

**Online Supporting Information S1.** The benchmark dataset  $\mathcal{S}^{\text{Bench}}$  includes 504 proteins, classified into 252 secretory proteins of malaria parasite and 252 non-secretory proteins. See the text of the paper for further explanation.

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(1)  $\mathcal{S}^+$ : 252 secretory proteins of malaria parasite

>PFE0065w, 337 bases, D1F677AA checksum.

MCSAARAFDFFTDLADEPTQLQDAVPETTEKLAEVVSDAATNVTDAVSDTASGIGSLV  
GEAASSLGNLVGEAASGIGNIVGGAASGIGNIVGGAASGIGSLVGDAAASGLGNLVGDA  
AEALATTELKDVIPENTESTTDLVPSEVSPPPVDDYLDGDFSSFFREFLESTPCWQRRM  
AQEALLNEYEVESPAESMSPILRVQFFADFAKQAVHVAKQNYLYVVIFFVFINILLF  
INFYNLKGKRGYYLAKKQKKEQMLEQNPEQNPEQNAQQNAQQNAQQNAQQNAQQNAQQ  
NAQQNTQQNTQQKTQQNPQQNAQQNTQQNTQQQSTTKSTTKTVARET

>PF14\_0142|serine/threonine, 304 bases, DD282E30 checksum.

MALEIDIDNVISKLIEVRGTRPGKNVNLTENEIKILCLSSREIFLNQPILLELEAPIK  
ICGDIHGQFYDLLRLEFYGGFPDANYLFLGDYVDRGKQSLETICLLLAYKIKYPENF  
FLLRGNHECASINRIYGFYDECKRRYSVKLWKTFFIDCFNCLPVAAIIDEKIFCMHGGL  
SPELNNMEQIRKITRPTDVPDNGLLCDLLWSDPEKEINGWGENDRGVSFTFGQDVVHN  
FLRKHELDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFDNAGAMMSVDETLMCS  
FQILKPVEKKKAAN

>PF11\_0014, 218 bases, B689E139 checksum.

MFKKNNNKIKNGVENGTYSYHNGGIQFRMLAQNNNTNKKSNNGNTLTNILLKDKGEGK  
GKKKNPDDQISDLVNLVDNMNITQEKKEIKNLTLYMNSDDIKEKNKSINELKKYSN  
NEECKEHMDNYLMYLRMQNDIKCLKRKNFNNIWINININFFVIIIMIACVVVGLIEAS  
SISYPLCIFPVFMYMLVRFPPDMKMGFKKIKETCTNFFQKKKK

>PFI1820w, 1315 bases, BE84B9BB checksum.

MAPKNGSRNGKLLSLRDVLENIGSGIKDKRKNQSKYTDKLGILTKAKFVDGLSSRYG  
YVRDSGDGISCNLSHKFHTNITIEAARDPCYGREQNRFDENVESYCNNDKIRGSGKIFD  
GRVCVPPRRQHICDHNLEYLNNNNNTDDTDDLLGNVLTAKYEGQSIVNNHPHKETS  
CTALARSFADIGDIVRGIDMFKPNQDEVWNGLRVSVFKKIHDNLSSEVKNAYPDDGSG  
NYFKLREDWWTANRDQVWKAMTCVAPENAYFRKTEADGIGISSLILPYSKCGRDTDP  
VVDYIPQRLRWMSWSEYFCNVLNKEIDEMNNQCKDCEMSRRCNDDSEGGKCKKCKEQ  
CQIFKELVSKWKNQFDKQSMKYMELYNKASTNITKQNSSAPERGYRRNHRRRGYDDDT  
NVQLFLKKVIENNECKVESLGKYLDKTSHCGNYNFNYDNTPGSNRSNAFEITPEKFKK  
ACKCKIPNPLEKCPNEENKNVCTRFDKVYSCTSLSFKNLSEWNNNSGVKNKENDNNGV  
LVPPRRRNLCINLFSKKDYKMKDENDFKEDLLNAAFSSQGKLLGKKYSNYSNEAYEAMK  
FSYADYSDIVKGTDMMNDLKKLNKELNTLLKETEKGDISVDRKTWDDNKNVWNAML  
CGYKTENENQQLNSSWCNVPDDDYIDQFLRWLTEWAQQYCKEKLKAHIINTKCKDIV  
EGRKHKSMVDITDVECKRLFIDYEEWFRYRYNQWGLSEKYIKIKKSKNSGVNIPSEE  
CAASYVTKHCNGCICNLRDMEDIHKNINNQNELMKEMINI IKFDTDQYRTQLQNISNS  
MEINPKSVKTAVDTTKDIVSYGLAGTMGVAAIGLQAGDFLGKKIQDLYNEFMKPVEKK  
LDTSSKNLNIYEDPNIMVPAGIGVALTLGLLLFKMRRKAKRQVDMIRILQMSQNEYGI  
PTTKSPNKYVPYGSQRYKGYLYVEGDTDEEKYMFMSDTTDTISSESEYEEMDINDI  
YVPGSPKYKTLIEVVLEPSKRDTQNDIPSDNTPSYKLTDEEWNQLKDDFISQYLPNTE  
PNNNYRSGNSPTNTNNTTSHDNMGEKPFIMSIHDRNLYTGEEISYNINMSTNTMDDP  
KYVSNVYSGIDLINDSLNSGNQPIDIYDEVLKRKENELFGTNHVQKQTSIHSVAKNTY  
SDDAITNKINLFHKWLDHRDMCEKWHHERLAKLKEKWENDNDGGNVPSGNHVLNT  
DVSIEIDMDNPKPINQFSNMDINVDTPMDNMEDDIYDVNDNDDNDQPSVYDIPMD  
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>PFI1830c, 2264 bases, C8CE2A8E checksum.

MALGRPGGEDKYKNAKDAKHL LDSIGEEVYKEIVEKDDAEKYKEALKGKLSQASIWRE  
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 GSNKGNEGACASFRRLNLCKKNMEKIPTSSTKHDL LADVCMAANYEAQSLIRDPKPKYK  
 LKYSDSLCTELARSFADIGDIVRGRDLYLGNPQEKGRDEL DKKLKDIFKQIHDDVT  
 TNGKNKDALKTRYND DAKGGHFYQLREDWWIANRHTVWEAITCDDDDKLGGSYFRAT  
 CGSGN NATLARDKCTCNGDVPT YFDYVPQYLRWFEEWAEDFCRKKKKYVDIVKTYCR  
 GKDKNSEERYCSRNGFDCEKTKRAIGKLRYGKQCISCLYACNPYVEWIDNQRKQFLKQ  
 KQKYIN VINGAPVSRRQKR DARNENYDGYESKFYKILKIDYQNVEDFLKKLSNEEICT  
 KVQDTEGGKINFENVNSGASGTNVESQGT FYRSKYCQPCPHCGVKMKDGKWETKGEDD  
 KCN IKLYRPKGGKDGTP IKILKSGEKQKEIETK LKAFCKTQNGGGGSDDCGGNSDSSL  
 CEPWQCYQPEELTKDDQGEEDVDDLEYENEVINAGGLC ILKKKKEKKT DNDPDEIQKT  
 YNDFNFVVAHMLKDSIYWKKLQRCLQNGNR IKCGNQCCNNDCECFQKWKQKKDEW  
 DRIKQQFRKQDFRKQGENIAGGMLGKEIESPDFVLQEV LKLEFYKEKSEGDGSAQDTEN  
 SLDEEEAEELKYIREIIEKKNQEPAGANGQKTIMDKLIDYEKDEAKCKDCQETQPQP  
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 VVTTKETTVEDPKVCDIVKTAL ENRENLDACNLKYVKGKNYGWKCVPTTSGGDNNT  
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 QEDLLKWF IETAAIETFFLWHRYKKIKEKEIEEK RKRENGELPFLARSTSVEMKALSG  
 AGGGPELTGSGSDDPNDPNNIYSGKIPPPFLRQMFYTLADYKDILFGDKGEKNGYS DI  
 INGDKEMAQKEQNIKTAIESVFKPSGSSPPAPGKKNPVQTPKDWWTKYGPSIWEGMVC  
 ALTYKENSSGGEGKTIEKVKTADDKDLFDTLKGKYS DYEKVKLEDTSGAKPKDPKASP  
 SGEKTTLVDFISRPPYFRYLEEWGQNFCKKRTEMLGKIKEECRGDRGGHQYCSGDGHD  
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 ADDKNIYEKLDYTSANFLEAL KHCKDGQTGGEKKSNDQDNKINFNDPKTTFGPLEY  
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 IKEYLKNSEKSFKDSYLFKSLRTEEWECRFNKEKKMDVCKLNKFDANIDLNEYTTFKV  
 LIVYWLEDFLYSYYILKKKIELCTQNK EQTCSEGNSKNGCVCVKKWVEKKKKEWDQIK  
 KHFNREQKEGDDMKSSVKMFLEDLQHLTELNKIMKPCTEL YHFLKSLGCTETDSSE  
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 CKNVVDTKKENDETGETCTSED TITKETVETDSTDGPKEEERIAPSAGDDGATRGPQ  
 EPSPKADSGDDNPETPQPKPPSNVFDNPHVK TALMSSTIMWSIGIGFAAFTYFYLLKK  
 TKSTIDLLRVINIPKSDYDIPTKLSPNRYIPYTS GKYRGKRYIYLEGDSGTD SGYTDH  
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 ASGNNTTASDTQNDIQNDGIPSSKITDNEWNTLKHDFI SNMLQSEQPNDIPNDYTSGT  
 IPTNTNITTTSRHNV DNTNTTMSRDNMEEKPFITSIHDRDLYTGEEYNYDMSTNSGN  
 NDLYNGKNLYSGQNNVYSGIDPTS DNRGLTSGKHDSYSGIDLINDALSGNQPIDIYD  
 ELLKRKENELFGTNHTKNTSTNSVAKNTNSDPIHNQLEL FHKWLDHRHRMCEK WENH  
 HERLAKLKEEWENETHSGNTHTS DSNKTLNTDVS IQIHMDNPKPINQFTNMDTILEDL  
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 DI

>PF10\_0001, 2241 bases, 319C507C checksum.

MAAQSSGGGGGCGEEDKDAKYMFDRI GKEVHDEVKNAANVFKDY LKGNLTISTIFGEE  
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 KSAGACAPYRRLSLCNKNFPNMNSKDSLKAKNDLLVDVCYAAKYEAE SLIPYHDQYKL  
 TYGDSQICTVLARSFADIGDIVRGKDLFLGHNRK KLEERLEQMFKNITHSNAAKLS  
 VLSSKEIREYWALNRDQVWKALTCDEENKLG NAYFHATCSERNGGCSQAHEKCRCP  
 MTS DGKPNQVPT YFDYVPQYLRWFEEWAEDFCRKKKIYVDIVK KYCRGERDGEKYCS  
 LNGCDCTKTVRARGKLR YGNRCTDCLFACHRYENWIDNQRKQFLKQRNKYTEEINGTS  
 TSSRTRRSARGGSDHKGYEKI FYEKLEGEYRTVDGFLELLNKEKACQEVKDSEGGKIN  
 FSEKHSNGSNDETGT FYRSEYCQPCPYCGVRKTKGNQWENKSKNDQCNIKLYRPNPG  
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KQLTTDQGQEDDDDEDYDKDVRTGGGLCILEKKKEEGEAKSQNEPDEIQKTYNDFFFYYW  
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 KQAGVAIGLDAFVALRGRCTEGGADSONKTTIDKLLDEEAKEAKDCQSKHKDPCPKPQ  
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 DGQTGGKKNKTHFENPETTFGPLDYCKTCPPNKVSCNVIRGRSGGRNGCNVKDNEDKW  
 KEVFDGISGNGGKSSTIEVEMIDRRGPYMKKEYMKNPFPKTSRLFKGIRKEQWECK  
 VTNDDMHICKLDQFKENINLNPYTTFKVLLHYWLEDFLYGYYISKKKIEKCTQKEKNA  
 CDEETKKNVCVKTWVEQKKKEWKEIKKHFKNREQKYGQGNDIKSKVKMFLETLIPLM  
 DLVNNKGKHESLDAFLKS YECKCAESSGKKGKKNIVLCLLDMLEKKATPCLSSTSD  
 SSETPCENTPTTLDDDDPLEEENPVIHPQICGDIPTTKETVDEADACKRAEEPKEPAP  
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 SGYTDHYSITSSSESEYEEFDINDIYVPGSPKYKTLIEVVLEPSGNNTTASGNNTTA  
 SGNNTTASGNNTTASGNNTTASDTQNDIQNDGIPSSKITDNEWNTLKDEFISQYLQSE  
 QPKDVPNDYKSGNSSTNTNITTTSRDNMEEKPFIMS IHDRDLYSGEEYSYNVNMSTNS  
 MDDPKYVSNNVYSGIDLINDSLNSNNVDIYDEVLKRKENELFGTNHVKQTSIHSVAKL  
 TNSDPIHNQLELFWLDRHRDMCEKWNNKEEVLDKLKEEWENDTSTSGNTHPSDSNK  
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>PF10\_0406, 2215 bases, 274CBE87 checksum.

MVRTLDPPEELRGIEDTTAKHALDKIGEKIYEKAKKNAEQYRSQLHGRLSDARFEKAP  
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 CAPYRRLNLCVRNLENISNYGKINNDTLLADVCLAALHEGAAISSDHGKYQETNNDVN  
 ANICTMLARSFADIGDIIRGKDLYRGVNGNDKLEKNLKKIFGIIYEGLTKANGKKGQK  
 PAKDHYGDDENYYKLREDWNNNRLMVWYAITCGAPKEAQYFRKTCGSGERTKDNCR  
 AIHGVPTYFDYVPQYLRWFEEWAEFCRLRKHKLQNAIKNCRGENNEKYCDLNGYDCE  
 KTIIRGKKKLFEGADCKCTVTCDFVFWIKNQKQEFQKQKNKYAEEIKKAKADEETSS  
 RNINNIYEKDFYERLTKTHYGSVNEFLKKNLEERICKDEPKVKEEKADAVDFTKDETNG  
 TFYRTTYCEACPWCGAEKVNGQNGKGGKWEPKNEACSQEEERIFDEQNITEIPVLTPE  
 EGQSGILKKYSKFCNGATGEKSKNGNQIETWKCYDENENKKGNGAINFCVLQNDK  
 IGKKEEKSMHYHPFFWKWVTEMLIDSMYWRKELKSCINNKRGKCKNKKCNNDCKCYES  
 WVQQKENEWKLILQHFKKQGGFSIFGNDYNYALKALLDVKEILTNIKDTYGNVKELEG  
 INNMLEKENENNEQEASGGNNSQKNTIDLMIHQKEAQNCENNPDKCENTPGVRS  
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 TSGSGVTATGGGSGEPKGRHRREANPAKASDSNQGAI CVPPRRRRLYIQKLHDWATAVS  
 PQASGDKATQAAEPQASDKAAQVTEASASSSSSESNVQTTTTPASTSSPSNSRDVDLVK  
 AFVESAAVETFFLWDRYKKENTKRQGGGAGGLGGVPGVELPELPVSNSVEKTPQTQLA  
 SGIPTPFLRQMFYTLGDYRDILVRGGNTSDSGNTNGSNNNNIVLLASENKQEMENIQ  
 EQLKVFFSNSGNQSSTVGRNPSQSRVTPASLWGDFAQYIWNGMICALTYEEKTSGSDD  
 KGVKIEQNEGLKEALLEDKTNEPKKPQYQYKTVLKEENSQTQPITPGSSSPSGGDI

NNPKLTQFVERPPYFRYLHEWGQNFCKKRKGMLENIKKECMKDSNSGSTGKKVQKCS  
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 GFYDLSICISSGIFKGIKDIWECGNVCGYNVCKPKNVNGETFEGQANGKNQIIFIRA  
 LFKIWLEYFLKDYNKINAKISYCKENGGTNICIKNCADKWIKLKEEWGKIKEHYLEK  
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 MYMYVWKKTKSTIDLRLVINIPKSDYDIPTKRSPNRYIPYTSWKYRGKRYIYLEGDSG  
 TDSGYTDHYSBITSSSESEYEELDINDIYVPGSPKYKTLIEVVLEPSGNNTTASDTPS  
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 SGKNKIDIYDEVLKRKENELFGTNHVKQTSIHSVAKLTNSDPIHNQLELFHKWLDHRH  
 DMCEKWHNHHERLAKLKEEWENETHSGNIHPSDSNKTNTDVSIIQIHMDNPKPINQFT  
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 EKYPADVWDI

>PF11\_0007, 2182 bases, 8B10CD8D checksum.

MEPHGGSGGGGDVIDHQSAKHLSDSIGKIVHDQVEKEAADYRSSLQGRKDATYSKKP  
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APKYKTLIEVVLEPSKRDI PSDDIPNNDTPSSKITDNEWNTLKHDFISNMLQNTQNT  
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>PF11\_0008, 2994 bases, 7EBE2595 checksum.

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 RGSSEVCIALARSFADIGDILRGKDMYVGYDEKEKNRRKQLENKLDIFDNIYKDLTK  
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 TKSFTNPKCGHGDNEVLTNLDYVPPQFLRWFTWAEFCRIRKIKLGKVKNECRGETSG  
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 KYFIQDFNNVKDKINRCTKFEKGDNTCIKGCKHKCECVEKWIKI KEAEWKKINQHYN  
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 KTLGDKTSKSYAEGCKWKYGMPLGLGWLNCNKEGEGEKGEDGLCIPRRKRLYVKDLE  
 TFSDHTTVGLREAFIKCAAVETFFAWHEFTKEKEREYKEEKQRNGELGFIDENDQIPK  
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 SSGKTPTAKKTPKEWWEKNAKDIWEGMLCALS YDTKTKIKNEELRKKLIDPKNSNYM  
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>PFL0935c, 2256 bases, D24E0D92 checksum.

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>PFL1950w, 2646 bases, 66BA7C93 checksum.

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>PFL1955w, 2287 bases, 354FD5D3 checksum.

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>PFL1960w, 2359 bases, F2654D48 checksum.

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>PFL2665c, 2268 bases, 264CB658 checksum.

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>PF13\_0003, 3346 bases, 23006AE1 checksum.

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 EANRDQVWKAMTCPTKNGNIQCGATPHDDYIPQRLRWMVEWAEWFCQEQSRLYEELLR  
 DCGSCTTGKCNNDKCAKCDKQCQEYKTKIQPWADQWNEISNKYQILYWQAKIAAINGG  
 TEKSTTTKDDKDNVIDFLQKLHEANYGTRGPPPEAHPDRRPRRAATSKSDVYETTAG  
 YIHQEARTRECLGQNVFCNNNGNNEYAFSLTPHEYKHACKCNENKASSPEELGRSDSF  
 DDHQTPRPEEDEVHSSEEGEEDESEDEEKEEEVEEVHDGADEKAGAVSQPEASPTTKD  
 VVKPPCDIVKELFSNVDTLQKACSTKYGPGKNYGWRCIPTKTSNDVTGEDGQGSRRVV  
 RSTPESGSNSDKNGATCIPRRRRRLYVVGKLEQWANKHNTETSVSQGEATEARGSEAPA  
 PGGKESSSGKETPSDKLRTAFIESAAVETFFLWDRYKKEWLAQKKAELQNGGLDLYS  
 SGDGDPDNPQNKLLNGVIPPDFLRLMFYTLGDYRDILVHGGNTSDSGNTNGSNNNNIV  
 LEASGNKEDMQKIQEKIEQILPKNGGTPLVPKSSAQTPDKWWNEHAESIWKMICALT  
 YTEKNPDT SARGDENKIEKDDEVYEKFFGSTADKHGTASTPTGTYKTQYDYEKVKLED  
 TSGAKTPSASSDTPLLSDFVLRPPYFRYLEEWGQNFCKERKKRLKQIKEECMDGSDKK  
 YSGDGEQCDRRDTSNEVSADLEGRSCGNSCRFYKWKIKRKRKEYDKQANAYSKQKTKY  
 EEGSKGAGLNDHNKEFCVKLGTCTDAAAFLNRLKNGPCKKDNENGGNDINFGNTEETF  
 RPAENCKPCSSFKINCRNGNCRSGDGDTEKCKNGGTITGNTMTGCTCTEDVMHVSD  
 KNANEFEGDGLDEACENAGIFTGIRKDEWKCRKVCGLHICKQEKNGAINDQQIILVR  
 ALLKRWVEYFLEDYKKIKKKLPCIEENGNGSTCINGCNKKNRVGEWIKLKKDEWTKI  
 KNHYLEKNKEGDKNVTSLVTNVLETTLVTQIAAANDKREQTSLDKLTSLGCNCPENSR  
 KNDGNENDAIDCMLNKLETKIHECKTQHENSVENSDQHPNCGGNPPPDEEDLLLEE  
 NPVEQPGFCPTPQQEPEPDDKCGKLEEKKDEKKEQPEQPAEEDGGAIVPSGPPGSEPE  
 ADKGPVKPAEIPKPQEPDLSPAVIPLSVTSTLAWSVGIGFAAFTYFYLLKKTSSV  
 GNLFQILQIPKSDYDIPTKLSPNRYIPYTSYGKRGKRYIYLEGDSGTDSGYTDHYSDI  
 TSSESEYEEMDINDIYVPGSPKYKTLIEVLEPSGNNTTASGNNTTASGNNTTASGKN  
 TPSDTQNDIQNDGIPSSKITDNEWNQLKDEFISQYLQSEPNTEPNMLGYNDNNTHTPT  
 TSHHNVEEKPFIMSIHDRNLFSGEEYNYDMFNSGNNPINISDSTNSMDSLTSNNHSPY  
 NDKNDLYSGIDLINDALSGNHIDIYDEMLKRKENELFGTKHHTKHTNTYNVAKPARDD  
 PITNQINLHFHWLDRHRDMCEKWKNNHERLPKLELWENETHSGDINSGIPSGNHVLN  
 TDVSIQIDMDNPKTKNEITNMDTNPDKSTMDTILDDLEKYNEPYYYDFYEDDIIYHDV  
 DVEKSSMDDIYVDHNNVTNNNMDVPTKMHIEMNIVNNKKEIFEEYPISDIWN  
 >PFC1120c, 2169 bases, 2B420EDA checksum.

MGRPKRAPAAKEPDYSSAKDAKELLDMIGQTVHSKVHREDANYRGKLYGLLTQAQFSN  
 KERVHINNPCLLDYNVDNVTSNVIDPCEHKSVERFSEVSGGECDEKKIKSNGGACA  
 PFRRLHVCDRNLEQIKPHTITATHNLLVDVCYAAQFEGKISGYYPRYQTKYKDSGST  
 ICTVLARSFADIGDIIRGKDLYEGYDQKDKQKVKLENKLDIFKNIYNELTSTNGKK  
 GKKQALQARYQDDGSGNYQLREDWWDANRAKVWYAITCGAGTSDKYFRKTCSDNTSD  
 TNEKRCVSTDPPTYFDYVPQYLRWFEEWTEEFCKRKKKKLEDVIKKCRYDENNERKY  
 CSRNGFDCKDIRAQEKLVKGYDCHKCSVACDDFEPWIKNQKQEFQKQKGYTKEMQK  
 YANGTTTKETSNPINNLYADDFYKQLQEHYPSVDEFLEKLNEQQICKDEPKVKEETI  
 SRVDFKNVDAFSYKEYCDTCPWCGTEKKQDGTLYRYKEDVECRNQPTTPLDNTKSTDIO  
 LSFTDKGNPKILEKFKNLCEENNEKTINWKCHYKEKNVYKDDSDKDYCVLQDGNQNIK  
 DQTIMSFESFFWSVSRMLNDSIKWRNQHSKCINNKKETKCI EGCKKTCECFEKWVGQ  
 KKTEWRKIKHHFDQQENLKGDRDNITLKYLDLIFKEKIKEAYGDERESKELEKLNN

IEGSQQAGDTEHSEFAVDVLLKHEEEIAENC IKYNPEDTCPTSDTGSRRASDHHDPPP  
 VIPRNDFEDEKDKQPEFKDPGRESEDDDDDEDELPPPEDEAKEQEEEEK GAGEDAASE  
 AEASGPKVEVEGKPPCDIVQTLFESTKNLSDACGLKYGPGGKEKFPNWKCISSGSDTG  
 STTKQNDSEGSEGGHRSKRHTESDSTTTSSGSVCVPPRRRKLYVGELTKWAEEARKS  
 STSPQPGESGVANASASSTSSPTDATQLLRDAFIQSAAIETFFLWHKYKAENTRDNKS  
 PLGNGGVAQFFGSYSGSESEEKTPQQWLQSGTIPTDFLRQMFYTLGDYRDL CVGVKED  
 VINALKASGDNPTNKLTIQQISEKIKNVIEKSGDTPSRTPPGQQPSDNDPKSWWKLHA  
 PYIWNMIYALTYDTNTASGEKKIEKDDAVYKKLWDEANNKPKKDNQQDYTYEKVEI  
 KEEDSGQKASTASQTPSPRASGENKPTTLDSEFVKRPTYFRYLEEWGETFCRERKKRLE  
 KIKVDCEVEENTGARGGTTKQKYSGDGEECSKIVENKDKIFKDLEKPCATPCGLYKR  
 WIRRRKDEYNKQKSAYNEQKTKYENGNNKGGGNGVCGLQENAADFLKKLGPCSKTY  
 NENGVGKTDFDDDKTFKHTKHCDPCPKFNVNCKNCNSSGGGKVECNRNSGTTTITA  
 SDIKNGGDSTEINMLVSDKFTTKFEGDGLKACKNANIFKSIRKDVWKC VNICGV DVCG  
 LKKGDNNGELDDKQIILVRALIKRWLEYFLEDYNKIKKKLKSCTEKGEGSPICEKVD  
 TWITEKRKEWKT IKERYVDKYTKENDGSNDLTTFLQQGPFYSLVEEAKKVVKCKDEQE  
 KLWGCTGNTTGHAQDKCENGDFITNLISKLQEKISECTSQSSGSDCTLSTENPSTTLD  
 DEEPLLEVDQNPEDAQKMPIKICGDVIPKEEAKEEGGCTPDIKKEEEKKEEKKKPEQT  
 AEKPAAEKAKEEKPAQDEAGPPADPLPAREPFDPPTILQTTIPFGVALALGSI AFLF  
 LKKKTKSPVDLFSVINIPKSDYDIPTKLSPNRYIPYTSKRYGKRYIYLEGDSGTD SG  
 YTDHYS DITSSSESEYEELDINDIYAPRAPKYKTLIEVVLEPSGNNTTASGNNTTASG  
 NNTTASGKNTPSDTQNDIQNDDIPSSKITDNEWNTLKHDFISQYLQSEQPN DVPNDYS  
 SGDIPLNTQPN TLYFDKPEEKPFITSIHDRNLYTGEEYSYNINMSTNSMDDIPINSHN  
 NIYSGIDLINDSLNSNNVDIYDEV LKRKENELFGTNHVKHTNTHNVTKSSNSDPIDNQ  
 LDLFHTWLD RHRDMCEKWNKKEEVLNKLKEEWENETHSGNTHTSDSNKT LNTDVS IQI  
 DMDNPKPINQFTNMDTILEDLEKYNEPYDVQDDIYYDVHDHDTSTVDSNNMDVPSKV  
 QIEMDVNTKLVKEKYPIGDVWDI

>chr4.glm\_42, 117 bases, AAECA4F7 checksum.

MYTGDDLPHYTKLREHWWEKNRKGK VWEAMQCGYKHGRDPTDSEKDLAICDRKDN DY PVG  
 NDRKEGTEYQFFRWFSEWSEDFCQKQKQLEEELEEELEKGCPTDMCTSENEKKQQMHTS  
 M

>PFL1970w, 2188 bases, 6948D14 checksum.

MAPGSGGAASSGEEDKDAKHVLDFEFGQKVHDEVKKEAKKYIDELKAGVSFASILGEES  
 AHTTEPCGLDYSKLIKSGSGGVAARGHPCGNGSASASDKRFSKERVDEYDEKKIGCS  
 NSEGACAPYRRLHLCNKNFPNMNSKDSKAKHDLLVDVCMAAKYEGESLKVYHEQYEV  
 QYPSSGSTMCTELARSFADIGDIVRGIDLYGGNNKRRKQLDDKLKEIFKKIHENLGTH  
 EKKHYENDTANYYKLREAWWALNRQDVWKALTCDAHGTYFRATC SERNGGCSQANDKC  
 RCPKTS DGKANDQVPTYFDYVPQYLRWFEEWAEDFCRKKNKVENVKKQCRKKNSSD  
 DRYCSRNGYDCEKTKRAIGKLRYGKCTECCFACNPYVEWIEKQKEQFDKQKKKYDEE  
 IKKYENGAPRSSGGRAKRAAPSNINYEYEGYESKFYKILKGDYGSVDAFLEKLSKENVCT  
 AITDGGRISFEKVNTGSTGGSVRDASGGDSGTNNEKEGTFYRSEYCPYCPYCGVKKKN  
 GNEWKKKDTDQCKNIKLYKPRDDKGGTPIEILKSGEKHDDIETKLKAFCKTQNGSDGG  
 RGGSGGSGGKNSDSSLYDPWQCYQIGELTKDNKAGGEDDEDDDDYDGLVTNSGGLCIL  
 KNNINKKEKPERSSQKEPDEIQKTFHDFYYWVAHMLKDSIHWRTKKLDKCLQNGNKK  
 CGKKICNGDCECFKRWVEQKETEWGKIKEHFKTQKGFDEKDNSSPSGFTLRMTHDVVL  
 DGVLKEEFLKGDSEDSAQDTQNSLDAEEIQHLREMLKETGFDGGSGIGVAKEQKTLM  
 DKLIEYEKGIATKCLQKCQETQOPENPARSLDSVPGSPSPPADPSLDTARGPNHEEEEE  
 DDDSGDDDEVLDQEDQDEAEADPDGESSTAETTQOEAVAPTTQDNAEKPCDIVD  
 KLFQNP EQFKEVACKQKYAKNNSRLGWKCVTPSGDQKATSEGNGDANRRVARQTS ESG  
 EKSGDKDGAICIPRRRRRLYIQKLQEWAKTVGNTVVS GEPQTQGEASSPSDKESSQSD  
 KLREAFIQSAAIETFFLWDRYKKEWALQKLAELQRNGDL PFFTS GAGYGMTAVVNGAQ  
 PTASPGHSNGLISLPSLVTDSDNPQNKLNDGTIPPDFLRQMFYTLGDYRDICIGVKED

VIKALKASSDKNIETIKKAIDEILSKQSRNNQQSGQKSGTTPQTWWDENAQHIWEGMV  
 CALTYEDNGEKKIEKVNDANGTDLFEKLLTKYQYKNVKLDENSGTEAKTNEPSSPSSD  
 NTPPTLLTDFISRPTYFRYLEEWGQNFCKERKKRLEKIKEDCYRNGGREGPIKFDQDE  
 TFRPAKNCAPCSEFKVKCNGRVCTGGVTKGNCNGGRITAENIQNKRDGNGNIHMRVID  
 SNTAVFNGLDEACKTSGIFKGIKIRKEQWKCDNVCGYEVCKPENGNENENKNQILLFNAL  
 FKRWLEYFLEDYKKIKHKISHCMKNGNGSKCTNDPCNKCKCVEKWEKKEEWYIVKK  
 RFNGQYTKENDDAISSNLNSFLEPLVTQIAAATDKAEHETLEKLEKSLGCNCPDSSQK  
 KGDTPKDIVECLLNKLOQKATSCQEQHSVDVDPKTSCTSSPVEDEDDTLDEETEVEKAP  
 EICKNVVDTKKENDETGETCTSEDITITKETVETDSTDGPKQEEPPAATRPTKPKGRKP  
 ROPKEIDFPTPALKNAMLSSTIMWSIGIGFATFTYFFLKKKTKASVGNLFQILQIPKG  
 DYDISTLKSSNRYIPYASDRYKGYIYMEGDSSGDEKYAFMSDTTDVTSSSESEYEEL  
 DINDIYVPGSPKYKTLIEVVLEPSKRDTQNDIHNDIPSDIPNSDTPPPITDDEWNKLL  
 KDFISNMLQNTQNTPENILRDNVDNNTHTPTTSHHNVEEKPFIMSIHDRNLFSGEEISY  
 NVNMVNSMNDIPMSGKNDVYSGIDLINDSLNSDQHIDIYDEVLKRKENELFGTNNTKK  
 NTSTNSASKLTNSDPITNQLELFHKWLDHRHRMCDQWNKNKKEELLDELKEEWNKENN  
 NSSAKTYNSDNKPSHNHVLNTDVSIIQIDMDNLKPKNEFTNMDTNPKSTMDTILDDLE  
 KYNEPYYYDFYKDDIYYDVNDDDKTSMNNDNNLVDKNPNVDSNNSTYNHRNPADINKN  
 FVDKNNQNQHPIEKPTKIQIEMNINNGELVKEKYPISDIWN I

>PFF1550w, 296 bases, CC6E1856 checksum.

MLLFNFLINVLVLPHYENYQNNHYNIRLIPNNTYRITIKSRLLAQTQIHNPHYHNDPE  
 LKEIIDKLNEDAIKKYQQTHDPYEQLQEVVEKNGTKYKGGNDAEPMSTLEKELLQTYE  
 EVFGNESDMLKSGMNTNVDEKSSTCGCTDINGVKLAKTKGRDKYLKHLKHRCTRGICF  
 CSVGSALLTMFGLAVAKKAAVDAILPVYVAAIKKCVSSSSLFHIFHGGSLTTALKATE  
 ACASVAGPDIVIPATGAAIGAFPPYGI AALVLLILAVLLIILYIWL YRRRKNSWKHEC  
 KHLCK

>MAL13P1.7, 308 bases, B14DA43F checksum.

MKMHYLKMLLFTFLINILGSPHNENYLNHYNISIVQNNTKRTTINSRLLAQTKNHNP  
 HYHNDPELKEIIDKMNEEAIKKYQKMHPYKQLKEVVEKNGTKYTGGNDAEPMSTLEK  
 ELLETYEETFGDKKHIMLKSGINTNQYDKSIDESSTCGCTDNNKAKLETTKGKDKYLK  
 HLKEGCTRSICFCSVSTVFLTLIALAFAKKA AVASLVYYGEAFQNCVSSSSLFYIFDS  
 VSLTTAIQTASKCASLAGATDAGGTAAGAAMGIFYPCGIAALVLLILAVVLIILYIWL  
 YRRRKNSWKHECKKHLCK

>PFA0090c, 289 bases, EEB69262 checksum.

MKMYNLKMLLFTFLINTLALPHYDNYQNSHYNINLIQYRAQRTTINSRLLAQTKNHNP  
 HYHNDPELKEIIDKMNEEAIKKYQQTHDPYKQLKDVVEKNGTKYTGGKDAEPMSTLEK  
 ELLETYEEMFGNESDMLKSGMSPNVDEKSSTCECTDINGVKLAKTKGRDKYLKHLKHR  
 CIHGIGFCSIGSTLLTLIGLALAKKA AVDALASYATSHKICVDSINIFNMIAGSAVCA  
 ADLTVPAATSAATIFVPCGITALVLLILAVLLIILYIWL YRRRKRSWKHECKKHLCK

>PFA0750w, 301 bases, 5FA740FA checksum.

MNMYYLKMILFTFLINTLVLPHYENYLNHYNVSLIQSKTKRTTIKSRLLAQTQIRNP  
 HYHNDPELKEIIDKMNEEAIKKYQNTTHHPYKQLKEVVEKNVTKHVGNDTEPMSTLEK  
 ELLETYEEMFGNERDIMLKSGMYQNDDDGSDSSTCECTDTNNSELAKTKGKDKYLKH  
 LKHRCTHGIGYCSIGSTFLTLIGLALAKKA AFDTLNVTFHGVSYSKCASSISIFNMLD  
 GPSMFAGGTACSAADLTGNAAFAAMGALYPWGIAALVLLILAIILYIWL YRRRKNS  
 WKHECKKHLCK

>MAL6P1.15, 231 bases, 9AE3A1AF checksum.

MFHYIYKIYIFTIILCASNLFNNVVEIGTYKLSYHNGGIQFRMLAQKNTNKKPFGNT  
 LTNILCKDKKKKNDLPQISSLVSLVDNMDITQEKKDKIKNLSLKYINSRDVKEKNESI  
 NELQKYSNNEECKEQMDSYLMHLRMQNDIKCLKRKNLWNNIGINSITLSLIIIMIMIA  
 CMFAIYSTAQYIYVPASFLLIIFIYIVARYFPDMKIGFKKLKTKLNTFFQNKQITK

>PFB0025c, 304 bases, 54C3D0F0 checksum.

MKMYLKMMLLFTFLINTLVARHYENFVNNHYNVSLIQNKTKRVTIKSRLLAQTQIHNP  
 HYHNDPELKEIIDKMNEEAIKKYQQTHDPYKQLKEVVEKNGSQNRSGHVAEPMSTLEK  
 ELLETYVETFGEEASNIMLKSGRYQNGDDVSDSSSCDCTDINNAKLEKTKGRDKYLKH  
 LKGRCTRGIYFCSAGSALLTLIALIAAKKAALSAVASYAGFKNCMSSIATFKLLDSST  
 LLSSFLSMKACVVGATDMAGTIATPAMAAFYPYGIAALVLLILAVVLIILYIWLYRRR  
 KHSWKHECKKHLCK

>PFB0065w, 298 bases, FC694BAB checksum.

