>contig15437 Frame-2F

MFTIVFLLAVAFAEVASSNSNADANPGPQAKELTPVLSSPTPWAMDNMHAFRGAYDNTPA

LEEREATIPRQGIEKTAKVVEESTSFLKVLKNILLWPFQKTRSTFKLWRFKRWMKNENEF

QADVIKATDTHTRYLACNIMPERWHQLMSEEKAIPQKNPFFHRGFTPESFYVYSKKLVGI

SVPSHHTVVRKSIDKTIRKMEPDLQNVVKERLERFESMFLDEHIPVAELVPFMTPVTVKY

VVEKTAEAQNFEEVLFAHDKSKWLEHRVLKRFLEFNKLYETRVESILYPLPK

>contig20006 Frame-0F

MRLTISRNTTKFWLILFILASDLPVDEFLQVN

>contig44040 Frame-1F

MKKKMLVISVVAALAIVVAVIVIAVTASRSHSSAKSEEPGDASNTNHKSRGPKPLRQIFR

ERASSGSLEEDEEKTDPLTETYTVSALAIGDWGRTIVKNGGSCCSRRKSFTVLDYNAMEY

VAILLGQAAAVAQPRPSVVIGHGDNFYWDGLHGATDQAYRFQQTFEEKYNAPSLAGIPWV

NVMGNHDYGGASFICTDGEQAIKCSSTSVLLEALDQKFRLQSQYVSPLDNRWIMPDHFFV

HSLADPASNVTIDIFNLDTNDADSHGAQQICCQCYGYSGKDDDSCENVKRGDSLCAGGDT

GLFDACMKKLKEWGDDSRSKLVEAAKASKATWKIVNTHYSPYNHYAPEPAEKWRELLEGL

GIQLFLYGHTHGEKHDYAAFKTHFIENGAGGGIQNESPSGIPPYAEEYVENIWAAGHYPY

GFFSLSVSPTWLQVKFNTFDDSWSMTADVDATKVGGIAINHCWYIPQHGGRGKSCKDAEA

QSDGSL

>contig59503 Frame-0R|Blast-NhaC Na:H antiporter (NhaC) family protein [Phytophthora infestans T30-4](gb|EEY66397.1|) 4e-07

MHPIIVAAVAIILCATNGAHTSSIRLQMPSVILQQVNFDASIELLELKNGSV

>contig31034 Frame-2R

MRTSFLIFVAGATLLIMTKATTTADPTKKTAVPAIEKPRHFKSISYNELKHGQSNPTVVR

RYVAA

>contig42393 Frame-1R

MLCGMGDFALGRCGLLLSFILNSGPVTIALVLTDQMGYCTPSADCCNFCVQRRLFLQFLD

WLGPLG

>contig54655-0 Frame-2F0

MPPMFVMWLPLLMPLAILLSIFLTRYACTRSRNAASKNTIIGIFHPYANGGGGGERVLYC

TLLALVQHSRRVN

>contig32524 Frame-0R

MKLIICSAIVLAVSALSGQNERVCEPTPVYLDPYYVIDEKHTEKSMCTTTKFLTNSIAWN

TTFTVANDDLSVVKSYVRAQLVLKDLQIASIQSIPATISHAYTGESFVSTDVLDMYIGTK

SDTTTMSQVTSMTKETSMIHLPSPSIRILVVLATYGNGSLTWLVTKLLTVQIGNDKFDLY

EGYLDGFTVYTFVIYTGTKAFNGDLIEFIKRLPQGKTIDESQYLFSVQGGSQIFCGTNAM

YEATEFMVDYKVKTLAM

>contig40774 Frame-2R

MNFGSAFLALLARLLAVRLASATKFGSAAEEALIGVPALVAELAFSTRLLSAVDLDVPVR

IVLAREATSSASAVTARTTLFSAVTTFLIKGGFPIAAETKLDLCSRVSLPSSCTRPPRLL

GFCLLVGRNFGGGLSLCTGKLMSSSPFGSSAELALC

>contig17177 Frame-0R

MARRTRAGLLGLAIVATLATVATRELHGSLDVFPSMKVRVTCKRPQQFFGKDNFVFFANP

VVSTNEAKVLYDGYATIENDGKIVTYIYVNGTGYVIRSDTDVQCLSSLPFYSIVSALNNA

TFISRAIIDGKLIVCTSGNLFKTVFAGAEVAI

>contig13251 Frame-0F

MGQSYSKTKLLAAIPLLVAAALLIASMNVPLAFGSTERSVVSRRLAAPNVASTINHDEHL

LAKLAREISEKWNNLFFKKSDSIPSNPHDLLETIQVLERNTNTHLANQPIKNKGYPAIAK

ALLDKYDLIPLASKIAQFKEYGPEDLKPLFDGTLKVILSRMEAKKISVYDVAASIQAPIK

WWVFKNMPQGFFEGELLMVYAKTDLELAAAMATRFDSLFQTLYRYKQEILPQRIVDACTV

TLSKSVETLIRELGLHNAGNNLFRLPQMHALVILASTMNLPNYGFIHLWEELLKIYPNGK

LLKLARQKQNVQSVSPSVQSFVTFVLEREALFKSRAIPSNQMRVVRGRVRQGKRIAKTT

>contig15433 Frame-0F|Blast-putative GPI mannosyltransferase [Phytophthora infestans T30-4](gb|EEY68034.1|) 2e-14

MKLHEKMRRKLFQLAIVFIVLPNVLCAFYFSRCH

>contig43557 Frame-0R

MKVAMHLLASYALSAVRALEVHNDDALVKNLPGLLNDLSFKHYAGYMHLKTEEKLFYWYT

ESQTDPANDPIVLWLNGGPGCSSLGGFFTENGPFVAQDDRSVKVNRYSWNRKANVVWLES

PAGVGFSGSVQEPHYYNDDIVAAKTREFLELFFEKFSELQNRAFYITGESYAGMYIPYLI

DMLVTKPLRGVNVKGFAIGNPFTDNLIDGNAYIDY

>contig58287-0 Frame-1F0

MVKLVCALIGVKGVFSVIIDEKELVADLNKAIKTENSNIIKCDARELKLFLARKGDAWLS

G

>contig58287-1 Frame-2R1

MFEFSVLIALFKSATNSFSSMITENTPFTPIRAHTSFTICISSFSFEL

>contig04427 Frame-2F

MVPCFSTVVLFIAMQLAAAAARTTTTSNVPQVAPPLGTRKVTTSRLKVNNATLINNEAEE

QERGFWGFWRPEETKLLRKFQTHQKKTITWNFALTKKFEKLGQLIHYRTKSEEAVATELI

KVIGEAELARFTDKQVSQLLFAPIYETIQSGLLKYWRSNERSVASIVQLFEIDPILLSQT

RLHEDVMLSAMIFIDQFPMNTVLKYLNPDNKHDHLKLIATLSERFNINAPEWIRIHYKNK

QTEVVKPLYAAAIAPVKEMVEVLGLKNAESISLSQIRMLLGFAQGSWRKKLNEVIEALPD

KCIYEAANELLNEPLNDFNRKFLGQVGAKFSKEFPNQPNPFLDPLAAQPHPNTP

>contig04492 Frame-0F

MYRPSSLRLVIFAAMTMTSGSQLVGTGTPEVHPPLKTQACTTSGCTDEDTSVVLDANWRW

LNKGGKNCYTGNKWDTTICTDPKTCASECALDGADYKGTYGIVTESDSLTLTLVTEGKYS

TNIGSRVYLMESDDKYKMFKLLNQEFTFDVDVSNVGCGLNGAIYFVDMEADGGMKRFPTN

KAGAKYGTGYCDAQCPQDIKFISGEANIIDWTPSKTDKNAGTGKYGSCCAEMDIWEANSI

SNAYTPHPCTSKIGGSHRCTTPKECGAGKNRYNGLCDKDGCDFNPFRMGNETFFGPGPKF

TIDTTKKITVVTQFLTSDKTAAGDLVEIKRFYSQNGVTHEIASSTFPALKGMNSITDPHC

SAAKKLFGDPDDHKIKGGLVQMGEAMKSGMVLTLSLWTDHAAQCLWLDSDYPVGADPSKP

GVSRGTCSKSSGVPDEVIAEHPDANIVVSNIRFGDIGTTVKGLPASKRTKKAAVAPPGEV

GNEAEVGNEAEVGNEAEVEAGGDAYSMPGTSCRRRS

>contig13698 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58939.1|) 2e-61

MISSVNSLVASALAATCVSGHGYMYKPAAFFSPESGDKTQYIATIDSSGTDFLGVYNTAP

NANVEAYTKAFAASKYKSLKELIDDKAVITVTGATLTCGNADPAAVPQPLPAQVEWVHSS

GEGFTASHEGPCEVWCDNERAFQDDNCPAHFTTAPAQLPYDKTKCTGASFLTLYWMAMHG

PSWQIYVNCAP

>contig17805 Frame-1F

MPSIFAIFAATAALIFAKVDGHGKMTCPVIRSVTKLFRESCGALINIGDEQLTIAPLENL

AGFKQADFPPSPTFNLMNGCRGTVYEKGNNVTNLKAGKPFDFKYWIQAPHPGYMRLSVVK

PTTDSKGIINYKVYKEVMKLDSFATNGGDQSAPATMPADVTECAEPGECVLQMYWHSDRD

SQTYASCADITVTGGSGGKPSKPATPAKSVKQAKPAPSTPPSPTPAPAPAAVKANPSISV

TQSEVGADAEHTGK

>contig44328 Frame-2F

MAFLNLFILLSLANYKNAGF

>contig14735 Frame-0F

MRRSTWLGTVLAALLAAVPPLMVYARGVHVKLKASWPTSPFFPLMETSEFLADENPLYFW

QFLEQLEERTSYVELMSSDVDALAELAVVVAEFVAPGLQNVLELMLATRTYSVKVEMFRQ

LGLDSGVRPCGVYADTWAVFYREPHCVEAVACSVVDLDDSLRNMKQKISKKTCIAAGFND

IELRVDHKYPYVASTNEEITPMTAILYGLVGTTSFHAFHSTLVNEAKQSNIQYIVRHYPR

DSPLETLLQGYGVALDIKNMEYKTIDDSRMAGGDETAANGENEVDEDEDKDIDDEEVSGF

LFKPLLARHVAIAFKLKQFHDMLVKKSEQDQELRAWHLKDLGASAVRAIVDAKNSLKRLE

TLSQDFPIQAKRLAFSQKLISTELREEIASTRMQASMRGLTNKFIMNGIAIDPTERSFNV

FDFMKTLKTEWSVAKQLASLTLNQTELEDMLTHVRETNQEQPIVRIHVRGSMDGTTPLYL

NNIETDANSADWPSDINVLKRPAWSLIFLRKNMYECVLVMDPLTGTGRAALSHVEFLQAR

NAPIQWALLISSKELIASNTFDGRQALVEKYKTLKGTDKANPWHFTKLLMLAQAKEKCSK

VTIDGEKKQAKGGDDDTSNEKEKVDQVRSMKIVSGFLQRVGNDDSSIILIDRLVEAYAEA

AAEIGSPEENEDEAMACLSSDQFDDEVLSMTEFIILKHLPLNSFIFNGVIQKDLDIQGAI

MANFGRDQPLYINMAYRDMLNNEMDLIEQLLMEQNAYFAYLSIFESSRDRLGDKEVDLPN

HLVADDVDGRLKAAAQQAISYLHPRGSRNLPKKQTVIFPVYLNDPRDADHAYRVVKAVLE

DSDKSLRVGIVPQISSDVKSEGVGELLAAILAITGDSDNEVYLKFVLEALTCIVKKKSVE

ASRGKLKEIWKGTADSRDENDSIYIKVLTLLSQKPGKWLSTKQRGVLTRFNALLRSRFPS

TFTDESLSKSALPYIFVNGRQVDLPRHSLSDEDVATILSFDLKHRSQPVAKALIKRSATL

NAKEADKLSFSIMKTTGIVDKYVKIDRTSRMEVNENSLNTVRLDGDPSLQVTAYVDPLSE

AAQVMSSLLCMLHSQLNASIELVLIPANEYASFPLQRFYRYLFDKKLSLAETSVEFRKLP

VQPILTMKIDTPEAWNVQTFLAGDDLDNLRVDPESLAAVRSTTRAVFQLESLLVYGQCSD

ITFNMYSPPNGLQLVLEREVGAQLLHRDTLVMQNLGYFQLQATPGVWSLHLAEGRAAKLF

DIINSDTELRLEARPITVFDFGSHMHQFLVRKKAGMEHEVLLQSIEDAVSEDTTKTDSNT

LSSSHGEGALRSYWNSLLNVMGKNDDNLDTISQAAVKEVNETSAVHQNSTSLPQKRRTGE

TIHVFSVASGYLYERFVKIMMSSVLKRTNNPVTFWLLENFLSPDFKKSIPILREQLGMDI

RLVTYKWPNWLRQQTEKQRIIWGYKILFLDVLFPLGVQKIIYVDADQVVRADLKELWELD

LEGKPYGYTPFCNSRNIGFQFWRQGFWKDHLRGKPYHISALYVVDLSLFRQMAAGDMLRA

VYSQLSADPNSLANLDQDLPNYMQNQIPIFSLPQEWLWCESWCSDETKATAKTIDLCNNP

QHKEPKLDMAKRIINGELFDESWTELDQEIKDAEGKHA

>contig19602 Frame-0R|Blast-unknown [Glycine max](gb|ACU16228.1|) 6e-50

MKISISLLLLLFCISTCFSSPVSVSDGVFSSDLALIGRNLLQAKKPCPVNFEFMNYTIIT

SRCKGPRYPADLCCQAFKDFACPYAEDLNDLENECSSTMFSYINLYGSYPPGLFASLCRD

DKVGLICPASAPGTARNGVGADTNNSHIIRNPSLLLSLTATFLILFFRWF

>contig21582 Frame-2F|Blast-putative membrane protein [Hyaloperonospora parasitica](gb|ABG23234.1|) 1e-08

MPYQVLPGLVVISVAFSLMGVGFSVVNQWEARSKMQ

>contig28282-1 Frame-2R1

MLSISCFAASMAMILCTTSQIVSADELPVGAFYKPNPEEVS

>contig59080 Frame-2R|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 4e-37

MQLVTRWVLGLMTFCGLLFFSDSVGLRFGRDVSRFFLLICACQFHLLFYMSRTLPNVYAL

V

>contig31263 Frame-0F

MANSRVNISALAVAVFFYFTDAHNNMITPPGTYPKNFYNKNNPTGIIDPKVLPLPAGMTY

NAGADTNTDAYFKA

>contig18603 Frame-0R|Blast-phospho-2-dehydro-3-deoxyheptonate aldolase [Phytophthora infestans T30-4](gb|EEY69972.1|) 1e-25

MIQMSLVLVWGARMPTVRVARLAGQFAKPRSSDIDVVQGEQVP

>contig28385 Frame-2F

MMSWMRFTALYTSLSVAQGVAHARGMGKLFVCNSRESMLFMIRKEVRKQPTCTHLKNRSL

FVSFVASEPCIRAKTVMLRSTVVDFIKRTIGRQEDTKRRVTN

>contig11902 Frame-0F

MRLNVMALIYLVGIDFSLAFSLTISRSNESDITSRERPSESTDDIYVQTTPPQLSLHPVF

RTKIKSEEERNCFPFDFNWASWLTGKLASIWASFQLRPIITALEELPTVTNPNTALPLDL

DKWLANVEKLRAEKGFSLDAETLNVLLRKKYNEKDLMSVYVWLLKFQHYQSLAKKELVAA

ASDSTLRIAIYDAFSSFKFGPAYAFTFFDLSRLLHPKDGKYDLAIRDWFRFVNLCINVDA

SKKEAFSIKDLFYILTNALPESHRSENNDKLKSSKYNQLLKIIDYLKLEKLPRLASAMED

LMGLNKNQLDKIRKHNV

>contig44324 Frame-0F

MVRIGTATRMLPFFWAMEAAALHTRDLEMLLDQNLLIESPSESVYVGHPSPCMLDLKMRK

RKLKEVSLRACLSLVGIPI

>contig54750 Frame-1F

MDADLTTKRLLLHVLVAICVVCGRVLGLKKQCDSSYS

>contig56976 Frame-2R

MLSRRLFGLIVVGAFALSVHAVDRSKFRTCEKTQFCNKFRNLQRQELPTKFHVARASIQT

DSYANLVRFVVEDVAQRESVALSGSLAFVLNADKSKVPVVRVRLQEKFEDPKDLKTRWIS

DDILMLAADETRPIRQVSSQEAGFKTPFVEENVLLFAPEIQGAVHVVAALKFGKAPFGVD

LYLDGEKVVSSNDNGLFHYEIRHSSNAVVQSDEVADQLAVDAHQGKTIVDYGEDGLAIYD

>contig59186 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56451.1|) 1e-07

MSAPATRLECLFLLVRDGSCAQIRENAAEKLGEV

>contig13697 Frame-2F|Blast-cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY65526.1|) 0.0

MRFVSPFLFLSGLLLADARKTPLEYEREFSAWMEIHRIAFADALEFAKRLGNYIANDLYI

MEHNVENAWTGVTLGHNEFSHLSFDEFKHRMTGLVMPKGYYEQRLASRIDGLWSDVQVPE

SVDWEELGGVTPVKNQGMCGSCWAFSTTGSVEGAVFVSSGKLISLSEQELVDCDHNGDMG

CSGGLMDHAFAWIEDNGGICAEGDYEYKAKAQVCRSCNTTVKVTGFQDVNAQDEHALKVA

VAQQPVSVAIEADQKAFQFYKSGVFNLTCGSRLDHGVLAVGYGSDNGQKFWKVKNSWGAT

WGENGYIRLARDENGPAGQCGIASVPSYPFATLVPNTEQIRKTPMINEKSRAASLDEVVD

LLFDKHIDIDTHANTLADFFSAAKITQCGDAGTAIIHFSHLAVNPSSPQRGQPVSITCNG

KPKRDFNAASYKLEVKLAGMQVFGHSGALCGDTHIPIPLGLGHIDVHGFACPVTKGTTTD

LLVEVNLPIIAPAGIYEILLTSDDGSNSPLFCLNVELDLTASEQTAKKSHVYEPILFV

>contig29191 Frame-2R

MRLLDVLVAFVILAATSSAMNSAAQLTPSVDTQLADRKHSTEDVRRKLRGFNPITYLSLK

IKENVAKKVLSKVFS

>contig53437 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54074.1|) 8e-19

MTLSNGSCMLFMCFTAILMATTALADPHEIQTTDFTEEFGDDFEDVYAVSAIGELKMHLQ

FDLEHQLVAGAEFTPRGIVTIVTSASNP

>contig18477 Frame-0R

MISKPKTVPLLYLYLLLSHAVVTSIQMTASSDGPHASKESLQNLRQVAHVTASSLSNESP

ENLRQVSNVTVPPPSHNFLENLQTHHPVVASPPMNVIPENQAQNSHGIEERSPSTHGILD

AVNALATSLKVDQFPRNGILKIVPKHFQKHRVQSLKDSKLISFITKFEGEILYDVAPNPH

NYNRLIEWIEGIKKEFRWRPRTAYSTIAVILSEELGTLKTCEVIAALKQHHSAETHLIKT

ALFQHWRNKDMDLVKLLEKDRWTSSEDVIKTLRNPGFDVINEFTSILEKEGKELRLDSFV

KKLHDSRLEDQVPKIIELGNAAYRDNIRVGNGFVTVENHLLNGWINKLRNEYSKSRIDEL

LRWVSVPPNSVDTITRTYKHLKLLFDAGYYKSLEDVVHDLSKSEEELKLFVVLHTMKSKT

NDHNVINGLLEQFRVKWQTSARTSNLEIDFFKLLHLDDVGSIRPKIYGIPSSPDLWKAFQ

DVLAGTKVSTESVLLSIPDQYKSNLANYEYIFKSGEFITK

>contig26205 Frame-2R

MAIGGFLKQLLSTIGILVLSTLLYFSWSRALIKRVVRAPGQGPSEKVMQHGFFTAQVAGY

ADDGKLAVTAKILGDGDPGYRLTSRLIAECALSLAKHEMKTLPGGFYTPASAFGYKLIDR

LQTKKLLTFEYTNTASK

>contig27219 Frame-1R|Blast-dimethyladenosine transferase, putative [Phytophthora infestans T30-4](gb|EEY60865.1|) 1e-133

MTIMVLLKQLTGAVSSFGSVHARCAFSNSASLLRSTPHLKRKLGQHLLVSDDILGQIVAA

SKLSSTCCDIVRVLEIGPGTGNLTSKLLQLNPILIVHAIEFDLRMVEQLKLRFPAEINAG

RLILEHSDFEDFRFGEQTDSTQSEKRLISACVANIPYHLSSIVVSRLSNYMHRFSTTFKC

AVLLVQEEFALRLLAQPGDKIYSRLSANTALVADVTSIVKVPRKHFVPPPKVESRVIKLV

PRAATTPTLPSNEAYFFPKFDALLRLCFERKNKTLRALLLAKTARSQYLLNENAQIDTEN

EYQVITERVEAALLATNLTSNRAVKVSVSEFIHLMHELHKRGIDLRPSQTRHFRN

>contig31850 Frame-0F

MKITPLSALVLQSVTLLPRKMVGIPINCRLQKHIPDDKSEVTTNHSCFVIIQVINPTEIG

FRFRMRRRDDNSEERTCEADIECHCSRRFVIEVPRIHALVSDSGDHGTADVLNDLLAMEW

ETYFGSRGSLRINEFHLGFIAGMEQVKMELSCPPVNFYIQPFPEISASGLASGEQNGGTM

KLGFGKERDLSTEAPKFVQVTNTPFKSQTLHVEVFQYVPVAIVIQRADIASQQPISGVEV

EVIITDENEELCFEMNDYVMVVGLLRTLVQWTELMDISIKKHKIQCMFLSEGNFCVTVRG

RVLDGDGQRAGNEIRAYEPLHVHVRLKD

>contig34611 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60537.1|) 6e-71

MGLGRFFLFGLALLVAMVALAWPQIEQFLISSGYSCPYPFSMLITGKGAENELAAEAKEL

PKYTLDQLRMYDGSDETLPILLAVGGKVLDVTSGAKFYGKGKSYSMFAGTACTRALALGS

LKPEDVNDDVSDFDEKKLKELSETKTFYYEKYPIVGELAFL

>contig36558 Frame-0F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY65662.1|) 1e-33

MHQKATFLLNGLVLALLCNTVVSRSSNCTGTPLNQTSGGRNLQLDTEFGVLLLAAVNKER

VSRGLSPLCMNMKLQSAAQKHSKDMASNNFMSHTGSNGSSMSKRVSAAGFKWTAVAENVA

AGQIDVMAVMKAWMNSAGHRKNILSRKFNMLGCGYAYKARTNLKHF

>contig40164 Frame-1F

MRTPIFFKIGWGIVPPVVVILLSILLLSHTSTSFTMPVSLATNVNGTNGILMSATDYWAE

DHPYKNQSLWKRLPNGKVVANNDSGVRSFANFRDAVEAKTPWISRWVLSPEGRHTLKKDI

PRLLMYNLVSPMDYGKSIRSDNVRRRRNKAIGMFAADNLALPLIKSLGRVAWNLIQKHYV

GYFEDELFTQRLKLMNSSEIIKEFNLTLSDEAIANAQEQEDRPNTTCPFIYDGESQRSAH

YAQYTSAFVPYEGYS

>contig55889 Frame-0R

MLKQFQLLRLLIVSALHSKQYLETSTACSSNCSGKTVVASSYLTTTLTHGPYFVKKHAAR

SFIFETFKKLTFDDRKWVASINNPPICKLIFPCL

>contig10764 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61989.1|) 1e-168

MQLRVAVLALAHLIKLASTSSVRALDGFGNAVAWWSVLKLPTHVQFPNGTVLPTPCDCPV

PDCTNVPTAGWSALNSRATGLCYLYADSKMPQFQHFRDLGYECIGQGGNDPLSHTLKQNE

KSSYWALFNDQFNGIAANYDSNAFPNVRKSKHVCGGDDLFSAHAKGAVAFQNDGSGGYFL

QTSTPNYPDPTRNDSFVKLGCQTDNNVEFAQHMVAMSLQDKELFELGNKLQLARLCSSNY

YRDQSLRELLASTHLLKDGREQINTTATAFYHALLDPNLPIQHPSDPMKFEFRLKLTNEF

RKIKSFVFEPLGKFQKLLTCLSNEKEEEVRVLVKSPRAAVPPWALVAEMLDSDISVASWW

DGSYGIPTICAGDIYSDTPLKFCLNNSATGVELNGNGGAPYNIENLMQAT

>contig36117 Frame-2R|Blast-ribose-phosphate pyrophosphokinase, putative [Phytophthora infestans T30-4](gb|EEY69327.1|) 0.0

MFALRSTATRLTPALAVFLGGATLGMTQSSFALAEEKRDLRDLEFGVPHDRKRVDPFSPF

FPSDKHPCTHAGMFIPGCHELKIFSGSSHFELADDIARRLGTRVGKIKLGRFADGEVQVQ

VGESVRGKDVYLVQSLASPVNDNIIELLLMVSTMRRASAKKVTVVLPYYAYKHHRRANPA

ATSLNSKFIQSPAADIAKMLEVMGVDRVIAVDMQMRVEGHEACFFSSDIPVETIETIMAG

VEYFATQVHLRRPLVVLAPNPECLRRARIFQKGLNKWLPDSPARFAVFFHGTGKKGSGEQ

STADIVGDVKGADVIVVDDLVDTSETLSKLTNLALSKGARKVYCFASHPLLNGNAERLID

ESNVSQVVVMDTIPADPKAFHTEKLKRLSVAPMLAELIQAEHFKAHSYIDKVNSREDFKY

VYHY

>contig58261 Frame-2F

MRNYLFKAIALGSLAFVSAQEINIDEIEPLPGLEPNTTMNKIILQFQPQLHVSSGCQPYP

AVDSAGHTSSGLGLWKMGTKCNGSPLGSQVYARTDKFNGYTAIMYAWYFPRDYVVRPTGH

RHGWEHAIVWLGGYG

>contig13165 Frame-1F

MRINFVPLIVTALIVAGADSALVPPATASNLRNALDAHSNVQSPAAPCADNRVRNEADER

MENMISPLKKIFQPSQSKLKKLLAKVVEADNFWAEPIFVDELNQLVQEHKMGSRSLRNDL

FASWEKSGLSFEDMQHELQHTKPMLSIKDLTILHDYFRHVYTKRNPILDASKGNKIHKYI

ILLVDAQRKSDTKNVATANLNDLLATLKFHRVTVSEAFKLLYYGQSASDVIQSQYLTVLE

QYITLLNKPTTLLKTLASHFGEASVAEALEMVSRTRVDLKDFVTKLQSEQFATWDKLCNP

GGGRYSKAIRDVVSGFDDLLNLKSALLENPRFLALWKYIKRARVSGNSLSLMETVTTGMD

EKIIYLSILADAAEHLSSRKLAIELQNEGIADLVNKYDDPVKFFRQLQLGTKPVETLQSK

NLWMFQRYLEAKNVQDPHMTILEALVGCYREIPVAKALGTASKDMQKLIRLLRAKLFSWW

FQTRHYSPSIVVRMFDLEKNGINEASYTILKGYTSYFNAKQKVEDNFIATLENGMGGKKK

LARVLNSQSNGDRSSKALLKMLFEGLATSHANVIKDLQIGSTVENIVLSDDFWMLEEYVA

ALKRSRDVDTTPVALLIKFFDNSIVAEGLAHLSKMEIKKERVHQLQRDQFAMWLKDLSWV

KAQFTTTRMTMRFRLLSIDFCNSLTEFLKSCDNGSKFDTIMMALTENLDMYLTFVAEAIK

ADKVLLAKQLKKMLILYWMKQKMNFESVKELLTSVDEGVKNSFLEKYRLALRR

>contig42329 Frame-0F

MFRTLFCSLSLVTSTTCCRHTTGTSVPHLLGNSVATSCKHSKSTRRYVSSRDWCVYDCSR

SFAVSMAPRRDKHESNGCDSRR

>contig07187 Frame-2F

MIRQLEVLLLNVAFFFFRHTLGFNYQPSRCAKTKTDDRSPSQLVIACDFFFIILMQGFGL

>contig26201 Frame-0R

MRLRGSLVALVATIALFSHGEASADSQAAPANFKHVRSPIQTPPNIEMESVPSLQMTRSL

RVDENRSGVPNPGAVEKTVANFVQVRNKSLGKLAMEIKNNPRYPPKSITKK

>contig59034 Frame-1F

MNFYMRILVLTFVILFVSSSSSSPAITLS

>contig59203-1 Frame-1R1

MWYESLGVFVVLRFLNTSSTADGVADVIVLLVCEDAILFDVDEVELLL

>contig10153 Frame-1F|Blast-uroporphyrinogen decarboxylase, putative [Phytophthora infestans T30-4](gb|EEY57967.1|) 1e-29

MGEVTTTSLAIAVSAAAAAAFILHRQNEAKKHSIKQKLPFPMTRTPLVRVPLDDLPKLKN

DLLLRALRGDRTERVPVWCMRQAGR

>contig26703 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 2e-20

MCTLLEWSVSGSILAIVQANSSSLVLWEPTKIEQHQLVELPCKDISYLKWSTSPNSLM

>contig34209 Frame-0F

MISKVKPIPLFYLVLLLSYRAVTSFKMAASIKATPLSKDSLDNLRQGSHDVAPPLRNNFL

YSFGQDFLVVATASGKSSVDNLRQDSRVIEERNDEFMKLEDIVKTVAKTFKSKGTNG

>contig42590 Frame-2F

MPIPNSSKAIQALQLMHPSWPRTALLCQLVLKVFGLPPSNLALIDGSPWLCCHIYKLALS

DHRTHKQYRLSGRVQGG

>contig29303 Frame-2R|Blast-hypothetical protein PITG\_06381 [Phytophthora infestans T30-4](gb|EEY69865.1|) 2e-42

MAGRVIQSAAQRWLGDKGTWPVLVTCVAAAGLCTAQCVRYLAGHPDVNWNKQNRQDIFRY

KEEKGADWQSHRRKIATLHKNAINEAKGLNK

>contig38143 Frame-0R

MRVCHFALLAAAISITITLASTADELTTHNEGTNFVTRLRVPSDKVIAHDDEERVLSRVK

GFLQKMGLAKKPSHSLKNANVALSNQNDFVATKTFRNWVDSNSAYILPTTPSLMGELKLS

DIGMAKAL

>contig51780 Frame-0R

MYPPLHYIVLLALVTTSISKFFHMKLMPPAHRTTHHRAEILATAHVTIGHEVDVSVRLLP

KVRVHLTSS

>contig25043 Frame-1R|Blast-polysaccharide lyase, putative [Phytophthora infestans T30-4](gb|EEY62246.1|) 2e-17 NOT\_ORF

MPQAFKFIIILVVAISVKVSFTELFLIKAGKVYDNKMKTFDRSNIKSNG\*DDGGATTSVF

IFEAGATITNVSIGVDQAEGMHCFS

>contig39998 Frame-1F

MTDHVVACFITELALASLSHLSTCMMHLFSLSLAFMATVATVSAGSPYQENPLKPILFAA

TYTRDEGWINGTGKGIYTYQFDTTTGSLTPWGVTPVGINPIFVLSTTKVFSTGQRVIYAI

NAVNENSAKLPGTQTGYVSALTLQHDGTLKLLNTLETLGGSPTHISLSPKQDHIIVSCYG

GSLTMFPLKHD

>contig45755 Frame-1R

MVLFGALLLARSLCAAEPRLHGYTICEAQ

>contig49197 Frame-0R

MHFLNFFIVLPRSTLCKISSSLHPLENVFFQHLSLRCKSRFFIQLCFVSDTQKRLSDYVL

KYDPHCSSAQMIL

>contig05035 Frame-0F

MKASQFILFMSGAIFHLGGIHTSFVGKLASLHEQRFHLNTALKTACQYPAFIFLRFSRSH

AQVFARMTAKSAKLNATNKK

>contig24896-1 Frame-2R1

MLWPASLHMPHLLCNGVLGSFRSKALALATNSNSDGFL

>contig27466 Frame-2F

MKSLLASMTLVFFSAMRLNLETSSAHRALDTSASRRLSTESALSSVFIPINVDDDSSDGA

EPLPTHQLAALPLPNRRPSLFNPAFGTFVSSISTKRRNSMIPGTTNGDSTQKHDAILQNS

SNTSTREQDEETTKPPLNFFYNHEVQSTPSKLRRENTSHCVHDYSSPAVEKLHEVISATR

SSICGQKFDRCELEFSNDYVKLAIWEERETRWKGSIKYAHMVRFCFAPVGRPPYILLLQL

DSIRGRSDFASFYDPIFAKVWEDNEARKQISSKLYGVVFYFEEELDYIRCQSMSDKYPKL

AHLFHESLSESEVRECVRLDASSRLRPRVDYKSSTFKTTGGRNLALLVGNQARSAIDSVA

SFFRPTSRPSVLENENFSVISDSGNSTRGKALDFTQKHHEESATDMAETKITLLNDHESS

NGKKSLGSIANAASELLKSYTQQDVTHERGLTMTAPFSIPQDENTSATIESSIRPATSRR

EADEMKRRQFESRRNEVLLTYPYDGSDASGRISVTLGDVDRLAPGEFLNDNIIDFYLRFL

WRHLSMWQQLHTCFFTSHFFTQLHGTNGAFELNQAGPDERFARVARWTQKETNLFEKRFL

FIPINDSF

>contig46575 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62203.1|) 1e-34

MCRNCRRLFFRPLAIAADTSAFCSRDCQSTFEYRRYLQNTAKKCEP

>contig12717 Frame-2R

MKISYTTFAATILLTNLSTISGAEITNFGPTDTEGHLPMSESSRSPTPLVQEETPTMTVF

MSNSTGEGTGEPVVNEINGMQPLPASESMTGLSDLLNVNAVEEPLGVEEPKVGEEPNVEE

EPKVEEDPKVEEEFLSSEELTAGEEPKVEEEPNVEEEPLSSEELTAGEEPSNVEEVKVEE

EPSSIEEVKVEEEPLAVEELKVDEESKGEEELKGDENHEGDEEPKGEEEPKGDEEEDSSD

DSSQERKNVNEEDPMKSEE

>contig31758 Frame-1R

MIFFALLAALATLIKAVAAKDGSCVLIDFTAADAEFAELNAALVSPSVKKQLGSMMKRID

PIEKENVTLDDASFGALGLGLTLSTTIESLSVSGLSTIALLNVDVKDSNSVSIKAGSPGK

VNFTSKMTIHIKELHATIEAQVRFVLVKPKFKIGIEADMFACAPKVPESQCSNLTVAGLQ

SDFVSLSSKSHHHASILKKLLMKFKKASATSFSLKFESVTGLTTKFDSPNALVKTLIRVL

PEYSEATISPTKSLYQKLGPNLNEHVPLMLNTMIASKLEPFFGATCLSEEQSQAF

>contig35475 Frame-0R

MLMFKILCVLRVSQALYTESKTWKCLTFLKSIRFFHVFDSSKSSLKLSIMHLCNCKTTIL

QFTVEQRDYWPVTILAPDVKSLRNKNLYVKLL

>contig37712 Frame-1R

MAKLLVWGDALFLVRCEFGELEVQRILVCADKKSTLRRCSVKIDKATVLPPDARLVATKE

VVDTQLAIRYPVLVIRASGEGAKEFLADPSPVFCKSQRPSEGKNTDTTLVDKS

>contig39677 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54965.1|) 3e-47

MALVYALGIKGMYIEIRGGLCLFLAFQLAYTGKLSRRCPVKTRGE

>contig39974 Frame-0F

MIAKHKRSASLCCLFLLSCYHIVTCVQNVAVVEAPDVDNSRQLRSSVELDERSIQVPEGL

ANSMKTLPERVGSSLRSRSARMKNKAATWRWIRRHFPQSSVRLAKDKVEAARKAFPRTMT

NISPNFLQSDAFNNWVKLIRRSVKGTREEVDEILIAALERKFG

>contig41919 Frame-0F

MSKGGGGKSSQLHWINVFLLAIHHCCIELLLCLLTDCATCGISLC

>contig46011 Frame-0R

MRHHNSSLLAAAIVTLMAFGSAITGPVKDFETKALRLVSDTRDAANAVRLLKIADNEEKR

YSLNDDDGNQDNSSKISDDSSDDASVSSSELPQWSYDDALYKRQMAMERHNDTGTLLRKG

KEANNFSF

>contig51622 Frame-0F|Blast-brefeldin A-inhibited guanine nucleotide-exchange protein, putative [Phytophthora infestans T30-4](gb|EEY53921.1|) 5e-24

MSWLYPLLTDLVSVLNAEVRIALSSVFGKAVRKLLPSL

>contig53637 Frame-0F

MFKKLSTALVLSAFELSITTVNAGLLAYGICQTGCNAVVVACYAAAGNCVCRGWHSVRHF

WL

>contig57776 Frame-2F|Blast-cyclophilin B [Phytophthora nicotianae](gb|ACR82294.1|) 6e-46

MASSSKFLLILFLTALMLALKADTSLKTTNQVYFDVSIDGKHVGRIVMGLHGETVPKTVE

NFRALCTGEKGVGKSGNPLYYKRSIFHRVIPDFMVQGGDFTNFDGTGGESIYGAKFPDEN

FKL

>contig05600 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 2e-68

MLSYLAAVASAAALFSGVVVGDPFEARARAMVDTFTPAQLLGQMCQLTLGTVMNSTTREL

NETLVRQYAKQYVGSYFNTYWDQGINGRYGYNASEFRALINRIQEITLEETNGHPIIFGI

DSVHGAIYVEGAVMMPQQINYGASFNPDLVYKIGQITARDTEAAGISLIFGPILDISHSK

LWARTYETFGEDPRLASVLGAAIVRGIQSYNQS

>contig26706 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56097.1|) 4e-21

MCTLLEWSVSGSILAIVQANSSSLVLWEPTKIEQHQLVELPCKDISYLKWSTSPNSLMVN

L

>contig36387 Frame-1R|Blast-elicitin-like protein [Phytophthora infestans T30-4](gb|EEY70305.1|) 8e-53

MKTAIVSAAALIVGASYSLASDCDVAKIESQLFPNATKGLANCGNATGINIFAVSQFPTL

DQVTLLSENVDCANYLNQINQVANVEIQCNVTIDGVPINFGKLIASFLTGKTGNETDTDP

SPTEVPSSSASKLMDSDSSPLPTSPRPNVSANAPSPVPAESSGASRNIAVSFISCGLVTM

VIALS

>contig37713 Frame-1R|Blast-hypothetical protein PITG\_12147 [Phytophthora infestans T30-4](gb|EEY59574.1|) 2e-33

MTSALFELVACVYVSKVYCSNPHLLIHARQISCLLTADSHSHIWSILELDSGPKDTLRCD

YLTTEGIDIDRVTCCCFISNLKKCQFSACNDLINWNVRTTTRLCSRKLMVSALVVAGTTN

NTVLVHANGRVLVSYVLPARPADIWLLDENCENQNYVFCVRCDDVKRSFFVLEFCSNVQN

DSMDLLLSFNNVGHGYAGYFTNYSLSDSRQVLLLNSIPGLVHTDDNAIVNNKLSIDTYVD

YGQLIKRSVLITQKTSAAKTKLTCHRLRLHTEEKSKRAIHYLKRSRNEKNGNLINSVVKE

VG

>contig39975 Frame-0F

MRRSQELVRVFAAVYLISSVSAKLDERNRKMQRDRSKVVGNERAKGSFRVDNVVEEDTSN

QERISEGYFAALAE

>contig46065 Frame-0F|Blast-unnamed protein product [Candida glabrata]emb|CAG59469.1| unnamed protein product [Candida glabrata](ref|XP\_446542.1|) 2e-16

MKVITSLVLLAAISVKTSAESFSDYSLDDILDSTTILSHSSSSTAPTSTSSPQTRTASSD

STSSESTTTRKPSELSHTPSTKSLSFENSSTKPPSALFNSTTKVPVKFSNSSSKSKTTST

NISNVKSLSTSTERVSSSLTDATSKSSTSTPAAEKSTSSKAVRSSSGSANDFMASLSS

>contig54549 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69208.1|) 2e-21

MTLSLSVGRGRGMTMPAWMRKKMFAIICLMVTIEWSGANCFAVTVKKM

>contig08983 Frame-1R

MLRVVLFLVAACAKTSYSHTVALSTRNSQYIASKANEHATIPEDINLNRRLRKAAVITEV

AETLESIIEAFNPLRTLRSDVRSEMSSKTKLEQDAMLKEPSFYFRMLKPFSEFRIRACFE

VYEIDTLILFGTSPHLLKQYIQNGIPRGILPESVTVLATTGEKLKRFQRQFDIFFNPPTG

SKPSKPSRAWPYARGPQVQANFKKIYSSDHIKFLAYAFHHLDDVNILAKLSSSIIYRFVL

DNFKECRATIRYGTVEDWYKHPMLNKLLRVH

>contig39675 Frame-1R

MLLGVLRSQMGALTLSAGAGSAFLNNVARATLSTSSIANETAAGDEMAAFLSSTTPVEPR

TVKSMKRAIRASPRKLAYLAQQIRGLSANEAILQMKFSPKRKAEIFQKTVQNAINLADIK

YQLEPENLMVAECFVNKGTYLKRLRIMGRGRSGVMHHPHMHLTVVLREFDPTKKPLNHYM

TKKLAREKAKKETTTA

>contig42268 Frame-2F

MVASLLFILALLTAFVQPSPIYQTAGTVRNIADEKFRPASQFDNKVWDIERDDASIFVPS

IDKVHVAAELGSVTLIAMPPLLNDGEDLVIQWSGVERPHQADFLGLSCGPKAHDKDFLVT

VDITAATEHELDGSKLSNSVRFSSLYMMRCNYTVEYFNFQPKGNFFALLAQTEVGMVDAF

TAPKHGHIALTENTDEMSVMFNSASREKPAVRYGLDPATLNKHAEGTFQTYTAAQMCHRP

ANLTSQQWFRDPGIMHTVILKGLKLGTRYYYKFGSDKDGYSSVYSFVSRPDVSVKSAKFI

AYADMGVNSAPAATSTAVRSFQEVMDGYDSFLLHFGDISYARGHAHIWDDFFHLIEPYAT

RVPYMIGIGNHEYDYVTGGNNDPSGAAGDDGRMDFHPSWANYGEDSSGECSVPMYYRWGA

PLNGNAIYWYSFDYGGVHVVQISSEHDWRRGSKQYKWLEQDLKNVDRKNTPWVVLTSHRM

MYTTQIGDKADRQVAQHFRDEVENLLWRYKVNLILVGHQHSYERSCAVRNGKCTKDNKGP

VHIIIGSAGADLEKQGFSSELGEWSVAHVGEWGYLRFNSTEESMNIQFVLNRNGVVYDQV

VLTRWE

>contig42710 Frame-2F|Blast-metalloprotease family M12A, putative [Phytophthora infestans T30-4](gb|EEY56337.1|) 1e-156

MTVWARSYMFMMLVVSVTAKQEATMLSTTFDILNEEASSTAPSRARGKNCESNGVVLRHR

TLKYYGENSYVACSNGVVGCYLIERVHDKATEVACPTTDLQQRIDRETNYRELEKRFKKE

AQRDDDNDSNRKLSLVVVSTTRIWDGGVVCYQLSKEFPFNKTHEDYIYKAMNRYEESTNV

RFVNTAKCKKEKLSHCDSCVNYVDFKHPTVGRDCNSSIGITDDGPQIMNLADRCFEVDDD

LKTVYGSAMHEIGHSLGLYHEHQHPKRSIGVLWDSIEQSLWSEMSIRELSVGGPYDVESV

MHYPRSYGFCQPNICSKSVEKNCVKEGTIFCNLNDDDNCIEITEAMCNETATNAIGQRKY

LSKGDLAAINELYHSAAWPLSKSKIRD

>contig16394 Frame-1F

MMPVPSELVITQHRRILLLFLALLAGVTIVMAATTAPNAVAGVFRRRLREVPNALVDGQN

DERNSSPSIAVRQIAEKSLASAKTKGILPKNFEEFAENFSKNNYSGNDDLDHRMYAFLNA

LTKNKREALEYVFSPNWLQKPHALRFYNFLVNRWSKQKLGQNLHLDGISRE

>contig22340 Frame-2R

MRFAFVWLVVMIVASVAGSDTTNSTRKALATKETVTSVVVTPSVPQRRRLGWSSKISEWS

TKFGQNSFIQKLKAFFQKHWFFKPAKIVKTQPVDNPSFPR

>contig40582 Frame-0R

MMPFFTSTIIIAIAAAAVSSAHRIHHTRVMRGLQTDTSINHSSMDMITSEMSNSTMDMQS

SAINNNLSDDDYRCPVCGMSTMNMGYNNLNHVGFVNGQIIYTCGMAARSFGDYGFDLTDT

AYLAANIAEFIVNPSDATNYAECRSSCDECTNGIKDPLTGDNVNTSNYQYVCLSNGQKIY

FASAANRVKYLNNVKLEPRYLVNNIICQNTTCADGESITALSAAAQAFVPETTSTNSSDS

LGETGGTNAVIAVKAPMHTVFALTCVLTAISCMT

>contig48461 Frame-0F

MLVGSGRSHCAGASSLILLRGASCHCEVENDFSALLNLMYHSNGLLGADQSGSTYVRLCA

RSFVGANYQLGRVRFPTFPAMPILEN

>contig12894 Frame-2R|Blast-lectin, putative [Phytophthora infestans T30-4](gb|EEY59218.1|) 2e-23

