

**Supplementary Table 1s.** Phylogenetic analysis of Pectin methylesterase inhibitor gene family gene list

No	Name	Uniprot ID	Amino Acid Sequence
1	CmPMEI1	A0A1S3AXX1	MAKSLSLLLLLLILTISAFNGGASNFIKSKCSAATYPDLCVQSLSSFASITQORNPROLVQOTALAVLSRAQST RSFVWKLTKFSGLKPREERAALKDCMEEVGDVDRLNKSVVEELKRVSGSKKKDFLWHISNVETWVSAAMTDE NTCSDGFAGSALNGRIKSSVRGRIVDVTRVISNALSLINKY AETQS
2	CmPMEI2	A0A5A7T9V3	MANLKISLPLLITLIALHNAATTGSPSTSIFFIESSCKVTRYPALCVOSLSTYANTIROSGROLARTALSVLSKALLA AAFVAKLKGKGGMKGLEYYQAVKDCIENMGDSVDRLSQSVKELGDLRRTAGRDFLWHMNNVQTVWVSAALT DETTCLDGFAGRRLDGQTKAGIRRRITLVAQITSNALALVNRFADENH
3	CmPMEI3	A0A5A7TTZ6	MKPORPLILSLLFAATLHFLRPVFANEDTRNSSNATANCIEFIRTSCGITLYPDVVCYTSLSRYANDIQODPASLTRI AITISLANSRRMAAYVSNLSHAGDYGADRRAASALHDCFTNFDDAVDEIRGSLKOMRQINDVDAPSRFQMSN VQVWMSAALTDQETCTDGFEDVADGPMKEDVCAKAEEKVKKHTSNALALVNSFVEKRIP
4	CmPMEI4	A0A5A7UKZ9	MTVLSLLLLLILSLSLAAHGGGGAVSODLIRSSCLQARYPTLCIRTLSSYAGSVKTPRDLAQTIVSVLSLAQN LSEYLSDSLKASRQORAADVDDCVDQIGDSVEELSNLTVLRLHPCGDDRRKFRLEMGNKATWVSAALTNEE TCLDGFKEVDGVEKLDVKKRRIVKVAKVTSNLFMNLRLDSDGNSGTGKEDVGRGGDNDK
5	CmPMEI5	A0A5D3D1R1	MMRPPSTRASIAALLALISILPWLTHSAKTSYVOEACRVTLHODLCIQSLSPFSSTAKRSPTKWARAGVSVTITE AKKVAALLGRLKNNKRMKGRNRAAVLDCVEVFDAAIDELHRLSLGVLRLSRNFDQSQMGDLTTWVSAALTD EDTCVEGFEGERGKVVCLLRNRVVKVGYTSSNALALVNLKATSGFETALNM
6	CmPMEI6	A0A5D3DJE3	MESQILKSSLTLLFFFILTTFTPSAVASSSSTVRPVKPHIRKACKPTYPRLCETALSLSYASOTKRNOQELCRAAM VSSLKAQAQNTSIIKLSRRKMSAYETEYIGDCIDDLKDSVDELRRASTAIKLSRSKDVDFQLNSIKTWTSAAL TDIITCTDGLSGSGWVKNKVKKEVKNCSINVRQISNALSLINNFYAK
7	CmPMEI7	A0A5A7T3U1	MDOINALKGYGKLTHHNLDEHOIPPPSPKPNKFPNNHNYSLPLRFAAASISALLLTAIISLIVGVYTHNSTPDN KSSNNAAHTSIIICNVTRYPNSCFTSISLNSPPDPPELILNLSLQVSLNELSNISRWVKTLGAEGDGGAAAALK DCQSQIEDAISQVNESVAEMRGGSGEMITLESKIGNIQTWMSAMITNEESCLDGVVEEMDSTSFEEVKRRMKKS IEYVSNLSLAIVANIHVILDKFNMPHL
8	CmPMEI8	A0A5A7UBK3	MKSIAIAVAVFLVISLCOFOILAOTPOTPTTSGGNDLITKCSSTPHVEMCKTILQSSPNSKGADLYGLAQIVMNTA ASNVSNIYESINQLONGTIVDSFLDSCLDCELYQDAIDQIEDSVTALEFKAYNDVNTWVSAAMSDAATCDM GFKEKKQGYQSPIAQMTTFVDQICKIILAINKLLSQGNSN