MLLFTFLINTLVLPHYENHKNHYNVSLIQNNTQRTTINSRLLAQTQKNPNHYHNDPE  
 LKEIIDKLNEEAIKKYQQTHDPYEQDKDVEKNGTKHVGGHVSEPMSTIEKELLETYE  
 DVFGDKNHVMLKSGRYPNDDDKSDDSSSCECTDVNNTKLEKTKGKDKYLKHLKHCIG  
 GICSCSVGSFAFLTILGCAFAKSAALTAFASESTKTCISSVAIYNLFQNSTMLSALKT  
 VGGTCANGAPDIAGTVSTLASAAFPPYGIAALVLLILAVALIILYIWLYRRRKNSWKH  
 ECKKHLCKR

>PFB1020w, 297 bases, 48BE8E16 checksum.

MLLFAFLINTLVLPHYENYLNHYNVCLIQNKTKRTTINSRLLAQTKNHNPHYHNDPE  
 LKEIIDKMNEEAIKKYQKSHDPYEQDKDVEKNGTIYTGGNGAEPMSSTTEKDLLETYK  
 EVFDDESMDLKSQNVDEKSSTCECTDINGAKLTKTKGKDKYLKHLKGRCTRGICV  
 CSVSSVFLTLIGLITAKNAVAVAVTSSFNEASKICASSISVLHMFTHESVTLSPSVT  
 AAGGVECFSDLAGTISSAAMGVFEPGIAALVLLILAVVLIILYIWLYRRRKNSYKHE  
 CKKHLCK

>PFC0025c, 296 bases, 8AE79126 checksum.

MKMYLKMMLLFTFLINTLILPHYENYLNNDYNSFIQNNTKRTTIKSRLLAQTQIHNP  
 HYHNDPELKEIIDKMNEEAIKKYQQTHDPYEQDKDVEKNGTKYSGNDAEPISTLEK  
 ELLETYEEIFGNESMDLKSQNVDEKSSTCECTDINGVKLAKTKGRDKYLKHLKGR  
 CTIRGIYFCSLGSVILTYIGTTAAKGAISTAGAGSKNCIYASIFHMLNHKSMSSALT  
 ALGTVGCAADYASGATSASAIIFLPCGIAALVLLILTLLIILYIWLYRRRKRSWKHEC  
 KHLCK

>PFC1105w, 301 bases, E53AEAD5 checksum.

MKMYNLKMLLFTFLINTLALPHYDNYQNSHYNINLIQYRAQRTTINSRLLAQTKNHNP  
 HYHNDPELKEIIDKMNEEAIKKYQQTHDPYKQLKDVVEKNGTKYTGGKDAEPMSTLEK  
 ELLETYEEMFGNESMDLKSQNVDEKSSTCECTDINGVKLAKTKGRDKYLKHLKHR  
 CIGGICSCSVGSFLLTMFGLHAAKVAVAVLSTYGKTSTCSSVLSITNMFNPATLQS  
 VLCATNGCTIGASDVVLPATSAAMGTFQPCGIAALVLLILAVVLIILYIWLYRRRKNS  
 WKHECKKHLCK

>PFD0035c, 289 bases, EC93E16B checksum.

MKMYLKMMLLFNYLINTLVLPHYENYLYNPYNVSLNPNNTQRTTIKSRLLAQTQIHNP  
 HYHNDPELKEIIDKMNEEAIKKYQKTHDPYEQDKDVEKNGTKYTGGNDAKPMSTLEK  
 ELLETYEEMFGNESMDLKSQNVDEKSSTCECTDLNGVKLAKTKGRDKYLKHLKHR  
 CIGGICSCVGSAILTMIGLAATKATIIKFLTVPPLSYNASTSPVTIYNMFGITAWG  
 PDAVGSIPTYSIVALQPWGIAALVLLILAVALIILYIWLYKRRKNSWKHECKKHLCK

>PF07\_0130, 296 bases, 6DA97408 checksum.

MNMYLNMMLLFTFLINTLVLPHYENYLNHYNVGLIQNNTKRATINSRLLAQTKNHNP  
 HYHNDPELKEIIDKMNEEAIKKYQQTHDPYKQLKDVVEKNGTKYTGGKDAEPMSTLEK  
 ELLETYEEMFGNESMDLKSQNVDEKSSTCECTDINGVKLAKTKGRDKYLKHLKHR  
 CIGGICSCVGSALLTYIGTVAAKAAIAKFAEVPKNCITSISILHMLTYDSMSSAIK  
 SVGTAVCVADLAGEATTVSAIFVPCGIAALVLLILAVVLIILYIWLYRRRKNSWKHEC  
 KHLCK

>PFI0045c, 293 bases, 40F75134 checksum.

MLLFTFLINTLALPHYDNYQNSHYNINLIQYRAQRTTINSRLLAQTKNHNPHYHNDPE  
 LKEIIDKMNEEAIKKYQQTHDPYKQLKEVVEKNGTKYTGGNDAEPMSTLEKELLETYE  
 EVFGNDNHMLKSGMHPNDDDISDTSSSCECTDIDNAKLAKTKGRDKYLKHLKGRCTRG

IYFCSVGSALLTTIGVCATKAALIAKFAEVPKNCIYTTISILDMLTYESMSSALKALSI  
QACASDLAGTAASAAMGIFYPCGIAALVLLILAVVLIILYIWLYRRRKNSWKHECKKH  
LCK

>PF10080w, 303 bases, 8F509C3 checksum.

MNTYYLKILLFSFLINILVLPQYENCEKGYHNGSLVLNNTQRTTINSRLLAQTQNHNP  
HYHNDPELKEIIDKLNNEAIKKYQQTHTDPYEQLREVVEKNGTKIRGEHAAEPMSTLEK  
DLLDTYPEEIFHEESHMLKSGRYPNDDDKTNEKSSSCECTDINNTKLTKTGKDKYLKH  
LKHRCRSGICTCSVGSFLTLIGLAAAKKAALAYFSGTTKTCVSSIPIFNMFCSSVA  
TSLQAGGATCATGISDIAGTVSTAATTTIFPFSIAIYVLIATVILIIILYIWLYRRR  
NSWKHECKKHLCK

>PF10\_0395, 305 bases, F88CFD2B checksum.

MKMYYLKMLFNFINTLLLPHYENSQNKHYNISLIQNNTQGTTIKSRLLAQTQNHNP  
HYHNDPELKEIIDKLNDEAIKKYQKTHDPYKQLKEVVEKNGTKIRGGNSAEPSTIEK  
DLLEKYEDVFGDKNHMLKSGRYPNDDDESDDSSSCGCTDINNAELEKTKGRDKYLKH  
LKGRCTRGIYSCSVISAFMLGLTAAKTAAGALAEYAAYETCLSSIIPIFSLPGNST  
VFSALQAGTEICATHASDLAGIISTPAMAAFEFYGIAALVLLILVVVIIILYIWLYRR  
RKNLSLKHQCKKHLCK

>PF11\_0516, 308 bases, 5DEC1408 checksum.

MNMYYLKMLLFNINLINTLVLPHYENYLNHYNVGLIQNKTKRATIKSRLLAQTQIHNP  
HYHNDPELKEIIDKMNEEAIKKYQKTHNPKYKQLKEVVEKNGKKYTSGNDTEPMSTLEK  
ELLETYEEVFGDEKDITLKSGINSDNDRSDNSSTCECTDINNAKLAKTKGRDKYLKH  
LKWRCRAICFCSVGSFLTFIIGLAAARATDVAALNITFNGINYSIYATYVTILNMFN  
EASMIAAIQAGVGATVDGLADMLTPAAASASAI FGGFGIAALVLLILAVALIILYIWL  
YKRRKRSWKHECKKHLCK

>PFL2610w, 295 bases, FDA89D8A checksum.

MNMYYLNMLLFTFLINTLVLPHYENYLNHYNVSLIQNKTKRATINSRLLAQTQKNHNP  
HYHNDPELKEIIDKLNNEEAIKKYQQTHTDPYEQLKDVVEKNGTKYTGGNDAEPRSTLEK  
ELLETYEEMFGDECHMLKSGKYQNVDEKSSTCECTDINGGKLSKTKGRDKYLKHLKHR  
CIGGICSCSVGSFLLTMFGLHAAKAAALAEFTKYGTTYSACKSSITIIYSMLSSDSMIA  
GSTACFTDLTPAATSAGAI FDFPCGITALVLLILAVILIILYIWLYRRRKNSWKHECK  
KHLCK

>PF14\_0007, 293 bases, D4D81FE2 checksum.

MNIYHVKMLIFMFLINALVLPHYENCQNDHYNKSLLOKNTQRTTIKSRLLAQTQNHNP  
HYHNDPELKEIIDKMNEEAIKKYQKTHDPYKQLKEVVEKNTKXVSGHVAEPMSTTEK  
DLLETYEEMFGHKNDIMLKSMPNDDNGSDKSSTCEYTDNNTKLEKTKGKDKYLKH  
LKHRCIGGICSCSVGSFLLTMSGLYFAKAAVLKYIASVGGPPYNACASTINIYNMIAGG  
SACVSDITGTAASAATAIFPCGIAALVLLILAVVLIILYIWLYRRRKNSWKHECKKH  
LCK

>PF14\_0767, 299 bases, 614309B0 checksum.

MKMYYLKMLLFTFLINTLILPHYENYLNNDYNVSVFIQNKTKRATIKSRLLAQTQIHNP  
HYHNDPELKEIIDKMNEEAIKKYQETHDPYKQLKEVVEKNGTKYTGGNDAEPMSTLEK  
ELLETYEEIFGNESDMLKSGMSPNVDEKSSTCECTDINNIKLGKTKGRDKYLKHLKHR  
CIGGICSCSCTLGSAALAYIGTVAAKVAVIGSFGDTVKNCISSISILHMLTYDSMNLAMQ  
SVNAAGSVTCVSDLAGATGTAYAIFVPCGITALVLLILAVVLIILYIWLYRRRKRSWK  
HECKKHLCK

>PF14\_0771, 297 bases, 5ADD9117 checksum.

MLLFTFLINTLLLPHYENYLNHYNISLIQNKTKRATIKSRLLAQTQIHNP  
HYHNDPELKEIIDKMNEEAIKKYQETHDPYKQLKEVVEKNGTKYTGGNDAEPMSTLEK  
ELLETYEEIFGGQKDIMLKSMPNDDNINISNKLSTCECTDINNMLKESRKGKDKYLKHLKHR  
CIGGICSCSVGSFLLTILGFATAKAAAMKAVADYTAFTKTCVSSISTFNLLDSSTLLSSFQA  
ISTCVEGATDMAGTIATPAMAAFYPGWIAALVLLILVVVLIILYIWLYRRRKNSWKHE

CKKHLCK

>PFL2635w, 295 bases, C0913FCC checksum.

MLIFNFLINILVSPHNENYLNKHYNVSLIQNNTKRTTIKSRLLAQTQIHNPHYHNDPE  
LKEIIDKMNEEAIKKYQQTHDPYKQLKEVVEKNGTKYTGGNDAEPMSTLEKELLETYE  
EMFGNDSMMLKSGMSPNFDEKSSSTCEYIDIHGVKLAKTKGRDKYLNKHLKGRCTRGIYI  
SSLATVILTIALYAAKTAALNYIVGIKGSYSACASFVTIFNMLSRESIIAVLETSAG  
FCASGAGDLGGTVAANALVAIYPCGIAALVLLILTVVLIILYIWLYRRRKNNSWKHECK  
KHLCK

>PFD00655w, 343 bases, F13392CB checksum.

MNTYYVKLLLFTFLINILVLPNVCTKIHYYAVNIKNYYIFNIYLLIFFFFENYIN  
NHNYNIIILIQNNTQRTTIKSRLLAQTQNHNPYHNDPELKEMIDKLNEEAIKKYQQTHE  
PYEQLKELVEKSETKLTGGNDAEPMSTLEKELLEIYEEMFGHKNDIMLKSCMYQNDDE  
KSDKSSSCCTDTNNAKLATTKGKDKYLNKHLKHRCTRGCSCSVGSVFITLIGLLVAKA  
AAVDAFKIVTASIATCSKCASSITISNMFNNASIVAALQKCGVLVATNGVSDGVGTAV  
GTATTAFNPYGIAALVLIILVAVALIILYIWLYRRRKNNSWKHECKKHLCK

>PFF1590w, 376 bases, 2F309D2A checksum.

MKIHYINILLFELPLNILIYNQRNHYITRTPKATTRSLSSECELYAPSNYDNDPQMKEV  
MDNFNRQTQORFHEYDHRMKTTRQKCKEQCDKEIQKIILKDKLEKELMDKFATLHTDI  
QNDAIPTCVCEKSVADKVEKNCMKCTQNLGGIVAPSSGVLGIAEGALYVWRDAEIVA  
AIAAAKEAGAAGAAVGIKEGIKVLNRLNTDFGLSPVRIKELESVINGTNYTDVTFI  
YEAITYTYKRSCVPVDVSVRFTVADTDLTFCESVWNQTLAVSQRNMGTSPLPPIIQKTA  
QKIVSDANFTAAATAETATEEATTTTLTAKNTGEVNATYMGYQTPIIASIVAILVIVLV  
MIIIIYLILRYRRKKKMKKKLQYIKLLEE

>PFF1545w, 360 bases, 78C68906 checksum.

MQNYKKCKRLYYIIFLFFLFISFSFFFGIKGKNMVTASHKNKLYMKPHTRTTTSRVLS  
ECDIEKSIYDNNPDMKYVKENFDRQTSQRFEYKERMINKNRQKCKEQCEKDQIILK  
DKIDKPVEEKIEKVCLRCGGLGGVAASVGLGTAVNVWVWKTAAAMDAAIGDAITKGLT  
EGAAMGATEGVAEVIAGLKALNIDKLFPETLGSFISATNYDKASYIFNIVNMKYKGT  
KILVPGGLSNPSNSICDSIQTWSLVQGSNHVNVTTDVAIGKEVVKVVTGAKTIAEKTA  
KMATENVTKGAIKTNVAEVNATYASCQTAIIASVVAAILVIVLVMVILYILRYRRKKK  
MNKKLQYTKLLN

>PFA0065w, 192 bases, D8D323C5 checksum.

MLAQKNTNKKSNGNALKNILLKDKSKKGSKKKNPDAEISDLVNLVDNMNITQEKKDKI  
KNLSLKYINSRDVKEKNESINELQKYSNNEECKEYMDSYLMHLRMQNDIKCLKRKNLW  
NNIWIVSTLLLIIMIACVYWLASTPPPGLFCLPFIVLIFIIYIVARYFPDMKIGFK  
KLKTKLNTFFQNKQITK

>PFF1565c, 377 bases, B7EB3A8C checksum.

MKIHYTNILLFPLKLNILVNTHQKPHTTARHTQKIPTTRSLSSECELYAPVNYSDPQM  
KEVMDNFNKQTQORFHEYDERVQNTROKCKEQCDKEIQKIILKDKIEKELNEKFSALH  
TDIQSDDIPTCICEMSMADKVEKGCLRCVGVFGGGIAPSVGLLGGGLGIYVWKPALKV  
AITAALNANSVKIAAANAAGEAMGVKTVIEGLKALNVHGLCPDLFESIGTKIHYTNA  
EEIAKIIIVAKYRATCNLSTGTSSTQAMCKQFDYTFGMRI RLSPVEYGGPPASAIPTD  
VKKVAGAEQAAEAKAANVRTTISSKIITEETDVINTIYMSNQTAIIASIIAIVIVL  
IMVIIYLILRYRRKKKMKKKLQYIKLLEE

>PFF1575w, 377 bases, F5B3BE9A checksum.

MKVHYINILLFALPLNILIYNQRNHKSTTHHTLKIPTTRLLCECDLYIPNYDNDPQMK  
KIMENFDRQTSQRFHEYDERMKTTRQKCKDKCDKEIQKIILKDKIDKELTEKFATLQT  
DIQNDAIPTCVCEKSLADKVEKTCLKCGVGLGGVTPAWGLISGIVYTGWKAALAAA  
KKLAAEAGAAEGASQGAAAGATRLIELIQSTFQVQNIAGQSLESIFTAQTYYTDVSNIT  
KALFNEYAEICLPIFTDSVPVVRGVRYNISSP ICTFVEEGILATSRDKGGSPITFIEKK  
VETMVSKAEGVATARAADVAAAKTAEFEATKVGAVEATYAGYHTTIIASIIAILIVL

IMVIIYLILRYRRKKKKMKKKLQYIKLLEE  
 >PFF0025w, 372 bases, 9A7E10FA checksum.  
 MKIHYTNILLFALPLNILVNTHTKKPHTTARHTQKIPTTRSLSECELYAPVNYSDPQM  
 KEVMDNFNKQTQORFHEYDERMKTTRQKCKDKCDKEIQKIILKDKLEKELMDKFATLD  
 TDIQSDAIPSCVCEKSIAEKAKEGCLRCGYGLGSVAPMIGLTGSAVAVNVWKTAEELAAA  
 MELAKQAGAAAGIKAGHLAGTKVVIDQLHTLGIYFVGGKPLESIIHVTNYMNVSVIYD  
 KVYSHYTTLCTPRFVIDRPVGFIFSGPVCNLVQPNHQGIWVKSSAQAIKKKVEEAV  
 AEGTQAADVAKNTADEVTKAAIKTSTEIDAATTTYTPIIASIVAIIVLIVLIMVII  
 YKILRYRRKRKMKKKLQYIKLLEE  
 >PFF0035c, 349 bases, A3929809 checksum.  
 MKIHYINILLFELPLNILIYNQRNHNSTTPHPPNTRLLCECELYAPATYDDDPQMKE  
 VMVKFSKQTQORFEEYDERMKTTRQKCKDKCDKEIQKIILKDRLEKQMEQQLTTLETK  
 IDTNDIPTCICEKSMADKLEKECLKCAQNLGGIVAPSSGVLVGVIAEGALYAWKPTAIT  
 AAKKAALAEATDAAIEAGMNAVSLKIEELGTVEFKPSEGFVNLSSIVNKLTYNNGDALV  
 ESAKNVIGGLYSNGKGGNTIFYNTTIHTKSGTLYVGNFGDIGRAAHDAKLASETTALT  
 KAKVGAVESTYGGCQTAAIASIVAIIVVIVLIMVIIYLILRYRRKKKKVKKLQYIKLLN  
 E  
 >PFA0010c, 331 bases, B68A13E0 checksum.  
 MKIHYINILLFELPLNILIYNQRNHNKSTTPHTPNHTQTTRLLCECELYSPANNDNDAAE  
 MKRVMQQFEDRTTQORFHEYDERMKTTRQKCKEQQCDKEIQKIILKDKLEKELMDKFATL  
 QTDIQSDSIPTCICEKSLDKVEKGLRCAGVLGGGIAPGWSLVSGLYAVWTNYVTQ  
 TALQKGIIEAGVKAGIEGLRDFSGLGKLIPIISVIQNLINHTNYDIAKTYITFVKSVNST  
 KCAVKEHSFCFSTYISNENALSKRAAGIAEYAADMAKITERGVLDAAATPGLTTYNAI  
 TASVVAIVVIVLVMIIYLILRYRRKKKKMKKKLQYIKLLEE  
 >PFA0020w, 372 bases, 9BA3921 checksum.  
 MKIHYTNILLFPLKLNILVNTHTKKPSITSRHIQTTRLLCECELYTPNYDNDPEMKSVM  
 QQFHDRTTQORFHEYDENLKEKRQKCKDKCDKEIQKIILKDKIEKELTEKFSSLQTDIH  
 SDAIPTCICEKSLADKVEKNCLKCTQNLGKIVAPSSGVLGISEAALSVMKTTTEIAAA  
 MELAKQAGAAAGLKAGHLAGTNAVIEQLRTLGIYFVGDKLETTIIDVTNYMNVSVFIYD  
 KVYSHYTTSTPSLVNDQLVGTFTNTSDPFCNLVHSNLQGSFYRSSAQTIIEYKVEEAV  
 AGAEQAATTKTAVMTPIYTTEFTAKNIAEVEAATTSYYPPIIASIVAIIVIIVLIMVII  
 YLILRYRRKMKLKKKLQYIKLLEE  
 >PFA0030c, 359 bases, 22FD456E checksum.  
 MKLHYTKLLFFFLLNILLTSYHAHNKNKPSITPHHTRSTTSRLLSEYDTESSIYDSD  
 DEIDSVKEIFERQASQRLREYDERLQEKRQKRKEQRDKNIQKIIHKDKMEKNLAEKIE  
 KGCLRCGCGLGSVAGSIGLFGAVAINIWKPAALDAAITAALNANAVKIAAANAAGEV  
 IGKALVIAELQKMGISTLKGQTLKSFRTISYKNVSSITKAVYGQHYEICVYDPSRNL  
 LSSFGDVRHIGICNSVWKQISAVSQRGQYISHEEVIKRTVETMMSEAEVSAKAAAKT  
 AEAANKLAIIEAQEQVMEATIYNWYTTIGYTLAILIIVLIMIIYLILRYRRKKKKMK  
 KKAQYTKLLNE  
 >PFA0040w, 344 bases, DFBE05D6 checksum.  
 MKFHYINIFLALPLNILVHNKRNMKTIICTPKTKQTKTHRTLCECELYAPSNIYEND  
 SEMKEVMEIFDRQTSERFREYDERMQHKKRQCKEQQEKDIQKIILKDKIEKELTEKFG  
 ALQTDIRTEDIPTCVCEKSVADKTEKVCNCGKTMGAVAPAWGFVSGIGYVAWTQYVA  
 AKILEVGIKKSQVSLDKVMEIVTQIHSLTAEIPKFSAAQILSSGNFTNNISLIDMV  
 QYLRNNMYGVIESQKCFERFGFILD TMGKNTLKVFNRYHIQVEAVKNAVDAEAAESL  
 KLATNTSILTNTIIASVIAILVIVLVMVIIYLILHYRRKKKKMKKKLQYIKLLEE  
 >PFA0045c, 350 bases, F099FA87 checksum.  
 MKIHCINILLFALPLNILVNTHTKTSITPLHTPKRPTTRLLCECELYSPANNDNDPQM  
 KEVMENFIKQTQORFYEYDERMKTTRQKCKEQQEKDIQKIILKDKLEKELMDKFATLH  
 TDIQSDAIPSCVCEKSIAADKMEKGLRCAGVLGGGVMPGMGLIDGSLGAI SVLQPLE

IAAAKDAAIAKATDAAIEAGINTVVSIIKGLLASFTEKEVLVDLTKIVTPSTYNNGAI  
LHKSAMALANKSCDFEGRGINSSFCNTLYNGEKTTFEPFAKAGIAEYNATYTLQKEAL  
ETANVDMVKATYASYQTAAIIASIVAIIVVIVLIMVIIYKILRYRRKKKMKKKLQYIKLL  
KE

>PFB0960c, 80 bases, 5048123B checksum.

MLAQKNANKKSLGNTLMNLLLKENKKTNLDPQTSSLVRLVDNMNITQEKKDKIKSLTL  
QYINSDDILEKNKSINELKKIQ

>PFA0050c, 358 bases, A3347A0 checksum.

MKVHCYNILLFSFTLIILLSSSQVNNQMNHYNTAHMKNTEPIKSYRSLCECELYTSM  
YDDDPEMKEILHDFDRQTSQRFEYNERLLENKQKCQECEKDIQKIILKDKLEKELM  
DKFATLHTDIQSDAIPTCVCEKSIADKMEKECLRCAQNLGGIVAPSSGVLGIAEGAL  
IVWKPAAIKAAKAAAASDAATQAGMNAVRLEIKKLEMFTEGKPGYVDLLPIVKES  
TYKNGSALVDSAKKLFVESGKLEGLDRMPVFYNTVIDYPGPSNIKGFSGKIGSDAYEAA  
FTSQKGTLEATKVGEVNTTYGGCQTAITASVIAIVVILIMVIIYLILRYRRKKKMKK  
KLQYIKLLEE

>PFA0080c, 369 bases, 3EEC82A9 checksum.

MKDHYINILLFALPLNILVYNQRNYIITPRHTEETNRSLCECELYSPTNYDSDPEMKRV  
MQQFVDRRTTQRFHEYDERMKTTRQKCREQCDEIQKIILKDKIEKELAQQLTLETNI  
TTKDIPTCVCEKSLADKVEKTCLKCGGVLGGGIAPSVGILGGIGEAIMSAWKVAALKA  
ATEYALTEGAAGAIAGNAQGMVVINFLKYWGVNEFFSEIFESILKISHYSKVKDFA  
DAIITKKAQICADGLLKNPAMCRKIDIKFGLSDEYGTPIAGPPNIEIPQKISGLVEQA  
DQAAVEVAKDTSQSVAAKITEEQTAVINATYTSWQIAITASVIAIVVIVLIMVIIYLI  
LRYRRKKKMKKKLQYIKLLEE

>PFA0095c, 343 bases, B857FA0E checksum.

MKLHYSKILLFSLPLNILVTSSYAHNKNKPSITPHHTPITTSRVLSECDLYMPKYDND  
ADMKSVKGTDFDRQASQRFEYEERIKDKRQKRKEERDKNIQEIIEKDRKDKSFAEKVE  
KGCLRCGCGLGGVAASIGLFGGLGIYAWRSAALVTAIQKGEASVEAGEAAGTKAGKE  
FVIAALQKMGIFTVGDQRLVSYFSTTDYTSALKISSDIQKYDPSSCFDFSGARETF  
CTWVKVKSDAAVNVERSTVSTNALVEKAVGTIVTDAKTVVERAVETATDEAIQRSIGV  
VDAKYAICQTAAIIASVVAILVIVLVMIIYLIILRYRRKKKMKKKDQYTKLLNE

>PFA0740w, 368 bases, DB5AFB4 checksum.

MKDHYINILLFALPLNILVYNQRNYIITPRHTEETNRSLCECELYSPTNYDSDPEMKRV  
MQQFEDRTTQRFHEYDEKMQSKRIQCKDRCDKEIQKIILKDKLDKELTEKFATLHTDI  
QNDAIPTCVCEKSLADKVEKTCLKCTQNLGGIVAPSSGVLGGIGEFEFELSVWKPAALAA  
AKEFAEKAGAAQAGAIAGNAHGMKIVIIYLLKDWGIQCCPEIFNPFVAKNIYTEVANIS  
GDIIAKYSKACADTVTGGNSMCKAFCLKLGTNIAHGRTLSVDHIVQLKIKGLVERAD  
QAVAHVTKTTSETVTAAIKARETALIEGRFESSITSINASIIAIIIVIVLILVIIYLI  
RYRRKKKMKKKLQYLKLLKE

>PFA0745w, 336 bases, CF2C6B28 checksum.

MKLHYTKILLFFFPLYILVYSKNKPSITPHHTQTNRSLCECDTQSTNYNNDEDIKSVK  
EIFDRQTSQRFEYEERMQEKRQKRKEQRDKNIQEIIEKDRMDKLLAEKVEKGCLRCG  
CGLGGVAAGVGIFGTVAVKELTKASTVAAIAAAQEAQAAKAVAGAEAGIKTVISGLQ  
KLDISTLNGQTLVSYFDTTDYTNFKTIAHAINTQYDPSPCVLRSGASESFCSWVRAN  
FFAPQEISGKVSSTYESIEIGVTSIVSDAKKAAAQVKKATDEVIKNSTAAAEESTYAG  
CQTAAIIASVVAAIIIALVMIIIYLVLRYYRRKKKMNKKAQYTELLNQ

>PFA0760w, 379 bases, 6A7A4EE6 checksum.

MKVHYINILLFALPLNILIYNQRNHKSTTHHTLKIPIITRLLCECDIYTSIYDNDPQMK  
EVMDFNFRQTQRFHEYDERMQGRQKCKDKCDKEIQKIILKDKLEKELMDKFATLHT  
DMQSDSIPTCVCEKSVADKVEKNYMKCTQNLGGIVAPSSGVLGIAELGLSAWKTTAL  
KTAIAAAEQAGAAKGLAAGAAKGAATRLIELIQSTFKIQNIAGKSLGTFIDATNYNNGP  
FIYQAIYTKFEMSLCLPVFPGVDPVPGAVRDPFCNLFKVFPTNGSSNRDSIINAIE

TYVQPFVSDAKFTAATAETAETATEEATAVLITKKTGEVTTTTYASYQTAI IASIVAILVI  
VLVMI I IYLILRYRRKKKMKKKLQYIKLLEE

>PFB0030c, 370 bases, 95750CA1 checksum.

MKVHYINILLFALPLNILEHKNKNEPHTTPHHPNTRLLCECELYSPANYDSDPEMKRV  
MQQFVDRRTQRFHEYDERMKTTRQKCKDKCDKEIQNI I LKDKLEKQMEQQLTTLETKI  
DTNDIPTCVCEKSLADKTEKFCLNCGVQLGGGVLQASGLLGGIGQLGLDAWKAAALVT  
AKELA EKAGAAKGLAEGNAHGMIKIVIHHLKELHIDKLVPGICEKISSTGHYANITNFA  
NTIIQQRGTMCGASGKNLGKDMCTKISIKLGTLPDGI R PGLPDKDAVTKVLNGLVEQ  
ADKAAAHVTKTTSESVTAAIKARETALIEGRFESSITSINASIIAI I VIVLIMV I IYL  
ILRYRRKKKMKKKLQYIKLLEE

>PFB0035c, 387 bases, B17C84C checksum.

MLFLKILINVFFLFVSNEREKYDCSKKYFYNGKIIAHNKNKQYISARTPTITSRMLSE  
CDINTSIYDDDTEMKFVKENFDRQTSQRFEEYNERLLENKQKCKEKCDKEIQKI I LKDK  
KLEKELMDKFATLQTDIQNDAIPTCVCEKSLADKTEKFCLNCGVQLGGGVLQASGLLG  
GIGAVAVNAWKDAALEAAIDFATEAGAAAGVAAGEAAGKAVVIKSLKYFRVDVFFPKI  
FNSIGNAIPYYDAKTIGAAIAEKHAQNCALVSTNEGAMCYPFEVNLGIREAITFTQTG  
PPAKYAIPTVSEIVEGAEQAAKAAKAAEKGVTAAIKAKETRLLLEAGFNSSISSINA  
SIIAIVVIIILIMV I IYLILRYRRKKRMKKKHQYIKLLEE

>PFB0040c, 330 bases, 1744E1 checksum.

MKDHYINILLFALPLNILVYNQRSYYITPRHTE TNRS LCECELYSPTNYDSDPEMKRV  
MQQFEDRTSQRFFEYERMQSKRMQCKEQCDKEIQKI I LKDKLEKELMDKFDLHTDI  
QSDAIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGAI AVNEWTKAATAAATQK  
GIEAGINVVIDTLKRLFNIEVVTDLKWKTLIT AQNYTDKILVGDVIRKLGNTLCGGSE  
DTAGGFCLFTVKANTLPQAINGHVTKAISEGTAEVVKVTEAEMGKVTT SAGAYSTGII  
VSVVAIVVIVLIM I IYLILRYRRKRKMTKMQFMKLLNE

>PFB0060w, 361 bases, DC6A3F8 checksum.

MKVHYINILLFTLPLNILVTLYHVNGQGHYSSTKHPISSTKSSKYHRS LCECEIYTSI  
YDNDPEMKVMQDFDQOTSQRLREYDERLIKNRQKCKDQCDKDIQKI I LKDKIEKELT  
KQLEALEVDITTEDIPACVCKKSVEDKVGKNCLKCGGILGGGIPGLGVLAGAYAVNSMV  
QVAMDAAKKAAIAEGAEAGIAEGIKVAIQGVPKFLLYTLNGKELQAVINANNFQNP  
FFYGEIMAEYVSWKKS DMVNSYGLFSFIEESCENNPDKIMK FILANSNDIAK DAKGAA  
TKMTTQTTEALTLKKTAEATSTSAIFSNPIVISFIVLV I I V L I L L I I Y L I L R Y R R K R K  
M K K K L Q Y L K L L L K E

>MAL7P1.58, 231 bases, E657A87D checksum.

MFHYFYKVYIFTIIICASNLFNNDGVEIGTYKLSYHNGGRQFRMLAQKNENEKSNNGT  
LKNTLLK DENKKGSKTKKLDPQITSLVNLVDNMDINEEQKDKIKTTLLEYINSDDIKK  
KNKSINELKKYSNNEECKEHMNNYLMHLRMQNEIKYLKRKNFWNNIWI V VITLLSII L  
LIAAMAMNTFPGFSAFLVTFVLSNLMIYMFARFYPEIKVQFKFKETCTNLFKKKSK

>PFB1005w, 316 bases, A74C5597 checksum.

MKMHYSEILFFSLSLNILITSSYAHSENKQYITPYTPNTSSRVLTECDIKMSIYDNDG  
DMKSVKENFDRQTSERFEEYDERMKDKRRKCKEQCDKDIQE I I V K D K M E K S L A K K V E K  
GCLRCGCGLGGVAASVGIIGPIAVNEVKKAALVAAAQKGIEVGMAKAIEELGKIVGLS  
DFSYNWSAMITATYYKPMKLVNIVNSANSMCTDSNPAFTSLFCKASYRINSEVSS  
RFTEVISQEAAKAASAAGEAAKNAEKAQIALVNEESAHL YSAIGYSVIAI I I L L V M V  
I I Y L I L R Y R R K K K M N K K L Q Y T K L L N Q

>PFB1010w, 368 bases, 5AD29E74 checksum.

MKVHYMNILLFALPLNILEHNERDHNNTTLHTSITRSLCEFE LYEPANYDNDQEMKEV  
MQQFEVRTSQRFFEYDESLQSKRKQCKDQCDKEIQKI I LKDKLEKHMAQQLSTLETRI  
TTDDIPTCVCEKSMADKVEKGCLRCGCILGAAMP ELG SVGGSLLYALNTWKPVALKAA  
IAAANKAGMAAGIKAGDAAGMNVVIVQLGKWGINEFCPEIFESILKINHYSK LKDFAS  
AIVA EHDKICAITTSGENSMCLPF DIALGLSDAKGTPIGPPASQAI PKMMNQLV GKAK

GTADFMANKVNSETYSKIITKQADLIEAGFNSCTTSIYASIIIVILIIIVLIMVIIYLIL  
RYRRKKMKKKLQYIKLLEE

>PFB1015w, 348 bases, A329AFE3 checksum.

MKLHYTKILLFFFPLNILLTSYHAHNKNKPYITSRHRQTSTSRVLSESDPYMLNYDND  
DDMKSVKENFDRQTSQRFEYEGRMKDKRRKCKEQCDKDIQEIIILKDKMEKSLAEKVE  
IGCLRCGCGLGGVAASVGIFGTAVKELAKTATAAAVAAAQEAVKDAAMAATIKAVGA  
AAGKEFVIAGLKQMGVSTLDGKELGTYITATNYTNVKNIAHAINTQYEPSSCLITVPV  
DSKPICTWVRAKEGAARVIQKQFSTQETIKVAVTSIVSDAENVAAAEEQQATKDAIK  
ASTLAVDSKYAICQNAIIASVVALLIIIVLIMIIYLVLRYYRRKKMKKKAHEYTKLLNQ

>PFB1040w, 345 bases, 69DAC979 checksum.

MKLHFPKILLFFFPSNILLTSYHVHSKNKPYITPRHTPTITSRVLRECDIHKSIYDND  
EDMKSVKENFDRQISQRFEYEEERMKGKRQKRKEERDKNIOEIIIEKDRMDKSLAEKVE  
KCCLICGCGLGGVAASVGIFGGIAISELKKAAMIAAIIASAQKTGVLAGEAARIIPAGIK  
AVIAGLKRMGISTLGGKDLGSYFATTDYTNFKTIARVINSEYQTDSCLIIGGPATDKSK  
TICNWVRANFVAPQDSPGKGGSVYKSIETAVKSIVTDAETVAQRAVENATEEVIKNST  
AAAESTYAGCQTAAIIASVVAAIIIIALVMIIYLVLRYYRRKKMKKKAHEYTKLLNQ

>PFB1050w, 327 bases, 64F55E9 checksum.

MKVHYINILLFALPLNILIYNQRNHKSTTHHTLKIPIITRLLCECELYAPTNYSDDPEM  
KRVMQQFVDRRTTQRFHEYDNRMKDKRQKCKDKCDKEIQKIIILKDKLEKELMDKFATLQ  
TDIQNDAIPTCVCEKSLADKVEKVCFRCGLLGGGIAPGWGLVSGLYVGTNYVTQT  
ALQKGIEAVISYLEQIPGIKGLPGFNLANIVNPNYSSGGLLTTAIDAAARPICSVNH  
SKTPAFCSYATQNGGSIIAKVSVDANAANAGIDAASAEANLAPKTLTLTNTIIIVSF  
VAIVVIVLVMLIIYFILHYRRKKMKKKLQYIKLLE

>PFC0030c, 359 bases, F6F19D39 checksum.

MKLLYSNILLFALALNILLTSYAHNKNKPSITPHHTRTTTSRLLSECDTESSIYDSD  
EEINSVKEIFERQTSRRFEYEEERMITQRQYKEQRDKDIQKIIHKDKMEKNLAEKIE  
KGCLRCGCGLGVSIGLFGAVAINIWKPAALDAAIAKAITEGTANISAAGVKAGEA  
TGKVLVISGLKKMGISTLGGKNLESYFATTSYKVASIAQAVYEQHFCEFGYLKEG  
FTPVGDPSTRDIHFCQSVWQQTSVVSKTGHYISPKDVIKRTVETMVSKAEGPANAAAEF  
VKATETATIKAAEETIETASTQLYSAIGYSILAILIIIVLIMLIIYLILRYRRKKMK  
KKAQYTKLLNE

>PFC0035w, 374 bases, A00E6632 checksum.

