGPREADGIVS YLKKQSGPASFEIKSGDDVVGDKKVVVVGVFPKLAGSEFDSFLATAEKLRSDYDFAHTSD AKLLPRGESVTGPVVRLFKPFDELFVDSKDFDGEALEKFVKESSIPLITVFDKDPNNHPYVI KFFDSPNTKAMF FINFTGESAETLKSKYREVATSNKGQGLSFLLGDAENSQGAFQYFGLEESQVPLIIIQTADD KKYLKTNVEVDQIGSWIKDFKDGKVSPHKKSQPIPTENNEPVKVVVGESLDDMVFNSGK NVLLEFYAPWC GHCQKLVPILVEVAVSYQSDPSVVIAKLDATANDFPRDTFDVKGFPTIYFRSASGNVVLYE GDRTKEDFISFIDKNKDTAGEPKTEDKTAEATKDEL
BrPDI1-3	Bra017948	MAMKGYTLCSILVFSLFASCVRSKETKEFVLTLDHTNFTETINKHDFIVVEFYAPWCGHCK QLAPEYEKAASELSSHVPPVVLAKIDASEETNKEFATKYSVQGFPTIKILRNGGKAVQEYN GPREADGIVTYLKKQSGPASLEIKSADAASEVVGDKNVVAVGVFPKLSGAEFDSFMATAE KLRSDYDFAHTTDAKLLPRGESVTGPVVRLFKPFDELFVDFRDFVGEALEKFVKESSIPLIT VFDSDPNNHPYVLKFFEIPNTK ALFFLNFNGEGAETLKSKYREVAASNKGHGLSFLLGDAKNSEEALQHYGVEQRQLPLIIL QTVDDKKYLKTNVEVDQIESWINDFKDGKASPYKKSQPIPGENNEPVKVVVAENLDEMV FSSGKNVLLEFY APWCGHCQNLVPILDEVAVSYQSDPSVVIAKFDATANDFPHDTFDVKGFPTIYLRSANGNI VLYKGDRTKEDIISFIDKNKDTAGETKTEEKKTKEVKDEL
BrPDI1-4	Bra008311	MAFKGFALFSIVVLSIFASSRSEETETKEFVLTLDHSNFTETINKHDFIVVEFYAPWCGHCK SLAPEYEKAASELITHNPPLVLAKIDASEESNKGIANEYKIQGFPTIKILRNGGKSIQDYNGP REAPGIVSYVKK QSGPASSEIKTAADAAEVVGEKNVVAVGVFPKLSGEEFDSFIALAEKLRGDYDFAHTLDA KLLPRGDSSVAGPVVRLFKPFDELFVDSKDFNGEALEKFLKESSIPLVTVFDSDPSNRPYV ASFFDSSATKVM MFVNFTGESAESLKSKFRKVATSYKGQDLSFLVGDAEGGKGALEYFGVEESQVPLVIIQTP DSKKYLKANVVVEEIESWMKDFKDGKVDVFKKSQPIPAENNEPVKVVVAETLDDIVLKS GKNVLIEFYAP WCGHCQKIAPILDEVALAFKNDPSVIIAKLDATANDIPSEPFDVKGFPTIYFRSVSGTVVAY EGNRTKEDFISFIEKNKPTTSHVEDTTSSTKTEEPKKIDDASDTKDEL
BrPDI1-5	Bra015665	MASNGFAMLSILVLALFASSIRSEETETKEFVLTLDHSNFTDTINKHDFIVVEFYAPWCGHC KSLAPEYEKAAAELSSQSPPIFLAKIDASEESNKGIANDYKIQGFPTIKILRKGGKSIQDYNG PREAAGIVTYV KKQSGPASAEIKSADGAGEVIGEKSVVAVGVFPKLSGEEFDSFMALAEKLRADYDFAHTL DAKLLPRGDSSVAGPVVRLFKPFDELFVDSKDFNGEALEKFVKESSIPLVTVFDKDPSNHP YVSKFFDNPATK VMMFVNFTGETAESLKSKFREVATSSKGQDLAFLVGDAESSQGALQYFGLEESQVPLIIIQ TPDSKKYLKANVVVDQIESWMKDFKDGKVAAHKKSQPIPAENNEPVKVVVAESLDEMV FNSGKNVLIEFY APWCGHCQKLAPILDEVALAFQNDPSVIVAKLDATANDIPSDTFDVKGFPTIYFRSADGKV VVYEGSRTKEDFISFIEKNKPASHSEESSTTVRSGEHKTEESAAKDEL

		MASSTSMSLLFLLSFLLLATSRAENAANGSDLDEELAFLAAEESKEEQQHHANSHHDQYR DFENYEDLEQGGEFHHGEHEGGGEYHEEEPQLPIVDEKDVAVLTKDNFTEFVGNNSFAM VEFYAPWCGAC QALAPEYAAAATELKGVAALAKIDATEEGDLAQKYEIQGFPTVFLFVDGEMRKTYEGER TKDGIVTWMKKKASPSIHNITTVEEAERVLSAEPKVVLAFLDSLVGSESAELAAASRLEDD LSFYQTTSPDIA
BrPDI2-1	Bra007120	KLFEIETEVKRPALVLLKKEEEKLARFDGNFTKAAISEFVSANKSPLVINFTREGASLIFENS VKNQLILFATTNESEKHLPTLREVAKSFKGKFVFVYVQMDNEDYGEAVSGFFGVTGTAPK VLVYTGNEDM RKFILDGELTVNNIKTLAEDFLADKLKPFYKSDPVPETNDGDVKIIVGNNFDEIVLDESKD VLLEIYAPWCGYCQSFEPIYNKLGKYLKGIDSLVVAKMDGTTNEHPRAKADGFPTILFFPG GNKSFDPITVDV DRTVVELYKFLKKHASVPFKLAKPSATPEQVITTKKADEKTESDGAKDEL