MLHSAVTVISLIVLAFIASISGEPLPSLTFTPPFEHVNSAGRRQISESFTYGGATDVKKN

FIRLTPDRQSKRGFIWSQQLIDRNELTTILTFRI

>contig16641 Frame-1R

MRPIRKRRRQSKRLRILCVLACLNFLRLSNLLSEHTSDKKVIQRKNYARRPTNTERLGTC

ACLRSWWVQKQGHKDTPNVNKDCNGVYRY

>contig51693 Frame-2F

MVKVIWGPVILMCGLALHACKETAQAREEPAPRAVNASATGEQLLSNFEERAGNDMYLLK

PFSKITHAIAQDIFDTVNTVQKNLMGEEVESFTFAHLSKWINDIKKDYNAMSQKDRDAYK

AMYDALAAYYSVVDRARIIATCQLAPKLQRHMENMRSFVLNDLVAQEKSPEQMYNMLGFD

AKDPYFLKDPLLELFLTYLDRNHSKNYKIVRDKLMEAYVGDKQKLMDLLKENGQIAKKLK

YIVP

>contig58764 Frame-1R

MIEQVLILLAVLLALRVWLVIIPRRIKAPISSYLDPLFHQLHVDNRKKRRQVRVMAVLGS

GGHTTELLKLMKNLKRDVYTPITFVVAKTDNTSQAKTELDWKP

>contig19281 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 2e-11

MLRSLLAVALYLTTVNALFADQAGEFDWKFENIGRVQFVAFEDSVNREPNSVVPKN

>contig34914 Frame-0F

MKVPTSFIVAVLTTLSVCTASESSELSPEQMPLVPPTSTDTAEEMPLVSPTSAETTEQTP

LESSSSTEEMSDTALTDWKESLTTDLNNPSSDATQP

>contig41961 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62019.1|) 2e-13

MNYVVAALLLLMKDSQDAMALYLEKFSMQEAAFWLTLALIRHRGMAELWKPKMP

>contig48643 Frame-2F

MCFMRLVLCVLQLLWKLVGVPLRWYYALKVKYNNNRNVVLLKKKMAIVRFCHLHFLLVIE

KLKREMKDRTREEMQQMVVALGALQQKKGTRVTLPAILATLRKIQAIEGRLKSEKFEEYL

TDINQGGRYEDDIDSGLPAAWTRLQDVYASFVRIQATIIRQQTPKKTWQLQQENVDGRHV

RQLSSSKDSTKEVLLELQELTRQLPQGFTADMFKSLGNAMHGSSGAVERGAELELKTHSL

ITLPSIPVAYENSYTPQKRHNIPRR

>contig02853 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57692.1|) 1e-118

MPLGRHITISALISTSANLTVAVVYSCALAQVRVHGTPVRCQIYREQVATVLNAMDHTHT

NETVTELTESINKRNVFPEDSRDMGYVVREPIINATFGDIRFRRGKARRVSVRSLGWDMK

VFIDGIYSVPLDYGVQAVMKVADEPKYVLRTVDFSSLPSSAPRK

>contig19282 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56921.1|) 6e-12

MLRSLLAVALYLTTVNALFADQAGEFDWKFENIGRVQFVAFEDSVSREPNSVVTKN

>contig19549 Frame-1F

MATGMLICSAVAVSARCSPLETRNQYDEDYQGYPRSSKDTRASSVDFTFERAHERNPPLP

PPQEPLQRSRARSFSYSQAYGPDGYNPFNGNKPFAPVPHHRVPPQQATGPEISQAHRTLY

PGSNMMQPPHTGVRLPRVSIPTDSPMHQFQYGPPMPYRRYSDAFAVPPYQDFYPDDQQEN

QSHQNNTGRGMRSYSIEYGNYTMTRQMRSQSMEGLQIFASAPPLEYPSLNRSNSAGGGFD

WLRKQIDLSPPLPPDMRGCSVNGTSHFPPPPPEAYYDVEFKRGRQEIFAGRASFKPGEYV

KVEADRGEDIGRIVQRTADPSKIGSGEFGSPGEEFIGRCKRHDLLTKKIICVANQRECDM

LN

>contig48903 Frame-1R

MFFPALAALALGVAGATSMSNALQTMSFNGTSVASRRLDETSAAFKKVAEALDGDKLRNI

FGHDMLNNVPHEVAYTQIQNHLKHLEHLRAELKDQAVLALMEKHYGVPAVSRYVEKTFSD

PNSMKGKVFNVA

>contig51691 Frame-2R

MSPSLLSLRWRCSLPLLGVFVSLLQVLARYNCGGHHVPLIRTHFGIHAYHGDFKHSSRTN

RHIQRFIFVTSAYGHRLRLTRMPTRSPLLRHPNVITRLGSRGPLRLSDNRIPKYS

>contig02629 Frame-1R

MPRRRLLQLLPLHRRLFCILPSLQSPPVPITRFTATRYYRVSSSNESTKNRRDSSSASWN

QLVLALRTFHSLERHFAVPFSFVIPTCSLWPKELHQLPLGVKVHRFLQSVSKSTVKKPPP

QTPKHIAQLQELDDMGFPLYEWHDYQFQEVCLPALQTYQELYGDLFVPQKFTVPDNSKAT

DGNLWPRATRGFKLGLAVAKLRKQMQQQKQRAQQPQRQDSKTSMRAVLPPLAPRHVEALN

ALGFVWRVRDTKWYDFFLPGLRKYKEIEGTADVPLAFTVPLHSLDPRWPKALEGYLLGRH

VYMVRAGKYATQVRECLNELQDLGFSFRLMDKVWTESIYPALHVFATQYGHCDVWQDFVV

PYDDLWPMKSWGLKLGDTVKNIRRGAYNTQVKTVRSELNAIGFV

>contig19377 Frame-0F

MLSAVLFLVAACAKTSFGHSVVVSTRDLKIYASNSNEYSTIPEDFDSKRRLRGAVNNINR

IKERDAAILSEILGWNINSKLSKNFQRWKKMNPRVMENDLFKIPETYKRLLEFTKSLSKK

AATKPVSFETLHLLGVRPQQLKERIPSRTAVIRKGKVDRYKKYLNNAFYNPVRRKKPFDT

SRLDDGKVEQAFRKLYNDNVLELLKTAFFNIVDVEKLAALASGPVYRQALEADPKYKEMM

SSIPLERWPENSILKKLIAIHEFFLKTDD

>contig23857 Frame-0F

MVRVYVAALAAIFALSASATLHLTLANASSVTTEEGDGRPQGKLRVNAATNVESDERFLD

GLKALVRGFYDLTPFAPRFQKDTYSNLLLKLNLSFEQFSGKDTLQLRRFYDAARRHNKVN

PTNPVSVYTGLVEKYGEFEIVNMVYSLKHAQSSKSRDVLKRLGKEEKWYWKDKKDAGKMY

AEALDLGNEFTVKNMVSKLSKLEQFLNRIDQKASEEQLKALVVADIERVKTKKESVSPSD

VEM

>contig47607 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63149.1|) 1e-24

MARSFRFARLRGALGTAVACGLFESDTMTHANSCMLRLRELEIGVTVQADENEGSVAEKF

VKQAIDLLRRVSLDMATCVE

>contig06757 Frame-2R

MKTRHPSQIVGLRSFSLAVASSLSSRTARADLLTLRRSKKCYQTWKKIYKNTSFAIFEKW

MRLVYSIEWFRTKQLRARKLKGQRKTK

>contig09828 Frame-1F

MNLRVLVLAVFLAATTRGDLATDDVNSTSLRLPSIEKRADGYGNAFNEEKVLNLRQITDP

SNFPNAHKKHLVAAVSKFWVKPRIPQEDLAQQTFKVFHVERVKSNLFTSKRWIKWVERVK

VAIPDRTKRDEELTRIMVEEFGLPLFFQKLHEASKNPETSETAKYFERLEYDRLLKNKVF

PEEFREQLGLQHLESDIELTRYYLKFRSRFLMLATPVEELKVPKLLKEVMDEPTKRTIEL

FGEFGKEEPDMVAKMFELKFNNEREVEHPLFNIWIDFMMAYLDEKFVASATFLQTFRLLE

SSAAAGNKRSLQIKETFSRRWISSDRSLKDVAKMLQLGKNQADSSWINRLELQLYMSYMR

KYILTHRKADPMLSWVLSKLVGLKHERSRKYQTRFVNFFRDNFQPSEVLTILRLDNEGGQ

IKNRPLVEFGLQYVASFLLKNPKAEPSILKTLKLLCHQGNSDDMFAFAKLWVSLETTPET

FLKILGIKKIDASILNHDLRDLWLAFLAHYGARLPSQALPHEMLQTINHLTTSAMMDNRT

SREALAKIFHFWSRKDLTQDDMFKMLRLHTFRPHYFINPLLSTWDMYQLTFVTMHPTEPQ

QQLSDMIFRCFNVNDVEKLTAGAKHIPDMLHSKVKTVVKELQDKVDHFFGRT

>contig34965 Frame-0R

MKFILLISPLLSLVRSFSFERADESQALVDTNTKAEKYGYVAAIHFEGPESKAYCAGTLI

APRFVLTSSLCLLTSMHDVYVSLGSTLRPRGDTHEFESIRVVRSFVHPLMTLEEGDLTPE

HDVGIFMLATSSKNQPANLPAAKGSVGKPGAMATTFDWNYQDGKQDFHSLNAETTKVIRN

DKCSQIYDDVNQTTVEHYVICTGIASCKGHMGSPLVVNGTIAGVMTTGLGIEKCGKVPPL

FARVSIELEFIDEVLNGGDPGEMTSLLTDGTGFPLEDLFQI

>contig46296 Frame-1R

MMNIFANSQFLILLMIAGRGSIHARPCTSTDLGVFNDVSNQVSQCRQDSQLNFLIPPHMS

LTKTEQSALCKSKACQGMIGSMDDLDIPMCEATFDLKNMTLQMSLDKFVAACDTSTPAPS

PMKRRKSLESSSFNDSDSKTRRYENVATAI

>contig15134 Frame-1F|Blast-PpiC-type peptidyl-prolyl cis-trans isomerase, putative [Phytophthora infestans T30-4](gb|EEY58608.1|) 1e-103

MRHKTLTIVATLQLWCLVLATEKAPASVPIQAHASHILVDTEAQADELNAQLSATANLSV

MFAKLAKEHSKCPSGRKGGDLGVFGRGQMVPEFDKVAFGGEIGVVHKVKTQFGWHLVLVT

RRIDGVEEPSMLYDIKQALYKSMPFLGPLLLVLFVAYGIRKSQSGPRARAYHILVKSEAE

ADALYTEIAASMDPKLKLAEMAATHSTCPSGKKGGDLGMFGRGDMVPQFDKIVFESDVGK

VAKVQTQFGWHVLLCTERVGDAKKLK

>contig24660 Frame-2R|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY58368.1|) 2e-26

MRFLSYSLAACATFVVTTYGDDCNGSPNARTTPPPGAVVVDSTGKYAGSVTTINLGVAQL

QASSSPQSLFIFPGTFNEQIFIGKDVKSLIIQGYTCDTTDYTQNQVTITHSKSQNDLPSS

VTS

>contig32605 Frame-0R

MTWSSLTCFLLALIYTTATIKALDWNILNHDDDSTLTLNPNYSDEILSPETLNEMMGSDY

LDRVKEMIYSRKNKIPDSSSEI

>contig40514 Frame-1F

MLLSRAISVLALLACIRCGVHAQNTEQNLKTQLTTDSAMITSQRLLRTSVDFKDSEERWP

TESSRIRSAIKDYFREFPEKVSIAMAIRQIDAHGVRHVEKVLSQYKFPAADQGNIRLAII

HHKAPK

>contig54542 Frame-1R|Blast-ubiquitin-specific protease, putative [Phytophthora infestans T30-4](gb|EEY64041.1|) 8e-30

MVSLLRVLLVHPSLHCAGIVRLVHMTFNGLKLTKRWDALNAVSTQILDAIYAKIIPKDTK

S

>contig55057 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69102.1|) 5e-11

MLYSLLAVLVVLHVSYKFQRFQQALRQHYQMIAVLNLPTPLVIMKSEYTQDEKSDQGG

>contig06755 Frame-1R

MVSIRVGMLMNNAFVALFVFVLAIHYQLFNRFEHT

>contig13560 Frame-1R

MFCCFSFLVCSLLNFDQCISTKLFHFLLLPLLPLDALFLFF

>contig32604 Frame-1F|Blast-riboflavin kinase [Phytophthora infestans T30-4](gb|EEY53210.1|) 4e-35

MPITGLMTVLRLQATVVEGFGRGGKQLGCPTANLSSKDLGDQLELLPTGIYCGWATVDGI

GPYKAVASIGWNPYFKNK

>contig38277 Frame-1F

MSRLTFISSLALLVTSCKAQIRANDEICVMGDFNYCPVDDLTPSALDRSIVIFPGGATRC

AFDDFSVPGANYTTNSTYFFQVFPAPSKTKLMLYFQGGGACVDEATCSFGVQCMFQTFNA

NAKPLSNGVLDRSNVENVFNDYNIVHLPYCTGDLHVGSTMKSDFGSTLNSSLNRPECLGH

NMSLHMVGYNNTMAVLEWAVTNYPNPEEIIISGYSAGAIGAQMVSGLVADIWHVKEKNIR

YSVLSDSYVGVMHNEEAAGKILSTYGMCDLDLKLTNSLQDACKQTTVSFTGIISHLITAT

TDVQWLFIQSMYDRDQRFYYQLQQDGVTGHPFTSLVSGEDFYSKMMAMIDVYKNVSNDIS

TFYVNNSQHVFL

>contig44753 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65867.1|) 2e-57

MQSNTQLTRLMKAALLQTLLHAIRTGSVEGVKVAIERGVQVHYLDSRHRNLVMLAIKCDT

DSRLRIVIILLDAGCDMNHKDQLGWSCLHYA

>contig59474 Frame-1F

MCKIGLLPILPASMSASSTLSPHLQAMKPLASTATTSAVPMPTAMVGALNKRPSTSVSPT

PRSPLKKPRTIPPNRGKATAAEVAALSAAASEMVSQELAQASVADIRKEADVLTHTSIEL

GTERRIMTEGRVRMVEQLRCQKEAWVEKDLFNSEKLRMQIRDVSRRAGVELGSQSSDVMA

YALHVYLKQVIEEMVEISKQRSDVQAQSLEALQKAQQMGTLMMSGRSGPMELTATDILRV

SCEDSYTKLRQEDLMLRSQLLEDAKREEQIERERAKKRKKVDRSKLTQDERDEADMDIEE

LARKDLRERLLQQDKSGLLKVGGRVNESIATKYIQRPIDNQVTMEDASYWLMSQKPYIRP

KLFVRAEAARIVTKSLL

>contig22259 Frame-0F

MKSKVPTFPHFLVLVNALSLLASLDAAPLRDAAASHAISVPSKTEDPSSRIEERMINVPY

FIQKMSKVPEKAVEDVSEAAVKVGENEIEHDKSIKELYNFLVDVEHRKPTFEEAALTKPL

EEEYTRLKFVTEATDISNTKDSTEKNHKHQSDVPETLSANEASTIAKLILNNPNNLNLPS

LKSFLDSYPGLYYQVLSVELEKTFSHDIESLSNLLKQGGDIGMILQVHRLNNWRKEIDSS

SFSPLFEVPEFEGCLEYLTSKDFENWIDLITRINVDAAPYKILLRELKNRLSFDQLAQLL

LGASTEREFVQLVGKNLERELFKSWLDHCTQEQVRELLKIEKLNTNELFKSPVTRFICCT

SLKVRLLCRQNVWSG

>contig24419 Frame-1R

MFLMLTILVAFHLVRAATPLMARQDVLPRANVSARNDKVTRMNTTPIALIKSGDEERLFG

LFKSKEEIAQASKSKIERKIVKLVERFDKKLEPTELPKLKYVMKKLKSVSSSTSKTSHED

LVSHLAGKLKAKLGLKKLYLYIQGGKGSTAARELEQGLYQSFGKLFVESSANAFSLGNKE

TTTLKELFENPLLEAFISYSRATIGKEFDLYVALSLILEYEDELAKMVNEIMVMKSSVYQ

PTAKILNDGLNYPIAEMFHFLHLDKAVENPFDDALLPSAIFYAEQYSKRHPNEQTFIQQM

AIIYGKEKLHQNIQAALKKGPPTNGVVTKIQAMQSLQKTSTKAAKPIRNTNSMSPQSFEK

PVDGASTNDHVASTTLKTADDHIVSTRPKTASPLHTFFAKIRGWFSRIWAKLRGMLRTKT

ADNVVSDDHKLRRH

>contig44084 Frame-0F

MRIDYISLLVIATVVTNANSASLRRSPIDTSKHSYDNTHDFSTQETDVWHKEDERMLNLL

KSYIKSPVEAASLTKPLLLSSKRIYEPNSFEGLAEVNNLARYIDALQLKDRQTNDFVDAK

LNFLVYYFGYSAVARELMKVEQSLGADYIWKLLFRNKESLPGNSKEYLDVIDFGILYQFI

KVAQRHDEMKELPQLVKRYFVVKQKQMSPKHSGYDFSADVEVNAFKLMFTDVPTSSVITA

MRNKYVELEFPDENSVLQMLAKIYSTFHNEDKQQMLDYFFLSYLFVHNNENSRNFIRKIR

SDLKSVSAKTDIMP

>contig45205 Frame-0R

MTFAGVCVVRSPPAAVAVVATVVETIDHLRASASFTCSPFPSIKARHVAAAATTNQSCDY

D

>contig51271 Frame-2R

MKSHILACGLFRIAMSLQKARILNHTSV

>contig53844 Frame-2R|Blast-myosin-like protein [Phytophthora infestans T30-4](gb|EEY53382.1|) 7e-75

MARTLYASIFLFLVSKVNSMSSMIQQPIASSTRTNNKNTPPCIAVLDIFGFEEFDINQFE

QFCINYANEKLQYQFLQDILLTEQQAHIEEG

>contig20638 Frame-1F|Blast-gamma-glutamyl hydrolase, putative [Phytophthora infestans T30-4](gb|EEY53659.1|) 1e-141

MKLKALMIYAAIGLPITTASDRGPIIGVFAHPSSYHGDYIAASYVKWVESAGGRVVPIPY

SAPKPYLEQLLPQLNGLLFPGGAAAVNDRAEWLYHQALGLNDQGVHFPVWATCLGFEWLI

QLTTNDTDSLTKSLDSMNITLPLNFTESARTSRLFSQASLEPFSWLGEKAITMNNHELGI

TPERFDQYSSLAKFFNVLSTNVDRKGIEFISAIEAKRYPVYAVQFHPEKNSFEYGEYEDG

IPYEVINHSREGVAAGNFFATFFINEARKNKLRFKDPKVERKALIYNYPTSTITYPGFVE

SYIFKHTYQMGFWSVM

>contig39179 Frame-0R

MAAPLAATCIPVWAIHRICVNNFDMNCKNIKNSRKRFFVTIFLSGVDCLKNAKCRCR

>contig45868 Frame-1F

MKLATGLILAAISVHGACGGSPLYLRSSDVDTSASTGNANIANEK

>contig08248 Frame-0R

MFQRFSLRLAGVFLLIGCGSTLEAIDTNSDTFGTRHSTDMNQPSAAISSNTRSLRLLKAN

AMGLNGLEGISHSILPNKNFFQNFNLEKLGLQRSALIKRNAVDNALKYRGGRIRPGLEKN

GFPNSVRTKRYSENNGYRNSVRTRVN

>contig14124 Frame-0F

MLAWILALLLVLAGAGYLHLQQQVRAKQEACKLQKEKEELAREHLHAFPNKKAKHKLPKV

DVTAELKKKKEQASAAERSDTEHSSILHVLKGHKYIVTAAAYSPNNRFIATASLDRSIRI

YFRDTLKAKKPKVHQINLEYDHVTAMCFSPDGRNLVIATVNGHVKVYQKLRIKPDIFADF

PISHSSDVHSVHMNDIGNWATIITCASESDTEVKFWNLRGELLQIVNTNQVANYHCVGSK

DNRYVAVAAYTPEVKIYEITREKAGNFKKANKIMTLQGHRAGVMDLAFNGSDTLAVDRVV

TIYKDASIRVWNIN

>contig15453 Frame-0F

MGNVCYRRPTITHLRFRLAGRPSFGWLLVCLLAYLRRCAIVPTYFQFQYLTTRPIENKRR

HAGASGQLFTCSITKYCITISNDVLMS

>contig17666 Frame-0F

MNISATIIAAATIVAGVTGNTVHTSRQLILGGHTAESSQQYVVGLCDSPSQNSFCSGVLI

TKSHVLTTSTCVDQVWDGISMYAAIGARFNTGLNFSNGMQNGEHIKVETIQIHPEFNNDT

TSYDFALLTLRKASQFTPIQQPTADAKPGMYLKAFGSGSPTYPDTLLQVVKLEVWSNDRC

DDTYEIDDSMICAGGENGKSTCIGDIGGPLVHETKSGDVLIGLVSMAECGNEGTPDVFSR

VWSARDWLIECIESDMLL

>contig58696 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61720.1|) 2e-08

MVLLPRVLAGLALLLGTTRGYDINVYNQCSGDLPLVHVRPGNVNTEWVASGGSTVKTIDP

>contig07279-0 Frame-0F0

MPCNWSIVFVVSSLAVELRRGFVLDTSSPFVAKFILNQ

>contig08249 Frame-2R

MYPHRVLALATLLACIVNGPSVASESNKPNFDTNDKAALRLRSNSAATTNADTEDRSFWR

IEKTITEKLRSKIDKQVTLIDILKKQPNEESKIIRDLKRLDKEIKPLLETYKHELKTIRE

IIQDKTMKRDSLADTLGVPKVGQFLFSKQYRKLRKISKEIKKLEERESKMKASFRRSW

>contig11979 Frame-2F

MLRIGILCVAAALMISDNGPCATHLGGLPKRNGGFGDNVAAERSLQPTNGEERAQEIKIN

PNTFEARTILHPYESYDDSSDSSDDKRTKYIHRRDDSSDYKRTQNRFKPSDSSDYDNKSL

RRSYQKSGVNSWNEAGNMRQHDHKNGGDSWSDNGKTGRHDNKISLDTWADKGNTQ

>contig13601 Frame-1F

MLFLHSSLILKFAVCAIFLYSSICCLCHFHYMTGENEEISLWRAAQNNNISLLWQITDKK

PISEVQVLLNLPHPIKGTTPLMVAATKADGTKITRTFIEFGAHLDVADNCKYKNSALHYA

AYNNRSDQLELLLAAGANMFALNAKGHTALDVARLRGRKEAAATLTSRLQVHCDWLYLRS

KSVLGFWKRRWCVLLACNVKQTSTELCIFRGPNKAHPKAVIWQDTLAHTCTPFKSEKGNG

FELDTQIVYQNLGGRRYSRYRSSGRTHVHKPNLQPIEFLFACDSEAARDAWMDALGGQLC

GGDSTNTAISSSYMGSPHRMSRVSRDASVDATRLTGRTSPVDIINGIDAPTQATVPSLMI

TQGPYRASAPTFIEDDDGHIWGDLSWSRAVFAQESHVYPIATVITLSGDPNEPQPVLVDR

CIVCANNSRDSVCVPCGHVAGCLDCMRAVTYETSSCPVCRAHVDGVVRI

>contig14316 Frame-0F

MVKLVLCFCSLILLSSFVLVACNEHAADDEVPESNNVTLLSKEAVQGFSEERIEVPASFS

QTVAQFFGKLKGKIWHVTEQMTNLFKRIVPYWYLKFASNKPEAIRKLLKAYKVDSATSLS

DPGFLQWSALVRKVYKLDFLEANDQIFTAMIENLKPQNMVKLLADAKHNAQWTNVATRYE

DVLFNRLITVEGLKIEDMVNNFKVFRTWGEEDKTFLIRFPKFDKMKPKEKLPLIDFFFTM

AKNVKHSEFDDSLYNKVLWHLKTSNVEPNGVPDYLSISAIQGDVLEHPRMYAWESLLPID

SATSAKKYDSMYLYLKKNMDAERLEKLLTQERQDNEYGKYLAANLQEAAKRLKDPLKTKP

LNLEA

>contig26678 Frame-0F|Blast-disulfide-isomerase, putative [Phytophthora infestans T30-4](gb|EEY66147.1|) 0.0

MMGSGALLLCAASLLASVQSMYSSDEDVKLLDAETFREEVLADSGVWIVEFYAAWCGHCK

EFAPEFEKAAKALKGVVNVAAIDCEEHEEFVNEFAVRGFPTIKIFGENKSQPVHFNGERT

AKGIVDAALTITRRIVKARLLDYTEKKKQKPKAEPKKASRSVRSSVITLTDETFDEKVLN

SGNIWLVEFYAPWCGHCKALAPEWEQAASNLKGFVKVAAIEGTANEQKPAEYGIEGFPTI

KLFGPNAMGPEDTATYEGERLASDITEYGLAAFDALGGNFQIKELGSASDVVDLCEGKSS

CVISILPHITEGGKKARENHLNTLQEAAKLVRGKPFRFGWMQGGEQLEFENRFELTFGYP

SLVAINLERKRYVVQRGAFTAETIGQFLERVIQGRESTVSFDLMPEITTTEPWDGKDIIL

DEIEDDDEDDDIMNEILSNVAGRDEL

>contig35726 Frame-0F

MHLIRSVLIVVAALVAISEGKSIRGTDYGENLQQGTDANMANTIEDRRSGGIGREPYRAT

GIGILTPFMYSSDTPNLDRKREHFARKVHAAYMKMQKDNQAV

>contig36455 Frame-1R

MATRLLTLLPVAGVVAWSGNASLMRARHQSHGERNFQFITGTMNDIIMETLETGDLVFFQ

RKLTALQPLAALHTWIMRKHLRSRFDHCGWIYVDRLGRKYIVEETLNKVQCRPYSARILT

SQATEISVLTLNVE

>contig59265 Frame-0F

MLALSKIIKAVVIASILIGSSSSFPMAKISSATSNDQSRHYGSEHGNGRLLRGAGIALHG

DEE

>contig30924 Frame-1F

MVISALFLLAALALGDVGATSISDALQTLPNSGTSVVSRRLDGTFAAVKDLVATAVEGNK

LMEIFGKEKKVVGDTPSEFYEMADYAPHQDAFKTLYSHLEHLTDHDNAATDHALLLLMEK

EYGMPAVSRYVSKALTANPNSNEVKR

>contig36526 Frame-2R|Blast-DNA-dependent protein kinase catalytic subunit, putative [Phytophthora infestans T30-4](gb|EEY69219.1|) 0.0

MKNVPLWTCLQWSAQLMALLNGPIRRTVLVILEKMAEKYPIALFYDFMVTCKSSLNKFDV

DLHRLEVLLTNSVMEKFVAALRLLHHPELRLKEGLKEISELVEDNRTQDAHHKVTRLWKD

CFSLDRPLLGGQIGRYNREWSRKAKRDVEKIMGKDGSKMTAKSIKFAREWIMKHFGVTPG

TYGITRDMKAHLGDFAEWLEEFDHSNCSLELPGQYTSYWGPPDSSKHVKILSFDSVLGVL

ASKQLPKKLTVHCSDEKEYTFLVKGGEDLRLDQRIEQVFGVMNQIFKADPRCRDQRLCLT

TYEVFPMTQDIGLLEWVDGTLTLKGVIEAQMQVDERCIDLKSDKSKKLDLFNTIAAKAYE

SFHRKQQGASFSAKIVAPRSKDVVDQFHRVQAMIPADLLRRQLLALGLNFEAFLLVRDHF

LKSLAVFSACSYILGIGDRHLDNFLIDLSSGRVIGIDFGVSFGAGASVLP

>contig40488 Frame-2F

MKLLFPLLLNLAAVQAVVRAEGSIRYPLDADISPPIDDKKGTEDDMISDFMVALNQPFQA

SGEWLQRLLSPDKSNTEVLRIVFTENESDKNDSAPDSKRACLKALEKIHGQDPLDSVTGV

SLDLFWSIFRTGTEASCDDLETTDLVRECNVIVESAYVMELVSEGKTDLEVCDIMSVVPD

DNRADKLSCKLCKRFVQMVDEAIVQEGQEVQQVRDIIGDLCDAMSPDSKCHSFLKNYDAI

VEWLKHDTEPLVVCARIEMCLKKSDNNNEALALDLTLDDPRSTNDKAMVVAGIQENDQSC

LLCSHVASVIFHVKNVFPNQLLMMKSVLIAVCETASPESYCELMVAKYDRMVELVQLGRH

PLDVCADIEICLKKPEGGAEMVDLTLDSERTCVYCDAATTIVELVMQESPEQIDQIREYA

DIICGMLGDDSPCHKYVNQMDVVVDHLKKGVHPRDICKTLKYCSGALLDRPFELQMMRTG

SHDIAGNEGNYKLAMLKDDDLNPPRHVESCLFCSRVATVINYSNHASSEHLAIVKFIMTS

VCAFMPLKFKCDITEKYLNDMVKMDNEGKRPHEICRSLGICGGEHYGEEGASVIAYEMKS

VVAASEWPSGNGTQCSYCQLATTVAKIAIQQYGTDVSEIRAYADLICDMLGSDNPCHVYV

KEFDYVVDGIAKGMSAKAICVELQFCPALVTQPSSSEKSAFGELLNGPMVLSSDGCSFCT

EVANVIELVVVENPSLVAQIRQIADVTCSLLPIDNKCHSFMTQFDAVVDLLKLGELPNVI

CQNLMNRVADPISTTTKIAGRDVISDQNHNVVKDTCAVCSGLVTELTVAISEQPERVKVI

RETAGLICQILPADDKCYADLKIFDSALSDIKSGKQPQAICHLLKYCASTDNSGSLLSSL

LDSAGANFLSPTKLSTCRDTTLLLESLISRHDDLAVFKNKTNSICQLIPESSKCELLMNH

QDKIIESLEKHESVDAICTRIVEYEHAAGLLEQSSMCVGCLFCEYTADLLKHTMDNEKVV

REVKVTLQTLCAVLPPSAHCDALSSKFDELLSRMREGESPSEACHSVDLCDQVLSHSSSG

EENLIIHASDHGRQSTGNVMEVQ

>contig24744 Frame-0F

MTKFAVLLCVAVATASALEDTPVSLCRDATYTSPASRGAVCAGAGGSPAGTACPMKGDVA

TADCYDYLPSWNGSACVAPEDARCTVVNGNTWGCVLKSIGCGNVPTPCPVVSLSQAPTMD

SQSSSSITTAEDALVNALPESPNTDTLMPATPVAPVLPNSAALASIPCPLTPLPDIETAA

TFAASTSDFIDPAAPALVSALPMTTLP

>contig29173 Frame-0F

MTYSLTNLFFFALSENASAPIYHLRSFCAI

>contig29779 Frame-0R

MTMYCLVRLVAVVKLFVLSWQCCDYGRNWKEQIRAG

>contig32829 Frame-2R

MRLIIFQSTIVGLCVFGVALCTAKHMSGLVKCAIQSKLLTTTNISSRLHCFSRSSQGGIW

VLSIFSLQSSSFKDRTPFRHFEPIARFIERLLHSPPPHPASKMRTPKGLISKKPSRQKTC

LLQHSMSLWPTSHPRKLQLP

>contig45953 Frame-0F

MVKIRGYSVVLGAVESALAQHPLVSTSVVLTEGDEGEDKRLIAYIVPEDWDKVPSASNLR

EFLNVKLPHYAIPSVFVQLNVLPINSASGKLDRKLMPSLEKAKKLRNESIDQSIEPKNLP

QTETEKKLALLWMDLLRLEHDNNLHRKASFFDVGGHSLLSTRLISSIRDTFGIQLTLADI

LSSPELCAIASHIDHLLLQCTNDTQSD

>contig52287 Frame-0F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY54007.1|) 2e-07

MGGSVVSSSLWLALPTATVAAVLVYLLLPDERQRAIRGLPSPA

>contig32961 Frame-0F

MVPLTQVCGLAALFAAGQVKAVPIGTDVSDTGRVLTIMDESFPGYGAFREAGATSTSIPL

EKKILPGKAHGKRMDRRLELTKTADMDKLESVFGLELELDITKL

>contig33676 Frame-0R

MSLRTLSCPYVFLLMTVVADDASRRLQTYAQPSDYASLMLERVNLERRAQRLLPLCLNQK

LQKAAQRHSNDQAANNFMDHIGSDNSSASQRITDARYEWRGIAENVAAGQIDVIEVMNAW

MNSEGHRLNILGDYTMLGVAYAYTSVGPYNHFWTQNFGLSNTEECDDGSIPSSPPTFQAP

GGSVQDSKASGPSVYIMPINPPREYRGRSSSSALTPTLLVQAVAAVLTTIVLFDLRNIT

>contig33962 Frame-2R

MRTCFLIFVAGATILLSTKASNPEDDVEDRGSAIGQVRRILRPKTINYGALEPGRSNPLY

NDPRNRPTKYLKLP

>contig59179 Frame-0R

MRLASLLLVVFSTAAICVQHCVKAKFAAVITNTEISHHHPLISPDTKRFYLKGLNDDAQD

ERIISRAVDYM

>contig23722 Frame-1R|Blast-hypothetical protein C56C10.11 - Caenorhabditis elegans(pir||T15851) 2e-13

MPSGVVAPIVLLLLLISRIHGFHEDPYKVLGITRSASDAEIKRAYRLLALKWHPDKNRSD

PMAKQQFMRIGAAYEKIINPIASTKPKQWRQQQ

>contig24749 Frame-0R

MKVWQDQRMQIHLQACTVLMVVLGAIDICRCSKFALMYAQAWSNLDMRKSKFLVAAISVS

VSRLVIA

>contig25557 Frame-2R

MNVHLLVLALVAALASTNAQTLGDSIVAGVELDPETYANAVADSVANITATNTATTSPST

STQEDNAEPDTAPIPTDNDSSNSGSDESEDATADGPQASAPASSDASRRLLGTCVTVLVV

AIATVL

>contig33679 Frame-0R

MSSLIFTCILIGAQVSLQEARRIHYTSVELR

>contig40008 Frame-2R

MYVPCRIATRLKVSTKLVTWLSVLSECCSPDIANNVIDFVSAVCVVSTTPTYLSQIVRNE

NIQLLKTLHLEHTDFPLWSLKRSLLTLTFKVQYSRFRITLSTQNASLERHENSSLFNEPS

YRFAENFSQAPSEAVYLV

>contig42086 Frame-0F

MALLSARHHGSQLLLLALIAATLVPSETLNEHKPHCADFRQYCAWNSSTSSCTFTKSMSF

VCGPRQSLEAPVSISTEFESLMDANVVSTSSFAGDSTTKELAVAGFTCHWDVAGDLHFAP

RVSVVVEGDDCLLHIGSGQMVRLGAQATLAASSLSVEASFVHLDEQAQISASYSGMFRHQ

QGLFTGTDVFGASYGGGGGQRLIANATMLTEQTTWGFFDARLQTVWNEFRGQKEAILKQS

SSGWQLASLWTTEKDDINSPAFDKALNETSSTSAYGSIVPFLLGSGSRAVIVRNNSKLIA

TVNGGGRIQIKASKDVVVMEEASIEANGGRAINGVSGGSGGSVFIAANALSVRGTIQAKG

GDAFCSADAVDRGITHCYPAGGG

>contig50427 Frame-0F

MSSSQSMNVTILLFACCVLLNKVCRVSTVVRTGSWTKHRDST

>contig52670-0 Frame-0F0

MVMTTVFAILVVVSALLLVEAQQDGCRCKRTMKGREHLHPTRNSLPILSLDETQELEQLP

K

>contig23723 Frame-2F|Blast-DnaJ and TPR domain protein [Aspergillus flavus NRRL3357]gb|EED47073.1| DnaJ and TPR domain protein [Aspergillus flavus NRRL3357](ref|XP\_002383253.1|) 1e-13

MPSGVVAPIVLLLLLISRIHGFHEDPYKVLGITRSASDAEIKRAYRLLALKWHPDKNRDD

PMAKQQFMRIGAAYETLINPIASTKPQQWRQQQ

>contig52288 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59832.1|) 7e-93

MVDATILAPLPFMLGFCTLSELQQLAQVSKAVSKICEFEWRLRTIASFGELRFTTCSWRR

CFLLRSRFQRKKAFKHVTARIYLMNNRGETRYFSIARGTPLMCSRERAVVYSHCKRMFDL

SLRINRSIQEISALIDMISVEETRELLSEHINLMTSVASLRGSLNFESELFSIFPAPVLL

DTNSLLRVTHTFEDENDAEFLQSSLMMMQVWASIDG

>contig10502 Frame-0R

MLHLGWLTIMSGIALLVSGIEEASKFKANAQEHGLMIRFTSLTADQERRLAEERSIGASL

VDKLTELVDAFQDSAIGRFVKRFRVTNKNSTNLGENAGQVVNVYEAGTVSSKPLQSEPFR

KWANSINNYL

>contig12298 Frame-0F

MSSFAFQRASKRVVLITAGAITVSGLTIVSAKEPKRLVTPITCDDGSTISPYETPTRAAQ

LQRLKREQFDVLVIGGGATGSGCALDAATRGLNTAVVEANDFAAGTSGRSTKLIHGGIRY

LETAFLKFDYLALKLVYEALEERAFFLSAAPYMNRPLPIMIPIYKWWEVPYMWVGAKAYD

IVAGSQRFVPRSYYINAEEAMFQFPMLRKEGLKGAIVYYDGQMNDTRMNVSIALTATQNG

ATIANYVEVLQLLKDEDGKVQGAHVRDTLTGDEWNIKAHAVVNATGPFTDTIRQMDDSTK

DKICVPAAGVHAVLPDHFSPHRMGLIVPKTSDGRVLFFLPWENGTLAGTTDSQSDVTMLP

SPTTNEVDFIIDEANRYLAKNVTRNDVKSAWSGIRPLVKDPRHANGSTAAISREHVVEVS

ASNLVTIAGGKWTTYRRMAQDAINKLVETVPELQTKAFPCKTKDVGIIGADRVGEVCNKK

FDKITVTLREKYNLDKDIAEHLMRNYGTRALQVAEIEKSGFLDRKPSDHPRRLHPKYPYL

EAEVVFAVRQEYALKATDVLGRRMRLAFIDSKVSTELIPRVVHMMGELLGWSKARREQEV

VECKEYLKTMHN

>contig13482 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60272.1|) 2e-95

MRFRGLLLLRLSLHVCVALLLTIHSSQLGSSLHYLQRAAANEWVRLLFYVDVVKKIAPDE

TMVETLPHFLLEVEEMIAANANDEFFAGGFAARASALPVGLLFTINETRQHLHGVVRNYI

RLADVALDSFLVYSNNTRSQLPPPLLTVRSSVNDDTSESLFSITNESVSSQWPPALRLGS

ETARQQDTRHFFDTLDAMEMKMVVGMRQKAKEKEKTGKTEMLYEWTVVMRYDLLNQGHLE

VTMNYALSYVPLLDRQRTIGERRMPPVLSDTGVVFDWLTLTTIGL

>contig47825 Frame-0F

MAIITSLLLLIPSAIAVATASIVSNAGLPTDWCRNGPAPMTKYTAYNNAFNTDVKQCSVV

TRQDGQK

>contig51996 Frame-0R|Blast-multicopper oxidase, putative [Phytophthora infestans T30-4](gb|EEY66763.1|) 9e-27

MGFKHFTAIVMALKALNVESTAADCITYDWRITSIYSEYDGVYIPSLGINDRPADKAIIE

VTLGQEVEVHVTNQIHEPTCLHWHG

>contig54797 Frame-0R

MLKKPRDICSLHRSSLLISLCTPLAYARLFCSKSLQLLILDPTCT

>contig12488 Frame-0F

MKNVFAPIAIALAAVVPTINATSYACEAGLLNYNFFDVNSQATAPNTVCSSVTENSETAI

HWTSSFNVVDPNAIHQAPSALVKTKFAPVAIDTIHEAYAKFSFETPDPKDNCTAAIMRIN

TKRSKDGSASFVHVVFLATYNVAQAVSPSMKWFTTVFVSGNHFDVYMEKVDDLTTFTYIP

SQNVMNFVGNVLDFLNCLPKDSTTFPLDLHSIEAGFEMYAGRSYFNGNLEAKIIKLA

>contig19863 Frame-1R

MKTALFTTVISAFALISAPARASPIDIRRKLILGGSVVKGHEKPYMVGLRSSETGKIFCG

GALVSSTHVLAASRCTMKDIRWASIGSHTRSGNNDGELLKVMSVMNHPNYSLNIEFSHDF

ALLELERPSSFAPVKLAAADDSDFKEGAMATAIGFGLTSEGGVMSEKLQRVNLPLLRDDE

CEKSVRIDDSMVCAGGVISADVCDGDTGGPLVLEAANGHGNDVLMGVVSWSRNNACGRGP

YYPGVYARVSRARKWIDSLATKSCFISGK

>contig28445 Frame-1F

MRIDYISLLVTATIVTNANSARLRSFPIDTNEPISGETQDLTNQENNAWHNDDERMLPIT

SADKYASAPLLPFLNKAGHEEGSVMTRISQGLKTLVKWMAQLLEPNIKGELANVNTLAQS

LNEVAGKSHPQYIYVKGLVNDLVQKEGATKVAQALLDDNQYTTVGAKEVWKMLMKDAELP

VENIEHMLRKKGYLDLADLDLLIALMEAKGDKRNEILKLVKSDAYKKAKKDAEVDHENFI

KVISHRSLPHMQ

>contig36082 Frame-1R

MWQVIYLCSLAASLAQAQTSQENETCIMSDSNLCPVDDLTPSALDSSILIYPGGATRCAF

DDFSDPNVSYTTNSTYFFQVFPASSTTKLMLYFQGGGACVDELTCAFSLQCMFETFSANA

KPLSHGVLNRSNEENSFNDYNIVHLPYCTGDLHIGNSVKSDRSSGLDALLNMPECLGRNM

TLHQNGYNNTKAVLDWAVENYPDTDEIIITGYSAGALGAQMLSALVADTWQVNENDIRYS

VLSDSYVGVLHKDEAGGKILSYYGSCDVDLKLTDSLQDQCEESSLSFIDIVTHMILYTPS

AQWLFLQSMYDQVQRYFYQLVKDGILGYPFPDLISGEDFYTKVTAIMDEYKNISDNISTF

EVNNSQHVFMTDNEYYDNVIRTPGGDSLGDYLEKWLVANSSVDDDASTSASSGGGDTNQS

AAIHLQHALLLTFIVIIAMLVQ

>contig08246 Frame-1R

MSCVLALLAHNVFVKKCLLATQFWVSSSSKDRKTH

>contig16050 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60308.1|) 5e-18

MGFCFWTIVFISWVLLFQMKWKDFGWQSLVMVVPEEDVNLGW

>contig21056 Frame-0F

MKTLVASFTIALMLLALPTSVNAHGQLIFPVPRLITQQYRAKCGALDGAGDQELQYAPVE

LLKAREQADRPSAPTFNMMNGCRGTIYEPNNTVTPLVAGSPFQVEWFIQAPHPGTMVLSI

VKPSTDSNGTITYVSVSKLLTIDPFAVSSADKTNTLATVPTNVTECETPGKCALQFYWHS

DLASQTYPTCADITVTKSTGFTAQESETIAPTPDSPAVLNATPESTSPAELSTPPSTTSP

AEGFSAVKPLDTTTSTPAMPLMVNKNCKVGRGTARARN

>contig41560 Frame-0F|Blast-signal peptidase complex subunit 3, putative [Phytophthora infestans T30-4](gb|EEY54545.1|) 9e-81

MHSIWTRANNVFFTSLMALAIMCTLTSISTFLHESNPVVRRLEMTELHSLRNYRDKTDRA

TLSFNLDADLSSVFNWNVKQLFVYVMADFESASNVRNQVVIWDTIVQTKEAASLLQFQNE

SVKYFLADQHDELRGANVTLRLEWDIMPVCGRLFIHSSDNEFAFKLPDAYHGKVVKARGH

F

>contig49739 Frame-2F

MVMPLIVFCTFCHFCQGYRLRAQTHLLRCMSALCHSCQDYRLRAQTHLVTLHERFMPFLS

RLPPQGTNASIKFLINIF

>contig06191 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53087.1|) 1e-149