MRITIKMKVHYINILLLALSNIANTHOKPSSTPRHIQTTRLLCECELYMHNNDNDP  
EMKRVMQQFHDRTTQRFQYDERLQEKQVCKDTCDEIEKIIILKDKIEKELNEKFAT  
LQTDIHSDAIPTCICKTSMADKVEKTCCLKTQNLGGIVAPSSGVLGIAEGALYAWKP  
NALQTAIEAALKAAADDILVGGIEAGKQVIGGLDALEIEKLGIGSWEPYFTEGYCIN  
VKSLASIIYEKRQTLGCATKSTLDKATCEQIGISIGTMQHDGTYGAPGTTPIETVLNG  
IVEGTKEAADVAEAARESATNAIKVQETRLLEAGFNSSISSINASIIAIVVILIMV  
IIYFILRYRRKKKKLQYIKLLEE

>PFC1100w, 317 bases, AF4895F6 checksum.

MKLHYTKILLFFFPLYIILVTSYHVYSKNKPSITSHHTPITTSRVLSEKDLQSSIIYDND  
ADMKSVKENFDRRTSQRFEYEEERVKDKRQKCKEQCDKDIQKIVLKDKMEKNLAEKVE  
IGCLRCGCALGGGVAPIWGLVSLWYATWSQYVSAKVLEEATNAAIKAGIIKAIIEGLK  
ELQDLGKLVGDKWSNIVTPETYSNPNLLSRALQRVNIAMCYSESNENVLFCNAIQRRP  
ESVFPASKVAADAGEAGKAVYLATEKAELLKIAPATNALTTAIIASVVAAIIIIALVM  
IIYLVLRYYRRKKMKKKLQYIKLLE

>PFD0015c, 370 bases, BB7AC3A7 checksum.

MKIHYINILLFELPLNILIYNQRNHKSTNLHTQNNRSLCECELYAPATYDDDPQMKEV  
MVKFSKQTQRFHEYDERMVEKRMQCKDKCDKEIQKIIILKDKMEKELMDKFATLQTDI  
QSDAIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGSVAVHVWPKALEAAIAK  
AIAEGTADIAAAEAAGKARGMEFVIKALKHFGVENFFPGICDTISSSTGNYTKVTEFV

NTIYSKYNGTCNLMRSSINPTACYTIETELSIKTGGAGTGDHPPLYAIRQMIKGLAAE  
ATEAAKAAEAAKNAKLTAAIKEKQTALIEAGFNSSITSINASIIAILIIVLIMVIIYL  
ILRYRRKKKMKKKLQYIKLLKE

>PF14\_0761, 820 bases, EC7D59F8 checksum.

MGIILNIYIFFIYLIYVRSHFSQPTSSEYEGYSEICEKARNANESSVYCMKDYKRNSS  
KMYMKHIMRMFIEKHNLDNKIALIEHECGEPQNYMTYDTFLRKILSFNNSLNKYDGI  
NIPEKIYNEEMNGKFKLLGLYGSNSINWLVADLGAMLSGVTTLMVHSHKFSMDVIVGI  
LNETKLEWLCLDLDLVEGLMERINELPHLKNLIILDTVAKQGIINSTIEKNKNINLKG  
NGNLNMMNKKGNLDSKNLEDVRLGPIKYDKEKLEKFKSLKERYHKYLEKFLLLDDVI  
NNENTNFKIKNEDPNFVTSIVYTSGSSGMPKGAMLSNKNLYNQLYSLYNHSVRKTYNL  
QYHLSYLPISHVFERTIAYSIIIFLRGTVHIWSKNLNYFSKDILNSNSVIMTGVPKVS  
RIYTNIMTEINNLSPFKRCIIKKIISLKKSNKRWLVNFLENLFHISSKIKEKVNPNL  
EIIILNGGKLSPDVASELCNLLNIKYCQGYGLTETGGAI FGKHVEDLNFECIGGPICP  
NTKYKVRSWETYKATDTLPKGELLIKSDSIFRGYFLEKEYTKNAFTNDGYFKTGDVVQ  
INKNGTLTFLDRSKGLVKLSQGEYIETDLLNNLYSQISFINNCVVYGDSDMDGPLAII  
SVDKYLFLSLKDDNMLEMTGVNEQNYLDKLTDDNINNNIFLDYVKEKMLEVYKETNL  
NRYNIINNIYLTSKVWDTNNYLTPTFKVKRFYVFKDYAFFISQVKEIYNNKLGKCAPI  
SVNSENKDEEKKNDKSKKKEEKDSEKLSNESTSNQNKNDMGKHEKYVENKKVKLGATYG  
TRQKEMNK

>PFD0025w, 382 bases, 9FE01EB5 checksum.

MKIHYTNILLFPLKLNILVNTHKKPSITPRHIQTNRLLCECQLYAPQNYDNDPEMKRV  
MQQFHDRTTQRFOEYDERLQEKRVCKDTCDEIQKIILKDKLEKELMDKFATLQTDI  
QSDAIPTCICEKSLADKVEKGCLRCAQN LGGIVAPSSGVLGIAEGALYAWKPKALEA  
SIKTAIAEGTANILAAGVEAGEVTGKELVIAGLKKMGISTLDNKSLESYFATTSYKNI  
TNIAQAVQKLYFETCADCSSGKVYLYGDANRHIPICVSNVWNQTPAVLTTKKGISTKE  
VIEKTVQTMVSDAEGVAADASAASAEKELTAAIKAREAEVINTIFMSKQTAIASVVAI  
LIIIVLIMLIIYLIILRYRRKKKMKKKLQYIKLLNQ

>PFD0030c, 380 bases, 2856DA57 checksum.

MKIHYINILLFELPLNILIYNQRNHKSTTHHTLKIPTTRLLCECELYSPANYDNDPEM  
KEVMEIFDRQTSERFHEYDERMVEKRMQCKDKCDKEIQKIILKDKLEKELAEKFVTLQ  
TDIQNDAIPTCVCEKSIADKVEKGCLRCVGVFGGVMGFGTIGGTALYALNQLKPAV  
FKAAIKAALEEGAAEILAAGIEAGDAAGMNVVRYGLRYLHVHELFPVIFDSFVKTRPY  
NEITSIANSILLKYGPTCTGLDNNSPPACTKFQLNLGIHKKIGAMIDTHGTPASTAI  
RQGLEGILEEATQTAEAAAKIAEKGVAAEITARETALIEAGFNSSITSINASIFAIV  
IVLIMVIIYLIILRYRRKKKMKKKLQYIKLLEE

>PFD0040c, 329 bases, B7ECC245 checksum.

MKIHCINILLFSVPLNILVNTHKKSSIRRLHTQTTRSLCECELYSPANYDSDPQMKEV  
MENFIKQTQQRFDHYDDRMKEKRKQCKERCDEIQKIILKDKLEKELMDKFATLHTDI  
QSDSIPTCVCEKSLADKTEKFCLNCGKTMGGVAPGWGLVGLWYATWSQYVTKTAIQK  
GIEAGVKWGIQELKVFHSLYRLIEVSQIQSFINPANYAEKTTYFSFVKSVNSTKCVGK  
AVNTEPFCNFVSLNGESALS DRAAVIAKDAAYMAEVAKEGVLKEGASVTSSSLTTGITA  
SLIAIVVIVLIMI IYLVLRYYRRKKKMKKKLQYIKLLEE

>PFD0045c, 309 bases, 912265AF checksum.

MKLHYTKILLFFFPLNILLTSYHEHNKNKPYITSHTPTTTSRVLSECDLYMPNYDKDA  
DMKSVKENFDRQTSQRFEYEEERMKDKRQKHKEERDKNIQEIILKDKIERSLEEKVEK  
CCLICGCGLGGVAPFVGLFGGLAVNELKKDAVAATEAGIKKAIIEGVGSIFYLEEGS  
PIPWMNKIHAGNYNQKMPVLTIVNSIYNNCEDDPSSAGSLFCQASKSFIEERQRPVFT  
KTISEMAGNAEAAAGKAANEKYAEMTSVGTICSDPIVISAIVVVTIAVILLIYLIILR  
YRRKKKMNKKLQYTKLLNQ

>PFD0050w, 367 bases, C055BE31 checksum.

MKIHYTNILLFPLKLNILVNTHKKPSISPHHIQTTRLLCECELYMSNYDNDPEMKSV

QQFHDCTTQRFQEYDERLQEKRQICKDKCDKEIQKIILKDKIEKELTEKFSSSLHTDIO  
 GDDIPTCICEKSLADKVEKGCLRCAQNLGGIVVPSSGVLGEIAAFVAVNAWKTEIAAA  
 TELAKQAGAAAGKIAGEAMGVKTIIRIFEKIFSIDKLGTTLSFFTTTRYNDVKTIA  
 SVIDTEMNTSCVLNSFGNHAI CGLRTKLDLVAKPGQVMVIQKDAITRMITDVVHKAEI  
 TAEAAKTQVAASKTAAAIKTNIEAIEAATTPYYPPIIASIVAVVVIILIMVIIYLILR  
 YRRKKMKKKLQYIKLLEV

>PFD0055w, 375 bases, DADBDAE checksum.

MKVHYINILLFALPLYILDHKQRNHNSTTYHASKTKSIKTHRSLCECELYAPSDYDND  
 AEMIRVMQQFHDRTTQRFQEYDERLQENRQIYKDTCDKEIQKIILKDKIEKELTEKFS  
 ALHTDIQSDGIPTCICEKSLADKVEKVCRLCGSILGAAMPEVGSIGGGLLYALNAWKT  
 DAIAAATKAAMIEGAAQGA VAGEAAGRNAIIGALKRYFHIDNLNGTSLKSFFNSTSYS  
 DVTTIASAIDTQMTASCDAFSGKIVNQAFCDVRKTLRIVADPGKSFVKQKDAITGAVT  
 QLVEKAKDTASFKATEVSSATSSKIITKQNALIEAGFDSSTTSIYASIIIVILIIVLIM  
 VIIYLILRYRRKKMKKKLQYIKLLEE

>PFD0060w, 329 bases, 768BE855 checksum.

MKVHYINILLFALPLNILVINQRNHNSTYHTSNTKLTKTHRTLCECELYAPSNYEND  
 PEMKELMENFNHQSSERFREYDERIQDKRQKFKEQCEKDIQKIILKDKIEKELTEKLS  
 TLQTDISTNDIPTCVCEKSLADKMEKTCCLKCGVLGTAVPELGLIGGSVIYSAAQAAA  
 AKLGVAKAIELMKKIYNLGNVSFIDWTNLINVGNYSHRMSLVGIVNKVNNMCQIKDPE  
 GNVVFCFAKQNMRRGGAGKFAQTISEQAGNAAIKAGETANVKFAEMTSVGTIFSDPIVI  
 SATVVVTIAVILIIIIYLILRYRRKKMKKKLQYIKLLEE

>PFD0070c, 347 bases, 17A82B13 checksum.

MLLCLFLLNKL LLLLLLLLLLPLLLSCKNFQSNGYISPHTRSVTKITTSRTLSEFDKYKNN  
 YDDDPEMKELMKRFNERTAVRLKEYDEQKKKKQKIYKEKKDKDIKEIVKDKIQKQLT  
 KQLSKLEKVTDTDDLDFKGNKNEKKVATKGGKGRKNKKT LGQTLSEWNILPNIDMYEWI  
 PFSSKEAKVDCNIKNIKQALTRVGYIGPNKFVTLGSKDGKDAIDMDNLFSSIMSSSNA  
 LYQKYIDKDDTSNGSSFFKQSGFLSFALYALWEIFEHIVLPVVTSMLLNGNDSSESQVS  
 GVDGHGHEVAHGVS VLYESFIALYTIASILLILYYILKYRIRMEKKEKYMKILQD

>PFD0640c, 376 bases, EE86FAAE checksum.

MKVHYISILLFSHPLNILLTSSQVYNQKNPYLTPHKTNPKSVKTCRSLCECELYAPSN  
 YDNDPEMKKVKQFDDRTSQRSEYHKRIQENRQKCKEQCEKDIQKIILKDKIEKELT  
 EKL GALQTEIRSDAIPTCTCQKSVGYKVEKTCLKCGGILGVGVAPSLGLLGEIGGLVI  
 NNWKNTPFYEAFAFAQKEGIAAGKIASDAARIDTVISGII SNFEVHTINGSTLANAI  
 TLET LKDDTILTKALHFEYGSMCVNTPPTDDKLICAYGMRAGLVQGKSASPEAVIRSSV  
 KTL LKNADNVASQAAQT TANETTSGMIKAELSKIASAGANTYSAITYSVTAILVIVLV  
 MVIIYLILRYRRKKMKKKLQYIKLLKE

>PFD0645w, 346 bases, BE191C17 checksum.

MKLHYFKILLFFAHPLNILLSSSHVHNKKNPYIITSHTPSQESLKTCSRSLCECDLYT  
 SIYDNDPEMQKVIQEFDNRTSQRFEYDRMVKNRQKCKERCDEIEQIILKDKIEKE  
 LTEKLGALQTEIQSDAVPTCTCQKSVADKVEKTCLKCGSVLGGGIAPGWGLVSGIGYS  
 TWTHYVATTVAKAATDAGIKEATEALGRIYTLNEVTVINWTSKITATNYYKPMELVEI  
 VNGVNNMCGETGVAGNTSFCLAAESIKPSDVFTRIISRQAQEAATYAASKAKDVTTAE  
 FANSASSTATLTNTIIASVVAIVIVLVMIIIYLILRYRRKTKMKKKLQYIKLLNE

>PF10\_0323, 355 bases, 5404EC34 checksum.

MKVGKIFFLLNILVVFHFIISCLCRNGQTTGRNLLALKAIEQDLQKKNRKNLILYS  
 LGSAALIAALVVTGIGLNMVMKKNVDSEVQEIIDEKDEKVKEKPAEKKT TVKIVSK  
 RVPVKS KSSNGKSKARTVNSEVSPKLDDEKEDLLKFNNDLLLAESLKEKLNPKYDE  
 NTQGNDSFKNINEPRKLASFSLYDALADASEQKNKDAESSTGQIPTPTESHGIGSDG  
 KKDTSTNDMDPLNPGSSKRNSSEDKPTSESKGTTPESNFDSKTP EIKEINEPIIVPS  
 YYPTTGPNPNTHGPPSRRISTSRSSGSSNRSSSGTSTRSKGPSSPLRDS SGRSSGRST  
 TPRVRKE

>PFD1010w, 346 bases, 523A1C6 checksum.  
MKLHYTKILLFFFPLYILVTSYHVYSKNKPSITSHHTQTNRSLCECDTQSSNYDKDTG  
MKSVMQQFVDRTSQCFEEYDERMNEKRQKSKEQRDKNVQKIIKDKIEKSLAEKVETG  
CLKYGCGLGGVAGSVGIFGTAVAVKELTKAAITTATELAKEAAKDGAMAATIKAAGAEA  
GKKFVIAGLGKLVSTLDNQILESYFATTKYTNVTKIARAINEQYNPSSCLTGGSGAD  
NSICPWAMENFFAARKIPGKVSSTYNSIEVAVKSIIVSDAEPVATAAAQQATEEAIKNS  
IAVVDKAYVICQNAIIASVVALLIIVLIMIIYLVLRYYRRKNKMKNKKAHYTKLLKE

>PFD1020c, 261 bases, 82EAD003 checksum.  
MKVHYINILLFTVPLNILVTLCHVYNQISLHIRNHTPTTKSRLLECDVYTSIYDNDP  
EMKNVMENFNKQTEERFHEYNERMQEKRECKDQCEKDIQKIIKDKIEKELTEKLEA  
LETNIKTEDIPTCVCEKSVADKVEKACLRCGGILGGGLEPTVGLLGTVVVNQLTKTAT  
VASIEFVTQEGIKAGIKAVVHNLINVLHLFDVTRDIWLTTLINSKNYNTVSGLTAAKT  
AKEAVGTTCLRNTPRPKPSCDAIFNKSJV

>PFD1230c, 324 bases, 18130BCD checksum.  
MKIHYTNILLFPLKLNILVNTHTKKPHTTARHIQTNRLLCECELYMSNYDNDPEMKSVM  
QQFHDRTKQRFQEYDEMLQEKRQICKDTCDEIQKIIKDKIEKELNEKFSALHTDIQ  
SDAIPTCICEKSVTDKFEKTCLKCSGIFATAVPELGLIGGTVVYDAAVKAATKAAIKK  
AIEEVGKIFFLADESTMQWTNMINAGNYSKMSLVSILTSLNNGCQDGEAVAGPLFCT  
ASNALTESGNPYVFTRTISEKAANAADAARKAASGKFAEMTSVGTIFSDPIVISAIVV  
ISIAVILLIIYLLIRYRRKIKMNKKLQYIKLLKE

>PFD1240w, 324 bases, 1702F03A checksum.  
MKVHYINILLFELPLNILIYNQRNHYITRTPKTNTRTLCECELYAPSNDNDQEMKEV  
MQQFEVRTSQRFFEYDESLQSKRMQCKDKCDKEIQKIIKDKLEKELMDKFATLQTDI  
QNDAIPTCVCEKSLADKVEKTCLKCGLLGGVAPGWGLISGLGYVGTNYVTQTALQ  
KGIEAVISYLEQIPGITDLPGFNLANIINPKNYSSSSLI IQAIDAAAGPICDVPVNES  
LKFCVLSSYNESTIIKQVSGGAESAAAFGEETASAEVAKFVPKTTILTNTITTSFIVI  
VVIVLIMVIIYLLIRYRRKKMKKKLQYIKLLEE

>PFE1630w, 318 bases, EBEF7208 checksum.  
MKVHCYNILLFSLLLHRLLLSSSKVNIEMNHHTPHIKNREPTKSYRSLCECELYTYI  
YDDDPDMKEIMNDFDRQTSQRFFEYNERVKNRQKCKEQCDRDIQNIILKDKVEKSLS  
EKVEKGCLRCGCGLGGVAAGVGI FGALGTYGWKVAATATAIEFATQEGIKAGIQAAIE  
QIKITVFNSSLNVEWLNFINASNYSIAGLVEAVKAAVSTERTSELSSNTMDRVRNA  
LSEAENWFSPAVREGTQTTASTITTTVQRTQLVDVTATSTYSYMAIAYSVIAILIIVLV  
MIIYLLIRYRRKKMKKKAQYTKLLNQ

>PFF1555w, 370 bases, 70CBC0B0 checksum.  
MKIHDINILLFALPLNILVGSPQKNPSIITCHTPTNRSLCECDLYMPDYDNYPQMKKV  
IQQFEDRTSQRFFEYDDRMVEKRKQYKDKCDKEIQKIIKDKLEKQMAEQLTTLQTDI  
QSDALPTCICERSIADKVEKNCMKCTQNLGGIVAPSSGVLGIAEGALYAWKPTALKV  
AIDKAIAAGAAMGKAAGDAAGATEVIKLMKTTFYINELNGKLLSVFTAQNYTNFPNL  
PHVIYKQYKTTCDLFAINTSSDPICKISKTFNFIAESGQAPVSEEAVIEAKVTEIFTK  
ATDVAATETTNVTTTQTTILETAKKGAIETTTCMGYHTTIIIVSIIAILVIVLVMVIIYL  
ILRYRRKKMKKKLHYIKLLKE

>PF07\_0003, 331 bases, AC58A1A5 checksum.  
MKFHYFNILLNLIPLNILIFSSHVNDQKNAYNSSIHHAPKTKTKIPNIRLLCECELY  
AAPNYDNSEMKVVMQNFDRQTEQRFNEYEERMLKNRKKCKEQCDKDIQKIIKDKIEK  
ELEEKLALETNINTNDIPTCICKSVADKVEKTCLKCGGILGTTVPQLGILGGISTH  
MLTTAATSAAIDAGMKAVVDKLDKDFVIGFRGNTVDLTPIVNPSSYNGNLLLENAKNL  
TKTTCMPNSAGKVSTLCAQIQNSGSISTFNGFAEAGTDAYNTTWATKTAEINSFNIAM  
MASIIAIVVIVLVMVIVYLLIRYRRKEI IKKKLQYIKLLNQ

>MAL7P1.57, 346 bases, B8831DE9 checksum.  
MMFHYFNILLCSLPLNILLTPSYEINMKSHNRSTLHTLNAKPIKIHRSLCECDLYTST

YDNDPEMKEVMQQFDDRAAQRKFKEYEEMLOYKRRKQCKKQCDKDIQKIILKDKIEKELT  
 ENFSALQTDISTNDIPTCICEKSVADKVEKTCLKCGGILGGGIAPGWSLVSGLGYMAW  
 TRYIAAKVLEEGIKKGLEVGLVKVTEIATQMIGDVNKVPSIDILQKITIGNFSDGVSL  
 YDIFKTIIDSTMSTELETQGYDFSLSVQSIADDDPAKWKWCSQKVADVNTAVADGEASV  
 LTEAAPVTSGLNTAIIASIVAIVVIIILVMSIIYLILRYRRKKKIHKKLQYIKLLQQ  
 >PF07\_0132, 366 bases, 91AD532D checksum.

MKDHYINILLFALPLNILVYNQRNYIITPRHTETNRSLECELYSPTNYDSDPEMKRV  
 MQQFVDRRTQRFFEYDERMKTTRQKCKDKCHKEIEKIILKDKMEKQMAQQLTTLTKI  
 GTDDIPTCVCEKSMADKMEKDCLRCTYGLGTLAPTIVGLIGSVAVGAWKPTALKAAIVA  
 AOKAGDAAGVAAGEAAGKKAVILALQHFKLDNLFPEIYNAIVKIRHYADVKNFSVAIV  
 EEHSLKCQSLDLKVTNTPTCETFEFNIGMRI PDSSFVEPVDQVVPEVLDLVLGNIKEV  
 AEAKAAEVAAAKTAEFKIANVGAVESTYGCQTAAIIASIVAIVVIVLIMVIIYLILRY  
 RRKKKMKKKLQYIKLLKE

>PF07\_0134, 382 bases, 5FE87B17 checksum.

MKLTLYNLILSCYIILNILLSSQINIQWNLYNTTQIQKTKLTITNTRLLCECDLYTPS  
 NYDDDQEMKELMQQFEDRTSQRFFHKEYEERMKTTRQKCREQCDKDIKKIILNYKIEKEL  
 SQKLVTLTETNIDTDDISTCVCEKSLSDKLEKTCLRCGGVFGGGVMPGFGAIGGTALYA  
 LNQLKPTAIIATAIEEAIKAGASNISAAAFKASEAAGLAKVITELKALSVEKLIPGILN  
 SIFSETHYTNATKIAEIIILTKKSVTCGLSSPGNPICHEFGINFNIIDPGNGFFFPDKT  
 GITQKVTEVVEGAKGAAANASKVASERVTAIIKAHETNVINATYAGYEITIIASIIAI  
 LIIIVLIMVIIYLILRYQRKKKMKKKLQYIKLLKE

>PF10\_0023, 276 bases, AF946D51 checksum.

MIKDHNNNEMSMNFYTYKKMINDNSTSYSSSKMEPEPESNRYIKGKNINIFPLLKFTVFT  
 LLIWIVTFINNYGNMNDGCRMTDLSTSRFLSEPLLEFDTVFDVFKDTFLKNMGCSDE  
 ETKNIRSTMKQYFDNIDMNALSKEKENGNGFFEQIGNNENTLERFMKKDISQLKCINV  
 ENAEEGEEIPKPYTVEEVDPNPNKGEIGNMKFNSNFIRRSVITLKKIGTSPTFLITM  
 TAILLKNDNFKTALLLMVALFLKGVNFALDLKAYNDKFHFIFKFK

>PFB0120w, 106 bases, C401A844 checksum.

MKLSKILYFFAALLALNFIAPRDYNSMVEAKPAKKLTPAERKKRNQNIMIYSSIASAV  
 ALLIGGAVGLGIHLHKNNKGDNKKGTPGAKKNDNKAVNPSISSTMYRA

>PF07\_0138, 339 bases, FF0904D0 checksum.

MKIHYINILLFELPLNIIYNQRNHNSTTHHTLKIPIITRLLCECELYAPSNDNDPEM  
 KEVMEIFDRQTSERFHEYDERMKTTRQKCREQCDKEIEKIILKDKLEKELMDKFATLH  
 TDMQSDAIPTCVCEKSVADKTEKVCLNCGKTMGAVAPAWGLISGLWYATWSQYVSAKI  
 LEVGISEGIKEGLTQIMKFTISLYPKANLPNITVTQMLSSGKFTNNVTLFDMVQHINN  
 TMYTTLEAEYEYSKFCGVVSSMAKYKNITFNRTYGYSTAVTEAVTQGKTNAINTLTPA  
 TNTLTATAIISMVAIVVIVLVMIIYLILRYRRKKKMKKKLQYIKLLEE

>PF08\_0138, 375 bases, 469C0E39 checksum.

MKVHYINILLFALPLNILVSSKNTYIKYNTLNKLIIRAHRTLCECELYALSNDNDP  
 EMKEVMQQFDRQSSQRFLEYDERMKTTRQKCKDKCDEAIQKIILKDKLEKELMDKFAT  
 LHTDMQSDAIPTCVCEKSLADKVEKGCLRCGGVFGGGVMPGFGAIGGTALYALNQLKP  
 TALKAAIAAANEAGIAAGKIAGDAAGMKVVSFGLKHFRVDELFPDIFKNFVNTKPYNE  
 ITTIANSILENYRAICTGVENIKAPTACKTFEYKFGIFIEGSRKPGPPAYNAIPQGLK  
 EISIKAEQAAATASKNASETVSTAIKARETALIEAGFNSSITSINASIFAIVVIVLIM  
 VIIYLILRYRRKKKMKKKLQYIKLLDE

>PF08\_0105, 388 bases, 66769F checksum.

MKVHYINILLLYAVNLSILLISSHINIQKNPYINALHTLNTTKIPTNRFLCECDLYTS  
 IYDNDPEMNMVMQQFDERTSERFHEYHERIQEKRRKKCKEQCERDIQKIILKDKIEKEL  
 TEKLDALQTDINTEDIPTCVCEKSIADKTEKYCLKCGYGLGSVSPNVGLIGAIAVNVW  
 KTGALIAAKNAIAEGAAAGKAAGEAAGIATAIDELYNNFFLTILGRKSVQDVITAKN  
 FWDPAFIYKVVKLESNNVCFITPQPQTHASFCSLESRLRNTPDFFEKYVVAGTQTVVSK

SSNAAAQATKDITEQVTTAAIESSKNTIEAACFTYHTAI IASIVAILIIVLIMVIIYL  
ILRYRRKKNEEKTTIYKIIKGIVMFCCRYIKRNLIIFYVIS

>PF08\_0104, 332 bases, CB5FD5D3 checksum.

MRIHYINMFLFSLMFINLLNVNKNHYNTTLHTPNNTTKIPTTRLLCECELYAPSNNND  
PEMKQVMDNFDRHTQQRFFHEYEQRMINKNRKECKEQCEQNIQKLILKEKIQKELKEKFS  
ALQIDISTHDIPTCVCEKSVADKTEKFCCLKCGYGLGGALTAWQIFGYTGIYGWANYAA  
LLAHEAGVKAGIKVVIDMFSTYPGLISLPGVDLTKMINGSNFNIPMELVNIVKGLSNG  
LCKTPNKHLFCAFTNMEKQSLVSFANSASQSGIMEAASVQGAKVAIKTTTADFSYN  
MIVSGITIFVIVLVMVIIYFILRYRRKKMKKKLQYIKLLKE

>PFI0010c, 376 bases, C63A9389 checksum.

MKVHYINILLFALPLNILIYNQRNHNSTTHHTLKIPIITRLLCECELYELANYDNDPEM  
KEVMQQFEDRRTTQRFHEYDERMKTTRQKCKDKCDKEIQKIILKDKLEKELMDKFATLH  
TDIQSDAIPTCICEKSLEDKMEKECLKCAQNLLGGIVAPSTGVLGEIAALAVNAWKTEA  
IAAATKAAIAKGTAKGLAAGAAKGVAEVIAQVESQFRLSTIGVKELGSIFNASNYTNE  
TFISGYIYAQYQGSQCGSLSMLLGKSKPFCTFVEGRIFATSVRVGRSFPEDFIKTTV  
QTIVKNAKTAEATKAQVASAEKAAVLETSKKAIEATTPPYTPIIVSIVAIIVVILI  
MVIIYKILRYRRKKMKKKLQYIKLLKE

>PFI0015c, 359 bases, 9D20BEC3 checksum.

MKLNITKILLFFFPLNILLTSYHVHSKNKPHTTPHHTPTTTSRVLSECDTQSSIHNDND  
EEINSVKEVFDRQTSQRFEYQERMKEKRQKRKEQRDKNIQKIIQKDRMEKNIAEKIE  
KGCLMCGCGLGGVAGSIGLFGGVAINIWKPAALKAAIKTAIANSADKIAEAANSAGIQ  
AGKEFVIAGLKRMGISTLGGKDLGTYFATTSYKNITNIAQAVYEQHFECADYPLWSV  
RVPSSAAKHDFLFCQSVSNQIPSVSQPKQYISRIDVVQKTVQNIIVTKAEGVAADASAV  
KSAELTAEITKEQTTAINTIFMSKQTAI IASVVAILIIVLIMVIIYLILRYRRKKMK  
KKAQYTKLLNE

>PFI0020w, 343 bases, 3C03B2D5 checksum.

MKIHYTNILLFPLKLNILVNTHKKPHTTARHTQKIPTTRSLSECELYAPVNYSDPQM  
KEVMDNFNKQTQQRFFHEYDERMKTTRQKCKDRCDKEIQKIILKDKLEKELTEKFATLQ  
TDIQSDAIPTCICEKSLADKVEKGLRCAQNLLGGVAPGWGLLSGFDYVTWSQYISGIA  
AKAAADAGLKAGVKVGLVNVVKIVRNTLGSAGEVPPMDWEKLIIFGNFSDGVTLHAIF  
KNLDNMMNGYLDNRKYSQFSMVVQKFAGNFKPITAKYSKEVAEVTKAVADAKTGVLTK  
AGNATSSLSTGITASIIAIVVIVLIMVIIYLVLRYYRRKKMKKKLQYIKLLEE

>PFI0030c, 367 bases, 56182295 checksum.

MKIHYINILLFVIPLNILIYNQRNHNSTTPHPPNTRLLCECDIYTSIYDNDPQMKAV  
MENYNRQTSDRFKEYDERMQGKRQKCKEQCDKEIQKIVLKDIDKELTEKFATLQTDI  
QSDSIPTCVCEKSLADKTEKFCNCGYGLGSVAPSIGLLGGPGIYGWKTAAALAAATKD  
AITKGLAAGEAARIKEGINAVIAGIKSTFSDKLGGEALKSVITAQKYNKVALISESI  
YSEFSRSGCDITSSSFLKNPFCTSVYEGIDAISSGGNGVSPEDFIKRTVQSMVSDANG  
VANAAAEIAEATEKAKAIKTSTDAIEAASTQLYGAIGYSILAILIIVLIMLIIYLIILR  
YRRKKMKKKLQYIKLLKE

>PFI0035c, 381 bases, BA6B98F checksum.

MKFNYYNILLFSLSLNIFLLSSQVYNQRNHYITRTPKTNTRTLCECELYAPSNDNDP  
EMKAVMQDFDRQTSQRFEYNERMMKNRQKCKEQCDKEIQKIILKDKLEKELMDKFAT  
LHTDIQSDAIPTCVCEKSLADKVEKTCLKCGVVLGGVTPAWGLISGIVYTGWKAAAL  
AAAKLAAEAGAAKGLAAGAEEVGDVAVILGLNSEFGLSTQAVQKIGLVINGTNYTNVS  
MITEAIFTKYKGCMSLSPGASPGSFRILVTDPKFCNLFLKKFVPIGSLDRNAITNA  
IEKKVETMVLQAEVVAEATKTQVTSETTAELTAKQTTAINTIYMKGQTAI IASIVAIV  
VIVLVMVIIYLIILRYRRKKMKKKLQYIKLLDE

>PFI0050c, 309 bases, 967AAE89 checksum.

MKLQYYKILLFSLISLSIFFSSSYAHNKNKRYITPQTRTTTSRVLGECOLYMPNYDKDA  
DMKSVKENFDRQTSQRFDEYEERMQEKRKRKEQCDKDIQEIILKDKIEKSLEEKVEK

CCLICGCGLGGGVTPFIGLFGGLAVNEMKKVAAVAATEVGIKEAIKELGKIFELEAGS  
 NMQWTKMINAGNYSQKMSLVEIVTILKNKCEEDEALAGPLFCASKAATESGEVFEFS  
 GNISRMAADAADAARKAANEKLAEMTSVGTICSNPVVISAIVVVIAVILLIYLLR  
 YRRKKMKKKEQYTKLLNQ

>PFL1945c, 105 bases, 3AE846D5 checksum.

MKLFKILYLIAALLAINLIAPSVCNENVEGKKKKKGCPLRNFNQEFRRKHHKAILIS  
 SVVSAIALLFGTAYGIGLHLNNTFKSILDLGKKRSASRSPHLKLLK

>PFI0065w, 378 bases, C08A936C checksum.

MKIHYTNILLFPLKLNILVNTHKKPHTTARHTQKIPTTRSLSECELYAPVNYSDPQM  
 KEVMDNFNKQTQQRFFHEYDERMKTTRQCKDKCDKEIQKIILKDKLEKQMEEQLTTLTLE  
 TKIDTDDIPTCICEKSLADKVEKGCLRCGSVLGGVMPGFGAIGGTALYALNQLKPAV  
 FKAAIKAALEEGAAEILAAANAAGNAKGMIVIHGLKLFVVDKLFPEIFNPFVAKNIY  
 TEITNLASTINSKYSTTCTWLKSGATAHPACNDFQLGLGIHLPNGSTLGIIPPYTAIRQ  
 GLKGILQKATQTADAVADAKSAQVTAATKNQTALLEAGFNSSITSIYASIIAIVVIV  
 LIMVYIYLILRYRRKKMKKLLQYIKLLEE

>PFI0070w, 350 bases, 2AE7E7B0 checksum.

MNVHYINMLLFAFPLNILVTLYHEYNQRNHSATFHTSNTKPTKTHRTLCECESYSPS  
 NYENDPEMKEIMEIFNHQTSERFREYDERVQNKRKQCKEQCEKDIQKIILKDKIEKQL  
 AQQFSPLQTNIDTNDIPTCVCKSLADKTEKVCLNCGKTMGAVAPAWGLLSGLGYAGW  
 SHYVAASILEEGIKKIEASLIKITEIATHIYQVSTADIPKITTTQILSSGHFTNNVS  
 FFDMVNYINNYMNTLESEGYSQFCWAISSMASRKPITAFNKTYAIYSEAVTKAVTGA  
 ENGVIADLAPSTSSITTTIIASIVAILVIVLVMVYIYLILRYRRKKMKKLLQYVKKL  
 KE

>PFI0075w, 365 bases, 8E5CCF5B checksum.

MKVHYINILLFAFPLNILVTLYHVNTHKKLSTTTCDIQTRLLCECELYAPANNDNDP  
 QMKEVMDKFSKQTQQRFFEEYDERLQEKQICKDKCDKEIQKIILKDKIEKQMQEQFAT  
 LQTDIQSDSIPTCVCEKSLADKFEKTCLKCGVLGGVAPPELGLIGGTALYGISVWKP  
 KAIASAVEAQKAGEAAGKAAGDIAGVAEVIISGLKSKFSLDTLFGTTLDFKITTKNYV  
 NETVISGAVKLQYQVSCATDPLGETSVLCFYKTIGEPNATAAVVENAKIVVTDIAIQEA  
 SEVAFKVTASKTAEFKEINIATVESICNSYNTAIIASIATIVVILVMIVIYLILRYS  
 RKKMKKLLQYIKLLNQ

>PFI1805w, 371 bases, 794CF712 checksum.

MKLLHYCKVLLFSVPLNILVHNKNKSYITPQNTRNTRLLCECELYTSIYDNDTEMKAV  
 MGNYNQOTSQRFFEEYNKRMNKNRQCKCKDECDKEIQKIILKDKLQKELMHKFATLHTDI  
 QSDAIPTCVCEKSLADKVEKTCLRCTQNLGGIVAPSSGVLGIAEGALIVWKPAAIKA  
 AKAATAAAKAAASDAATQAGIEAVRLEINKLSVYFNGTTGFVDLTPIVTSSTYDNGLV  
 LVECAKKLIGDLSNGRGGYTGFYNTAIHTESGELYVGNFVGIGKAAHDAKLASETTA  
 LTEAKVGAVDTTYGGFQTYITASVIAIVVILIMVYIYLILRYRRKKKNEEKTPVHKI  
 IRRINIMCLAFFIDIFVYEILLV

>PFI1815c, 369 bases, EF13EBCB checksum.