BrPDI2-2	Bra002464	MAFRVFLLLSLTALLIFSAVSPSFSTSDVDDEDLSFLEDPKEEHDPTKPLTSTESELDEFNEG EEEDPEMYEGDDEEEGEDLSDLGNPDSDPFPTPDVDEKDVVVVKERNFTDVIENNQYVM VEFYAPWCGHC QSLAPEYAAAATELKGDGVVLAKIDATEENELAHQYSVQGFPTILFFVDGEHKPYTGGRT KDTIVTWVKKKIGPSVYNLTTLDDAEKVLTSGNKVVLGYLNSLVGVEHDQLAAASKAED DVNFYQTVNPD VAKLFHIDPEAKRPAVVLVKREAEKISHFDGEFVKSDLASFVSANKLPLVSVFTRESAPEIF ESAIKKQILLFVTQNGSEKVLPEFEEAAKSFKGKLIFVSVDLDNEDYGKPVAEYFGVSGNG PKLIAYTGNEDP KKHFFDGEIKSDKIKTFAEEFLSDKLKPFYKSDPIPEKNDGDVKIVVGDNFDDIVLDESKDV LLEVYAPWCGHCQALEPMYNKLAKHLREIDSLVIAKMDGTTNEHPKAKAEGFPTILFFPA GNKTAEPITVD TDRTVVAFYKFLRKHATIPFKLEKPAASTESPKTAKSTPKVETTETKGNPQSTTKSTESDL KDEL
BrPDI2-3	Bra020239	MASRVFLLLSLTALLIFSAVSPSLSADVDDEEDLSFLEDLTEEVKAPAKPLTDDFEGGEDD DDEEEDGEHFSDVSNQDSDPFPLSDVDEKDVVVVKERNFTDVIENNEYVMVEFYAPWRG HCQSLAPEYAA AATELKGDGVVLAKIDATVENELAHQYSVQGFPTILFFVDGEHKLYTGGRTKETIVTWVK KKIGPSVYNLTTLDDAEKVLTSGNKVVLGYLNSLVGVEHDQLAAASKAEDDVNFYQTVN PDVAKMFHIDP ESKRPALVLVKREEEKISHFDGEFVKSGLVSFVSANKLPLVTVFTPESSQEIFESAIKKQLLL FATENGSEKVLQEFEEAATLFKGKLIFVSVDVDNEDYGKPVAEYFGVSSSNAPKLVAFTG NEDPQKHYFEG EIKSDKIKIFGEEFLSDKLKPFYKSDPIPEKNDGDVKIVVGDNFDEIVLDESKDVLLEVYAP WCGHCQALEPMYNKLAKHLRSIDSVVIAKMDGTTNEHPKAKAEGFPTVLFFPAGNKTSS EPITVDADRTVV AFYKFLRKHATIPFKLEKPAASTESPTAAESTPKVETTETKGKLESTTTKSTESDSKDEL

BrPDI3-1	Bra014319	MSMNPKLSVSTFILLLLLTFLLIPSHSSSSDEESDDDLEQLLAVDEQSQEDRPQHQQSEAET VSKAQRIVLELTGDNAKRVVDGNEFVLVLGYAPWCARSADLMPRFSEAATGLKEIGSSV LMAKIDGDRYGKVASELEIKGFPTLLLFVNGTSQPYSGGFSAEDIVIWVQKKTGSPIITVNT LDEAQIFLNKYHTFVVGLFHKFEGSEYNEFVKAAKSDNEIQFVETSDNDVAKLLFPQLKT NTVFIGLVKPEAERYTAYDGPFKM EKLLEFLGNNKFPLITRLTESNTVWVYSSPVKLQVMLFSKAYVFQSLAQPLEDLARKFKS KLMFIYVDIANENLAMPFLTLFGIEHANKTVDFCSGLADGTVSRYYRSEPVPDNVDDFPTI LLYKSGEKEKPV ITFLIEQSYKPSM
BrPDI3-2	Bra018958	MSINPKPQSSLLTFILLLLLTSAAYSSSNHPGSDEESDDLEQLLAVDEQLQQDLPLHHQQSE AETVSRAQRIVLELSGDNARRVVGGNEFVMVLGYAPWCARSADLMPKFSEAATALKEIG SPVVMAKIDGDRYGKVASEMEIKGFPTLLLFVNGTSKAYTGGFSAEEIVIWVQKKTGAPI VTVNTVDEAQRFLKKYHTFVVGLFNKFEGSEYNEFVKAAKSDDEIQFVETSDSEVAKLLF PEIKTSDVFIGMVKTEAERYTSYA GSYKMENILEFLSKNKFPLITKLSESNTAWVYSSPVKLQVMIFAKADDFQNMAQPLENFA RRFKSKLMFIYIDITNENLAMPFLTLFGIEHANKTVVAAFDNKLNSKYLLESDPSPTNIEDF CSGLADGTIPQY YRSEPVPDNENASIVTVVGKTFDELVLNSQENVLLEVHTPWCVNCEAMSKQVVKLAKHF KGFENLVFARIDASTNEHAKLQVNDYPTILLYKSGEKEKPLKISTKLSAKDMAVFINEELK PRGGSAKDEL
BrPDI4-1	Bra000454	MAKSQIWFGLASLVALLVVSAVADDVVVLTDDSFEKEVGKDRGALVEFYAPWCGHCKK LAPEYEKLGASFKKAKSILIAKVDCDEHKSVCTKYGVSGYPTIQWFPKGSLEPQKYEGAR NAEALAEYVNK EGGTNVKLAAAPQNVVVLTPDNFDEIVLDQNKDVLVEFYAPWCGHCKSLAPVYEKVAT VFKQEEGVVIANLDADAHKSLGEKYGVSGFPTLKFFPKDNKAGQDYEGGRDLDDFVGFI NEKVGTSRDSQG QLTSKAGIVESLDALVKELVAASEDEKKTILSRIEEEASNLKGSTTRYGKLYSKLAKSYIEK GSAYATKEVERLGRVLGKSISPVKADELTLKKNILSTFVASS