9	CmPMEI9	A0A5A7TAE5	MENPLAKSILFLLCVPTLJQLANGLDIVOHYCKLAAKTDPYDYKLCVOTLKANPNSEADDFKDLVMISINOAK ANATEIRSEISELMKRTSEKWKGYSLNCLKSCLELYSEAVSDLKALRGLKMEDYETAKTAVSAAMDAPVSC DGYKEKDGESVPLSETNDGFFQLVAISLAFINMC
10	CmPMEI10	A0A5D3E196	MKFFSAILLVLCLCAAQRLDAASQANKEGIEKIEKMCQOTNYKDLCVTSLTSDPNFPADKMGALVALRLA SSNASDISIKVMLNETSNQEPAAVQGLFDCLDEYLDASQQLDDSAIAIIAKAYGDVEKVVHAAVADVRTCE NSFPTKPSVLTNRNEEFIKLCDIALSISRIAEEN
11	CmPMEI11	A0A5D3DQ82	MGMKNFISLIFFAIPLIFFHKNVSLASADOTLIQKTCNTLYYKLCMSSLKSDPSSLTADTKGLAIIMASIGAA NATATSTYLSQLPSTSSAATNANNKTKLLRQCSEKYAFAAEALRESLKDLADETYDYAYMHVSAADYAN VCRDAFKGFPAVSYPAKLRREEGLKRICRVVLGILDLLGW
12	CmPMEI12	A0A5A7TAH1	MKPKFSLSPFMTTPLPCLLLFIMFNIISTIVVADLVOKTCKCETDDPNVNYNFCISSFRAHSGSDSTDLRKLGA ISLSTIQKLNSSLEYVEKLLQNKKEIDSYRRVRLNDCLDVSYDAIVNVEEGKKAYPEKHYDDANIKVSSVMDA ARVCEDFREKEGVSPLTKWNEKDLQLAALALISVNMYP
13	CmPMEI13	A0A5A7TEK0	MSSLSHSILIPCLFLFMLIFSFPITOSSNNNNNTSSLYKTCASSEODPNISDFCITSLKPAATKHRHGDTSLLR LGLMITYLIRHNMSSTRHHIKLQRKKGPDFVKLCLDCELELYSDAIPMVKQARKDYKAGRYADANSKISS VMDDCSTCEEGFEEKEGVVSPLTNRNHNFAELSAIALSINML
14	CmPMEI14	A0A5A7TCY0	MAIPHYFSVFLSIFFFSFLIIQSSKTIKTADLIYKTCCKKISREDPNISFNFLCSTLKLATNHSRCTDVRHLGLLSIG LLYRNVITSTCHHITKLVKNKLLDPFVKSCLDCELELYSDAIPVQAMKDYKSKRYDDVNVVIGSVMDAATT CEDGFKERKGVASPLKRRDENAFELGAVLSIMSILVR
15	CmPMEI15	A0A5A7U1K7	MSFTYTHRYIALAFSFKRVLENFEPISANDIVSRCTETSAAARDPNVRLDFCLRSLAAAPGSDTADLYELGAISIRLI GRNATSTQRYIERLLKNEKKKSSSDSYRPRSDCEELYSDAVETVGEAAAEYGRKRYDEVNVLSSVMDAVT TCEGDFKEMESRVSPLTRNGDVFELAAIALCILDLRP
16	CmPMEI16	A0A5A7SYM0	MGENHLVSFSMVFLFAAVFIGQAHGSSLCDKAAPPALCRSTLKGASDPTSALKNAIKHLIFETTRAKVSSLRIGS LKSLLVYCKQNFDDAIDLETSLAYMQKKDIASLKNLSAAMTDYSTCDDAVIESGEQKASRVLNTDNLLEQL AANCLYLASLLK
17	CmPMEI17	A0A5D3CVX8	MAKKQSVSFPVFLVVATAVVVLFAGQAQGVQDICAQAEYVPLCRSVVKGASDPTVAIKTAIQHLSFETKRAKT ASSILGNKQAIDACTONYNSALDNQKSLYLOIKDLPSLRVMLSGALSFFVSCDVAEVSFTGVVKMAKNV EKTDALQHLAGNCLHIASLLK