MKIHYTNILLFPLKLNILVNTHKKPSITARHIQTTRLLCECELFSPQNYDNDPEMKRV  
 MQQFHDRTTQRFHEYDERMKTTRQECKEQCDKEIQKIILKDKMEKQMAEKLSTLETKI  
 NTDDIPTCVCEKSMADKTEKFLNCGKNMAAIAPWWGLVCGSGYAGWLHSAMAAIDK  
 AIAEGAAAGIKAGHLAGTNAVIEQLRTLGIYFVGNKQLETIIDVTNYMNVSFYDKVY  
 SHYITLCTPRPVNGHLVSNFNFSRDFCKLFHQKDLVSLDIKSVKAIKKNVEEAVAGA  
 EQAAKAEVSNVTATKTTEFTTKNIAEVEAATTSYYPPIIASIVAIIVLIMVYIYKI  
 LRYRRKKMKKLLQYIKLLEE

>PFI1825w, 367 bases, 9E7FDB7A checksum.

MKVHYINILLFELPLNILIYNQRNHNSTTPHPPNTRLLCECEWYAPSNYDNDPQMK  
 VMQDFDRQTSQRFFEEYNERLLENKQCKEQCDKEIQKIILKDKLEKELAEKFVTLQTD  
 IQSDAIPTCVCEKSVADKVEKTCLKCGVLGGVTPAWGLLSGIVYTGWKAALAAK

ELAEKAGAAEGASQGAAAGAVEVIKSIKTTFGIESLGVNPLQSLFNAENYMNAKFISE  
 SIHSEFISSGCGAILKPPNKPICTSVYKGI EATS RKGKVKPIEFIGKKVETMVSQAKD  
 VAEATKAQVTSETTATLTDLKTGVVQTTYMGYQTVIIASIVAILLIVLVMII IYLILR  
 YRRKKMKKKLQYIKLLEE

>PF10\_0003, 345 bases, 361D0614 checksum.

MKLHCSKILLFLLPLNILVTSLSNVHNNKLYNTPHHIPTTTSRMLSECDLYIPKYDN  
 DADMKS VKENFDRQTSQRFE EYDERMKGKRQKRKEQRDKNIQEIIEKDKMDKSLAEKV  
 EKGCLRCGCGLGGVAASVGLFGGLGIYVSKSAALATAIAEGAETAKAAGEAARI PAAI  
 DAVIKGITKVFVSTLDGKELGTYITATNYTNFKTIALAINEQYNPLSCII PDPGADK  
 SICPWVMRNFFAAKDSPRNVVSAYNSIEVAVKSIVLEAQSVTERAAKKATEDVIKSSI  
 AAVDAKYVICQNAIIASVVALLIIVLVMII IYLVLR YRRKKMKKKQOYTKLLNQ

>PF10\_0006, 361 bases, 32F0C016 checksum.

MKLHYSNILLFFFPLNILVTSYHVYNKNKIYITPHHTTTTTLRLMLSEYGVHTSIYKND  
 ENMKSLKENFDRQTSQRFE EYEQRMIRKRKKYKEQCDKDIQKII EKDKMDKSLAEKVE  
 TGCLKYGCGLGGVAGSVGLFGGFGIYGWKTAAALAASKNAVAEATAKGVAKAIDL VKS  
 TFDVQNIAGQPLETVLNVINYTDVSNYHLIYSQYKTT CISTSSSTPVTGGPETFCISI  
 WNKSLSGLGSNVVFEETKVI EATVKTIVSSAEKVAGEALEKATEGVIKTSTATIEST  
 YASCQIAIIASVVALLI IALVMII IYLVLR YRRKKMKKKAHYTKLLNQKIYSFKILN  
 PFLCCMNSRCLNT

>PF10\_0393, 359 bases, E94B9A9C checksum.

MKVHCYNILLFSFTLIIILLSSSQVNNQMNHYNRAHMKNIEPTKSYRSLCECELYTSM  
 YDDDP EMKEIMHDFDRQTSQRFE EYNERMKNRQKCKEQCNRDIKNI I LKDKIEKELK  
 QQLATLETDI STDDIPTCVCNKSVADKVEKTCLKCGGVLGGAVPELGLLCGYGAYELV  
 KVAIGAAEKAAIAEGAKAGIAEGIRVAIKGIGAFNIEFLDGKTLAEVITGKTFNNST  
 FFVEKFVQ EYNTVCLSSTTYQDTLFCDYGSMFGGKVDNITAI SLNAKNTAIKAGQAAA  
 KMTTETTKALTA EKTGEVTSTSAIFSNPMVISFIVVVI I VI ILLIIYLILRYRRKKM  
 KRKLQYIKLLE

>PF10\_0396, 378 bases, 59FE4D31 checksum.

MKFNYTNIILFSLSLNILLSSRVYNKRNHKSIILHTSNENPIKTHRSLCECELYSPT  
 NYDSDPEMKRVMQ QFHDRRTQRFHE YDERMKTTRQECKEQCDKEIQKI I LKDRLEKEL  
 MDKFATLHTDIQSDAIPTCVCEKSLADKTEKFCLNCGVQLGGGVLQASGLLGGIGQLG  
 LDAWKAAALVTAKELAEKAGAAAGLKAGDIHGMKIVIEGLKALKVDTLKSGIFNSFVN  
 NSHYTEVTGLAIAIDTEMNEVCSATYIGIHPICVVREKLGVI PKAGGTMVKQKDAITN  
 VLKQALEKATQSAEALSETTAEDVAAKLTAQKTGAINTIFMSNQTAI IASIVAI VVIV  
 LIMVIIYLILRYRRKKMKKKLQYIKLLEE

>PF10\_0397, 348 bases, E777225B checksum.

MKLQYSKILLFSLPLNILVSSSYAHNKNKSYIAPHIPTTTTRVLSECNLYIPKYDNDA  
 DMKS VKENFDRQTSQRFE EYEERMIKNRQKRKEQRDKNIQKI I HKDKMEKNLAEKVEI  
 GCLRCGCALGGVAASVGLFGGLGTYGWKIAATATAMELAKEAAEQAGAAAAADAGKNA  
 VIAGLKELGVQNIAGQPLVSYLTATNYHNATFISSA INNQYSPSSCIVSSGTRSGPV  
 ARETFCTWVMQKSTAAANVQRSSVSFNDLI I KTIENIVTDAKKAAGEATEKAIEEVIQ  
 RSTAAVESTYASCQSAIIASVVAIVVIALVMII IYLVLR YRRKKMKKKAQYTELLNQ

>PF10\_0398, 350 bases, 41D60D38 checksum.

MKVHYINILLFVIPLNILINDQRNHKSTTHHTLKIPI TRLLCECELYTPANYDN DPQM  
 KEVMDNFNRQTQ QRFHE YDERMVEKRMQCKDKCDKEIQKI I LKDKLEKELMDKFATLH  
 TDIQSDAIPTCVCEKSVADKMEKGCLRCGSILGAAMP EMGSIGGSLLSALS AWKPVAI  
 EAAEKAAIAKATDLATQAGMREVVLKIEQFLKNFTEKEGLVNFTSVVNKSNFKCPTAL  
 FQANELLSDSCIPDEVTNRTSTFCSTIAYGEKTT FEPFAQAGATTFQETLTAKTPVL  
 QARYTAAVKTAYGGYQTAI IASIVAI VVIVLIMVIIYKILRYRRKKMKKKLQYIKL  
 EE

>PF10\_0399, 326 bases, F0FF1EC6 checksum.

MKLHFPKILLFFFPSNILLTSYHVHSKNKPHTTPHHTPTTTSRVLSECDTQSTNYNND  
 EDIKSVKEIFDRQTSQRFEEYEERMQEKRQKRKEKCDKNIQKIIQKDKREKSLEEKVE  
 KCCLICGCGLGGVAASVGFITIAVNEWTKAAEIEIAKIGIMNKATSAGVAKGIEATID  
 GLKGMLGFGNLRGVDIPAMVTEKSFNDANLLVPSIQKAYNSCSQIPTGSAKPPFCGA  
 VETNMQIVFSSAHSIAMESGELATKTTATLSPQFISDEITLXKTASTNLVNVITYSVI  
 VIILVIVLMLIIYLVLRVRRKKKMNKKQYTKLLNQ

>PF10\_0400, 372 bases, A7F45BD7 checksum.

MKFSYFNILLFSIPLNILINDQRNHKSTHHTLKIPIITRLLCECELYSPDNYDNDDEM  
 KRVMQQFEDRTSQRFHEYDERMQSKRMQCKDRCDKEIQKIIILKDKIEKELSQHLSTLE  
 TNIDTNDIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGAVAVNELKKAAMAIA  
 IKDAIAEGLVAGETARIQASIKAVILGIKSKFRIDTLGGEVLESIIITAQKYDDVSLIS  
 ESIYMQYQSTCLPQYVGHGADLSKPICHTVYTLDFVQGVHVPGLQGSIKKALEKIV  
 AEAKSNAVSETANVTTRQTAVFESRNIAAVDATYASYQTAIVASVVAILVIVLMLII  
 YLILRYRRKKKMKKKLQYIKLLKE

>PF10\_0401, 295 bases, 57990E94 checksum.

MKLYYFKILLFSLLLNILAHNKNKSYIAPHIPTTTTRVLSECNVYIPNYDNDPDMNSV  
 RENFHKKTEQRFHEYDKRMKRNQRKEERDKNIQEIIEKDRMDKSLAEKVEKGCLKC  
 CGGLGGVAASIGIFGTIAVNEWTKAATAAIDLAIQEGIDAGVKVIAEIKATNAFKS  
 IWYVELSSFINGSNYNTVDGLSAATKAALDSIGKRCTSSIVDRACNGILNNSDGWFSS  
 IAEAGKQAATAATESAKTTKLVDTVTTTSTHLYSAIGYSVLAIFIILLVMVIIYLILRY  
 RRKKK

>PF10\_0403, 370 bases, BF2901C3 checksum.

MKLHYTKILLFSLLLNILAHNKNKSYTTIHTPITTSRVLIECNVYIPNYDNDPDMKSV  
 KENFDRQTSQRFEEYNERMIDKRQKCKEQQEKDIQKIIILKDKIEKELAEKFVTLQTDI  
 SINDIPTCVCEKSVADKVEKTCLKCGGVLGGGITPGWGLISGIVYTGWKAALAAAKK  
 AAIAEGAAGLAEGIKEGIEVMKGLCRDFRLSEVDVKKLGLVFDGKNYNNTEYIFKA  
 IFSKFDESCMPSSTGAVRGASEPICNSVWSKFVFTNRSSSRNSIINAIKENVETIVSQ  
 AETTAGATKEMVTQEVTSAAIKTNTTAVNATYASCQTVIIASVVAVVIVLVMIIYLV  
 LRVRRKKKMKKKLEYIKLLKE

>PF10\_0404, 334 bases, 3EF5E9E3 checksum.

MKLHYTKILLFFFPLYILEHNQNKPYITQHHTPTTTSRVLSECDIPTSNYNNDDEDMKS  
 VKENFDRQTSKRFDEYEERMKDKRQKRKEERDKNIQEIIEKDRMDKLLAEKVEKGCLR  
 CGCALGGVAASVGLFGGLGIYVSKSAALATAIAEGAETAKAAGEAARIIPAAIDAVIKG  
 IETKFGVSTLGGQKMETFFNTTLYTEVSKIADAVYNQYAATCITSGNGARGPICTLAW  
 QYSESRGNVVSAYNSIEVAVKPIVSQAETVAERAVKTATDEAIQRSIGVVESTYAIQ  
 TAIASVVAVIIIALVMIIYLVLRVRRKKKMNKKLQYTKLLNQ

>PF11\_0009, 340 bases, 4B8DCDDF checksum.

MKIHYTNILLFPLKLNILVNTHKKPSITPRHIQTTRSLCECELYAPANYDSDPEMKRV  
 MQQFHDRTSQRFHEYDDRMKTTRQKCKDKCDKEIQKIIILKDKLEKQMAQQFSTLHTDI  
 QSDAIIPTCVCEKSLADKVEKGCLRCAQNLLGGVAPGWGLLSGFGYVTSQYISGIAAKA  
 AADAGLKAGVKVGLVNAVKIVTNTLGSAGKVPTMDWEKLIIFGNFSDGVTLHAIKFNL  
 NVMNGHLDFGKYSEFSTVVQKFAEKFKPITAKYSTEIAEVTNAVADAKAGVLTAKGN  
 ATSSLSTGITASIIAIVVIVLIMVIIYLILRYRRKKKMKKKLHYIKLLEE

>PF11\_0010, 323 bases, AE4AA79C checksum.

MKIHYINILLFALPLNILVNNQRNHNNSTYHTSNTTKTIKSHRSLCECELYAQSNYEND  
 QEMKDVIKEFNDRTAQRFEYNERMQVKKQCKEQQCDKEIQQIIILKDKIEKELTERFS  
 ALETKIDTNDILTICICEKSVTDKFEKTKLCSGIFATAVPELGLIGGTVVYAAAVKAA  
 TKAGMEAALVGLSVNGLRGLLGEKIKDLVTTTTFQCPNALMGLVQNVKDTQCVGAAA  
 QSQVFCCKLLPESTSRIIQKAAAAGREGAEAYNTTFSSTTITAFITDPIVISAIVVI  
 SIVVILLIIYLILRYRRKIKMNKKLQYIKLLKE

>PF11445w, 1364 bases, A5B7A430 checksum.

MIKVTIFLLLSIFSFNLYGLELNEKVS IKYGAEQGVGSADSNTKLCSDILKYLYMDEY  
 LSEGDKATFEKKCHNVIGNIRNTFSNKNTIKEGNEFLMSILHMKSLYGNNNNNNAGSE  
 SDVTLKSLYLSLKGSONTEGESEVPSDDEINKTIMNFVKFNKYLLDNSNDIKKVHDFL  
 VLTSQSNENLLPNKEKLFEQIVDQIKYFDEYFFASGGKIKVKKGYLKYNFLDIYKQPV  
 CSAYLHLCSRYYESVSIYIRLKKVFNGI PAFLDKNCRKVKGEFEFKLMDMELKHNHIV  
 ERFDKYI ISDDLYYVMKVFDLKNVDKI QVSKIDDINNLNIYEHKETMHLSAKNLSRY  
 IDIKKELNDEKAYKQLMSAIRKYVTTLTKADSDITYFVKQLDDEEIERFLIDLNFFLY  
 NGFLRITEDKHLINADDVSPSYINLYRSNNIVALYIILKTQYEENKLSEYRAHKFYRRK  
 RVSNITNDMIKKDFTQTNALTNLPNLDNKKTTTEYYLKEYENFVENFQPDLDHIMKLQL  
 FFTMAFKDCNVNQNFTETSKKLWFDLLYAYDKFGWFYIHPNEVINSINKTDFVRHVLV  
 SRNFLKNNQDLTFLETQVAKIVEI INLSLEVDKSPDSLDFSI PMNFFNHKNGYHVMN  
 DDKLKLTSYEYIDS IANNYFFLSEYKNDVFRGTGNNFKLYFNLPNIYSLAYQLFNELA  
 ININVITNVPLKYLKYNASYAYFTLMNMIGKNHDIYSKGSRFVYASYILGLVFFIES  
 HIDIARLKPDKFFFMKQSLPI IDHVYHKDLKTLKKNCTLLTDFMKINKNSQNYSLTHT  
 EEMIKILGLLTVTLWAKEGKKS VYDDDVS LYRKL MVSCVFNGGETIQEKLANNIEKS  
 CDISQYGIKSKNLKDMIDINLS IHKWNPAEIEKLAYSFVLSCKMQKLMYKPMNVEKLP  
 LEDYYKLSLAPDMVKTYHCYKLGKQAELLES IILKKKFVRFVTD AIDVYDFFYIKK  
 VLSSRIKKEYNEFLQDKRAFEKKELETILNNSPFSEEQTMKLINSYECHWFTSYENFR  
 ILWMHASSNLGTGTYLKNFFSELWQNI RFLFKSKL KIRDMEYFSGDISQMNLLDYYS  
 MVHSESHCQEKMQVLFITLRDSKEENRSEIAQKVKSAYYQCKLDYYKNHHSDFIHRH  
 PNDFLNNKVYVLKQPYLMSNVPLNPNPKKVSRLFVTEGTLEYLLLDKINIPECFGPCT  
 KLHFNKVVIKESKQRIYDMTINNALVPEIQPYNRRKYMTIYINEAYIKNIVSDALTSE  
 EIKRHDIQKGNIKICMGKSTYLTEPILTEEHFNLTHKPVYDFSSVKHNLKV FHMKNEH  
 LVSEDPNDDCFINYPLATINLGKHKKIYNK

>PF11\_0011, 327 bases, 3D96A0A3 checksum.

MKLHYTKILLFSLQLNILMLSSYAHIKKKIYITPQIPITTSRVLSECDVQTSIYDYDE  
 DMKSVKDNFDRQTSHRFEEYEKRMNVKRQKCKEQCDKEVQKIILKDKIEKELTVKFGA  
 LHTHITIEDIPTCICDKSLSDKVEKTC LNCGGILGTVPVPGWGILGSIGFYGFVNSIAI  
 DVAVKEGIKVLHELKEITALEILLNNKLEALVTPETYACTNALNKS IMAAKLTICKA  
 SPQPAPCSPKLFDL SVIAPKVHNATMEGINTAKAAEVNTWNTAFSSPAFFSNPIVISA  
 IVLICIAVILLIIYLILRYRRKKQMNKLLKYIKLLKE

>PF11\_0021, 330 bases, D3A17289 checksum.

MKVHYINILLFALPLNILVRLCNVGS PHKNPSITPKFPPNTRLLCDCELYSPANYDSD  
 PEMKAVMQGFDRQTSQRFEYNERLLENKQKCKEQCDKEIQKIILKDKLEKELAEKFV  
 TLQTDISINDIPTCVCEKSLGDKVEKSKLCKGKNLGGFIPGLGLIGGTAVYAAAVNAA  
 TKAGMKAALDELKSVNGLFQLLGENIKDLVTATNFNCKDALLRRIDTITTPLCKSDEA  
 VNNLYCSLKSGKQPMGFSKIKSKISNAAEWAASASDEAKAEALNATFTWETFFSSPLG  
 ISLLVTVCIIIIISIIYLILRYRRKKKMKKLLQYIKLLEE

>PFL0010c, 378 bases, BFE5F602 checksum.

MKIHYINILLFALPLNILIYNQRNHNSTTHHTLKIPI TRLLCECELYSPSNYDNDPQL  
 KKIMENFNKQTQQRFEYDERMKTTRQKCKDKCDKEIQKIILKDKLEKELMDKFATLQ  
 TDIQSDDIPTCVCEKSLADKVEKNCMKCTQNLGGIVAPSSGVLGIAELGLNAWKTTE  
 ITAAIAAAEQAGAAKGLAAGAAKGVAEVIAQVESQFHLSTIGVNELGSVINVTNYNNS  
 QFIFKAIFTKYRGSCLPSPDRLTVAAGEETFCRTVNALGFTRRNVDPSLLQDSIKS  
 VGNQIVTKAETAASTETAKVTASETATLKA AKVGEVNATYMGYQTP IIVSIAAIVVIV  
 LVMVIIYLILRYRRKKKMKKLLQYIKLLEE

>PFL0015c, 345 bases, D391267A checksum.

MKLHCSKILLFFFPLNILVTSYHVYSKNKPSITSHHTQTNRSLCECDTQSTNYNNDEE  
 IKS VKENFDRQASQRFEYEEERMKEKRQKCKEQRDKSIQEIEKDKREKSLAQKVEKG  
 CLICGCGLSVAGSVGIFGTVAVKELTKAAIAKAVVVAKEAGMAAAKAEGAAAGKEFV  
 IAKLQEMGISTVGVQGLQSYFVTTDYTNALTIFRAINNQYSPSSCIFVSSGTRQAFCT

WVTEQSKSVANIREMLQNSVSYTKVTEKAVGTIVTDAKKAAGEATEKAIEEVIQRST  
AAAESTYAGCQSAAIIASVVAIIIIIALVMIIIIYLVLRYRRKKKKMCKKAIEYTKLLNQ

>PFL2585c, 375 bases, C547831B checksum.

MKMKHVYFKVLLLLFSLPLNILVTLHHVDKKTNDYRPYTLTYTKLENTITSSRLLCECD  
TYAATNYDNDPEVKKVMQQFDEHTTQRLLEYNEHMIKKRKECKEQCDKDIRKIIILNDK  
IEKQLKEKFSALQTDIGANYLPKCTCEKSLSDKVEKTCLKCGGLLGGGITPTVGGFFS  
TIVTYLLTDAAAKQAGILAAKKVSVEAGIQTFIQQLSDMSNLHVLIGHKLVNLITPKT  
VGNIMELSKTIHETLQSTCFAAEPRINDVMTILCSTDSYIFDAQYLQQQVANIATKAA  
EEGAKAGALASQNAEANTWSLGTISNFFFTNSAGIAFTTIVLIAIILLITYLILHYRK  
KKENEKTTIYKIIKIDMFYVVDVYR

>PFL2605w, 346 bases, BF2F294B checksum.

MKLLHYCKVLLFSLPLNILVYSKNKPYITPRHTPNTTSRVLSECDINTSIYHNDPDMK  
SVKENFDRQTSQRLREYDERLQDKRQKRKEQRDKNIQKIIHKDKMEKKLAEKIEKGCL  
MCACGLGSVAGSVGLLGGFGIYVSKSAALATAIAEGAETAKAAGEAARIPAAIDAVIK  
GITKVFVSTLGVQRLESFLTANIYNNVTMIARAINEQYNPSSCILPIGGSGADKSIC  
PWVMEKYLPQNIPEMTRGGALSMDVIETAVKSIVTDAKTVAETAACKATEEAIKAS  
TDAVESAYAACQTAAIIASVVAIIVLVMMIIYLILRYRRKKKKMKNKQQYTKLLNQ

>PFL2615w, 351 bases, D0F6F148 checksum.

MKVHYINILLFALPLNILIYNQRNHKSTTHHTLKIPIITRLLCECELYTPANYDNDPQM  
KEVMDNFNQRQTQORFHEYDERMVEKRMQCKDKCDKEIQKIIILKDKLEKQMEQQLTTLE  
TKIDTNDIPTCVCEKSMTDKVEKGCLRCGRNLGVAVPGLGVLGAYGAHSIVKVAMATA  
EKVGIQLGIDAGNAAGIKAVIEALNSSLNIDNLGGITLDTVLKGNFKNIDFLVYILT  
DKYNTTCTVSNTEVETLLCYIGKEKPTLPYTLIQSNVRKAVAEATEVATSTTEEMTTI  
YTTQELSKVTSTGAILSNPIIISFIVIVIVVIFLIYILRYRRKKKKTKKKLQYIKL  
LKE

>PFL2625w, 379 bases, C8627C7E checksum.

MMLNYTNILLFYLSLNILSSSSEVYNQRNHFITYTPKRSTRLLCECELYTSIFDNDPE  
MKSLIEHFNKQTQORFHEYDERMKTTRQKCREQCDKEIQKIIILKDKLEKELAEKQVTL  
QTDIQSDAIPTCICEKSLADKVEKTCLKCGGVLLGGVTPAWGFLSGIVYTGWAAALA  
AATKEAIAEGAAGAAAGTKAGIKAVMDVLYSDFGLSIEGVQKMGLVLSATNYKDVPM  
ITKALYSKFQVSSCLRGGPVPVPPVRPTDGTFCSAMLEKILAQENVVKQNSLEGSIK  
SVVNQIVTEAKSAAVSETAKVTASETETLTKATNIAAVNATYASSQTAAIIASIIAIVVI  
ILIMVIIYLILRYRRKKKKMCKKLQYIKLLEE

>PFL2640c, 326 bases, F23A4A4C checksum.

MKVHYINILLFALPRNILVNTTHKKLSITPPHIQTTRLLCECELFAPQNYDNDPEMKS  
MQQFEDRTSQRFFHEYDERLQEKRQICKDKCDKEIQKIIILKDKLEKELTEKFATLQTDI  
HSDAIPTCICEKSIADKVEKTCLNCGKNLGGFVPGGLGLIGGSALYVAAVKSSVELGIK  
MGMQSVISDLKVLWDLTSLIKAVIENFVTPTNYCNITSIIEFLQNKSSCAAKTKI  
TPLFCSTVEYQGPEELAKRVAGIVEQAQFAGAQAANEKFLLELTTSYAILSHPIVISLI  
VVVAIAVILLIIYLILRYRRKKKKMCKKLQYMKLIKE

>PFL2645c, 317 bases, DC255E02 checksum.

MKIHYNILLFPLKLNILVNTTHKKPSITPRHIQTTRLLCECELYMSNYDNDPEMCRM  
QQFHDRTTQRFHEYDDRMIEKRQKCKDRCNKEIEKIIILKDKIEKELTETFATLNTNIT  
NEDIPTCICKKSVADKIEKTCLKYGGALGGGVMPGLGLIGGNSVYIILANYETINAFIA  
KTIEELEGIPGITKLFGAKISQFVTPAVFRKPSMLVETILSEKKKLCLCAANKNELLC  
RGMNPNVPETLPKKEVAVNEVLSSVNDTWATATPTTFFTNPIILSAIAIILVIVIM  
VIIYLILRYRRKQKIKKKLQYIKLLEE

>PFL2660w, 350 bases, 8C4AED86 checksum.

MKIHYNILLFPLKLNILIYNQRNHKSTTHHTLKIPIITRLLCECELYTPANYDNDPQM  
KEVMDNFNQRQTQORFHEYDERMVEKRMQCKDKCDKEIQKIIILKDKLEKQMEQQLTTLE  
TKITTTDDIPTCLCEKSVADKMEKTCLRCAGVLGGGVMPGMGLIDGSLGAVISVLKPA

IIAAKDAALAEATALATQAGMREVLKIEQFLKLFSEKEKIFDLKLIVNKS NFSCGSS  
 LFQNAKELANKSCVAKPNGSYTSFCNSITYSRVEPFNGYAQAGITKYNETLPLQKALL  
 EKAKVDAVNTTYAAYHTSIIASIVAVVIVLIMVIIYLILRYRRKKMKKKLQYIKLLE  
 EE

>PF13\_0004, 343 bases, D2CDA707 checksum.

MKIHYTNILLFPLKLNILVNTTHKKPHTTARHTQKIPTRSLSECELYAPVNYSDPQM  
 KEVMDNFNKQTQQRFFHEYDERMKTTRQCKDKCDKEIQKIILKDKLEKQMAQQFSTLH  
 TDIQSDDIPTCICEKSLADKVEKGCLRCAQN LGGVAPGWGLLSGFGYVTWSQYISGIA  
 AKAADAGLKAGVKVGLVNAVKIVTKTLDGFGEVPTMDWAKLIAFGDFSDGVTLHAIF  
 KNLNMMNCYLDSGKYSQFSTVVQKFAENPRSYATPYSTEVEVTKAVADAKTGVLTK  
 AGNATSSLSTGITASIIAIVVIVLIMVIIYLVLRYYRRKKMKKKLQYIKLLEE

>PF13\_0005, 331 bases, 1A2D1D55 checksum.

MKIHYINILLFALPLNILVRNQRNHRKSILSTTKSELTKTHRTLCECELYAPSKYEND  
 PEMKEVMENFDRQTSERFRKYDERIQDKRQKFKEQCEKDIQKIILKDKIEKQLSQQFS  
 KLQTNIETNDIPTCICEKSVAEKVEKTCCLKCGEILGTVVPELGLIGGTVIYASQAQAA  
 VKVGVSKAIELMKDIYFLGQVPFFDLVAKITPSNFNDKMSLIGIVHDASYTV CETTNA  
 QDTLVFCLSKYSIGRRNPSMFLSVTANQAKDAAEAAGEAATGTFSEMTSVGAI FSDAL  
 VISAIVVVIAVILIIYLILRYRRKKMKKKLQYIKLLEE

>PF13\_0006, 345 bases, 25C777B1 checksum.

MKLHCŠKILLFLLPLNILVTSLSNVHSKNKPYITSRHTATTISRVLSECDIRSSIYDN  
 DEDIKSVKECFDRQTSQRFEYEERI QEKRQKRKEERDKNIKKIIEKDKMDKSLAEKV  
 EKGCLRCGCALGGVAASVGLFGGLGIYGWKTAAALATAIAEGAAGAVAAEAARIAEGI  
 KAVIKGIETKFGVSTDGLQGFKSFFTANTYNNVKNIARAINNQYEPSSCPI TVPVDSK  
 PICTWVRANFFAAKDSPGNFTSTYEVVETAVTSIVSDAEPVATAAAQQATEEAIKAST  
 DAVESAYAACQTAIIASVVAILVIVLVMIIYLVLRYYRRKKMKKKAQYTKLLNE

>PF14\_0004, 337 bases, EB7EF59A checksum.

MKVHYINILLFAFPLNILVNTTHKKPSITPHHTPKIPTTRLLCECELFEPANYSDPQM  
 RAVMDNFSKQTQQRFFHEYDESLQSKRMQCKDKCDKEIQKIILKDKLEKQMKQELTTLE  
 TKITTTDDIPTCICEKSVADKMEKGCLRCAGVFSGGVAPSVGLLGGIGVYGWKMGAPTV  
 AMELAKQAGIEEGVKTVIAQIKGISIFNPYLESVECSKYITKLNVDNVSGLMKAVQAA  
 IKSTGETCEANSGDIVCETIYNKVERFLPVVQAGKQATTTTTTETVKNAALDTIESTAT  
 TCTTAITASIIAIVVIVLIMVIIYKILRYRRKKMKKKLQYIKLLEE

>PF14\_0005, 339 bases, 7520AA74 checksum.

MKVHYTKILLFSLPLNILVTSSSNAHSKNKTYITLRHTPPIKSRVLSECDLYIPKYDN  
 DAEMKSVKGTDFDRQASQRFEYEERIKDKRQKRKEERDKDIQKIILKDKVEKSLAEKV  
 EKGCLKCGCLAGVATSVSIIIGPIAVNEWTKAALLSAKSSAIAEGNIKIEAGV NAGI  
 KAVIDGLKSKFSLDIVAGKALEDLVTKTTYLNKNLLSEPFHIQYQSMCVGPTADIDKP  
 LCAFNIKNDTTWALKAIDGNVEKIISEAIKTTDTVTSNVTASEIPSEALEKAAIEIT  
 CSNFHTAIIVSVVAILVIVLVMVIIYLILRYRRKKMKKKQYTKLLNQ

>PF14\_0006, 367 bases, 8345C648 checksum.

MKDHYINILLFALPLNILVYNQRNYYITPRHTETNRSLCECELYSPTNYDSDPEMKRV  
 MQQFVDRTTQRFHEYDESLQSKRKQCKDQCDKEIQKIILKDKIEKEFTEKLSTLQTDI  
 TTKDIPTCVCEKSLADKMEKVCLKCAQN LGGIVAPSTGVLGEIAALAVNAWKTTALKN  
 AIAAAQKAGDAAGKIAGESKGVETIIGILEQYYSIYELKGTPLKSFFATTHYTDISNI  
 ATVIDTELNTSCGLNSLANQAICGLRTRKLGVLVAKPGQVMVTQKEAITKMITNVVHKSE  
 ITAEAAKTEVAATKTA AAIKMNTAEIAEATTPYYTPIIASIVAVVIVLIMVIIYLIL  
 RYRRKKMKKKLQYIKLLN

>PF14\_0008, 316 bases, 8FD37C07 checksum.

MKLLYSKILLFALALNILLTSYAHNKNKPYIIPRYTPTATSRVLSECDIHAPIYYND  
 EDMKSVKENFERQTSRRFEYNERMKNRQKCKEQRDKDIQKIILKDKIEKSLEEKVE  
 KGCLRCACGLGGVAAGVGIIGAI AVNEWTKVATAAAVQKGIKAGIAKAIDDLGNIVGL

IQFDLIDWAAKIDGINFLKQNSLVSIVNEVYYKCIDIENSDFLFCSATKAWDQQKST  
LGLQIISNQAAEAAVAAGKAAETAEKAEIVLVNAKSSLLYSAIGYSVIAILIIIVLMI  
IIYLILRYRRTKKMNKKAEYTKLLNK

>PFC0120w, 1417 bases, D30708CA checksum.

MVSFFKTPIFILIIFLYLNEKVIC SINENQNENDTISQNVNQHENINQNVNDNDNIEQ  
LKSMIGNDELHKNLTILEKLILELESLEKDKLKYPLLKQGTEQLIDISKFNKKNITDADD  
ETYIIPVQSTFHDIVKYEHLIKEQSIEIYNSDISDKIKKKIFIVRTLKTIKMLIPL  
NSYKQNNDLKSALEELNNVFTNKEAQEESPIGDHGTFFRKLLTHVRTIKENEDIENK  
GETLILGDNKIDVMNSNDFFTNSNVKFMENLDDITNQYGLGLINHLGPHLIALGHF  
TVLKLALKNYKNYFEAKSIKFFSWQKILEFSMSDRFKVLDMMCDHESVYYSEKKRRKT  
YLKVDRSNTSMECNILEYLLHYFNKYQLEI IKTQDQDFDLHGMMEHKYIKDYFFSFM  
CNDPKECIIYHTNQFKKEANEENTFPEQEEPNRQISAFNLYLNYYYFMKRYSSYGVKK  
TLYVHLLNLTGLLNYDTRAYVTSLYLPGYNAVEMSFTEEKEFSKLFESLIQCIEKCH  
SDQARQISKDSNLLNITKCDLCKGAFLYANMKFDEVPSMLQKFVYVLTKGLKIQKVS  
SLIKTLDIYQDYSNYLSHDINWYTFLLFRLTSFKEIAKKNVAEAMYLNIKDEDTFNK  
TVVTNYWYPSPIKYYTLYVRKHIPNNLVDELEKLMKSGTLEKMKKSFLTFLVHVNSFL  
QLDFHQLNEPPLGLPRSYPLSLVLEHKFKKEMNSSPAGFYFSNYQNPYIRKDLHDKV  
LSQKFEPPKMNQWNVKVLKSLIECAYDMYFEQRHVKNLYKYHNIYNINNKMLMRDSID  
LYKNNFDDVLFADIFNMRKYMTATPVYKVKVDRVYHTLHSITGNSVNFYKYGI IYGF  
KVNKEILKEVVDELYSIYNFNFTDIFTDTSFLQTVYLLFRRIEETRYRTQRRDDKISVNN  
VFFMNVANNYSKLNKEEREIEIHNSMASRYYAKTMFAAFQMLFSTMLSNNVDNLDKAY  
GLSENIQVATSTSAFLTFAYVYNGSIMDSVTNSLLPPYAKKPITQLKYGKTFVFSNYF  
MLASKMYDMLNYKNLSLLCEYQAVASANFYSAKKVGQFLGRKFLPITTYFLVMRISWT  
HAFTTGQHILISAFGSPSSSTANGKSNASGYKSPESFFFTHGLAAEASKYLFFYFFTNLY  
LDAYKSFPGGFGPAIKEQTQHVQEQTIERKPSVHSFNRFMELVNGFMYAFCFFAIS  
QMYAYFENINFYITSNFRFLDRYYGVFNKYFINYAI IKLKEITSDLLIKYEREAYLSM  
KKYGYLGEVIAARLSPKDKIMNYVHETNEDIMSNLRRYDMENAFKNKMSTYVDDFAFF  
DDCGKNEQFLNERCDYCPVIEEVEETQLFTTTGDKNTNKTTEIKKQSTYIDTEKMNE  
ADSADSDDEKSDTDPDELMISRFH

>PF14\_0766, 359 bases, 59B06ECF checksum.

MKLHYTKILLFFFPLNVLLTSYHAHNKNKASITPHHTRSTTSRLLSEYDTESSIYDSD  
EDINSVKEIFERQTSRRFEEYEERMITQRQKYKEQRDKDIQKIILKDKMEKNLAKKIE  
KGCLRCGFLSGVAGSIGLFGAVAINIWKPAALKAAIAKAITEGTADIAAAGVKAGEV  
TGKVLVISGLKRMGISTLDGKDLGTYFATTSYKNITNITQAVSSEYVQKCISASSGSV  
RFRLVDAQORDIHFCHSVWKQTSAVSTPKKGISYKEVIERTVETMVSKAEGPANTAAEI  
AEAANKLAIIEEAQEKVMEATIYNWYTTIGYSILAILIIVLIMLIIYLILRYRKKKMK  
KKAQYTKLLNE

>PF14\_0769, 348 bases, 671F7E7B checksum.

MKVHYINILLFALPLDILEHNKNEPHTTPNHTQTTRSLCECELYSPANNDNDPEMKRV  
MQQFEDRTSQRFFEYDERMVEKRMQCKDKCDKEIQKIILKDKLEKQMVQFSTLQTDI  
QSDAIPTCVCEKSIEDKVEKGCLRCGSILGAAMPGLSVGGSLLYALNTWKPAAIIAA  
KEAALAEATDLATQAGIDTVVAQLKIEGLLASFTVKQRLVDLSSIVTSSTYNNGAILH  
KSAMELASSYCHFEGTQSTPPFCSTIKYGQTTNFVRYAKAGSAAFKTEFASKSATLTK  
AKVGAVEATYGGYHISIISSIVAIVVIVLIMVIIYLILRYRKKKMKKLLQYIKLLEE

>PF14\_0770, 344 bases, 3759350F checksum.