BrPDI4-2	Bra004455	MAKSQIWFGLALVALLVVSAVADDVVVLTEDSFEKEVGKDKGALVEFYAPWCGHCKKL APEYEKLAASFKKAKSVLIAKVDCDEHKGVCTKYDVSGYPTIKWFPKGSLEPQKYEGPRN AEALAEFVNKE GGTNVKLAAVPQNVVVLTPDNFDEIVLDQNKDVLVEFYAPWCGHCKSLAPVYEKVATV FKQEDGVVIANLDADAHKSLGEKYGVSGFPTLKFFPKDNKAGQDYDGGRDLDDFVTFIN EKVGTSRDSKGQLTSKAGVVESLDALVKELVAASEDEKKAILSRIEEEASNLKGSTARYG KLYSSLAKKYIEKGSGYATKEAERLGRVLSKSMSPVKADELTLKRNILNTFVASS
BrPDI5-1	Bra015375	MNKTRVFTILSLVFAFSFDLSNALYGSSSPVLQLTPSNFKSKVINSNGVVLVEFFAPWCGH CKSLTPTWEKVATTLKGIATVAAIDADAHKSVSQDYGVRGFPTIKVFVPGKPPIDYQGAR DAKAISQFAIKQI KALLKDRLDGKTTGTTTGGGSSEKKSEPSASVELNSSNFDELVTESKDLWIVEFFAPWCG HCKKLAPEWKKAAKNLKGKVKLGHVDCDADKAIQSRFKVKGFPTILVFGADKSSPLPYE GARSASAIESFAL EQLEANAGPAEVTELTGPDAMEEKCGPAAICFVSFLPDILDSKAEGRNKYLEMLLSVAEK FKKDPISFVWVAAGKQPDLEKRVGVGGYGYPAMVALNAKKGAYAPLKSGFEVKHLIEF VKEAQKGGKGNL PIDGTLEIVKTEAWDGKDGEVVDADEFSLEELMADD

		MQNKSPLTLLTLLCLSLGFLNLTNALYGSSSPVVQLTASNFKSKVLNSNGVVLVEFFAPW CGHCKALTPTWEKVASVLKGVATVAAIDADAHQSAAQDYGIQGFPTIKVFVPGKPPVDY QGARDAKSIANF
BrPDI5-2	Bra005546	AYKQIKALLSDRLEGKSKPSGGGSSEKKSEPSASVELNSSNFDELVIKSNDLWIVEFFAPW CGHCKKLAPEWKRAAKNLKGKVKLGHVNCDVEQSIMSRFKVQGFPTIMVFGVDKSSPY AYDGARSASAIESFATELVEASAGPVEVTELTGPDVMEKKCGSAAICFVSFLPDILDSKAE GRNKYLEMLLSVAEKFKRHPYSFVWVAAVTQPDLEKRVNVGGYGYPAMVAMNVKKGV YAPLKSAFELQHLLEFVKDAGAG
		GKGNVPMNGTPEIVETKAWDGKDGEVMEEDEFSLEELMGGDDDANVGTKDEL
BrPDI6-1	Bra018672	MKLGARLIAFILLLSLTIVLTKAEVITLTPETFSDKVKEKDTAWFVKFCVPWCKHCKKLGN LWEELGNAMEGDDEIEIGEVDCGKSRDVCTKVEIHSYPTFKLFYNGEEVSKYQGKRDVES LKTFVVEETEK
		AAEKAQLEDKEL
BrPDI7-1	Bra034408	MRSLGLMYWWISFLALSISLSASSDDQFTIDGTVLELTDSNFESAISTFDCVFVDFYAPWC GHCKRLNPELDAAAPILAKLKQPIIIAKLNADKYSRLARKLEIDAFPTLMLYNHGVPMEYY GPRKADLLVRY LKKFVAPDVAVLESNSHVKDFVEDSGTSFPVFIGFGLNQSLISGLGRKYKKKAWFAVAKD ASEDVMVSYDFDKAPALVAQHPAYNEHSVFYGPFEDGFLEEFVKQNFLPLILPINHDTLKL LKDDERKMVL
		TIVEDETHESMGKLIKALRAAAHANRDLVFGYVGVEQFEEFADSFHADKKAKLPKIVVW DGDEEYEQVNGIETVSHEEDHLTQVSRFLEGYREGKTEKKRIKGPSFMGFINSMIGIRSVYI IVFLVAVIMMLR
		SLGQVEEPARVRTAASDGQATSVLEGETSEHKPRDKED
BrPDI8-1	Bra001793	MVSPTKLKSVDFYRKIPRDLTEASLSGAGLSIVAALVMMLLFGMELSSYLEVTTTTAVVV DKSSDGDFLRIDFNISFPALSCEFASLDVNDVLGTNRLNITKTVRKFPIDPHLKATGGEFHS GLASHHINHGEEI
		KQEFPDGAIQLTNGGFQSLSHHFPLLIVNFNAPWCYWSNRLKPSWEKAATIIKQRYNPDT DGRVLLGSVDCTEEPALCRRNHIQGYPSIRIFRKGNDLKEDHGHHEHESYYGDRDTESIVK MVDELVAPIHPETHKLALDWGISNDTAKLLKKAPVTGGCRVEGYVRVKKVPGNLVISAH SGAHSFDSSQMNMSHVVTHLSFGRMIDTRLLTDLKRLLPYLGQSHDKLDEKAFINQHEFG ANVTIEHYLQIVKTEVITRRYGQEHSLTEEHEYTAHSSITQTYYLPVAKFHFELSPMQILITE NPKSFSHFITNLCAIIGGVFTVAGIIDSVLHNTIRLIKKVELGKNI