18	CmPMEI18	A0A5A7V7V7	MGKNKEIKMVYNSCLFIVSLIGVLLFTINVASSTDVVSTICPKTSNPQFCSSVLKSAGTTDLKGLAVYTLNLAHT NARKSLTLANSLAKTTTNPQLKQRYSSCVESYDEAVGDIENYQKDLALGDFNGVNIIVTSGAMTEIDDCQDKFA QPPKDTSLLLKNGKTLNDICSIILVISNLL
19	CmPMEI19	A0A5A7VHV0	MANNSCLIIVSLVGVLLFTIISNVASSNDVSTICPKTSNPFCSSVLKSAGTTDLKGLAVYTLNLAHTNAHKSLLT LAKLLATTTTNPQLKQRYSSCAESYDETVDIENAQKDLALGDFNAVNIIVTSGAMTEIDDCQDKFAQPPKDT LLKNGKTLNDIYNIILVISNLL
20	AtPMEI 1	Q9LVA4	MAKOYLFVLLSISYLLSLELTAATAASQTGASKKAINFIOSSCKTTTYPALCVHSLSVYANDIOTSPKRLAETAI AVTLSRAQSTKLFVSRTRMKGLKREVEAIKDCVEEMNDTVDRLTKSVQELKLCGSAKDQDQFAYHMSNA QTWVSAALTDENTCSDGFSGRVMGRIKNSVRARIMNVGHETSINALSLINAFAKTY
21	AtPMEI 2	Q9STY5	MAKOIFYTLFLFLLSTAILTASSAPRAAITSKRAINFQASCKATTYPTCVNSLTGYANSIOTSPRRLAETALNV TVTQAQSTKVFVWRLGRFTSLKKREIQAVKDCIEIHDADVRLTMSIHEVKMGCSAKGRDQFWFHMSNAQTW TSAALTNANTCSDGFAGRVMGDRVKNVSRARILNLGRGTSNALALINAFAKKY
22	AtPMEI 3	Q9SB37	MARNFELSLILFVLYLSTAAVIMARNLEEESGDTEFIKASCETTSPDRCFOSLSSYASEIKKOPRKLAEALAV SIARAKSAKTYVSEMTDYKGIKROHEAVADCLLEEMGDTVDRLSNLSKELKHLIEGDSGEDFWFCLSNVRTW TSAALTDDETACMDGFGGKAMAGELKSLIRTHIVSVAEETSNALALINDFASKH
23	AtPMEI 4	Q9STH2	MEPKLTHLCYCLLLFPLLCOSTIAKSSSNPSSSINFIIVSSCRVTRYOTLCVKCLAAFADKIRRNENOLAOTAL AVTLVRVQSTTIYVGKLTAKRIKREYLAVKDCVENLDGLEMALQSMRELKQVGRSGRDRDEFLWRLSNV ETWVSAALTDETTCLDGFDFGKVMGDIVVKS AIRRRVVHVARVTSNALALVNRFAARHKIS

Supplementary Table 1s. Continued

No	Name	Uniprot ID	Amino Acid Sequence
24	AtPMEI 5	Q9LVA3	MGESFRLFNHHHFLTFLLIIIAMLKL VHTTTTTTTTTNTFEVFKSSCFITTYPRLCFSSLSHSLIQTSPKLMHA AALNITLASAKVTSAMMVRLSNSRLKPKVEVSAMRDCVEELGDTLEELRKSIGEMCQLSGSNYEVYISDIQTWV SAALTDVNTCTDGFEGEDMDGKVKVLRGRILVIAHLTSNALALINHFASHIG
25	AtPMEI 6	Q84WE4	MAPTQNLFLVAIAFAVIFTASTVHGRHNGAEDIVHSSCEHASYPSCVRTLSSYSGPTITNRRDLAQA AIAKISLSHAQSAAKKLA VVRDSVGGKKQEKAAALVDCVEMIGDSVDEL SRTLGV LKHLRVSGGS AKEFRWQMSNAQTWASAAALTD DDTCLDGFQGMDDGEIKTEVKQWMTKVARVTSNALYMVNQLDETGRGKPHD VHL