MKLNHYTKILLFFFPLNILVTSYHGNNNNKTYVTSHIPTNTSRLLSEKDLQSSIIDNDP  
DMKSVKENFDRQTSQRFFEYERMI PQRQKYNEQRDKDIQKIILKDKMEKSLEEKVEK  
GCLRCGFLGGVAAGVGI FGSIAVNELKAAIAKAVVVAKEAAEKAGAAAAAEAGKNA  
VIAGLEEMGISTLRGNVFETLFTANTYPNASEIALAINEQYNPSSCILPIGGSGPSET  
FCTWVKVKS DAAPKIPGKVSSTYEVIETAVKSIVTDAKTVAETAACKATEEAIKASTD  
AVESAYAACQTAI IASVVAILVIVLVMIIYLILRYRKKKMKKLLQYTKLLNQ

>MAL6P1.251, 302 bases, C1223008 checksum.

MNIYYVKILIFTFLVNTLILSHNENCQNNQYNISLIKNNTQRTTIKPRLLAQTKNHNP  
HYHNDPELKEMIDKLNKEAIKKYQKIHEPYEQQLQELVEKKGKTKPVGEHGTEPMSTIEK  
ELLETYEKMFGDKDIMLKSGMPPNDDDRSDKSITCECTDINNPDLTKAKSKDKYLKR  
LKEGCTRGICTCSVGS AFLTLIGLAAAKKAAVAAFSAPYDACVSSTSFLFYIFDSGTLA  
SALKVGS TCASVATDMAGTVSSAATTAIIPFSISIIYVLIVITVLLIIILYIWLYRRRN  
SWKHECKKHLCK

>MAL6P1.315, 371 bases, 5440266 checksum.

MKIHYINILLFELPLNILIYNQRNHNSTTPHHPNTRLLCECELYAPATYDDDPQMKE  
VMQQFEDRTSQRFEYDERMKTTRQKCKDKCDKEIQKIILKDKLEKELMDKFATLQTD  
IQNDAIPTCVCEKSLEDKMEKGLRCGGVVGGLIAPTFGLIGSVAINMWKTTEIAAAT  
KAAIAAGKAAGKIAGEAAGKKAVIEALKYFGVDDFFPEIFKSILKMSRYTDVTKFGAA  
IAEKHVLNCAMSARGGSVNDSTCNAFEIKLGLFEAETGKPNGPPAYQAIPOKINELAE  
EATQAAAEAAKKASESATAAFETAKEAIEAASMQLYTTIAYSILAILIIVLIMVIY  
LILRYRRKKMKKKLQYIKLLEE

>MAL6P1.8, 323 bases, B5DE572E checksum.

MKIHYINILLFALPLNILVNNQRNHNSTYHTSNTTKIKSHRSLCESKLYAQS NYEND  
QEMKDVIKEFNDRTAQRFEYNERM QVKNQCKEQCDKEIQKIILKDKIEKELTERFS  
ALETKIDTNDILTICICEKSVADKVEKTCVKCGRILGTAVPELSLIGGI AVYAAAQ SAT  
MKT F ISETIDVLNRIGGMSQLFGAKISQFVTPSIYGKPMNLVIPLQEA INNACKCPDM  
GDKILCGGIERSFEQNL PARIAYAVNQVDTANDTWATATPTTFLTNPFVASSIAIM  
IIVAVLIIYILILRYRRKQKIKKKLQYIKLLKE

>MAL7P1.2, 371 bases, 1F5B9110 checksum.

MKIHYTNILLFPLKLNILVNTHTKPYITHHTQKIPTTRSLSECELFSPQNYDNDPEMK  
RVMQQFHDRTTQRFQEYDENLKEKRQKCKDRCDKEIQKIILKDKLEKQMAQQFSTLHT  
DIQSDAIPTCVCEKSLADKVEKGLRCGSVFGGIAPSVGLLGGIGEA AISAWKVAAL  
KAAARYAASKGAAQGLAAGIQAGKVAIKSLEKLGVKYFWTGMSS EILKMNHYKEVAN  
LTDVIY TAKLKVCDLTFDDFVNMCEQFDIKIGVYTEEVKNALLPKYAVPNALNEIVS  
NAETTAKEVFEAESTRIAAEITEQQTAVINATYSSWQIAITASVIAIVVIVLIMMIY  
LVLRYRRKKMKKKLQYIKLLEE

>MAL13P1.8, 422 bases, BAF51114 checksum.

MKLLHYCKVLLFSLPLNILTST\*NVCMK\*\*KIYVSFYFLFNIPYTYLLQIYKIINYN  
\*I\*HTYIYVMNSL\*VHNKNKLYITPQHTRTNRLLECELYTPYDDEPMMKVLHDFD  
RQTSQRKFKEYNERMQEKLKCKEQCDKDIEKIILKDKIEKQMVDFSA\*ETNIDSNDI  
PTCICKKTLADKVEKSCLKCTQNLGGIVTPSSVVLGGIAELGLSAWKTTALKVAIEAA  
KEGGAAGLAKVQAMGFANFFEGMKS GFCIKELDIKLLKAVFIQQKRENFTKLAHSIY  
VQYNNKCGLAVAKNSYHTCNFGKALKCTELCSQANCSNEATIADGVN KILSTAKSAAA  
NETANVIASETAAIEATKKGAIETT CMNCHTPIIASIVAVIIVVMVIIYLILRYRR  
KKLKKKLQYIKLLEE

>PF07\_0001, 359 bases, 8ED8230C checksum.

MKLHYTKILLFFFPLNILLTSYHAHNKNKPSITPNHTRTTTSRLLSEYDTESSIIYDSD  
EEIDSVKEIFERQTSRRFEEYEERMITQRQYKEQRDKNIQKIIHKDKMEKNLAEKIE  
KGCLRCGCGLAGVAGSIGLFGAVAINIWKPGAITAAIEKALELKSAYISATAEAARIL  
AGKEAVIEGLKKMGISTLEGKDLGTYFATTPYEKVASIYVAVNEQHFEKCAFGSLKKE  
FIPVGDGSRDSLFCQSVWKQTS AVSQPRQYISPEEVIEQTVQNI VNKAEGPANTAAEV  
ARESATNAIEVQQTNVINAI FMSKQTAI IASVVAILIIVLIMLI IYLVLRYYRRKKMN  
KKAQYTKLLNE

>PF13\_0002, 348 bases, EF586AB7 checksum.

MKVHYINILLFAIPLNILIYNQRNHNKSTTHHTLKIPIITRLLCECELYSPVNYDNDPQM  
KEVMENFNKQTQORFEYDERMKTTRQKCKEQCDKEIQKIILKDKLEKELMDKFATLH  
TDVQSDAIPTCICEKSVSEKVEKGCLECGGILGAAMP ELGSIGGSLLYALS KWQTTEI

ATAIAAAQKAGIDAATQAGMNAVRLKIKEWYVYFSTEKIVDFTSVVKESNFSSASALH  
 ESAMNLLNNYCNFNGLNRRGYFCSTIKYGDKTTFPFAQAGTEAYNATLPTKTA AFET  
 KYIDGVNTAYGGYQTAI IASIVAIVVIVLIMV I IYLILRYRRKKMKKKLQYIKLLEE  
 >PF11730w, 1340 bases, E26DCF16 checksum.

MIWFIQPTIFYIIFILARNIQCTYKGDNINEIKSILDNDELNSLSNLENLLLQTL  
 QDELKIPIMKGDLDKYLNMSNFKILNELNADGAEKPYI IPTSNCSANDIVKYEHTLKT  
 QITLEYKPEISDMLKRKNIVVRTLKI IKFMQTPMSAYKNTNNIKQS LLEMNKLFNKE  
 KKLNEHTINALRLRDRI FNTNNLTHRS IKKGISTYMPIDTKSDI IDYDDLLEFTNHPSI  
 ELMENLDKLANYYHIGIFNMIGSHYIAVGHFITLKLALKNYKKYFEIGSLKYLNWQSI  
 LKFNQSDRFKVLDLICDESSWYEGQMKRREQYLKNNIFSTSEECVLEFLIHHMNKYQ  
 MELYSKMHKLSLNVQIYLENKHLKEKFLQFMCSRKECNIYESDRFKQE QEKGIEFHD  
 NNNYKFSQENDPVSKVVDPFNLFTNYFYFIKYYSVFNSDHI IYMHLNFVGVNLGN  
 AYVSSLYLPGYYNAIQLSYKDQVGLKELYQNLVKVEKCYIRNRKNRSFSHRIASIFR  
 HKKFDSSKCSICEGTLTYINDQSQDKMSMAQKFYIFVTKILKVNNISSFITNMNIYED  
 YSNYLMHDLNWTFLFLFRMTTYKDI PNYSISNAMYLNKDEDDTKRMTMVT FQWMPST  
 IKRMHNYRIRKYVSIYLLLEELEKLI DNKLIKLEKLCITFLIHLNAFLQLDFFSYLNET  
 PANLQHPFPISMMIEARFKDWF IQYLTGFFFFIN YDDANTRYNMPENMKRGTFIPPKYS  
 KWNHILKRFIDEAFLMYFNQKHALTLFKYHNPYINISNKIMLMRDTFELYTKNYDQLIF  
 GADIMLLRKTFSCTPMSTKVWDRVKYYLHNIIGNPINFYKHGLIYAYTLNKAMLKEV  
 NDFEVIYKMNKDLFSETSF LQTVYLLFKKI QGT YFSHRNDVSMNNIFMFNVEKNYS  
 KMSQADREKEIHESMASRFFAKNLFVTFQMMFVIQISNDVDKLDRIY GKADMLRLSVH  
 DEPFLRFAYAYYGS MYDKLTNVFFPMNIKKPTIQLKYGKTFIMANLYYLC SVLFSMYN  
 LNNLGLLCEYQAI G SANFHSYKKMSQFIDK KFIPLVFYTLKARTEGIIGKEWYKMFVN  
 DFDGKSMANTWPYFGYYMGGNMLYRNILYFPNHLPEELRKQTKGVELQQPEYEPSVHS  
 IDWQVGYAISHGLSLSFFTFGMMKAYAYFENVIFFLRNSIRIFDRFY SILENYVCMYI  
 KRLFNKLTVDKLLKAMS RAYTSTKKEGAYE EAMVSRVRNKENVVQEVQEDKGTDITPL  
 PTFDIMDSKQNTNYMYNDNEDYFDDLDDNEQFLNSKDLLYYDDGIDRTKRYELIPLQR  
 YRYDPF

>PF07\_0136, 342 bases, 605765EB checksum.

MKLLYSKILLFALALNILLTSYAHNKNKIYIKSHTPTTRSRLLECDLYMSSNDNDP  
 DMKSVKENFDRQTSQRFE EYDERMKDKRQRKEQRDKNIDEI IKKDRMDKSLAEKVEK  
 CCLICGCGLGGVAAGIGI IGGITISELKKAAMATAIVSAKEAGMAAAKAEGAAAGKEF  
 VIAGLKRMGISTLGGKDLGTYFATTDYTNFKTIARVINSEYQTDSC LIGGSGAEKPIC  
 TWVRAKEGAARVIQ GKQFSTQETIKTGVENIVSNAETVAGEASKKATEDVIKSSIAAV  
 DAKYVICQNAIIASVVA I LVIVLVMII IYLILRYRRKKMKTKKLQYTKLLNQ

>PF11\_0515, 314 bases, 8E73441A checksum.

MNLHYTIILFFCLPLNILEISSYEINKNKPYISPHTPTTLRVLSECDLHTSIYDNDSD  
 MKSVKENFDRQTSQRFE EYEERMINKNRKRCKEQCDKDIKKI IVKDKIEKSFAEKLEK  
 CLRCGFLGGVAASVGIIGPIIVNELKKTALVAAAQTGTEAGIDKAI EVVISKYGVNK  
 LYGVALEKSITSNNFKNVMFYIQAIQHRYNTMVCSAEPIDDIGPLCFLKDSLNDGVLF  
 TKSISASAQKV VADATEKATLVTKAEVSAAEATS VNLYYAIAYSVIA I LVIVLVMV I  
 FLILRYRRKKMKMKAQYTKLLNQ

>PF11\_0529, 349 bases, BA3A9B4C checksum.

MKIHYINILLFELPLNILIYNQRNHKSTTHHTLKIPI TRLLCECELYAPS NYDNDPEM  
 KEVMEIFDRQTSERFHEYDERMKTTRQCKDKCDKEIQKI I LKDKLEKELNEKFLTLQ  
 TDIQNDAIPTCVCEKSLADKVEKGCLRCGSILGAAMPEVGSIGGGLLYALNAWKPKAL  
 EAAIAAAKELAIT EATNAGVKT VSEINKLLAKFKQHEILFELKPIVNSNFSCGSSL  
 FQRAEELASKSCVAQPNGSYTSFCNTILNGEKTTFKPFQA GANTYEKTLTTETPVLQ  
 ARYTA AVKTAYGGYQTAI IASIVAIVVIVLIMV I IYLILRYRRKKMKKKLQYIKLLE  
 E

>PFD0120w, 329 bases, 49EF20B1 checksum.

MKLHYFNILLFSLPLNILLSSSQVYVHRNHYSITLYTSKTPKPIKSNRSLCECDLYK  
 PNYNNDPEMKNLMENFSKQAQQRFNEYDEHMNEKLQKCKEQCEKDIQNIILKDKIEKE  
 LTEKLSALQTDISINNIPT\*ICEKSVADKMEKNCLKCGGIIGTAVPELALLGGVSTHM  
 LTTAATYAAIEAGMREVVSHIKEFLTNEEYLVDLTPIVNESNYNCGTALFEAANKAV  
 STSCLTTKPGIISPLCSAIKTTGKNTFNHYAQYGSAAAYNEKLNAEMVGVTSFNAMMA  
 SIIAIVVIVLVMVIIYLILRYRRKKMKKKVQYLKLLNQ

>PFD0125c, 301 bases, D75BE51E checksum.

MLLFAFLFNFLSQRVKCINKIGNISLIKNNQTSISTKSRYLAEIERPNNPHYYNDP  
 ELKEIIDKLNKEAIKKYQKNHDPYEQQLKEVVEKNQTKVTGGNDAEPMSTLEKDLLEIY  
 EKLFQDKSHIMIKSNIYINQDDKSNKNDKSCECANYKKYNQLLSSYSVDDAYLHNLK  
 SGCVACVGTSAISSIITGLYGISAASTAAIEAIKTTSSATIITKLTSLFGINFFSQT  
 SIESAYITAGITSVEGELYAGLVTSTFLPYGIVAIVLILVIVALIMLYIWFYRRRKSS  
 WKYAYKNHLST

>PFD1220c, 304 bases, 950FA7E1 checksum.

MLLFPFLFNTFLLSQNVNQCNNLRNKS LINNYTQRKILKSRCLAEIERPLNPHYQNDP  
 ELKKIIDQLNEEAMKKYQQSNDTYQLHELLEKKEKTSRNRSEQEMSKIEKELKIY  
 EKMSGDENHIMQKSDMYTNEHKSNDKNDKSCECINKNSTDKLSSTNKVHDNYLDNLK  
 TGFVGGVLVVCALSSALVGKYGIAAAASAAGVLAQAFINALPSISSSQLTNILNGINFF  
 YETSIKSAFTFGGITSVEYEGAASLASSTFLPYGIAIAIAIIVLTIIVIIIVVWLRKRR  
 KNSWKHECKKHLCT

>PFE0015c, 347 bases, 41B4B257 checksum.

MKLYYFKILLFSLLLNIVLTVSSYI\*IKKMIIIYIYIYVIFYLYKYTIYIYIKNIYNH  
 K\*LIITYMYTLHSL\*SRNKNKTYVR\*RRPTTASRVLSECDIETSIYDNGADMKS VKEN  
 FDRQTSQRFYEYERMSKKRQKCKEQCEKDIKQIILKDKMEKSLAEKVEKGCLMCGCG  
 LGGVAASIGIFGPIAISELKAALLAAIASAQKTGVLAGEAAGIEAGKEVIIGGLNAL  
 KIEILSIGPWETIYFAEGYSINVKQLATVILRRRDAVCSATGLTPPGDTCNRISISIGT  
 KLPNGQYAAPGDPVINVLNGIVERTKDAADAAKTARETVTTGITEKETAAINTIF

>PFI0265c, 897 bases, 1EE18E4 checksum.

MRSKHLVTLFIIITFLSFSTVKVWGKDVFAGFVTKKLTLLDCNFALYYNFKGNGPDAG  
 SFLDFVDEPEQFYWFVEHFLSVKFRVPKHLKDKNIHNFTPCLNRSWVSEFLKEYEPEF  
 VNPVMKFLDKEQRLFFTYNFGDVEPQGYTYFPVKEFHKYCILPPLIKTNIKDGESGE  
 FLKYQLNKEEYKVFLSSVGSQMTAIKNLYSTVEDEQRKQLLKVI IENESTNDISVQCP  
 TYNIKLHYTKECANSNNILKCIDEFLRKTCEKKTESKHPSADLCEHLQFLFESLKNPY  
 LDNFKKFMTNSDFTLIKQSVWVPIFDIYKPKNYLDSVQNLDTCECFKLNKSNLIIFL  
 SFHDDIPNNPYYNVELQEIVKLSTYTYSIFDKLYNFFFVFKKSGAPISPVSVKELSHN  
 ITDFSFKEDNSEIQCNVRKSLDLEVDVETMKGIAAEKLCIKIEKFILTKDDASKPEK  
 SDIHRGFRILCILISTHVEAYNIVRQLLNMESMISLTRYTSLYIHKFFKSVTLLKGNF  
 LYKNNKAIRYSRACSKASLHVPSVLYRRNIYI PETFLSLYLGLSNLVSSNPSSPFFEY  
 AIIIEFLVTTYNGSEKFLVLYFISIIISVLYINEYYYEQLSCFYPKEFELIKSRMIHPNI  
 VDRILKPIDNLMKSTRYDKMRTMYLDFESSDIFSREKVFTALYNFDSFIKTNEQLKKK  
 NLEEISEIPVQLETSNDGIGYRKQDVLYETDKPQTMDEASYEETVDEDAHVNKQHS  
 AHFLDAIAEKDILEEKTQDLEIELYKMGPLKEQSKSTSAASTSDEISGSEGPSTE  
 STSTGNQGEDKTTDNTYKEMEELEEAEGTSNLKKGLEFYKSSSLKLDQLDKEPKKKKS  
 KRKKKRDRSSSDRILLEESKTFTSENEL

>PFD0080c, 560 bases, 92E64A7A checksum.

MKIISNLGSMNITLHLCFFGFLFVILNFTLDNSNFSNGGDILLNRNLSEEKAEDDYK  
 KSSSCSSLASTTKRSPSTASTSTSLRSASTASTASTLRSASTASTASTASTASTASTA  
 STASTASTASAASTTRSASAASTTRSASAASTTRSASAASTTRSASTASTARSASTAS  
 TASAASAASTTRSASAASTTRSASAASTTRSASAASTTRSASAASTASTASTGSTSTT  
 QSPSTSTSTQSPSTSTSTTQSPSTSTSTTQSPSTGSTSGSTTRLPSTGSTIRFPSTG  
 SSRLEDYEKEGSNVDITEEEEKEAESVDDNNKEGNE SDNIYCMLCSSNTRGFGCDCKD

AANYILKNLDLYDEHEAKKHASDRTKTFSKELSKLFKKLRTKDPNMFNKNKIVFQDLS  
 KKHTWDKYELHLPGLAHGKYNNERDVELNKKLIDLEDGFTDTQYIRKLYSLINENEKE  
 KFDDIKRKILCYCASKNKS LHRTPEESEQAWKYVQKLIKLYYNDFDKHFEEKVFLIWLA  
 LSEGFDFVEYKMLIAANRLLWRKLSDKVQEESKVMIQD

>PF08\_0036, 759 bases, 7130638B checksum.

MDIHAQENQGTGIRFSWNLWPPTKAEAAKIEVPLGCLYTVLKRTDDSSVKLVEYEPLKC  
 KTSNCILNPYCNIDFRNKTWTCPFPSNIKNPFPLHYAEHISEKNLPADVMYSNIEYIQP  
 SNVGDIPPTFLFVIDTCLLEEELEQLKDSIQQCISLMPGDAYIGIITFGNMCYVHEI  
 GFNDCLKS YVFKGNKEISAQDLQKQLNLGSRNDPRSSTTSASARRFLQPVSECEYNIN  
 MLEEDIQKDNWPTPPDQRAKRCTGVALSVAIGLLECCCNQLSGRVMFIFGGADTTSPG  
 KIVDTP LSESLRHHLDLQKENSARHVKKALKYYVSLANRAVASGHAIIDIFACSLDQI  
 GLYEMKVCCEKTNGFMVMADSFMSNVFKDSFKKIFETDSTEYIKHGYNACLTVICSKE  
 FRVCGAIGACSSNKKTANYVSDTCVGEGETCEWTICALDRQSTIAFYFEIVNQNLASL  
 PPDRQAYLQFQTLYQHPSGRRLRVTTISYRFAEPNIAEISQGFQETA AVIMARFAV  
 LKAETDEPIDVLRWLDRKLI RLVSTFADYQKDDINSFHLSSSEFSIYPQFMYHLRRSHF  
 LQTFNASPDETAYYRSILLRENVMSLIMIQPALLQYSFDSPTPIPVLLDAQSLKSNV  
 ILLLD SYFHIVIWYGEMIQWREQGFHEKPEYEHFRQLLNAPHEDAKSILEDRFPPIPK  
 FVLCNSGGQS SRFLAKVNPSTTHNSLSGSTFGTSSNESYIINTDDVSLKIFMDHLVK  
 LAVQT

>PF10\_0013, 231 bases, AE9D5F4E checksum.

MLFSFKYIYFSSTFLLLVLQSKTKYIQNFVNIQETLNEKCSSKYIRLI SEQTSDEST  
 SKSIKNCKCVNKRNNKNE DNHELQSKSRSLKGTELDVTSYNKSKHTQQNNLGDLSKRT  
 KNNITNISSKKNETYLF DENTNEYKLRNTLR LMNERYADSI VDTMDLNDKTKDKFKKF  
 LHLYMAKENPDKQRKLYEQIESDIEKYKKNHVICSIVDFENIYDSFYFLKYEDRYIT

>MA17P1.87, 1036 bases, 8866E66A checksum.

MHGSELKTCIGVCDNNNNKNYEQFRKLKSNNDTIMRREHLGEEKREMNGDGKELTILT  
 NKRTYSNDNYKNNMNNRRSCSKISLLKYNEE IFKHQNDKCNDENNDMSDESHNYLYND  
 MYNDQYNDIHDDMPNNINNDIYNDIYNDKQSELYNDKSSDATIYNDKHCHMDKVQKHK  
 NDNKKNKLVLSGISYQMKNAMNVFGEVKEHIKYTASEAKKNMNYPFCKAPCNIENLR  
 NTIFINEEEIVINKNIYKNI FNKKNIEKEQOGKNKKENEELFSCNQSDIIKGNYNFGI  
 DIEMVYVNEQNKIVVYAYDKETKKKI PCTYKWTRVYYNKECELVEKNVYPHKNVILYD  
 ENEYELTCEDIGTKIYVECSINNEQINVENLSKFYLN GSTNSENCNYEEGVIDQKRI  
 EHKNKYNI DYNQNNRND SHAVLHIGNDKSINDS NGLSSLKHCVTKNKNCDEEHSRNH  
 VLEKSMYLLHNYYNKNGKEKDDNNNNKKNIYMYKEDTPPIKDLSSDAYASYESSIL  
 NKNSSSTIVLNNDKNIYNNKKYQGVAIGEIGPLNINEKTKKMLERI IENDTIRYPIYI  
 IKKVYNDEETCNDFINNDDMNRNKKDDTLKIYND DNSLDSFTVNSNIESEHDMDIYML  
 YIHKNEIKI IDHNNMNMHNNVNNIMSNVKSMDKIKKNMWTHKFHYIYPYVHFMTGKHK  
 QNNKKTDFQLYINEKEYYICKCLYKRHRDLIAIILRYMHANLYIINDYIFNNINQNF  
 KTRVKNIFENIDVNYILQNINKELLINRKITQKCYLKINKLQSEKNMLEEELKSTIQA  
 FQSQLDNVKFKFDENDLIQTNEKLMKEIKILQEKYRNVDLFFKNKT LISDIEKYKLL  
 EENKSKVNEDDNLLNENVQMCNIYNEEKKNKTELENKLGKLSIKLETLNNSLQEEKI  
 QRNINSESLKEMEELKRNNKDLQKQNVKISDEMNL LITEKNRLTKLVDLSLTKDIEKSK  
 INKNVKSTDNKMDIDQDKEKLFKEISLLKDENELLKRIKKLAKMSTIRT

>PFC0525c, 440 bases, 61EA65D6 checksum.

MKNWPIDEDINIYEEKNHTNKNYVNNFEMSDQKDEEEYSHSSNRSEDEDEERTIDNE  
 INRSPNKS YKLGNIIGNGSFGVVYEAICIDTSEQVAIKKVLQDPQYKNRELMIMKNLN  
 HINIIYLDKDY YTESFKKNEKNI FLNVVMEYI PQT VHKYMKYYSRNNQALPMFLVKLY  
 SYQLCRALSYIHSKFICH RDLPQNLLIDPRTHTLKLCDFGSAKNLLAGQRSVSYICS  
 RFYRAPELMLGSTNYTTHIDLWSLGCIIAEMILGYPIFSGQSSVDQLVRIIQVLGTPT  
 EDQLKEMPNYADIKFPDVKSKDLRKVFPKGT PDEAINLITQFLKYEPLKRLNPIEAL  
 ADPFFDEL RDPCIKLPKYIDKLP ELFNFCKEEIQEMSMECRKIIPKNVYEEFLMVDE

NDNNIINDTISNDFNESNLDTNNSNNKTHVIES

>PFC0140c, 783 bases, 97CF3B28 checksum.

MRTNLQCCCKLQSQELALTNCGFINIGLYNNLKKSVKSNVYSEVGNMVLILRGDGNIG  
 REEIALNTCQREFSRIQLKELVEINILDKENKNDLVNFIPIIDSIELEVNLVFKPDRLI  
 EMEDEKLEDEVFKKYFLNHILTKGQILALKYNDILLKCIKDLKTADFDEIKRLNNSNN  
 NNNNRNSSGFSGYFNKWSPGFNNADNQNLSYNRYERGILFENTECEIFTSISDGGKLCI  
 ESKKVLKQNI IKNNFNFEELGIGALDEEFKTI FRRTFASRIYPNYI IKQLSIKHVKGM  
 ILYGPPGTGKTLIARQIGKTLNAREPKIINGPEILNKYVGQSEENIRNLFKDAEMEYK  
 QSGENSLHLHIIILDEIDAICRQRGNVGSSTGVNDSVNVQLLSKIDGVNSLNNILLIG  
 MTNRIDLIDEALLRPGRFELHIEISLPNKEGRIQILNIHTKNMRMSNKLSSDVNILEL  
 AERTPNFSGAEIEGLVRNTVSYAFERHINFNDLTKPINADDIMITKNDFMKALKETKP  
 AFGAEEDIIGNLLCNGIINYGKEYENIENTCKLLIKQIVDNENTKLMSILLYGENSG  
 KTTISAYIAKCANFHFTKFITPENLIGYSEIGRINYINKIFEDAYKTPLSLVILDNIE  
 RLIDYTRIGPRFSNSILQAIMVLIKKKPKKENQKILICTTSEYQFMKDVGLTKNEFV  
 NIHVPLLSTSSSIKNVLQHRNQTYHDFPNNEIEKVISSNIIKNIAIKNLLMIIDMASE  
 ASDDKNITSDVFLKIFNDCGLLLDDDDTDY

>PFC0810w, 192 bases, 485A247B checksum.

MFIINWFRDILAHGLSQQSARILFLGLDNAGKTTLHMLKDDRVAQHVPTLHPHSEE  
 LVVGKIRFKTFDLGGHETARRIWRDYFAAVDAVVFMI DTTDRSRFDEAREELRHLET  
 EELSNVPFVVLGNKIDKPDAASEDELQHLNLF SNITVHNNMKGGSGVRPVELFMCV  
 IRRMGYAAAFKWISQFLT

>PFB0640c, 1460 bases, EF4D3FDC checksum.

MALKSINISGNFEWCPFEYKNYLLCFNSHNLLYSNNNSLNNYIYLLDINLNSEIRNL  
 EIVNKYNFEDALKYDNDVIKGGNKNNKNNKNNHNNNSVNEYVTCFEWMNSNFFVDIN  
 NNEELSKGIIVGGLTNGDIVLLNAKNL FETNRNYDNF ILSKTNIH DNGINCLEYNRHK  
 NNL IATGGNDGQLFITDIENLYSPTSYPYLDKNNLQKITCLNWNKKVSHILATSSNN  
 GNTVIWDLKIKKSAVSFRDPHSRTKTSSLSWLSNQPTQVLI SYDDDKNPCLQLWDLRN  
 SNYPIKEIIGHSKGINNICFSPIDTNLLSSGKDVTKCWYLDNNNFDI FNEINNSANN  
 IYSKWSPYIPDLFASSTNMDTIQINSINNGNKMTSKYIPTFYKKEAGICIGFGGKICT  
 FDNSTNNMSNVNMMNVMNMMNINSFNNDNSCDGEYDSNKGKNKSTQKKFLIKYHIYP  
 TDMELISEADNFEKYITSGNYKEFCESKINKCDDHEKLTWQILQLLCTSQRGDIVKY  
 LGHDINNIVDKIMQTIGKQPGFIFKTLIDEKENNNNNNNNNSTNQMYQNDVLLHNDPN  
 LMNNYLLKDNMNPIMLNNNNNNINNRGTNVMYSNGQNLGDTNHNEENFNNGNFDID  
 PEKFFRELGEKTENEKIKQNEEDISGNDEHLLNSSIKGKENKTKNKKSGLGTDDNNDN  
 GDHNKNEGSNINGEHVSEHILNEKNNTNWNNGIEAIIKECVLIGNIETAVELCLHKN  
 RMADALLSSFGGEQLWHKTKTIYIKKQNDNFLKNINYVLDDKLENLINNVDLNSWEE  
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 KKTSLNLVLDIVEKMTILKMI IKYENFNSIMNQKISQYAEELLANSGRKKAAMTFLCL  
 IQHDQSIESLILRDRIYNSANHVLCQQIKPPI SPFQIVDIKPSPNVYQNNMYNNNNNN  
 NNININSSSNNNNNNNNKVLSSMHHPMQQFNQCNVNKMYTSTSNII NNNTMNSNFKS  
 VIPPPLPMNTQMNSTSSIQPPSPVPTKFHTQI INNTMNSRSSIATTTKNYPTSNLN  
 SVIPTSMNNMNTNISHGNNVTPPYMSQTNVAVPNMNNNNNNNTMNP TYPSPKFPNY  
 NLNSQVQONSIIPEKQLTSPMFSSNSYGNINKTHTTNAVPPPPNVTS SVVTPPMP SN  
 QLNNTRSSFADIQNVVSPRNKNQSISSSTANLNYQHDNQFNKRECMEQPVPMTNQSS  
 MFSMNTMQKKNVPGGFQDNTSQMNYGMQPTGSPSSSLSTTSPIAGALT VTPGMPVP  
 WPIPTTTQQLGSTTQSTANENKKIQTATKEQNGVLMNRNHIENIKKTI SNLLNIYTSQ  
 ESVKKKADDVSSKVYELFEKLD CGAFNEQINDSLLNLVNCINANDFKTTNKIIVDL SR  
 NLWDGSNKAW

>PFB0095c, 2441 bases, 3A86487C checksum.

MATIKKYHIRGRKNILIFLLKIFLFSPLIWILYSEYFTVVKNYKIDNVYNI FEIRL  
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KLKEQKKNDAQKAKDLTKKESQDSSSEKSLKEKVNGEALKEKENKETLKKKELENQKE  
KEEKNKIKDNNDEALKNGNDKDDKIVPKKPESVEKDLKEMELKEKEFIKQHLKDYE  
ERKEKRRNWI LRSLRRDKLREIEQLEKLNAQLESAINELKERRASRRPMMVKMQRGMK  
DEVDEWIKKYDDEQAENGTKDEEIKDKGDGYEEIVETKFGMRENALGELDEYEERY  
EKKRYLLKEDGEGDLKDVEEKLEETGYGFREKFPTRILVKRKRNKEQKLLKEDKEKK  
LIAAEEPDDKIKLKDSDDKVVVPVKNKSSFPDKFRAPDKKRTMFRYRLSELFPIVP  
RKDNELAVSGDCMDSKVNKGKLLKSTFNPFKRRRNKLKERKMQELHKFKKNYKKYQKLL  
EREKRENPGEPLNTPEIHVIRPSDLMDKGENKSAGHPFKYQPTKGLKEYEESHVAKD  
YQLEHEPPTKLPEYEKGHVSREYQLDNEVRDELPEYEKGHVSREYQLDNEVRDELPEY  
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NKARENLEEYNETDLAKGKEVTNKARENLEEYNETDLAKGKEVTNKAHENLEEYNETD  
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KELRNKGSGLKENAELKNKELQNKGSEGLKENAELKNKELQNKGSEGLKENAELKNK  
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NNDLENDGLKHKPNQGQKHTELNKNLKNKPTDGLKNVKDDELSDNESDNEKSKKNL  
RGKKN

>PF11\_0507, 5507 bases, FC3EA3D3 checksum.

MKELESEEFPEKYNIEDMEETEKENEIEKIMDENKETEQTTEGNTTEEFVQEKELNQE  
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EEQVPKELPQEEIEEIVVEELPIDEHLSSSEETTIVTEEDTFKGGQLINEEKPVEEKSVSE  
EIPVEEKSVSEEIPVEEKSVSEEIPVEEKSVSEEIPVEEKNVSEEIPVEEKNVSEEIP  
VEEKNVSEEIPVEEENVSEEIPGGIAIEDVPVDEETVTEEITVDEKIYDKLPNEIET  
VNEEMPVEDETLTEQISSSEHERVPEEIEEEKPFTEGEETESLTDEIVEEGVVTDDIPE  
EQIITEKVQEEEEFVTGELSEEDIINEKVQEEDESVTTELPEEDIINEKVQEEEEESAY  
QEIVQDGSVTKDVEYKELVNDDVRDKENFVIEEDPFGQLINEGLPVEEEFVTKELPV  
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SGEVDETEYVTEEEVEEETELVNEEVLKEEGSASEKVVKEEGSASEKIVEEEGGSVTEETA  
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 SVTEK  
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 EEKESAS  
 DEHEQEDVSVNAQV  
 TYEK  
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 VEDGSVTEEV  
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 EEE  
 SATEE  
 IIRDET  
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 VLEKEGS  
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 GSGTND  
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 GSVIEE  
 VVEE  
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 KLKEE  
 ASAIEE  
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 DVLE  
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 SFTEE  
 VIEER  
 SLIEE  
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 EDRL  
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 IVD  
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 VEDG  
 LATD  
 EF  
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 QSII  
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 DEGS  
 VTEE  
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 EGSP  
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 VEGV  
 SVIEE  
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 SEEI  
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 TEEMI  
 KEGL  
 ENEV  
 ILDE  
 DSIT  
 EEAL  
 EKEG  
 SVSE  
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 EMG  
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 ILKE  
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 DEVP  
 NSKE  
 VQEI  
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 EEI  
 VED  
 GLTT  
 DDLV  
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 VIEE  
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 VGS  
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 ASI  
 TEEV  
 EKKE  
 SVTE  
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 EESV  
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 LVSEE  
 IVTE  
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 VAQE  
 IVEE  
 DAP  
 ATEE  
 IDEI  
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 VEE  
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 EIVQ  
 NES  
 GT  
 EEI  
 LE  
 KVSAS  
 QEIV  
 QDGS  
 VTEQI  
 IEEQ  
 KPVT  
 EEV  
 NEE  
 ESIT  
 HEI  
 IQEE  
 SHV  
 EKVV  
 QQGS  
 VAE  
 EVV  
 ENPV  
 SVTE  
 EIVE  
 KEGSV  
 TEDIG  
 QEGY  
 VAE  
 EIVE  
 EEE  
 FDN  
 EEI  
 LEE  
 SVAE  
 EEFV  
 EEF  
 VEE  
 GFD  
 NEEI  
 FVE  
 QISD  
 SEIV  
 KEEN  
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 EVLE  
 EEGS  
 YTEE  
 ILEE  
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 TEEI  
 LEE  
 EGS  
 FT

EEILEEEGSYNEEILEEEGSYNEEILEEEGSYNEEILEEEGSYNEEILEEEGSATDYF  
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 AIEKILEEETATEEIVEKQVSVTEDIIVEKEGSVNEEIIIEEASVAEEIIQGGSFTEEIV  
 GQEESEATEEVIDEEGLISNEIEEEEEKSVTEEMIEEVEEVSVDDEVVEEVSVAEEIVEE  
 ELVDDEILPEELSATEDVIEEVRSVTDEIVQEEVSCCEEILEQEVSASEEYVDDKSVTD  
 DFGHERSVIQDVENTESVTEEIAEVDKSVIEEAVEKQGSVTEEKVQEGVSAIEEIEE  
 LESVTEEIAEEDKSVIEEAVEKQGSVTEEIVEEEELDTEEVLEDKSVTGDVVEQEGSG  
 KDESEAKESFTEEVDELKSVKEEDQETEYISREIEEESATEQHSEQELSINKEVVETE  
 SLTKDIEEEKSTTQEILEETQSVNEEIVEEERDTDEVLKEKVPSEEVIEEQASTTEE  
 FVEERSSTDEIVEVEDLFTTEEVKEREKSVTEEIVEEGSDTGEIVEEEGSDTEEILEEG  
 SFNEEIVEEEGSIITEEILQGSVTEEILQGSVTEEFVGQQGSVIEEIVETESAIEERVE  
 EESATEEVDERESVTEVVEEVS SDEVVEGSIIEEVIENEGSVTEEILEHEVSADENF  
 VGQAVSVIEEVEGTESVTEEVVEETESVSEEIVEVSPTENVVQQTDSVIEEVVEQKEG  
 SFNEEIDIRELGDDGVEEREKISTEEVVGQDKSATGDVEEVSSTEDEEEVSSTEGLEE  
 VSSTEGLEEVSNTEDEVVEVSSTEDVEEGSVAENVKETSITEEVSVEEDIITDKVSVE  
 QEVMAEASVEENILTEVPVEEEMTEKLSVEDKALNEKIMSEEEIVIEDGNVHEVPA  
 EVSVTEEIPGVEETTNNESHVKGENVVNEVVDDNSVNDEIQFDDDSSIEIYTVDSKD  
 VFHKEENYDSFREEVRSDENIHI FRKKNFVKKIENEKSSVGHVPTEYTSKENIAEE  
 VPSHIMFKENVTEVPKEVKYEENTVEEVFEEVTSKENIEEAPGDINSEENIEEVP  
 EVVTSEEIVVQNDVNNINTNIDHMFDFDLDDILKIPEAQRKLNKLRTLVDVHLDVIEK  
 MQRDEWKKNRDFLYICLKEINKLSEDTLMKFYGSNKSANDNDTVMVIKILKDKWG  
 TGRIVDTIANSLNKSNSLYHNLYIEMEKDLLINKTETFNKWSKQHWNKLDNWKEEKW  
 FKLFRDLKIDMRNTYESDQNDENNEESMNELSDELIKNNTSDNMRNEQKTLKKNKE  
 YSNLSKDLGLIEKQKIWKSWIVKNVNNIENWFDEMWFKNVVNELKEKNDVSNVLQEN  
 ASEASVENYISDVEDSKDMTNSINDSEKSKIVASSSKTTNEEYIILSRKDLIYNIIVM  
 VHMMVLDQFKYDELKYAKKRFLNRSIDKFIKEKKIKDKETVLDYYIDDIKRIVEDTS  
 HVNNIKEKAIDHYTSHDWFRLLRQGNKAQNSISQEVLDILTEKYKKLISEEDNKKENN  
 NNDDEVKPELKDNIKCEENVSFNILLRRSNKKDQLPLEEKKKNKNGDLNNTLTESDGKKI  
 NINEAIEESKNGNEDKNSGNMEKSRKPRDRRTERKEKDQDLRVQLLQDYENIFEQIQN  
 MENQNKDKNKKETKNILKTSIDLKDLLREYKKEKNIINQSEKEFSVNN

>PF14\_0358, 184 bases, 2046D0B3 checksum.