MVFMSIRNYLSRELLAACFFVMLLSSTLDQYPGEVDPLPYNCDYELHTREQEARYNKTQQ

LIRNTKLFEPPQIERLFLDQALGAEDMAVSQDGIAYVGLTDGRIASFDAAANRLGNFSRT

GRHVPGCGASDMEGICGRPLGLIFASATPFSTFMNRIPSSKPFPGDQVLLIADAYKGVFL

FDANGKRTLLFSRTKEEKLNYFNGIAVVHATGEVYVSASSQRFQRNQTVLDFLERNPTGS

LVHFDPRTKQVRIVAKNLGYPNGLTLDQKRLGLLVALSFQSKIVRFDFLTKQMTDFAFLP

GDPDNISIEKIGLGTKEKEVLMVAMVSHNDGSIIHQMRESVKVRKLLSLLPTWVTMSLVH

KVGFFASVDLDTGDINFVYEASQGQTPMVSGVRRFGDHIYLLSWARSYLTRIPAALLQ

>contig08247 Frame-0F

MFQRFSLRLAVVFLIIGCGSALEAIDTNSETFGTQHSTDMNQPSAAISSNTRSLRLLKAN

AVGLKGLKGIIHSILTQKKNLSKFEVEELRTSTLGATQKKYGG

>contig13117 Frame-2R

MRVFRILTAASFAAVASASCDPSKWQPPYDGNYKTSSRVAPDKLNVHLIAHSHDDPGWLI

SVDQYYVQRVQYILDTAVEELLRNPDRQFMFVEQSFFQRWWHEQGFEVRSMVKQLVKEGR

LDLTVNGGWCMHDEATPHYIAMIDQTAYGHQLLMDEFGISPRIGWQIDPFGHSATQGSLL

SQGVGFDALYFARIDYQDYANRKKNKELEFIWRPSKSRGKASQVFTGEIIDHYCPPSKFD

FGENANEIQDDAALHDYDVCDEVEDFVKNAKMRGDASKGNHVFIPMGCDFQYDNSRHWFK

NMDKIIHYVNQDGRINVLYSNLSYYTDLKRKEGLTWSIKTDDFLPYGSARNDYWSGFFTS

RPTLKRFARVSNTLLQQVRQLNAVYQSHHSAQLVALQRAVALVQHHDGLSGTEKQSVTND

YVLRLYDGIVKAEKELNEVLFVIGEKESYHFCIMTNTSVCDVSTQNKNFEVLVHNALAHT

SIQTLTVPIMHNSAAVTVLSDDAKVRDQNVYVAIPVHPETLVAPYSLVFSAELKPLSSYR

FLVKQEDLNDEQVSAETHAFNDNVVVLENSLIRAEINKTTGLIVNLANKKKNIQIPLSLD

VAYYQAYQGDGAKSGAYVFRPDGNKTYPITDNKHDGGARDTAGVTMVNLQTSAGARTSVP

RVAFKISSWVTLEYRVNDDDEFLEIEWTVGPIPIDDNKGKEVILRFDSLNSIASDATLYT

DSNGLEFMKRVRNHRDTWNLTLHDNEEMVAANYFPITTGAYIKDAKHQLNVVTDRAQGAA

SLVDGQVEVMVHRRLLADDSKGVSENLNETESVYDFASKQHVTKGLSVRGSFFINVDSAE

DGMRSIRSKMESQFFRPLSIYRKSVPSEVEAKVPWLLVGEFPENVGLTTLSELTKQCLMV

RLTHLYALDEHLTLSKPVTVDFSTLFTVRKMVVSVVTELVLTGTKEMVAEDKGFDMQWQT

IDDANNLSTRSLPVKGTSVTLQAIEVRAFRVCFAKATENQAVVDGRKVESWDEADNSLST

ALQGLAEIIAIE

>contig24021 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57770.1|) 3e-23

MSRWAALEAVAFLLALFVPAFGTSTAETVAQRIANDDDIELSKVFGGHSGYAFSDMANIR

LEQTLSAITIRGAKRIDAISINIKTPVEKTWSHGGHGGTENTLALEKDEYIVSMVIHWGR

KHSRKSIFYLKFTT

>contig31953 Frame-2F

MRRILLLSLALTFKLVRTQEHRFPKLHGPQSPHLPQHRHTTTITTPCLSSPYRTQQVI

>contig40104 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56945.1|) 2e-70

MDVWALGIVLYVILCGTHPFDPTNEATDFELQERIRKGTFDCQSPRWKCLSPLARDLIQR

MLTVDPVQRISASQVLQHEWLTSL

>contig47181 Frame-1F

MLLLRQAHRDLLKCLPLLVFFCVPIVGNAAPLLGYQFPKQLLPWQFWRPDQRTQFLQENV

EARSKTYPTLMKLLQQIKHKDDTLQEMLAIANKSGSDGLRPTQVVELVPFFEGPAALSAL

SSEHIHVLAEGSALFPSFALLNRLLLKTQLEKRLSRRMEALSVDDQQLLTGGVDDLSLSE

LEFACHERGIVTQYG

>contig54790-1 Frame-1R1

MSFNAFGLAYVLSLSSVASSTSSIPQRERRVRLLRASSTSTSYARFIDVMPILSILL

>contig21928 Frame-0F

MRSTKCYFAVTIVLFYVALLARSSFVHIKLHSSYVRHRSEQLQILEMAKIIDWTGRGLNS

WSQVERNLTSAVDNLNVSDNALGEIVFTQTFENLQTLACSNASISQIKLNGTFLKKLSAS

RNRLASFRDTVLVASIKEL

>contig29007 Frame-0F

MKQKRYHEFIIGQLCLLLCSSYRADDGKVNLIDSHYACLDEKTTFRLILRGNGHLYKVEG

KIKADEANIEAEDRRTWKCRSVFPHPANDVLLHLTMTGGLSYRPFKQPLREVLSSVLTTT

M

>contig29771 Frame-0F

MGNIIRNSAILIWLELAWSHNVDPYQVLLLELITSRDAHYVDIAKIAAAPYEGEGIRAVA

LNLEMALAHHWYKEDLKDEAVFAILGLDKLTETDVIKSPFCETWFYYYYLKNFYSSVGNI

KMLKSYFKDDIFVLILFASVKRNDDLENAVYPLMEEALISKNIDPVQLFRIFCLDEARGQ

LFENLFFKFWAKYVKSVYPDVNPAKIMVNIMVNAGYSINTLEEIIGRVIHASSRELESSV

PLLRNAEFAPDLWAVVLEAKQKQ

>contig17757-1 Frame-0R1

MTIGRCHSREVWAHQTAVLLLVLVTFELDSFPTFYQPG

>contig15305 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56132.1|) 4e-91

MALHRSFQTARRFPLQSFLRSMHVLIHLQVSAASYSVPSTSTRVVPNVTDNAIHTLFERA

IAQRHPTQALQCLAQLHTSPGAPLLQKLAILLARQKKTSRHDVLRAFEILRGVYRLPCLK

PDDYTKLASIYVLDACVRHSMLDHAMELYDEALNQAVVLDLPAYDGLLKALVKQKRMEEA

MDVLRALVRGEDLCPMETTFVPVLIKLIETREYDEAINVLQQGQTRGVVFTSTTFHPLLT

LAEEDTVSTDSLIKFLSFIEDAWEECKDFDVEEYEDDLND

>contig17422 Frame-0R

MTWMLLSVAFCASVCHSPGPVDPLKPLFPEMPS

>contig20415 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63977.1|) 4e-57

MKNSTKALFRMQRWLFVFSASRLIGIAASRATFVLWPQHINATLSLSISPDNSPFVEASH

GGVLSTFDTKFDTKSKVALDPLIDAIEIKWKPATDVHSSTFNRFLASSSRFDGINAVGIH

LHVDLRKGVRWIEMNTTFHKRIEENVRKVLDNIVPSVQILPNFLKDFLAKSFCNHATWKS

SNSPERIFHEDASKSQTLCYSSSFPFWPENDNSSFFHNLFQKSNANTGIVKHSITERALL

EAHRNLRTCRQEPIIAALKLSRRETSPATLEATFFGSYIVRFCRSGAADRTAVQVRRSTS

DNFFVTPIISKHNIYELEYAWLQRKGKAVSVESVLTTPIEVQVTQPVAAALMHAAIIGEG

FHRRYVIDVKVLKHEGCGKATRNNTILLRVPISNTAYIDLDELRRMERFNELKLVSFTKH

IEIERPSPVSAQHVIVLEFP

>contig20460 Frame-0R

MPPRVALVLSLFCAVVTCGLADYGPKDSVTILTDKNFKKEVLQSPDYWLVEFYAPWCGHC

KTLEPEYKAAAKKLKKHARLGVVDATKHQQLAQKYQIKGFPTIKEFGATKKRPQDYRGGR

TTSEIVQYVMNSPEAKKLGVSSASVVTLEIEKAHAFFNQKLPSAVFFGSPKKGKKSAKVP

SWLSEVAESFSEGKKKRKQPKVQLAFVPGSDTKMLSHFELTEDQLPTVMYVYPSSQKYVV

SDVSKLDKAAATKFIGDALANTEVAEKDEMLPIVSSFPSPGVATKKPIVALKALDATLVR

NCVAKRGKMCVVVAKADIKLVRALAKKYRRDPFLFLSSKVDDPTYHSLSNFLGVKTAEVI

VVKPGRKVKYSALTDASDERAISEFLDKLIDGSNPLSLPSGDLTILEAALSGSPDDATNH

EEL

>contig34047 Frame-1F

MGGKSTLLRQTCILTLMAQIGSFVPASRCRLSPVDRIFTRIGASDRILAGQSTLFVELAE

TATILNHATSHSLVILDELGRGTSTFDGTAIAYSVVEYLLSEVQCRTMFATHYHSLVEEY

ADNDNVSLGHMGCIVDSENERKVTFLYKLEEGMCPKSYGINVAMLAKLPNEVIECAAKKS

EQFERSLKANTELESVRLAQKVRELLAEGDADIEKLRQLWEYARSITLYARN

>contig42745 Frame-0F

MEKHQLLTLCRVKYLSLRVLRLASSSCVLAAGPVIQASNASPAAS

>contig41935 Frame-0F

MNLIRAMFVAALVACTRNGVHAKASEADLVTLLTTNSEIVTSQRLLRTSAEPDDNDERAI

NIPFITNYNQRTRIKAPLKELK

>contig38224 Frame-0R

MAILQILAILLFGNSNLPRNNKEAICFPIFTRPREAMGTPFPKEAILPCRAIVQPISELS

SHEATLDVRPTSPTPRRDNKLPSWMQTS

>contig38703 Frame-0R

MLGHARRRRSTLLKHLFSSAAIADAVLTREFIYASLYAKEAGYFTTQHREVLHTPAQGID

FGNLWGAGEYRSVLAQLYKESPEAWLTPVEIFAPHYSHALARYMLNSPFLRQELVIFEIG

GGSGSNALHILNYLKEHMPDVYARTKYTLIEISPVMAKRQHKCVTTVHPHQCTVINQDIL

TFADTHAPVSSHCFFLALEVLDNLPHDKVTIKNGKWFETVVKMQSDVGIPVLEEAIRPLN

DMLIRQTLHYFGCELPLHVSYKNKSGLAQRVRHMLGKESPALTSAFIPTGAMQLLNTLRS

AFPQHHLIAADFDSLPAPNLNELSDVKAIKHPLSPTATSAGALFAGNAPLVASKVTG

>contig39340 Frame-0F

MLSKTLVLLGLCVDLQMVNARGIAMGMGPRRRLGSYKNIDHHPYKNDHGYKMDSNDKGYD

YPYYRRRLEEKDIKSTESSDYGYGKDDYDHKGYKHD

>contig56783 Frame-0F

MHYLLLLSLHWLSSLQDAHVGF

>contig15640 Frame-2R

MLHLCCCLFVACGKYYPPLRLFNGHLQTLFFAFDESGPL

>contig38296 Frame-2F

MSLSRTPRYRTPRMLCAVFFILVAVCAKSSYGHNVSVSSRDSQHIALKSDEHATIPKDVE

AMRRLRVAMTTDVVMHGGIVGKLKELLPNNDISNPFSKTRPSKTVTNSYGFNDVVMLDRT

>contig40394 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58240.1|) 6e-86

MSFTGLRFFLSLKLTVSVVQLNVPTSERCEPTRRKRVAYKHIYEDKTFSIGIFILPPGVA

IPLHDHPGMSVISRMLYGSLHFKSYDLVKDNAIYSGSKQPARLCVEKIITAPYTMEVLPE

SGNLHELIGGDDIGCAFLDIITPPYDVEEGRNCTYFRVVDSISSQHTENEKLWLLEKHEP

QDFVVVTETYCGPHISSTLN

>contig49850 Frame-1R|Blast-glycine dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY63500.1|) 1e-40

MRLQRILSIRRGTLLRAATARAMATSSGYAPSDGFLQRHLGVSSAKDITAMLSTVGFDTI

EDLVSATVPAEIRLTEPLNLPPPLSESAALAKLKTLATKNQTLKSFIGMGFHDTITPA

>contig19313 Frame-0R

MNADMVVLLALSGLLFVGALTILLFFCRVQRDRESLVFIQETVDVYREELNDSFNEQALW

RCGVCKFLNHPERKLCDLCQTLRGAGRVVTDSKKHTSSTGPSSHSKNNGNSALVRRMSAI

GESETFSSGQVDNAIGGSLERPSGDFMKLLTG

>contig38222 Frame-0R

MAILQILAILLFGNSNLPRSNKEVICLPIFTRPTEAMGTPFPKEAILPSRAIVQPLSELP

SHEGTLDVRPTSPTPRRDNKLPSWMQTS

>contig42735 Frame-0F

MNFIAALVFAASTCAYVNATFTVASSTTEARISSLNHVSHARQWTINAATARDSLNSIDL

DLAGRVYVSYASSLPRGVLGYVHVLGDSKSVVNAVTVSNGDADDDDDDDENEGDLHVVMS

TSAEATRGYLLTEIVVASSGIVSKLKSTRSAQVVVQDGVLLTSSATEEVQIKASGSSAVY

VAAPSATVSVRVFQLEAKGHWKATDYCRESNSDGQSATRSREYGQDFDPFVVGRDGLP

>contig50390 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68374.1|) 1e-115

MLLMPMARVLVVLVATNAIFSQLPCATVDATGDASMPRSFSAMTSNGQSFNRSKSSFESV

KDDDIVVGTIRIDNEDAETHRNVDGSKKLWESSHNNVGAHSSGHSGTLALVNAALKLGSV

LNATSTIEQTYVNWLGNPYGSIYSSRACWRKAHIAKMCPLGYNSKLGMCWTQCPYSYPLE

CGLECIRQNDDCGTAVFYKVAVVVQTAISLSAWSIYGDMEKWDKGVKVAIKCIKYMISII

KSLVRYIRYIKVYNPEATKDKILSILYQIDNVIIDLPVTVAYCIGKRASDDIKFVDTVLT

TAEYLLYDIISNGDFIISTWKEFMRFMKKLALGDSAASLTGEEIKALKSALKSNTTCGYD

LKRLLDRTWMTVAELRLLHPEMSEDEIRVTVSQSNLMLNDIPI

>contig09795 Frame-0F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 1e-107

MKVYVLPLVALASLAINASATSVANECSGPGAPPHPPIMEDPASSPESCSGEHARTTPPA

GAIVVDITGKYEGSVKTLTEAIANIPDTTEVTTVFVFPGVYEEQVVVEKIKSPLVIQGYT

CDTMKYSANQVTVTQAKAQAHVPAEITDNRNFLTSTMGFKSQSGVKVYNLNVANTAGKIE

KDGQAVAVYVDNTDYGFYACNFTGFQDTVCANKGRELFVKSYIRGAVDFVFGQRAMAWFE

SCDIEAISKGYITGNGNQNETVVSEFVFNKARVFGSKSKSTMLGRPWREYARVVFQECEL

SDVVDPKGWSAWDDKM

>contig17859 Frame-0R

MRFAFVWLVVMIAASVAASDTTDSTRKALATKEIATSVVAKPSAHQRRRLGWSSHVSEWA

SKMGEKPFIQKSKALYRKFRPAKLKKTTTQRPDVPLYAQSGTIPIPKKSSVSEPGMFTAT

KLDDPPVLPLASIPVVEPIKPPVSMSASVPDVKPIEPPRSKHKVRFDLSDKNPEENAVRT

PMKRPVSALTPV

>contig38197 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63726.1|) 2e-44

MMTSALAWQILPLMMGLYAKVSAQRVPRRLPGFTLGKGSADAGVQLESFVDLLCPDSKSA

YPGLKKIVEHYEADEFRVRFVLFPLPYHQHAYTTAEAAFAITTSLGDKTFTTWLETIYAN

QA

>contig51585 Frame-0F

MIVVGVLLALAIVLISAAHVPIYEEHSTSASLVPVNISKASALPSQVHVALAGEVEVRSY

LTTEASNRMPSEIRLGMTISWATGLKTATSLVRYGVSKDNLSTSQQTEGSCEQYNFCYYT

SPWLHHVTISGDKLTPNTNYYYQCGDEDGGWSAVYSFKTAVPVGTESSQTFGIVGDLGQT

QYSMQTIHHLQGYHSNMSAIICAGDLSYADSEQYRWDRWGELIEPLIARMPWMVAAGNHE

MEVPCQLGVSEFVAYQTRFRMPYVESEKLQIRNLYYGFRVGLVHFIVLTPYVDSIRTSLQ

YKWVQQEFLRVDRTLTPWLVVIMHGPWYNSNTAHQDIEPHLIMKENMEDVLYRHKVDVVV

AGHVHAYERSHPVYKEQIVQNGPIYVVLGDAGNREGLAPMYYDPQPAWSAFRQADYGYSL

LNVINRTHAVMQWFEDQEEGDAVLHDTVVLTTSEYRSS

>contig34493 Frame-2F|Blast-beta-secretase, putative [Phytophthora infestans T30-4](gb|EEY54529.1|) 1e-125

MRYPVSTLVAMTTALQSLPTTMAVLQQKLYGLPSGLAYYVEINIGSPVYSSSSSPSSINS

FNLLVDTGSANTAVVTAQCCALTNEKVFSCQASSTCVDEGASISVRYISSSWTGEKVRDT

FSGQGLGLIESMPFAQILVEDNFVTVGYDGIIGLGYESIASPSDETSMPYFDVVSTRNGL

NDVFSMQMCGTLQALSLRNVSTEDTSFLYAGELLLGGTEGPNGQTYHQGDIVFTPLVHER

FYNVIVTDIGANGQSLGIDCESINSPRAIVDSGSSNVAFPSSVYTAVIAELRAQVAQVAS

MDDSFFSDDSTCCSNECDPGNLNSFLYRLPGLTISLALENNESQQMTFTIP

>contig39098 Frame-1R

MRQMVALLLVTLTSFIAESVQLTIVCTSSADCLNGDTCVAGDSAIPIQTCVAGAVCGGTS

SGNCPSDTTSGQLACIQRNSIYQCVSIERCDQYFGGASCSGGCSASGVACSGQGTCNLVS

TDANGRPGFSCSCNEGFSGDKCEDVSRTDFDSSTTSRTTSNAMDSSFDAASQDFSLLTSS

SQARSTSTTSNVADPGSVANSEVDLTDSVSSRSGSPSGSSFV

>contig50009 Frame-2F

MIVHPAVRRLLGLWLIECSDRARGSVSDFCMHWLACVQRPESDGLHVEAEWTLLSQAVNA

FVCAGYALDAMPLLLVLPIKRELMPRFFELLKKLALDSKHASMLQLHAELVIAWQESHRK

>contig54904 Frame-2R

MGRLRDDSKAITAYWWVCFSARTFACITMHVHDASLIACHNWLAGRSWNHTNFKYNLRWY

NRYEPKMTSEYRHQFIPQHRDLKFLMIHIVPFCT

>contig18840 Frame-2R

MPVPFKLITAVAIAFLLIGSSASPPMAKTSLAVTTNQGRHYESKEVDGRPLRGAERALSL

NQEERGRFSLLNKFRKLFKRKPKKKLTRTE

>contig51098 Frame-2F

MRRNACVLCLRVILNIVMLAIDLRSELLDNQITITDACAYMSCCMRNRRYVARRSASSEW

LNSYAAI

>contig56033 Frame-2F|Blast-mitochondrial 2-oxoglutarate/malate carrier protein, putative [Phytophthora infestans T30-4](gb|EEY67662.1|) 4e-35

MHDGVQTHILASMVAGLVATTACAPADVVRTRLMHMRDHEYTSATDCFVKIIKYEGLRGL

YKGWVPAYMRLGPQTLLT

>contig59403 Frame-2F

MIYFFKMVLFLYLLRDPVFASVTKPAVEK

>contig23333 Frame-2R

MRVHVVLLYLTLYGVITTLALHASDELSPNSLSNRFLRVDSTVHEIASFKGPSDRSTEAR

STTPFRTFYQNTLYGFAKSLHLKPKWTLSLSYLLREHDETNMVRRFTEYLTHHHQFSFKV

KEKLIKKLVNKLRHHHELTNLKAILLKLQDEPKSSAAAALLLQRIHHIEK

>contig37243 Frame-2R

MEQRALMQLAILASMATVTAFVALTLYLKRTAADTKRPRVPSSASKPPQKTLVCQSADSN

IVIAASLVEHDATLATEKYKSGDFSGAVKLYSVAISKCEKQQPLDIRNLKVMYSNRAAAY

EKLQDHENVVEDCTKALLLEKRHLKSYLRRAKARACSGDLRGSLVDYVCLLVISEENQEQ

VDENLVQEISRIHSTITAKEIEDARQNKQNPIRYLPDQFFVTSYFSSFHPSDDENDFLAE

KPSEEYTSELEALDTNESTRYQRGLLLTKRGLALKKVKNYDLAAKDLDAACKLVDPENEA

YYTAQIENGTFYHLRGEFDVARNAFEKALAVKPYSIFAKIRMGGLCFDQKNLTKALEWFD

EALSEKPECSTAYFHRGQLHSIDLLPDESSNELSMATALSDLEKCISIAPDFSMAYIQLG

VSHARNGNFQGAVEYLMTAARITPEVPEIYNYIGETYMQMLQAPGSPVDLNSVEEMFLKA

IELDPTYPMGYINQGNMLVQKGTEYGHQALMLFEKAVEMCPRSKFAYCHLAQVYMAMQDY

SRAIEQIDKAVAFAFSKDELNELFAIRVTAETHQKASGLLQ

>contig46188 Frame-1F

MWRLLYAMFITAFGICLICLVVLGHIVQDNSIANNGIKGLESTSQGLLA

>contig53090 Frame-2F|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58600.1|) 6e-46

MIALIFLAAIVAGTYADKYFTGDGTAYTLGQTSAGNCNMMSALNFATTEYAALNNEQWDG

LQNCGRCAQVSCDDDRCDDTSKTIVVQILDRCPECKYGDLDLSPSVFTAL

>contig57326 Frame-1F|Blast-putative elicitin protein SOJ5 [Phytophthora sojae](gb|ABB56000.1|) 2e-18

MNSNIAFIAAALAFVASVNGDGQKCSFMEETMALARMAPLYNNEDLKQCSQKSGFSMMDS

KTMPTPEQKAAMCATNECHAFIGAVGGMNPPHCILKIPGGGLEVDVSQMCGTFEKDCA

>contig01010 Frame-0F

MKLHLSFVLAAFGFVLNGGANALNVVMPGSNYDPYLSDSPGAIDVCKSAADVDADLRALQ

PYVVTIRTVMNMKCDTKFILQSAKALNVSVYLVLALTTVSPTFEEGKMKLQELMSSEFFS

IVSGISVGNNAIHEKILDMSTAFQNLETIRKMLREQNRTLPVTMTEDPETYDNSNLAAMV

DTISVSVSPFLDGVGVNQAVSDILRRLQSVRASGQRLNKPVVLVQIGWASGGGEESQNLQ

ATPEAQAAFLSNLHQVCSALKIPYSYYTAFDRRIQGVPEVQHHFGLFQEDRTLKSSIQNL

VIPMRTSLHIKNERSNLYLYEFLDGLYMKSVSTDPLETVRSNWYYDTTTQLVRSVGSDKC

LALYQYVSGGYPTMATCSPMDGNLKWIYDSNTRLLQHASQNLCLNTDMAMGYSLTVYACA

PGNPKQEWIIENI

>contig13592 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65535.1|) 7e-10

MAGNRHSALWNLALQLLVGLLVMPYLYKNEAV

>contig55091 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68982.1|) 3e-13

MTLESHVFAAALGALIPSLLLILQMEKLWAQELPPQCSGVLDSIF

>contig06779 Frame-1F

MRWGLKPLLLRNAVSLLATSRLGSRSSARRESTSRFFRRDGLVSYHVSWTRYNY

>contig23464 Frame-2F

MRLTCFVLTTSTLTFVAAAVPCSEQSLHQGATMLLNAHTDAELGGVGAGKRGDVGFQYLK

PAEALLAAQALAHDDFDLAAAQVFRILEYQKPDGLLPHLVYGPSVSSELRWIPSNRTFFP

GPAFWQQSSIEQRRKVHSASEFETSTISAPPVAADVVWEIFQLAPYDSMVGGKATAVQFL

CHVYEPLRKLQKHLFSTRNGTAPDSLLLTRHPWETFSSLSPHWIAFLADLKTAPDYDTIV

SSIPEEASARFAEGASAIYSAKDAVRNLYEPMIYLASQARHDEALFESISSAKSGIEAAP

FGVKDVEFNALVLRSSRGLENIGRVLIEHSFACKKFALTPKEVLNDIKESHVLIQKLEGA

LIGNNNTQGLWNTSADFFADSSRVSWTSLHSLREFLPAYAVELDSIKKCV

>contig43224 Frame-2R

MSRIPLLLSNLFLRASSDYIICSNSLQTLLNVSLPARSCHTQY

>contig45657 Frame-2R

MNLLMGLRRFLGLGLLSAVLRFFTGVSSSSSSSSSGMSSSDASSSSERLRSSSSSLDDIV

ASRFRPLQCAPSNVNINSQLMD

>contig12618 Frame-1R

MKSTWLALVLMLLEAHALAKETLNAFNEPTSDLSLLLKHRNECALLGFDVEALDCRLCDT

LASFLAPVAAKAQTNGAKAVQKVTQECHECCSDLSKVFEAEGRRFYKAVLAVNQYRLKRY

PKVANFLEHQAKQIKRLEVEEANLRLPMLLFYDKVGEKVEEISVAHWDENSILEFIERKL

LPDDEAEEAVVEVEVDATNL

>contig16683 Frame-2F

MLRLIYLTTAIVLLLIQGACAQTRFLGALCGGNGPTNFYTDEGDYKKLTGVMFRSGKRID

RVGLFYDGSKEPKAFGGTGGVWRQLKFENGEYVKSLHLHSILYKGGYRISYIKFITNKER

VLEGGIKTDNITISTPEKNYRLAGLSGTHGNEVNSLQAVWYIR

>contig18317 Frame-1R|Blast-mitochondrial inner membrane protease subunit 1, putative [Phytophthora infestans T30-4](gb|EEY53724.1|) 2e-59

MRAALRETSTVIAWLARFGGVSFCLTQLVDTIKCSGPSMLPTLNQNGDILLLDKFSPKLW

KLQPGEVVIAKSVSDPRRTVCKRIIADEGETVCVRTRLSSSEVEFHKIPKGHVWLEGDNK

HDSHDSRYYGPVPRALLEGRVLMRVSY

>contig41939 Frame-0F

MRLALFSTVFFGTLLASTKASQERFPCRPACAKGETCKLQKVLCVTTPCYPIATCVPNET

IKPACTKICSKNELCQIDSATSAQYCLNPCAFTLCGANTTCEIEQVQCIRAPCPSTVVCK

PIETDPSLC

>contig48006 Frame-0R

MRTTFFLTVVIAMFCACITAIETLEGPTTTGREPNIADATPTVVARALRGAVAFNEDRLD

LEGLTNSVATLFDGALHEINPELVRTAKALTP

>contig49434 Frame-0F|Blast-apoptosis-inducing factor 1, putative [Phytophthora infestans T30-4](gb|EEY59276.1|) 1e-13

MFMMWRSWIRSPFPAAALAAGISTLSLSSSNDPVPSPSDVPLEGPDALSPPGPPSAGGEK

LHLARRFTRRK

>contig52791 Frame-2R

MRQFSTLLTLLLSASPASARLVHYEWDITRLTNTALFDGVLGKFGYG

>contig16949 Frame-2R

MRVGDYLVVVFIAWIATCFSFSSANNVAQVSEQGEGKQLLKGSGLSITIKTGVNSEERRL

GGVYKSTASKLASIVKFSWNRILSPVLESASHLF

>contig42247 Frame-1R

MAKLLIIATAVLAFSLALGEALDRDKLHEVMASVHGNHNYTVHYDDVEENRQELKCYGNL

TREINPVCGSNGKRYTNLSMFNFRKCMMKVQEDEEIQVTDMEFCKDAELEDMAPNMKYIS

>contig56035 Frame-2F

MHLKYFVAILAVNLRAVSALDLIEQGLIDPSRRWPEPFRSFPANQLVDESHGALRTSRDL

AQDDDNETRMISLTSMRAPITKSVANAQKGPMRNAVFDIVAERISQLEHSLANKDTVVAK

NAEKFFDKSTAETNPVAETSTAAKARSSVAETSDAAHVKPVGFSHDKPSGIEYRGDDEVA

LFFAINYELGPISTDENICFYADYNIYYNLKSKTEDVIFDRALFDKIDPAYLYQQFRRFA

SIDENNQLIWKEYITPEALGENAHAAFTKALKNVKRDNWEHHFDSIVRVLRFLKLIEENQ

GTADPYVEHAMDILSSWSINIDNLDDTVESLIGLKTLRPEIHRILEDKRLKIKKNMEIEN

NMKAKKAKKKEAKKTKKVADANQKKKGN

>contig04479 Frame-1F

MLGLIYSTTVTVLLLVQCSNAAVIRDTPFGGAGSKCQKAKDPSRTVTGLMVCAGKRVDKI

GVYYQGVNEPETLGGPGGECHNYMLGKDEYFNSYDAYAGLRNGKWRIFYVQFNTNKGNQL

VGGTKTTKKAYTTPYKYKLAGIEGCYGDEVDKINGVWNPI

>contig09322 Frame-1R

MTKYTLATSTLLIAFAVIVSAHDGEDHSQATDDDVSTECESNVSTSFIDTIDNSSYFNTC

VEGTTFNVTSVFDALNFTEPEFLTFCNSSTCLEPIHRLMGSVDCLITYMGEPRDLSDEIS

KLHDECHEVLDAANLTMNMDGESTAGGATNNTGSTTPEDGTASNPATLIITLGSVISATV

IAA

>contig31286 Frame-2F|Blast-Annexin (Annexin) Family [Phytophthora infestans T30-4](gb|EEY59586.1|) 2e-32

MNCLACVTILIVCTVRLALQPDVAIAILFERTMRGLGTDEKGLSAAVIRYHGMQPHVELL

YENLYGRSLEERIRTETDANYGDLLVSLLHIPIDMCDALKTIAIVEKL

>contig52209 Frame-1R

MALLAVLLLASIVATPCTAISAADSISSAVVNVKNSEAAFYVSSAAAEGWGESLEAQKLK

DGASHAYYPLVYNVTGLVNGFGCTSKEMLLKESSNGSLAASNLSSASLLG

>contig57097 Frame-2R

MRPSSAIRLIGVALLIVNYSSSLATQDTHSATVATVASSDPVESIELVSTTTRSVRSLQT

EDDDPSNESGLTEEARGILATLTDSLGKKLNLHNGAVPTTSRVSKDLTSKPEELLPSIAK

KAL

>contig09323 Frame-0R

MATYTLATLTLFVAFAVIVTAHEGEDHSETTIDLSNECASNVSTSFIDTIDNSSYFSTCV

EGTTFNVTSVFDVLNFTEPEFLTFCNSSTCLEPIHRLMGSVDCFITYLGAPRNLSDEISK

LHDECHEVLDAANLTMNMDGDSDAMDNSDSTPPGANASNSPTLLITLGSIMSATVIAAFL

V

>contig11757 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58463.1|) 4e-65

MVLFAVIAGAAALASASLAAPIFPEPKPLPYDGSFNDLTVANIADKYHTFTFNMRNKKEN

AKVEKYVKIDQKARVPAYNNDTGVAYIAVDDTSIFKNQTNFRRSELSQFIKTNPKGKTFI

RASFMKEDEFLNPRQWQMFQAESLIFQIGVDASVEPPQVIYYNNHEWVPKWQTDFKTKTW

YNFGVAISKDPKGDNHGWSCTPAWETTNSN

>contig24850 Frame-1F|Blast-polysaccharide lyase, putative [Phytophthora infestans T30-4](gb|EEY62246.1|) 3e-90

MLQAFKAIASLVVASTTVAGLPVPDGTWPKSTGLVSFDEPYVVKSGETYDGKMQTFDRSN

IKCEGQKESGAETSVFKLEPGATLRNCIIGKNQMEGVHCFEHDCIVENVWWDDVCEDAFT

IKGGKASSVTKILGGGARYADDKVFQHNSVGTVVIDGFFAQDFGKLYRSCGTCSTNPAQR

FLKLSNVYADLTIIKAKRVDPNVSIVMMNENYKDEA

>contig44287 Frame-1F

MASLMSRCRSFWLASLAILACYLSFSKVYSEKNFIKVPLYKHQESAQLSDRLARQQIRAQ

RRALEESAATFDNVSVGVLALSESHLGVGFGTHYAELYLGIPAQRASVIVDTGSFFTALP

CSTCVNCGSHTDGFFNISKSMTAKYVACKDFQYCTSCENNRCILS

>contig48496 Frame-0R

MLAACLFTIFRQISSSKCAIEAFYCLHIAYTSTAKDLTTLKAATYCMSVTDILPTFLSTA

SDQAAI

>contig52374 Frame-2F

MKTPTIAMMAAMLLVGASADVMTNTSLTSESTAATNASTTPGCFEVSVENDATYCIQGPI

CSGPALRPAGSLCPVRGDVATADCFGNLPSYSAQGICALPMDALCHIGKTGAWSCVIPTS

GNFSNENTSAADGMMNATMTSNTTATITNTTVSTDTTKILGCTEVSVENDATYCIQGPVC

SGTAANPAGSLCPVRG

>contig52424 Frame-1F

MPECFNIALLHWAAYHVVLAPSILTLTDVLRRKWQIFTDTTRLARSLS

>contig54978 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54011.1|) 1e-31

MWPPAAKLSHLRGTLVLLEVVAMMCSVMHNTDPDANSSTVRTWMAERAQFCL

>contig55380 Frame-0R

MTSRSISMRLAPLIELIASVERAFAAVTKRQINDAFLALQR

>contig46530 Frame-2R

MIRMRVRWHYLLQYLLQEYTHALAAFCVIFSTFAHGDAHRGVPVDNYRVSSVRDVKSLKW

HV

>contig48068 Frame-1R

MRAIVFVTAAIVLISACDDVWASEAVARMEERSVYPLSLFDQLKFLLCGLPPVKMFKDNA

ASALLPLKSSVFADIHLTWWERIEALFLPDYLKRFFMSYASLDWYFASWYDCLSADEITN

QLKEKYPGKARFIDKIVKA

>contig52302 Frame-1F

MWRPFGLLYVFQVVSLSVTFEAISNVKAADVSILSSTSSSSSNANGGWHMKAVTSIQARV

QGDAPIWNDKARMWLSQYGDTIEAAYRNNLDTV

>contig43288 Frame-1F

MAFVAAAVAFVAVVVAAVALVYVRQKLVGEKTKVVEDTIENASQEEDEGSDQDAKLDGPS

IAPPTPTVVAERMAKTPIAAMKATVAGTIIGAERSFENNSGMEPFSEV

>contig14621 Frame-1R

MSVKCKLATRLNRLNLLVSLVLLACSKIATVAVAYSVEANRRFRALPSFEATTRSQRNEE

RAAVKTLSKFIRFKKSAAQKLFEEEALLSYLGKLKHKMMFAKVENDLLRDQKWWIEAEGV

ALNELMRDAKTFDVNSRNFQHLAFVVNHIASKMPRIDIRKIFLRYVENLGEAKAATIFLK

GEVTLPKYAFERGVLESLLTKNEVSPADAFRFLAPRDLTDVQFTVERLELWTTHCDPLLG

ENRYNVLAKLLLDRYDETKLVSTLNISKRQSATIDSVLSAVELGRAANAK

>contig17053 Frame-0F|Blast-peptidase family U48, putative [Phytophthora infestans T30-4](gb|EEY66429.1|) 5e-57

MPLLMTSALFLGSLLANALRLLHVSRQFHSNGFWFAIKNSALYYSITHERLPSLRTYVMG

PLTEEFVFRSCMVPLLVCADFTVKQIVLGGPLIFG

>contig21319 Frame-2F

MRLAAALSALLLHAVPTAAQESTQDVYITPSLSASNNVTGLPGGNEICGSTRVRKPWASL

TAQEQALYLEATEMAIADGGVSAFADIAADSLSQAQGQYSCAFLSWHRRLLIAYEAYLRD

LDTRFACLTLPYYDVHTAYVRTINGECTNIWECSDIFLALGGAGNVSAQVSVLADDSVNA

TGVALIGAPYSNSC

>contig24855 Frame-1F|Blast-serine protease family S08A, putative [Phytophthora infestans T30-4](gb|EEY68685.1|) 3e-15

MQVCFLSLVLAAIVQTSASSVIIDQRGLEFVSQDAFCAYHCSSVHVAVAYRHLSATSECV

PRNCDTYLRTHPPERRLPA

>contig48427 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69089.1|) 2e-23

MTIYDPPHLSFLFAMMLTAVAFVLRSYPAVMHLEESLRVISIFIGPSPNLIFSEACQFGS

IRLLDWIWSISCTTPSTRLRGWSLTDYLRSDANYHNWQFSKSLYVAVSRDDLTMVKWLFA

HFSGCEASEHAVDVAMSKGYLKVLFYLWIHRSRRL

>contig51331-0 Frame-1F0

MLILLHGSLIMCRNGATANGASLSDSNLGICLKSCGDRVVQLSTRSLNIAISSDEISLTK

SY

>contig53179 Frame-1F

MKVLHLLLCTALAISRVSGATIRATASSPAAASPTTLTETSTAPLTATSTETVTT

>contig54707 Frame-0R

MTRLIFIQASCMNSGLAEVVTSDVRITGLNYGSTATVGGS

>contig04316 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53884.1|) 1e-95

MLWSYFVLMPTVAFASANGFFKGEGTAYTLGNVSSGNCNFMYDPGVNGNYAALNNDQWDS

TRNCGRCAQVSCDDDRCSDKITTEVVYLLDRCPECKQGDLDLSPSVFKKLTGSDPSRYNI

KWQFVDCPVKGNVQYCTKSGSSSSWLAIQPTNFANGVASFKIENQDVTMVDSCYYYLLAN

GANVNMDAVNVEMTSISGETITDTLKLEVDKCIEGTMNFNGGETHQSSNDPKPSELPPTI

APAPVTPTYPVVPPITPEVTPPESNPIQVPPVSTTDFVPTPDIVPTPEQVPTTPVPVLTP

ELVPSLETVPASESVPTTPVAAPPTPEQTDAYNTFDLIGASNTNYKAGLVTLADVPASDV

SVLQSNEGDVGHTYPGPNLLPESLNLANNQAEKGPELTVGPLNSEKPINLLTEHLGSNQY

DAGNVQVPGDSGLSSQDQTQQLPVIPGSGNYKAGTVLSDVPVQMELPVLLSEDGKSKTSV

LLSNDDIDMPNNQQNDKANPLKTEQV

>contig15448 Frame-1F

MKFFICSAIALAAAASAENAPEPTCISGQYQDGPYYFISSVPAPPARSCLSMTANRSTAI

SWNVDFSLPGIVDDTYWSESHVSLSLPSVKMEYLQTATVKFEYTSFQDKDLSAIAHITML

LQANVFDRGSLVVVMLCQSGPDPTWLGIFKKEVQVDGVSYSLFEGYVNTMLFQTFVPKSC

TTAYIGNTKAFLNQLGLSSSHRLATIRAGFMIRSGVDAVLNVNNHYMTYTAAVDPSARMF

R

>contig21678 Frame-2F

MVSCLLVICLMERTTYSLIMEAKKVASAKVQIC

>contig23113 Frame-0F

MKCALLSSLAAAGAVCIAVTATECELNSIENTLRSNSTIGASMGPAQMKCKEDTGVDIFA

ISDFPTKATALKIQKSDKGCNVVINLVNVYANTDAQCTIEINGINVTYGRLISDFLDGKI

GNETDTSSDSSNEIATISSESESGSTSSSSSDQIITSGASTKVLSLTTCGAITAIAFALR

>contig32047 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68748.1|) 1e-32

MLQSLVALCVARLAMGATQHSLLSILRRLPEELALTLLANMIASKTLTDDRLATFFMISR

RVLNLSGCCSIRNSILRQIPFRCPAL

>contig40688-0 Frame-1F0

MNWILFVASNPFPCMADLVEADAVGSFDLNATGKAEQLRQDGNEAFRRREFLKAKDLYTE

AILLQSGHSVLYGNRSAANH

>contig48943 Frame-2R

MSIPIALILTNAALAMKVVTLQMLTDPFALEHSTNACVKAAYRYASSMDVADPTGF

>contig57486 Frame-1F

MLSCKTFLEIFAVAVALSTYTDNAARAHAAECEMTYGENTVPVETNPASTTPFVPNIAAD

TASSTVASVEGTVAE

>contig21561 Frame-0F

MLGAPAFGRLLVRQSVSVLGLTALGVVATITGRDTEMHSLGEKGLVVVVNSRDSDDKSTR

LGAGRRLILKQRSKHQAQ

>contig41242 Frame-0R

MRWHRTLPLLHLLIASLLFLIAHNLLYLIFAMSYYACGMWSLPQNE

>contig52084 Frame-2F

MKYLLCLVVTIAFLGSTNSVTYPQVSPGTCLGCVCPPPAGLTRIPHCRPCCQGTPAPFS

>contig54176 Frame-1F

MLRVLRPAVSLQVRAFAQPLLLFNGARSLRTARGGTRRQKDHIARIAKLEAMAQEREYAQ

>contig59063 Frame-0F

MKAKQWNKFVCILTLHLSADVWIQPQYARHRYQEEDSHSHSKEL

>contig15639 Frame-1F

MGNVISGLASRPTLALLLVCVGHKAFSHIIFSRFLRWYIAETPRLVYKATDGNKKLLSHC

HTI

>contig19947 Frame-2R

MTTHRSLSETFLLLFMSSGLELLDAEQREDAMVVAADLEKCYTQLVGKKLLTGSTKKEAN

EAEQESVLVLTDLLLSLLSQDSSAMREIVTQVFRSLLPLLNRECLTTMINVLLSTREGNV

EHEDEGDEFAPITEAEDVEQEQDVSLSSDALSDAVRKDEKLLALHGEDLALAAFVGQVKI

RSQRKKDLKRARLQTMHFQLRVVDLLQVFASQRPEQSKSAIEKHDALVLSLVAPLFCVLT

QVETADSKQLVLRDRIQAVLLHKVLRVKDKLPCSESAQMEALNALRQLVELFRTTPMDKD

HSGKVASAAVVYLVRVVCTGKAEIEVLPIVHTAVFDAFTKKRSRFPRASFQDLLTKAPIV

GARLLLEPLVAVAAATNNKENADVSVARTAVDEFSQFEVFRLLTLLLRGASKLPVSADML

NSINGVCDTLKSALVRRLAPDSVHHLKAKRLKIVLLFALQIVKFWRTLEDQRAHETDVRD

VVAAVQAVNFKSPVIKNLIKHVSESADVPLVVRNGFETDKKEDEENELTRKAKPSKKKRK

RSITLE

>contig34357 Frame-1F

MPLRRWSQSKRHSLVPNLHLLIVRCQAHCCHLQTVGSSHICKWLYATCHSYCSKAEQ

>contig41238 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67179.1|) 2e-09

MWTSLALTFISVSCAATGITSFTLWRSWDLQVSSVRWLFFIF

>contig50175 Frame-0R

MAFIFSTCAVAAALSLVTAQPSFIYKFDASLAAGIDGSIIVKYASADSSTATITANLDFS

GVDQSKIAAFDGNCTEAVTSWKWHIHTKWNSTQTSDSYKQCSKAATDNHYDP

>contig53174 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62398.1|) 1e-19