26	AtPMEI 7	F4HXW0	MLTRNKEEINRVKNLKLMGRQLYTTTTLVLYLVTLLFCRTISAVRFPPEOPTTDDLD FIRTSCNTTLY PDPVCYTS LAGYASAVQDNPARLAKLAIGVLSRAKYTAAYLSKLSRRAASA AVHDCVSNVGD AVDOMRGSRLQRLREMN HRRPGDPAFRFQMSNVQTWMSAALDDEETCTDGVTEEMEDGETKTAIC DRVADVKRFTSNALALVNTYANN GA
27	AtPMEI 8	Q9SI74	MNLSQTOILHL SIAILLFITSSSSLSPSSSSPSLSPSSPSSPSSAPSSSLSPSSPPPLSLSPSSPP PPPPSSSPLSSLSPLSPSSPSSPSSAPSSSLSPSSPPPLSLSPSSPPPPPPSSSPLSSLSPL SPSSPSSPSSAPSSSLSPSSPPPLSLSPSSPPPPPPSSSPLSSLSPLSSSSSSTYSNQTNL DYIKTSCNITLYKTICYNLSLSP YASTIRSNPQKLAVIALNLTLSSAKSASKVKNISHGGGLTR LEVVAVADCVEEIGDSVTSLODSIRELDSINYK DSAKFEVMMSDVETVWSAALTND DTC MDGFSLVKTA VKDLVRRHVVEVARLTSNALALINMYSASTQENFS
28	AtPMEI 9	Q9ZNU5	MVTVSQSHHTTFFLFFTFELLIFGSSISAVRLLPRNTTTTNDLDFIRTSCNATLYPDPVCF TSLSGYASAVQD SPARLAKLAIGVLSQA KSTAAFLSKLSRSAAKYSYSGDGHOTASAVIRDCV SNVEDAVDEM RGSRLQRLRDMNGRGGGT AARRSVETFRFQMSNVQTWMSAALDDEETCTD GFEDEMDEGLIKTTVCDRL EEVKRLTSNALALVNTYANN GAP
29	AtPMEI 10	Q9SB38	MLRFVVLSTLMVFINSNFPKTAATPPGTYNHTTYVKTACNSTTYPTMCYNCLSSYSSTIKSDPI KLCCTSLN LNVKSAKNATLVVSNLLOKAKAAKSHEVLSLKDCVDEM KDTIDELKQAVAE MKYVRGGGKTTEEHLKNVKT WVSSALDDEGTCTDGFEEGRVNVETKVKVKAISELKTTSNTL ALLTHYLSY
30	AtPMEI 11	O81309	MAANNKLFVLLSLFPLIIFSATATSSKDYDTKAYVHSWCRTTLYPKLCVRSMSRYVRSRAV QNPRLARFAL KASLYRAKYTKAFLKKEVKNLETTLRPOYYASVHDCLDQIRDSVNLQSLA IAELDRVSRROGKSQGDHLWHIN NLQWTSTAL TDAETCVSOPFGRMSKLLKATIKGKVK NVEETSNALAFIEHYAARYRARRP
31	AtPMEI 12	Q9FHN2	MSOVLVSLTIVVFFASNIQKTSGSASSYSONHKTFVKTACNSTTYPDKCYKLSYSSYSSN KSDPIKLCCTALNL NVKSAKEATSVVSKLLKMSQKSTAGRKGKMLPEALILKDCLEEMK DTIIEKQAITEMKNLQDGGSM AEHITNVRTWVSSALDDEGTCTDGFEEVKVNETK KVKVVEELATTTSNLALITNLRY
32	AtPMEI 13	Q1PFE5	MVTMMRPTLLILLFSTFLPOILTVDPLLPNSGDFIRLACNTTLYPDLCFSTLSSFANSION DSNRLARVAISLTL HNTLHLLSYLQNA YNRDHP TPVLRDCFENLKDVAVDGMRGSMKQ MKELVSASGSI ESFRFQMSNVKTWLSAALTDEYCTDGFKDVHEDDSIKDDVCSR VDDVKKLTSNALALVNRYADESIIN
33	AtPMEI 14	O49297	MKLSLHQPLLFFFLASVLP LILTVHSQSDSD FIRTSCNTTLYPDLCFSSLSFSSSVHNDP ALLARAAISVTLTKT LDLASYLANITTLQPE SNEDGAHHTAAA VFDHCFDNLKDAVEE MKGSMKQREL VSTGLESFRFQMSNVQ TWLSAALDDEETCTDGFKDIHDEPRKDDICAR VDDVKKM TSNALALVNRVCDKAIH