MDKSKSSIEKELNRIKQDVSLSAFSLFSEMVOYCLYKSKRGYRIEDCLHEMGLRVGY  
 KLNEYLTYKNKVKRSINIINILTFISKHVWKYLFQHSSDLLKSQDSIYEYMICDNIL  
 LNKFINVPKDYGNINCAFAAGIVEGFLCSSEFQADVTAHTIHEGDDNYNTTIFIKFY  
 PEVVEREKNH

>PF10\_0159, 824 bases, F57509CD checksum.

MRLSKVSDIKSTGVSNYKNFNFSKNSSKYSLMEVSKKNEKKNLGAFHSSKILLIFGII  
 YVLLNAYICGDKYEKAVDYGFRSRI LAEGEDTCARKEKTTLRKSQKTSTRTVATQ  
 TKKDEENKSVVTEEQKVESDSEKQKRTKVVVKQINIGDTENQKEGKNVKKVIKKEKK  
 KEESGKPEENKHANEASKKQEPKASKVSQKPSTSTRSNNEVKIRAASNQETLTSADPE  
 GQIMREYAADPEYRKHLEIFYKILTNTDPNDEVERRNADNKEDLTSADPEGQIMREYA  
 SDPEYRKHLEIFYKILTNTDPNDVERRNADNKEDLTSADPEGQIMREYAADPEYRKH  
 LEVFKILTNTDPNDEVERRNADNKEDLTSADPEGQIMREYAADPEYRKHLEVFKIL  
 TNTDPNDEVERRNADNKELTSSDPEGQIMREYAADPEYRKHLEVFKILTNTDPNDEV  
 ERRNADNKEDLTSADPEGQIMREYAADPEYRKHLEVFKILTNTDPNDEVERRNADNK

EDLTSADPEGQIMREYAADPEYRKHLEIFHKILTNTDPNDEVERRNADNKEDLTSADP  
 EQIMREYAADPEYRKHLEIFYKILTNTDPNDEVERRNADNKEELTSSDPEGQIMREY  
 AADPEYRKHLEIFHKILTNTDPNDEVERRNADNKEDLTSADPEGQIMREYAADPEYRK  
 HLEIFYKILTNTDPNDEVERRNADNKEDLTSADPEGQIMREYASDPEYRKHLEIFYKI  
 LTNTDPNDDVERRNADNKEDLTSADPEGQIMREYAADPEYRKHLEVFHKILTNTDPND  
 EVERQNADNNEA

>PFE0040c, 1434 bases, 40B01CAC checksum.

MEVICRNLCDKKNMMENEGNKVKKVYNNSSLKKYMKFCLCTIICVFLLDIYTNCES  
 PTYSYSSIKNNNDRYVRILSETEPPMSLEEIMRTFDEDHLYSIRNYIECLRNAPYIDD  
 PLWGSVVTDKRNNCLQHILKLEMQESERRKQQEEENAKDIEEIRKKEKEYLMKELEEM  
 DESDVEKAFRELQFIKLRDRTRPRKHVNVMGESKETDESKETDESKETGESKETGESK  
 ETGESKETGESKETGESKETGESKETGESKETGESKETGESKETGESKETGESKETGE  
 SKETGESKETGESKETRIYEETKYNKITSEFRETEENVKITEESKDREGNKVSGPYENS  
 ENSNVTSESEETKKLAEKEENEGEKLGENVNDGASENSEDPKCLTEQEENGTKESSEE  
 TKDDKPEENEEKKADNKKKSKKSSFFQMLGCNFLCNKNIETDDEEETLVVKDDAKKK  
 HKFLREANTEKNDNEKKDKLLGEGDKEDVKEKNDEQKDKVLGEGDKEDVKEKNDEQK  
 KVLGEGDKEDVKEKNKGKDKVIGSEKTQKEIKEKVEKRVKKKCKKVKKGIKENDTE  
 GNDKVKGPEIIIEEVKEEIKKQVEDGIKENDTEGNDKVKGPEIITEEVKEEIKKQVEE  
 GIKENDTEGNDKVKGPEIITEEVKEEIKKQVEEGIKENDTESKDKLIGQEIITEEVKE  
 GIKENDTENKDKVIGQEIITEEVKEGIKENDTENKDKVIGQEIITEEVKKEIEKQEEK  
 GNKENILEIKDIVIGQEVIIIEEVKVKVKKKVEKGIKENHTESKDKVIGQEIIVEEVKE  
 EIEKQVEEGIKENDTESKDKVIGQEVIKGDVNEEGPENKDKVTKQEKVKEVKKEVKKK  
 VKKRVKKRNNKNERKDNVIGKEIMKEDVNEKDTANKDKEIEQEKEKEEVKEKEEVKEK  
 EEVKEKEEVKEKEEVKEKEEVKEKEEVKEKEEVKEKDTESKDKEIEQEKEKEEVKEVK  
 EKDTENKDKVIGQEIIEEIKKEVKKRVKKRNNKNNENKDNVIVQEIIMNEDVNEKDTAN  
 KDKVIEQEKEKEEVKEKEEVKEKEEVKEKEEVKEKEEVKEKEEVKEKDTESKDNVIVQ  
 EIMNEDVNEKDTESKDKMIGKEVIEEVKEEVKKRVNKEVNKRVRNRNRKNERKDVIE  
 QEIVSEEVNEKDTKNNDKKIGKRVKPIDCKKEREVQEESESESESESESESESESE  
 EESE  
 GLVHRNCKKKEKKYNNGELEYYKEKQNEEYFDEEYIIQSKEHNTLNTFPNLMALNEDF  
 RREFHNLISIHEDTDLMELKRIILYNLFLEYNPHMNNKQKAELDCKKFSEMNVVHQILNY  
 EERIRMYEENAARGRLNTVILDPIITFNVIIFGDDTMFKFIDE

>MAL8P1.17, 483 bases, 9A2B6023 checksum.

MNRKYFSSFLFLISFVFEFVSRSHGDLFNHFVTDIHDGELDKFITKNDIVLVMFYAP  
 WCGHCKRLIPEYNEANMLNEKKSEIKLVSIDATSENALAQEYGITGYPTLILFNKKN  
 KINYGGGRTAQSIVDWLLQMTGPFVSHVEGNIEDVLKEKKINVAFYLEYTSEDNDLYK  
 KFNEVGDKNREIAKYFVKKNDKHNKLCFRDTDEKKVEYDEKTPLEEFVTSESFPLFGE  
 INTENYRFYAESPSELVWVCATYEQYNEIKEHVRLAAQELRKKTHFVLLNIPEYAEHA  
 KASLGLTEFPGLAFQSNEGRYLLKNPKESLLNHNAINFFKDVEAGKIEKSLKSEPI  
 EDDKNAPVKIVVGNFSFVDVVLKSGKDVLEIYAPWCGHCKKLEPVYEDLGRKLKKYDS  
 IIVAKMDGTLNETPIKDFEWSGFPTIFFVKAGSKIPLPYEGERSLKGFVDFLNKHATN  
 TPISIDGVPEFEDGTSEEL

>gi, 339 bases, 61B6687B checksum.

MVSFSGKSVLSAAVFAVLLLDNNSAFNNNLCSKNAKGLNLNKRLRHETQAHVDDAH  
 HAHHVADAHHAHAADAHAHAHAADAHAHAHAADAHAHAHAADAHAHAHAAYAHHAH  
 ADAHRAHHAHADAHHAADAHAHAAYAHHAHAADAHAHAHADAHHAADAHAHAAYAHHA  
 HAADAHAHAHADAHHAAGDAHHAAYAHHAHAADAHAHAADAHAHATDAHHAHAADAH  
 HATDAHHAADAHAHATDAHHAADAHAADAHAHATDAHHAADAHAHATDVHHAADAHAAD  
 AHHATDAHHAHAADAHAHAPAHHATDAHHAADAHAHAHAHAHAATHCLRH

>gi, 264 bases, 9E5D1B5E checksum.

MVSFSGKNKILSAAVFAVLLLDNNSAFNNNLCSKNAKGLNSNKRLRHESQAHAGDAH



GEMLNQKRKLKQHELDRAQREKMLEEHSRGIFAKGYLGEVESETIKKKTEHHENVNE  
DNVEKPKLQQHKVQPPKVQQQKVQPPKSQQQKVQPPKSQQQKVQPPKVQQQKVQPPKV  
QKPKLQNGKQKQVSPKAKGNNQAKPTKGNKLNK

>PFE0360c, 893 bases, CD113355 checksum.

MIYLGKKLLSCTLFVYFLYIHFFLLKQNNFCDVKVRERILEESINNDLSSKGENLHIY  
EKTNSVSVQTFIKKKERKNLSDNNINDKINNNNNYNNNNNNNIEDTTYPTGNEKKENI  
FLKIFRYVKNWFPIKSSNNLKKTNINYEQVQEENEFSKYILQNNMSIETTKVCLIGSG  
GDSSHDLIKQFLLHNNVKYNRNYENDNSLNNKSGSISSYKYYSEEIQEPIIIDRDI  
CNKKKNCKESTLNYENNPKTIGNIIIQSDILKNEKIFNMNRHFVVCYFGSIPKTNI  
KINQSTLIQHLIKCLDYCKMEGVQYIYIGYNIYAANNKLEIMKKLREHKIIIVTSSG  
KIYDDDNNDNNNFYNDNIYNNNIYNVHNDDEKIKNHIKKKNKQNNYLYEYQRTQKD  
EEQKSNSSLYQNLNENVISISGLIYTDSSKKNKNKNYIYDNEIKILDQKGNKLNRYI  
SLFYFSYDTDIYEKIESDIIDDDHDLVSASFVNTLVLMHSINLKLSLGRLRKILNKS  
VKREELRHLNRAYYHDMNMTFEDSLNQRKRSYKIFYLELKNKHKVLLSDANLKS  
QDNLVNYNEEDHVKNVEQETSVERDIYKNNENSNNKRNKMDMDEGKGTIYQNKESHK  
YNIHYPYNRKIQSLLNDNTLNHKPYVVSFLNMSYYNEDIKRNRYNIYDDPSYTYDQGIT  
YDDNYIIDDHDIHTRKKRKISYDGEDNDYHMYDDRDNLFHSNLGNKYEDDGNVHRE  
KEKDLEPRFLYDPFANIENRDLETVQELSELREKKSNNFYSRNHDNSSNMKRRRKEKK  
KKLKKVLRKYDKIGNLERIRRKKRRMIHKNKINKRRNMKRKNNELEERRNKQADKN  
SSSGNGKKGKINGTRNSPKIKFKR

>PFB0100c, 654 bases, C155B129 checksum.

MKSFKNKNTLRKKAFFPVFTKILLVSVFLVWVLKCSNNCNGNGSGDSFDFRNKRTLAQ  
KQHEHHHHHHHHQHQQHQAAPHQAHHHHHHGEVNHQAPQVHQVHGQDQAHHHHHHHHH  
QLQPQQPQGTVANPPSNEPVVKTQVFREARPGGGFKAYEEKYESKHYKLKENVVDGKK  
DCDEKYEAANYAFSEECPYTVNDYSQENGNIFALRKRFPGLMNDEDEEGKEALAIKD  
KLPGLLDEYQNQLYGICNETCTTCGPAAIDYVPADAPNGYAYGGSAAHDGSHGNLRGHD  
NKGSEGYGYEAPYNPGFNGAPGSNGMQNYVPPHGAGYSAPYGVPHGAAHGSRYSSFS  
VNKYGKHGDEKHHSSKKHEGNDGEKKEKKSCKKHDHDGEKKSCKKHDNEDAESVKS  
KKKSHDCEKKSCKKHDNEDAESVKSCKSVKEKGEKHNGKKPCSKKTNEENKNEKT  
NNSKSDGSKAHEKKNETKNTAGENKKVDSTADNKSTNAATPGAKDKTQGGKTDKTG  
ASTNAATNKGQCAEAGATKGATKEASTSKEATKEASTSKEATKEASTSKEATKEASTS  
KGATKEASTTEGATKGASTTAGSTTGATTGANAVQSKDETADKNAANNGEQVMSRQQA  
QLQEAGKKKKRGGCCG

>PF10\_0321, 561 bases, A10BE752 checksum.

MLKHVFFCYRWRAEYGWVKSRLNFLCGASCYSSNINMDKIIDENKYEYIKNLSQELR  
ILSENCCVKKVDDVIIWSEICRHSIEKYNSFKYFDALLLSSFDKMNIVDKSLYKTF  
DVFQIKQISYLKPEHFILLINLYCRVNIIFPRVLFTEIFHGIKCYCNKLYPDEYVNL  
FANLKIANKDLIKTLCKSIIKNINLFDYIHLTNIVGALRSLEITDDIFYVIDQKQK  
ELKFLTVOEIFDFIKKIKLLQYSWKLYEQDLMKEFLFKVYNFKNEKDVDQLDDPFVCL  
NFLVSKGLLQGNNTNIKKNNNKKNNNNKNNNNKNNNNNNNDNNNDNNNNNDNNNN  
DNNNNNDNNNNSSDFIDDINCGGANFLVALSKWCANQVYHYPSRSTKRPTSYQLIK  
LYELMKEFNIHNSDFIEKAIYRFVITRGGLENNRDKMFKPTSYQKGRKYIFTKDPQID  
HINYEKNKEHSYSHYNLKDHTTDYEQQNMHYQTYDYNDENHNMNQKTLSEKHKRIKL  
SMEKKTQNKETHSNSRYCNFKLRQRPKRIKNSPAPIKV

>PF14\_0607, 1068 bases, F6C99CD9 checksum.

MLMLYLHILLCIFLNNPVLVTNENFFIKILRSQEKKIENEVSLYEKLNRRILFEGSD  
DFSNDLKLKSLLSFQKKIDNTIRKKQKEENKLLKFFQQAIKNGNNIYPVGNPQGFEEK  
EREEKEQEKTYMNNVINKINEQKGNYYEPNKNINNKYTEDLTSNGLLYNKDKIKNQFN  
NPHQEKFIRKHEHEREHEGKNEGKNEHKNEHKNEHVHVHEHNSKNYEGNPPKNE  
YPNINFTNILNSIDFYKKIDLKKNYFGYNNNETLNQNMKEQKNMQNHVENEKNNMIQ  
ANNQVDENQNNHQYNNNFHNQKNDNLKQDTKDNSSEQTYNNSNNNIEDNNHIKFFISK

DIEKKKNKQNDINESVYNAIKNKNLHLRRNNIKEIFDVDDLKNIKSFLGIKSNIHEA  
 FENQKLI IKNCNYESFGPELCSVDEKAKEMLWKYEKKKNSAFLFIILFTLFFSLIIQN  
 IVYFIEKKVRNSKDQFRKDLLNTAFRQISLITIIINLTIWGILOQTNIAEALDEVI FNDI  
 LPRHRNIDGVLHNVEPLLEVI FEKILFISMNFLICYSFIVSIHFVTRTILKWFSESD  
 NSDVSSVAKEVKESQRKCFRNYFFFFRNVNRNSKYLAHRYDFSENVDAISIPGLDPNGY  
 YYYEYMRASLLKYNVKLIKIPNAVILFLIFVCISLRPFYNI RLKAEVIFLNVLSLICI  
 IGLISLFFVYLYRIDTKLLPRDISKYLLNKYHIETCDKNKRDVTPYYKLLKQESVYPSA  
 LNYFFYKTTFPNKHEQLFLLWGNGPSLINFI FQTLFCFCFLIILSCWIFLLRVDNITWF  
 QLYSYGSL SICVILVFFFILKYIIYYNVMVTKTGYLIDTKLLEQVWEYERSDNIKRI  
 SEFIDAIIKIKSTLHALKEGGEIFWRQLLIKSSSTVPSNIQEKMFSIWIGLDEENRGIID  
 SSKILKFLKSQGINLTSEHDIREFLEVFDNRNKNGLNQEEFFVLI IIVKQILVELLDI  
 NAVQSLFEEVYGI PWKSLSSIDVNSLKKILTELNLKWPHGKIRNLIDFVCENKKT KYV  
 SAEYFIKQLINIEEVTLPFHVSS

>PFE0355c, 769 bases, DD515F98 checksum.

MINRQYFIWYIFIFNIINKIYFENIRYVKNYEVVIRKKKNIERGIGNDFAFIRRYYS  
 RLLSDVSYKNNSIKGKNRVDKEGDIKKYDNNDDNKMDNSYDYKNKSIKENETKIRKEQ  
 VISLDRYNRNINEKEEIKKKIKDIQRKRLIIYFKQDNTILSSRNYKHIFMKVLSSCG  
 HIEKLTFINFYLYEFPKSIINEDMLLKICLRLLESRRINVENDNQISHTVQMKSYNNN  
 NNKWDNINSKNNCIYQIKDKIKDLPNVSPSASTFTSISTSPYTLKLRDRNKYANDKNH  
 IFKINHSNKHKNNNNNNNNDYHNNNKSNYHSHSSAKCQTQRLNKKMIGTNI LDGYDI  
 IQMEEGLNLSHNYELNDVNVCIIDTGDIDENHIDLKDNIIEKKT FMKHSYKKYNIDGIN  
 NIESDNIDGINNIESDNIDGINNIESDNIDGINNIESDNIDGINNIESDNIDGINNIK  
 SSDNIKSSDNIKSSDNINSSDNIKSSDNINNVHTMLRNKLYLKKKKECSNYNTSNDGHG  
 HGTFIAGIIAGNSPKGKGIKGI SKKAKLIICKALNNNAGYISDILECFNFCAKKKA  
 RIINASFASTTHYPSLFQALKEQDKDILVISSSGNCSNSKCKQAFQECNLNIQKLY  
 PAAYSADLNNIIISVSNIIQQSNGNIVLSPDSCYSPNYVHLAAPGGNIISTFPNNKYAI  
 SSGTSFSASVITGLASLVLSINSNLTSQQVIELFKKSIVQTKSLENKVKWGGFINVYD  
 LVRFTIDSLPKDKDE

>PFI1735c, 713 bases, B0829D2D checksum.

MADYSSNEEETPKKEKKISKLEDMQSPFDYKRFFRKYTIFAPFILVYFTLMFFVNSTV  
 QNGTMLLNSIKENANSKLPALLWNKIIGKGNDEVNFEKMKMIEGNKSGNGEEHNKHK  
 RRQVDNQEDDYDVDEYGNPKSGAPYKSEEEHAEQQNYGEGHGDYEDKNEYHGKSNIE  
 NNKDFPEQGQKDEEKEKEAKKKAEEFEKRKQLHEEEKRKARETQQALHKKLQEQQLR  
 KEQEKKKVEHQKLIHKIKTQGDVDPVAVQKVLNKYNQKEKDEEQQILKIRDLQVQLRHI  
 QQRIQSLKSTNNGQPKTKDEYLQLKDLQKEYYDKEQDEQNMIHLEHLQGEMQYLYEE  
 LQIVYDENQAKTAQAKDEQHELKPOAEKDASKLTTTYDQTKVQKPOAEKDASKLTTTY  
 DQTKVQKPOAEKDASKLTTTYDQTKVQKPOAEKDASKLTTTYDQTKVQKPOAEKDASKL  
 TTYDQTKVQKPOAEKDASKLTTTYDQTKVQKPOAEKDASKLTTTYDQTKVQKPOAEKDA  
 AKTENQNGELLPOAEKDASKLTTTYDQTKVQKPOAEKDASKLTTTYDQTKVQKPOAEKDA  
 LAKKESEAPKGSSTSDKNTTENQLNAEAQSEVQKQKDYWKSKNESQTETNNTWKKD  
 SWKKKTEEQQNAEAQQEVKSPYEKYSYNKETKQNDKYTLNKEVQKPOAEKYTYNQKVK  
 AENTESEKSLLESSVFN

>PFI1740c, 119 bases, EE3E66E0 checksum.

MKMYLAEIFSSGKESLLSLKDTLGSSNFSPLKPEGLECLPQVLFVIFLLLCTGIF  
 MHNKNKEHHHEKSHNNGQNSNVPKNSFQNNKSQNHVQKSKVENQKVPVAQGSQHKSA  
 VNA

>PFI1755c, 326 bases, 3375A313 checksum.

MQTRKYNKMLSKVETKQFIYILFFLCLYLNTFNKYTTSYEGSSFRQLSEPVEEQDL  
 KKTNAESSHIEATTSQATTSQATTSQATTSQATTSQATTSQATTSQATSSQESDEQGLTAPSL  
 NLEETQSNKVRNKIFNFPIPSAEGTVSKEFKNQPKTEYEKKLFEWQHLMFEHSNWV  
 NITVQSCQVLVQGLTSLDDYDAKFKSWSAMVELLGEFRITLNFESNNMFEALLNELRE

ARKENPNENLTPEEEEEKWDLIKQTKLEKDIEWKIYQILTWKYWNLKEFPGV DIPDPSV  
PSLDFDATYDVLGDILEDEDEDEDEDEDTAKPSTSSS

>PFI1760w, 214 bases, 2D32C81E checksum.

MGNFFIISYNKHCIGQIIHMLYFICLIFILYNRNTCLRRIAKCGRNLSELNLDLRTDY  
DEREININKNIPSPVKFSKLEYKLRNEWDELEIDEHDDYMDVTVECFEKLLENDKNL  
ENYQENYEIRALVAYMLHELRRGYINEQKMKFKNFLHKLKEKRINEPIDTLNNDQDE  
WNKIKNGKIKSDEEWKSYQLQQTWEYLIKMEYYKNKYSQNV

>PFC0435w, 1294 bases, 60D44EDC checksum.

MKVGIIFFCLFFFVVLGACNNVKERIFKNIKKRTKFIILNEPIVDLSFSENLFHTLLF  
DLDVDKNLYTLDESLLNLENLNYSSIFRLLVDTYKNIKENEDDNKNIRYIFLGTSSFR  
IHPLNFEYFLRKLNKYIYNGNIYEKGNVDIRGILEEYNKEIEEKKLEKQKLNKIKDN  
NNNNNNNSKFSKGDGDNEDFNKNLDYNPSDKLYNNDDIDVHELLEEIIITKEKRFFL  
NDDDDNDSNDKYILKTDEVNKYKGGFFIGYGFNDIIPSVIHHYNFDKNFLFPSSLNSGII  
LDITLLKNIYEVSNIILLSNNEKDQSIHIDYIYEVTKYIKENLRVRLTHSENVCLNEEQ  
NIHLLDNDPNNFEIYKYYQVLNLFKDYNKNTTEEKQYEKIGHENVRHEETSSEGNENLN  
RNTKHNNNDNNNDNNYSEDAIAELLSYFNVFYPISTCMCYSIRSKHESLMDYDKYHM  
INLENDIKLKHYIKETEEIHFNSIEEYKMKLNRINYKYDTLLEEHEENLVTHKNILIGI  
KTSINTEEERIPHINKTYDNKENTQIIFNFTFNYDNKLKEKNTFGFYNNSSLQNALEND  
NIDLDIYMSDKESQKYDNLVFNKSVTSKEGLCEKLNKMIYYYYEYVMKNSEKKYFF  
IADDDTFVNVKNLIDVTNLTNLNCSHSHKMYDKYIKSYDFVKENEALFLQNFPPKTL  
FLYSYLKDTFAKTIQTLKKYDYVPKYCQGGIILSKKHKNNSDDDDHDDHVGKQNNDS  
NHQDIEKNQVNVINNNNNNNNNKAKSIPYILGRRYSYNTFSTNSNEYFYDYLTGGAGI  
LINDETAKRIYECKECTCPSTNSMDDMIFGKWKELGILAINFEGYFQNSPLDYNKK  
YINTLVPIYHRLNKNRTTKESRMYFNYLVNYNRNDKEQNKDIYVDYLDNRHKNMID  
NVFHYFFYVNMVDEKNKVVTKIEHNADMNSKKNKSKNPQKLNNTQGDKNVNDENVND  
DENVKGDENVKGDENVKGDENVKGDENVKGDENVKDDENVKDDENIKGDDNNYNVNDM  
ENIDDIINMVESVDDDMERNKKGTKGKEKDDKNHNNKEKATDVKKSSVPTNNIDKNE  
DTTKYVIKMKNEKIYNRMQESGKYKQLFDINKFFKKEIEGHPYFQIKKKNEKAKKEKE  
KMNQLKKQKDYTNNYFHTSNMQGNFNQKMGNYQNQENEENDFFDQRPEIEEDAINPM  
DYEEYEMENLSNFEDDGEPEYDEYDDYDDFVNTINADKCLKINDQNKHLYEQIKDIAQPPV  
NFQNDQNSNTFDFDTDEL

>PFE0060w, 408 bases, 737D8C83 checksum.

MLLFFAKLVVFTFFFWLLKYGKTRSYPKSGHKGHTKLNQPVVRTLADFNDMFANQKNT  
FNFLKHINHYNKNEQDTNNTHTPNHDEYSHNLPKNHEESNANMNNHNSFNDKSVNKKEA  
FDQFLQTLNLYEIMHKEDESKEHQHNYKEGPSYEDKKNMYKEILKGYNVFFENYA  
NDTESNVHNPKEEVHKHEEIHKHKRKLHKHEEVHKPEEFHKPEEFHKHEKVKHEEVHK  
PEEVHKHEENHKHEENHKPQMVGQAPPEKEIRQESRTLILGSFPQAGEILREDLWNKE  
DNKFSYALDPNDYASIEDKLLGSIFGYFKKNHDLVVKHLLQQINTYKHKYMELKEQYI  
NEVMKLLKIYNKSIMVIFIASCISILGPVMLHMHQNNPEEFFATILSFSISLGLHNLL  
LT

>PFF0845c, 2394 bases, 36DC08B0 checksum.

MGPAPRTATTTYSSAKDLLEDIGESVQKEAKKQALGRSESVLHGLLSNATIKGVKNKA  
TKPIQLEYEYHTNVTGGFDKNNPCANRLDVRFSDIYGGQCTDNKINGNDDDETTGGTCAP  
LRRLFLCDQHLSHMKEGNINNTDNLLEVSLAAKYEGDSIINNYPDNRDKKEGICTAL  
ARSFADIGDIIRGKDLFLGYTKKDEKEKEKVKQKNLKRIFNEIYKKMQDPAKSHYSGDS  
SDFYKLREDWWALNRKEVWKAITCKAKNDAEYFRKKDSGKHCSVQNCCKVDGDPPTN  
LDYVPQHRLRFDEWSEEFCKRKRKQDKLISLEKCRGKNKDKYCSLNGCNCKTTVRGKKK  
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KEYFETLEKEHRTVDTFLKLLNEEKECKNHPEVGEKKTFFIDFNDNIETFSHTKICEP  
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>MAL13P1.413, 249 bases, E8F5558E checksum.

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>MAL13P1.356, 2223 bases, FE89FDB8 checksum.

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>PFF1580c, 3954 bases, 4E8196CB checksum.

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>MAL13P1.1, 2162 bases, 8AE29CB6 checksum.

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>MAL7P1.187, 2595 bases, 3B9AD333 checksum.

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>PFF0010w, 2879 bases, 44511BE2 checksum.

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>PFF1595c, 2238 bases, 21C71EA0 checksum.

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>PFA0005w, 2163 bases, FF481D5A checksum.

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>PFA0765c, 2203 bases, FA7A87C0 checksum.

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>PFB0010w, 1711 bases, BE834973 checksum.

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>PFB1055c, 2199 bases, 46227279 checksum.

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>PFA0680c, 186 bases, 95132A2 checksum.

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>PFD0005w, 2646 bases, 588715EB checksum.

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>PFD0020c, 3467 bases, 941CB843 checksum.

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>PFD0615c, 2209 bases, B21A2120 checksum.

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>PFD0625c, 2277 bases, A473F6DB checksum.

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>PFD0635c, 2326 bases, 12A4625E checksum.

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>PFD0995c, 2152 bases, EE782057 checksum.

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>PFD1000c, 2201 bases, C010679E checksum.

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>PFD1005c, 2181 bases, 4B98EF82 checksum.

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>PFB0985c, 229 bases, DB6FFAD2 checksum.

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 >PFD1015c, 2193 bases, 723BC224 checksum.

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>PFD1235w, 3553 bases, 58745069 checksum.

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>PFE0005w, 2207 bases, 2E213C1D checksum.

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>PFE1640w, 3164 bases, D990C2B0 checksum.

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>PF07\_0049, 2275 bases, 3869900C checksum.

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>MAL7P1.50, 2267 bases, E423C7B8 checksum.

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>MAL7P1.55, 2239 bases, EC964FD checksum.

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>MAL7P1.56, 2192 bases, 14751040 checksum.

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>PF08\_0142, 2120 bases, E2B4BBD2 checksum.

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>PF08\_0141, 2858 bases, CDCDBFBC checksum.

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>PF08\_0106, 2231 bases, BB909D18 checksum.

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 KEWKENENTNSSLTHTSNIPSGENSIKNVLTNDVSIQIDMDNPKPKNEFTNMDTI PDK  
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>PFI0005w, 2270 bases, 24AEEC12 checksum.

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SGGDGGGSSRKKRVARSSSSSDDNNGYESKFYKLLKEVGYQDVDSFLEKLNNEEICKKI  
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DNNIHSDIHPSDIPSGKQSDIPSDNNIHSDI PYVLNTDVSIQIHMDNPKPINQFTNMD  
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(2) S<sup>-</sup>: 252 non-secretory proteins

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DQSEYGVPSILKLLDACDNYIEEPKRKTDL PFLMSIDDVLQISGKGT VATGKVEQGT  
KLNDQVEILGIKEKSIKTVITGIEMFRKILDTAQAGDQIGIMLKNVKNRNDITRGMVVT  
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 CIHNNNDKCCIHNNNKCSNNMNEKILIDVKQTFQYLFENKLITIPYEQEKNYEYHVFN  
 KIFHINFC DINKIFTFQYINQINPNILMKYNI TQKINIFKKLYHNYKGNITTDKQT  
 SFFTLFPFITILLIFKDIEFNKNLQNLVVEFIKYIFLMNINLQQYDLFVYDILKDDDP  
 IACTELFSYVQSASSIMEFIFNYSLVQYIYVKGFLPDVLLMIFAFCINSEINLKIHF  
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 >MAL13P1.184(Q8IDW2\_PLAF7)

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 NDVEIINQVYTLREPNHTFLNLILOYYRNRLINRNFKNYNEYSLKDCILNEPRR  
 VNYFLKNFLHKILPYFFKELQFIESYISLITLRKKEKKSVENTIKKNLENYNHKDEIPK  
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 NYFNLKRMKNSLLNKDNFFYCKEKKLSFLHKAYKKNCTFQNYSLKRKSNRDSHKLFS  
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 NHYDNYGGDNNNPCNNNDKYDIGKYFKQINTFINIDEYKTIYGDIEYKEIYELYVER  
 NIPEYYERKYFSEDIKKSFLFDIDKYNDVEFEKAIKEEFINNGVYINNIDNTYKKN  
 ILIMKKILHYFPLLKLNPPSDLKLLKQYLPPLAHELKIFLFFIVNITGGHFSSVLS  
 SLEIQLLLLYIFNQPYDNVIYDIGHQAYVHKILTGRKLLFLSLRNKKGISGFLNIFES  
 IYDKFGAGHSSTSLSAIQGYEAEWQVKNKEKYGNGDIEISDNANVTNNERIFQKGIH

NDNNINNNINNNNYINPSDVVGRENTNVPNVRNDNHNVDKVIHAIIGDGGLTGGMAL  
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 I IKMDNENNTNEHYSSRGDTQTKKKKVCIFNMGSMFLNVINAIKEIEKEQYISHNYS  
 FSIVDMI FLNPLDKNMIDHVIKQNKHQYLITYEDNTIGGFSTHFNNYLIENNYITKHN  
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 ILIKKKRRKKKRIYEQKHLASYSSKLERTTNGNKYINTYDGNEEENIFVHEEINTAY  
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 YVCKSCIIDIEEKSLYALKIREEEKEKDSNNISLYKEKSRHIQIYDYEDMQEYIMKK  
 KKKNEKNEKNEKKKKKIMMRNFKNSISGTKPIINTPYEPLKNNYQMINFTKRLFLS  
 NPMKIQEKGFELNRYYP RRVNYPMKEKLTGSGEYIWAYAININKNSQYKDVVLKKFLI  
 TKDEETSELNAMREYVFGIILKNCNISRFIYFKEYEINETVNKKKEEYIYFWLVFV  
 NEGYSLSKHLFDTSSSTLGLVTPSALWWSIKKQNI GMLVLKDLLRQILNGIYIAHKKG  
 ITHRDIKMENIFVSSTTPFTVRIGDWGSAVEYKNEHFSFIPSKDEETNGYQPPESLFG  
 HMKNNFMRLPYDMWSIGIVFLQFILGTKNPLEVKDKESERLKKIFSKYPIDILKEA  
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 YNRPNHIYRKHFFSTKSSYNSLYTNNNNNFIMNKLKYIITNDLINIKKQSFHNIYNI  
 SDKYKSLISLPSSPLCSDGMCLHKYDQAYDKKNITQPNDTGLICLNKYKLFSENQKN  
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>MAL13P1.209(Q8IDS5\_PLAF7)

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>MAL13P1.22(Q8IES4\_PLAF7)

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 PDYLNVEAGVGEALILKTMSEAYSRTESSIKKDLQQIEDLGI AENCSCKMRTIFPLP  
 RLTIQSVFHELKSI PNLI GSN SQKKREVIKKLLVSAKTSEAKYIVRFLQQLRIGVN  
 SATVVQALS YAFILTRPSIPDDIIKRGKEINENLINGKLDGTNNLINKSNNKTEEWLT  
 QSGDRNCIKEENLNDELLSKDDINKCENMDSLINERIRNEKINKPNIFYNLIEKVG  
 TRLLPLFFKELKNIYCEENNDIDIFECMEKSVKSALCELPNIEIIIQNLLNGDDMNTL  
 SKKCTVKTGIPVQPM LAKPTKGVQEVLD RFNNTFTCEYKYDGERAQIHYIDKDNIKI  
 FSRNLETMTEKYPDVIQIIKDQIGENVKECIDSEVVAYDIVNNKILPFQVLTTRKRK  
 DVDIENIKVKVCLFPFDLICCNGIPVIKEPLAVRRKLLYSLKSKDGVLSYATHSEM  
 NIEDIDMFLQDAIENNCEGLMVKTLVENASYEPSRRSLNWLKVKDYVEGLSDSVDLV  
 PIAGYYGKGRSGVYGAFVLAAYNSETENFQTVCKAGTGFSDEILSTLYETLSEKIIP  
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>MAL13P1.220 (Q8IDQ0\_PLAF7)