MLGVYFLGLVLFDELTSFKNGKTRTKKPLKMKRRRRRSSVEQRQRASLSVSTRKAKSPCC

AVESSAPPSPHTSQ

>contig54603 Frame-2F

MTMRRRRRNSLLLSCLTLLLYKYDTNAAKADYSIDLTGIASGTAYTLTVNIGTLGSSSDN

N

>contig55389 Frame-1F

MVLVALSAAFTIIITFIDQATDTMRVQVAIKTAMFSSLIKSTSVDSSSTSTSVCSDTPTS

V

>contig09617 Frame-0F

MRHFSHLLKPRPWLVAALPAALGVTYVSKQQEKSRCKSFIPTSEFLYEPLSEDRASKDSI

EFNTKAPLSKRMEALILRVQDEICAGIEAIDGKTFHEDSWEREGHGGGGRSRILQDGNVF

EKAGVGVSIIHGTLPPAAIKEMTQPGKDLKEGVALPFYACGVSLVMHPHNPMAPTIHMNY

RYFEVETGYNDAQGKAKTIGWFGGGTDLTPSYLFEDDARHFHAVYKTQLDKRDLSLYPAW

KEACDKYFYIPHRQECRGIGGFFFDDLTDTSEEHFQLIRQCANSMLDAYVPILNKRKDMP

FTPQQKEWQQMRRGRYVEFNIMYDRGTKFGLLTPGSRVESILMSLPLTARWEYMNIPAPG

SWEEKTLQILKHPVNWLDVPALDLETLSTKELL

>contig22931-0 Frame-0R0

MSSLFASTGLVCYTGLALQLMIG

>contig26342 Frame-0R

MIAIIVCIAVKVAIFAGISSVRGHGNFVKPAVVFTDGYVMNGFSATLDNEIWGLYNHDKY

GHGVNATLTFFINVFPFKGYNSLGALIVENQEVLDAGVDAECGRTVFKESKRSELPRSEL

EFSGFTHPGPCEIWCDQAKVVFAYDCQTEYPGVPAKIPYDHAKCVHANRMTIYWLALHGD

PWQVYTNCAWLQGGKGRGSPPVEKGQNTLKKGGGSNLALAITPFNEMDTIAPELDGKLKG

EDDVLEKTTEPPSVEIISAKCMRRRE

>contig33036 Frame-2R|Blast-1,3-beta-glucanosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62229.1|) 4e-50

MGCNSRVQGLCAAIVLCTVIAVSSTTAWVAPIITKGNKFFNSVTGSEFRLKGIAYYPRPN

DGEMANVSNYDWTTDEHEAIWKPHLKSHEGPRCKYDSSLLGGPKQVS

>contig36930 Frame-0F

MLNVFRSFGLVVVVSSTSGTARSLTSVSSGSRCPADYLWCIVHPLLPRT

>contig58457 Frame-1F

MYFSWQCLALDLFVWYATRSYLFGNSVAQSLCVVVAVFDRACARERVTTHLFITCLCSKT

LFLAVGSSFCSCVVA

>contig19651 Frame-2F|Blast-phospholipase, putative [Phytophthora infestans T30-4](gb|EEY61139.1|) 1e-136 NOT\_ORF

MRRSFFLRNVVLPPLVAAESVVRYVVIFPSHIVFPSRAEIEDRTDLFFEGSTTRVQMLVE

HLYSATEVLDQHLSMVQWNILGRGPYESLSSSRRSEVIRSVYQRMRLLVSYYKRFEFLAT

IKVQNEMLYMDLHRAFPDVNGFPLFSHEIALNQELTKDLADQNLTTFPIWFYKKLHYTKG

HGQGAFSTGLLHGQKKGNLKDYSLNNGATKASGDSSRGWIEFPPNETRRLERKY\*WYHQK

KKKSLGPIGPNSVVLVDEGRHEVDLESMRMTPVYWPPLEEIVVCRSQWVYAQRHYGLAPY

RAETANILESAFVYYLGFYSREKERLMDIEAQKPRGFLSSRARLSDAVLASRVEKDCT

>contig32313 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65817.1|) 1e-45

MLGKRTIVHSLAFIATADIADGEELFLNYRYNPDRPLPEW

>contig49669 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59939.1|) 1e-24

MMGYFPLSILFIFPPPSTSTPFDLTRLHSSFISLVEQDYPILIGELYTEPKSGVISVMQT

AKHRDNGAYQIKFETNPRYSMTTRQAIQSRSWELMPSSKSKLEL

>contig50245 Frame-2R

MCPLRYILLLLSLLVAMIGLSQAMTDQEISALTEDEDEVGSKNKKQRSKARVLVDMLNGK

YLFDTYMARRSLTTMKID

>contig50829 Frame-0R

MRQKLWGKVVLLSALRGTSSSDVLASSPTIQAVGLRLDEAVHPCKDIISCSFCCCNGHWS

TNPLREHHGIKQICDESGA

>contig17322 Frame-2F

MLAAGASQHLLQPCFTLLFHLMPWPLEGQGQGQPQETNYQICQERNRDQSPPSGL

>contig33539 Frame-0R|Blast-hypothetical protein [Plasmodium vivax SaI-1]gb|EDL47246.1| hypothetical protein, conserved [Plasmodium vivax](ref|XP\_001616973.1|) 6e-22 NOT\_ORF

MKTILAIIAVLCFVAAVALSEEPTVKVGVPTEADHVKSDAGVEAGDVVPDLQENHRGGHH

GGHHGGHHGGHHGGHHGGHHGGHHGGHHGGHHGGHHGGHHRGHHGS\*LGCHGYNRGGGGV

CGGMW

>contig38039 Frame-2F

MLVLIGIAAGALVFIGSLLAVFMLLRQGGSFERMAQEAVGLPVSLEEQKLLLYDELLDKA

NSFEQRPAPIGINKLLEGNIVSVKDLVTVGDVVKLHDISCGKPCGGIFQNLAFDANEMIW

RYLPQGPFNSFTELKNFYLKEEKDSRHFVLLRSNSRLPIGMVTLGNHSPRDLRIELMNLW

LSPAFQGTAALTEVVLLLLTHLFEKGYRRVEWQCDGHNVRARRAAHSLGFIFEGVMRKHR

ILKNCNVDTVVFAAINSEWGLMKEHLQNRLQQKKVSSSVAH

>contig40128 Frame-1F

MTVIFFTWFATSGLLSWSKAAISASISAMYSETCWSTKMKFSLSITNVIGLRSSVMSFIK

>contig47312 Frame-1R

MEISSIRVILMLSMIWGVRARHGDVPAAYVKAITEDEYDI

>contig50626 Frame-1F

MIWRVLAAVAVTLTTVDAALQSAGICYSAWHHPSVTPENVHNDLIIVGKYFSSIRTFQTL

FSSVNIITAAAKANIQVAVGVQLTDP

>contig50653 Frame-1R|Blast-endo-1,3(4)-beta-glucanase, putative [Phytophthora infestans T30-4](gb|EEY66016.1|) 4e-16

MKFTLLMQAAMGVASTASAVMEDITMSLAGSGFEQGTVQAFNDRSTLNSNDYMAPFSTED

ISNLFQRNGNLTKLAPIVNVASNLLDKPLPTNKWWGNL

>contig59126 Frame-2R|Blast-dolichyl-P-Man:Man(7)GlcNAc(2)-PP-dolichyl-alpha-1, 6-mannosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY58713.1|) 1e-36

MQLVTRWVLGFMTFCGLFFFSDSVGMRFGRDVSRFFLLICACQFHLLFYMSRTLPNVYAL

V

>contig07258 Frame-0F|Blast-cytochrome oxidase assembly protein, putative [Phytophthora infestans T30-4](gb|EEY64598.1|) 3e-73

MRESPLAWWLFGTAGLVACTLSVGAAARLTRAGASTLYWKPRFMYSPKTSSEWHEEFEVY

RDFCARYQRTPMTLENFKQNYRWESAHRELGQLTALAFVGPLTYFATKRMIPIPAQAPLA

LVAGLGATQLYIGRELVQRNVYGSKRGKTEQEEEFEGASFFLPF

>contig13260 Frame-0R

MLRCCLLFSLALGLSSAAVVRIPIIKRNDDEFVSSLLHDLRAAHRPTIWGPAANLPIETQ

TITVKDTASVVIRDFQNAQYYGSISIGTPPQPFSVVFDTGSSNLWVPNRKFGSHRVYDHD

HSSSYKPNGTTFDITYGSGPVSGYLSQDALQLGKLTVPDQFFAEVNVTKGLGPAYYLGKF

DGLFGLAFDTICVDHLKTPFHRMIQQGLLDEPIFAFYLGDKKDGELTFGGVDKAHYQGEI

EYVNVTSATYWSVQLDALVIKGQKFTDVNKAIIDSGTSLLAGPKDQVAKLAKLVGAHKFI

LGEYIISCSGEAPDITFVLSGKTFTLTKADYTLKSGPICLFAFMGIDIPAPAGPLWILGD

VFMRKHYTVFDWGTNSRKPRIGFALAT

>contig17325 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53794.1|) 8e-08

MPTQHWLFRMVWKLWILGSGSSCHVVGDESWLDDSEDTDGMCVQPDGQPLRKKGNLKSSF

PFQKNRS

>contig21364 Frame-1R

MHLNHVVAIFLVGAVTCFTETIEGSKRRGEIIRERLSYPVDVAIASRALRHTVASQVEDK

GKEERALWEEIAECFLQAQLGRGNIYRSLHIAEKMQNLKEQLLEAFQNLKPSRMKYVKQQ

LLEIEANPALHNSRYEAWLNYDINPQEIFEARPGHDFESWLGYIKFYRLKGRDFSEDDMV

VLLKKHNLIEEAAETFILMDREFFLRSVVRPMLAYMVTQTDVSDIVLTTWLGNGVHPNVV

IKILFPGRFMNFDSDKLVYGLKYIQMFRKFFRKFSDDELSIMLVRAESNSKLLEKLEMLH

DPSGNQYDINEVIEKGLVYVRMSVELDKFLLKGQLPDISALSQVELDAKDNFFRHWLRCV

SIKFPSKPSSVEDLYALLMTHGEATNEKLTDIFDTLQDEHSMDEIS

>contig27339 Frame-2F

MSRSMVYLPAFTLAIAAVIVPQIQHATAGSLYYGPYTVSGTDDKISKSAPFYGAEIPDED

CAIEVQEDPTLPDVRTIATVPVIYAELLSNKSRAPIEPVYTKVGKKIMAEESECNDAYTD

ETTQWMENDERSMKQSERTSKGCVSGCDAFGAQQDEYDDTRRLQSEKVVKYMTKLGIKRR

LESEANRDIEKLENFYGVKMQVKLEYLPTVCVHSMAPWAGPFWPTFEDSINVIWRKSDPS

PAEK

>contig27898 Frame-0F

MTRFAFVLTTFSILCGHVFAQGRQGPIPMGPRARNREQFGNGVGMGGGGMNGLGGAGGGA

GGIGQFNGGGAGMNQFNTNAGNGLGQFNGGFGAGGNGAAMNQFGSTLNGQMGGGALGAGA

VGQGIGTNGARNNGFGNNNGPATPAPTMPNGEPGPGNDNGAMQGGAGAGPRGAGGFAGAN

GFGRGAGGGIGAGGQLGGGMGGMNGRFGGNNGVGGLGGFGGGFGGGAGGMNGGAFGAGGL

GGIGAQGQGGGLNN

>contig34058 Frame-2F

MNSAMAVCCSSLFRVNSMATTAGSAYDRTHAVDRSPIQRHSND

>contig35804 Frame-0F|Blast-elongator complex protein, putative [Phytophthora infestans T30-4](gb|EEY68724.1|) 3e-19

MFALGSRDQSISLWWLAQGIWCRACAPVCFEAAVTA

>contig39923 Frame-0R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY67925.1|) 3e-64

MVKVSRTPLAMIALAWSCLQFASSAEDLCSITPSSYTMAKTTHPHLASALTTIEQYAIVA

WYTDRTSEADRSAMLSSITTDCSEDSRMTIAVYGIPNKDCNAGLSTSGSVQSTTDYESFL

STLSTAVKDRKVLYIIEPDAVGLLAENGCGQSSGYLDNLKIA

>contig46806 Frame-2F

MVRVYVTALTAFLAFSASVSSTSKLARANPRPVNTDHSDAPAQLRLRGYTATNVETDERV

VLTEIYAFVRKFMNPLSLPTEEMVAIVNRMKDLNTPVKEVLRSAELQQLSDLVKS

>contig49025 Frame-2R

MYPSSASLVGNFMFFIFVAIVDEVLQQTRQDKTRTIRF

>contig51338 Frame-2F

MRVFSLGNAICLAFAIIKTSVTARRAICATELNAAALKSSYNFQSLSPATPPSDSGAPDV

NGE

>contig55363 Frame-1R

MPMQVTVQSIVSTTLAAGVLVIGPALHGELHQILLT

>contig34059 Frame-0F

MSRFAAFLTTTAPSTHCFHLGLIYVIVCYVACSDGVNSG

>contig35221 Frame-0R

MAPRCLKMSLHACFFFMAACVRHALSTAIQSASV

>contig44643 Frame-1F

MFQPPAAAIPTNWLGWTWLGVLIGRGLTTCRPRRPYYEAVRTCAKIGLMRLKSRHIL

>contig48184 Frame-0F

MKVAIIIAHIAATIASLSVLPINALNEVENYSQQLGAGSFRGTDSSQQQTAQESITQMDF

TQIQTGSRSSEQTNKKEDDGNDKKDGVEDSDDDSRKKTEKSEDGDKDEKKKDGNEDVTQE

DIKRDDKKEDKEDDDKNEEEDKKDKDENKKNKAEDKKDGNGDDKKDDNNDDKKDGNNDDK

NDGNDDDK

>contig55087 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64569.1|) 5e-17

MMRRPWTLLHLDWLGTLDALLQLVIIWPLETYEAVAILPVSFLRRHVPVLGGA

>contig03775 Frame-0F

MVCASYKSLFATVALMAMDSTDGVGTCFAPWRNELVNFNTLKADVLLIGQTFSSFRTFEV

RMGGVNIISVAAAANVKVSVGVQMNDLAAVDLEIEAVCKGYAENPQAVEAIYVGNECLKN

KDFGTVSAEQLVKYINQVKACTGGAVPVGTVQRINEWMTASDIDLVASACDLRGSNIYPF

FTPGTQTPIEKFKIQFDQLASKYDVNTIRVTETGWPSSGEVAFGNTPSLEVMQQYLNDFT

EWSKGKSESFWFMMFDSTVSYTGAEYEKHFGVFTVDGKPKVVLPPMTPSGKTFDKLPLLN

NSSLTTGDSTSTPVQQPIGLTPDVGGTGAGSPVQNTPVVETPVQNTPGVGTPVQNTSVVD

TPVQNTPVAETPVQKTPVVDTPVQDTSSPNNPVQNSPGQDTPVQQDHPFRSESPCSERLR

SEHSGGQPWC

>contig13631-0 Frame-0R0

MRTCYYLTLAAACLLSVSDVGAAVLRQTSTPVDKLGVLIESNDYDDANNNLRASKSDEID

QPQTNTIDFQALRRPKQRLR

>contig22293 Frame-0R

MDLFRMLLIAVISLFAIACALSRFEMRLDNVHFTPTNLDQFHHGRFLRSFVPAISPESNL

DNYADEKRLLSQPRLRDAAKTALSSLKKKIFSWIKLFLSWLSAKVDEYTPMGIKTTYWLD

NNKNPGYVEAAMGLDTVPLGEREKHPLTPVFEKYTKAYEKKFVKRVIRENISTYSFWRWL

KLDQIVNTTDDMPEAELIAALQKIQETKGFKLYEKYALEYDKLKSMSDCFDKKATRLEKF

ARALIWATSYQRRSNVRTFLNLRA

>contig30126 Frame-0F

MNFRSVITAATVAVVSLLQLSTTEGQVHLRVSVHSSKNICYIKCEPGQFCPLG

>contig31976 Frame-0R

MRTTSFSLSTAMRPWHSRHTFLVPLLLLCAFITAQDIPLPKSPRPPISLASRVTGEANNI

VISRGVGRRRSEGFSISHDIADNTGITTNVANVLKFTPKYVNLGRAETCVPQRYDVYVEN

TGSLPVRLERVECTHDAFFLLTDLNG

>contig35806 Frame-2F

MSRNHDKVSTSLTLGLGLLAATMTLVTASSMGLVGFLLGREYPQRKVRSLSLEKRSKTSM

EQEHRRRLRIPSGTASEDVKISDKKAIMDVRIAGIRPLIPPAILIEKIPLTTKIVQTINR

GRQGLANCLRRLDDRLVVVVGPCSIHDPDAAIDYAERLLKLKKELNKDLLIVMRVYFEKP

RTTVGWKGLINDPDLNGSFNINKGLHIARQLLAAINELGLPAGCEFLDTMSPQFISDLVS

WGAIGARTTECQLHRELCSGLSMPIGFKNGTGGDLQLAVDAVVAAKHSHCFLSVSSQGLA

AIVETSGNDMCHLILRGGKSGPNFEKEHVDDASARMLKANLVDNIMIDCSHGNSLKKHKN

QITVAANIADQLRCGDYRIVGVMLESNIEEGNQSLTPDEPLVYGKSVTDACMGWETTVMV

LHDLAAAVRERRAIKHQ

>contig38474 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67103.1|) 1e-22

MTLLLAPILVLELNGVFHERNTSEAFLSGTPGMPQYTDLLLSGVISSALIAVRFASANIF

ASLARVVLSPKKRLVKDRIDRFASVLFKL

>contig57464 Frame-1R|Blast-conserved hypothetical protein [Lodderomyces elongisporus NRRL YB-4239]gb|EDK44744.1| conserved hypothetical protein [Lodderomyces elongisporus NRRL YB-4239](ref|XP\_001526365.1|) 2e-09

MHWCAALRVLHYLMGTQSHGIVYTRSDGNKPMLCAYCDANWGGDKSTRRSTSGVLIFAR

>contig03468 Frame-2F

MKSLISVLLLATSTYAATCETEGQVVLMASGDDNVALVADSSCEQQGVDVSKNALTATSF

GIEKVLSAPDVRTI

>contig11856 Frame-2F

MVKACWGSVILMCTLALHPYNEIAQAQEESALRAVNASTKGEVLQSHFEERAPSYMDLAR

KAAGFAEKIHYYISSVPNFANSNEKVQNMYRNWHISQKESLQKINPAMRNNKVLEALSDE

FQLKFSNSQRAVIISACQGMASIQIKR

>contig14091 Frame-2R|Blast-1-acyl-sn-glycerol-3-phosphate acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY63610.1|) 1e-149

MAVFHLYSALHLFWILCNSSCINFLQFCLWCLVRPFNRILYRHLMCFVAQSLWVDVASTS

FPQTKLAVSGELPSNPSKPVILIANHQVDADWWYIWQAARHQKAAGNIKIVLKDPLKYVP

IIGWGMRLFDFLFLRRRIDEDAEHIKQYMQTLVSDAFPFWLAVFPEGTTIHKEYVAKSHA

FAAQENRPKLERVLLPRTTGMQIILDAVAEAKPDIYDLTLAFPSYSGEVPTYQMGYTRQF

DTEVPSMKSLLAGKQPLGRVALHSQRYSYEDVAKDLQGFLDARWKEKEARLTYFMKHQAF

PEATPPVEVDLS

>contig16501 Frame-0F

MVFPALFLLIAFALGDAAATSMSNSLQTIPFSGTSVVSRRLNLDPVTVEKAAQAINVEHL

LDIFGKEKEVVGDIPSEFYKIADHTKHQELFKRLGSHLKTLPFDDAHKDHAVISLMEKKY

GEPAVAKFVNKALSLDPKSTEAIRFQSAMLDRWDKEGLNIQEVAKKMTPKDFKLSKETLE

DFPREMLMRYAVKVGGSEADADFVASAVLVVQFINKINTEEKLSALLPNLKAIQDLSSSD

IARCFHVKKDATADILDQPMGFVFLLFNRLRTSQDPFEKLGRVRSLYGKDGGLQPSAKNF

WPTTKDVDFPSKMDIFVENVLPTTFAGKIRYFFRRMWFKLVSIFKKKSTPAVVSNHEIPK

SEIPETTVTDVVDDTSNILKTPVNDDIAATSERPSSVGRSTVINAADNTGGDASAISKSP

AAASAKDLRDVSKKADDVKPKTGAEATNDVKLETVRAPSNTKPENSEGATPVVNTDATST

RKLRH

>contig42908 Frame-0R

MTDWRVNPFWLPWLLLLWWTQSKSWLRRWIKYWLLRPLMRLGIQLVDESDEKDATIFLES

DGQQSSDSALPGGLVNSGNLCFVNAVLQSLAAIPGFLNGLDRAVRTRSQLIRAPQTDDSQ

THKVLVVETLISIMRDLSINSHKEECKANTEAKEDYGQRLTREDKQQKSRRFRAALSRCT

SLVSSAASRQEQQDAEEFLTFLLELLHEVLRVPAQSIRSNEDEHSRFLELEKNLSLRLKC

FNPNDPRSYVQAV

>contig47154 Frame-1R|Blast-small cysteine rich protein SCR76 [Phytophthora infestans T30-4](gb|EEY61402.1|) 2e-15

MTGICLWMFWACCWLHQWHILVVPIYGAE

>contig51719 Frame-0F

MSVVFAIIGAAIGVIAVAVIFLTLVRRSKAAHDEDEDEITTTSAAYKKSQGSTNTTAAAA

AYASYNGGNQTGNGSDVGADTARGISMNAMNYYNQQPSANSSVPSPRVAGRAIPSQPVGV

SQSCSTSRPFGNNSSYAASGHDAMG

>contig11051 Frame-2F

MLRLIYSTTVTVLLLLQCSNAATIFKDEPFGGSETNCQTAKDPSRTVTGLMVCSGDRVDK

IGVFYQGVDEPETLGGP

>contig56638 Frame-0R

MKVVQQVATALLTLSLTAASIINTEQIFSPTIGGNNDSM

>contig56744 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70346.1|) 7e-20

MSSCSGVTMCLAEGATLCNVLAESCPPCLYVLTGGEYSCYSRNPTQKCPYPSTYAECDKL

NPTPLNTTLSNTDNPNDEARSITPSNPSTTAEISTNPLVNTTTPSFESPRIPTN

>contig18453 Frame-0F

MLFLFLFLFMLGNPWTSMATALLRRPCIRVEPIRKVYPSMKRFVSLSSIAPIPSDGNSQK

HVVVGMSGGVDSSVAAVLLQRQGFRVTGVYMKSWDSSDEKGKVACPVDEDYADVQKVCEQ

LGIEAQMVNLVQSYWNQVFQPCLEGYEEGLTPNPDILCNREIKFKAFTEFATKIGADYVA

TGHYATLQLEKHDHVPQLFAAHDKTKDQSYFLSSVNGNAFANVLFPLGKLTKTTVRELAE

SEGLCTATKKDSVGICFIGKRKFANFIHQYIPRQDGYFYTVDGVRLYTHEGFTAYTVGQG

ARLQGKSAKWFVVAKRKSDHAVIVAKGTRHPALFTDTLFASATAFNWIAGEMPQELYTTG

RLRCLYRVRYRQDLDECTISFVSAFEAQEAASKLHDWQPKRVATDTKRSYLRVDFDHPQR

GVTPEQSLVLYRNDGLCYGGGPIAVAGETYLEQKKMLAEEATDWRR

>contig23770 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59902.1|) 2e-12

MEYFAVCLLVFLVLQGFAKAQSDTVTCTTPADCAWGETCVAGDSETSVQACVP

>contig40355 Frame-2F

MLFSVFFFLVATCVKSSYGHSVAVSTRDPENIALQLHEYASIPETIETIRRLRGALAHDA

TAYDERMFFENAANKMYAIAQKTRLSAAAVKKLIPESQEKKLLSYYLTKMKGFIKDREAL

YSITSSYDELALLGVTPDLFRTRLLSVESPEVAAARAIEYEEYIKNICFVSSEKNPCKTV

TELVESNKFDKIKELMEKHSIAELLIGALTNLNKVNHLDKLTTRIQLKYVLENTPELGPL

LSRDVNELLKDPSVSKIFSRFLTFVYGIPS

>contig40607 Frame-1F

MYTLILMVSVLRTLHARATQYLSTYEDLDSLNNAKRNEADIASSLFTPQKLWKVMGEGPL

EGLKRWYALIESHLRCEFDYSVNEVPCLCGLYGLDGAATEEVAAADNSNDVAFETSTTDD

YN

>contig47655-1 Frame-2R1

MFSLRLKYSVGPISIVATLLPFETALCSSSLSFRRLLKTRERRSVSGAEGVGMLAVACDT

DPEDGCIISTVTSLDMNVGCGSLELVNT

>contig50181 Frame-1F

MVAKRNDTTFLRFAMVFLGWALLASIHTVAMAADALKESNEVTDTVNGTKDFHARPHLRT

LLVSTAEGTSRDERSDKWHPTSQNVLVRYISPSIIKSTGFRTLVKVLRSDN

>contig54574-1 Frame-2R1

MVSFSRQILASFMLSRCQSERITSYISDVDDIIEDHLPTQPEDEQDDSQELPKMTVVDAQ

KALEMLETFWLQQDGDALGFLKSIQQMKDRV

>contig59357 Frame-0F

MPPTGLAISWHLALQCSFGTLSSLDNSRCCLGLLQCFHGKD

>contig18744 Frame-2F

MNRIFPPGQRWLKLLLLVLVMLPMVQAMDPSKDYYKVLGVKKDVSDRELKKAYRKLALQY

HPDKSENADDKEAAKEKFVEVSEAYEVLSDAEKRKEYQDARQYQSTTGAGQAGGFGGQKS

TTEDDLASFTKMFEGIFGHGFGTKGGFGGGTQEFQFDGFDGFGSTRRSMPSHLQPRQPKT

LFGPDSIVKTLSKKKFQAKTRDTSGSCGFMNSTCQVRNSVARMKTSLVICSKKCTWGR

>contig45993 Frame-0F

MMLTVMVVATTSFLAAFCVSILSTATRLYSIIAVKIQAPVDGFNSRMRFARNVGVHDQNN

QK

>contig46835 Frame-0F

MSRLVHLQMSRRWYLLLVFLFILISATYANSFIDIFSNFIENFRAEDPTPTPEEAPFASI

PLVSHDESSCAAPPIPSSPPSPVILENRHILFVTIAMKSHAQPLLRVASAMKEQGYRVSF

ATHDSGREWVEAYKLPFISAGSFPISSDNLREKLQAISRDTSRLNGLVTMFKDIYVEAAS

PMYDALLLKLKNTEFVPDLLVLDIATIGAQFLAQKLQIPYVLNSPSLLFDSGSVPNYVPA

YGTGFRQDMSLWDRCVNLLYPTLLSMALTSPFMVLNQIRDDVGLPLFRSQNDLFNGARII

LNTAFGLEYPQPLSP

>contig50326 Frame-0R

MLVAFKLAVARLHKKALALVLAMIVDCADSKLSF

>contig56746 Frame-1F

MVKARWGSVILMCSLALHACNEAAQVRGESVSHAVNESIKRQESRSHFEERATDDMSFVG

PISELAQKAIAEIQSGLNGQIIKNARGNVESIRNSVMKWVRWTKKSASISKSATENDQSK

QLFNVFKAHFSEVDRARVIIASLNSGANNSRFQRHMRHMRDFMMEEWNAKPREQVYNMLR

LDATHSDFLTSSMLQLFVKFLDKYHHKNYNILRDKLMKAYVDHRQILRDRLTNDTGIGKT

LLGIIPPNYWNSPTFYPAILLLEENELAHLSVTELVRSPKLDSWCSFVRDKNGEDPYRIL

IKKLLDEKFELELATELEAALKQEPPGDFYWKLEQLEN

>contig08155 Frame-2R

MRPPLVLGMFLTGVCVRFVLSVIVIDVPPSTAQEEYIFPRVPKESTTKIKAVGDRRLQVL

ERLLVKKTLLNVADDIADKKATWEQVHLDLKDVGWSDTNIVHGLRVQLEEKNPATLDRAV

KMGAHILFSKSTSEDVKTEVFKGWKALGLTPTKVCDNLVMSDVDADLKTLMVLRYHALFR

EKQEASQIYDIVTAYDRLALAERLLKDDQLEKWILHPKPQYEEMAKSLHDIYKRRISFIR

GDPKFMIVLHFNEKSPVPELFRMLYYFRAISDPDTLKRILARLQTSKVLTAESRDELLLA

MKESISMEKIGTQLNELAKDS

>contig17335 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70538.1|) 1e-57

MLLAVALTTLVLLTSSSLSSNVGSIIELQPDHALQSQRGLYGIPQFFHVVGLQPASVYDI

KVSYLATQPSLIVVHVERVLLPSLLINIDELNAIDRAQKKDLMAPTRRKLLTAPKFRLHP

IKLKEHKSVQYRLESIDNAIEVEFSLLAEVEGVRHPDSVSETNEYLFDIVVEEVLLGVFP

KHTLVLIGWLMILLYISKKWVLPFLEKKIALGFLKDRVEVEVT

>contig18745 Frame-2R|Blast-homoserine dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY63706.1|) 0.0

MAKPLIVGLFGCGTVGAGVFDLLHSPVRRQKFAAMGVNVLISKICVQNVSKDRALKHFSA

SETIITSRFSDILEDKSINCIIELMGGTNEAKDVVFGAIKAGKHVITANKALVANFMSEI

LQLLQEHPNVHFGYEAAVAGGIPIIHTLQNAYNADHITEIAGIMNGTTNYMLSKMEAEGV

AYDVVLKEAQELGFAEANPSADVDGFDVQSKIAILAKLGFGGSIRPTDVPTVGISRVSAA

DFEYARMMESTIKLLGVAKLLQPANDVTGQPQEVTVYVSPVLIKRTHVIASISGATNLVN

IRSTNLDSTAYVGPGAGRYPTANSVLNDIVQLARGDAPLDPFKASVPLTLQPDYEARFYV

RITVADGLGIIRHVGQLAEETEVSIYSILQAPIVDRSNVQFVVTTESSLLSKVRTMCQKI

AALPFVRDEPLYLPIM

>contig22832 Frame-0R

MKIFSTAVFLSLVSTCVDAIYGGVSIQSGNGEVMVTMRGQGNENLCGGTIIGSSHVITTT

SCAKKQIKDVVVNGTSSVDVSPGASVYKIKSISIHPDYSPGSGKFDLAILQLDGQSQVSV

ARLPTTDALSQFGSVYGWDSSESPSSVNLLTVSLPIVPIAQCKLDTGKNDLDETFICAGG

EAGKGVALLDAGGPLTTIGPQGIRVNVLLGVLSEPRGLGKVSIFVRVNTAMKFIEDVFKQ

HGDTFQTCC

>contig24070 Frame-2F|Blast-anaphase-promoting complex subunit, putative [Phytophthora infestans T30-4](gb|EEY69744.1|) 3e-61

MISKKRYLLLSVACVGRWSVETLAAKLDVSNDALLKHVSVWLNHGLVAFATERTELIAST

SFQGTGRDDNTIVEELETAVSSDAQAQEDLQLLESYLVGMLSNFGSLTIQQIHNMLATFA

RSGAQPYTKTISGLSVVLEKLVNRGKLEIVGGQYQLIQ

>contig24423 Frame-2F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY63451.1|) 0.0

MMSPLKFLTHPVVIGLIVAAAGATLVALSNRYAVDFDDDKEDKVRPVPYLPGGHPILGHT

LLMARNLDRFQDWLVETSVARNGKPFVLRQPGKNDWFFSARPEDFEQILKVHFDTFIKGP

QVRELLDDFMGENIVIINGHRWKFQRKALVNLFTAKAMRDHMIPIVKKCAMVLQQVFAKA

ARKGEVLDIHRIMGRFTLETFAEIEFGAQLGLLKSGQGHSFEMAIDDANHISLERFAVPM

WVWKLKRWLNLGSERRLRQDMKVISTFVTNCIAGAIQRRQERLLATARGEPVKPVAKDIV

SILLDNFDTKGEPVLPQDVFNISLAGVLAGKDTTGDAISWLMHLLHENPRVENKLRNELL

AKIPKLATDESYVPSMVELDGVTYLEATIRESLRLKPPAPCVTQHCTQDTVFPDGTFIAK

GTDTTLLYHASALLPSVWGPDALAFHPERFLDEHHKLVVLPPLKFIAFSAGPRICIGRQL

ALIEMKVVAACLLSRFHLTQLPGQDIRGSLGISFGMKNGMMVTVEPTPGVAARA

>contig24988 Frame-1F

MHLRLVVAVATFFPCVTSASPMASELNAPHLVTNDEAALRLRGRTTNEDTENRSFFWMTT

TEKLRRTLEDRMAIVGKLNKEPDQFSKYSKALKGGDSKIEKLYQKHKRELDKLQKIIQDK

RTMKDNLSVTLRDPKIDRVLRLKTAAAEDKLTEEISRLMNRKADMEAGLA

>contig45853 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY56330.1|) 2e-17

MNSRRFTIFVAVTLVAFCSAAMDPVRRDGMLRVVGEVHSNRYVVVNSWEKRAKKHPHCVD

TGAVDKNPVCASTGVLYMNKDVFEFHKCLIEAQYGDVITVAEIDLCKKAKREDDEHTNVY

YDVS

>contig45992 Frame-2F

MMLTVMVVAATSFLAAFRGIRTSILSTATRLYSIIAVKI

>contig53003 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53261.1|) 9e-31

MTLLLPFIFHPSASIRALMYYIILLLTCSADNFIPNRVPVDLTNNALATTNEDAKVPDLL

KSSFGLYSSRWTRCC

>contig54392 Frame-2R

MMGVKIIAFARIAVHISLAITLTSVASKRNSPRRQSFFIKNHSLHIRLAFGSIGSRSNRP

SMLIRPFFLRQKVPMQIRLFRSQ

>contig40439 Frame-1F

MKLFGFGAIALAVSASLLHAEETCDNKSFYLGSYLVINDLANIKGSMCISADLKSNSLSW

LTKANASPIEYGSPTGYDHAPCYPRVQRNLGYSPLSSVSSLHTSMWYEYTGSANDASLVT

LNLLIGSKPALVPALDILKTPSIQIMVILSVHGNESPTWLNTKIVSIEIGIYAFDLFVGE

IGGVTIYTYLARSVIVKLDVDVTEFYKKLPKEYIIDDSQCLIALQAGTQINGIVNAELKV

LDFSVDLMLK

>contig44259 Frame-0F|Blast-ribose-phosphate pyrophosphokinase, putative [Phytophthora infestans T30-4](gb|EEY62052.1|) 1e-144

MSRFYIQAKSLVTRNMVALMAVGTVGMLNGGRSSRAEHSTTLAEANKVATNSEWYPNTTT

KHWHFYKGKMTKASAKSVKLFKVADTPIADEIASYLGVELNDMEVKKFNDGETSIIVNEN

VRGKRVYIVSSTTTVDRLMELLLAISAMRRASAKSITAVIPFYGYARMDLMHKGREPIAA

ADVARMLETMGVDHVVSVDLHSAQIEGFFKPQIPVDNLQAFPVGAVYFSEQTLGDPIVVA

PHSAAVNRAAMFRDTLSRAIDESVPLAFVIRKHQLDEDQPGELVGDVNGKDCIIVDNLVD

TGSTLVKTAKVLKANGAKTVSAFAVHARYSAHAMQTLESCEELDKLVTTNTIPARYKLDK

IPS

>contig57453 Frame-2R|Blast-peroxisome assembly protein, putative [Phytophthora infestans T30-4](gb|EEY69439.1|) 3e-24

MKKFELLALTCQLANLLIFVRYGKFRSLPERLLGLKLESIMPSITPRAINFEYMTRQFIW

TGL

>contig07952 Frame-0R

MPSLASMPQAQLFQRIFILLYIYALLACSNSITVVAVAVRAVAIKARPHIGKHHDPNRVS

ALVKNEERFLDLPHISDSFYEAKLTQKAKALLKNSEFVKMYDELRKEAGFSVHTSNIAIP

LPQHPISNQELAEMLYAAKERVQDVLKVPLFKKWSLHFGAEDMFFELRLDVDKFHYEFVH

NPKFTIWVEYAQYLNLSVKEILDVIGKHFNLEYFLLRILEDYPVPKAKTVLTTLAEEMLS

KRVVEPLSPQKTHMDVYDYLISVKEERVENHFLRPGAPWFVEYARMHELTNWPHEVIKTH

SIRL

>contig21556 Frame-1F

MLGAPALGRLLARQSVSVLGLTALGVMATITGRDTEMHSLGEKGLVAAVNSRDSDDKSTR

LGAGRRLILKQRSKHQAH

>contig38529 Frame-0F

MTKYKCSSLICSLLLLSCYHVVTSIENVALIEAPVLGKSRQLRSSVELVEGLLLTSDKLA

KVIGTLPKNLAKEWLATFKWGINHFKILLAEDKVAAAGKIFPDDSANPIMTKLFESDAFL

WWEKLIRRTVDDTQEEVDTIITSALVTRLGKGRAIKLFTEAGFEADAINAKWLALLYHAL

DDEDMPKLFKEIVSSGGFDKNSVEFFIKLCARENNKDAAYEIINSLLQDKKEYREVYQKF

DGVVETYRTKWDSLKSVYFKAVSDPKLDKSVSPMQRLRNLYQTEELDPVSVASKIAD

>contig38626 Frame-1F|Blast-lipase, putative [Phytophthora infestans T30-4](gb|EEY57047.1|) 1e-55

MRLLRPLVLILQSLVVSSATPVWQHSFPLDQAPSPIIVSSLSSDGAGFLYNETTALYLAH

VTSISYCQSRHIIEWNCQPCAFVRPLVGVTVFEDTKDNFQGLVGYSELYDAIVIAFRGSM

DVTNWLDNLTFIKTRAYVHFPSVMVHEGFYWAYRSVALQVTKALRKLQKEHPFASLMVTG

HSLGGAVATICAFELEYIEKISVKALYTFGNPRVGNIHFSLKMKNTSMDSVRVTHFRDIV

PHLPPTWTGFKHT

>contig43134 Frame-2F

MLTRCTMFCSVTAIYATSLVRKTPAFELLLKFGPALSQEPVIEKTHFDMSFQ

>contig43509 Frame-1F

MRPCSIRFRSLNCFELLWQAYASVASPYLLSDSGRVVKM

>contig43783 Frame-2F

MTDWRVNPFWLPWLLLLWWTQSKTWLRRWIKYWLLRPLMRLGIQLADESDEKDATIFLES

DDQQSSDSALPGGLVNSGNLCFVNAVLQSLAAIPGFLNGLDRALRTRSQLIRAPQTDDTQ

>contig48588 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60766.1|) 3e-11

MRSRITLTALLTIAFSLRLLQVRAAACAEICYTTELTGFGPGGTAGCTC

>contig51191 Frame-1R

MLEWTRPSNLNATALAGILLCYPCVYTMAAGTKATHISSEQLNCLAMCPLYLLQTSIL

>contig51726 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60668.1|) 3e-47

MNFALVTGLFVACYAAFFLQNALDTWVKHHWTAPVLAGLRQSSCCTTYSDAVVYLHKRSV

AIGA

>contig05755 Frame-1F|Blast-methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64588.1|) 3e-33

MALSVVLFIGSSKAWIHDLVKIGQSMTVNGGMEPHTDVGPLISQAAKDRANALIQASSDH

GASILLDGRHVVVPKYPHGHFLGPTVLDHVTTDNPAYMNE

>contig12759 Frame-0F

MRVGAILSYLVGVLVSTTANKTYANCNPVCSKNETCETKSVQCVTYPCNPISTCVTKPMP

EPKCTLKCPEFETCRFDALDNSQICLGPCATVRCGSGYTCVAEKGKCNSPQCPPVARCKL

VN

>contig22169 Frame-1R

MQLRLLLPIFLLGTSNCVVFNLNASSLEVTKIASRDSTSKSVAKNTPNFKTLPKSNATST

FDGVPFATKNEEERGWWSQLWYWILHKWAWWRRPTPSNTINAIPAVKIFKKKEWVGKDFE

NWLRRAVKQLRKEPYTKFTADNIHFHL

>contig23683 Frame-0F

MMELALVHWTLNTLRARGFNVVFPPDVAHYKFVEGCGFQPRGDATQIYSIAHSDLCLTAT

SEITLAAAKSNEILSTSLLPLKYAGFSHCFRTEIGHGGRQTRGIYRIHQFSKVEMFAFCA

NEIQAQAFLEEMVDIQTTMYAELGLHFQLVDMATEDLGAPAYRKFDLLAYMPGRDEYGEI

SSMSMCTDYQARRLNIRHKDLKAEGSKPSFVHTLNGTACAVPRLLISLWETYQQKDGSIV

IPEVLRPYMGGQEIICRTA

>contig36348 Frame-0F|Blast-pantothenate kinase, putative [Phytophthora infestans T30-4](gb|EEY68288.1|) 4e-14

MQALSFLLFSTAVAMFCLERKRHRYREWCQRLTHKKLSESSDLGTSFGLDI

>contig39334 Frame-2R

MIDRRYHRSLQVLSWVACAAMTSKLVLFTEFGNRRGHGKHEHVFSG

>contig46325 Frame-1F

MILMKVVTYRAHSTFTSPAPCIPMMMSLLVVLFICRASVKFSRKAKVHVQAPIFDSHGIL

ENSSSFSHTRCSMRLFYGRRVITDFPIVVFT

>contig51725 Frame-1R

MVAAFAFWMVATIIVQAELTTATLQDHGSMENAATTSWPSLRVHFSVKRSSRKLHGQSEF

MIVADPVVSIDDSTRVLYNTFG

>contig53679 Frame-2R|Blast-serine/threonine protein kinase [Phytophthora infestans T30-4](gb|EEY66337.1|) 5e-32

MFGMDPVLSGSLCFLVLAIAMYLKFIREQPWSDEEFLDRKKSSVESDDMMPFLRSSSSVG

RLETQQQKRGPGKGRQQLHQKQQVPRQTQQQRL

>contig14433 Frame-2R

MMYHIQLAVSIVFCVACCGGHAIRTLAE

>contig43868 Frame-0F

MTTFNSPIWLPLWCNVALWSAEHPVDLQNYRIRVNCRLAVAFIDSPILTYIMCT

>contig44717 Frame-2F|Blast-unknown [Phytophthora infestans]gb|EEY62661.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|AAN31499.1|) 3e-37

MISSWLLFSSAIMAVAMAAHIKVNHHHRGHHQKFREVTVIPDNGICPNGGDVLLCQSASF

ACQDDGTGKQKCLNRDDSFLDSIDSKTAAPWMQCSLTNASLPSLCL

>contig45857 Frame-2R

MKVPLEWLAAWQVIHWTCLGAGATAALLLLLHSATFRCKRRMTDLLLGGIALADLCFVTL

EALKQALHTSYFARYRRKDEGLEEFHYTTGDFILTLMSRFSFFKSLCWIANLSLLMRLGA

LKALQVKKNLLISSLVSFGYGCMHAT

>contig47437 Frame-1F

MLQHFFCALCVLALLACLHFVAAAAVANRPLLKMQQNRSLASSVKGVKGLIDVFGSTLPK

TAVVGNDLLRIEGDVKNSVKNAVESWSTISSNFLKMTLDEEN

>contig50716 Frame-2R

MGQVLMVKAFGLTLAACSSGLAGISIYGSDIEIQITYLKNRVLIAVPHVLGTCAVATKAT

EMSDIAIALLTGGEIPNNEERNLNLIFGLSSTTCSCKSVPRPC

>contig57656 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63563.1|) 1e-24

MSILLAGLIGFQARRTVARISIVAGGDKLRFTTHKFF

>contig16487 Frame-2R|Blast-cysteine synthase, putative [Phytophthora infestans T30-4](gb|EEY69413.1|) 4e-70

METWSVPLWRWSLCAAMATLSLWKMGELVISSGSSWCRLFKKKSQKEMYPTGFSGLIGNT

PLVELTSLSKATGCQILGKAEFLNPGGSSKDRVAKEIVEKAERQGLLKQGGTIIEGTSGS

TGISLSLLARARKYRCIIVMPDDQAKEKSHLLELFGAEVVFVRPASIVSAKHYVNVAKRL

ELKTEG

>contig18056 Frame-0F

MSVAVAVMSVAIAAAIRNICLAAINLNGFRCDYCVSLDLVIIRSSSNHMRFFLCTVGTFS

LHVVAKSIPRACFSPTLQELAFCNTSLSIPERVEDLLRRLPLNEKVMLLTARASPKGNLS

SIGLPEYNWGANCVHGVQSTCGTNCATSFPNPVNIGAIFDPRAVFNMAQVIGRELRALWL

EGARENYEAGPHLGLDCWSPNININRDPRWGRNMEAPSEDPLVNSNYGVAYTKGLQEGKD

PRFFQAIVTLKHYVAYSFEHYDGIDRQAFDAVVSPYDFADTYLPAFQASIVHGKAMGVMC

SYNSVNGIPMCANEYLNTHLLRDTLGFQGYVTSDSGAIEGIYRQRHYTKSLCEAGRLAIE

SGTDVNSGEVYSECLAELVTKKQLSEEVVNKAIRRTLKLRFQLGLFDPIEDQPYWHIAPS

EVNTATSKYLSLKLAQKSLVLLQNHGMILPLAKGKRVAVIGPHAMAKRALLGNYLGQMCH

GDYLEVGCVQTPLEAIQRSNGESKTLYAYGSGINDTSTADFDDAEAVARKADTVVLFLGI

DTSIEKESQDRVNIEIPMIQMELLKRVRRAGKPTVVVLLNGGVVGIEELILYADSVIEAF

YPGFHGAQAISDILFGDAVPSGKLPVTMYPSAYIDRLDMKSMSMTQFPGRSYRYYKEVPV

FPFGWGLSYTTFTLALDKGMDSSEIIEITRDQYHTVSVIVSNDGNYVGDEVVFAFFRPLN

VDVTGNASLLNQQLFDYRRVSLRPTQFHKLSFRIQQSTLALVDEAGNHVCIPGFYEVTIT

NGVHERVTFAIQLVGEPEKLHLISKYVDRGSLHEKDVTLSVP

>contig26747 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53680.1|) 1e-154