34	AtPMEI 15	Q9LZI3	MKTPMSSSITFALVFLLSLNPTSSLSKRESYVONACSVTRYODLCAKTL LPEASVAKNSP SKWARAGVSAIT DNKDVL RHLLKTRLSITGKRDRIALSDCRELQDSLDLHKS LAVL RTLRASEFQQQMSDLATWLS SSDLTKDCTDGF EKTSTRSSSTVMIRKRVTTSMYLS SSNLALLNKLAANGL
35	AtPMEI 16	Q9LVA5	MAKQYQALFLLFSVYFLFSSVLTATVNPAGTTT KALNFIOSSCKSTTYOSLCVETLSVY ANTIKTSPRHLLDAA ITVSLNQA LFKFISHLRKSOFOILODCAPSTDFSTDCRCSVQAL QEVVNCNSWTDCLFHVKNAEVCAISGES HSVENTCSSPFADPGKISARGRISDAVRKSL HTRFSLRQEIINAKMLFEAFPNKH
36	AtPMEI 17	O22244	MTSSSSSPITFTLLLLL SLLVALNPNPNSLASTGNSINTNDIVTOYSTYVRNACNVTRY NRLCVRTLWPF AIVARNNTSKWARASVAVITTDTKRVLRLLLKTORS AVGESERIAL SDCREL FVDSLNDLYKSLAVLRTLNADEFQRQIS DLATWLSAALTD DDTCLDGF EETSSRTRTRVMVRRKATKCMRLCSNALALLKLA FDFGL
37	AtPMEI 18	Q9FFW0	MKLSOVFYIIFLFLVSOVKS TSDMIDOTCKSCAAKSTIFDYNFCVSSLNSPIALP SPTNLSLALVPMLOALDN ATATASTIQLLISDDDDGFRSACL RDCLELYEDATDRLEE AVRVFITRKELGTVNVMVSAAMESAVTCENGFR ERDDGGGGGGVTTWTSPIG DENHKLFEFGQIALCIFNMLSSSVTSLSF
38	AtPMEI 19	Q9FJR7	MKFLLYLVTFVLSNGLANGQTLIRNSCKKATATSPKFYKYNLCVTSLETNPQAKTAK DLAGLVMAS TKNAVT KATTLKGTVDKIIKGGKNKMTAMPLRDCLQLYTDAIGSL NEALAGVKSRNYPTVKTVLSAAMDPTSTCETG FKERKAPSPVTKENDNLYQ MILIPLAFTNMLK
39	AtPMEI 20	Q9SAC5	MAGRDTFQLRFAA VAASAAYLIFLMAGQVAESRMINICSHTA YPSLCRPLVKRVTS PRKATHRTIOALEAKTK LALAETARFKNGNOAVSTCYETLGD AVYNLASARKSIRK RDVPAMNTYLTA AVSDYGACVDGFIETQOVNAI QNAVVDLRKISSNCLALSTLIR
40	AtPMEI 21	F4JHA1	MKMAGRIFLLFLSVYVTVAIADKAF CVASLTSRPEAATATAPKLGVI ALSIASSNAS DTSFYIAKAKLKOKNLEPA LEDTLDDCKSNYLDVAQLDDSLAALMQNSFIDV DIWLNNTAISDGEACENALNDRAGNDAELARRNTNLLKCKDALLNTILTP
41	AtPMEI 22	Q9LNF2	MAANLRNNAFLSSLMFLLIGSSYAITSEMSTICDKTLNPSFCLKFLN TKFASP NLQALAKTTLDSTOARATOT LKKLQSIIDGGVDPRSKLAYRSCVDEYESAIGN LEEA FEHLASGDGMGMNMKVSAALD GADTCLDDVKRLRS VDSSVVNNSKTIK NLCGIALVISNMLPRN
42	AtPMEI 23	F4I1W9	MKQSAQVFLFCIVLISFVTGNANS GMISDLCKHSDDPNLCLSSITSRPESGEFAGT SNOIEIIAISAASANASATSS YIKQKLSNEDLEPAIEDTLED CQKDYQDAVEQL DDSIAMLADAHTD VDVWLSAAISAIESCGSALGSRAGND AELSQRNEVFLKCK NALMINKMLT