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 LGDTCTRGCKFCSIKTSSNPLPPDINEPFNTAKAICEWNIIDYVVLTSVDRDDLDPGGA  
 SHFAKTVELVKFSRPDILIECLVSDVQGNIDSVRKLAFSGLDVYAHNIETVKRLQKYV  
 RDKRANYDQSLFVLKTAKEINPQLYTKTSIMLGLGETKKEEVIQTMYDARKNNIDVITF  
 GOYLRPTKNHLSIVQYIISPQMFEEYKKEGLKMGFKYIASGPLVRSSYKAGEYFIKNLV  
 NQRNKDKKN

>MAL13P1.253 (Q8IDJ7\_PLAF7)

MATTNKKLQKIMTQPINQIFRFFTNKTVVQIWLVDKPDMRIEGIILGFDEYMNMLDQ  
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>MAL13P1.281 (Q8IDD3\_PLAF7)

MIFIYFFFVTLIIINLNTIESKYLFGYSYNGNPKCPINILYDKKYIYSFILNNNKRNT  
 YNSRIKCAKSSIIIPNEIVEGKVRFRFAPSPTGFLHVGCCRTFLYNYILSKQMNGSLI  
 LRLEDTDIKRNTKDSLDEIIKDLNWLNLTWDEGPDVGEYGPYKQSEKIQLYKKAIAHQ  
 FVNEGKAYFCFCSKEELQEIKEKSKMMKKYIYNRKCRCRDMNNEQIKMKLEQNIAYTIR  
 FKSPKRRKIILKDILKGDIIIDEVLEDFIILRSNELPTYNFSVSVDDYLMKITHVIRGV  
 EHSNTFKQILILETLNADIPHYAHIPVITTEEKKKISKRNNEYLIRNLREEGFKPEC  
 VVNYMTTLGWGSIKKEIYTMSELIDTFNIHKLKSSVVFDIKLLKWMNKKYMLQDN  
 ETYVREAEYMINNINILSSNEYKEFVELCVDIFKYEVHNYSELKECILNALKYEHVN  
 DPLNTDDIYLKQVSFLLYDWRKNDVKDNTTEYLEMKMIDDFDSLIDDIVKSTNLKKNQ  
 VLLKIRLLLTQSKGIPFIYLIKLVASARKHNIIPNYFSLKKRFLHLKLNLFKF

>MAL13P1.301 (Q8IDA0\_PLAF7)

MKTQTLNLMNINGKRKFLGTNNKIYRKVIINPTSEDDIQKFCRNYFRIYNFSLYNFIR  
 RLISFDAILVYSLFLTUVYIFSEINHGETTKYLFIDTAISLFFNIILLIVIESLFLK  
 LKDVKNANSQYYLRIVPKMSYFEKVMTKDIKVGNIIRIFQGDEFPAADVILYKNNAN  
 AIVDSFKIDGLFRKSIKYAVDKYKIDKDYKMLSEINGVIRCELPNKNIFCFQGNFKL  
 DKHPRSLLLNYENFALQSSVLKGAEYIDAVVVYTGADTKKNLNIPOKIEENKTFCIKM  
 NNIVYYLIFMYFVFLVLSIVIKTIFFFHKNSFQNSRDSFLSMLEDFVGLYILVLPIMM  
 YSEKSLIYIIQSLRIENDLRMRNTDSEKPKVFNKNKNDSLGNVDLLATSRNGVLVKKR  
 ELLVSCVINNVMYGKKDIICSRTNFKLPTLNILDSEKRVSNLLNLDERIFKDPENIF  
 FPTRDFYSFLKLFENKISSIYNPYSSSLNLLKEKYKNYVNEEILNKNVKLTSFVKSQ  
 LTIGYNQICEDDELSYNCYEIKEDSQKENIQSVKIEDFILGLCGCNRIIYNEKSLDI  
 SMNEYKSDNFMETYSKFEETENEEYHENDHDEYHNMEHSDDENINSIEYEDICLYNIIR  
 NTGFSIYCYKNTLFLYNLMKECKVYFLTCYHDFLRSNKFSMCILKCGYSINNEKEGGI  
 LYVRGYDFNILPYISKEKNNIKKIKNVIKIYTLNLYLVIIILCKKQISNEDIKAYIILK  
 SISKKLSFKFYDLIKLFFLYDLEVIGIIGLKNQLREGVKETFNDVINFDIKSWIFANE  
 CSKDTYLTALQCNLIVSSNLFLINYYNLKNTHEEGANILFHNFISSLYKLKSNSYAV  
 VINDESIKNIMTNVESMKIFLCIAMRATVVLFCVLQNETKGKIIRTLYALTSPKLTVL  
 GIGTTLNDAYLLKYSSISVFLSLNEHVNIYINISDYVLQEFKFISELLILGRLNRFLS  
 CKVFLWIIYLKITVVSFYFFHNFNDYFSGSSASSILYTQTTFALLHYFLIIAFSAYEI  
 DLPYKFVRRLPYIYQLSRRKYFLNNNIILLTIEAILISLTSYYILRLNVFHLITHRE  
 FTFHIFILNVFITTEKILLSKTWHIYFFIMAVLIIGILLIYVNIFTLVDCIKNGKCE  
 FSLFQMENIYFWTSLFPILYINFIFDKLMKYIKNRIYPDISDYLRKYFLRRICCHNND  
 KFLSQRKIKGINKFVNFEKNDILLKYIPTPKIYKIKDDPTYNKSRSKFLYDTRFKV  
 IDINVKYRNQQLNLEYKTYEKGNKLLRIIVILLFLIYIIIFSSQTIIDINTKSNIHY  
 ITMFYIIYFVLACVLLIYIRIRNKATSTFFFFLSRFLICGFCIELYDNISNDILNVL  
 ITYSFTVSYIFFMSFKILEALLVCISILLLTFGVYEEKNKNMIDICTHFCSNPYLSIN  
 NLDHMNISCLCKKQIVIFLISLLSFTLICLSMKYEIFYLKKKFLFRYKQKVNLAQOI  
 EILHTMLPNFLVEYLLISDPKNDGIMVGKNISGEDRGIISVIFCDIDDFQNMVSTLQP

HVLVETLDNLYLYFDKCIKYFNCIKIETVFESEYLAASGLSEKKNALDKIMYDTKCAI  
 KLAIAQLSAKYIISYKVLDTREHFSNDSYDYINKNISLKGIGHTGKAISGVIGSV  
 KPQYALFGDTVNTASRMKSTSLPDHIHVSYDITYKYLKEDNTFIWKERKVFIKGKGKMK  
 TYLLVDIILDDVKKRKGESLNYYSSSNLLLSQLGSEAVSIYEEREDIKEGSMDI IKESSR  
 DI IKEDSRDI I KEISTNISKSSSRNISKSSSRSDI KEQG I IDKEDLIFKINRMKNK  
 IDSRYSKRIDKESRDKISDKTNHVLDEVVKHSDIHLLNIEINNKRCKMKMGDTNNENK  
 LIGDIFNMYDKKIYIYKKNYKSKSMENISFIKHYRNTKYKKS DYLLLDNKGESKFK  
 RNTSYVLESPLHLIGDIVDNNIKRKKKKEIKTIVSDDMFTSPVNIKEYNYNEQERKK  
 EIVGNLSYDKTKKIFPFIKFTKEGRIKKKIEKKEKKEKKNNNNFFLYNDYSSYSSP  
 KYGDNENNFVIKYIRERKDFQKKFDHPNFNF SKFLHNYNPMKNKNKNKNKNVRNE  
 YPNYTSSSKDGVSYNFLSDFSSDNEYSSDNEYSSDSEKYYKRFKKNKKI IKFDDL  
 FTKIYIKKRLLQMNNDYVKGKGLKNKGMERNKTKYKNVNEITKMKYFVNNENRDH  
 EVNKEDISKSMQYFLHISKHKKEQIEDKKKTHKYFHKNVECVYPYAGNNINHNFSRN  
 EKRKYSINLYDHLDEQEKIKGKKKYFNKDKELIGSINKQTERPKPKKNKKNIENKDK  
 KKIRMITNKTKEKHSNSIISVEEQNMNHNNSLKKKEVNFTGKNEEYLNRRANTNCSLGI  
 KEMEDVYEFHSNNIYNNQTSYSDDINNTTKLKGGMNNTNDISKNGKKNLGGKISF  
 FSMNKNYHESEIMNEEDKNMNLNLTQSQIINKDKYNYFTHCPSLKKKSVFTKINNLF  
 KNYFKSIDVHEKFGFSKFKFHSKDSDDIKGNNNKISKNRYNNNNNNNSNYSNIDSG  
 KYSHNNKNHHNNNNKYHHNNNNKYHHNNNNKYHHQNNNYEKHHHSNNSRVMLSKGEK  
 TEKNENVDYAYQFDNYDKLLKLLTSLNLQLNKNVKNFNMFYKFNDEELEEEYTRNY  
 YREIINIDLTKKLIIFIFTEIFLSLCNIIELS FYEKLRYNDSIVI IWLIRSIYLF I  
 ITYIWIILKTKLKEYKNNSSKMMWTFILNIFLCSWGIILIDLSCIHYSMMLGNKNER  
 ALFFMKDASELIICIQLIFIKNMLFKHKFFFFVFFYIFLIYSFSKLF SIHTCQTHICC  
 SIILFISINILYFWYSEYLDRIQFLVKKRNRMEKISQDFLTKILPRQVLEEQNDNL  
 QLYTKHEKIAFLFADIVGFTKWSKTVSPKEVLKLLQKLSKIDKDTIKLGLYKLFITIG  
 DAYVATSQPNSITDESEALEGILNILKLAKLILHNINTIKIQFNKHDFNMRIGLHYG  
 SCVGGIIGSVRIRYDMWGLDVLIANKIESNGIPGEIICSEQFRHFFIQNEPQA  
 >MAL13P1.322(Q8ID64\_PLAF7)

MIAKSYVYRDSSSDGNKKNNDKIQTGFLYNEKKNKLEFKRRKVNKINKKLTDDVK  
 SNIFKKIDTFEEASFKKDKVSKRYLNNEKEKEYYKDRDNKIKKNNIKDKHVNQKYN I  
 YNSSTSPDNSDIDNLYNHKENKNNHKYKNSDYSEDSINISINIKNDES NKYNLSNKQH  
 HNRYSNKTFEKDEKQKDYKKNNDKILDEIWTKEDEFVDSFYNMDIEATYEKEKKM  
 INNLKTRINSNTGKKVNQKNLDNNLWELNKLKQGGVTSTYNKLQLEKINEANVTNEIK  
 KIVLRTVNPPFIDKFKSYNKR FVNIEQRNNFDDQKSEKKS DNINNDKYYSNKPIQS  
 TSYSTVVKDETCDFVKAACKGSEFLKYFKSENEKSKARDRYWEISNSKLGELLKLYKN  
 KKKKNKNDNTSKEDYDNISYNSSENKEDDNGSDVFDYKDKIYSSLFNIENNNKDKKN  
 TLKDKHEELKLKESLPIYKSKHELLDAVYNNNIIIVGETGSGKTTQIVQYLYEEGYH  
 RNGIICCTQPRRVAAVSVAYRVS YEMNVDIGSLVGYTIRFEDNTTKDKIRYVTDGIL  
 LRETLDNKELDKYSVIIMDEAHERSINTDVLGILKNICLKRNDLKLIVTSATIDAKK  
 FSAFFGNAPIYNIQGRTFKVHIEYLRTPCNDYIECAVQKAIQIHVSDNNYDNNFGDIL  
 IFMTGQEDINATCYLLSERFYEYVESYKESKNNKDTINKIKNILNEDNNNNNNDSNI  
 KKKVDGDNNTNDHMIYPFYIFPIYSQLSSEQSKIIFKDYDLRKIIVSTNIAETSLTLD  
 GIKYVIDTGYCKLVYNQTIGMDVLQVTPI SQANANQRSGRAGRTGAGICYRLYTENT  
 FLCDLYQNNIPEIQRSNLSNVVLLKSLHVQNLFEFDFIDVPSKESIINSLHELWVLG  
 AINNEGNTDIGRKMVQFPLDPPLSKIVIYSQNFQCTKEILIVSMLSSPSIFLESKE  
 NNESIESKKEKFTVPESDHLTLNIIYLQWRSHNYSYSWCTKNFIQYKALNKAKEVYSQ  
 LIDIKTLNINKVSCDNKWELIRKTIICSGYFHNAAKLKS FSEYINLRTNVSCHVHPNS  
 SLYNIGYTPDYVIYQEI VFTTKEYMRNVTTVDPEWLCELGPLFFYMKNV  
 >MAL13P1.324(Q8ID61\_PLAF7)

MPRLVIFYFLIFVFMKINCINYSFSKRKINYHLIRDKQENIKYKYLREDEKLNLSRR  
 NRTRKTKETNGGTQRIKRIKRIKRIKRIKRNLSNIFYNKNDYMIKKINVPRTYFIKN

MGNSSLKGCYKEKKTIFNIYNIYDDKNIMNPKNFGNEDGNLLNKLGN DYSDKDSYNK  
 NMNDKKQIVLDNKNEKMYIENMKKNLSRTDEVYKYVEEMELKKINIKGVDIQYRLYN  
 LEEGIYIVDKENYEKIKKKLWDKDELKKAKENFEDTFDIKKQGIKDEDWIMLPFEYEEN  
 KNIKLVKADFDNPTYDYILTYDKERNYWEYKRRNYKMFKNTVHETPPYKSDLEED  
 KRYYGKEIIIPKKKLDNDFRQPMLSDVMTSGCNREPLGFESWRFVKYPYGNLIESQK  
 YSKLYCVKKNDKDKPMSKYHYLGNSNLAVSEICLGTMNFGNYVNEKLAHELFDYAFEE  
 FQVNFDDTAEIYPLPASENYGHSEEILGNWLEAKGKANRHKFVIATKICGRTDKLPW  
 MKKYKIRTEQKNILNKRNADIYNDNNYKGDHYITNSKSNEYSHRNNNHMLDKEDNKNG  
 YDKLKEKEEELYLKKDYDKINKFEEYEKERLDNSANLITLNKENINSVDNCLKRL  
 KTSYIDLQLHWPDRYYPDQSSGDFSHVLYDYNKYDDFIPFIEQLQALDELKKKGI  
 REWGLSNETPFGLLKFYELCKHLHISPPVSVQLEYNLLCRNDVEKGFPEICRPQNTNI  
 SILAYSPLCAGILTGKYLEYTDYTTKGRMQKFP SYMKRLRGS IATYI IRELYYLSQKY  
 YFPNLTVAALKWVYTRSFITSTIIGVSDFLQLRENLYSLTNEVLFTDKLEREINALHW  
 KFRDPIRIIQ

>MAL13P1.335 (Q8ID40\_PLAF7)

MSLFNLITLYYVMQKYAKTPKISILTKILNYLILYIYVIMFLHFFSTSEVRTILRFL  
 NKNIEFHAVEKSYMENCNNLANISVRILKRKIEHSKNIYIYICIYDKIDWFVCAHLWG  
 WFAKGMIRNFFLLNINSVIFELIELRFQHILPNFYECWWDHIFLDVLSCNLIGIVAS  
 ILFMKYFNIELYDWKIPDKIKPNKKNIIFPTIDKLCRKVFTNSSTLLILIFLSFITNI  
 IDLNVFFLKAIEIQLHHVNLIVIARTFAIGFISGKACKEFYRFLKEGMPKRAFYIFLE  
 IIIILSLEFLLAIRWKDTLISDKSDLTGINMVWLFITSTLSSILLLLLYVNESLI

>MAL13P1.338 (Q8ID37\_PLAF7)

MSAIGMPQHILILFQARPMLÉFYKPIKKKKPKEYSGLSDFLNYFEEGEAPPKIKVESF  
 KERKEKKKKEKMAYNELILKEKRKEYDPFKNEDLTS DPKKT LFIGRLSYEVSEQLKK  
 EFESYGKIKTVKIIYDKNLKPGRYAFIEFEHTKSMNDAYKLADGKKIENRRILVDIER  
 GRTIKNWIPRRLGGGKGPARGSEEKKKIIHNINWTALINKDKYRNDKRSDELYKNVP  
 LYNERNNDDDEDDGISSTMRDYKHRSDDHRRGSKRDRRHRSSRSESSDRHHHKHRRR  
 DRSRDDRDRNYDRHGRHDKHDRHDKYDRNDKYDRHDKYDRHDKYDRHDKYDRHDKYD  
 RHRHDKYDRHDKYDRHDKYDRHDKHNSDNPNYDNSTKDDIRKENEINDIQHNDYENREH  
 NEGFVYESITSIEDCDD

>MAL13P1.35 (Q8IEP6\_PLAF7)

MSNNTTTHNINSINNVNNDNINNDALNPNNDYLDKNTNFTNAHFKPSSYVNGAGKNM  
 DSAGNIIPNINNNIQYHMPINPNMPYGVNPNYNIHNNKMINNPKNMYNAPYPLNMNTI  
 PINSYGGAEKFTHSVRIPIYPTPQNMLYNTMNYMNSKAYIKHLKYNKVIPTDPTIPP  
 ETLYIKNLNDRVKTDEMKNLKDLFNTYGEIKDLIVMKSFWRKQAWVVYDDKECATK  
 ALNALQGYVLFVKIMQINFSHNKSIDIHAKRDGTFVERSKEPKPKKILEREQKQKEIF  
 EQMHKNYLEMQKNFNMLNGNKEINKPEIIDLSQMDKQTLIAKAQAKANEDKNKKNEE  
 LPNNNIFSSYYQMNNIAPVQNYPVVMPYKILFVENVVENVDTQAFNDLDFKNYAGFVEA  
 RIIPQRNVAFVDFDTDETTATFAMKAVQNYELQGSKLKISYAKRYFFI

>MAL13P1.47 (Q8IEL5\_PLAF7)

MRYAFGTSYLTCEFMGINKAMKKFVFKKNKYSSLHLFERNEINNFQINIMDRKYVHSIK  
 EEKKKEESEDYLSMGDNIEKRYSLALYNVAKKQNKINEISNDMLFIKNHLLKDTTFQ  
 KFLHTPNIEKKEKIHFIKNECKTLNKFNIITENFIESLFDISKRISFLPKIIEEFEFLL  
 LKQRKEIKCVVYTANEIDNNYKQKIQDSILIKLNKKLPIIQYKTDPIYILGGLILQIG  
 NQVYDFSASKIDKIKTNFSQ

>MAL13P1.56 (Q8IEK1\_PLAF7)

MKLTGKCAKYIIFTVLIILANILYDNKKRCMIKKNLRISSCGIISRLKSNNSYNSFN  
 KNYNFTSAISELQFSNFWNLDILQKDIFSNIHNNKNKPSYIHKRLMSEKGDNNNNN  
 HQNNNGNDNKKRLGSVVNEENTCSDKRMKPFEEGHGITQVDKMNNNSDHLQQNGVMN  
 LNSNNVENNNNNNSVVVKNEPKIHYRKDYKPSGFIINNVTLNINIHDNETIVRSVLD  
 MDISKHNVGEDLVFDGVLKINEISINNKLVEGEEYTYDNEFLTIFSKFVPSKFAF

SSEVIIHPETNYALTGLYKSKNIIVSQCEATGFRRITFFIDRPDMMAKYDVTVTADKE  
 KYPVLLSNGDKVNEFEIPGGRHGARFNDPHLKPCYLFVAVAGDLKHLSATYITKYTKK  
 KVELYVFSEEKYVSKLQWALECLKKSMAFDEDFGLEFDLSRLNLVAVSDFNVGAMEN  
 KGLNIFNANSLASKKNSIDFSYARILTVVGHEYFHNYTGNRVTLRDWFQTLKEGLT  
 VHRENLFSEEMTKTVTTRLSHVDLLRSVQFLEDSSPLSHPIRPESYVSMENFYTTTVY  
 DKGSEVMRMYLTILGEEYKKGFDIYIKKNDGNTATCEDFNYAMEQAYKMKKADNSAN  
 LNQYLLWFSQSGTPHVSFKYNYDAEKKQYSIHVNQYTKPDENQKEKKPLFIPISVGLI  
 NPENKEMISQTTLELTKESDTFVFNNAIVKPIPSLFRGFSAPVYIEDNLTDEERILL  
 LKYDSDAFVRYNSCTNIYMKQILMNYNEFLKAKNEKLESFNLTVPNAQFIDAICYLLE  
 DPHADAGFKSYIVSLPQDRYIINFVSNLDTDVLADTKEYIYKQIGDKLNDVYKMFKS  
 LEAKADDLTYFNDESHVDFDQMNMRTLRNTLLSLLSKAQYPNILNEIEHSPYPSN  
 WLTSLSVSAYFDKYFELYDKTYKLSKDELLQEWLKTVSRSDRKDIYEILKLENEV  
 LKDSKNPNDIRAVYLPFTNNLRRFHDISGKGYKLIAEVITKTDKFNPMVATQLCEPFK  
 LWNKLDTKRQELMLNEMNTMLQEPNISNNLKEYLLRLTNKL

>MAL13P1.67(Q8IEI1\_PLAF7)

MYVKCFYVIQILFIIIFLKCHCYKIKCFNILDNKKKYYSFREHINCEHIRNSVNRNN  
 LSNVLLRRRTKNALVKELYVSKLKDNYKTHTNFIRTNNIFLEEDKKIQECNINNIINN  
 NVDIQENVEKYNILYKNQLDDINILYILLFNTLMIYKKKYDFFMNENYIRSYYYIYKN  
 NLGRDKKIYNTKNYFINTFSITWYNTIKPYMNNIFLEILNIENTLGNKIIFYIDIKQE  
 LNKNRDEIINTLYNIYKGNFRKRDKKPIKLLFIGSNEYSNLCFKIILLIKRLRNDII  
 LDNVITKSPRRKGRNLILKKSNEDEAIKNNINVFYDCLKNNIHMQLQKKMDLCSISI  
 SFGEIFNCNFFKTIKSNIIFSLHPSLLPFYKGASPIQRSLNNEILYGYSVFLTTLNID  
 SGNVIMKKPFWFNSNYNFNDIITILFTQGTLSLLKNISYLANYNKDI PHKNIYNNNIC  
 EETKNNLNQNHVQNKYDSEINIHNSENLENKNNSRNNILPLNINNVLNYYNNKMYIQND  
 YNINNNYAPKIKNDEKYVCFFCSTSLFIHNKIRSFINWPKAECTLFLQNEVIKPLEI  
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>MAL13P1.83(Q8IEF5\_PLAF7)

MDELEVAAILCLYGNEHSNINKNDAQKYCENFQNSADCWKYCMSKFLESNKLEVKFFCI  
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 MNDAFKYLINLIMLNNDINIKTIHINFFLKLMMNMFSEYIDNVCSNKSIQTTTNIKEA  
 IKENDLPIIIIECFYIMNMNIPESTSLSIFTLISKYVPWIDINYVVNDKILTYYIYQTLN  
 TTNSITEASYSFLTSLIRKGMNSANKIQFIESINIICILQNTPKITDLTFDVKNIMT  
 KRGELINYICLLEVESIFEINKLKDYQMNMLKYNEICTKAADMFLVLPHALDIFSVN  
 DFYIASTVEKFFSLFFTKFKNVIDVGSCANSIMKSSNDYESSKNNISNNINSSINSN  
 INNNNANSYKISIDKLVFINTLICTIVNKFEYPECIPDDYDEEEEDDDEFSTFFNF  
 RENIEKLYQRLILFDKLLKAEIEIKNAI IYLNENYDNLKWNNIESKLYAFYVTTSIYCE  
 YKQGSTNTSNNLNNMI TNNQNKNNI IMNNSLEHFKNIKEANEVNI DYNLLFDCLIE  
 LLKNRKI LNSTNYHININLMEIFQRLNLFFIKPNYIEYALHIFLTNGIRSNNNKIAK  
 KSVHIFKKFLKTNSSVISNYIKDILQLLESYLDVPYIYPKMDINNNILNNNNMILDDN  
 TIKYIYTFLYSNKNYNHEYQIDIYEIIGLLLLNYDFNKFKKLSKTDGMSIQSNNNLS  
 NNLNLNNNDNSININNNNNNTINSNNNSNDGLNQNISEEMIANKYDRIFFFKGILN  
 KLENLSAVKNLYLNSTKTQHDNICASFISSVIKICIGALCKNVNINITDILLNDLDN  
 TLGIIISESELEFYNNYIVRDSVLFTYRILSNLFDKLSLNYTVKILPYFYNISYNNMIM  
 NKLQKSSVDNQNANTFNMITPTSYSQVDGTTNNPMKTSNTHHEELKYLYNELNELSIL  
 VCHLISTHKEKSFDTFVNPYIYNITQIHMNIWKFINVQSLEMQREQNAVLSPLLLILY  
 NISVNIPATIHSEFMSFEHIALNHKQFCDFSNDDI KSKIADAITSILLISLNYKNTS  
 DINICLYSAQTLNMLNATCMTNPSEVLISKYPIMQIIDTLCVTLKSLDYADPKTKRI  
 MQEVMNIFRLFCGFKVSANCLPNKIESSQICLQNSLLSVFKNNPNDAIILIQAINAN  
 NQQQFRQILSNIVA

>MAL13P1.84(Q8IEF4\_PLAF7)

MNKMSTKIENPKYKLMKLIKGTFGKVYSAIDMSTQEAVAIKRSPKWRNKVSREVDL  
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 GIKDLHKNDFAHRDLKPDNIDLIDLSSNIKIEICDLGSAKKVQRNIISIPYICSRWYR  
 APELLCGSMFYTTTEVDLWSLGCIIFELINLCPLFPKGFKKDEYSEECSQIINLIEVIG  
 SPQMSFFENIKDHTSKKNTLLIKELCELNIKPLCWDEILGNILEIENPNERLNIDAVL  
 SNPYFSTLNK

>MAL13P1.95 (Q8IED5\_PLAF7)

MNIVILLILLITFSIKHSNTYKLNKNTYIPINMYHNNKNILRSQKSKLFLNFLSNNQLA  
 NSNKQTCFFKSNIKSSISNIDNYDYIRKRYINTSNKNKLFYNITLRTNDGEKKIECNE  
 DEYILDASERQNVLPYSCRGGSCSTCAAKLVEGEVDNDDQSYLDEEQIKKKYILLCT  
 CYPKSDCVIETHKEDELHDM

>MAL7P1.113 (Q8IBN8\_PLAF7)

MNKHDQKKRNKQHTDNVMGKKSkgfIKNKNIGESGNEKKRNNNFNNIWKKKKRSGN  
 SEKQVDILGLLKGdSENmNDDDDNNMDDYNNNNIKGDYNNNNIKDDDDVDDDDYDDD  
 DDDNFdenKNCNDNCSSKHkRNVPSKKEHDILELNNINFNETRKKMINYKNI FDGKFC  
 DLKYILSESLINTLEKNEFIKMTSIQKMSIPLFFKPNDIFLKSMTGSGKTLCYAIPSI  
 EKILNMKEKVKITRDMGIFVLVLSPTRELAIQINNLFCILTKPYPIVASCITGGEKK  
 KSEKNRLKKGISILTCTPGRLLDHLENTKSLKLTFLKMLVILDEADKI IYLGTDQDKIKL  
 IYDMIRKIKQEEFSKVHKKKKKEENEVLHDHINDTNMSDMNNISNDHSNDYEQFILDKF  
 QMIFISATLNHAMKTLANYCLTNNTMWIEKEKKNINGGNKNDETKQKSNDMISCMNR  
 ENSPLNIHNNDDNDNDNDNDENNGDNNNNNDNNNNNDNNNNKNNDDDDNNNTYELPEQ  
 LKQYCILIDMKQKFI CLIMLLDCIEKKKKPVVFLSNHHSVEYLQIILLKNIYWPTDVN  
 KKNIEVNKKLNEKITPVLEREDEKLLRKHLEQNILNNNYNNNYNVGNI SYKNINLEE  
 IQNEDELNDEPGNLYNINADKHKRIYLFNNVNIYILHGNLSKEDRLGNFMDFSKTNNS  
 ILLCTDIISRGIHFDSL SVVIQYDPPQILEEYIHKVGR TARLNKQGSAYLFLLSQKQ  
 FLNILKNKNIQLKIILGNTIINHFKKFCIPNFLKSVGKDILNFLHNMQTIVKSNNTL  
 MEKGTSAFLCTITSFYSTSKNLR SIFNAKDIHLGHLAYTFLEKTPKQISKYKKEQNY  
 INIKKQTVLSKKEKRLKSKQFQKKQKRK

>MAL7P1.118 (Q8IBM9\_PLAF7)

MKLLYRKRDN DKMIIGLITEEDDDLWGVYNLLSLNDEIESYTSRKVQKDIGNNSYVTE  
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 DHIHREKLEECTNIKNNCEIAILLIDCGRANMYLLTQQLYKTVFSINKIIHKKKDKNN  
 SSSYKKSLENFFNIVLKNLYSSINF EKIKCIVLGGPGFFKNDFFSYLYEKSDMKNDKN  
 ILTLKNKFLIVKTSNIFKNSLNEILNDENMKKQILNLKVVSHVDILNKFYKIFEKNE  
 KICYGPDEVKYASKINAIDSLITDKTFRSCDVKTRKEYVQVVQYVKN TGGQVYIFSD  
 NHTSGEQLNSLTGIAAILKFPIFYDINQAHEKGQSTKEDYIKREDTQNGEHMTNI

>MAL7P1.122 (Q8IBM9\_PLAF7)

MAPKKKEEPPKLLLGRPKNTLKMGLVGLPNVGKSTTFNVLTCLNIPAENYPFCTIDP  
 HEAKVTVEDERFEWLVKHFNPKNVHAYLSIFDIAGLVKNAHLGEGLGNNFLSNIAAV  
 DGIYHVRAFENEDI IHTEGNINPVRDLEIINSELIYKDISHCEKNLEEVTKVLNRNK  
 KDKVKQNEHDVLT SVLNYLKEHKWIKDGTWKSNEIEVLNEYNFLTAKPVVYLVNMSEA  
 DFIRQKNKYLAKIYNWVQEKNGGTII PYSAEVEQKILSMDEEEKQYFETNNIKQSML  
 NKI IKTGYYEINLIHFFT CGHDEVK CWTIRKGT KAPQAAGVIHTDFEKGFI CAEVYKY  
 TDLVEYKSEGEVKANGKYLQKGDYVVEDGDIIFFKFNVSSGGKK

>MAL7P1.130 (Q8IBK9\_PLAF7)

MKRSFRS IKTLRVNYFMKNKRIYHSSNNTYDEKEKRFNEQDNEWWD DDFDNENNT  
 QENKTCIKTRWKNIFDEIIGKNIYSLHDYNKKRFD FIFKNYEFLYYKNIKDHMNKKEI  
 NILDIGCGGGILCEYIKKNIFYFLLKNVDNVDLIKDIQINIDGIDVSEKLINVAIKRQ  
 QINRDYTKHLHINLNYMNC DLNEYVNIHNNNKLKKKYDIIISSEVIEHVPNNKKNIFV  
 SYINKLCTKN TLVVFTTINKNYLAYLYT IMLGEKIFRMMKKGTHDYDKFIDNKQLDKL  
 CRDYNLYNIKTEHVLYLPFFRNYFQTYKLNLLYLSSFIYSGNNL

>MAL7P1.150 (Q8IBI5\_PLAF7)

MKFLQIIKHLKLQNKKNALDNFVNCRTYEHISNINKLFLNNSSTKEHSEHGQVKHEN  
 FLNSTLKYEENSQNGSTNNLKNNGKYNMYVSEGNVNIINEEKYKDNNISSNNTQYNNNSS  
 NSGSLNDEGPLWKEHIDDVVNENKKKKMNRFYLDQATTMIDPRVLDKMLPYMTYIYG  
 NAHSRNHFFGWSEKAVEDARTNLLNLINGKNNKEIIFTSGATESNNLALIGICTYYN  
 KLNKQKNHIITSQIEHKCILQTCRFLQTKGFVETYLPKPDNGLVKKLDDIKNSIKDNTI  
 MASFI FVNNEIGVIQDIENIGNLCKEKNILFHTDASQAAGKVPIDVQKMNIDLMSMSG  
 HKLYGPKGIGALYIKRKKPNIRLNALIHGGGQERGLRSGTLPHTLIVGFGEAAKVCSL  
 EMNRDEKKVRYFFNYVKDYLTKHLDYIVFNGCQINRYYGMMNISFLFVEGESLLMSLN  
 EIALSSGSACTSSTLEPSYVLRSIGISEDIAHTSIRIGFNRFTTFFEVQQLCINLVKS  
 VERLRSISPLYEMELEKKNPSNDDIPKFIWT

>MAL7P1.151 (Q8IBI4\_PLAF7)

MHKIKVLELYCGIGGLHYSLLQAFNNFVHANKITEKKCDTYKDGIHNMHSNNKSIEIH  
 KYHDCCTLCLNDLFCFISVDLNPVANQTYFHNFKDSTILLTQTRDVHKFFKWKCDSDM  
 KQSNGSTHNEHEKTQKKKNKKKNDDDEKNNIFNINKNYIIQTDINNIMPEFLNNHHF  
 NILLISNPCQPYTRQNQKFKEINLDDLFCKNNEYKQNVNNNI SNNNSFYSNHNGDEN  
 HQFNVDNINIDELNNYIYNDKDERTKSFIHICTLLTKVDFKNLPEYIFIENVKNFELS  
 SSIYFLYCIKNNYSFQTYLLSPLQFGIPNERLRFYCICKKKNYDFKHANNLSGINYI  
 KDKNLNLYTNSLIPKNYLHKNNIHEQKNNQGDYNNISCEENVIFYTPNLITYLDVNNN  
 FNITNNIWNHINIYNNYLDNYQVQNVQLQKNASYCFDIININKKTTTCCHVANYYYHHH  
 HQKKKENVNNISPDEPTKHMNAKGNAMCFTSNYGRYIKGSGSILYNNRKENSNCAEQ  
 KTKNKETNVLTKENNEYVHTSNYTCNSISNSDNDTYETRRKKNCMKKYEQNVRYFTPT  
 EISRLMGFKMKTNNKNINQNEKGKNTYGNVFWNIDHINHTCAYFSNVHYCDVQKNAC  
 LLTYQNVNTLNNNHTYQNC HQKNCLCHEFVFPNFLTDRQKYKLI GNSVNVIVISYIFH  
 VHNI FEHIHI

>MAL7P1.159 (Q8IBG7\_PLAF7)

MDRYINIDVRNMNNISDTDGSPNDFTSIDTHELFNKKILLISLPGAFTPTCSTKMIP  
 GYEEEYDYFIKENNFDDIYCITNNDIYVLKSWFKSMDIKKIYISDGNSSFTESMML  
 VDKS NF FMGMRPWFVAIVENNILVKMFQEKDKQHNIQTDOPYDISTVNNVKEFLKNNQ  
 L

>MAL7P1.20 (Q8IC21\_PLAF7)

MSIFVECRKNIRGLNKCLFLYKGVNRIRNRYNLCSYVNKDVENYSRYFKNSCSLILSS  
 GTGGTEACDFCNMLYMYIKYLCRIKRNKNIKYEVIDISKNEVGIIKVEIKIDGEYSF  
 YNFVSEKGIHRLVRNSPFNAQNKKMTSFVKVDVIPTLNFNDLNVINFLNTAEGVGSS  
 SSKLTKESSDKKQNKKNKHQLKESDNNNNNMNNSYNGGNNKMNDVINKSDLVIQTMR  
 SGGKGGQNVNKVETAVRILHKPTNISVKASERTQLLNKRNALKRIYEKLLYLQTEAL  
 KNKKYELANKSLTHFGEQIRNYVLYGNKMIKDTRTNVSTDDIDKVLVYQGEIDIFIDAY  
 QKNL

>MAL7P1.21 (Q8IC17\_PLAF7)

MLKNFEVNSPKKLIRKIEEETYEEDKEEYLITNLTENKKNMPSVIRIPRDLNKFLSN  
 EETTIKYNENIKSSNNKMNKEQKLT SFKMDNKYDMNSEEKISAMDNIVLDSTYQSDST  
 HESISFFNKIKGQNYTIDNINENENNNSSNGDSDDSDNDDSDNNSYDNSDYTTDDD  
 KPIDESLLKSFKNKYVDVYESNVSNNEYITFIKNHTKNELEHFLQRRKLHHTNEMKVN  
 DIINIDYDKLNEKNIIPYFLTNVFDMEQKKKREKMKLELEKRRKIMEEKRKTKTQVDD  
 KAKTKNDTHINEKKKKRNENNKVDTKKSVENFTKAANTQKIVKEGKMKTEDNDNSYD  
 EYEDDNSYENKNRRNKKNTNSNENQKINEDNEESYSDSYNDEFDKEDIDINIYNDPT  
 LYGIEGSSDYSDMKSADNHTQEDDTGKEQITNNNSKTPKGGKKNIDEKNSEEEE  
 KLDDIVDACTQRLISYDYSSLNIKEIVKPNKIKSLSSYIPIQENLDNLDHIQKLQY  
 LIKNLPYTHIKEKRSLYHYNIKQFIKWKVYLLNNINICLYGIGSKFHLLNLTNICTLN  
 DGNKCIILGFEDEINFEEILVRILEYHYKYKSSKTLKSFLLYELIQRVNDSNVPLYF  
 IIHNLNNTKLYPYEYFSFLSQYENIYFVCSIDDVSEFELNMNFKNISSINFYIKCHT

WLDYRHEILRQWNKFLPEWVFNKKCEEIDIKKNIETILNALSINHKRLFKIIASIQLE  
 NLDKGIYGVESKESLLQDKRIFTVGASSIRINSLLEFVSHNVITETRLKEGNTFLKIN  
 ADKEELKRISEEL