		MVSPTKLKSMDFYRKIPRDLTEASLSGAGLSIVAALVMMLLFGMELSSYLAVNTTTAVVV DKSADGDFLRIHFNISFPALSCEFASVDVSDVLGTNRLNITKTIRKFPIDPHLKTTGEEFHSG HGSHDINHGEE
BrPDI8-2	Bra035770	TKEEIPDGSVPLVSSSFDSFSKHFPLLIVNFNAPWCYWSNRLKPSWEKASSIIYHKYNPETD GRVLLGSVDCTEEAELCKRNHIQGYPSIRIFRKGSDLKEDHGHHEHESYYGDRDTDSIVK MVDELVAPIHPETHKLDLDGISNKTLKHLKKAPVTGGCRVEGYVRVKKVPGNLIISAHSG AHSFDSSKMNMSHVVSHLSFGRMFSPRLLTDMRRLLPYIGQSHDKLNEKAFINQHEFGAN VTIEHYLQVVKTEVITRRTAQEHSLVEEYEYTAHSSIAQTYYLPVAKFHFELSPMQIMITEN PKSFSHFITNLCAIIGGVFTVAGILDSIFHNTIRLVKKVELGKNF

BrPDI8-3	Bra019071	MVSTSRIKSVDFYRKIPRDLTEATLSGAGLSIVAALSMLFLFGMELNNYLAVSTTTSIIVDR SSDGDFLRMDFNISFPSLSCEFASVDVSDVLGTNRLNVTKTIRKFSIDSNLRPTGSEFHSGE VLSHVNHDEAGEEVVEDSVSLTSRNFDTLLHQFPISVVNFYAPWCYWCNLLKPSWEKAA KQIKERYDPEMDGRVILAKVDCTQEADLCRKNHIQGYPSIRIFRQGSDLKDNAHHDHESY YGDRDTESLVKMVIGLVEPIHLEPHKLALEDKSDNASKTLKKAPSTGGCRIEGYIRVKKVP GNLMVSARSGSHSFDSTQMNMSHVVNHLSFGRKILPQTFTDLKRLSPYLGQSHDRLNGRP FINQRDLGPNVTIEHYLQIVKTEVLKSNGHAMVEEYEYTAHSSVAHSYYLPVAKFHFELSP MQVLITENSRSFSHFITNVCAIIGGVFTVAGILDSILHQTMTLMKKIELGKNF
BrPDI8-4	Bra010413	MISPRKIKSVDFYRKIPRDLTEASLSGAGLSIVAALSMLLLFGMELSSYLTVSTTTSIIIDRSS DGDFLRMDFNISFPSVSCEFASVDVSDVLGTNRLNVTKTIRKFSIDSNLRPTGSEFHSGEFL SRVNHGDESAEELVEGSVSLGARNFDTFLHQYPISVVNFYAPWCYWCNLLKPSWEKAAN QIKERYDPEMDGRVILAKVDCTQEADLCRRNHIQGYPSIRIFRKGSDLRDDNAHHDHESY YGDRDTESLVKMVIGLVEPIHLEPHKLALEDKSGNASKTLKKAPSTGGCRIEGYMRVKKV PGNLMVSARSESHSFDTSQMNMSHVVNHLSFGKRILPEAFSDLKRLAPYLGGSHNRLDDR SFINQHDLGPNVTIEHYLQIVKTEVLKSNGHAMIEEYEYTAHSSVAHTYYLPVAKFHFELS AMQVLITENSKSFSHFITNVCAIIGGVFTVAGILDSILHQTMTLMKKIELGKNF
BrPDI8-5	Bra030465	MVSTTKIKSVDFYRKIPRDLTEASLSGAGLSIIAALAMVFLFGMELSTYLAVTTNTSVIVDN SSDGDFLRIDFNVSFPSLSCEFASVDVSNVLGTKRLNLTKTIKKVPIDPYLRATGAEVHSTS GLHLINHGDEDHGNNTYAAIPLTGATFDKFSHHFQILVVNFYAPWCYWSNRLKPSWEKA AEITRQRYNPETDGRVLLGSVDCTEETTLCKRNHIQGYPSIRIFRKGSDLKEDHGHHEHES YHGDRDTESILKMVEELLKPIKKEDHKLALDGKTDNVVSGIKKAPVSGGCRIVGYVRAKK VPGEIIISAHSGAHSFDASQMNMSHYVSHLTFGKMISERLLTDMKRLMPYLGLSHDRLNS KWFVNEGQFAANVTIEHYLQVVKTEVVSRRFGQEHSVIEEYEYTAHSSVAHGYYYPVAK FRFDLSPMQVLISENPKSFSHFITNVCAIIGGVFTVAGILDSIFQNTFRLVKKIELGKNI
BrPDI8-6	Bra018881	MVSTTKIKSVDFYRKIPRDLTEASLSGAGLSIIAALAMMFLFGMELSTYLAVTTQTSVVVD NSSDDDFLQIDFNVSFPALSCEFATFEVSDVLSTNRLNLTKTIKKVPIDPHLRDTGEEYHPT PDSDLINHGDEH HDDNTYAAIPLSGGTFDKISHKFPILVVNFYAPWCYWSSRLRPSWEKAAEITRQKYGPEN DGRVLLGSVDCTEEPTLCTKYHIQGYPSIRIFHNGSDLRGDDGHQEHDSYHGNRDTESLV KMVEELLRPIKKFDGTTNHAASRIRKAPVSGGCRIEGYVRAKKVPGELVISAVSGSHSFDA SRMNMTHFVNHLSFGRLISDRLLTDMKRLLPYLGLSHDRLNGKWFVNEGKFAANVTIEH YLQVVKTEVVSRRFGQEHSVIEEYEYTAHSSVAHGYYYPVAKFHFDLSPMQVLISENPKS FSHFITNVCAIIGGVFTVAGILDSIFQSTYGIMKKVELGKNF