43	CsPMEI 1	A0A0A0L8D7	MAKSLLLLLLLSILTISAFNGGASSFIKSKCSAATYPDL CVQSLSSFSSTI ORNPROLVOTALAVSLSHAQSTR SFVWKLTKFSGLKNRRAALKDCMEVGD TVDRLNKSVEELKRVSGSKKDFQWHISNVETVWSAAMDEN TCSDGFAGSALN GRKSSVRGRIVDVTRVISNALS LINKY AENQS
44	CsPMEI 2	A0A0A0KR60	LHNAATTGSAATSFIESSCKVTRYPALCVQSLSTYANVIROSGRQARTALSVSL SKARLASAFVAKLKG GGGMKGLE YQAVKDCIENNMGDTVDRLSOSVKELGDLRQT AGRDFLWHMNNVQTWVSAALDDETTCLDGFAGRR LDGQIKAEIRRRITLVAQ ITSNALALVNR FADENH
45	CsPMEI 3	A0A0A0LB27	TEFIRSSCSSTTYPRLCFSSLSVHANAIQTSRLLATAALSVLS SVKSTATOILKLS HSHGLPSRDVSALND CLEELSDSVDSLAA SISEMPKLRGTNFDLAMS NVQTWVSAALDDETTCEGSEFGQKT VNGGVKAEVRTKIVNIAQLTS NALSLINRIADLH
46	CsPMEI 4	A0A0A0L8D1	MGISNSKSLILFQILQ LTLIHSAITPQSSTEFIKSSCSSTTYPRLCFSSLSV HANAIQTSRLLATAALS VLSVSKSTATOILKLSHSHGLPSRDVSALDDC LEELSDSVDSLAA SISEMPKLRGTNFDLAMS NVQTWVSAALDDETTCS EGFQGKTVNGGVKGVVRTKIVNIAQLTSNALSLINQIGDLH

Supplementary Table 1s. Continued

No	Name	Uniprot ID	Amino Acid Sequence
47	CsPMEI 5	A0A0A0KP63	MENPLPTLLPLLLLLLIIISDQTOILSVAASSTLPRKSSAGIRTNTEYVRTSCSTTSYPRLCYNSLSVYAGKIKTNPKT LALAALHVNLAARSSAASMRRLAKTRGLRRRDAISAIDCVVEEVGDSVFELORAIRELGRPRGYDFMGLISDIE TWVSSALTDEETCMGEFGGRRVNGVSVKAKVRRHIVRVVAHLTSNSLALINSYASSAAVEEGVLP
48	CsPMEI 6	A0A0A0KPD9	MKPORPLILSLLFAATLFLYLRPVSADETPNSPNATANCMEFIRTSFGITLYPDVVCYTSLSRYANDIQDPAASLT RIAITISLANSRRMAAYVSNLSHVGDNGADRRAASALHDCFTNFDDAVDEIRGSLKQMRQINDVDAPSRFQOM SNVQTFWMSAALTDQETCTDGFEDVADGPMKEDVCAKAEEKVKKHTSNALALVNSFVEKKIP
49	CsPMEI 7	A0A0A0LWR8	AISQDLIHSSCLOASYPTLCIRTLSSYAGAVKTPRDLAQAITSVSLSLAQNLSSEYLSDSLRQASRQORAADVDCV DOIGDSVEELSNLTVLRLHPCGDDRRKFRLEMGNKATWVSAALTNEETCLDGFKEVDGEVKLDVKRRRLKV AKVTSNALFMINRLDVTNNGGGFTAVE
50	CsPMEI 8	A0A0A0LIP3	MKSSYFPLPVKAILLILLINOSNIANSOPINDTOFIKTTCCOSTPYPDLCSSLSDSAATHSSCHLMTVAALTVALT HTRSTSSAIESLAKSSNALTPRDSYVIRDCIEEFGSDSVEELKMAVEELKDNKNSRSETEDIRTWVSAALTDDDTC MDGLVGDAMNGNVKESIKEMVNVVAQLTSIALSLVSLK