MMGMHTLPTLLAGNLTSGRAFMWQGDLEPMAQKKFENFGEFYQLYPEFKHVFVGDNGQGD

VRAAELIVERFGSDALEAAFFQRVQPMEKMFNYHSREDLTRWRKMNILFFDTYVGAAVEA

FGMKMIRLSGLKKICDDAGHSFANIKSWLTSQSRERARLQLNCDLTAANALISKTLGSSS

LVMKPQVFALNSVVRTSMGRGIVRKYRGIDGIYCVDLTDWPSLTHHKRVQAFLPEDSLTA

YVSSDFSIIPKSSLNYVKFYRSPPVRILAAHTLVKTLFGIGRVLSYRAEDNIYTVSIPGD

QTVLHIVAYLNMDSLQPVD

>contig27119 Frame-1F

MTTLVALRVLCAAVGVCFGCYVLARGGRFNNDSIVKGLEQEVERQKQLRAQERAGRTKAE

RDAREALQRRQEAVGYNLDAIAYVHSCFSDRRGTPRQGGLVKNSRARITFKRSIPPASFE

SLEQFSHLWVLFIFHENTNLVTKAQKTTFSAKIAPPRLNGKKVGLFSTRTPHRPNSIGLS

VVKIESIQDRYIEISGHDLVSGTPVLDVKPYVPADHVSGYVVPDWVAAETDVTLRTVDFT

LEAMASLTELINAKLSLFYETVTELRTAIEQMLILDIRSVHQGRG

>contig28334 Frame-2F

MSLKPKHPMLFFYLFLLLSDHVVTSLTMADSIMALPSVENHSEKLRRGPDVVENRGIEAD

VARAAGKELAISPECLTHLALLDKKKYKFKLPSFLRTVKITRGKNVKALEPFGLNVRKKL

IKNPSSLEPFANWFNKIEAKYRKNPTDAHLVVITDLSSQFGDGLVVRFLTDVGNKYKEVY

FKLTIALFEFWAREKVDLFELLSRMPLQWEGDASNVAKTLLDPVFSVWFIYSKHIGLDTG

NSAFLALKKMLARHNLDSQMNDIINAGLQIGKQIAERDNNELSGMLNYFKLQLEKDTDPN

VLFESLTLVPSLENLIAAEKVYDRIVSVCHYYGDEMSRAKWLVNSVSTENKLNLFFVMLQ

ANVDKSRKTFSGLVLNKLALFWQNWKSSTNIVALNLFDQLRLRDLPDNSYSPGQLIRLRY

WKEFMYLAYGDNIKQNPSHVLYDVYSARVMKALHDVESLAGVPKLKDLQRAWAIDFRKQ

>contig28864 Frame-0R

MCAIMSSILDSIVATIFVCFAEDPAALQRSHPEEHARLVNAWTRLQPDLLTFPTHMV

>contig30142 Frame-1F

MKENLKIVFVGCLVLARACWSCCLHSKWP

>contig43687 Frame-1F

MTFAAVMEMSTVKITLALAVAWGVLAKHGKADKEEHLEIYLCAPIGIEIGEKILRSLRVQ

SPRISFSGCKKHYELEQAGRLWSQLLHFKLT

>contig44912 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59939.1|) 8e-52

MNASYVSTLDAITALFIVLISRARGHDDDVKCSTFVNARRRLEPPMPPNYSGNAVFKALS

NFTNSELQPQTKDNAKVSPETLGMVARRVRGSILQCNDAYLRDGLNFLAEQKDDAVAQIG

THVPFGPDIMFTSWLHIGMYNAEFDGVHPWLASCPQVPG

>contig45227 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69381.1|) 2e-44

MPRTLIRFVLGLICVAFLAPQALQSQELQTLGGVAESHNNHKIEDDGLVVRCRACGAPVA

KKKDYIDFHDTINTVGSRYEAVLGDDTELFTFANPSRTEVELAGFKEVSAIEGDTYTKKS

SFFDNYSWQDLRCNHCKKHV

>contig45726 Frame-2F

MAQCYVTLLMVALLFLYSMHIALKQSVGTVSQKSETISRTTRLLRAHGMSGSVALRTKAL

FSNARLDTSIHEYLAAINSIDKHEAPAFAKKFLHSPEFKEYVHNVRQTNKNDPFKA

>contig46411 Frame-1F|Blast-cell division protein ftsZ [Phytophthora infestans T30-4](gb|EEY60941.1|) 1e-170

MASHRTLLVLLTRRSIALSTHRPSPLLNSVRWLHDTRATSDTAKLNGNSTSAFNVPTSMP

PRNSKRTSEQRKRSKTAARVAVASKISAGTSLNEEANKVKEQGNIRPLTSALKDGKPWIT

VMGLGGAGSNAVNNMIASQLEGVEFVVANTDCQALGRSLAPRKITLGKNITKGLGAGSKP

ELGKCSAEQQNDEIQQMLHGSNMLFITGGMGGGTCTGAAPVVARIARELGILTVGVVSTP

FRSEGPNRTRLANAGVKELAKYVDTLIIVPNQNLLALADKSTTMLNAFRYADDVLLEGVK

GVTDLIVRPGLINLDFADIKTILSNAGRAIMGSGTSSDNSRARKAAEQAFVNPLLGDLPT

ESAHGLLVTIRGGQDLTLFEVDEIMEIIRSRVHDDANII

>contig52902 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69435.1|) 3e-75

MGGMLGQLFMLFLGDHARMNGWDVSKINFVGFGSPRVGDIGFAARLRVLFDPQQLLIVMH

PSDAVHAFPPTAEGYVDACIKIFLRESGKGVGRRAAGPFSLLPVTKSIDRAFEHAHKANT

HNKASNPACSFCKSKAHRTSQHRCRYCIERGSHRG

>contig09815 Frame-0R

MVSPVFGFTFAILAALSTGEMDQCEPTDPTVASGVPGNTMLYHRGPCPALNTLANCGYLN

YSGQSLTRESINRAIVDVFNQDIAIVTALTASLKEPISLSDLSRRALGEHDGSLVHLNSC

LGIDPMFADKDLFTDLINRGQGDKLCAKDLGEAYLNRRTTAQCYGTPPITEQEIAQSYAQ

GSGILTTFGTGECISKAHATAFLLNEVIPSGWTKRSTPVTADAASKVASEIKRAAEMRQ

>contig19955 Frame-0R|Blast-strumpellin, putative [Phytophthora infestans T30-4](gb|EEY66160.1|) 0.0

MCEALYLYGVILLLLDRKISGPTREKMVIAFYRSKGESALENIDEVCKLCRVTGYLPGQS

KPAQYPERYFRRFQPPEEVVSMVIGKLQSDDVYLQEPCFPHRTHRSTRLAAQASMLYVIL

FFAPDILIHEKASMREIVDRHFNDNFILTTYMGAVADLSLEWAAYPAARLALANTLEPSN

IVQITKTKAQQTQRSIKELNYFLTEGVLTEMYVLENLDPLLNCIRNANVTIRWTMMHSRI

QPVIPMMDNATAQREIFDKGSDPDKLITLLLKVSQLEWKLKQMFGALLASKEDRWQRCMK

ETSERLEELSDYFSGEKPLTRVERNEDLMKWFMDLAEKVKSLDYVDHIKAGRRIKRLIEA

LGHVEQFDQIDTNLQVKAYLEESREFLTEMVRTVRIRDEVMGIIENVSDLSYGWEIITDF

MKILHQRVKNDPSSVILLRAMFLKFASILDVPLTRIHQCGSEDVISVAEYYSGELVDYVR

RVMEVIPQSVFRILAGIIKLQTDHMKPIPVKFENTLLKNHAQLNERYRLARATNEVSKYT

EGILAMKRTLLGIIEVDPRQVLEDGLRKELVFRVSLAFHEVLNFEKNTSKECNEIFVNLA

SNLDAYRLSFEYIQDYIGIYGLRMWHEELSRIINYNVEQECNRYLKKKVYDRASQYQSRA

IPIPRFQPSSEDMSVNFMGRLMHALFTMTDPHLTIYSPQSIGWFSEDGTEVCGIGAFSVL

HKSVGLLGLAGLDRMLSFRIVHTLNNLVKFWSSAVTPYFPLLDQLSAALVPEWKLLEHST

KLYDAALRKVEKIMSKLLKAVLIIGQAALIRRQISSELSFSSRLDANLLATTLDTLNSSL

LNDIRAHYRDPKTKPYPGSDGNPLLVELNKYLENTGANDPFQKIYVTVAEPMEGLAAMFM

LFVVAYMPKLQYNRNFGALNRVGKNPIDGEPLLVGILTILKQFHPSYTEIFLAYLGQFVR

TKVNDIFAEKADKKVKSSSLPIELSADVVNTLIFMLEFARCAKIKRSILDGHVPSYVFDA

IQL

>contig20700 Frame-1F

MFRSFIMICSILRVEATTLGEVITHFSKIVELRSEFATSLLECLKAQDYAIMDLRRELRA

YDSRQTGKIDVDNLRTVLCAFGFRLARFRFNTVAKMLFELNGTKVEYGQLLVLLANAQQD

IAREHLQSSQVRQHPLLQRSQTTLEGVGNATFRANHANASGSERQAPSVPPSMEHSESPR

TSSVNTSRLRRLSLYRVSNTLRPSKTDSRARTSTLESSDTSQRMTQNELRNTRSESAASM

DNLPSHTVYTVL

>contig25466 Frame-2F|Blast-peroxisome biogenesis factor, putative [Phytophthora infestans T30-4](gb|EEY70091.1|) 4e-08

MTTRGAFLAPVLVPVKNCFANLPPDFVNAFLGGPDHV

>contig39773 Frame-0F|Blast-glucanase inhibitor protein, putative [Phytophthora infestans T30-4](gb|EEY60885.1|) 4e-08

MMNIIATIIAAATTFAGVTGNTVHTSRQLILGGHPVTDSSHQYVAGLRDSPYENTFCGGV

LITKLHVLTT

>contig43291 Frame-0F

MQRHLVTAIFLVGVTACFVTTLHAINLKNRDDYRRKLNAEPLLR

>contig44719 Frame-1F|Blast-unknown [Phytophthora infestans]gb|EEY62661.1| conserved hypothetical protein [Phytophthora infestans T30-4](gb|AAN31499.1|) 2e-37

MISSWLLFSGAIMAVAMAAHIKVNHHHRGHHQKFREVTVIPDNGICPNGGDVLLCQSASF

ACQDDGTGIQKCLNRDDSFLDSIDSKTAAPWMQCSLTNASLPSSCL

>contig55872-1 Frame-2R1

MVSIKLFATVAAMLAPVLSVRGHGYL

>contig26851 Frame-1R

MILLPIQMPLFNFIRLLLRATFSHALHFACGLDRHFLSLFRDIVPKAHKAVALGEDCMIL

AQTHACTHVVLGTTLANNDVAGHDALASKLFHAQALGLRVAAIFCRPSSFL

>contig27328 Frame-0F

MAILILIALFASSTVSKSTLPSFSSSLDTSYVVQLHGNRDDFSLPGDGSKMRTQLMATES

GQHFECFLPPLHSNTESKEAISLSVPQSPNANEAEKEKSDAFLSFGRAAAEKMKPKCIVY

VGKETNAFYEVCVGLSVQFTDMISFFSPKESLSTVDVEVDAASATSTNKGKDEVLFNKDF

SGFIADSIQPLLRYDYFVLPEVQARVKSHEKPLYTQTFGSDVQIQVQFICNISSQDDGVI

AVQWTGTPREGEARKVAAFLVGSGMFCDPKYSDADPSDVTSVRSLLQPLEIERTCLTRIE

GWWTYEFCFGRSLRQFHRDGDGRIEIEFSLGTFDVAGNLDLERLGSALVSEPIDATHEVS

RPAYLELYDGGTNCKGFESRAPRKAKVFYYCSQGGLSHHILSVKETQTCSYTVKISTPVL

CGHPHFLNDIQKSDQGVEILHCFPVAEDAIVIAE

>contig30517 Frame-0F

MIRENRFPVCLCALNLLEMLLCHLKLKRPLPLVCPCCGTENAELETSQQLSRPHLELLGF

TALMENAFSLASSLFSNRFAYAEGGSAELALAHVFSHSMLVMDAVWKQQLQQDPSTNLMR

FREALVETRKRIVAFLSRQCLPLTLTELDTWGSRQRARCHIFPTTPLR

>contig31910 Frame-2R

MLLSRAISVVALLACILCGAHAQDSEADLGTLLTTLDSSMVTSQRLLRTSVDLDNNEERV

KWPFQNLVTDYLNQKAIRKSLVNQAKKTVNAHDENVLEEAVKKEINAGRVKNVKQALSKL

KNGDPAKAKLQRLYNAEILRNLPKTHNSGQVRISRDKVSR

>contig48323 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54280.1|) 2e-23

MILISRSLAHSITMLSALVRPTVSSALRQRHIFGEHGFLSRRSLSSLNKWGKTNEYIDAR

IVNIVEDGGNVRTNIPIHQAIEIAQSQGLDLVQVSPVGKQPAICKLFDTKKRLYELRKAN

KNATKQQKPKPDKEVLIGAKI

>contig48587 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60766.1|) 4e-10

MRSRITLTVLLTIAFSLRLLQVRAAACDEICYTTELTGFGPGGTAGCTC

>contig52566 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66749.1|) 2e-20

MQLRFALVLNALFTLGVVAESKGKVVKLSVGVGCEFSSYSALPVATASKPSYRLQLDPGL

GRGIYVLLFTQFSLPDDDLVIVR

>contig54494 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67728.1|) 6e-27

MFFWRNMKTLLIMAVILSGVLHMLLLPVEWICTLFLRPETVDASVRAFRYAAASTIPFFL

ISV

>contig12336 Frame-2F

MRYHLMSAPLKPTVVLFHLVMLLSSHWIACLGLVAFDDSSVSSDDSHDNLRQGSHLVVSR

LDEDSDNSMQQVSSVDEDRMDPNSEMIAVLAKKTLSGKSFWKVPYRTVRSGLKRMVMPQR

YIDNPYKAKSAFKSIQYSKGDFVSKFARFDQVVMEGYSKAGLKETEASEVVVKVLNDEIG

PWRAAKLLKNLESVNPELFGRTRLALYRYWNVKQLSFVDFEGGKISSMLGKGETEKAKER

IFNCFSEYFKYAGQAAGREENSAYKSLMEIIENLGYGHVLDGILRSFSQPEINELLDNGR

RIALDYLKKQHEKYNTPSAIIKAVPYWDKGLILMGQPFFRLRALCKTHVKVEDGAVSEVE

LQSKWLIDQLDDWVFDKKLFFVMYPMRRDILAATVLKQLSHRWKGEVASSIAMAQDYIKS

MLEIVELKGTWPMYSIEYHAFQDFIDLAFDKPIPVQIKEAFNGQEGVDELIYKLNNAF

>contig35861 Frame-1F

MISRILLLTAVALLSSTNFVVAAPNEKSLAALEREKSDSIRTMRNFDTISTAGSTNTSRG

QGSPDGKIVSSNVNLEERGPGVLRTIWLAITEPINSYFRLRGYKPSDLLALEKNGSRLQR

WLYSTYASHFERVSKMSKKAANQ

>contig39267 Frame-1R

MLCSLMFLLASSIDLKGLNVVSLKKEECHNIHFLICSDLITPKATSTKQLTSMLDQLKIV

LSRPMNSTTTRVEKHYDDLPQSSLKMADPSTAFERSGWSYI

>contig44894 Frame-0R|Blast-glutaredoxin, putative [Phytophthora infestans T30-4](gb|EEY55291.1|) 2e-67

MSGLAKLVATFTAGSAVGVAATVMMFRQPKHTKRLPILYVYDHCPFCVRARMIFGFKKVP

HELVFLANHDEATPIGLVGSKQVPILQLSDDHAFPESMEIVKYVDERFGGPAVLAPSANR

PELARWIEESAGVFRLLYHPRFHAAPFPEFARLESREYYRKKKEKSIGPFQDALDKTAEL

VEQANGFLEQLAPLLRSTHSFNETLSYDDIDLFGRLRGLTLVRDLDWPSKLRNYIEHMSE

KADIPLLDNMAMH

>contig53388 Frame-1R

MSYRSSRVLAIAARASAARAVLPACTSRLQTASLSTIYDRRTPFEDINRHRSDAEQRIAQ

VPIVEVAGSIAVCDGGGGALGHPVEYIQLDTRKQNTPQTCKYCGIRYMMKVGYHGGH

>contig55100 Frame-2F

MWSFQSLVGSLLWVARCTQQDIASAVHKATRQTHQQ

>contig56291 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY70228.1|) 1e-35

MTAVVLPGVCFVALVCIALRLTRDHKKDA

>contig41726 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60672.1|) 4e-59

MKQGALLLLLLTVLGRTLAVQDAPMPQPARAHCRVFVVLARTRTRVLVLQNAYEQDGINV

YDHFPLLPSIIEDVFDATLKDKYRSDEIYQILRPAFDQAVKWLLNRVDPSLCFAHFVMAE

SETTPDSTSQDKTVATRVIERLDWLRVRAKRDKHFPFALNVPSIKPQDDHESVISSGDLR

VVPSTWRLYFYVVGTNYFSGKVAPSLSPV

>contig48325 Frame-0R

MPWRGSSCTIESHTPAICTVLAIFSIASALALGEIKKGPALSLADYSWKMRYIFKYFLKR

LIFVVPFSDSGQIGKR

>contig56102 Frame-2F

MCFSIYACVLSLPQGGGLCVTFEAVINLLTLLVNMSCNGLVRGYTDLESWMVFLWAILPH

>contig09389 Frame-2F

MRLLNIALATVAVATAGPRFSVSADSQTLSSFQTGVATVDRARRILLSSRSEEGTHLVSQ

PSTIPDEERFWGSKKKKRKKKKHKKHKHKHHEESGSQSLSDVPDSSDSSDPRVKKKRRFF

SFRGR

>contig12648 Frame-2R

MLSKPKTVPLLYLYLLLSHAVVTPTKTTASSNGPQASKESLQNLRQVAHVTTRTLSKESP

ENLRQVSNVTVPAPNHDFLEYLQTRLPVVASPPMNVIPKIHTQDSHGIEDRLLDIGEFRD

AVNTLAKSLQTDQFRPTGIYKYVPKLFQKPQIISSDDSRLLNSLIREFKSEIRRDVIPFP

HNNVRLIKWIKKIKKSFPVRRSAAYSVIAVILSENLGNFKASEVIAGLMQHHSHDFQLIQ

TALFQHWRNKNMGLKNLLEEEEWTLSEDVIKTLRNPGFSVINNFASILEKEDKQIAFVSF

MEKLHDSKLEDKVEEIISLGQRAFPEYVRTPDGYVMFHNDVLAQWIMKLGHEYVRSNI

>contig13838 Frame-1R

MKNLHWLIVLLALGLLTYIETKSVEIPISNTNVHAHGRLRLLTSSTSSQAQTFNEERAFE

ILEKVRQVFHRVLEKIKDSRFWRFVSRKRKNIPHPVDSDPAEKLRAATDRVAPASSSTIV

RFSKSINKYRGDQSINPLKTTAFTVLLATTRTKHADDIYTFLIQE

>contig13944 Frame-0R

MVFSYALIGMAAVASTFVTASPKSLVPLPWDGTGTDLTVETLTKKYQDHILIQRNGGNNG

KPSDYVTINDSGRLPAYTDDQSVINIGVDAKAQFLTQTQLIRTELVRNVTANTKGTTFFR

MSLMKKDPFIHPFPWQLLFTETHIFEIRVDATKSPPMLIYLNNATWDAKHEVEFVYGTWY

NFGIGIKAAASGKGSVLDFYMSEGHADLVLITSHEVSMQFPDFHEFHVGCLAYFDKVVPP

MVPGQDIFSYNGVRILDEVSTSSDGSNLNVPTQMDPTGGSSEKLPAKQSPINPPKCA

>contig22287 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61896.1|) 5e-08

MKSTFEVTVLLAVTGVTNLCMLPAICSLCRRQLVFEAFI

>contig46414 Frame-0R|Blast-Ferroportin (FP) Family [Phytophthora infestans T30-4](gb|EEY68156.1|) 1e-07

MLVIGALMLIPITGCLYAARLDSCDLLEVLKKPLLENQEQHDLKPFRQPRRVKMYLYARH

LLSAWG

>contig51256 Frame-2F|Blast-exopolysaccharide phosphotransferase, putative [Phytophthora infestans T30-4](gb|EEY53591.1|) 0.0

MKSFLALLGFALTVATFLLMRQEPNPPARLADLISGIPLINGSRCDVANLEKLRHSSIVY

TWVNGSENCYNKRRERAGMLHGGTSRDKEMGELKYSLRSLLKYAPWLEGPIFIVTPGQIP

NWLDMSNPRIRIVDQDDLLPKQKNQLLNCDTNVIEQYLHKIPGLTDIFIYMNDDYLFIKP

VTPDRLFSCDGGIRVLTEINHIRHVPSQKSNAWLASVRNTVMLTDQTYGGQHVYNFLKHA

PFVYSRLAFEEIHKKFSKELDKMLVHTVRHPDDLNIPLLHHIYMQEEGSKLLGIPMELNP

LTECDEWLLVRIKDNIDDSLNEQFKMALENKGSEVMLALNDEFSSPKTAELVNRFYAKLL

PDPVFFELPEGQHLSVV

>contig22028 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66543.1|) 4e-47

MHGSSFVGSSILTTFLAIFCRAFTPFQARVPGSEHVVYLNVNGCYEFWKDIDIPLLHLFD

QQHPALYLPFLAIAGNLVANGVPHILVLGVSLGLQFSPLLDGVTH

>contig26741 Frame-2R|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65627.1|) 1e-10

MLLWFGALSSAAALFSGVIADAPFEARARAIVDTFTPAQLLGQMCQLTLGTVMNSTTREL

NETLVRQYAKQYVGSYFNT

>contig30221 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68691.1|) 7e-68

MAALALARSLRVCTGQPAPLLMRTFASATEPNIHPRFSVVDHPVTADSIKPEDYFAIIKL

AGTQYKVVQGDIVIAEKIKNAKVGEIMDINEVLLLGNVNQTIVGRPLVEGAKVRARVEEQ

TVDAKIDIFKKKRRKNYRRWNGFRRQITVLRVTDIVPINAEIA

>contig30971 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60063.1|) 1e-100

MTCSQMQAIVASTTATVCLALYVLKLRAEMTTLGNRKEKTAVGSNKIVYNADGDRLWTAE

ALIAERRSIFPTDYDSDKKVPRDVLKKMLTAANWAPTHGRTEPWRFVVFEALEKRLELGQ

LMATWYQTNVPANKFLQSKYNKMISNCSVSSYVIAICLKRQKSGKIPEWEELCAVACAVQ

NMHLVATTHGVAAYWSSGPPITLAQEMKDYLQLEAKDKCIGLFYVGMPKEDAKVPKGTRK

PIEDKVTWV

>contig31077 Frame-1F

MQLRPTIAALVANVAVSTHSVMVGAVACAEICYGTELTGFGPGGIPGCSCSGLQQGARTG

DGSCTCGQCYEKAQGKVFGFAINADGMCTYGTDCGTCDFSLSWTAGTDKPANVTSTPEVP

FVPATPAPALTTEVTPFVPATVAPSDTVRQ

>contig38856 Frame-1F

MTMRNLLPVVLFATILHQVTAFDSIPDIGGILQSTLSNVTDKLIGTTKEASFQSFFDYNG

EYFAPFGTDEPSKELYVQNDSLKDIVPIINVAPEALKVAIPTNDWWTNLIHVTDSMDVSN

YAAWANPYAVKLPREAPYGLQTFYSFSYREFGDEVNGTVRYYNHSFHNDLTLSSKEFFSC

QPVYEIFEWDEGGAKVRTCDEGSGK

>contig48583 Frame-2F

MMLSINFILLGFGTRAVVSKATEPCSTLTFDIEYIGGDVGSVLSASITGCCNLCSQHESC

KAFTWNGVNGGTCWFKSSSEHSKASIGSISAAIQQLTSELWHMSPVKVIQAR

>contig10442 Frame-0F|Blast-hypothetical protein PITG\_09602 [Phytophthora infestans T30-4](gb|EEY55650.1|) 2e-24

MSLKSIVMAVPQLLTATLLLYYACTFSRQSSAFVHPMVADSCLHQCVTSFMLASLIFSAF

HLSQSLCCTSPVF

>contig24764 Frame-0F|Blast-small mechanosensitive channel family protein, putative [Phytophthora infestans T30-4](gb|EEY57764.1|) 2e-13

MVMRSVLVVGLLSLELVAILSGFTV

>contig26322 Frame-2R

MNIIHTLGAFTITLAAVEAGYSKESDNNTPVPLVVIPETEVDASLKTLQFSIPSTKHPDN

LSPTIPFDKICPFEMAQPSDARITEKAAIKFRPQVTISQGCYPHAAVNEAGQISKGLQAP

DPTYAKCGDPVQGTQVYGRSAWFGRVWAIMYAWYFPDSPIDWQHAIVWTNNPNVSSPVIL

AVTVTDSKGEYSSKVSPDIDGKTTKLIYKNRGLDLTDKDGECQNLVLWHQLTVDAQEKLN

DDKSFGDTRVPFNDDYFLLSLGKAWPFP

>contig40700 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57235.1|) 2e-15

MKFILALTAAAVFSLTNGQIDDYNSEVLDFVNKIRTASGKKNLCFNTKVAAAAQVVAKDL

AYYQIPQEFTTEVHSVKSVLTANKVQVKGSKEAYGVGIDSSEAMVNQWNITHRDVLLSDF

SFFGAGFVENKILEFNQYWVIGVVDIMDGACE

>contig44393 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60457.1|) 1e-12

MARGNTMRGARMLLRFFNFAFSVVALATLSRAFVGSSYYGYSSMLG

>contig54370 Frame-1F

MDTAVKQFRALLSECVFISAAAAASTDVENADIRVKSVVIPVGLSADQLQYWNCFCGDSA

SSD

>contig54406 Frame-0R|Blast-histidyl-tRNA synthetase [Phytophthora infestans T30-4](gb|EEY67043.1|) 5e-25

MASTCVMIGASRLSVADVCSVAALGAFVTLDMKSEAFSTSPKFTMQLVSSTSSSSALPTV

RRAVLVLFLHRLLQAKSVENAHYVAMLLNHPGKTPAQVRYVDLPVGLSQEEQQAFTNVPI

ELLAETALAVGGAISLLPLADAVAAITCETMRADSAAFEADFVDVVRPHRGIVTSAHNLR

MMLDGSKYINSLDKDGAESGTVALRYIPQYHGP

>contig04453 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56120.1|) 2e-08

MSVSFLSVATVLTTVHARTDIVAQLYGNTAITAPMPPQSLNSALEELVVSVANFTQYPAA

>contig13659 Frame-0R

MRVYAVFEVGTLVCAISSVAVAKSAGFKALVKNFFHGGDATGSDTSDRTNTDDRTCLYDW

ESLTCQPESKCSIQYTFGDVTPSQACRITDSGDHTKTPQQFHLAFAGTEPGTGMAISWTS

FAEEDAPGVWIGTAPDKLVLDVDGAIDIVMYYSDKK

>contig22967 Frame-2R

MAPPVVIALFRSLLRSTQTLQRDILAGRLLYNAVRSGAIASYAGIKTDWQREQLFLHCFD

DVKVLKRRTQDDRTYAAIVRAGFVSPVNDKAALNARIDAAFITLKRVDDHNALLQKLIGQ

GCFQPKDRTSAIKFRIGDIIQVKNEKRGVIFAWHMTLKNAAIGPEVVYDVLPHSPGHSFA

SKLYNVPQDEIRLDETPKAIIHSALLLYFDGFDSTRHIPSEALLARYPSDFSKNIQVADR

IVATPSIMHVQSADENELLKYLRCDDSTIVQFAMASLEGKWIGEGGQNAQDHVQRAIRLW

MRRNGVKLVKCFNKSCTMYPCMHTRGTNLPWSSIRAVILAKHSKITKLP

>contig23209 Frame-1F

MEGGLLAILINVSFVAFLATAFFFMRHKLIYKHTQRLRDLAEPLLGIPLSQNDHRLDTIT

REAEKGFDTCIVCEFENFKNALFCSLCGECFEKNQAPYHDLKLKKRCRKGQQESKRNVTS

ALSRCFTARQLRVKKRKEWTRKLDVEGHMFWFRKKETSDLITPASAGKVLYFVKLNANRK

MPEQVKGPEAFESKVAIVEPPTLKVFEDLVSMDIVLASKADAAVRATGEVLESDTQNGVE

CRREILEWAAKDFPSKYAYFVRTTAALLVPPEVEFLKLSIHRDYIFEESMEHLGCIEERN

IRSAMRIHFLKESGVDAGGLQREWLTMLTERLMDPKAGLFKMTHGDDRAFYLNVNSRYDN

GMEHLIYF

>contig27429 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58746.1|) 1e-18

MVVTGMLGSLGGFLWAYQISSFRLQGYKANSGEVQRYITSKPE

>contig31066 Frame-1F

MQWMEVLCTKPPLMILVGWVSQVARTLFQRYERYGHLSSEYPAEFHSLAAEYEGEASRFD

VVRTSESEFEVIDQQTSAGRIVNFAKQTCTCGEYDVSQFPCLHVFLAVTHAGMLRTDVIP

HIFLMTTLKTLYAGRITPIDISTVPSDEITIPHPLPKTRGRPRKVQQIQQFGDPKQEKLA

CSVCGIKGHNKRTCKQVTSIPTPICEDQTDDIATDTNDTFLVSPYGDALSFENSTLEGTD

SESHVSDGQPLCMSSSKRRRLAQNDSAEDKSSDQDEEDTTGIVLV

>contig47746 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62662.1|) 5e-71

MHFLACVVGTASLVAAVSAVQPSIKYYVHVVADGEDCDYLDNVLPMCASKNFVCRMGPGH

EMFAEAPSCIAYDPNNMADNPFLIEESASAPWGVCNPVAELKRRIGDPPVCKRDFTCQCL

QGASSSCICAPPDAVDDVNGAARCENESLACAEDKYCHYLKEGGMECGQKPFNS

>contig50229 Frame-0R|Blast-axon-associated SH3 binding-like protein 168 [Procambarus clarkii](gb|AAD23372.1|AF091267\_1) 3e-16

MMLNKLIFALYLASVALYGITVEASTEVAETVHYNARSAYDRKARYSDDSSSDDINRYAG

RDYSRGYKYGSDRYVSRSRDSKYGASRYGADRYARHSHYRDSKYDDGRYVDDRDASRSRN

GNYGAGSVVGRNAGANAGNQNTGAGLQPIAALNTATGVSASAGTMVTAPVGDKSKDINGN

NVVNGPATTSLTTDQKTSDSVTQNSSDPAVKMTTNPATQNTLDPATQNASDAETQKTTDP

VTQKPADPATQKPTDPVTQNAADPVVQKTSDPVTQKTGDQVTQMSAPGPINTLEYHNLRS

>contig51554 Frame-1F|Blast-SCP-like extracellular protein, putative [Phytophthora infestans T30-4](gb|EEY64509.1|) 5e-19

MLAVLVVALLTMNAHVESFSAEDQAIWIDRHNFFRSTGLPWAAGNMRRVGWSADLASSAA

STA

>contig00005 Frame-0F

MIVPLKLVLAAVVAGYASGEQEPLPVEGRREAINYNDEATTTILPIHHNISTITDPALLT

GLGPVVRGGQGPTLNNPEETEFKTTSLVINHNALKDTDPNIFRGLGPRQRIGLEPSLAPC

QPLPVPAY

>contig06807 Frame-2F|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY58144.1|) 1e-38

MKLKPFLVSTVFMGVFVDAQDNLQVELPAEPEKPPEEWKPHWIKHKDVKPFPELPPTTVA

EKAALMFKPQLKIITGCHPYPAVNEQGEVSGGLQAKGGQSSGCKGSGHGSQVYGRSTWYR

GIWVIMYSWYFPKDQPAPFLGHRH

>contig09745 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61720.1|) 6e-07

MVMLPRVLASLALLLGTTRSYDINVYNQCSGDLPLVHVRPGNVNTEWVASGGSTVKTIDP

>contig24014 Frame-0F

MIEVAWLLSFLSAREEATLQLLLTHGLIAFFMPSFTTTKEELL

>contig25589 Frame-2F|Blast-cytochrome P450, putative [Phytophthora infestans T30-4](gb|EEY63452.1|) 2e-14

MLRQWFVKYRKLSPVGPAGLVLLAGAAVVATYVITRSSDDDVNIVTPLSDHDVNPDESKE

KPKEVPYLPSK

>contig34716 Frame-1F

MALCFLVLQLSYHVVTCLNMAASTGDAPPSDNFLKNLRQGHLIGPPPLRESYLDNLPQSP

HVEEDRYIEVDSPDALVKKVALALKFSLNFPEHEKAGLLDGFRSFLLKKVNNVHKATVSF

RSNVRDSLKMNSPDYTEFLKWCVAIERSLPGRPEKAYAIMSVVLSKELGNWHAARVLVGL

KEINLFRSQKVFQALLHLWQIKELNLAALLSEVELGLLDTPNKVIETFLNPVFAECFEYA

YDMERAGKESVYDSLMVVLKQYNLDSQMDNIIAAGVERLHHAVTSEVEKLRRILHYLVFQ

LNKKTNPIPILESFIIPHGSSNAISRTYDRLAKACHPHGNDEAKSEWLINSLTGSLLEPQ

LLSSCTR

>contig37043 Frame-1R|Blast-mitochondrial-processing peptidase subunit beta [Phytophthora infestans T30-4](gb|EEY57641.1|) 0.0

MMSRLFLVRQPLVRAQSSAAAAASAYPSYVLNAPATEVTTLPSGLRVASEGSHGETATVG

VWIGAGSRYENAENNGAAHFLEHMSFKGTSKRTQQQLELEIENMGGHLNAYTSREQTVYY

AKVFKKDVPRAMDILSDILQNSKLDEAAIERERDVILREMEEVNKQQEEVVFDRLHETAF

MENGLGRTILGPMKNIRNLQKSDLQDYIAAHYTAPRIVIAGAGAVDHIQLVELAQKSFGT

LPTTPAVAPTLEPVRFVGSDVRVKDDSIPLAHVAIAFEGFSWTSEHSFPLLIMQTLLGSW

DRTSGAGMNMSSKLGQVVAEKELAHSYMSFNTCYQDTGLFGVYAVADKYKLNDLTWYTME

ALVRLVHKTTDEEVERAKTQLKANMLMQLDGTSPICEDIGRQMLTYGRRMSPAEIFTRID

AVDAAAVRNTADEVVNDKEHALAATGPIHELPDYNFIRRRSYWLRY

>contig38644 Frame-1R

MKTLLKIIKALCVIVGVAAQSASGVLFCSSLNGPYCDALDAGFVEAPPHARQNLDVDAE

>contig48045 Frame-0R

MLPATRSFMRLPRVVFLSIVYPKGVSSELVLFNRLEFKQSLRRRIEPISSRNNHPVPHSV

IAERFYRVTATLHEAYYPPLPRTLHQRPYIT

>contig09272 Frame-2R

MNPMTSMLAILVAFRSARAATPLIPTLDVLPRANLSARNDKVTRMNPKAIASTEIGDEER

FKWFKWFNSNNAHGTKIVNDVAKLFKGSSYPSHEVVVQAFKSVNSLEDRRDLMGQLVGKV

TKKIGLENFYLYLKGGEGTEFANELERGLYKSFGKVPVESSAKTFLLGKGTTTEEELFHK

PLLDAYVSYSRATFSKFEFYVAFSLLLEYDNKLAGMVKNAKKSAKSNRATIDIIEKGLNY

PIKEIRNMLEHDYVSKNPSDDAVMRGVIRYAEQYVQRNPSKLNHIEQLKLYYKPERIDEL

LPAVVPASPSKTFFARIRDWIWAKLRWMLRSNKVDSVARDDHKLRRQ

>contig11246 Frame-1R|Blast-Dual specificity protein phosphatase, putative [Ricinus communis]gb|EEF45324.1| Dual specificity protein phosphatase, putative [Ricinus communis](ref|XP\_002517161.1|) 2e-13

MGRSRSATIILAYLMARYNLTLTSALQELRRVRPQAQPNSGFYNELLIFEGKQKRLRE

>contig22309 Frame-0F

MALSASLGQARWVVFYFFNFLPSPLSRGQACIEGMETVQPGNGVFFSIRTSRIYESSKYS

GGCRS

>contig30351 Frame-1F

MELIQLLLRLLLLMVGNVTIYQHLPHNYLSPSTHIPHISVNSMTGSRKVSRTCE

>contig48389 Frame-0F

MKFITACVVLCSIAVVGHSTSFDFQS

>contig49463 Frame-1R|Blast-chitinase, putative [Phytophthora infestans T30-4](gb|EEY67716.1|) 2e-91

MFKVITPMFFLGMILVESNYCSQQSLPDVSSPESSSAPVASVTFRLGLSRFLDQRQFQEL

FPDAIDLYKFDGLVNAAKRYTEFANTSDDTNDRLELAAFLAQTAHESDNFKAAEEYARDT

YTVWQYCDNTTYPCAPGRKYYGRGPIQLSWNYNYFLAGRDLGLDLLNVPELVATDDTITW

MTALWYWMTPQNGRVIHDVVTDVNGFSQSTAIINGGLECGSNAPNTANELQRIQYFMRFC

EVLGVQPRGNTSCNA

>contig49539 Frame-0F|Blast-carbohydrate esterase, putative [Phytophthora infestans T30-4](gb|EEY54423.1|) 3e-60

MSSTTHRVVFAILVLAYFRNFVRTFHQHCTLLLRNEPRLTWSKNILAALKYTSIGQLVAG

CEYLLCFEKHRLAARIGRSLVCRPRNCSVNCRYGPYDRNVLDIYGVQGRKQTIAAKPVLV

FIHGGAWSFGHKWQYALVGEYLALQGILVAVMAYRTYPNGSIVDMVEDVENA

>contig56733 Frame-1F

MKVGGALGPVVVAVLVALLLHVYNDFVPIDSYYPSATANASIDSYFSDSYYQAQALFRLT

AKSAGATLFSLPLEHLQPLNLSIDIAVMKGSKDRVLLHISGTHGVEGFAGSAIQAALLER

AAGTVRNNENQPTVVFVHALNAYGFAHLRRFNEHNVDLNRNWLTQEEFQERQAKDPNERG

YLDMYDVLNPTQIHGIRNGFWFQCIQTLITKGFDAAKQAVVTGNYHFPQSVYYGGTKLEP

SLLLLQTFLSKHINLKTIQKFGMIDVHTGLGAAGVDTLLLKAGSNISVAQSVFRGPEYQN

QVVFQDDSNHPVTRGYEGTGGFVFDGVAKMLNPEILQNALFVCQEFGTVPGVFILKATIE

ENTMYHYHSSISRLPYAQKLRDVFYLHQSSFWKTEVRRRGIEAFDRLDAYLTAS

>contig57107 Frame-1F|Blast-hypothetical protein PITG\_12566 [Phytophthora infestans T30-4](gb|EEY60231.1|) 1e-137

MAIGGALSALTTWLWTSSNTTPTTNATTLLTSAYDGAMATFNVAKRMRRVQQLQLKLLSG

NAATCTHVVFCINGFMTQSDDPTKNWRVWTQTNEDVAVFAVLWEAGDAAAWNKFCMHATD

NLRQSSIVNVVAHFTENPWHSAQIKAERVGVLLAQMFSQRPALIRNRKISIFGHSLGGAV

IYSAFQELAKLRAERRHRITFDI

>contig57969 Frame-1R|Blast-hypothetical protein PITG\_00592 [Phytophthora infestans T30-4](gb|EEY57994.1|) 7e-10

MDTALMSFVNCLGAIIMVSVVCFHYLTAKPTDADL

>contig13757 Frame-1F

MKVIAAFILLSSASAPAVAFTDTRIMIESTYTDVLGLNDLAKTAYKERGGKYMGTATDLK

QLDDTFYAEKLGNISEFGMITPTHAMTWEATELTQGVFTYENADKIVAFANKAGSGVRCH

TLVSHDQVPEWVQVLEKAELLKAMSNHITQLMTHFGNSCTAWDVVNEAFNEDGSYRESFW

YKKAGKEFISVAFQTANELKVKLKLRARLFYNDFNINVANNKSDAVLAMATDLRSRKNWV

EGVGFQSHYTTDDIVAGAKIFDNFRRFTVNKMDIAVTELDVKTSTATPTVKEQQTQVGII

TNVVSACKKT

>contig22586 Frame-0R|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY54022.1|) 7e-32

MVILMGLLYSSVFYQFDETNAQLVLGLIFNAVLFV

>contig27930 Frame-1R

MCVTVFTVSASLVSITAAAKSRERATETAATIVVARDAEAHLVRSFFVPRYEIEMITFLD

MLTSEGIEYGGITTCAKHLKIT

>contig28997 Frame-1R

MAILSMHQQKSQKHWVCSALQLVFPVASASASTLGTPMVVAMDIDQ

>contig31924 Frame-2F

MRLLSVTLLTIAALLSGVEASRTLVQTTTAVPTKPNVPATRPAKIDYSRLRRPDKHNVYK

GKPLKRTVNRGS

>contig37625 Frame-2F|Blast-amidophosphoribosyltransferase [Phytophthora infestans T30-4](gb|EEY65962.1|) 1e-142

MALSATFLSKITCLICVETWELATADTRPLVPAQVLRHSRFIPTPRTASHSPHNGNLTNS

HELVDQLANTNFRHVNTDSDSELLLNILASELLKRVDQILDTEMVLDAVTGVFQRCRGGY

SAVVLINGFGIIAFRDPNGIRPLVYGTRQTQYGSDYVVASESVAIATLEFKLERDFAPGE

AMVIKQTGEMTTRKCVANAKLSPCIFEHVYFARPDSFIDGVSVYQ

>contig40429 Frame-2F|Blast-RecName: Full=HAM34 proteinemb|CAA34853.1| ham34 [Bremia lactucae](sp|Q99074.1|HA34\_BRELC) 1e-89

MKFSQILVLAAIAVAAISAQDAAPATTPDTATATTPAAATTTTTTTTPAADAGTASTEQT

TTAGPEAAGATNGTTTTPPADGTQTATAPLDATATEESSASGEMTPTVGTDTSDQVSDST

AAGPSTPEGSMTGTSTPKASDSSSSATDTTSGASHTTMAVACATVMTVGAYFL

>contig42962-0 Frame-1F0

MKRRVILTYFMLISVPLSGPSKLV

>contig45596 Frame-1R|Blast-cysteine protease [Phytophthora infestans]gb|EEY64276.1| vacuolar-processing enzyme, putative [Phytophthora infestans T30-4](gb|AAY43369.1|) 5e-30 NOT\_ORF