BrPDI9-1	Bra026786	MSLIHLFLLVSLVSLEADATTSFSSGSRSILRDIGSNVIADHKDNAVELNATNFDSVFQDTS AKFAVLEFFAHWCPACRNYKPHYEKVARLFNGPEAVHPGTVLMTRVDCAAKMNIKLCD KFSIKRYPMLFW GPPSKFVGGSWEPKQEKSEILVVEEWRTADLLLGWINKQLGSSYGLDDQKVGNDHLLPNI SDHEQISQAVFDIEEATEEAFDIILSLKAIKSSETGASFIRFLQLLVPHHPSKRCRKGSAEILM NFDDLCPAGECSYDSGVNNTLRNFHICGKDLPHGYYMFCRGSKNETRGFSCGLWILMHS LSVRIEDGESQFAFTTLCDFINNFFMCDECRRHFHDMCLSVKTPFKKARDVVLWLWSTHN KVNERLKKDEDSLGTGDPKFPKIIWPPKQLCPSCYLTSTGENIDWDHDEVYKFLKRYYGE KLVSSYKKNTGGVSKEEVVVAAAEEMSVPRNALVVPVGAALAIALASCAFGALACYWR TQQKNRKHHHNPHYLRRYSSNYLVMNTFSNIESEREKER

BrPDI9-2	Bra014330	MSLAHLVLFAGLLSLVILASSSSSSSSSPGSRSILRDISGENADQKDRAVELNSSNFDSVLSD TPAKYAVVEFFAHWCPACRNYKPHYEKVARLFNGPDAIHPGIVLMTRVDCAMKTNTNLC DRFSVSHYPMLLWGSPTKFVSGSGEPKKEKSEIVVIDDARTAERLLKWINKQTQSSYGLD DKKFENEHVRTNITDYKQISQAVYDIEEATAEAFDIILSNKVIKSSETSASFIRFIQLLAAHH ASRRCRKGAAEILVNYDDLCPS GKCSYEASGGKDTLGSFPICGKDLPRGYYMFCRGSKNDTRGFSCGLWVLFHSLSVRIEDG ESQFAFNTICDFVNNFFMCDECRLHFNDMCLSVKTPFKKARDFVLWVWSTHNKVNERLM KDEASLGSGDPEFPKIIWPPRALCPSCYLSSDEKSIEWDHDNVYKFLKSYYGPKLVSLYKE KSVVGSKEETVSATAEDLTVATNALVVPVGAALAIAVASCAFGALACYWRTQQKNRKY CRGEAGTEVLEAELLMFP
BrPDI10-1	Bra001092	MDLHLPILLLCVIAASCFPSGLASSPVDSSVCNHEFELFRFDLASKCPPSLRPSPPIEVDGDS LDRLMALNHDDGNAYVSVLFYASWCPFSRAVRTKFDMLSLMFPQIQHLAVEHSQALPSV FSRYGIHSLPSILMVNQTLKARYHGRKDLTSLIEFYDESTGLKPVQYVAEGEPATTLDATD GSLITWLRNGTSISEIFKRDPFLVLSLLFICIQVAILVFPIAESRMKALWASYAPNLNLERFG EVSQVFSRALHMVDVRRLWLKLR
BrPDI10-2	Bra031969	LVKTRSFHERAKNAQAWASSLASVSLGQTSSDQS MDLRVPILFFLLSTIYFPSVLASSSPVDFSVCNHEFELFRFDLDSKCPPSLHPAPPLQVDGET LDRLMGLNYDANGYMSVLFYASWCPFSRAVRPKFDMLSSMFPLIQHLAVEHSQALPSVF SRYGIHSLPSILI VNRTSKARYHGQKDLTSLIEFYEESTGLKPVQYVAEAEPTTSLDSTDGNLITWLRKGTSIS EIFRQDPFLVLSLLFICLQMAILVFPIAESRMKALWASYVSNLNLERFGEISQLFSRALHMV DVRRLWLKLRLV
BrPDI10-3	Bra036758	KTRNFHERAKNAQAWASSLASVSLGQASSDQS MDLRVPFLLLIAVSCFPSSFASSSPSVCNHESELFRFDIHSKCPPSMYPTPPIEIDGDSLDRLM ALHHDGNAYVSVLFYASWCPFSRALRSKFDTLSSMFPQIHHLALDHSQALPSVFSRYGIHS LPSILMVNQTSKARYHGRKDLTSLIEFYEESTGLKPVQYVSEPEPTTSVDATDGNMITWLR KGTSISEVFKGDPFLVLSLLFVCLQAAILVFPMAEQRLKALWASYVPNLNLERFGEVSQVF RRAVHMVDVRRLWLKLTLVK
BrPDI10-4	Bra036429	TRSFHERAKNARAWASSLASVSLGQTSSNQS MEKGILLLVLVILFGNLMFTAVDGVSVRAPICAMRSVKDYALGFREQSCPFYGDELADRP HFVVVTEGDERWLQTALDMIHKNKCDYVALLFYASWCPFSRSFTPSFDLISSLYSSIPHFAI KESSVKPSTLSK YGVHGFPTLLLMNSTMRARYRGTRMLDSLVAFYRDVTVSELTRKLLGIETLDKTSLEKSL LVPHLGNENNTEPENCPFTWARSPENMLRQETYLTLATVFVLLRLLYFVFPALVVFAKFT WPRIAQNMRLES