51	CsPMEI 9	A0A0A0KAX0	MLRAPSRRASIIALLALISILPWLTHSAKTSYVOEACRVTRHODLCIOQSLSPFSSAAKRSPKWARAGVSVTITEA KKVAGLLGRLKNNKRMKGRNRAAVLDCVEFEAAIDELHRSGLVLRRLSRRNFDAQMGDLTTWVSAALTDE DTCVEGFEEGEKGVTLLLRNRVVKVGYTTSNALALVNKLAASSFETTINM
52	CsPMEI 10	A0A0A0L671	MESQILKSSLTLLIFFFIILTTFTPSAVSSSSSTVRPVOPHIRKACKPTPYPRLCETALSLEYASQTKRNOQELCRAA MVSSLKAAQNAATSIISKLSRRKMSAYEAEVIGDCIDNLDKDSVDELRRASTAIKSLSRKSDVDFQLNSIKTWTSA QTDVITCTDGLSGSGGWKVKMLKKEVKNCINVVROQISNALFLINNFNYK
53	CsPMEI 11	A0A0A0LVF4	LIVGVYIHNSTPDNKSSNNAAHTISVCNVTRYPNSCFTSIFSLNSSPODPDELINLSLOVSLNELSNMSRWLKS VGGEGDGGAAAALKDQSOQIEDAISQVNDVSAEMRGGSGEKLTESKIGNIQTWSSAMTNEESCLEGVEEM DATSFEEVKRRMKKSIEYVNSLAIVANIHVILDKFNMPHL
54	CsPMEI 12	A0A0A0M1H8	MKSIATAVAVFLVSLCQFOILAOTPOTPTTSGGNDLISKTSSTSYSEMCKTILQSSPNSKGADLYGLAQIVMNV AADNVSSIYENINQLONGTSVDFLSDCLTDCLESFQDAIDQIEDSVTALEFKAYNDVKTWISAAMSVDATCDS GFKEKQGYQSPIAQMTSVDFDQICSIIISINQLLSQGNIN
55	CsPMEI 13	A0A0A0KAX0	DSWGIDEQQADEKEKQGPSVCVKVFEATIDELHRSYGLVLRRLSRRNFDAQMGDLTTWVNTALTNEDTCIEGFE GERGKVVNLLPLVLKLR
56	CsPMEI 14	A0A0A0LHE9	YGLDIVQHSCKLAAKTDPPYDYKLCVQTLKASPNSKDAEFKDLVVISINQSKANATEIGSEISELMKRRSEKWG QYSLNCLKSCLELYSEAVSDLEKALKGLKMEDYETAKTGVSAAAMDAPVSCEDGYKEKDGDEVSPLEINDGFF QLVAISLAFINMC
57	CsPMEI 15	A0A0A0KY96	ILLVLCCLMAPORLDAAGAAQEEGLGMIQKMAQOTNYKDLCTITSLTSDPNFPADKMGALVALRLASSNASD ISESIKVMLENETSQNNEPTVQOALFDCLDEYLEASQQLDDSAIAIAKAYGDVQEWVAVAVTNVVRTCESSFPTK PSVLTTPRNEEFIKLCDIALSITKIAETN
58	CsPMEI 16	A0A0A0KJ03	MGMKNFSISLIFFAIPLIFFHKNNGVSLASADOTLIOKTCNTLYYKLCMSSLKSDPASLTADTKGLAVIMASIG AANATATASYLSSQLPTSSSGAGANNKTKLLRQCSEKYAFAAEALRESLKDLDGETFDYAYMHVSAADYA NVCRDFAKGFPAVSYPTKLRREEGLKRICRVVLGILDLLGW
59	CsPMEI 17	A0A0A0K9X7	MKPKFSPFMTTPLPSLLLFIIFNISTTFVVDLVDKACKKCEIDDPNINYNFCTSSFRAHSGSDSDTLRKLGAISLS LIQRNLSSEFEYVEKLLQNKIEIDSKYKRVRLNDCLDVYSDAIVTVEEGKAYKEKHYYDANIKVSAVMDSARVC EDGFEKEGVSSPLTKWNKDMFQLAAIALSIINMHP
60	CsPMEI 18	A0A0A0LUJ3	MMIMISTSLFSFTIVFILIFSSFSQTYSNPHNIIQETCKKSAASTPNLYTKFCVTSLESDDRYSRYANLHKLGLISMD LLRHNVSTRREIKKLLRNKKMEEFIKGCLNDCVLEYSDAVPTLKEAKREYKRNRYKDNANIKVSSIMEAPTTC NGFKEKEGIISPLTKNNSDVFLQALATLTIINMHLHDIQ