MPITSY\*\*FPSSLPSIGL\*LWLALADSNYWHQSDVCHAYHVVRHHGIPAEKIVLMMYDDV

AWHKLNPFPGQLSIGSFPQSVTREELSSVNLYKGCNIDLRGAEVTPETYLNVLT

>contig49538 Frame-1F

MSTLFLRSRRLLPCLAAPALLLSTSPARLEASDTDSASPPAVDFVGVFVETESARRLSQK

FPSKFGAVSEPLVVVLRFQPSIEEQEAFAPLFGRTAKLQVKGLAEDDHVQTVLVEVTTET

GESLEYEGSAEPAHLTLSTSAAGLSAGYSSVLLERLRASDKLRYLLKDDEEKKHWSGELP

IFESEHLPLFSPFPAVEAKLVKEQDELVLEGTICLSSRFDVASGECLAPKAEFGFCKFMK

AGPCGKEFIAWETCLDQCKKRGDDFLETCGPQTLGLRDCVEANPEYYHVLNEGPGEQDSE

LQKEQDSKNLEFPETDE

>contig50154 Frame-2R

MLLAARCASSASPCWLAPMLRMALILMAIKPPSRLTCLARFARPRHHSVTQAPVAAVSQS

PPSSQDRPRRALVRACLYSFRARACA

>contig14328 Frame-1F

MCPEFVAIHATFSAVVELAVANVASALDATPHFRVVVEEGAVVMTARNLLEDSVHIDHFH

AYEAPANTPHQKKDSFFDVAELSLELHTDSGLMIAMAAPAYFELSSTGRLVPKATEGRDA

GLYIQTATGEVVRPILESDELLLMLGSGIEDWIETSPPLRSVLHGMQYPRAVSTVGKDGN

QGPPVFRSWFGKMILLPAHQQMKNTGSTFGHYANQTVRYLMQHENQNTVFSVACPPHRHL

EASSVGTCLVKTCSLKSTSSSSDLKASCPITCNHVAPADVALCSKHCDCIDETKPGTTCW

MLCVENLATDVCPGEQKCNTGPSREQLAMTCPGGLISPPSVAPLSPATAP

>contig25081 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65208.1|) 7e-59

MKTLCDFIILALLAVTTFSVAEANQSPGSNWHYSTPASLTPTVITPKPLSKVVNFVDIQS

FSPNSAFNVKKDTVGYSDDSDDSYDNNGFSSYSNALATVAVPDNINIGSTANTRDKILAT

YRNWIGPSIGKPSDPAFDKACWRKAYIMDTCPDGFNYNTKVCWAQCPMAYPVECGFECIR

QSDVCGAQIYAKFTSVANSFFSFQIMNVFGAFTKLPKTVGIGIKCARAMLGTMRAIVNYV

RALQVSNPQTSKDKILLAVYQTSYITIDLPVSIVMCMGRSYNWEVLDPASVALGTVQ

>contig25517-0 Frame-2F0

MKIGGIWVNFSIVAFDSVGMAKDVHRVATDSRVGRNLDGSKVALVAATVS

>contig27267 Frame-1R

MRGHNLRFLFLAVIAAAVVLLMAGKQRQCLELISIEYFSKQYIAAVSNVSDPDSRALRYA

SKPGIGTEERGIGSSLKNKLYDSAFKWALKFHMNPKLLLYLLNVPFSHPHAEMDRNFGRW

IHYVIKFESFQDEAHRFSESTFYKLLETKLTTEDMAMLFQSLETWPDGERLAGKMQAYMI

LNAPSRDVMHIAWNRVREPPEHVFRILNLENETIPDRDRLITEWLRYCRSYRETESAVAF

QGLRIPDELFYSELLRLLRKTKADEDIIAFLQSIRNIDGMETFTDHIEAVADRTLLTHEI

LLKRVEHPETFFNRLHLQNAFLAYNSNFLKWLSYIAVYNKQPGIAPFTMEKAFEFIRSSS

EVRRLDLYFGEFLEAKMKDVPELKEELRKMQTEVFKYWRSLNIKPLTLWNTVNVHKRGRL

NTPEMKNSFAYRSIQSYTK

>contig30883 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57175.1|) 1e-109

MSLSVNLANASLLLAKASNLLPNSKVCGPPQWRPDAASTSCLCCGNDFSIWLRRRHHCRA

CGELVCGECSPFCVRLPELGFNGRVRVCTDCHAQIDSPFNSSASMLSLSSLETATTSSES

SQNELIGDVEELLVFRSVDVLVHCSREKRLKLRYQYFVQSEAVSWLMDAGIMSSRTGCVS

LFLRLVKCGYVTLKPWSGSARSAFYYISEEITLDNRLSHYETAIHSETSRCYNCTQSFQK

SLAPADGFCSIDCKTNALINQLDSAHIHRFCD

>contig49335 Frame-1F

MREGFARVACGVALLIRRADTTTAADAAEVAMPEQVQSLEAALNNTSGVQFLRSPLMTAF

NEERDLKALVKKLLHIRTNKVTDVNVLEKKVLNDIIAGDDIEKSMKVAEYAIVYKINLFN

KESTA

>contig50948 Frame-2R

MVKVYLAAVAAFVAISISASNTSLANIVPVTSEDDDTFAPGRLRANAATNVNSDERGLLR

TLDTAVWSVIPHVPFLVPKEDAVMTVAASLNKNLEQALREDTLQLKVLKKFVKNHNYH

>contig58672 Frame-1F|Blast-methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4](gb|EEY64588.1|) 7e-34

MALSVVLFIGSSKAWIHDLVKIGQSMTVNGGMEPHTDVGPLITQAAKDRANALIQASCDH

GASILLDGRHVVVPKYPHGHFLGPTVLDHVTTDNPAYMNE

>contig03372-1 Frame-1R1

MTRTSDVAFVLVILVKSAIERCQLHIIWYSCSDIVAVFRLANFCVMLSKMSATKTLNRIE

NSKWPN

>contig19124 Frame-1F

MSSLGTISFLLHLDMLSQGVKNLPVKPNQESSKTITMISREMRDIFFEKVQLTDFGENYL

DMIFLMALPNNAGYTRSQQLVDELIANAVKENIHPADFAIMLQLNSIDPSEANILVLGVF

MRYLKSLNHDTPQLIIDLEENIGQVRLAMLLQAAKTPFDHEQSSIATSFQIDQFKIWQSN

RVNIVLMRNNLNEAEFYGTGSALYNNFLNAFTVYVDAVSQYIEMASVLSPNNLLASKQFQ

DWSENLLAKFPNDQAIVTKVLRHIYTDDELFASLTSQDSALTPTSQYLLEELMGIWAKDI

LASPRTGFFANRENNMYSLNAMAKYIDIMLKKPTITDSDLIDILSLDNLVANKFRLDITG

HIKASEEPINNYELGVFKRWRAGGCTVDRIEKLIEQLSSDGKVDIHKESLADTLVLYKEY

YSSLNYEMNDNDIRKEVSNELIALIAEAKENQENLFETTAYVRWSTVLQLRFPHDKVIKI

QALLGVYGDEELIALLDVPGNTNKIWRQQLLGELVAFWVDENEGTAILKIMREISAKTQS

PSIPLLEIFAKYIALQSREENKMRLVANGDVGGWDLLLAKAIQNAIVVKKSNTMVDLQVA

QFQRWVANNVDYKSVQAQFDEDPRKLLFSETVEPIVRAYELYNIDRNAFLVNVASHMTPE

NVESAINLEQLTMWHDFLAKYFPNHQYMFS

>contig25707 Frame-2R

MRTLVLMLLVAAFAAITLAQTTSSNAASSAATNSPPPMTAELAAIVECNTTQLDDGQITL

TSNQRAEQCEEALDLQAGTMLQVTTADATEMCETTSCRAALQELYNFLPNCRYELWGLQY

SAKRLLEYCGITPTNTTSAGRSRSSAGWSVTSSSASFADVGATEAPSTAAGESTPAAASS

DATTRMALTTFLMAVFGIITATVA

>contig29619 Frame-2F

MSGQKKTGYLLWGAAFILARWIHKHRELFLNKSVLEVGSGLGLGGITAARYATVSTLTDY

QADTCVALEYNVQLNKFFTHELNSLKPEVQVSLLNWDCTDSVEAVPKADVVIASDII

>contig46959 Frame-0F

MKYLLCLVVTIAFLGSTNSQNPQATQALSCQGCTCSLRNQSLSIACLRCCQP

>contig48041 Frame-2R

MQLFVLTVVVVLLAPITALTSNLETSTSEHADDYGTEARSLHWIKLLWTKARGGGGDKIG

AQSQKVSKLESAVANNPSLLLTIKAIKDNPKLQRIVRKFEDNSKFVEKFVDNANVRNLVK

NIENGQKLNPDSVRKLQSDIVAYKNMHYVEALG

>contig50581 Frame-0R

MTPRAATGPLARLVVTNIAAGFAHSLATTNEGAVFSCGYNDNGQLGLGSRRNSAEFQRIT

ALEKYFIQHIACGQQHSLACSSLRDSTKAIKGKNECSDRSGVCFSWGLGVLGQLGTGENL

SWLPAEVKLARPAVSVAAGSHHSVAVTDDGKVYTWGHSEYGQHGAGE

>contig57733 Frame-0R

MLLFCLKIATRTFLSPLPITSACVFYIHSNCIRALPTCTASVQVWCLTSLHVH

>contig59454 Frame-1R|Blast-phospho-2-dehydro-3-deoxyheptonate aldolase [Phytophthora infestans T30-4](gb|EEY69972.1|) 2e-23

MIQMSLVLVWGARMPTVRVARLAGQFAKPRSSDIDVVQGEQVP

>contig10605 Frame-2R

MVHSQLPGKSSAHVQLLLLLLGAVNTSVLSAGVILVANVFSSLCIACIKVGSFLPSTVNL

LLVGLLSRSCQVVSNYVDLYVLAPRKSTVRPLNEICRKKLLPS

>contig27382 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61490.1|) 7e-16

MARAMRWASLLSLLGVDLVCAVELIWEDFYESAMYHTGLGYQCSFVDKPSQMVRQHLQVY

LKGQERATEAVVGAIEAWEFS

>contig37620 Frame-2R

MATKISHVVLNLFVPFQGGIVAESGDTAHEDSSMIHSERAKHPLIVTDGTACVGGNVLSF

CDFFAHVNAIENDFSRVQMLQHNLQVLQKTNVKCIHANYLDVMLQLKQDVVFLDPPWGGP

EYKDLERVNLFLGGQPLHEICSRLQGSTKCIVLKVPSNFDEVKFSQNVPGKVVIRRDLKK

MHLVLLDFR

>contig49148 Frame-2F|Blast-Sulfate Permease (SulP) Family [Phytophthora infestans T30-4](gb|EEY58082.1|) 0.0

MLLFFVVGPNAVSYLPRCMAGCVMMHLGWDLLREALIDTYDQLDTLELGTVWIIAGTMTF

WGMNQGLAVGALLACLTFVMQSARTPTNAPIRGSMSAATLRSHAWRLTAELNVLDRACRN

IHVVQLKGHLFFGNISQLCDYVNVVLQDGGVTVGYNDKNALLPSVLGIERRPRPEIRWLV

LDFTLVVGLDSSAADRLTKLKYVCRTHECTLVFAAVPAAYRKFTDHLMALFGDSADFYVA

LDLDSALEYCENAILRAYGGVCCEPRTLEAPEAHEHDEEGLHVLQFQRFMPDQPRAIQQR

LLAYFTRQIIAKDTVLWRQGDPSDQALVLLEGALTAVVEEEAGTTENVSVGSVVGDMCFL

TGEKRKTSLVATQKSVVYVLDRANFATMIAQDCYLAFLFQGISLRYTSYRLQYVGNRIWE

TKCLPI

>contig53468 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY60560.1|) 2e-58

MPSIELAAVFGALFDSIFLMFMGYNPPASSIPDGYKWLYQLVPHRYTFQSLTALVLGDCP

LDQLQLIAEAVATNTTINVSGWPLGCQPLTDAPP

>contig57103 Frame-2F

MRFSLLSAVAACYIAVASSQPIDLDEVVPFPEIVPQSESDELMLKFKPQLHISSGCQPYP

AVDQNGYTSVGLGVSKVGTSCDGSPLGSQVYARFEEYNSHYAIMYAWFFPRDYMIRPIGN

RFSWENAVVWLSKEDHKLLAVSASGMFSYKKYEPVDNKNLDGDSFKLKYTYLVTSHHYLK

ATTEKGVKHDLVSWTNLTRPALHALQREDSFGDYPKMPLSDNLFGKNLEKAFPF

>contig07727 Frame-2R

MFIKRKTQLWHRFVTLLGIFCLLAWAKTDPIVVMASNAIANHTSRRLKKHHDGYHNRIAV

KAEERMFQIRSIFKGDTIADLVKVEQDLFQSEPFKNWWANSIKKGRSVKDLAAELVEHIV

GIAKYKFNDGNAEMDELKKSIIEVLTEKHGPKDPQDLNGLKDFFTNLGLNADTFEGQSFS

ILLKSFADYPKIRANDKAYYDTLFSMLSKIEQPLERIALHLLQERPKPGESTFAAKALSH

LLVRWHNEGKGLNDIYELIVVMPLQMRITWKDPLIFSGLRRMLKGCTG

>contig12800 Frame-2F

MAPSSRITLLSAFVQAAKVQARHFSVKAVNLGCFLPSQKQHGQCLSTFRFVTSSGGPKSY

GNKSIARIIALAGSIGVTSVIAQMEAGTDKNLEKRFEYAEAVDTIRQQVAEFRLTLRSFK

NRYPKEISINKIESTRICAPNGVSTIRIEFACPSFVNQEAILGRFLLQLHEASTFSSRQI

VEVIPTQLKELNKSIKTQPAVTYLYTNGSGSFQFLRNFSPKREITSKFIFYKDSYLTQAE

IDAVVGAYKEMYSLANVEAFNRYYLDQRQNSALIERSRSPTNIATAISG

>contig28485 Frame-0F|Blast-serine protease, putative [Phytophthora infestans T30-4](gb|EEY67871.1|) 2e-51

MRVTWGLWLSTGLFGCCFAALEDAEGLVFVDAAALCAFHCSHALLSPASQCSPELCGRRR

RTLEASDTSENPQQIDVLSCRNIEQNASTLAFSMTLSAADSAQVFEGFHHAFFEAYDAML

GGDSVTADACQLAFLQDKMLPTVEDD

>contig28694 Frame-1R

MHCCMPILVVSAYIALACVSNAELNAVDRRIPQSRALAILAETTTGKKSLRTENTSTSVT

EPRGLFDTIKQLWTRFCKWLASFMPAAEKVHMSPKAEFNGRPELSQSESNVVLDPTAKLE

KTRQDGPGTDTMPDTTKIKKSSSNKKKKSFFSFMKSSKRPRKSEKAQALKMQPG

>contig31920 Frame-1R

MVRIYVAALTVVLAFSASCSATSPLTLAKATPVTANGSGGRAQGRLRAHTTTNVEIDERS

ISDVIYAIARQVADHRSNLVQAPKRTYTTYLATLDLSLDKVLEQNWSELRLLYVKQTKRK

RPKDFVSMYELLVKKYGLLKLTDMMKKPDYISLSETDNFKYLYDEASVYWRKNSVLKQYA

SELYDSKGNSKTFDVTDFESLQPFFERIGRRGDYLEITAAEHEKWKTNKLRPT

>contig32983 Frame-0F

MKNAFVSATALIAAAAYSSAADCDISTIEGLLSPKTMKGLADCGNATGINIFSVAEFPTL

DQVETLSENVKCSNSFNQINQVANTEIQCNITIEGVSINFGGLISSFLSGKTGNESDSGS

GSIQIQLDDSMGSSLDYFASKSNSTSASSSSGSTVASPSQVLTFIAYGIAIAVGMCL

>contig38642 Frame-0F

MVQSFYLIALSVLVGMADLGASKKSNQAPNFLRENSSAQVRSAEDDDERAILNLPGRFYD

SLATATAVKELVAKRKNMKQVLEFLQIPLAATAEELVRHSNFEVFMLYCQMKMPKIFKNG

NPYGVLIKKGEPIYFSEEEFNGNLYFWLAEGYS

>contig44995 Frame-0F|Blast-CorA Metal Ion Transporter (MIT) Family [Phytophthora infestans T30-4](gb|EEY64528.1|) 1e-31

MLLRWATSRRSLVFLSPVTASKNAPPCTTLNHSCHYLNRLTCRSFKSLTPDKPLSVSPTV

HGKDLLSLVSRARDSHPLDWSEGVSSVEDVDQWDLMDPHYDLTTAKLTKLFSLFQPNGIK

>contig51658 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57216.1|) 1e-39

MVLPRKNVAQGLLFLPPVLVSVLLFFVCGASGVSALSIGMLSSFAFCDVWYFLRMGFDTL

RPAPRGSRKHLFAVSRIKGRIGLMDIDRNGHCNNARFLRECGFGRRDLW

>contig55795 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66324.1|) 2e-24

MLGSLLIFLKVWDPAALQRSSTTSLSPLASSAIFPFPDSLLLPSSRTKLRLAYGFATE

>contig57102 Frame-0F

MSIQRLGSLLTLFLTCACASDWLGISPELQQKLTSVS

>contig57810 Frame-0F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 1e-61

MGADSFGTGLLVLSAFPIASALYHSFSLSGRPYALHESDFVANKGVGLLRIETPAGLIDV

YVTHLVAN

>contig20437 Frame-0F

MQTRNFLVIALAAASQTAYGKAHIETISGPIEQHDNSQFAKQWTLQSDDYKNTLDSIRLS

FNGKALIHRANYLPEGVLGFVNVTGHSFAAVDAVSISHEDAYYDVADRFDDFDSEDVSDS

DFDFDSGDNLVGRYLDISVPSDRSSGHVRIEITLAPYRSVRRIKTERKANVVIENNVLIN

SGAKATLAIKSVDYSSVLVESPRAYVTLQVLSLKASNSASITYKAGYLVNVGLLKVSSIQ

HAAIAFVCDSIKVQRMQLKALVGGRMCFSAHQIKARKHDVDGKKMISMSNANKKYGTKGD

DSCRANDYRFL

>contig23915 Frame-0F

MRLHHILLASAVAVFSSRVLGAATQETRNLVAFDKLEGTADGPTDDDADVDAETTNKAFQ

SGATSDPADSPAVSTTAVAGSKSEEINSILTRLQSDLLDLIGSDDGSKPVDPNPLGENGS

KLTKLMNFSDPNFLKILKPLGLGGLIGADLNVKQEPEAPTAPENPVAPATPEAPLADDTD

RDELEAAVAAMIKKKKMQANGSDGPNDVDPTDPTLKKGLNDDETSGEDLLTTTKSSALPT

DDDGPDSTYLSSIAKTPVVPTSSDEDNDDDINSLNPTLDKKTGVANTKSSDTGVKSPTTA

GDGSGTDSDFDGKFDKLLQMSDSELDDLMTSDKNSSAAPYLAAAQKMLEPVESVPGENKT

AKGEAYLSKLDSMLKLSDSQLDDMLDSMDITSLEGLKKVAGTKDVAVSETTTTPPNTAKT

TPSSNTVSKSAPVLDDGQSDADVLFEKTPEKEDTLEVIPPAEESSYLKGLYALSDDDLKA

PAPAPDTKSPPKTIDDNSKTEDSMSDVEDFDTSECPTGFFGHIKSWWKNTVGGGDKCALE

RRLRVVV

>contig25603 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 4e-09

MVGMHMLSIVALKWSCIMVVGLAVICGIESVLEFLFLTFECSTFNELLNEVQLDLYLQEH

RMASDKELVRDK

>contig28675 Frame-1R|Blast-NADH-cytochrome b5 reductase, putative [Phytophthora infestans T30-4](gb|EEY59645.1|) 1e-136

MWSTVIMRFPARAVLLSRGALVTAGLAALAALSVPSSAVQCEEKSKVALSPKEFRSFTVR

RVETLNHNTKRITFALPSLDHVMGLTTSSCLVARAKVNGTTVVRPYTPTNVNGEKGFLEL

VVKGYPNGNLSKHIVNLMEGDSLELKGPYLKFSYVPNRYKRIGMIAGGSGITPMLQLVKT

ICRNPEDRTEITLIYCSTSEEDIILREEVEALMYLYPQFYVVHVLSNPSADWKGLTGFAT

KEIIEKHMPEPSNDNLVCVCGPPPMMYHISGDKAKNGSQGELQGLLKDLNYTSTQVFKF

>contig30234 Frame-1F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY69528.1|) 8e-12

MVTLMCVIVGVAGKAFPVDIDDSKFVGHLKKAIKQENKNEMDKVDAKKLQLFLANTV

>contig41195 Frame-0R|Blast-synaptic vesicle glycoprotein, putative [Phytophthora infestans T30-4](gb|EEY59841.1|) 4e-36

MGPPPHLAALLSVTASVMCTGAVASRWISHGTKDNGDALSKRSSGENASEAVPDISPVVS

RCGGDDDEEGEQSGLIRYDFLHREKNHALL

>contig53237 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60187.1|) 1e-19

MSALLAGFTMSTIIEVQIADATSEPVLIMYGTVCCLE

>contig55815 Frame-0F

MFRKIGVTLSPFAILSIAEAAEQYDTDKKMLYAKENLLKSRSDFKSKPRIKDSKTTASTL

LGTGPPKFPYLLSVSAGDNPAIVINTLLTGIKLVGPYEEPARDTIKRITAPASALGLAAC

WVATQYSNLKKKMYRHISKGLNLHVNGKVSAEDVMMEAILLALRDLQMDNIKESTKNAYD

PINSPTSEVNNRLVFLLRDFDLFSDEEAERWLRWTHLVLHENLVHVILHITSTVTPSKMQ

WIQERHRLGLSGDASGKWNDFIGILVRPAHGLVDCSSANEKLHDLAVRL

>contig57783 Frame-1F

MKNVFIPLAVALAAVPSYGQNFEQCSSDGFKAGSFNVSRSTFSTNVMCITYLGASDTMIS

WM

>contig58470 Frame-2F

MLHLWILHFWLACAFSCDRLCPHASAFCGSITVDVGVRTSRRLRRIRRGTR

>contig17632 Frame-2R

MPVKYYVFLHIAFVISRLTEGSAACRPMNPPSYPLHGPGGMAPPTSSIPGVQRPAGVSNP

NYFTDKKKGEVNELKNLLREVTIEKDLKRKREIIKKVIAYMTLGIDVSRLFSEMVLCVDT

KDLISKKMVYLYLTNYAQKNSELAIMCINTLLNDCRNEDPMVRGLALRSLCSLRLDSILE

YIHDPLQASLTDTSAYVRKTGVIGILKVYSLNPEIIKESDMIDTLYNMIRDRDPQVVSNC

LVALNEIMADEGGIAINQPIVMHLLSRISDFNEWGQCNILEIVAKYKPTGPDEVFTIMNT

LEQCLRVSNSAVVLGTAKCFFNLTQARGMEPIQDQVFERMRQPLLTLMAGGSHEINYCVL

HHILLLVGKKQQIFSRDYRQFYNRYNEPTHVKYVKIDILALVADGANVADIITELSEYVT

DVDQELARRAIRAIANIAGSSNLLVNTVPPQYLGTNVPDAYGQQAAEQLVEQTQDHILDT

MVDFLELDLDYVRDESLIVMKDLLRKYPDKRHDVFASALPHCCGRGSASSESCSRVDAWR

VRSRLASSAVRVGKAD

>contig19920 Frame-0F

MLWGLFLVAVVREALLILGVLRALQECGIHVDVVGGTSIGAFIGGMYAMHPNSLDLVEVK

VRQLSMRLSSIYEKLCDLTLPIASFFNGSRFNESIRALFYDLSIEDFMLNYFCVSTDIAK

SRMNVHRSGPAWKYVRASMSLQGYFPPIFENGSLLLDGGYMNNLPADVMKEEGGIKYIFA

VDVASESCTDFYDYGTTLSGWWVLWNKLNPFAKTVAVPSMGDVSAALAYVSSEQHKDRIK

EECVDLYLRPPVKDYGTLEFSKMEEIIEVGYKYALPRIKAWMTRVLDAEPDADIKKASVA

G

>contig23961 Frame-1F

MPRFATFAVTITTLLPLIQGFTNPITVKGYKLFDLTTGDAFGVKGINYYPRPNAGELDTN

NVDFFTDDHEEIWRPDIEHLAQAGANVVRLYAVDPSKSHDLFMCALRAKGMYAIIDLGAN

CENCSITLDEFPTCYP

>contig25178 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63589.1|) 6e-23 NOT\_ORF

MVTASRVLLPLVFLIKGLAHHSFLLDLNGISCAFYRVDI\*TF\*FRFVLRL\*TVTYLLYRI

SAENEKVLQFDFFLVAGDTGSSCCEIKPLGHTFFNTQLGQCLLAVCLGPELLVQWLQLTL

ALYSLHAMAATDDEW

>contig32123 Frame-1R

MPQALVATLSPDLWTQLLMFLTWRDTNAMCCVCCVLNRIVNEAKKWHPEWRCSVLGPSVN

SVESLKLLQRNHLQWADTRFTPNLVILSAASKDSTPWRKGKYWENAIAAIEKSRLLPRAC

RIVGVFSMNAVLGSTEEVEMNDKRDEISVTLSISVAHLPETTIEMATFDRKDLRRSQQGD

HIENPFLTLKANDSPAFMLFGVNDQSARQLTRILAKWHPTATIIGAVSPLQHCCVPVATY

CKVSTDYQKPKARKTYRVKQEKYLTFPSTLLLCLNGSVGIRTSASSGYHVITPVMRCERV

RAAQDVSQALTYDTVSVVGAVASNAGSHYRMLDLVEPSERYAIQEEGRPLNNFLVKTVRR

LETWSIL

>contig36219 Frame-2R

MVRSTSKGLTSCTVRSLMLLAVFALSACVATLSTGPNTVTRSSYRHLRELPDTTTSALSE

NRINSYYDSLKAMAQQLEVGILTAIDGLFDVLLAPIGRPTPKKALDMIEFEVMSSLPRFA

DRDYYYNEVFKKLLATYGESQLESLINHPDLVNNPIRDAMNARLQQFRALNRSPAYFPTS

LNVEEVRSEVNSVIPSSLHAM

>contig45503 Frame-0F|Blast-prohibitin [Phytophthora infestans T30-4](gb|EEY58193.1|) 1e-144

MSMASRFLNRVAGVGAAVSFGGFCLQECIYDVDGGHRAVIFDRKDGILEKSVGEGTHFKI

PFFQYPTILDVRSNYRLISSRTGTKDLQNVNISLRCLYRPNADKLSHIYAEYGADYADRI

LPSVGNEVLKSIVAQYDAVELLARRNQVSQQIAKEMNERCSNFFLLLDDVSITHLEYGPE

FTRAVEQKQVAQQDAERQKFVVMRSEQERQAAVIKAEGESEAARLVSDAVAKSGSGFIEV

QRIDAAREIAESLAKSRNVTYLPNQTGGNGGVLLGLQ

>contig49983 Frame-0F

MSILIALILTNAALAMKVVSIQMLTDPFALEHSTNACVKAAYRYASSMDVADPTGI

>contig55476 Frame-0R

MIPISAFWARTAIMTFPALHLLLQPWSRTIKML

>contig12320 Frame-1F|Blast-calreticulin precursor [Phytophthora infestans T30-4](gb|EEY70179.1|) 0.0

MLTKLVVALAAVAVTMARAETIFRETFDDADWESRWVASTWKPEAEVGKFEQVAGKFYVD

DDDKGIQTSEDARFYALSAKFAKPFNNKDKDLYLSYMVQHEQQLDCGGAYIKLLPADVDQ

TTFGGESPYSIMFGPDICGMNKKTHAILNYARPGEDAVNMDHKETLRTESDSDAHLYSFV

LKKDDTYEVKIDGKVIKEGKLAEDWPFQPEKKIKDPAQSKPKDWVDAVQIPDPEDLKPEG

WDDIPRTIPDPNAEKPEDWDDEDDGDWEPAVIENPEYKGEWKPKMIDNPDYKGEWEHPLI

DNPDYFEDDAMHNVAKNIGAIGFELWQVKSGTLFDDILVTDNEKDFIAHEEALFSKIEAM

MAKKKKIQDEEKARLDAEMKAKEAEKEDEDETDDEATEVEGEAKEDADKAKDEAKDEAKD

VADEKDEL

>contig19923 Frame-2R

MATVLHLAVVVATLALCMPLAVNAVPAELCSITPLSFEPAKTKYPKLASAITELEKYSIA

AWYTDRQSLADKETMLQKLVTECSEDQRMTIVVYGLPNKDCSGGHSTGGSVKTTADYEKF

IADLVKAVGDRKVLYVIEPDAIGLLAEKDGCGKDAGYLENIKIAIAALAVNKNAELYMDV

GYWTVKSETQLPVVVSAMKDLSASSKLRGIVLNTSNYRTTKEISELCSKFQKAMGNTEMN

CIADTSRNYLEPVDDEWCNVLTNGVGAVPTSDTKFKNLDYLMWIKVQGESDGVCNGGPDA

GLFYDKAFIKLWNQGYFVKELKMKPIGDGDSDVSQTDYSDADDPVQKTGLPEVGGESTVT

SEETSEIAPPPVMNCKLKRRMRKL

>contig39626 Frame-1R

MTLGRSFSVLAIHALGFILLARYTSVGVRAHNLQRLQDFRGHEYFVQFGLHQSEDDPVEP

PVYEDYFPNAILDHFAPVSKRLLWNQRYQVNEEFWGGHGFPVFLYIGGEGPLGPKAITNH

TFIYFLAEQHHALLVALEHRFYGRSYPTTDMSLPNLAYLSSEQALADLAHFHAFITEKYS

LIDTKWVAFGGSYPGNLAAWVKLKYPALFTGTVASSAPLHAKKNFYEYMEVVGDGLRYFG

GGACYYQVEQAITKLGKALDGAQDDREQVLALFSPCYPMTTELDDSVFATSIIGAFQDIA

QYNRIHEEVMTLSDVCKHFSKPGDAINKLASFINSTRVGNCLDSKFQGVPNGTIEVLGRD

QFDGKSSARQWVYQTCNEFGYFQTTSSRESPFYALRAVTEANIGSTICSLVYQMDRAPDI

ATTNLEYGSLDIFVEHVTFPSGTIDPWHALAVRNSTKLPSMTAKAVYIEGTAHCADMYYP

STRDSPELVWAHDQIAARVKSYLVETDRVVAVE

>contig41197 Frame-2F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY56896.1|) 7e-50

MFVLQQSTLALLLSFASVSSATNLQQMAPDFSPVVSSQPSDLVAHVNMERANHGLANLCT

NHKLQAAAERHIMDQFKTDFMSDTGTDNSHPEQRITDAGFEWQSVAESVDAGDANATDVL

NWWMKGENRENVLGKYTMVGTAYVYNEMTFNKHYWVQVYATSSSEHCDS

>contig51655 Frame-0F|Blast-GlcNac transferase [Phytophthora infestans T30-4](gb|EEY68842.1|) 6e-59

MKAPAKTLLLLLGGLLVIYGVAVGVESHMSIINTKLSIKLDPSVQHIPLDPAKEQLRPPP

VQIPASFDIFVGISVFRDGYRCGKTILTGLKRAKYPKRLYFGVVDQVDDGDERCMDEYCK

MAEAEWPGKGSCPYNDHIRVDLRKA

>contig54959 Frame-0R

MMASMAAAILPLFLSIVLRSLLSNPFPKLRLEFNQTILLISHTHCASHHHK

>contig17308 Frame-0R

MRPSGFVSLSQLLALPLFQSVTSEQIKEVVRTNAKKRFSLTTDESGATTFIRANQGHTLQ

VVQDEELLTPLDDPCAIQKCVHGTYLDCWDSIWNLGLSKMQRNHIHFTEREVMDEQVVSG

MRSNCNLLLYIDFSLAVSDGIKFYKSSNNVVLSPGMGKTGVIDRKYFLQAVKRDGTVVYK

RD

>contig22177 Frame-0F|Blast-aspartate aminotransferase, putative [Phytophthora infestans T30-4](gb|EEY66202.1|) 1e-102

MGFWLFPPSMGWLRSSMLVMASETYTSVASPIQHAARRAFVLDCVELASYKRKCQKTLQL

IGRWCAYQLQKMDVEVQVPEAGFYLFPCFRRHQKALSLRGIFTDEQMCAQLLQGTGVAIL

PGSAFGRAREEFFARLAFVDFKGDIALYL

>contig22748 Frame-1F

MVSYNGSSRAPTVSLSLLLILSVGNSLVASRRSIRPHLLQTRSMSLRTVNGAIASSRKQQ

LQQLQRIYCQGELLHEVQMQELFTDSKHFVDMPIKAQSSVSNVLTQFQELKASFDTKPKG

AEWKAQLETFVERHFDPPGSELVPIAPPDYKEGVVPPKIMKIRDERLRDWAMELHKLWNV

LARVPASASSDQTSRTSFLRSLPILSAPDASQNVLARQFNGENVLVVPGGRFRESYYWDS

YWIVQGLLVSGLHQTARGVVNHLLEYVAEFGFVPNGGRVYYLTRSQPPMLSDMVRVVSKI

EGVNETDNSAWDLQYLQAALPLLEREYEFWMQRGLHGHAIEISSGGETFVLNRYVAHSGM

PRPESYREDLYTASVSHINESDYSSLYNEIIAAAESGWDFCSRWFDDFSTLAATRTSQVI

PVDLNSILHRMELNVAKFYEVLGNPVASARFQDAAKARVKAMDAILWSEPDGCWKDYILE

SSMHSSVVSGSDYFPLWSGAFDASNSSRLDRIVTSLKASGLVQEGGIQSTTSITGQQWDA

PNAWPPLQDIIIEGLQAADTVSSRALANRLVQTWVKAGLIAWQETCLMFEKYNALQIGGV

GDGGEYASQFGFGWSNGVILTVLTKYQEQINLDDLAENARSNDTCHKFPNEG

>contig28698 Frame-1F

MVSRWKLLLVLLSCTSHALIAEVANAANHTYFRPSGPDVSGFPRPNSAPFHRSPCPALNS

LANHAYLPRDGKLLTPQLIHDAVVNVFHIDSTLAERFTHSLPPQLTLADLSVHGLIEHDA

SLVHDDAWSHHDPAYINSTLFDCLIAQRKNGILNKRSLAMARRERERQCKKENPTYALPI

KTQVAAYGEAALLLIAMGNYETETITVEAMTSFLLEEKIPDKFKRSPKPITTATVLFVAA

QIRLLALLLKAEVDTTDASAGF

>contig33052 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69371.1|) 5e-09

MVLQKLAMFSILMVLVPLSTFFGVRSLFRPG

>contig39528 Frame-0F

MWLVASTFTLVVSAWMIPAQATIEQEGGMIMQLHRRPTQNNYPERYMRRLTKEGNSPELV

PLHLGLGTHYTWVYAGTPPQRASVIADTGSAYMAFPCSECDGCGNHTDAPFNINNSSTLI

HVTCAEPSIFQCTSCEKQSDSCMYSQSYLEGSTWKASVVEDIVYLGGDASFKDVDMRNQY

GTHFHFGCQNAETGLFVTQVADGIMGLSNTGNNIVAKLFEENKIGRNLFSLCFTENGGTM

AIGHPFKSAHRGEVSYVKMLTDRSSTHFYNVRMKDVRINNKSINAEKEAYTHGHYIVDSG

TTDSYLPRTMKNEFMKAFKKHTGRAYQSGNSCKSFTISDLAVLPTIQFVMEADGDDEAEV

VLNVPPEQYLVESNGAYCGSIYLTENHGGVIGANIMMHRDVIFDVGNHRVGFVDADCAFE

GGNATLPPSIHKSIQCIGRNTSRRV

>contig41196 Frame-0F

MVLRATRRILQAALLVQVLQYKAVIVTSSDASPASFAQVASPATVKPYSVPSYNIQETVN

DEERAFGFDDRENAAPSPEDAAGNLITATPVPGTGDRPTYASLKSKYGSLVDDMREKMDL

GPVAAGPSAGSGSSGAAPAESTDVALTDTKAAAGAEAGSG

>contig49008 Frame-0F

MTSIEEVALARNLLSSVLAIALPSGLPTNVAALKAFSIQQKTLCDAFERHNVFGIVTDGK

ALMKWQTRLLDLVNGLAPARRIGWELFSFTMRQSPFERLESLCPTLLEHAVKAFKRHQSN

KSEDEDTVETTSAVCNVVQVLVQHINRMNPETRREALDLLSKLLPPLVTRIASKNQQSPA

FLAPFELLQTVLIVSPTSVRHHILKIETACVTALFSKSTSNDMLLSITNCLALLSNASAS

PQLVWTQMAHNALKRAHEYLDVFAGNSPA

>contig18535 Frame-2F

MKTLIVFQAAVTALVTRYIAAFDLIPSVGEFLQDTTEKLVGLEKSSETIEYFAPFGTDEP

SRDLFVFNDSLKEIIPIINVAKEALNQPVPTNEWWANLIHVTDLGSESNFAAWANPYSVK

LPRERPYGLQTFYSFTYREFAKKINGTVKYYNHSRHNDLTLSSGEFFKRQPVYEIYEWDE

VGAKLRTCDKKSGKCMYSALVSGMAFVSAKYDGLVPRIDSEHNITHVDDSTPGKFVLYLN

NSQTWVMYTSKPVSFHIERKVNFSVNATGSSLVADNEYFGTIRVALLPEDARDDIYDEYA

TCTILGGTVSMESRTSYSFDWEVEGTTCDTTGLLHFALYHHLESMVGPVTTYTTPGAIIL

NAATRGRMVGQVCTVPKWSFYEPEADFEVDFYPIDRPTPYIVEKIDLLNTLKKDITANWT

GWDVDSWYFNGKTFQKFASLCIMASDKLIVGDDTKLLKFCLQKLERLIEPVLNNTLTPFL

MYDTLYHGLISTSIFRNNNIYEEFGNSIYNDHHYHYGYYLVASAMIKHLDPHWTRLPELE

RIIWTMIRDVANPSKLDPYFPRFRHFTWYLGHSYSHGATSIDNGKDEESTSEDINFCYGL

LLWGRMTGRKDIEDLGSLMLRLNAHAIRTYFLLKRDNPIHPPDIVRNHVTGIFFDNLVFY

NTFFLDEVYAIHGIQMIPVSPINRLARTSVFVEQEWVDIVSKTSIVLDQNSNNTWLSLLL

VNGATVEPMEALRRLPMATMDDGLTLSWALYNAATRCRDDVKVNNPSGISITIELLGNFL

TIEAL

>contig18913 Frame-2R|Blast-fatty acid desaturase, putative [Phytophthora infestans T30-4](gb|EEY68973.1|) 1e-84

MSLAQGLAFFMIAQMSCGAFLASVFSVGHNGMSVYERNDKPDFWTLQVTTTRNITPGIFI

NWFCGGLNYQIEHHLFPLMPRHNLQKVNPLVKSLCREFGLQYHETGFCRGLVEVVDELAN

ISQEFLLEFPAI

>contig31422 Frame-1F

MISLSWHALIELFTGLPAPSLLDTIVIPDDKTPRVLPVNLDRLDVHLQKLRNYLAEIKQE

VVDRKERKRLYQLGQAEGIVCNFAIGNSVLWSRVDKRMRGNKLLVRWGPFSCHGGSSIFI

YDNASFNKRYI

>contig31880 Frame-2R|Blast-GPI-anchor transamidase, putative [Phytophthora infestans T30-4](gb|EEY65990.1|) 1e-41

MNMSRPNISVWSLILLALHAALGENYHRHTNNWAVIVDTSRFWSNYRHIANALSLYHSVK

RLGIPDSQIILMLADQMPCNARNCFPGQVFNSRTQKINL

>contig34465 Frame-0R

MLGLMMAGAIALVLLVALFVYKKTNQLVQDDDPGLERGRHDHTQGVAQASTVAANYHQNH

NMSPTGFSDDNYPPNPGNSQFDQEPYDHDGGRLTYNDPNLDMLTPRSQIALAHSQMSLPP

MAQTNSSHGTSQYSQYSSQSSSFYGQSMYSSGHSGNHFQSKYDSRHREDLASEDESDFGG

DSIQDLSNGWHGMGQKGSKKTTKRPDMSLDESFFEPKDSRSTSASDYHGQTRFQASGQTE

YRMSTADESRYMGDESFAATNSNYDQSHYNGDPSFQSSGFSEFEASGAPRRRGDSSNHDA

SSFYRTKDSRFTDASYY

>contig44880 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59509.1|) 1e-62

MLNFYDPVTIFVLRVFLVTILAEVAMSNRYIDVGGFEAYEDNDGQELTLKMLVNISAKKA

FNAWLRCGWLGRSSIIKQSEGRELVGLRRVILPGVEEQIVSAGPPDSSGRIPSVRYRIKK

SGPLLLRDHVAFVQFVADTTAPPSQPKTLILWNSKLTPSTVGSVLLCGGSISRLILRIVL

SDSLSKIPALLQQDQS

>contig47052 Frame-0R|Blast-calcineurin-like phosphoesterase, putative [Phytophthora infestans T30-4](gb|EEY62213.1|) 6e-46

MPVWQNLALALSVFFGYSAHARSLTATFDLLSYNDVYELQQDTVEGLKLGGPSRVVPIAN

AMRRANPNSLVLLAGDTISPSLWSARFNGQQMIKAHNAIGLDFASLGNHEFDYGLDNFLN

VSRTSNFT

>contig31665 Frame-2R

MAALHRSRLLLLLGLALLSLVANVHAFEFNFGFNGGRHDQVKEHEHVDFYEVLGLTMEAS

EAEIKKAYRKLSLKYHPDKNKGDEGAENRFHEISRAYEVLSDPQKRQVYDLEGFEGLERE

EKSADRPSSPFDAFFGGGGKQRGPDASVDVPVTLEELYNGATKEAQFTRSVICRKCRGTG

AKGGKTTTCKKCGGAGQILVQQKMGGFSMQMQQPCPKCNGRGKTFKKACPFCHGHKVVKE

NKVLVAEIERGMPSTHQIVFERESEQRPGIVPGDVIFRLHQVPHKNFRRVGDDLHYNLEI

SLEEALLGYEKPIKHLDDRTVLLASTKVTTPFEARTVEGEGMPVHNYPSQRGNLLVHHEI

IFPMTLSEELKELVKTLLPEDDPTVAVE

>contig46252 Frame-2F

MIKKGRLRSHKRVAKLGPNLLYFLAVLEVVRGLCSDIDLTGSNVPFPMMRDVMTY

>contig46502 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69280.1|) 1e-61

MIGPYFAQVPLSSTMKAVAFAVAAILPGARGWTDRWDYSQRFAIAGHAQLYCDGENQLAS

CCICKAIVNEVETQLNNTQNDYVMEVVFRISEEKKQIKYSRSEVRILDVLDDICDRLPLK

LQGDSHRTKRIMSDACNGFVGEYEDELTRTFFDDFTPAKDRMCGGTLQVCSHADKRLKHD

DL

>contig47880 Frame-2F|Blast-cyclophilin B [Phytophthora nicotianae](gb|ACR82294.1|) 3e-91

MASPLISVLVVFLAALALKVEAGKKPKITNQVFFDVSIDGNHAGRIVMGLYGNTVPKTVE

NFRALCTGEKGLGESGKPLHYKGSIFHRVIPNFMLQGGDFTSFNGMGGESIYGKKFPDEN

FKLKHAGKGTLSMANSGVNTNGSQFFICTTKTSWLDGRHVVFGRVISGFDVLDNIEAVGS

QSGTPSKKVVITESGEHLGNDIVAVE

>contig49095 Frame-1F

MNGCTSLLLKLMLVGVAMCLSFHTVGNLQNYRLDSLVNG

>contig57535 Frame-0R|Blast-crinkler (CRN) family protein, putative [Phytophthora infestans T30-4](gb|EEY60146.1|) 4e-07

MRNIFRSFGLVVIVSSTSGTARNLVSDSAGSRNTLDYLWCIVHPLLPRTAIDSDIMILPT

ILQGIIANSRPLFAWTAVQYMRKSRWSEGSNTANYLNALVGHLAPMFADMKPKRLHEFKI

GQLCLLLCSSYRAEDGKVNLIDSHYACLDEKTMFRLMLTPTGELYKVAEIKANEAKIKAE

DKRTWECRSVFPHPANDVLLHLTLTGGLDYRPFDHPLREVLASVSTTTM

>contig06710 Frame-1R

MHVYTSVSVVLVAVSVCSVPLVRSKALNVRDTVSHESQFEFVSKNTTGEENHSLRSAETA

HEDRMPTGFGKKLSNLLNKSSRNDLPFAISTDGEPLSKPLLSKSLNEKFSAIENEFKLLS

KNCQSMVPRLSRINKRDAERLIEWIEWFSKARDPPAMDPRTALEFLGLLTSFKVNSMNIV

TAFKLLSYNPKLVQFANVALKEMGSDWAFIETLFQSWKKNKKDPMKFLKLLPISDAVMNN

MLVMWLKHFQDYYDVSSKPTIQTIFESLKKPNPNLSSATLFYRLQWLLAHSTLEINETIT

RLMLSGFMDETTSRFMKETWEAQNIGFDKILDTMGILQNGHSVDSSLLRQCLVYADDWTE

KVSVAMINRKRDDLEKEIESKLHENVESARNAIVKRFNLEDETIKETLISLSRTEVIETS

DVNEILEIVSPIKKRVVHVKLKDSSPVTKKDVDIILNKLVPTKKRVANEILKNPFPTNK

>contig31666 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY53883.1|) 4e-99 NOT\_ORF