BrPDI11-1	Bra019406	LQEHTVGFLSRLCMYLKEPCKRSNLQGGAMNARAWASKSLATVSIGESSSSNSRASSASQ MALAINVSSSSSSISTSSFPSSDLKAPQIGSLRLSDRINVSSASLSLSGKRSSVKALNVQSITK ESMVPPQAASMVASEIREKVDVIEVEDFEELAKKLETASPLEIMDKALENFGNDIAIAFSG AEDVALIEYAHL TGRPYRVFSLDTGRLNPETYRLFDTVEKHYGIRIEYMFPDAVEVQALVRSKGLFSFYEDG HQECCRIRKVRPLRRALKGLRAWITGQRKDQSPGTRSEIPVVQVDPVFEGLDGGAGSLVK WNPVANVEGNDVWSFLRTMDVPVNTLHAAGYVSIGCEPCTRAVLPGQHEREGRWWWE DAKAKECGLHKGNIKESSNGNNAAVNGNGTTSTVDDIFKSENVVSLSRQGIENLMKLENR KEAWIVVLYAPWCPFCQAMEASFDELADKLRGGDGVKVAKFRADGDQKEFAKSELQLG SFPTILVFPKNSSRPIKYPSEKRDVDSLTSFLNLVR

BrPDI11-2	Bra013579	MALAINVSSSSSSAISTSSFPSSELKAPRIGSLRLSDRVNVSTASLSLSGKRSSSVKPLNVQSI AKESFVPSQAASVVASEVTEKLDVVEVEDFEELAKSLETASPLEIMDKALEKFGNDIAIAF SGAEDVALIEYA HLTGRPFRVFSLDTGRLNPETYRLFDTVEKHYGIRIEYMFPDAVEVQALVRNKGLFSFYED GHQECCRIRKVRPLRRALKGLRAWITGQRKDQSPGTRSEIPVVQVDPVFEGLDGGAGSLV KWNPVANVEGNDVWNFLRTMDVPVNTLHAAGYVSIGCEPCTRAVLPGQHEREGRWWW EDAKAKECGLHKGNIKENSNGNANANVNGTSSTVADIFKSENVVSLSRQGIENLMKLENR KEAWIVVLYAPWCPFCQAMEGSFDELADKLGGSGVKVAKFRADGDQKEFAKRELQLGS FPTILVFPKNSSRPIKYPSEKRDVDSLTSFLNLVR
BrPDI11-3	Bra034466	MALAVTSSSTAISGSSFSRSGPCSDRKALQICSFRLSDLSHVSQRRYSLKAESPPTRNDSLV TRASTLITPGVEEKEEDVEDFEQLAKKLEEASPLEIMDKALQRFGSNIAIAFSGAEDVALIE YARLTGRPFRVFS LDTGRLNPETYRLFDAVEKQYGIRIEYTFPDAVEVQALVRNKGLFSFYEDGHQECCRVRK VRPLRRALKGLKAWITGQRKDQSPGTRSEIPIVQVDPVFEGLDGGVGSLVKWNPLANVEG GDVWNFLRTMDVPVNALHAQGYVSIGCEPCTRPVLPGQHEREGRWWWEDAKAKECGL HKGNIKKEDDSTTADLAPAIVHDIFESSNVVALSRGGIENLLKLGNRKEPWLVVLYAPWC PFCQAMEASYVELAEKLAVKGIKVAKFRADGDQKEFAKQELQLGSFPTILLFPKSAPRAIK YPSEHRDVDSLMSFVNLLRSVRKHDDKELVLELMATLTRGRESY
BrPDI11-4	Bra029505	MAMAATVSSSGITSSAFSPSVISSEPKVSQIGSLKLLDRVSLTTPMSLKKRSSVKPLNAEPK RNDSMVPLAATMVAQVAEEVVETEDFAELAEKLENASPLEIMDKALEMFGNDIAIAFSGA EDVALIEYAHL TGRPYRVFSLDTGRLNPETYRFFDAVEKHYGIRIEYMFPDSVEVQGLVRSKGLFSFYEDGH QECCRVRKVRPLRRALKGLRGWITGQRKDQSPGTRSEIPVVQVDPVFEGLDGGAGSLVK WNPVANVEGSDVWSFLRTMDVPVNTLHAAGYVSIGCEPCTRAVLPGQHEREGRWWWE DAKAKECGLHKGNIKENANVNGESKPVVEDIFKSENVVALSRQGIENLVKLENRKEPWIV VLYAPWCPFCQAMEASYDEMADKLAGSGVKVAKFRADGEQKEFAKQELQLGSFPTILVF PKNSSRPIKYPSEKRDVDSLTSFLNLVR
ZmPDIL1-1	GRMZM2G091481_T01	MAIRSKAWISLLLALAVALSARAEEEPAAAAEGEAVLTLDVDSFDEAVAKHPFMVVEFY APWCGHCKKLAPEYENAAKALSKHDPPIVLAKVDANEEKNRPLATKYEIQGFPTIKIFRD QGKNIQEYKGPRE ADGIVDYLKKQVGPASKEIKSPEDATALIDDKKIYIVGIFAEFSGTEFTNFMEVAEKLRSDY DFGHTLHANHLPRGDAAVERPLVRLLKPFDELVVDSKDFDVAALMKFIDASTIPRVVTFD KNPDNHPYLM
		KFFQSSAPKAMLFLNFSTGPFDSFKSAYSAAAEEFKDKEIKFLIGDIEASQGAFQYFGLKED QTPLILIQDGDSKKFLKVHVEADQIVAWLKEYFDGKLTPFRKSEPIPEVNNEPVKVVVADN VHDFVFKSGKN VLIEFYAPWCGHCKKLAPILDEAATTLQSDEEVVIAKMDATANDVPSEFDVQGYPTLYFV TPSGKVTSYDSGRTADDIVDFIKKSKETAGAATTTTTQAPPASEKAAAAEPVKDEL