61	CsPMEI 19	A0A0A0KBR8	MFFSNFPITQSSNNNTSLLYKTKCASSEQDPNISFNFCVTSLKPAATKHRHGDTSLRRLGLITTYLIRHNMSNT RHHIKKYLHKNKGPRDPFVKLCLTDCLELYSDAIPVTKQARKDYKAGRYADANLKISSVMDDCSTCEEFGKEK DGVISPLTNRNHNFAFELSAIALSIINMLC
62	CsPMEI 20	A0A0A0K951	DLIYKTKCKISREDPNVSNFNLASLKLATNHSRCTDVRHLGLFSIGFLCRNVTSTYHHITKLVNRKLDLPFVKL CLDDCLELYTDAIPTVKQAMKDYKSKRYDDANVAISSVMDAATTCEGDFKERKGVASPLKRRDGDFAFELGAI ALSIMSLLG
63	CsPMEI 21	A0A0A0L7T4	MSITYMHRFIALALSFFVLFNLSISANDTLSRACELSAASDPNVRLDFCLOSLAAAPGSDTADLYELGALSILKI AWNATSRRYIERLLKNEKSPDPYVRPRLSDCEELYDAIKAVGDAAFYGRNRYEEVNVKLSVMDAVTTC EDGFKEMEGRVSPLTKRNGDVFEFTAIALSILNLRP
64	CsPMEI 22	A0A0A0KQ52	MGEKHLVSFSMVFLVAVFISQAQGSALCDEAAFPALCRSTVKGASDPTSALKITIEHLIFETKRAKDSLSLIGSL KSLGVCKQNFDDAVDDLQSSLAYMQKDDIPSLKINLSAALTFYSTCDDAVVESGDQKKASTVLSNDLLLQHLA ANCLHLSTLLK
65	CsPMEI 23	A0A0A0KQ68	MAKKQLVSFSPVFLVVA AAAAVVVLVFAQQAQGVVICVHSEYIPLCRSVVKGASDPTAAIKTAIGHLLFETKRA KTSSVVLGNEQAISACNQNYDLALDNLQKSLEYLQSKDLASLRVMLSGALSSVVSCTDAVAEVSSFGVVKMA KNVEQTDITLQHLAGNCLHIASLLK
66	CsPMEI 24	A0A0A0KCV8	MANNSSLIISLVGVSFTIISNVASSNDVSTICPKTSPQFCSSVLKSAGTTNLKGLAVYTLNLRARTNAEKSLT LANSLAKTATNPQLKQRYSSCAESYDEAIGDIENAQKDLALGDFTGVNIVTSGAMTNIIGDCQD
67	CsPMEI 25	A0A0A0KEW6	VVPSRATTPSNDVASSICPKTRNPPFCVDVVKLSAGSTDLKVLATYTLNLANENALKSTNLAKSLAAMTTNPPL KNQYLSCEYESYEEATSDIENAKSNLASGDFNGVNIATSGVMTSVSDCLDSFKQLRIDPSLLKDGKTLNDVCSII VISNLLP
68	CsPMEI 26	A0A0A0KHY0	TGSPNVLTITTCIPKTRNSTFCKTVLKPVGKSDAALLKVANYTLFAHTTTVEGLHHAORLATEATDPLLKORYS ECSRRFDVFTKGLLEEIAELAKGGYIPLSHATGAAVVEADRCVNMFKKPPPEPSKLEKAKNIGDICDIAVSVSN ILTEDIY
69	CsPMEI 27	A0A0A0KCV8	VTSSNNVSTICLKTSNSPFCLSLKSACTTNLKLIVYTLNLAHTNARNFTLANSLAKKTTIIPQLKQLYSSCV ESYDEDFARGDFNGVNIIVTSGDMTINIDEYQDKFAQPSKDTSLLLKNDKTLKNICTIILVISTPL
70	CsPMEI 28	A0A0A0LK13	MNCLNLTSPFAPALLAAFLSVTFPSHGIPHENLVITCSKTSNPSLCEKILNNSRTVSAANLPKLSLICSNLAKKQA DQNLDTFYKLSKNESDPEEKKSFEHCVKYHYHEIQSNIQKAYQFSQKIFRENVMNKLMILCCDISISVNVQCAA NGHHSVNV