MSLLSLVLFVALASPDTVLSTYQGYGTVYSLSTPSSGNCNFMHWPSEAVTKYAALNAAQW

NETMNCGRCAQVSCTDPSCSGMPSEIVYILDQCPGCAYGDLDLSPEMFQSITGQSYTKLS

IEWNFVECPVSNNVQYCLKTGSSEFWVAVQPANFISGVQSMTINHQEASLVDSAYYFLID

GKGKSVADLHSLQISITGVNGEVLEETLSMAADSCTNGHSQFSSSSSVYQSTSTSTSTSF

SSFSSSESTSTHVSQTIQDPSNTEVPVTDPPLPSASPIDSHNVTTNGIAIIDDSNRKPFH

SSCDSAN\*SPNDVSYDRIAVNCLPN

>contig40998 Frame-1R|Blast-hypothetical protein PITG\_08092 [Phytophthora infestans T30-4](gb|EEY54448.1|) 2e-32

MDWKPQRALVLILSVLVCWCRSDEILDMLSPFINFKELADQVAKETAESPVANKDVDHTY

PVASVEMDALMKMYRECRTQNSQAMRSWCTGFDEDYYRFESIESTNSCPRGVTTHPCTGQ

ILNTTKSPSKPDSKLLWSWKGLRCDVLTEPT

>contig46057 Frame-1F

MAICLLILATLNACLSMNAIASHSSGQLQRWDFWPPLVAGARITRYLSSQPRGIHLIRQS

FEPINLFQLQNNKLTINELLYGGILLKPIYPLDLTSNSAVQVAFQAGVKSIRAHANVHVS

PEITLVAATVYPLKVTGDNGESEMSILQESMGTNGQRYQFTSHVTFGFNYYLTLEDAKFN

LRHHIVVALDRESEHNVFQHTFSPLKKRILDETLEAAICGPGDDGCSTARVGPRILSYNV

WNTNPSSGVYGAGRRWKQYVKRLD

>contig50025 Frame-2R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY54846.1|) 1e-29

MILLIMAIVTLVPIPAVLFRLGEEPRQLRVDSVDRLLLARHLWNILQQQAVWRILLFVCT

SVL

>contig53460 Frame-1F

MQVCFKITALVMINALSISSLISAESSLGTAAFALKTPHMESHEAMRSLRARHTSTLNVD

EERLRLKLLRRV

>contig25604 Frame-0F

MFRTFSATTAVFIALGLATEGRLWQWIPASYTKLEESERKILSSAISTFFEMKKVAQLGT

VVVPCSVENNRKSAENLVLIHGFAGGNAVWAMNLEKLSKRFNVYAVEWIGVGRSDRPDFN

FKDYDSANDFIVNSFETWRQEIKLESFNLCGHSMGAIFASSYALKHPA

>contig30178 Frame-2R

MRPSMTIWWYCSLQAFLADARESEVNKIQISALDCIAFKYWTATLTRDPAKLKINKAADD

AADLWIGQRFSKKVLRKGLKKPLLSSIQPAFEAVPSYDNKNVRLRVVK

>contig37377 Frame-1F|Blast-NPP1-like protein [Phytophthora infestans T30-4](gb|EEY58144.1|) 2e-19

MVRLFIQVMVTGALLACSYYNQLATAAFAGQPVHTQIAGKEFGDKYGGQFDYRFSKNFGD

ILKGVTISTGKRVDSIGVIFQTPQHKQVKYSYGGDGGNLQTLMLQQRERITGIEAHSTVK

DGRKRISFIKISTNLNRSIQGGTKTDDVDKEDAENGFQLMGFYGRRGDEVNSVGALWQHA

G

>contig38332 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55552.1|) 0.0

MIAVAWIVMFLCLFNSSSALKSTAKSAAQARPRVVFSFTTTPRGIQELQPTVDALVHQEG

DGFKAIYVIIPHMYQNKVVDIPSWLLSDASILKRTNFYGITFSTGASSYDTKIQIIVIDT

DFGPASKVLGTLLVEQDPDTIIVYGDDDRIYPPQLCERALYYTHKYPNDAIAVLGGWISS

EDRLYCGRSLEIGVNSVSFVGGAGGVAVKRRYFGMGEATLLAFAVANMSKACFLGDDFYL

SHLLSRNSIRRRLVADSCWNVETLDETFSHGGLSHAPSNHSGGANVEHYQQCIRELGKDQ

DLSYDGEFGIACMFVLSRTWGMFRGLKNLMYGGKFVSC

>contig45963 Frame-2R

MRFYCVVAAAIHLACVALGSSVGMPKAIIESPLDSDTNTQVITMLRRTTAVALNKKAEPV

SRRLIRSLWRKFNDRILHLRSEKALARLSKVSS

>contig49141 Frame-2R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66701.1|) 5e-08

MLAMACVGGALSFLVLLVTASSIDSGANWFAREVFDTETCSSTPVIVNLSKAVQCRSCQC

SSFKSNNVTR

>contig01292 Frame-2F

MKVCTTILLAAVATQVVLGGGGGGISFPNENPYTPSGTGSGSNRQNDDQDGMKTTPPTLP

SSPLSTPMPTNPDSNSTPTGNNNPPTPDQTPSSPPSPPVEVPMSKNDPSNSPNLDENTPC

PTLSYNYPSPGPSDKPKDEASSPPTPTTPTANSPPASTPPAPDGNPTESGPPNPTQQDDD

SSQKPSGSHTGENIPSTPDVKNPPISSPPEESPSGPNAPPSGIPPVGTPNPEENTPCPTL

PYNYPTEAPSVPTNPTATIFPPVDPSNPAGSPPPGVPSSSPPTGPSPPGQSPPGQSPPGQ

SPPGQSPPGQSPPGQSPPGQSPPPATPPTGQSPPPETPPTANDPTATPPTVPTVPSPPGL

TPPGQYPPGQSPPAATPPTGQSPPSGTPPT

>contig23634 Frame-2F

MRYPSRAVALLIALSWLPGSHFDVSEALSSDPISPPSPLVETLNRENAAVRDLSDSALSP

LVPRAERRDALVQLGDIYFYGNSSLDTSVNGTLAMSLYAEAAALGAPRAQFHVGVALSYG

LWGFPLDEAAAMSHYYFAALGGDIGATMVLGHNHMLGINAPMKCESAARYYEVAANEAVA

RRERNVIHPIIYDVPHRRLKTVADSLHKKSSPDDAAVADYYQFSAEKGDPESTLNLATLY

FYGSRGIAQDVERAAALFQKAYELGAPEGAYHLGHIYNFGIGVPQNNATAFKYLQEAVKE

GSAAAHNELGRMYLEGKGTNRDEEKAVELFKAAIKQGSIEAFHNLGILFMQGRVSKDVAH

PEYDVARSYFLIAAYQGHTLSKHKLGHMHLHGIGGTRSCKQAVESFKTVAEFGEWDDVLN

QAYADFKNQDYEASFMKYAVMAQQGYEVAQHNAAYLLDSDFLTPSAFSTSHILTSSKTEL

KKDVIASTAVKLYRLAAQQGNVDANLKIGDYYYYGKGGHAVDYVKASAHYSIACKHSNAQ

AMFNLALMYEHGIGVDQDFYLAKRFFDKAHLAHNDAKVPVMLAMWKLRAHKALRAWMRWW

NELVGYNFSSNTTDVLPNKAELSAIDAVDSGLSLVFGEIKKWRESLDFEDYVVVLLVVAL

AIVVYIRSERHYLHVPPPQYI

>contig24965 Frame-0F

MRLRGSFVTLVAIIAVFYQGEGMDFQAASATFKHVRSPIQNPPNFEMESVPSAQMTRSLR

VDENRNGGQLGSDAKTIITKVKFPKKAFENLTMKIKHNPFYPAKHIN

>contig28297 Frame-2F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY64568.1|) 0.0

MKRTVSLVSAVMFMFSCGADALNVKMPGANYNSRKGPDWAPTASKCKTASEVQKDMFALK

GITDKVRIYSLVDCNQAELVLPAAKNAGLKVHLGIWTSKSHDYLLEELAKLAGLLDKGLY

DNNVVAMHVGSETIYRGEISVATAISYMNEIRNYIRGRGKNTPITIADVIDVYDANPQLI

DAVDFVSVNQFSFWERSDVNEAAAVTLDRLRKLRIIAAQKSKKIVLSEVGWSSGGWDPAA

GIASPANQAKFFADFFKMAHSHNFEYYWYVAFDSKWRVTNGGKEVEADFGVFKEDDTMKS

NFQQLTIGYNAPRAIRNTGTKLLLSENEGKLYMSGKSSNWLVQEQQVWFFDSATQQVRSK

SSDRCLDAYQGWNGGIVHVYRCMEHEVNQKWRLESSTGKLLHTKHQGYCLDTDPAQGHKL

QLYGCSPNNANQHWMMIDPANA

>contig30919 Frame-0F

MRWSQALVNVLAVLCLVALVASDLTERDRNDQSDRFKDVGFVRPKESLRLDNAVKEDALN

QERVGSNYFKNLFDDLGKQIDHHLPTLSKLYKSRAVSPDATVH

>contig40844 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65515.1|) 3e-11

MQIPKAAICRRRPFCRFLRSQNPLLIIPLLPAHTSAMPVANNSTFLPSCILQETELKSQR

KFKHHQHDVSRRLAERRSEPRFKHHRRHQNRANIA

>contig59370 Frame-0F

MFLLYSALTLQVASLFVDATATSMQNESLTVL

>contig12998 Frame-0R

MAPKTVVVAGAGVVGLAIARAAACRGLEVIVLEKNAQVGQEASARSSEVVHAGIYYAPTS

WKAHLCVKGREQLYAFCHAHGVPYSKCGKLIVAHSHQSNELRLLLQRGRANGVSDLKLLT

RSEVFAMEPFIECHEAVYSPSTGIVDSHGLMMALQGEAETYGAMVVCATAVEGGTFDLKT

KTFTIQVVQHDCKHEIQGDYFVNATGLFAPTLLTKVGVLNRPINSTSELPTVFNLFAKGT

YFKLQTRPFTHLVYPIPEVGGLGVHATIDLSGNVRFGPDVEWIDKIEYCPDSSKAETFAT

KIRTYWPDVRTEMLTVDYCGIRPKNCNAWPNL

>contig15252 Frame-1F

MRQRFRLRCGRRHLCATALLLLSLASAAESGEEADVLDFGPAHRVAEQRATELEYEQEKS

MDKIDVVDIAHQRGSQSRKSSQVSPHLKERSIADTFERDRDECVRETKTKKNPQGMHHMA

SKSVRKHQGFDSKIGKRQVTRIDLTLDVNSQNHSINKA

>contig29668 Frame-2R

MKLWPIVIFALTSIATTPAEKIDFEEVEPFPEFEPKTIEGKVALHFKPQLFIKPMRKSCH

APYPAVNAEGDTSKGIKVPFVRCWGSPLGSQIYGRMVEYEGYVAIMYAFYFPKDAILLVR

VHDWEYAIVWLDSLSVDAKVLAVSTQDTLTHETYHAPFPGYLDGPNFKLDYTRVYRAQHR

LVATAERGTAHNLVMWEDMTEKAREALNKSDFWLTSVPINDDHFQGYVEECFPFKRKAEQ

>contig30059 Frame-1F|Blast-orotidine 5'-phosphate decarboxylase, putative [Phytophthora infestans T30-4](gb|EEY55676.1|) 0.0

MPASFFSFLRARVSAVDSLLCVGLDPHITELPEATAIAAQAFCINLIQQTQHVAAAYKPN

SAFFEAFGAEGITALHAVIKAIPVGIPVLLDAKRGDISTTAAAYAVSAFEKLEAHAITLA

PYMGVDSIDPFVRGHPERGCFVLCKTSNPSANDFQTLSIGSRALYEEVAAKCQQWNSEDN

VGLVVGATDINALHRVRTLTPHLWILAPGIGAQGGNLEEAVEAGLSANGLGLLVPVSRGI

SKATNPKKAAENLRDAINAVRKKKMATLTVAVAKLNCNVFIKFALSFGVLKFGEFTLKSG

RKSPYFFNAGLFRTGRALSQLGRFYAEAIYNSGVQFDVLFGPAYKGITLVAAVAIAYADM

YGVDIPFAYNRKEAKDHGEGGVLVGADMTGKKVFIIDDVITAGTAIREAFDLLQTTNAQV

SGVCISLDRQEKVSSEDVRSAIDHVRESFNIPVVSIATLDSLVEYLETLDANVDTNASFL

PVIRAYRADYGVLQQ

>contig30341 Frame-1R

MSSFSKHVRLFVLAGSVSGITSVAVRHLFDTTCQRLQVFPAHSRCFFHCIQRTVQRETTR

GLFKASYSILKSGSVQSHHLYHIVHAS

>contig50404 Frame-1F|Blast-putative polyprotein [Phytophthora infestans](emb|CAI72305.1|) 8e-20 NOT\_ORF

MC\*ETVIILLTLYFAITAAKIIVSDRNNKFTSALRPSMLDLL\*TKLQMSNAAHPETNG\*T

KRVYRVPEDVLRSYALYFTS

>contig51447 Frame-1F

MSSTLLSFLFVGALWGCTNPFIKRG

>contig52749 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59445.1|) 3e-48

MDASIWFRLGLTYAAMGQLLQATKAYQRSVQIYTKEFDSAKGFNQEDVLELQKAYGITLA

ALAETFGELGDFNSAVQVFKTATAKFPNNANMHYNLANMRLARMESTGKKAFDIKVVQNL

ERAVLLSPDTLEFVNDLNLYLVAHDQQPDRVR

>contig10973 Frame-2R

MFMNITAWLTSVLDTLCSQAYGAKRFAKIVLYFQAGVQIISVRLGPIYHFNWYAETFLLA

MGQDAKVAQFAQSFSR

>contig21595 Frame-2F

MVCFLFKCALVAFAAAAATAEEEVPNPLFVALQANNDIGDITVEANPNLTPANSNAQSLS

SPFETTTTAAISDSISNVTTEMELPPETPDDADGSDNSVSDADSPAPSVTSSAS

>contig24673 Frame-1F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 3e-24

MRLFAYSLAVCVTLLLSTYGKDCKDSPNARTEPPPGAVVVDRTGKYEGSVKTIKLGVDQL

KASSSPQSLFIFPGTFNEQIFIRDHVKSLSIQGYTCDTTDYKHNQVTITHSKAQKDLASD

VED

>contig26529 Frame-0R|Blast-carbohydrate-binding protein, putative [Phytophthora infestans T30-4](gb|EEY58254.1|) 1e-24

MQLRGIITTLSLAALTTEASVLVTIFNACSENVELFDNVVIETITPGFATTRVLPEGFAG

MFRNGVNPQATLAQFSVAGGALLYNIGIVPTGNVG

>contig32807 Frame-0F|Blast-phosphatidylinositol kinase (PIK-G3) [Phytophthora infestans T30-4](gb|EEY55051.1|) 4e-55

MRAPTLIFVEVVPLQSAQPVGLYDSNRDHLRPFVFNTHP

>contig39820 Frame-2F|Blast-L-aminoadipate-semialdehyde dehydrogenase large subunit, putative [Phytophthora infestans T30-4](gb|EEY68241.1|) 1e-151

MVSLPPRNVFLTGATGFLGVHLLHALLKFTTTIVFCLVRAEDEDAALVRIKSALKEFALL

DEARNFHLEDRVIPVPGNLAQPLLGLTANTFKMLATEIDAILHNGAEVNLAKPYSALKSV

NVLGTQEVLRLAVTNGLTKTRVKPVHYISTNGVFPSTSNTPIFFESADISELSDELENGY

AQSKWVAERMCQEAALRGLPVSILRPGNMAPSSSTGQWNSSDFMYLLLKGCADLNAVPAC

SDWYFDMTPVDYAARAIVHFTALHPKEALGQTLHIQNPSLPIRSDSF

>contig45896 Frame-0F

MVAEVMALLRLFGVPYLVSPMEAEAQCAALEQLGLVDGVITDDSDIFPFGGQRVYKNIFH

HQKFVEAFSARDIENELGFSREQIIALALLLGSDYTDGVRGIGIVNASEIAASYPGLEGL

CDFKQWVRDYNVAEEAQRVASKKHTKSRQKSLAKDSATASDSDDSDNESIRARFQRVHAS

ARRKWDLGEEFPSKQVVQAYMAPQVDRSDARFTWSAPDMDALRKYCARAFGWDAAKSDGV

LKPLEEKARKDGGHIQTRLDRFFTSYKDQVHYAQIKSKRLRSAVNQRQSSKKRKAKLQ

>contig50407 Frame-0F

MRFRGTLAKDALVVLLDVAQSFARLGLHSSAKTNCVFTLTPETLTIALKSGGAELQSFAR

LQTTRLFHDVVVQSQAANHIGFLCDIRHFQQALTSGKDASAVMLRLLKRDGHNFLCLRTR

AVDIDIIQSIPIDVLSMSLVEHYKEPSVPAPQMAIEMPPLRAMRSIVDRLKVMHKTMTVE

ASKSGTLVLRIDTNTLTLQTLFAHLRYRDDLIEDDEEDEEEKNRRQQQRSSSVTVDSKVL

SQAILVDGQSTRSVLCCISENQAMVLHSILIDSFGSFTCYIPVLTPDL

>contig59398-1 Frame-2R1

MRRPPLINDFLLLLLSAANAMYSHLPSHTNCCAVSCGD

>contig22692 Frame-2F

MKLSRAYIAIPALFMLMDTSTTALDVKMHGVNYNMRKGADWEPDELRCKSPDQLQRDMFA

IKQVTDRVRIFSLVDCNQGEYVLRAAKTAGLQVHLGIWTTTSMNYLLRERDALGRVIDMG

LYDSNIIGLQVGSEAIYRREITPETAINYLNVIRDYLRGRGINTPCTIADVIDIYIEYPE

IPAQVDYYNINIFSYWEGVDVNEGAARTLDRIRAARKMAEDTGKQLTVAEVGWSSGGYNI

TTGESTPEAQAKFFADWYKVATSINLAYYWFSASDSLWRVTNGGYSVEAYFGIFQEDDTM

KSNFQALTIGAPRYYQAIRSDVTNLLLTESNAAVSITGTTNSPLAKEHQRWFFDPTTQQI

RSQSGDRCLDGYQPWDGGIVHCYRCMDNEMNQKWMYESTTGKLKHGTYTAFCLDVDPAQN

NKVQLQGCSPNNPNQRFTILDGASI

>contig23215 Frame-1F

MDSVAYSSILLGLLPEIMAKALTHRTMKAAGEIYLVPLTVEQAQSGRDALAKAIYASIFD

WLVAGINASLGAKAQQTTSTIGVLDIFGFESFEHNSFEQLCINYANEKLQQKFTQDVFRS

VQEEYEREQITWAHIAYADNSETLGLIESRMGLLALLNEEIVRPRGHEEGFVSKLSSAYC

KHKTLIEFPRISKTQFAIHHYAGTVLYDATGFLEKHKDALLTDLSDLMCQSHEPFPQMLF

QVRKEMEAAAPKHPLSSLGIRKAGADRTVGMQFKKSLNALMTTINDTNVNYIRCIKPNCR

KSASLLEDKMVATQLRCAGVIEAICIARVGYPNRLVHGEFAAQFDLFLTKEQQQQLQNDP

KTYGVLCCRDVVEQFHLETPEEYQMGQSKIYLQKGVLETLEYAKAQKLYAYVARIQARWR

GMRARVEYCNQRIAVRMIQRRVRVFIARRHFQRARVALALIQRVWRGLR

>contig23996 Frame-1F|Blast-alpha-glucosidase, putative [Phytophthora infestans T30-4](gb|EEY61906.1|) 0.0

MTWVHYYFYRAFACLGYLALVSSLLGSSTSTQGTHVKVGGGYVDGPGYSVTSASENEGVL

TINLALNKPSTSTPYGADLSALVVTVFMTEVESIRVKIVDMKKQRWEVPKALFSAGTLGM

NDTATSASEEPLYSFHYTKNPFAFQVVRKFDNYSLFDSSSTSLVMKDQYLEVSTAINKNL

SIYGIGESTRDNFRMSTGDKQTLWARDEPSATANVNTYGSHPFFLGVNSAGQAHGVLLLN

SNGMDVTLEKKSLVYQAIGGVLDFNIVVGPTPAKVLSQYTKLIGRPKLMPYWAYGFHQCR

WGYDSVDALHTAVSEYKRNKLPLDVIWADIDYMKRFHDFTVDPLNFPQARMASFLDKIHA

DGQRFVPIIDPGIPDDTKDYAFTKGLTMDIFIKDTSGKPYLGQVWPGPTVFPDFFHPKTK

SYWSEQLQLMYNSCEFDGLWIDMNELANFCPGTSCVRNSAETCPKQGNSSTMTVCCLTCT

NKKSRYDSPPFAIHNAGTYDAITSKGISTSALQYGGIRQYDAHNLYGISESIVTNAVQEE

LTKKRSFVLSRSTFPGSGVHAAHWTGDNAATWADLRWSIPAILKFGLFGVPMVGADICGF

LGPSNMELCARWTALGSFYPFARNHNNLDAPPQEPYVWPEVAKVGQKFIGMRYRLLPYIY

TLGYHAHVHGIPIARPLVMEFPTDIATHNINYQFMLGSALLITPVVTKNAKKVTGYHPSG

VWYDIFSYSKILSSGGLVTTKVSLYDMPVHIRGGKILAMHQAALTSTAGPPNIL

>contig27488 Frame-0R|Blast-small cysteine rich protein SCR108-like protein [Phytophthora infestans T30-4](gb|EEY64712.1|) 4e-16

MKLSFIAFLVGAVAVPVSVISLHLRLTMHSKIAEYLEQCEWEDKAVRCNQTYLFCLRTSS

TYGQCLKTNPGIGDRCCGVKHRGATWSRSCIGENVECKVDAKGEGTCQKKENRKALKMFD

HRKENAVDVP

>contig29756 Frame-1R

MKALRCVLLLSSVALLTCVETAVENAVATSQSLGHRSLLQSTMTSDSDLADERLLQGLIE

KFKGTWLGRMLAKTWIGKWLQPEVYLAHASNKQAAITNLFPRFNKKSLETSNPFESTKFT

TWYNIVNKQFKTNFRDGHMYMLETLKTTFGELKLV

>contig41707 Frame-0F

MIGSRFLALLMVSMFGVSSSTLSLSDCIHAFNASKLFTLQPEGDPSLVWFEYERFLLSPD

RTTPLLLFFISSSICSGGEVFEENFNDEKLFLVDQEVCLRHQMLVEAAMTLAAETVSTPQ

LPFIRIDVQTWPEMLQY

>contig50499 Frame-1R|Blast-resistance-Nodulation-Cell Division (RND) superfamily [Phytophthora infestans T30-4](gb|EEY58769.1|) 3e-20

MRVSAFSTLLLPAAMVSQTATATSPSSPVIASSSTSSVSGHVPWTLSDNASVLAGIRSQL

TTCSYSKVKECLHDPALMRELGLLVRAPGHCVAFDSSYVNVTTPSAAIPNRYYPTSVEDA

YRAGFANKFSEWSDSNREQFQVDCP

>contig59535-0 Frame-0F0

MLVGYDSRLLELFQCWFLMHLCSTLHLHLNDN

>contig07122 Frame-0F

MSLVLVGSLLLNIVTASVDTFRLELEKNGQYDIVSRIHEDGSAVVVVRQDGLLHLLYDET

IIGAEFQDSSLRDQTVYPGFTIMQCAAYLKRKPTKALQIGLGIGTVPTFLREMGIPTDVV

EISHAVVTQAADYFQYDWCTQEDDDEEELCIQGQTFVMDGLKFLASTSVALGIQTNEEKK

NPYDLFIVDVYTGRNPFAFVLREQILRIHKEWLTPDGVLVMNFVGYIKGVHAVAPKSIYR

TLQSVFQYVKCFPELEESTIEALNIVFYASNQPIDFILPSTGMYENPLSETHFY

>contig13556 Frame-0R

MGFGKIYVILLVAIAFITSIYAVAVAVTDDNPMAVLNNDLSDSNRLLLVANPIITNYFNR

RNLRQITQVPRKLANLGNGFHNVKETLNFFIKRYLLPWLYSSH

>contig16887 Frame-0F

MRAALILLVAFPASTVASSVMTAGMTGNWRSGEVTVADTEVLDGALKGDSFSQSVGDTRV

CHTSLKKVEKQVVAGTNYRFYMEGCSVQESTGTCAPSSCVKPECCMVQIFSQTWTNTLRV

TNITIGGSVCVSPSSESKETITFPI

>contig18711 Frame-1R

MEYARLCVSTFCFGLTGLTGLNADNYARHWRCMRTGRCCGNPCHIK

>contig21593 Frame-2R

MPSLKLLGVALAMVHLAVVNATYMASERKSFVSAFYANPDGRRLVEVKPVSWLGFGTYAS

TSENRRLGEHNEEERVFGMSGSTFSKLAKEPELLGVEDVLKTRFGDDFVQVFKKNDKATK

AMKDSLASFMKRSKAGDLTPDEVGKFANDMLAAVKNSKKWSKKKKFV

>contig26189 Frame-1F

MKLATILVLAALAVTTAKGGNPNSLRATDFEPVDVSKTENVDQLELDSLDATDNGSVESR

PLNGVNNEDSADLSTKSTVSSKSSKKGGEPFSLGPVYNDDLDNTLRTQDDVTKDGMLDPS

IEPTVASKSSKKGGEPYSVGNVYDDDFFGTTGDQDNDMDNDMTHSLRKETSQQNRRGWEQ

KDADYIDESSITDENIDAIMDKYAIAKASTYSSGSGYDIEGKNGMSPDDLMSNLKDFES

>contig26303 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58754.1|) 2e-14 NOT\_ORF

MWFTGIIGTLGSAMLAYQNSTLRLQGFGRNEAELERHLHKIRDK

>contig28015 Frame-0R|Blast-serine protease family S01A, putative [Phytophthora infestans T30-4](gb|EEY64173.1|) 2e-40

MKLNIVFLPAVFAALVNCISFTDPDERIFGGTIAELDKYTYIAALHPDGVRSNLTCAGTL

IAPQFVLTSGLCLEYTLVDVYVTLGSKFRSNVGIGNYEAIRAVEAFRHPRYILNPDTLDY

AYDVAILKLETPSTQQPAKLPAVDGSSNRPGVMATALGWGEMETGENANVLRAVDVQVIT

NKQCSRIWSTIVDKSFICAGNGTNKGINVGDWGGPLIVKDVVVGSASLSSNKNDSLHNLY

ARVSHALDFIHDILDGGSTGDVTELLTK

>contig32777 Frame-0F|Blast-glucose-6-phosphate 1-dehydrogenase [Phytophthora infestans T30-4](gb|EEY57587.1|) 1e-133

MQNHLLQVLSLVAMEAPVYAAGNDYSNYIRDEKVKVLNCIEPIKLENTVLGQYIGDQTLN

EPGYLEDPTVPNDSSTPTFATAIMYVNNKRWAGVPFIMKAGKALNERKGEIRVQFRPPPG

VEHMFPGIKIPVQELVLRLQPEEAVYLKINVKSPGLQTQAISSELDLSYAERYEGTEVPD

AYTRLILDVLRGKQAAFVRDDELHAAWKIFTPLLNEIESRKVQPLPYAFGSRGPKESDEL

VNSAGFHYHDGDYQWQPRVRTNSAL

>contig34285 Frame-1F

MILIGCAMIIVLTVAFLYRRVFRRPRQPYMNISSLEQPTRSIINSIDDEDYDGNDDDTNE

GPRIARHAQTSRSVL

>contig35299 Frame-2R|Blast-GPI inositol-deacylase, putative [Phytophthora infestans T30-4](gb|EEY53553.1|) 2e-63

MTASQLLLPLLAFSSVLLTALYVFDEVATRKYVSACEMTWSWPVFSPVKWRSTPSHDKYQ

FYRVDMKSARNSLSGVPVLFVPGHMGSYKQARSLSRHLWDTNETLFDIFALDLNDEPTGL

NGNYITDQALYLNDVVRAILKEYKRQHIKSKKQLNSP

>contig37275 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59177.1|) 3e-57

MAEPLFLLRIALTLLLLALSAFLYKWLKTPSTPALQTFSKRPKKRNKKKPAKKYASPGSS

SPPPQSPTQTPQPSVASAIPSALTAAVSPNYGDSASESDADDGLSAAQVLTTRKFKPKNL

GGTHLARTIKASLPPANALKFSIDQKVVARFQGGTQWFPATVMEQRKGNEYHLKYDDGEV

EYRVPVELIKAWPILSDDEVNTGRHSLIEEANKSAENAVAHEDSSGSDSSESDDDDGWQV

VGTSSAAKRHTRS

>contig44930 Frame-0F

MPHLGYTFTVAIVVCTTLQVLTSAATCTDDEQTTVDKLYMELSSSSACENLVFNSGVTSL

DYCMNRECLSVLSDAVDQLPDCTSNDEIDRKKGLATIITFCIGANELLDSSASASASTSA

SGSNNDFITSGTSKSAVVRGNMVFWLPIALYVFGAW

>contig51525 Frame-0R

MALLLSPLWIHAARNGNAFHSYSHGTV

>contig52502 Frame-2R

MVQPAKTILTLLLVAVAKSKCAHANPCTSIELGVFNDVRGQVSKCLQDSKLNFLIPPRTS

LTKTQQTALCKSKTCQEMIGSMDDLDIPSCEATFDNQNMTL

>contig14040 Frame-0R

MVSKPKTTPLLYLYMLLSHTVVTPIKMADSYDAPHPSEESLENFRHIADVTDPSLIKDSP

ESLRHVSHVTTPTLSKKSSENLRHVSKLTVSPLSNDAIENLQTNLQVAASPLLKVFPVNQ

TQDSHGFEDRSYYHDELRLSAISLAKSLDNSQFHPTGIYKYVPKFLRGSYLNRVEGFQRF

TLLWNDFRHDCLDKMTNNALNDKFLIKWIKKIKERLPMRQDEAFAIIAILLSDQFKVPMS

LRAIAGLIRDYPNDYHLIFTALKQLEKKEGPRLMTSFEHPNGPGMVVKN

>contig20861 Frame-1F

MKLQFQVFSTIALVASGGTFEFLDNLDQLESSSTGETSRDASYICQQYSFEETVNTSKVF

GGLGGEEFTDVKQVRYGVPLNKVILYSGERLDGISLIAEPVSDPFSLLHHGGKGGREQIF

NLETGEFINKFTVQTGRKDGSDRIRYIKLDTNRNRSFEGGTRAKDDFGLHQVDAPPGFMM

TGCHGRAKDEIDALGAVFVKVSDHICKSSKKT

>contig32325 Frame-1F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY63799.1|) 1e-45

MLNFTRSPLGLWLLISASFNNSVAKELLHKKPRKLQIYSSYDDYYQEMLNAVNAERAKLS

LSALCANEKLAAAAARHSEDMASNDFMGHTGANGSTLSERVSGAEFAWTKVAENVAAGQK

DVASVMQSWMSSKGHRDNILSADYIMLGTSYVYR

>contig33249 Frame-2F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63774.1|) 1e-131

MSGMHTLQVTLICAGDLAASDFGFMGMGGKSDPYVVFKLGRVSQKSSVVPNSLHPRWEPP

ETFQFQVDRPKEKCLEVHVMDYDRFLKDDCIGNANLALAPFLEKKQSEVVSYEIEVPPDF

DRQKRKSILFLEIKLTPNEQVDQMLELWENQRYHIVKKWTTDTLISGSNERKRWSSVTDA

NVSSDAFEKVAPKVPSHLRAEGWTLDVSQGDDNGWIYAPSFSGPWQKDPFTLAMVRRRKW

INRCTVVDK

>contig36905 Frame-2F

MNKFPSSIIVKLFLSVLLYGRREADVSFGRCCTMVRRKASVT

>contig42380 Frame-0R

MLRNSNARHLVRVMAVTYTCGSAYAARPHRARNKNDAARHFYTFWHEVTEIYPPIPRYKQ

LVEFALAVLS

>contig50233 Frame-2R

MRCYILVVPSLLALASSALPNLILTTESSLADASADSPLRSSSTSPDDHSERGN

>contig51036 Frame-0F

MKCLLSLAVIAGALTISAVADDDAAYFCDSDSYCEKTFPDTACISVNNYGDVVSKCTPNT

SKRPACRGATPGLCPSFQSADIGYLNAHCVFVSEENLSLSSSGSMSSSRRLMALAANTSA

VLSNSTLAASSMLSSLSASQGDDVMIPEGKNGMFSAEVDGVAVSGQFICLDVSDCANKAA

DPSTCEPTTCQSPDSKEVCTYHGTCTYKSKSKINKRSCMCYAGFDGDKCEKEVSNACDVD

CGTGGDCVDGECVCKEGFNGVEHNGKKGKPNQRCTRCTNDLACQNKNTCNTETGKCICGP

GFTGDTCGATEDSCTTRMDCGIGACQVLTNGSSACFCPMCNPTCNLCDINVDASFDCSTC

QANSATTMQSFNLLMVASMVVTILLTNLAL

>contig52738 Frame-2F

MTAQWSLWRLPLRAAALCIRCIPYFKANRFCSVCNFVLDGDVLAIKVDLLTCLTCNHYVH

AACEPDPNVAFHAFSNSSEFTLDVVMEMET

>contig11813 Frame-1F

MVKARWGSFILICSLALHACNEAVRVRGMSVSYAVNESTKGEESRSHFEERAPGDMNSIS

EILQTALSNIQSGLNGQLVKNEIEFVNLIKDALHDWVMGTKISLFDDWRVGTKNSASKAE

IEEMYQQSVQLFNAFKAQFSEFDRARIIATSLNVRAGRLVIDQHIKDMWELLMEEWKAKS

QEQVYNMLRLDATHSDFLTSSMFQLFVKFLDKYHNKNYNILRDKLMEAYVDNRQILRDRL

KNVKGIGKTLLGMIPPKYWDSPTFYPAILQLGRFEFVHLSVKELVRSPSLEAWCFLAESN

GEKPYRILVDKLLVERDNLEFTKELEAALKEEPSGNLYGKLKQLENALFQHWMDVVKFTP

IEFEKFLLLDTVKEDAFFRTPLSWIYLSYINFRGFNVRNTILQKLETKYGGVRQVIDVAK

EIDPRIASMVITMYYRHWKNLKNALMDLNLMDLNLTFGVLNGRWVAHWIEFVFESKKTQN

PTNYVISFAKRKYTEQGAAVLLISAIEKAPTIIVKELVLSVFLEYMKQTPAKNVLAGLGL

DQAGDNLFSTRNIIYWIIGTKPWNEARLKFDPFRDFYTEDKLLKLSSSASTAANSVAAVK

SFADEMIQYLEALSVEPPNKRLRTSAHTP

>contig21959 Frame-2F

MRTLRLTCVSLVLVCCGSTLATIETYQDTLFTATSTKPVKTSEQNLSGRSTLRSLKAVRH

DRNYDLEPLEEGRMMSQHPPSHVPLPASSKEVIKELRGRLRKRKGFKQPLRN

>contig36560 Frame-1F

MVKVDCLPKVALATCLSAAVASAANVNFINKCPHSVELYHSQLGSAVAKVADIAVGASTS

IYVTGPSHMYRHGQDPSATLVELSVDKHVWMDISIIPPMPAYCDSYIACKAGGKVGFNLP

ISIVPKTNNGSGSTCHGIECAADSPKTCADAYHFPLDNSKTHSCPMDTELDVTFCYVQLS

PSPPPYEQQSPVQQDYEQQSPVQQDYDQQKPDQQKPDQQKPDQQKPDQQSSDQQDPEQQA

PIRQDDSYLPLPTVIPVDTDVTQTLGNALTLGTVKSKYTYAGKNAGNVPGSYDRVTDLCQ

CKKERVTINSPVGPLSEAVTMVFRGPLILFDVAVYIMDTTTTKWLRVSSYSKKDQTVENM

TFMNNKNVDYSGQDRHSPQGYATADGMSKADNATVFNGVLKEAADVSKIGGGSGISTGVE

VNILTGTKCVDGGECVGFHGDNDYQGWVGGKKIFVTKVMMPHDTAPNQPAIWMLNAQVVH

SNQYGCNCRGMGPVGGCGELDLTEVIETNAKRDMITTHYYFYDGSILSPLGDNFAPRRHD

KPTVYLTIIDDSKDGLVKIVEVDDFDFSQVDITSLYQQLVDC

>contig48248 Frame-1R

MWCLLLLLSVALLTCVKPGSWDATTDATVESQVHRRVRLTTNSSVGQEPGYNEERLP

>contig57437 Frame-2F

MLHFSTSSYFLIVLPFKIVLATNLADRI

>contig16075 Frame-2R

MLLLTAVISLTFVVASANKPILDHSTLSSSPDANLDEHRLANSTSNTEERNWFMTLFKPW

KGLNENFGQIGKSLASDKSRTMLRDASTKFQKHKVFSPVVNVARDNPNFIVNVMQKGGDK

AIEKYVRQDPRKGEH

>contig16273 Frame-1F|Blast-1,3-beta-glucanosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY62229.1|) 1e-179

MVFSSCVQRLCAAMAICTAIAISSTTAWVPPIITKGNKFFDSVTGVEFRLKGIAYYPRPN

DGEMAGVGNYDWAADEHEAVWKPHLEIMKDLGVNTIRLYSVDPSKPHDNFMCACSDAGIY

VLVGITAPCENCSVLDYKPPACYPEDLFTRAQMVYNAFAVYDNTLGFSVGNENNLQVEHG

AHGTTTAPCVKAFLRDTRSYAASCAGAVRPVPIGLDIADIPPREQWIAYYDCAAEEDENT

RAEWLGFNPYVECDPTTHLKYSQSTGLKKLMTEYASVGYARPIMFGEFGCNKGINTIDGY

ENQRSFLDAKWMNEEEEMTAEIVGGNVFEFTTEIANLA

>contig29374 Frame-2R

MNFKQRELGSAPLQPVCMSLAWLPLSTFSLVLEYAVCGFTRDLGPERRSLHGRSLKDVAL

VSKRWYHAVDELVALIRRDTMQLTFKYGSRTEVMAIRRKVQLRGRLVRDLRIRMGRSDGA

RFVTGVWWWMEDRELPWNVILSLTPGLKRLDLRFMPLDSRHLIDLLEVAAKCCLQVEFLI

LPKKQNFGVTDNCKAIARLMEALKYAMARWYLKGKCGGLKQLTVPTREKTDTFRNSTKFI

EGVIEFCPNVWYLDGYKDTIDELNDVACDEKWMISLETWENFNKSCTHLREFNWILVPFT

DPFFQMFGKYVKPNLKILSLTPNMSWGWDNYLSQDELTNHATTIPDHELPANDVVALFNG

CPALIELKIRISMEKDEDVLLYAEVFGDKFWETVVSCCPLLQNLCFDDCSTYNEIQPVKT

IRSFTDRGLLALAGHLRLTTIKLPAVCCSGDGLFEFLQHLFRMKDFGGGTRTLVLSLAGP

TDYNNLPPHPFYVEIVRLLKCLAQTSEEQMGITTCCFKASLIIHNPQGSLVDQRWSYSYV

HNELKPILKKICETQLSLDLHIVLCRDDESTFRRIDNLELNWCLGSQQGDVFIEDEFAGS

AGSNYYSSDVEDDYNDD

>contig30163 Frame-0F

MRIVAVLLANGYIWATSVAQPTPTWLTDEKTVATPVSCVFRYVLPTGTNLPSAVIDQFPP

ALPITSEHETDTSRSTTDGSDDSLEPASTESDTMNLPTDANVPKVTIRNTSMATLNTTVL

VPSTSAPHAPTSLLNASTPATSNTTTPKSASKPPVLATNATKVLDVFNTTTTPQKSLNTT

SLEKDRRLQVTNVLPFTPENDSDASNDSSRDKPTTMDTIKASNATTPALIPTVTNSSSRN

ALSPSLIKSFVPINSSTESSSNGYIKDLESTATLATFQCDATFYNAWSRMGLQCGNVDLD

VASAISASVCSIYSGTSTSTV

>contig20925 Frame-0F

MRVAHMSAFVAAMGTLSASAKEYSFSEISTNEKNFIFGGTEADINDFPFVANLVDNLLQQ

PFCVGTLISKQYILTAGHCIRSDTFGIIARFGRNESTGVEAFSVPVVEGFRHPMYRKKTH

>contig22758 Frame-2F

MEVVSVSSAYFLVLFRSTYLKPFLELY

>contig24918 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61365.1|) 1e-95

MVTVVSLRRTFFPLVLLLNTRHVVKGHAWIDCFEKDWNKIYDQSASYIFGGAGGNGFCSG

YGAGYPGRGDHGIGPGYTHKMLQNEVEAGVPVCQTVDPNTYSDWRKRLSMAPGETTFFAY

LPNGHIVKDKKGVGTQHGIYWTGKPGTSLSTTREMKPEHLINGHTMNFDDGNCGETVDFN

NVPSGRAGDGKPCIGSFMIPPGTAPGIYNMVWYWTFWLNNESAYKDQNMAKGYFGAAYST

CFEVEVTSGGAQAPNSAPQASNPAPQAPNPAPQAPNPAPQAPIPASPSCTQTVAPGDAAN

GIGIMTDTNCKSGGLGCINYICRYCQVTMTD

>contig32917-1 Frame-2R1

MRLPFHVLALVTTYALSMTSQTSAESSLVRATVAHEQSHMESLEAKRSLRAQQTSPLNAN

DERISFKNLMGKIKGIVQKFYRRKTTGLRRIKNMKSVR

>contig33244 Frame-2R|Blast-metalloprotease family M12A, putative [Phytophthora infestans T30-4](gb|EEY56315.1|) 1e-132

MLLSVLLLMSTTARAWSRPAGCNLDGMEIDHGSMKYVTGRAHRPGSIYSRCSYGIATCFE

DRGLVDAPQWINSREVSCFESLQRRRLGVAIILEEDIWPDHIVWYRITGSFSDDELDMIK

MAVDVYANVDVNVTLKECEPVTMCNGKYVSIEQNEDACYGLVGYVNDGKPQIMNLGETCF

DGGPGNVVHEFGHALGLYHEHTHPEREVIVLTDLDLPVSAENYAKKSSQVATLTPYDPKS

IMHYGRAAGLCFPKSHYPLKAFCDVEHVRNCIQPVVQ

>contig43742 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61639.1|) 4e-89

MKSFLTSHVIALATYVSSVSAHGYLSQPKASYVPGSIYTDYTSLTNSSVNKGFDGGVYNG

APANNYKEFSKHWSATGYKSLRDMVDPIAPGYGFSLDTADPVDVSSYKEMWWQNNELKEG

FLASHHGPCEGWIDNKKVFHYDDCVTEFPENPAKIPTDYSSCKSSKCLFVFYWLALHSPK

WQIYKQCVPITNGG

>contig45447 Frame-0R

MPKSLTMAALSFNPPLVSSIQTIPVEFDYDYSCPANDLEAVVIFGMFLSYAPNTAATYEV

VVLLNTYGASKIAGNFVNTVTIGETLCDVYRSEDNTIFTFVVKTPTFDLKADAKLFLNNL

PINSNLVDMQYLVYIYGGSKIYRGTEAQFDVLNLSVV

>contig55172 Frame-1F|Blast-aspartokinase, putative [Phytophthora infestans T30-4](gb|EEY60689.1|) 6e-22

MSLMASSWVVLKFGGTSVSTAGRWRCICDQIRSHLESPSSPRVWVTISALSQVTNKLTRA

>contig58074 Frame-2R

MVFPVLFLLAAFALGDAGGTSMFDP

>contig59378 Frame-1R

MKAYPFPVLCLLLSLMLYAGLCERNIKR

>contig09068 Frame-0R

MAKGFVDFFALARGCVTNVCCGTNDAFVLDVAGRRVFSWGTYLGGREVG

>contig15335 Frame-0F

MLRSSIMPALVLLCFASAESTSPAISYRTYAEMTRFLLELNTTFPDIVQVSVAQETYGLP

YPKELQCIEDDEFNTLRHCKQYVVHLTNHSTVANDPKRPEVFISGALHGDERIGPNAAIE

LVALFAYGTSMYSTQSKKQPTVNTRRWLKELINTRNILVMPMTNAHGYSHHVRKELEVDP

NRDYNYMRSQGDCMQAMTSRVVNEIWRDHIFQLAVTFHAGTRAVAYEWGSPDHYLNGSKE

NMSEKSPDHMAQLQISSTLAKFAGVFPDGQLFPTGTMNDVVYGVTGGMEDWGYAASWENQ

FYKPNKQPFRPCEPTTFGGYPKEKTIYNNITHRAFNMLVETSNKKEPQAKDLGFSNELYE

ANVDFFRTEDLITEVVGHVPRNVRLALMMIELVQPMVRWIDGAKKPRNEEVVDVFPAISL

FASNANQVMKMGCSASAWMRNQVATCNVSRCSILDTRHSKVQLAWEVLGALTVDRTLVQI

SSSKTFEEDAILMETTAQAGITRRFYSFTPNASQTTP

>contig21839-0 Frame-1F0

MPFLLQLILLTALAVSVAFAIESEQSQHTRLRGLLDRIVSSESTPEPVRVLSASWEEGKT

GVPRQLVPISEKIMGGGTVVLFNDRRVPTVGEKESAVVNFDVRSIPNCVVSVCGEMSQWY

LGSKEKCFDLRIAPKSADRQENGLIRGLSAAYSGLRPVATTLYLKFDETNFIDGSKCEYE

ILAGTKTVREDQVASGSEAAIA

>contig40030 Frame-2F

MELWWLLLAARVGTEVGFARLVQDVACRTCLCLKTSQSRRDVKLRQRILSLGKFESASCV

LDALHEGDGALMIIC

>contig50479 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54957.1|) 6e-68