ZmPDIL1-2	GRMZM2G163421_T01	MAIRSKAWISLLLALAAVLSARAEEPAAAEAEAVLTLDVDSFDEAVAKHPFMVVEFYAP WCGHCKNLAPEYENAAKELSKHDPPIVLAKVDANEEKNRPLATKYEIQGFPTLKIFRNQG KNIQEYKGPRE ADGIVDYLKKQVGPASKEIKSAEGVAAHFDDKKIYIVGIFKEFSGTEFTNFMELAEKLSSD YDFGHTLHANHLPRGDASVEGPLIRLLKPFDDLVVDSKDFDVAALEKFIDASSTPRVVTFD NNPDNHPYLMK FFQSSAPKAMLFLNFSTGPLDSFKSVYYAAAEEFKDKEIKFLIGDIEASQGAFQYFGLKED QTPLILIQDGDSKKFLKDHIEADQIVSWLKEYFDGKLTPFKKSEPIPEVNNEPVKVVVADNI HDVVFKSGKNV LIEFYAPWCGHCKKLAPILEEAATTLLSDEEVVIAKMDATANDVPSEFEVQGYPTMYFVT PSGKVTSYDSGRTADDIVDFINKSKETASAVQATATASGKAADAAEKTEPVKDEL
ZmPDIL2-1	GRMZM2G134889_T01	MGSTTMSPPSFPVVLLLLLLATIAAAAGSNMDEEVVDDLQYLIDNSDDIPTNDPDGWPEG DYDDDDLLFQDQDQDLTGHQPEIDETHVVVLAAANFSSFLASSHHVMVEFYAPWCGHC QELAPDYAAAAAHLAAHHHQAHLALAKVDATEETDLAQKYDVQGFPTILFFIDGVPRGY NGARTKEAIVDWINKKLGPAVQNVTSVDEAQSILTGDDKAVLAFLDTLSGAHSDELAAA SRLEDSINFYQTSTPDVAKLFHIDAAAKRPSVVLLKKEEEKLTFYDGEFKASAIAGFVSAN KLPLVTTLTQETSPSIFGNPIKKQILLFAVASESTKFLPIFKEAAKPFKGKLLFVFVERDSEEV GEPVADYFGITGQETTVLAYTGNEDARKFFLDGE VSLEAIKDFAEGFLEDKLTPFYKSEPVPESNDGDVKIVVGKNLDLIVFDETKDVLLEIYAP WCGHCQSLEPTYNNLAKHLRSVDSLVVAKMDGTTNEHPRAKSDGYPTILFYPAGKKSFE PITFEGERTVVDL YKFIKKHASIPFKLKRQESRTESTRAEGVKSSGTNSKDEL
ZmPDIL2-2	GRMZM2G033829_T01	MGSTRTSHPSFPVLLLFLLATAAAAGSNKAEEVDDLQYLIDNSEDIPPNDPDGWPEGGGG GDYDDDLLFQDQDQDLPDYEPQIDETHVVVLTAANFSSFLAATRHVMVEFYAPWCGHCR ELAPEYAAAA AHLAVHHNQTDLALAKADATEETDLAQRYDVQGFPTIILFIDGVPKDYNGARTKDAIVD WINKKLGPAVQDVTSVHEAERILTGDDKAVIAFLDTLTGAHSDELAAASRLEDSINFYQTS IPDVAKLFHIDP
		AAKRPSIVLLKKEEEKLTFYDGKFKASAIADFVSANKLPLVTTLTQETSPSIFGNAIKKQILL FAVASESSKFLSIFKEAAKPFKGKLLFVFVERDNDEVGEPVANYFGLTGQETTVLAYTGNE DARKFFLDGE VSLEAIKDFAEGFLEDKLTPFYKSEPVPESNDGDVKIVVGKSLDVIVLDESKDVLLEIYAP WCGHCQSLEPTYNKLAKHLSGVDSLVIAKMDGTTNEHPRAKSDGYPTILFYPAGKKSFEP VTFEGERTVVDM YRFIKKHASIPFKLKRQESRRESIQTDGVKDEL

ZmPDIL3-1	GRMZM2G014076_T01	MRARWAVTLLLLAVLALTASAARLDLDDDDDSGVLDELLAIDEEAERGGLLDAEGAGE AVRRAQSMVLALDNDNARRAVEDHAELLLLGYAPWCERSAQLMPRFAEAAAALRAMG SAVAFAKLDGER YPKAAAAVGVKGFPTVLLFVNGTEHAYHGLHTKDAIVTWVRKKTGVPIIRLQSKDSAEEF LKKDMTFVIGLFKNFEGADHEEFVKAATTDNEVQFVETSDTSVAKVLFPGITSEEKFVGL VKSEPEKFEKFD GKFEEKEILRFVELNKFPLITVFTELNSGKVYSSPIELQVFTFAEAYDFEDLESMVEEIARAF KTKIMFIYVDTAEENLAKPFLTLYGLESEKKPTVTAFDTSNGAKYLMEADINANNLREFCL SLLDGTLPPYH KSEPLPQEKGLIEKVVGRTFDSSVLESHQNVFLEVHTPWCVDCEAISKNVEKLAKHFSGSD NLKFARIDASVNEHPKLKVNNYPTLFLYLAEDKSNPIKLSKKSSVKDMAKLIKEKLQIPDV ETVAAPDNVK DEL
ZmPDIL4-1	GRMZM2G128171_T03	MAISQISRIFLAILLLAAAFAAAPAALADGDDVVALTESTFEKEVGKDRGALVEFYAPWC GHCKKLAPEYERLGASFKKAKSVLIAKVDCDEHKSLCSKYGVSGYPTIQWFPKGSLEPKK YEGQRTAEALAE FLNTEGGTNVKLATIPSSVVVLTPETFDSIVLDETKDVLVEFYAPWCGHCKSLAPTYEKVA SVFKLDEGVVIANLDADKHRDLAEKYGVSGFPTLKFFPKGNKAGEDYDGDRDLVDFVKF INEKSGTSRDTK GQLTSEAGRIASLDVLAKEFLGASGDKRKEVLSSMEEEADKLSGSAARHGKVYVTIAKKI LEKGNEYTEKETKRLDRILEKVGNAYLARCLMKHPLLGQLTVQI