>MAL7P1.75 (Q8IBU5\_PLAF7)

MWKAANVSYTRYASEMADILRKCLKDPYSDIALERSKMHIRETIYKDGKPVSQELYEE  
 FEKAYKNLSRQKE

>MAL7P1.92 (Q8IBR8\_PLAF7)

MRNSDFFFFFFVLLNCFLNIPYVSNATSNIIEKNTSFVKKIYDDPYIKKDVTLQLK  
 NAKYNHINKKISKSKKNVKKKRGISFVSLNLNKILELQDKNPIKLSNIYAKDKSKFL  
 STCYENNKLNNDINNCNRFITISKQICDTPVGFNLNDNFLVKETGGLSSTCLVDNKPEYW  
 KIYNNHIIVESGEYFDLIRNETFLLQTSIIITKDICMNKTKIESSYFTYQNNHNSKIG  
 NPILYKGEVIGMEIKNIKVKDDVEGLFNVCSCYLDNEHHAYNKCSETNKHMQISSIR  
 IIKKIVHNINILTGKKLHINLQNYVTPYPIKSAFIIKKVEHYSCNNINNKSFNEIQEH  
 FYNNEKKLKFYNIFLYETDLQEFKEDIIFENPGMYLLCYTSNDSQSEYSAELSTILVN  
 GYDISKMNYLYLDLYENKLNLRNSVVLHRYNLNEKLEEIFFKKEETIQCSGEDIIYSN  
 NITETKSYKSDDNSDDVIIDTIYIYNINLNAYDQILEICSKKYNEYSLIGYTTIKPY  
 ILHNYKDINHLTHFNIPPDHVRTYVVDKKSNIITFFPQLLNIFNQNDINDMYMSFSCY  
 SSKNEIIITYSFDKNMTPFFFKYLKISDASSSILYITNKGVYLYVLKKSQLLFLYDI  
 TPEKVKKKKIIITNKKINDDYLELLLSYLDYDFTKCEQCLSPILMEPIYDEKQNLK  
 HIFLITSHPLAKLLIVGLDFKIIYKHDNNDVKNVVTIRGFNFSTSDVLKYSSFLITGI  
 SCGILKNESLDCFLIDQLNNTIIAIEYLQKQKTIILIDSFQGENKNELNYESINLNDF  
 VFSQSNSYLHTPRNAIAYSFGESYVIFVNESESNELNLLFYDKNKADNLSYITKINN  
 TYINDGAIENIYKFYDHKDLINRNVLLIMKYYEGDVYFMYIPLRNIANKLELAYDYPT  
 VIQDNGNTYTMKIKSEEEKMNALVNFQIEVHNVNKSKEYVTIDKYDGTIEIKLSEFVG  
 DSVNLTAKLHGFFLELNVNITFTVICSNMGKALNGICIPCPLGSYNNINEYIKNNNIY  
 ECTLCHNNSTTKNEGSTSSISQCLCLPGYELNNDLVCVCKRGTWKTKLSNSPCIFHCY  
 PNSYSLVQGSRSEEEKCKCKRGFYFVSKDSINFCDNCNIGYFCPGGYKIGEKKCPKN  
 TTNITQNNFSISSCKCDVGFEPFDSSNLNAYNFKNDFIFNDYKDFLDDVKSSQICVPC  
 KEGFYKNTVSEKCKRCSDNVYTDGLQSTSISNCKKCEKGYLQSESDSCICPDNHYC  
 PGAYINDPKYAIYENQKIPCGDKSLTIPPNLNVSHLNCLCKKGFEEIKTDDNEFDCL  
 EVPKNYYKSHLGNKEKEPCPENSVTLYTQTKSKVKCLCMPGYWDLKEFKCIKCPKGH  
 YCPGGYLKNCFNQNLHSCPKQKKKCPKLNSTTQTKESFSQSSCLCDKGYTINKEELR  
 ECIPCPINTYKDVISNAECTKCLTPYTDDGQIGSTKEEDCTCSGGFFLNHCLPCSDK  
 NTYCKGGKMIVNKNKTIHYGPSKCPNTTVSFETERPYNKGFCVCQKGFKHVYTTSD  
 FTKICAPCERGGFKTIIGDFSCESKCKPNSTSFVGTIETHCFCLENYFKNKICLNC  
 PDGAYCEGGFQKETLLYMKNYLLDTSKIKHIMPVPKENYALYKLKTNIYNTDWFIV  
 ECPIKEACLYNEKCHESMTNFLCCECKGYTNNFSLNLCIKCSGHIMNIIHMI FVSI  
 FILLFTVIMAYLNVFTGANRKS SVHSIVIKIAVNYFSCMKIFYVMGISELYFPVTFSSH  
 VNYILKNIKRLLKAKKNYGLYCILTNYFDLSHADAYFYGMVYHAFRPVFLAIIITLLM  
 FIVVEIYKYKVRNETNIKLNITDKIKELGKDKLHEEIMNELPSEALVLFRIPIPGD  
 SRFKRIKNFLEDMIPMYVTLFFIHTKTYYMLTLLDCKALYNDKFVEQYMSYVPSI  
 KCDLSKSYSKFFILGLTGLIVWGIGIPLMSYLVLYKNRKQLHSENI LFKYGFLLNNGFN  
 FQFWYWESIVFLRKILVLLISTVPIFKNAKIFGTTMWLFTI ISSIFLTLQVILQPFDS  
 RNYHILNKLETYSMAWTMTLII FVFLTISNTNVTINFYVLLFLLFFNFVFI AKILIS  
 LCYSYIENLRHMKKRIKLPFLRIFFEKMSKIAEEKDYKDPVVS LNTHDNSIQFTRKYK  
 KKYISCSFKNNMLTTEEKNYFLDVISNFIYFGVLNLFVFSYFMEFMLRLSIIIDNE  
 MLYRKGNGILKLIADPNKIDKWIKIKEREINKKTFERHKKILNLF SKSLFVIQNN  
 IKSIVYKGDKHTIISDYEVLINVLKYDEDFITDFKFLYDDNAVKSGLILSDLHLSFTK  
 IKMKDKELIKQLFSLFIAKKNIVQFERDIQLKNKIEQLTSLYDILIKSSEKKLTFRK  
 NVEDAVKGDPFYKILENELKSVNDRINNLIIENYRKLKDVDFEGMDNIDEEKMDLNN  
 DSEFFNNKLELSFKELKDDITENEQNEDISKKEKEKIYDETTNDDQTK

>MAL8P1.104(Q8IAU8\_PLAF7)

MDERTKIVDVWANNLEEEFERIRDIVEKHPYVAIDTEFPGIVARPTGNVLDYNYQTIK  
 CNVDLLKVIQLGVTFSSNGKGEPMNVSTWQFNFKFDLDSDMYAQNSIDFLKLSGINFEK  
 HQSLGIELLHFGEVIMSSGLVMNEDVKWISFHGICYDFAYLLKILTCSALPHNEAAFFE  
 LLNDFFPPLYDIKYLNNLNLIKQLSRTFSLQKISEILSVKRIGRQHQAGSDSLVTCKT  
 FFKLMEMYFDNKIDDKKYSGIYGLGSTIKNYNPKLDDHNNNRYHNHNNYNNHNYVK  
 NSNNNNNNNKYNNNSNNSNNSNNSNNNNNNNNNNNNNNNNNSNNSNNSNNSNNSNNSINSHH  
 SHNNNNMLMNAAPNNNPMSNYIDAKEYHPTGFNKEIPKLNKNDVMFHMYADNNQNSYN  
 NISSNINNIHGTTNYITNAIYSSDVTNNYVLNKFVNSPPSPSSSLSSPPHPPHPLPH  
 PQLLNTVKNVRLSLNTSSYMNSKSTDPIGINNHNNNNNLSSSSRSYMASYPSSGIK  
 NSLDTSKIMGPIYNDIPRINITGNLNSDLNNIANENMMNINGLTNGNNLSPTLSANNGI  
 MSPSLSNANGLLNLNNTNLNNSINNTINGSLILGGMNNNGHTNNNINNNHNNNGNAI  
 NMNMNGMGIMNSSMNISGLSTNLMMNLYGDIRSLGGSTSNINLNNINSMNELNLLKS  
 GSISNISNCDENMIGLNKNIYSTNNGPLIGNMINNNVYNANINYNNYNYNSINTNNS  
 NNSFLNSVNYNTAYAHGNNPISIPGGNNMSTNNYYSIQNKYSNFGKYSSNLNLYVNPL  
 SQSINEVKSMAGEDYCDIDKRSIDNLGSSKNSFANNKLLGKINNNNNNNIISSSST  
 SHHINFKNTISNNNSNINNNNLNINSTTSVHPMNNPNMNDTNNLNKRNMKNESFISD  
 LSTNKNELNMGDHSVGMENLNMMLVQNMNIKRDEKYKDEKINNNNNMSKNMMLNLNNS  
 SIVNVLNMMNSNDLIKNNNTTYMKNINMSISNINNGVTNTVLNTDLKVSSNLNQ  
 NGINVTNSTTYISANSLDNNNNNNNLNSGNNINDHGNNSGKGINHTNPTIINNDNKIN  
 VASHNKGNTSIDGNWINGPINNTNSNKYSEGKDKDANTEDNKIGYKANDNNNSN  
 NRNNNGKVLSSNNKNSKNGNNKNSKNSKNNNDPNKKASGDNLNEPDYKENNMMNNNN  
 NNN  
 NNSNN  
 TTNNNEQDKDDKNNMKTGEGNSKFSKQHGMNTRKNKNDKNNFVNSNLVNSNVEDV  
 NNFNNIINQRNHCNKNYINFIKEDQQEVDQKELHASNISHMLNEDNSNEIMDKNTSYN  
 NPYNNNANYKSDNIKLYRGFEKNSSHQLILKNFSSNSNMTENEGIMHDMNKMNPN  
 NNADILLGNEILLGIKNLNNYMPNVHNTERNNELNNNNTNMITNKKVNSCNDMLH  
 KQINNFNIININKVHNNISNSLFSNMSNYNVVSENVNINNNNSNTNNTANNFMNKK  
 SKANLVFNQSLINNLNLNLFYLNENSFNKINMNYSNINSTSYFNTNDNNMNT  
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 TEKYPGAVLETVDNNFGYPNYEYKTKDHKYFYDN

>MAL8P1.140(Q8IAP0\_PLAF7)

MNISIFFFLFLYSGSICAIHLWRHSEWRGRNVLGKCRNNDNMLWLDLIKKNKKVKN  
 KKNKNNNNNIISSSCCCCCCCCIYNDKYCFLFVNKKIDNNYKRIKKKEKHCKKRLKS  
 LNNEGGSNTYHNDVKNTLDYCEERLPSYHRYIDNLKTRKIIHPSIRIRNLDKKFMK  
 CKESYNKLYSHLKENDLFENFSYVGRQKKGILSPTYRLPKYIERPNYHKTGPIYVPY  
 DKEKKNKTNSDHNNKYDHYNCNYDNYDNIKSDKDIQIIKENCKFARELMDDVSYI  
 ICEGITTDIDIIYILNKCINNGFYPSPLNYHNFPSKSSCISINEILCHGIPDNNLLYLN  
 DVVKIDISLFRNGYHADMCESFIVPKLSKNEKKRKKFYDFIYLNNSFKTKYTKYILK  
 YHYDLTKNKVVRGKSFVTKKIKYAAPNSKEQNDLNDNDFDDNTTNVMNTSOKYCFN  
 DIYEDKIPSHNTNMHTNMHTNTQHTNMHTHTHNRNNSYYPNNQMHNNEKNTFNMSNNV  
 LQQEDELLEYFHKYYDQKIIFNKENNEIYEDIQKFIYQKSLNKTIKGRFDFDNTKM  
 STNDIKNFMYQKNLDLIKTAECTMAGISVCKDGTFPNKIAEAMDNYIKQVNKKNNKT  
 YSIVPHLCGHNIGKNFHEEPIIHTLNNDQRKMCSNMVFTIEPIISESSTNFILWPDN  
 WTIISNTKYHFSAQFEHTILIQKNGAQILTDKRDISPXYLWQQIN

>MAL8P1.37(Q8IB70\_PLAF7)

MKVGKLLKRRKNSGLLYPYFKNKSFRLNRYIFIKPIKSVKLNKKKKMLTHEICILNC  
 SEKLIDYKLAFLQNLILHHSKIIMKNKNEVQISNHLELKKFKNFKENMEKYDFCFILQ  
 HTPCYTLGSVANCSDILLDKENYIEELGDIYNNLYSNEIHLMNKCETIQDKINQSD  
 IYNENTNYFNNFLKHCQRKIPYRVNRGGKATYHGGQLVLYFIFNLKNYPSNYNER

IINKHYKYTNKENFPSKTSEYEKNNIYTNSNSKENISSIERTFDLRTTINNFQKIGME  
TLQKFNIKTHCKKDTIGIFYKDKKIISIGLKITKYISMHGLSLNFNLDNNFLKYL LSC  
GMNHNDYISMHEINEMKKKNYIYQKGKIASSSNILNELTLNITESLKKVFNVKVRNIK  
DIREMFY

>MAL8P1.48 (Q8IB57\_PLAF7)

MTLTVGKAGPASDFRKFMEKRLQIYLNNGNRQVVGILRGYDTFMNLVLDNTMEIKKDEQ  
IDIGVVVIRGNSISYWECLDKVNIK

>MAL8P1.76 (Q8IB05\_PLAF7)

MATLPASKSASKVALTSEVEDEGIKEHTFQEIEKLQDLGINAADINKLKGSGYCTILS  
LIQTTKKELCNVKGISEAKVDKILEVASKIENCSSFITANELVQKRSKVLKITTGSTV  
FDQTLGGGIESMCITELFGENRCGKTQVCHTLAVCYIDTEGTFRPEKVCKIAERYGLD  
GEAVLDNILYARAFTHEHLYQLLAISAAKMCEEPFALLVVDSSII SLFRVDFSGRGELS  
ERQQKLNKTSILSKLSEQFNIAILITNQVMSDPGATMTFIANPMKPVGGHVIGHAST  
IRLSLRKGGKQDVCKVYDAPNLPEVEECIFQLSDKGVIDATD

>MAL8P1.9 (Q8IAV7\_PLAF7)

MSSINIESYLENEILVITNDSRIFTGKLKGFQDTTNIILGNCHERIYKESMEKISLGV  
YIIRGDTVTLIGEIDEDVDKNILHQKIKPQMLKPVN

>PF07\_0071 (Q8IBS6\_PLAF7)

MSEENDATLIKKRNEKINEEQHNTTNNNYEEPLVYDFLTKEHDHENYNNFVRFCKDNF  
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IYDNDKPCNRYKKKKIKDYRKNLKLINIKKNRARINLIVIKKKYLNDNNNNNNNNH  
NIYNSNNFCSGERVQKNTIILSPFFMPVGTCCIKGLTLEDVNDICDYIILSNTYHLS  
NIYDMSIFEYNKDINNLIKFPNAMLTDSSGGFQMVSLSKRIKILEEGILFNNIYNSEVI  
KKNIKACNVGDVVKKTYESVCSMDHNDNNNDNVVVRDNVVVRDNVVVRDNVVVRDNV  
AHDIFDEINKNVCDETYNNTNEENSCKTKKYVDMGEDILLSPEISIRLQNFISDIIM  
ALDDVRSLEEDKNKIEEATHRTNRWLKRCIDIHKKKEEQSLFGIVQGGLHIDLNRIS  
MDYILRQKLNKYAVGGLCGGEKKKKFIIEIHHCSNEKNKKYNYLPTNKCRYIMGIGYI  
VDIIFCSLFGYDMYDCVYPSRTARFNTAVSFDGTIKLKQAKYKYDFSRLNCKCYVC  
LKYTKAALHYLISKRNTITNVLLTLHNIYFTLYMCHLMRVAIFSNKLNQFITTFLYNH  
FVVGKNGNYKIPCADDKMNDDKMMNDEKMMNDDKMMNDEKNINDEKNINDEKNIND  
EKNINDDKMMKSDKKHEQGSLENLMKSKNMIIEELKKNLPQWAIQALEYADIELMF

>PF07\_0073 (Q8IBS3\_PLAF7)

MVLIDINLFRKEKGGNPKIKESERKRYHDENNVKIVIEYDDKWRKCI FELEELKKNIN  
MINKEIGNKKKVDKNADVEDLKKKSLNIKEEIPKYQLKEKELKERNKYISKIGNLLN  
IKVVCSDNEDNNKIVKTWGECKILPACEENDNSIHDNVVNSNNIKRET LNNEVDNKKK  
IKYYYHYDLLRKIGGANFKKGIQVAGHRGYLTGAGFLLHNAILOYALNFLVNKKYIP  
VYPPFFMKKNIMEECAELDDFEETLYKIPSTSNSTLSSQQVSTSPTKISSQADIKDDT  
TCNSQKKTNI PSNEDLTRDDLFIATSEQPLCALHKDETIESKRLPLKYAGFSSCFRK  
EAGAHGKDIRGILRVHQFDKVEQFCIALPQHSNKIHEEMIQTCEEFYQSLNIPYRIVS  
IVSGALNNAASIKYDLEGFFPTSNOYRELVSCSNCTDYQSINLNIRYSDSSIKINDLN  
KNTNLNDEMSEYEHFLTNTFNNTENKYHVHLLNGTMVAAQRFLCCLLENYQNGEGIVP  
EKLRPYMNMDFIPFME

>PF07\_0103 (Q8IBK8\_PLAF7)

MWPVVMLLFGGGVLFVKKGLNYVKNQGIQLNGKRSFFPSGFNKNLNNLFLKNDLKGFE  
RNMSKSEAFKILNINPTTNKEKIREVHKQLMLKNHPDNGGSTYIAAKVNEAKDILLK

>PF07\_0115 (Q8IBH9\_PLAF7)

MRSKYNILIYKKKKKHLRLDVLLFFVYLI FLNLILQNKKFEAQP KDYEYIEILKNKNV  
NEETFVHVKRFEP TSSDLGNIGKEKILEQNNYNVKSINNVELRNDNMVINNEGVYNK  
YVKENEEIIGDNEKKEKRAKTFENNDFKNEKSFKPIIVGKYNLIYIFYSIEFICLLLF  
IFLHFLFLLSQWNINLFI SYKSLYSKNKEKYLYNLKNFCTHVYIEPCI IKSEEDN  
GIYDKNRYNMDCNFYKPKSELIELKKIDNDIYFFYKQKKYIFNYETFIFESLKHFDNF

NLSFYLNWKGLLDYPKGDINKMDIYNNKMMRDIKDRVTCNNIESVIKKLDILYALHN  
 DKKGNLNIIDEKVDDVNFNCNDFISKEKNVDNVYDMNKKMINIKYRGKTNKGNNNFID  
 VLKNDNMCEKDINKNDIFGDYKDDMDDTHNHNVDNRNIICSNKKKVDSIKNSIHNDVV  
 RDDNVNNNFYNFYKKSCEIPIYDIFVHNNVEKYGENIYDIPCPCFKELLYESMLSPF  
 FIFQFFSIVLWMLDSYWYFGIFSIFILIILESQLINKRIREFNMINGMKVDPQDVVY  
 RNLRWTIMKSNKLLPGDIYILTNDMTATDNNICTCETLLIDGTCITDESILTGESVPL  
 IKACIDKSVINNKSNNNNNKNENNNNNKNENNNKKKDNKNENNNKKKDNKNENNNKK  
 KDNKNNDNNKNSNNNSYRFIGDDNVERLNYKNFENNENEFIKDKCEDYESSNYCNS  
 LFCNRDLIKNKHKKHIVYAGTNI LMTKNENNKFNKGKLPVNGCIGIVLRSGFSTYQ GK  
 LVRTIINTSEKVNSSSIDSIIFLMILLLSICSSAYVVYSVLKTNEERNLYKLLLSVS  
 HIITAVIPPEFPITLSLAVTISIVYLYNMKIYCTEPFRLPFSGKTNICAFDKTGTLTE  
 DNMIVLGLFGLDDNLKRINEINESIINKQKIPFFSLSVIAGCHSICTLNNKLLGDPLE  
 KNSFLKLCVMKSLNHTYVYTNNINNNNNNNNNNNINNDNVVDKKYHKNNEKKIKNQS  
 LENFQIVKRFFFSSSELQRMTCIILHEGSQHDWYGDEYETDTCDSDEQNEEQYKNTKQH  
 VLRNNGHEIYKTTPYKESAQMLRKLKRKNNEYDTESSDDHADQNCDIHNNDIHNNDIP  
 NNDIHNKDIHNKDIHNKDIRHNDVHHNDICYKHEKEKKKKNRKIKNILFVKKKKENKD  
 KIVKQYLVVSKGSPEIMKRFLKKVPEHYDEVLSLSIKGYRVLCLAVNILDNNMYKEN  
 ISREEVEKDLYFCGFLTFCPIKVTTPNYILHIKNAGIKNIMITGDNALTACQVSQDV  
 NIVPKVTCKDILILKMNEVISYDLIGEKR TNMINMIDIMTTNNNHTCDTNQSDDVCKN  
 KINNVVKDLRYDHAI FKNDDIKDCIEFLTCLKNKETSIVILKNHVENLIRIEVNYNKC  
 SNILYFMNRENKKILPFIHNIEYIKVCEIIFSLCITGDIIDYFLEVYKNNLHIFNELI  
 RGVHIFCRMSPKNKEI I IKTLNKIGYITIMCGDGTNDMAALKAHVGVSLLSIKISYK  
 NRDGNRKSVLNDDRKSLLNNHNNMRMMNMYGDGRVKSVDNLRASYSEARNI INNNSN  
 NLGGINFRRSYEQMKLYNEKKKELDKMLQSLDDSLPLIKLGEASIASPFTYKGNDIKC  
 VKEIISCGRCALS KVMIMYKLMINSLITAFSVSILTLDGVKLSDAQTTIISLLYTCL  
 IVLISKTSPLKNITNYSPPNSLNFNSV IISLLSQI I IHFSILYIGWKLACVYREINYI  
 PDIKGFIPNLVNTCIYYLIYCINLSIFSCNYEGLPFMVPIHKNKEIVYIFAVNFFFL  
 FVLVMDIFPFLNYFFSLVSPNIRFKFFFFFLMLVDIFLPYLVTNLFKSLRFYIFHKY  
 QINI

>PF07\_0121 (Q8IBG6\_PLAF7)

MNGKKDDELIIEGEHNDKMKSPGKSLIPCIKEKFNETNLKMKIVKKVTFIDEHEDYIK  
 NKKEIECESESNSYCKKEDENDIKKKEDIDEKESILEQLNGNISNEKNGYHTYESKNC  
 DFNFKYDDTDNINMYEENIENDIHLNKNYYHYNKYMNLDYKDNITNEKVIYEKYDKR  
 EYSENHIHPSTIMNGFSSLKNQEEENYSTYENNNI IDNINENLNI SYYNQMNGNNDLST  
 NKEINEYINEKDEEKRGILKNESPDFNKSYNDSLNNYLSSSFVDILNTLKDVKNNENN  
 DGSYINSNGSYINNPENSNSNNNDTNLRYISCI LCGDSIKANTS KMCHNCILQNI ES  
 NSININKDTYLIYYCRECKRYLHNRWVYCELESKELLALCLKKVNLKLLKILDAKFL  
 YTEPHSKRLKVHVSQEEELINNFISEM E I I IHVVIKYTQCDDCKKKYTPYTYNTCVSV  
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 IYTDGKS AKSSSRVKLDKLVYAFVELYDESNGTTILTCTCNAKHLRPGDYVNAYDLR  
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 RILLNNCKALENMAITST

>PF08\_0011 (Q8IBA7\_PLAF7)

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 KPYNDVYEKGDNTYKYNKKKFYILDMFPYPSSEGLHVGHILCFTITDIISKFKKMNY  
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 KDWLF SRQRYWGEFPFLYKMKDKNGYMDNTKIKNDDHMNENNNHNNMMLSDCKDINN  
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>PF08\_0014 (Q8IBA7\_PLAF7)

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 ELLGQEKRIYNFFKDDSLYYILNRIHNIVRPSLELKHLLKKNFIEYINSFCSLKFETFY  
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>PF08\_0055 (O77370\_PLAF7)

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 KNININTNNDTNQMDQMDQMNKIKFVTHTTQDDEDNNDHLQIYFKNNEYLNQKYEN  
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>PFC0831w (O77370\_PLAF7)

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 TGDDYKNCNPNSSYKMMELLRLIKTKISKDEMKNIIIAFEPRFAIGTGQPVSYDILN  
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>PFC1020c (O97313\_PLAF7)

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 GYTLIEGHTDVKTLDNYHLRMFCIAFTKQRQNTKSTCYAQTSQIKKIRKMMVDIMTA  
 EASKVLLKDLVKKFIPESIGKEIEKQCKKIYPLQNVLIRKVKILKRPKLDISKLMELH  
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>PFD0230c (Q8I1Y2\_PLAF7)

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 ERFEEKEKRYIVFNEDRSLN<sup>1</sup>ILNEEGDINSRYSGYWKI<sup>1</sup>IYDEGLYIEVYKEDDSKEVY  
 FSFFKFKQKGDVSYSCNNLIMGVMNKYSLDNNI<sup>1</sup>WDMRYEENIEENIRSDDKNNNIHM  
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 YIKNIDSLFFSNEQLILCDIF<sup>1</sup>NQCGNGGYIYLSLKYAYENYLYTQKCFEKYKKKINYN  
 TDDLEIKSSLMSQDDNSLLCDQ<sup>1</sup>FDVFKIKNEKK<sup>1</sup>KNNEINIKEQITMNI<sup>1</sup>NDNKNQ<sup>1</sup>EY  
 TNNDHDHLLILSYQIQ<sup>1</sup>TDPNKKDDNKK<sup>1</sup>NIYGLNEDYILIDEQKYNNNHNND<sup>1</sup>DDDEE  
 YDIFKSN<sup>1</sup>SCDVKINVSKFEYLDIQDEELLK<sup>1</sup>KYIYNGPVAAAIEPSSEFIGYKKGIIL  
 GNFIKMYDGT<sup>1</sup>KNNAYIWNKVDHAVVIVG<sup>1</sup>WGEDTLPNFVKKNKLSKETMEHILTTWKEN  
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 NGDNDN<sup>1</sup>GDNNIINNTN<sup>1</sup>VIKYWKVLNSWGTN<sup>1</sup>WGN<sup>1</sup>SGYFYILRNNNSFNI<sup>1</sup>KSYILAC  
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>PFD0260c (Q8I1Y2\_PLAF7)

MEKGSILSFIF<sup>1</sup>FCSVVIFIRFIGYFFCNRYMTEEPYNNIFEI<sup>1</sup>IKPENLYSSLLLLSNE  
 KENDFPSSTNCNGYMKCIPFYNNV<sup>1</sup>SERWKRYNFIQLYI<sup>1</sup>IRSALNIHVM<sup>1</sup>SKYNNMLNKYN  
 KETNRL<sup>1</sup>LKRN<sup>1</sup>VENRINNI<sup>1</sup>SNHYLC<sup>1</sup>SGFKKENR<sup>1</sup>LFFLLFYKTIKMMKLYIRNLFMKY  
 IKIYYKTKHFEKNIET<sup>1</sup>NKVVYVERDNL<sup>1</sup>FDIERNNL<sup>1</sup>FDILYMLKRIDS<sup>1</sup>VKNIYSIIS  
 NNFLYVIRIIFL<sup>1</sup>PFEKIYFSLKSLIMIK<sup>1</sup>MMN<sup>1</sup>SSSY<sup>1</sup>YYYVNM<sup>1</sup>FSLYKKNY<sup>1</sup>KYEEIF  
 IHEQRVIY<sup>1</sup>PNEYLKNEMLDKYRRVIRIL<sup>1</sup>SGQHDNPFID<sup>1</sup>SLLINPEKIEKDDLDV<sup>1</sup>KQKK  
 KKIIEELK<sup>1</sup>KKKENTNTNT<sup>1</sup>STNTSANT<sup>1</sup>NTSTNTSANT<sup>1</sup>NTSTNTSANT<sup>1</sup>NTSTKESHIL<sup>1</sup>DES<sup>1</sup>KLET<sup>1</sup>FYR  
 DELDKMGKEE<sup>1</sup>IETYFKGNIDK<sup>1</sup>SLDEFHKIL<sup>1</sup>LEELNKMDKDELYEMYREELN<sup>1</sup>RIEQEK  
 IRNMNKEE<sup>1</sup>INKTYKDEIN<sup>1</sup>MNSDQVDKI<sup>1</sup>HREELEKIEKEKINKMDKDEIDKI<sup>1</sup>YREELD  
 KMDRDAI<sup>1</sup>YSMYIEDIS<sup>1</sup>NKNIKDLIKNEKET<sup>1</sup>NKDKNKKK<sup>1</sup>DIDINKKKKK<sup>1</sup>DIDIDVD<sup>1</sup>IDK  
 DIHKDHVEELYGEVKNKLSKEEL<sup>1</sup>DRMDR<sup>1</sup>DALYRVYLEELDRMNRDELYRVYLEELEKI  
 DKEEKEKIHREKL<sup>1</sup>HKIEKEKINKMDK<sup>1</sup>DQIDKIYEEELNK<sup>1</sup>MDSDEIQHVRRAILQDIQK  
 EKIQNLELEEID<sup>1</sup>RLYKEELDRMDREARYEIP<sup>1</sup>MRNLSRNEKDNIIHRN<sup>1</sup>IKNESN<sup>1</sup>QKNKK  
 ENVNVFI<sup>1</sup>IHDN<sup>1</sup>DSNNNNNNNN<sup>1</sup>RDVNNL<sup>1</sup>NNKHTNN<sup>1</sup>NYENVEVELVVRN<sup>1</sup>LDKDKGAKI  
 EDIIDYFNKEIKK<sup>1</sup>DKNVN<sup>1</sup>SNIVN<sup>1</sup>FLNSKVGKDNTPI<sup>1</sup>QHKKENQVDVVR<sup>1</sup>KNIQIIQED  
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 NAE<sup>1</sup>INNNEK<sup>1</sup>DKFVYEFYTSN<sup>1</sup>KKENIDKEEENN<sup>1</sup>IDDKN<sup>1</sup>IKIEIEPNYEINN<sup>1</sup>NFEEEN  
 KNEIN<sup>1</sup>VIIDKEAK<sup>1</sup>NMDK<sup>1</sup>DDSNNNN<sup>1</sup>IQKNNII<sup>1</sup>IKDNT<sup>1</sup>NVSEEVHITES<sup>1</sup>SKEIAEFFN  
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 SMDCISIN<sup>1</sup>KNDENNNNKEH<sup>1</sup>NYKN<sup>1</sup>DDDL<sup>1</sup>YLKKSVEEFI<sup>1</sup>PGFLSNINKV<sup>1</sup>DDLARI<sup>1</sup>FTP  
 SFIQNDIFL<sup>1</sup>NCIYK<sup>1</sup>YRND<sup>1</sup>FDKNN<sup>1</sup>IYSFPMKI<sup>1</sup>FLRKNSTKI<sup>1</sup>KGCSFQIDEDPLLYKDY  
 SEKESFLSNKIIL<sup>1</sup>NSNRNTECVLHASNEIV<sup>1</sup>GFQCGPPYKSYDNIQYRHL<sup>1</sup>TNKSNDIQ  
 KNIFGIYSNN<sup>1</sup>SSYSHLFKNI<sup>1</sup>FNNEHKLYNVGGYFQTEPINC<sup>1</sup>FEFVNDNINVEDILPG  
 AVPFPRFDL<sup>1</sup>IHHDLV<sup>1</sup>NQTRYILLNET<sup>1</sup>NQDKTISCTCNYFTEPNIVYTGKII<sup>1</sup>IKVEEE  
 KIYKTKKLQTEFNDI<sup>1</sup>INN<sup>1</sup>KEIYHEKK<sup>1</sup>MNHI<sup>1</sup>KEKKDEDED<sup>1</sup>MSFNKNYVNNY<sup>1</sup>NENFK  
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 HENKNNQDVINYEY<sup>1</sup>NVDDYHEVQDQ<sup>1</sup>DES<sup>1</sup>FKEEEDFIDFKENI<sup>1</sup>INDNTNHN<sup>1</sup>NTDLDD  
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 NHTHPNEEKRTFPKYISL<sup>1</sup>VYKEKN<sup>1</sup>DKNEKIDKTLTFI<sup>1</sup>KEFYPLL<sup>1</sup>RGGKDSDPENKQT  
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>PFD0462w (Q8ILW9)

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>PF10\_0053(Q8I716\_PLAF7)

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VNLFYRTSYSFHKMFVQNVWKYLVHNNYIYKDTYKGYNINEERYISEQELREGKYKI  
DNENI IYVEEENS YFFNILKFKDYLIDFYEKNEFIYPPYLRKQVIYTLKNELRNICI  
SRYNTKWA IQIPNEAEGTIYVWFDALLSYVSSMLYLHKIKKNNNNNNNNNNNNNNNN  
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KNYKEQNI ESFELFLRNNVGNLLYRVVSLCIENNYNMPVIKTNDYDSNII LNEWKDN  
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>PF10\_0149(Q8IJP3\_PLAF7)

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GHLHIEGLKMSKSLKNFITIKNMLTKYTSNQIRILFLLNKWDNFMNYS PNGESMVQCI  
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DALLAIQKLITEINIYMDKEKIQIGLLEIKHYINFIFDTFGLIYGDAPKGKYDKFDE  
LLQTLGTYRRNIRINLQSNAKLIRNILKEKNKNDLDPVAAQEKSELLHSEFINNIKA  
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>ABRA\_PLAF7

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EKE

>ABRA\_PLAFC

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KE

>ABRA\_PLAFF

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>ABRA\_PLAFG

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>ACT1\_PLAF7

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>ACT1\_PLAFA

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>ACT2\_PLAFA

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>ALF\_PLAFA

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>AMA1\_PLAF8

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>AMA1\_PLAFC

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>AMA1\_PLAFF

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>AMA1\_PLAFG

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>AMA1\_PLAFH

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>AMP1\_PLAFQ

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>ARF1\_PLAFA

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>ARP2\_PLAFA

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>ARP\_PLAFA

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>ATX1\_PLAFA

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>CALM\_PLAF7

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>CALM\_PLAFA

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>CATC\_PLAF7

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>ENO\_PLAF7

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>ENO\_PLAFA

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>ERD2\_PLAFA

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>GBPH\_PLAFB

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>GBP\_PLAF7

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>GBP\_PLAFG

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>GRP78\_PLAFA

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>GRP78\_PLAFO

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>GSHR\_PLAF7

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>GSHR\_PLAFK

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>H2A\_PLAFA

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>IPYR\_PLAF7

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>ISPF\_PLAF7

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>ISPF\_PLAFX

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>KC1\_PLAF4

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>KC1\_PLAF7

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>KNOB\_PLAFA

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>KNOB\_PLAFG

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>LDH\_PLAFA

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>LDH\_PLAFD

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>RS12\_PLAF7

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>RS30\_PLAF7

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>S230\_PLAF7

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EDFKTAQG

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>S230\_PLAFO

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>SANT\_PLAFV

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>SANT\_PLAFW

MNRI<sup>LS</sup>VSFYLF<sup>FF</sup>LYLYIYKTYGKVKNTDHEL<sup>S</sup>NIYGIKYYLRNGLSDKKNKGKQKYQ  
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>SERA\_PLAF7

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SESLPANGPDSPTVKPPRNLQNICETGKNF<sup>KL</sup>VVYIKENTLIIKWKVYGETKDTTENN  
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GNFNIEKCFQCALLVEKENKNDV<sup>CY</sup>KYLSEDI<sup>V</sup>SKFKEIKAETEDDDEDDYTEYKLTE  
SIDNII<sup>L</sup>VKMFKTNENNDKSELIKLEEVD<sup>SL</sup>LKLELMNYCSLLKDVDTTGTLDNYGMGN  
EMDI<sup>F</sup>NNLKRLLIYHSEENINTLKNKFR<sup>NA</sup>AVCLKNVDDWIVNKRGLVLP<sup>EL</sup>NYDLEY  
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SLDGKGYTAYESERFHDNMDAFVKI<sup>IK</sup>TEVMNKGSVIAYIKAENVMGYEFSGK<sup>VQ</sup>NL  
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FIHSVVI<sup>F</sup>NVDLPMNKT<sup>TK</sup>KESKIYDY<sup>YL</sup>KASPEFYHNLYFKNFVNGKKNL<sup>F</sup>SEKED  
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>SERA\_PLAFD

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GSSTGTVRGDTEPI<sup>S</sup>DS  
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>SERA\_PLAFG

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>SSSP\_PLAFO

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>TBA\_PLAFK

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>TBB\_PLAF7

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>TBB\_PLAFA

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>TBB\_PLAFK

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>TBG\_PLAFO

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>TBP\_PLAFA

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>TCTP\_PLAF7

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>THIO\_PLAF7

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>TIP\_PLAF7

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>TPIS\_PLAF7

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>TPIS\_PLAFA

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>TRAP\_PLAFA

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>TRXR\_PLAF5

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>UTP11\_PLAF7

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>VATA\_PLAF7

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>VATA\_PLAFA

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>VATB\_PLAFA

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>VPS26\_PLAF7

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>YCA2\_PLAFA

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>YDH1\_PLAFS

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>YDH3\_PLAFS

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