ZmPDIL4-2	GRMZM2G159369_T01	MAFPQISRRALGLLLVIAAAAAIVSPATADEVVALTEADFEKEVGQDRGALVEFYAPWCG HCKKLAPEYEKLGASFKKAKSVLIAKVDCDEHKSVCSKYGVSGYPTIQWFPKGSLEPKKY EGQRSVEALAE FVNSEAGTNVKIAAIPSSVVVLTSETFDSIVLDETKDVLVEFYAPWCGHCKHLAPIYEKLA SVFKQDDGVVIANIDADKHTDLAEKYGVSGFPTLKFFPKGNKAGEDYDGGRDLDDFVKFI NEKCGTSRDPK GHLNQEAGLVPSLNPLVKEFLNAADDKRKEVLSKIEEDVAKLSGSAAKHGKIYVTAAKKI IDKGSDYTKKETERLHRMLEKSISPSKADEFIVKKNILSIFSS
ZmPDIL5-1	GRMZM2G389173_T01	MRPAVVTVLLLVAAAASPAAALYSAGSPVLQLNPNNFKSKVLNSNGVVLVEFFAPWCGH CKQLAPAWEKAAGVLKGVATVAALDADAHQALAQEYGIKGFPTIKVFSPGKPPVDYQG ARDVKPIVEFAL SQVKSLLRDRLSGKASAGSNGKTSGGSSEKSEPSASVELNSRNFDELVVKSKDLWIVEFFA PWCGHCKKLAPEWKKAAKNLKGQVKLGHVDCDAEKSLMSKYKVEGFPTILVFGADKES PFPYQGARVAS AIESFALEQLEANSGPAEVSELTGPDVMEEKCASAAICFVSFLPDILDSKAEGRNKYLELLL SVAEKFKKSPYSFVWTAAGKQANLENQVGVGGYGYPAMVALNVKKGAYAPLRSAFQR DEIIEFVKEAGRG
ZmPDIL6-1	GRMZM2G073628_T01	GKGNLPLNDAPTVVASEPWDGKDGEVIEEDEFSLDELMGDSSSANDEL MDLGAPARRRLPIRLLLVSLTVLVVLTARSSAEVITLTEETFSDKIKEKDTVWFVQFCVPW CKHCKNLGTLWEDLGKVMEGADEIEIGQVDCGVSKPVCSKVDIHSYPTFKVFYEGEEVV KYKASMDYTRTNCSVVGTLRTRTSPAATRSRTKCRSISTCFVR

ZmPDIL7-1	GRMZM2G176443_T02	MAARVLPPPPLPLVLLLLLLPLSARDTVAAGEDFPRDGRVIDLDESNFEAALGVIDFLFVD FYAPWCGHCKRLAPELDEAAPMLAGLSEPIVVAKVNADKYRKLGSKYGVDGFPTLMLFI HGVPIEYTGSRK ADQLVRNLKKFVAPDVSILESDSAIKNFVENAGTSFPMFLGFGVNDSLIAEYGRKYKKRA WFAVAKDFSEDVMVAYEFDKVPALVAIHPKYKEQSLFYGPFEENFLEDFVRQSLLPLVVP INTETIKMLNDD QRKVVLTILEDDSDENSTQLVKILRSAASANRDLVFGYVGIKQWDEFVETFDVSKSSQLPK LLVWDRNEEYELVDGSERLEEGTDQASQISQFLEGYRAGRTTKKKISGPSFMGFLNSLVSL TSLYILIFVIALL FVMVYFAGQDDTPQPRRIHEE
ZmPDIL7-2	GRMZM2G007385_T01	MAMALRRLLLPLLLLVLLGLRPQSCVASGGGGGEPAEFEIPRDGSVLELDESNFEAAVRA AEFLFVDFYAPWCGHCKRLAPQLDEAAAVLAGLSTPVLVAKVNADKYKKLGSKYGVDG FPTLMFFDHGV PSEYTGSRKADVLVENLKKLVAPDVSVLESDSSINGFVQAAGINFPLFIGFGMDESLIVEYG AKYKKKAWFSTAKDFSEDVMVVYDFDKVPALVSVNPKYNEQSVFYGPFEGTFLEDFIRQ SLLPATVPINRE TVKLLKDDGRKVVLTILEDESDESSLQLIKVLRSAANANHDLVFGYVGVKQWEEFTETFD VKVSQLPKIVVWDTKEEYEVVEGSESFIEGDYGSQVSRFLEGYREGRTTKKKVGRGSPTL LGLNAVYILVL LVAVLVVLMYFSAQGEEDHQPRRAHED
ZmPDIL8-1	GRMZM2G067063_T01	MISSSKLKSVDFYRKIPRDLTEASLSGAGLSIVAALAMVFLFGMELSSYLAVNTTTSVIVDR SSDGEFLRIDFNMSFPALSCEFASVDVSDVLGTNRLNITKTVRKYSIDRNLVPTGSEFHPGPI PILNKHGDDVEEDHVDGAFSLSSRNFDSFSHQYPVLVVNFYAPWCYWSNRLKPSWEKTA KIMRERYDPEMDGRILLGKVDCTEEVELCRRNHIQGYPSIRVFRKGSDIKENQGHHDHES YYGERDTESLVAAMETYVANIPKEAHALEDKSNKTVDPAKRPAPMASGCRIEGFVRVKR VPGSVVISARSGSHSFDPSQINVSHYVTQFSFGKRLSPRMLHEFIRLTPYLRGYHDRLAGQS YTVKHGEVNANVTIEHYLQVVKTELVTQRSSKELKVLEEYEYTAHSSLVHSFYVPVVKFH FEPSPMQVLVTEVPKSFSHFITNVCAIIGGVFTVAGILDSIFHNTLRMVKKIELGKNI