MKCNADTSPAVYLFVLLFDVLTVTSLCPQFGSFRLNAFGSKAFAFLWNSTLKKLPYVCFA

DWSWLEDQSTGGKLPALAFCHLLATILLSNSPMDHYCQRSCKNYAAVVKHILCKLYVGGQ

AIQKSVDTVPSTSLMLAEWEITHIELHDLDSTFASILGLDGFFEVTEAMKTICWP

>contig58075 Frame-0F

MLIALSICTSPIWISGFVVLVARLLLRDTSTIEDEFHPDFEEEEVTSPHHPNSMYRRAHL

TNHYIQRE

>contig22486 Frame-1F

MSLGKRLKVLLLLCFSNISLCTAVGEQYQSLNGSEVKLSVRPSATTSKKDAKVFPDPDKD

SKNTITNTEDDVQEARSPNKKLLNSIARSVKGNPRQSVVSTIASTMERNPRLKVTRTSAS

STKRISREKKISTIASATQRNSKQQDNAEPTRSHVSVLFAMISNQITSEEYKKALKQTQS

NLIQQWQEKNTPPR

>contig33620 Frame-0R

MKFWTVPIASLFAAGFLQVHDQVRAQGKWQPEAISHNQVQPFPERPATTISEKAALAFKP

QLKVASGCVPYPVVNDKGEVSDGLRNSGKAAGSCRGSGYGSQVYSRSTWMADKWAIMYMW

YFPKNAPESGRGHRHGFEHVVVFVNNPGTEEPQIIGCSTSKDHRYAPCPLKKVFSKT

>contig37857 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65133.1|) 9e-29

MRLSSFKLQLLLPLWVGLGGYVWPQKQAPGKSLRSRRKARPWCVKRAWCDSLIYSNVVYA

LAAIFSFSCGQKCCGGLQMGAAIASVMFHRSKETKFLLLDALISGLLG

>contig38320 Frame-2F

MKKASRLSSLRLLLFIALFCIALLSGSFCLAESTESQNELERDSSNPVVDDLKELTGGET

FAFQAEVSRLMDILINSLYRTKEIFLRELISNASDALDKIRFLALSNNELLKEQRHLDIR

INFDKDARTLTIRDTGVGMTKEDLIANLGTIAKSGTAKFVEAMQGGSDDSSLIGQFGVGF

YSVYLVADRVRVVSKNNDDDQYIWESDANASFAIAKDPRGDTLGRGTEITLFLKSDASEI

LDQDKLKSLVGHYSDFITFPIYVNATYTESYEVDEEPADNEDDIEKNADTTSEDDEEKDT

EATSEADEELEIMEETEESNSSKTRTETRTVWKWERVNEVKAIWTRSKDDIADEEYESFY

RSLQKTDTTDPLTWIHFQAEGEIEFKSILYVPGQAPRDMYTRFESKKADIKLYVRKVLIT

DDFDDFLPRYLNFIAGVVDSDDLPINVSRETLQENKILRVIRKKLVRKILEMLRKLSEND

GEYGEEEDDETEVIDPSAEVDFKTSEESVKDAKIEVEEEKEKENATYNKFWEQFGKNIKL

GIIDDAANRGKLVKLLRFVSSGSDGKWTSLEQYVDRMKDWQGSIYYIAADNAEACEKSPF

MEKMRAKGLEVLYFVDALDEYVVSHISEFDGKKLVSIAKEGVKFGDDDESLIQKRDQLYA

DKFLALTTSLKALYGDKISRVTMSQRVVDSPAVMVTSQWGYSANMQRIMKAQTFSNGDKN

SPMYGTASAILELNPRHPIVCKLHELMVNDSQKEETKDLAWLLYDTALVNSGFDMSDTSQ

FSARVHRVMRSVMGIDSFELEPEIEVPEEEKDVEEVDNLDKAENSPSLDAEIYAEADDDQ

SEKDEL

>contig43278 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57474.1|) 3e-07

MQRKLYGLIELSSIFFRSLLASVPWCSMYQACA

>contig45702-1 Frame-2F1

MVSGGTYFFCILLMHVRLASTCLSYLVNGLLKSRWR

>contig48150 Frame-2R

MTVCIAVFILLGHGGTSVVYKCHERRTGTVRAY

>contig48392 Frame-1F

MKFIIACVVLCSIAVVGHSTSFDFQS

>contig48785 Frame-2R

MSCRCDTIVSLLLALLLGYHALSEPTILPEPQNPDSSTTSSSEAASRWNELYSESPVLSS

THASLHGSQAIVPTITSATDVSINQVEKHLDIVHQIELSVDKSLHHLENNEQFATFTTLQ

RQEIHHLHYELTTMQLNLRRLARGLNGT

>contig11045 Frame-2F

MLRLIYSTSVTVLLLIQCSNATTIKKDERFGGAETNCQTAKDPRRTVTGLMVCSGDRVDR

IGVFYQGVNEPETLGGPGGKCHNYMLGKDEYFNRIEASADFRNGEERIFFVRFDTNKGNQ

LKGGTNSGRVGVSAHPNFKLAGIEGCHGNDVDSISPIWISI

>contig40032 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY58205.1|) 3e-99

MAKTALYVFLFIEYTASLIPADVTQVHLGISGPSVGCANGIAVSFATNEAKPYKVIATTG

DSTITTESTYTNYAVTEPQYNYSYVSPQLHTALLCDLADTTRYTYTIGDSDFTGSFVSLP

HPGSDSKETIIGIIGDPGDTNSSETTFSEQAKTFEDKRFKLWSSWAISRMPMANICNGTI

GFGRNRTSLRSSRSRVSTVTTRLSRQRVI

>contig40762 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54284.1|) 1e-48 NOT\_ORF

MVRCSRVTKQASALTLRLSL\*TVVFVVLHVVNTTILVCSWRSCELIDPAAPVEETLPNGW

FGIRLDGPRWEKTRYCALCRKAVPGLDHHCTWLQTCIGKSNYAQFVTVACTGTIQFVLQV

TYAACCLLWLCDSSLEEIDTFG

>contig40946 Frame-0R

MASPHGFLRSSFHLRLVDFNLLCLAIASSFGVLLLRSRAIPKRIFDVRRALLRRSVASLG

SIYSENCSIFRLSTPQTELH

>contig41945 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54233.1|) 2e-45

MFTMSQMAVFVAAFMQTVTSHSSYSELIPNGENILKPLGHTETAYTGFGQLFSDEGTDWS

NVCNMTWPGGSVTCGEALGDPCCRWKNGVPDYTLTEPSLDGTICATSSDASSGDSSAATY

GPDTTESTVATKESPIQTDITFSSDAVTDSSEYCG

>contig42856 Frame-0R|Blast-serine protease family S08A, putative [Phytophthora infestans T30-4](gb|EEY60762.1|) 6e-55

MDHRKVFMFSLTLLLSSVQAFNHVLLVHLHPCLNARELLLSSELSRSERREKVFQTLTRS

VSDVQRSVSSFIEAQNEVNLTVSRLWIQNTLIVRYQSDHHGFHSVLKQNLRWFPGVLQVE

EDTRVLRLIEAHQDKNIASLDLEKPQSNIKLLHAPQLWNKGVKGKHVIVASIDSGVRYTH

DALR

>contig44137 Frame-1F

MRVACWALFAVSLVVSVLAKGKAKSKDNLTCLAPSAVASFESKIAELQESNAALQLQLET

AKAQLEDKAPNHEVDVSELQKEIHELKKNVASEKQGFTLELNSALNKLSTETKRAATLDN

QVTKLKKDLATEQAAASTASTELKAAVAEKARQAKKIAQLEKTIQSMDKKNKALLKDLSD

STPVDLSLASLLSSYYDEALVLAEDAAGIAQQKLHEQSDTLDFVQRPD

>contig45242 Frame-2F

MRLRSVCRSAKVLTPLFVTSLQLSCNAVQQALATRIDGNACILRECIHLRHLEIVSLAAG

MTFGKLSMRATNCPQRFVVTHDDHEQIVLSLAEQMRLNTFVGLSRLSHTCLFTNEEANGE

ADVLLNTLMLGCCPNIEELCLPGNSFGDYGATKVAEMLWSQVCPKLTRLDLRRNFIGEDG

IRILCHALADGCAPNLAELCLGGNTITDSSFHHILFAMESRQMRCLRFLGVEMNYLTAKS

MEMLGRTVGKLVCPALTQISYSDNSVDNDAAKRLLTTAIYRERVLRASKESNFICDSITS

EDESSSNEPLLSDEGV

>contig57119-0 Frame-2F0

MTKSYRNGVFFFHILYSSLMSFSCKAASLAAATSTAVAAVSGWSVVSAMF

>contig08448 Frame-1F|Blast-pectinesterase, putative [Phytophthora infestans T30-4](gb|EEY69622.1|) 1e-111

MKIYVLPLVALASLAINASATSIANECSGPVDVPIASPASCSGEYARTTPPAGAIVVDIT

GKHEGSFKTVTEAMASISNTTEVTTVFILPGTYHEQVVVDKLKSPLVIQGYTCNTMKYSE

NQVTITQAKAQADLPVEIKQNRNFLTSTMGFKSESGVKVYNLNVANTAGEIQKDGQAVAV

YVDNTDYGFYACNFTGFKSVVGANKGRELYAKSYFHGADNIVFGRHAMAWFESCDIETIS

KGSITSHGNQNESIKSEYVFSKANVFGSEKNLTMLGTPWGEYARVVFQECKLSDVVNPKG

WKASEEVNSTETVYFKEFKNTGPGAKFDQRVEFSGQLDMAKKMTETLGEGISNYWWVDSK

FL

>contig18719 Frame-2F

MREHALFAVCGVLAIASSALASHQALGAQASMFGFSGSTCKCKSTPRPCLFIHGQNNGYQ

AKALQPMSTMFGDMKDHAPCCSSIKYASLNTIDTPWTDDNLQATVCAHALSVSKSSDLDK

KIIANTILVTHSMGALIVAGALANAKCFLDKHTTWVSMSAPMMGTMASNYAQEVCTDDNT

QAFQKIFAVLGKCPVGVGMKSLAAMGGKFSNVDLNRAYVAAQKVYRKHVSAVMCSNSAFG

IVSTEQAGYIYLGFSAKHNSSEHDGFVTYDSCRGGLPRSQFTSSYKSRFYVSKCNHADTA

FRHADSFFRDSTKPVKWFECLL

>contig20082 Frame-2R

MASASSFNAALAVLLAVKYCRQNPLFHWKEEALPSMGRRAMKYCFRVDMLNLQQERCGEM

LLALLPSQLSLLNCQKDNILYRLKALLVTL

>contig22978 Frame-1R

MMLSHRNCVLHALRVLHTSAIVLLRLLSRGANRLHHANVLACCACRVHTFFYPQIRPLAN

AGSSPQPHERKANLPTNRF

>contig27102 Frame-2F|Blast-cyclin-dependent kinase, putative [Phytophthora infestans T30-4](gb|EEY57985.1|) 3e-94

MWSVGCIFAEMLLLKPLFSGRGELEQIDQIFKLVGAPNEHNWPGVNHDVPDASVRVRGKW

PKYSRLRDKFPLSATFSGSGCSLSKAGFDLLRQMLTLSPRHRISAKKALAHEYFMESPPP

KQQELMPTFPS

>contig36364 Frame-0R

MCMISGIAFAMLSALVDLRADLGLAQVSLVTLSVRAQVTRACSMAPLIDVDTCACSLV

>contig36423 Frame-0R

MTALLISLLQLVFLAMASMPQPLILRVEFQQQHNLPDTLQGPMTLRLSNHPASLAELHEV

LDRQLVAHLLDFRVDNRQMMKLNMTIEIYNQEKQRFVTLKEISQLGERRSRLSITLANAD

AVFPGHTCLALPSKNFTDIAGDNKIEIDGRVVFISEVANSGKGTGLTTWDGSVVLAKYLE

HNRHSGIAGSRVVELGSGTGLVGIAAAILGANQVILSDLPYVVDNLAKNVAETVKLAARI

GRPIESEVSVEVLDWFKPPTDLGDIDILLASDVVWVEELIPPLVATFDTLLRHSTAKTRI

LMSHQKRSNRSDRLFLIELNRYKLIRSRVPASNFHPDFFSDHIEVWEIVRAV

>contig37770 Frame-1F

MLCMKARRANKSWVWLFRSLNGCSANVKLGAKFKLSAMLYWKKNIDGQWYVEFARVKIPL

LGRIFFIVCLYNIMVKSDEFGEDDHHSSRGTSEMDVAIRLRREQELGQAEATVLKCRAEL

GYQLSNHLTGTSTRLERVAKDMAATKQQYEEQMQLWEHERLQLKQQLVKARGQRRVLVTE

IRNLRTQSEGQIAVAMAEASEARMVNTRLKKQNEILLTQIRTLLDEVNEHEKKCLTNLQP

REVDGQGAQVADALNKVTMPAVSATTAKSCNKNCFDGDYHSEVVAKDDHLPIPYTLNEKD

IAMLNGRAPVVNFANELLPTQQEQAPSLSIALRGHDTVFRARLVAFFEERDPDKVAEVDE

MLANYQGVEESLFESLELKYNFMELTRRIAQTL

>contig43746 Frame-1F

MHLIRTVLFVAAAFVAIADCKSFKGTDLDESSQQATNANLPNEIEERRGRGGGGGKGRGT

RGGREAYRANGIGMFTPFMYSSETPHLDRERDRFYRHMFAKYVKMKKDNQAA

>contig49490 Frame-1R

MVRVYVTALIAYLALHAAVSATSQTTLAGDSPVDAEETDTPVQRRLRAHAETNLESDERA

LVNLSEPLFYRAIRFLPLPKPDMAAIINLVKDLDLSSSEALNNNLAQLQHLKTLVQRYNW

CYYDKPISLFELLEKKYGAAVMEKMMETAKDDITDMSISKVLYKERQVYLKQFSRLGTKR

AMDLQ

>contig56090 Frame-2F

MVRVYVAALTAFLAFSASATVQLTLASDPPVNGTGRDAPASRSLQGFATINEKTEERDVM

EIIKASARAIKSHLSRPNVDIQASSVRELDISLNKVLHMNSEQLHQLIKRLKKSNKYPVS

LYEQLVLKHGALNVENAMRIAKSGKNDADVMKYLLEEEKAYRKNWAKAGTIYARELKIHE

DGVKAFETNKISELQAYLARISPDPSEDLQHQKLVKVLSEEYGGDKFLAPCIAQASSLGL

ETFSLKLALVSKWEKNDVPLDYVWWYFCKDVTAPTEEEAEMFSQFYGYAFVRSSKGKLLF

ETTALVEPNLMKVYKDSASDVALDMLIQIRLARRFQMGK

>contig56577 Frame-0R

MGLLIVLHLCAATLLGHAFAWDPQPDGYQVINGPDSPDALDTWRREWGQWKKMELITNRY

DPNDACTVYNLPQTQWTQRNFVQVFLMMTDRAIFDRDTQQYTVDKYVDNMMERVGPIDSV

VLWSGYPNLGIDNRNQWDHIRDLPGGLEGVKGVIADFQRRAIRVILPYNPWDIGTEDESG

LEDTVRMYTADITALSKILAALQADGFNGDTMYGVPKAFFNCSNPMVATPEGGVPSAYLN

HNPMSWGYIFGYSKFPPVLRPKFLESRHLVEVCARWSLDRMVEFQIAFFNGGGYVLWENV

WGIWNAMTEREDQTLKRMFAILRQFGAIVSTGTWTPYYNWKGDEVYASAFILSDDKALYT

MISTSEQSLSYELVLVANQSSTDVRVYDVYHGVELQKETGSASNRMVVKIEIEPRGFGAV

YATTSTNPDLTAFLRDMQALTLKPLAEYSMERQLLQQELVGGSTFLNSNSGMDSTTDMVR

ISGMKDWWFNVTGVQIEPVSAWTPTFAQFGTGVQFPWESRPWNNHSSILSIDDFMIDKYP

VTNAQYATFLKASGYVPKSLQRFLMHWENRQGAVASWTIPTSLEQTPVVYVAVEDARAYA

TFYGKRLTHDYEWQYVVSNGDKYDSYPWGSNLDRSKLPKLYHGKELPPLRPVGSFQSSRS

STFEVEDLVGYVWQMTDQFCDSHTCGILLRGGSSYYPVAATHSDPNWYFPQALDAQHHNR

FLMISEGYDRSPMVGFRCAKSVTS

>contig57794 Frame-2R

MHTTVLMAGFLVLLFKMDRKALAWDKEYDRDEVEGDDDDSFDFVTSKLEFIKNEDIVEVE

CDSQHCAANAATGVPSVFVRGLVTTKPKPKLILQEHARAATNIEKQFKGETLGYVTPWNN

RGYEWAKKFRAKLTYISPVWLQVREDTHRAPIITGLHDIDRQWMRDIRDEIKGNIVPAIV

PRIVYERNRLSSEDVSVIIDDILALMDEHDFDGIVFEIPVMAGTVDMLQQIARACQNADK

LLILVLSRSSQEG

>contig57808 Frame-1R

MWFAKRSVKHWRMAYLRWLLVLLGLSLLASIEIETVGTRLTSTSGQVHGHLKVLSSSSRR

DHERRLGEVWTTGIMGKMKQWFTRFVKKIKRTRLWQYLWPT

>contig57901 Frame-0R|Blast-Drug/Metabolite Transporter (DMT) Superfamily [Phytophthora infestans T30-4](gb|EEY54955.1|) 2e-14

MSGTLTVVFCAFLPLAICWTSPLETSVGCMLTIPLSAGLDLFIRHTSFSWQSIAGSVFVM

AGFGILECSSSSSVPLCIQEESRRPSAVA

>contig36310 Frame-1R

MRLGLLFTIAFATSLAMPTNALAVSDDVYKDRALTFDSPLTEEREHEDDDSTEPAKPVVH

HPKKKRKGFFAKLVEKLKL

>contig50512 Frame-1R

MTLLRLLTALVLLSTTMIEAGNLRSQHDDDGLIQSHSGSSSVGIVEQIRDEDAILDSALS

QDSSAINDAVLRDKTDDVRAWAQCGGLYYLGETKCQQHTSCKQLSDFISICFPKSRPTEN

IVRLEL

>contig50934 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66749.1|) 2e-31

MMRWPFAILLSSLATFGVAATTTGQMVQLLVGAGCKFSSYSTLPNATATKPSYRLQLDPG

LGKGIYVLQFTDFNLPEADVLIVRASGTGKSVPPAATLSGKNATGS

>contig54938 Frame-1F

MWHGNCNILSMVMLVAHRRWFLFMWLLALVLYINTTTATNAAIRAVENVDASRFKMRTNA

TM

>contig59308 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 4e-30

MAWSFGRILYSVMTLLTFTKGWFNVHREDAS

>contig15989 Frame-1F

MKFYVLTTIALMACTSVTGEMRISFDKNIKDVFQLSDDGNGGIKISKKPQMSYEDTGSNK

EEETNDDQENNDDEDNNNDGDTIDGDKRKCRPFGLNEGVQQSSTYGGPHGNEFSDKKMVM

PGQNVTSVTLWAGERLDGLQVVTAPPRGVSLTLKHGGQGGKDST

>contig27100 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59864.1|) 0.0

MTRGRHPLLLLLAVACLVALSMAGKDYYEILGISRDASSAEIKRAFRKLSLKHHPDKNPG

DESAAQKFAEVAGAYDVLSNEEKKSQYDRYGEEGLQNAGGGGNHDPFDIFSQFFGRGGRN

RREQEPSRGPDIVMPLRVSLAHLYNGKSLQFSIRRETLCHHCHGKGAAHEEDIHVCTECH

GHGVKTATRRIGPGFIQQYQTTCEKCHGKGKIYTSTCPICGGRKVEMADLNFDVDLDRGT

NDGFEIEFEHYADEIDGHPAGHVRLQVVTAPHPAFTREGDNLWMDMDITLRESLIGFRKT

FTHLDGRQVDVVRTDVTPPRFVTVLKDEGMPKHHSSKVKGELYIKYHVKFPDSLSEEQKV

GFRDFFAKVK

>contig27485 Frame-2R|Blast-glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54864.1|) 1e-156 NOT\_ORF

MRLLLLLALRVFPILSHRSLLTKELERHVHALDLVHVSTLSPEASTTRVLCWVNTFHGNH

DTRLQAIKQTWGRKCDKLLFMSDTEDLQYPTIAITAPPLHSMLWQKHREIVRLLLREVTE

DQYDWIFKCDDDTFVVMENLKTYLSSPAIQAAARAGPVLLGHRMTLPWWEMQRVFEPFEN

FHPDHVKIMLKVKEETQSHGGLLYTPGGAGYAMNWAYLKQLVAALDQPFCLPYEVVPDDW

AISFCMRHLGIIPLDTRDIEKRERFHQYDPKELYTKSHDAEAYDHNVFTSIYQEMNWFSD

HNGIGWQNGTNCCAPDSISFHYVKPPLMELFYEYYYGE\*NFADCVSILRSFDILILL

>contig38324 Frame-1F

MPAPSASTSLSLLLVALGVLLYFRKHPTTLFNFDVAAALLNRKKTKEPPEQFKRRGSLEF

KPVTVRILYGTQTGTSKKLAEALERTLFALNISGFHFQTSVVSMKDYDQDNLEQEAIVVA

ILSTWTHGQPPEDAKMLCSWITDMTQDFRVSKSWLNNVQHAVFGLGNAEYDEDYGRAAKN

LDRGLCDLGSSSLVTLGLGDDNVDQLKQFDIWMDNLIAAMCEYSSKIAEAALKKTRSFMK

PGKDEWLTQTEFRRQKRAKKTEVAAGNGEILKPNEEDLMNEQFLVDEFSDDEEHTKKMTE

ENNGMVDVEDIGNSMKESEAASLSREMVTPMQRKALTKEGYKIIGTHSAVKLCRWTKHQI

RGRGGCYKHTFYGITSYQCMETTPSLACANKCVFCWRHHKNPVGRVWRWKTDDAETLVKG

SIERHQNMIKELKGLPGLIPERWKEAFTVRHCALSLVGEAIMYPQINEFCKQLHDRHISS

FLVTNAQFPEKIAALNPITQLYVSVDAATKESLRAVDRPLFKDFWERFLACLEELKHKGQ

RTVYRLTLVKSYNMEGLNNYAELINIGQPDFIEVKAVTYCGKSDGSDLTMKNVPWHEEVR

AFCLALCDRVSGAYALASEHAHSNCVLIAKKKFCRDGVWHTWIDYQRFHDLIAKYYEDGT

AFTADDYTAPTPHWAAYDSKEQGFDPVETRFRRSKDGKVVEFAYQSTESGCG

>contig40936 Frame-2F

MNLYLGFMRFNIALNICALSSSSACTRECHSSPLTQ

>contig46242 Frame-2R

MAILRYSFLKRLFIQHTPFVRLITMPLLISFVLFFLAFARTAHGIDCPMEFLMKFAASPD

LALCTADTGFSLETIPTMTVDKMINVCKTMPCMKLMDELAAAKLGNCTVPGTNVSIQQDV

LGKFATACQETDSMSSTGSMGSAGSMGSMNGSVPLVDDESKADIADEEQSSERSPPSSST

SGAESLKVKFASAIVLLVVILA

>contig57381 Frame-2R|Blast-mannitol dehydrogenase, putative [Phytophthora infestans T30-4](gb|EEY56075.1|) 8e-47

MPTTCRICSFLSFVAVRGSCIMVGLPNDEIKFHAFGVVAKGLKFVGSNIGSIQNIKDMLQ

LASEKNVRPVIQKMPMDKVNDGVKLMRDGTVRFRVVLEN

>contig06799 Frame-1R|Blast-Endonuclease/exonuclease/phosphatase [Thermomonospora curvata DSM 43183]gb|ACY98716.1| Endonuclease/exonuclease/phosphatase [Thermomonospora curvata DSM 43183](ref|YP\_003300754.1|) 5e-20

MKLPLLLALATLYHATNADENDGCKYWNSEERTRVTTAYGGNGGTPYTDLYDASPGLRMK

SVTINSGDRINGVTFNVQLSYGAPVVLKHGGNGGSKKEITFSQDEYIKSFVLQTGEKDGK

NRIRYLKFVTSKNQVIEGGTRGNDPKNQLVQEVAPASYQLAGMHGNAGKEMDKLGFVYTK

LAANNCPAS

>contig11355 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68486.1|) 4e-76

MVSSTSLFALIAVVAPGANYVKAHGFITDPKPTWKDKESSEWVVQIPPFWKGPWDEAKGD

DGLLALFKELAPANNFKDLRSLFDGNPEFGEECGYTDPKGTPVDPPSNGAATLSRGIVHA

GSCEIWLDDKLVLRNDDCQSAYGDGTKQTPTVFKPVDYSSCAAGGCLLRFYWLALQNLDG

>contig41941 Frame-0F|Blast-glycosyl hydrolase, putative [Phytophthora infestans T30-4](gb|EEY61621.1|) 2e-62

MIWPTNYFKMACATMFSLFWGGATCAPTCIVDGMSVQEYLQSHYLNAMAQLALVLKGLSN

VVGFGT

>contig42290 Frame-0R

MRVRLVWVLLLSLATHEAVDANDNPTASTSRASTRDQDAVIQKIRGLRNEGMKLNDAHNF

RGAIEKLRDAIAALHDRVFGEARQTITDASEISQDAALYAQILNDYGSVLIRAKQYDEAI

EVLEDSIAMVQKIYGDSHPSLSLSLRSLAEAYMAKKEYKMAIKRYKTLRKHVKRGLGATH

EAYIEASLKIAEGYKKLHKNEKTLEVLENAVKAQGSEPNGLTTGVAELYMELSTAYVAMN

DIEKALRAAGTANVIFLQRDGKDSLSYAFSLNALAGVKMRQKEVDEAIQLLEQAHRIAVS

IYGEKDAITIASAKTLREVKEHKMDLQTSKDEL

>contig43367 Frame-2F

MYHAFIVVLSTGVVAVLVASSPFHVGSQGRVMWQNNCDLYGNDIKSISGIPDVCGDYCTD

TADCTHWTWTQANGGTCWLKNGQTASTSQSWGANCGYIIGRFSDSNFDSTAKHLMQFIDQ

NVNQEKKENFELLSDKQNYKSGYVKTGPNFSSSWSSYSSFGSVNKSPQTDLTFQLPTVTA

PAPVAPAPVARVDQAPVALAPVPSPFSPPPQKSGLMSSNYGLTEVETSEMLSSINAYRSQ

NGRASLTIDSRLMSAAYVHSQDQASQCKMSHDG

>contig48155 Frame-1R

MRRLSLTKWRLKTLVSSLLLSVSSCDASSRSMRSANPVISSRSYTSCVDLALSSALTSSS

SPLRLLAFRDQFVL

>contig48894 Frame-0R

MLSRWLCSLLLAQLCGHFAFSQPLHEAPASASIKLSLSSSPYDHQTQDLCTKFALICDFV

VQSCSFKEKNQLWLKNATNLDTNFKCVNNFSLLDQHNATLTKCIEEYSKDDSDRKHQAMV

CQELYSTWHQQNTCNQFHATEAKAATECSGFYSHRPWTQETLPLFCQDAFTMYKTMRHDL

DRFCERTSNSDAFWEGYVNYVASDTCKHYYDMMREANEQECGKSDREECQTKYQWYVDNQ

KVVETECYEIRASKAFYHGFYTWKKQQS

>contig56093 Frame-0F

MKNLFIPIAAALVALPSFGEATTYACERGVNEKQSFNITNTVTSEKNRMCSAVKGSSENS

IEWTSNYEIVEIDPYHQPSTGVAQYKFESLPLQDVSQVPVSFTYNFFNTSAISSAVIMTM

NTRRGAGGSASFNHLVVLASYNGARTVTS

>contig19226 Frame-2R

MLAVILGALLFVICKASGQHPTSSRYRYIPKYFSQRDPSQSPPASYPPHMGLQDGYTWHD

VHAEVAAGRLEGRNVKLLVFLRHGEGIHNVATNKYGMFAWDGYYSKLPEYLDSPLTKTGV

IQAGKASKMLDGEISMGLHLDNVLVSPLERTLHTYSVAYQNQQNIKSTVVELAREILGVS

TCDQRRSISEKRLEYPHLDFSKIKSDADPWWTSDHRETDAEIKIRATKFLNFIFSNTSSQ

SVGVVSHSIFAAALLGVINHPVYKIATAEFLPLLIEAFPPAN

>contig27186 Frame-2R|Blast-cell division protease ftsH [Phytophthora infestans T30-4](gb|EEY63068.1|) 1e-151

MKVPSARRLVTALCVLLLVGRGARKLRLFILSRLTRSRASSALKTIPTPSWRLLSVFLSD

LKTHSLGKVLLAGDHCVVQTKDTATTYKVLMPPRTDLTYLLDALVHSGVEFGSTAPSRVR

QFAPVALVLFPFLYLGLTYKMLSQMFSTDNHSVGKDGCQNVRRPEASPRIFFRDVAGIDD

ARQELEEIVDFLRFPAKYEAIGAKVPKGVLLCGPSGTGKTLLARAVASEAKVAFLFCSAS

DFVEMLVGRGAARVRDLFTQASQSSQCIIFIDEIDALAKSRGGVNSNDEREQTLNQLLTE

MDGFEGKGNGIIVLAATNRPEVLDPALCRPGRFDRHVYVGYPDVHGREAILKVHCRHVR

>contig29315 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65987.1|) 3e-10

MLLVAVFFAAELAPIYLTLDKRLLAMLSVENYEPLLDH

>contig30322 Frame-2R

MRLGKRVQILLLLFFSNNNSWIAVGGQYQSHKGSEPKRLVYPSATTFTKASYNAKGSQVS

DVDSIESTANDTDEEQEQDEKYYFKLSGATSRLLVPIKASKTQKMRKGKDFAVSQVQNFK

NTLYAYYQDVFTVKSSS

>contig30524 Frame-0F

MSRLLSLVLALLSAVTSALVIE

>contig35642 Frame-0F

MTLKPTLKACQCTFFLLWGVASLLCIETATVNATAPSTEGHRRLRQLVNPTLNETNYRSE

DRVFPSGVGLKRTAGIPFETRPFKMSKSEADAVIKRIYHHANEHIDIALKNSNILSSNIL

AKKHIERIIAEKVVALKSQPQSLPFGLAFQENVFKDWERRGITIEAAYEKLSLEHEINLG

VGDSVMEVWFSFACHLKKEKYSTQFLLSKLLEHFLFEPFALFNFLVRLHSN

>contig40642 Frame-2R

MGGFVLLVLLQSLVLERFVAEIAPQKLLTDRTWFSQVANVPVVVDALACMAVSDPLHPGV

AVEGYELVERLGLLGVCKHQQTPQMQWPVPDRNMVQIIPWTLLSSNVDRRHLTVCPLPGA

AKASQQFSAPPLPLPELVKKDADIRIPPNSPEGPMLEYHYATEEAERIYVNAHYRLKKKF

DA

>contig45689 Frame-2F

MVSFFYQIMATVVLLSGSSNAENIRNLATTGQVAYQFGLTHGSQAGGVPFSVQPAQNEQI

ATIRLNTGRR

>contig34811 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY59543.1|) 1e-117

MPYFLEAVLLCALASLHRAVPKKTNAPGLTNSNPFLDSCRAMHVVQNAVNVFAHAEICGF

NLPLRTNVVVLRKATFATRTAQSIIIKCIAWRVEQSVTDKFGALTHLSILFGAANAMKAT

METLLSVFQERVLLKMQLNVNSRRKRGWANPLLAKTYGKKFITRQCISKAEAKLLPFLSH

AVQELHDFLQNQSTVNNINLKVAKADWKCAASVWSEYKHHEVMLSDVKLVAACRSLQEEE

LTTTLLKDWRTALPFDTDDIASDFDDDEEVDELNEESLSEDEDDGFAVKSYASSIREKSA

AGLELNESEQRVIKLHDNEDLGFPTIVVNYKKQKTTRS

>contig37708 Frame-1R

MEILSMHPPKSQKHWVCSPLQLVFPVASASASTLGTPMVVAMDMDQAWDTTNTTHTTHTT

VVMLPRSATAAIRTQPLLRLPPAICAHKWRDNPSTILVTSNTTFQSRNKCCIL

>contig45396 Frame-2R|Blast-secreted RxLR effector peptide protein, putative [Phytophthora infestans T30-4](gb|EEY70235.1|) 4e-08

MRFILVIFMTAATICASWETISVEKDGEHDKLLVITSTTRYLKEDYGAVSNSRLLRVSVG

SNQSGTMQDEADIGEDSYMDTVYFKLWRLIGKTPGEVYTDSFGTMDPASAAQNPSYNRYI

RYKRYYNNHH

>contig14955 Frame-2F

MVQLIYPIILTVALLIRSSDQRAPTPGTLYGDFEGGSTNFWIGEDAPNKKTISGIRIYSG

ERINQVGLFFNKKATPEMSGGKGGKSTDLILEDGEFIKSVQVSPIKLPSQGRFRISYIKF

VTNKGRFLEGGKKTQSGRILAGGTDGPHHGQKLVGFAGRRGAEVDAFYAIWGNVY

>contig19901 Frame-1F

MRLLNIALATVAVATAGPGFSVSADSQTLSSFQTGVATVDRARRILLSSRSEEGTYLVSQ

PSSIPDEERFWGSKKKHKKHKKHKHHEESGSQSSSLDSSDAPDSSDAPDSSDSSELRVKN

EERQF

>contig32762 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66796.1|) 1e-100

MKLFVPLFASSAMLAAQVSANGVCYDPDHSAISGGMTAASVIEDIKMIKSHGFTSVRTYI

SKFGDTNLGLLLSNCNLTVALGVPYPHDDYEEQLDAAITAANNGDVSYIFLGNENLASAT

SVPEEMISIIEQTKLLVPDTVKVGTVQRNTEFLQNSAISGWSDLVCASDVLGVNIHPYFL

PETIAQNAIDVVKNQWAAMEDEDFSDKLMITEVGWPSSGTLSNCVGSLAGLQTFYDDYMS

WSSSMDESFYFQMFDTPYKTSLYEKSFGLLTSDALSKINFNPASQSGP

>contig42093 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63221.1|) 4e-07

MANTDLTGLYISCLLLLASVDSAILSKRAIPFVCYTEKDAVKNAAGINYFSRLKKTKAMM

LNAKLRRLDVAT

>contig47340 Frame-0R

MLFLCISSNLSIAVYVVYFSSSSALNSCCLDVLPTAFTSTLLICVMANLTRFKYLWYRLL

AGNLVNAA

>contig21604 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69376.1|) 2e-80 NOT\_ORF

MTRYSLVFAIVAIAVASSLCRGTELKELSSPRVEDLKQPLQRVAFGSCNDQSFPQPLWST

IAAHKPELWIWMGDNIYADMKELDEPHPFSISPRKMFVEASADVLIRRYNKLMANEDYAA

FVNRTPIIGIWDDHDYGINDGGKFYSYREQSQQLFLDFIGEPIDSLRRKQEVRCSISSYG

QFKKST\*\*FCYILLWRP\*QGIYTSYTIGSRDQTIKFILVDN

>contig39960 Frame-2F|Blast-tafazzin-like protein [Phytophthora infestans T30-4](gb|EEY53093.1|) 5e-73

MLWRGSRLVSSFSRSVFTFGSLSVSAGTVALYVDAPVADLGDGKYDGGRRSEIFPEWLHD

MARVPLFGAVTLGSKVYLQHFNRSTIKGVEILVQQLDQRPKGTSVITVSNHSATVDDPAI

FANMMPWRYMWPRNSRWSLASQEYCYTKGKLASAFFFGAKSLPIKRGAGIDHP

>contig58491 Frame-0F|Blast-Crinkler (CRN) family protein [Phytophthora infestans T30-4](gb|EEY65440.1|) 8e-12

MVTLLCVIVGVAGKAFPVDINTSQFVGHLKDKIKEKKFNTIKGEARTLQLFLANS

>contig25283 Frame-1R|Blast-cleavage induced serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY65993.1|) 3e-96

MFVLVFAIVSNSIGVLSQHLVLASPAGVPRPPPPLDPKSEEGKARNRSWLRWMVYLAWKN

GMTPLSIARFVGPYGPKLVQNVVHRRTSFMFENSAMRDGRVDLKELGKYLYHNWALKPSG

ERAMTTHLAPGAHAVRPLVDMLLPHRVKMPLTFIYGENDWMDYHSGQEIVKHFRNMGQAA

DLYRVPNSGHQMFMENPDEFSRTLIDSLTKDELTNMHSIP

>contig27182 Frame-1R|Blast-glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, putative [Phytophthora infestans T30-4](gb|EEY54864.1|) 1e-148

MLLILLLALRIFPIVSHRPDLLKALSNHVPAMELVHVSTLSPEAAKTRVLCWIFTYHENH

DTRLPAIKQTWGRKCDKLLFMSDTEDLQYPTIAITAPPLHSTLWQKHREIVRLLIREITE

DQYDWIFKCDDDTFVLMENLKTYLSSLDMQAAARAGPVLLGHRMTLPWWKMQKAFEPFED

FHPNHVAAVLKTVNETRKQGGLFYTAGGAGYAMNWAYLKQLKTILDEPFCLPYERIGEDW

AMSFCMRHFGVIPLDTRDAEKRERFHQYDPQYALYEAA

>contig44945 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57628.1|) 1e-153

MMRSIMLIAALARTSFASTGPYDGWAPHRYCNSMDGIEATRIPQLTSQQVKRVESLEQVQ

IIARHGARVPYAKLFCWDSNIHNPMGAQWNCTTTSVSSHDINLNENTAGFGRLYRKSYMK

GHNILNGDCVVGGLLPLGRLQHKSNGEFLCDSYVGDGPLKLFPTANLSHLELSKIYLRSD

DQERTLGSGQALIDGLFPVDSTRSFEMQRMLSWDVSDIAMDYISPNENICPYIGHISELS

SKSVEMEKHLQDTATVKIDKHFSNIVGEFSWSTVLECLSTARCNNLELPSGIDEETFAKT

YHEVEVRQGYYLLYNNSWYAKLAMQPLAHDMIRRLDDALTGNPDAFKLSVTM

>contig20735 Frame-1R

MIAQVLILLAVLLALRVWLVIIPRRIKVPISSYLNPLFHQLHVDNRKKRRRIRVMAVLGS

GGHTTELLKLMKNLKRAVYTPITFVVAKTDNTSQAKTELDWKP

>contig22782 Frame-0R

MAKIFRSPLAMITLASCFFQHAFASEKLCSIAPTTYTMAKTKYPNLVNALTTLEQYPIVA

WYTDRQSEVDRKGMLSRITSECSDNSRMTIAVYGLPNKDCNTKLSSSGTVHSTSDYESFL

STLTTAVGDRKVLYIVEPDAVGLLANNGCGQSAGYLKNLKIAIAALSANPNAELYVDVGY

WLLGNSTKASEVATIVKELSFSGVLKGIAINTSNYRSTDECMSYCDTFQAAMGMTTLSCI

VDTSRNYHGSPTTDWCNIKSAGIGKPPTSKTNISNVDYFLWVKPPGESDGICVTSTQSLT

GVTAGTFYAEGFQSLWDQGYFIDEKTKATIGGSTSDHVTSNDASVQFGAGSDVKDTSAND

SVIQTIGTVAPADTDSSDDSAVTTPATVATPIVTTLPPTTISPNATDFGLLQQTSACKPK

RRMREL

>contig25695 Frame-2F

MVRVYVAALTGFLALSASASATLQLTSVNESLADAYDSTAPARGKLRAYAATNVESDERA

FSNLLEHLKTLNVLFSPLSKERMEAAISKSDSSVVKHLSEDGAVNEKKLGIGRDGVKAFE

PAKVSKVKMILEDIFRKPYNKILLKVLSKANGGERNLVRNLAQAEMLGYKVFFLKSTLAS

KWERDGVSLMDVWSYICKDVKAPTEEEMKIFSHWCGYAFVLSAKGKFSAEETVIEKTLLK

VHNDNKNKKGKLAINMLAQIHLSRKFKVDANFFELYDPSPSSLKKLLLELEKSPRACDLD

VELYRLLKQAVTDDKFMKGIWDRSTKKPEQPNAKRN

>contig33098 Frame-0F|Blast-F-box protein, putative [Phytophthora infestans T30-4](gb|EEY63750.1|) 1e-19

MVASVIQAAIIVWARGRFVDANVSTELELLLRFVYSFSSGLRSFLKYAKYLSITHFASAK

KLLRHEYLQCVG

>contig55591 Frame-0F|Blast-polyketide hydroxylase, putative [Phytophthora infestans T30-4](gb|EEY56473.1|) 5e-17

MHKRSRVLVVGGGPVGLSTALLLEKVFNVPTRIVERKRSPTQHPQAHFMNLRTMEVFYAT

IPAFHDRLLAQAASSKL

>contig20736 Frame-1F|Blast-eukaryotic translation initiation factor 3 subunit C, putative [Phytophthora infestans T30-4](gb|EEY57814.1|) 1e-174

MMAQLGLCAFRCGLIWEAHACLSEICTGSRTKELLAQGLQSFRYGERDLEQERLERRRQV

PYHMHINLDLLETCHLVSAMLLEVPNMVNPNVTDRKRIVSKAFRKLLEFHERLVFEGPPE

NPRDHVVAAVKHLAQGSWRQSAELLVSLPVWDLFPGLNVAERVKAMVQHKIQIEGLRTYL

LAYSAEYDSVCLDRLMEMFELDEKTVHSVVSKMMINEELQAAWDQSSQAILMYKTERSSL

QTMALQYSDKLAQIVENNERMMDLRSGTSKEEWNNRRGGNDGRRGGNGRIGFSAGSNRRN

ETSNSRDGFRPRRGGGGGGGRGPRQQR

>contig28101 Frame-1R|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY56120.1|) 2e-64

MSVSFLSVATVLTTVHARTDIVAQLYGNTAITAPMPPQSLNSALQELVVSVANFTQYPAA

LQRAMLWSAGWVRAQPEAAILDESSSAATYVQVYVLCDRTMSDVFQSPHAFDDPTRCGIK

ECKSTLISFTKSTCDPDYVRSRALCAINPDATTFEFVPSLQTKNGPLWAMDGQIDATFDP

QLFQYANASSNTSTPLFLLTQKSAWTTMKDDDTCPNSAQFIAP

>contig29502 Frame-1F

MVSALRRMAPSVSPLWLFAALVVVAMSIYVHDLNVMLAVRRALLYTSLSSAFYPNDPVKP

VDCADAHRFLTDVMQVKGYHVLCIESTANDLLRVTGFKDGMHANSSVTTTMDLQTFQRAI

EVDMLQIPEPTDDNARKYKQLPAYFSPEGEKLKKDTLTFLQYRVVFLFEGGQFFWPGIKI

GHKTVVKNTFGRGDLVLETISMTPLVFSVEEFLRDDEIDIILELSMPHLATSGVSLQDGH

ENRPATDWRTSTMYWLDSSLHPVVKDIDKRTADLVKVPISHQEPVQVLRYERTQHYDQHV

DYFSPDRLRNSPDLIKKIEHGYKNRMITVFWYMSNVTKGGHTNFARSGGLPAPSSNKECS

SGISVAPKKRKVVVFYNLLPNGEGDPMSLHAGCAVEEGTKLSGNKWVWNKPRYNND

>contig34445 Frame-0R

MKIFNVAAAIAIAIASVGVNADQTSRRLIVGGESVIEGQFNYTVGIRAYANGRSNCGGVL

IHEFLVLTSVGCATNVSKELQPRFAAINQKIVDGTDSKTGEVIEVKRVIFHPMYDDIKVT

NEIALLVLENKSRIKPAKLGSDPKPGSKVWAFGWGRTDSSHDYPSRTLQRVQLEVKANDL

CDMYEMLTATNLCVGGEEGKDVCNNDYGGPLIAEGADKNSNDDDRVVGIIGLGSGNYGEG

CAIGVPSLSTRTSFALNWI

>contig41799 Frame-1R

MRTTFVQSVVIAVFFASATAIDTLIIPTTKGLEDATRSGVARALRGALSFSEKQYELEKQ

KHTSSYTDVVARPFHEEHSELIRTAKALTP

>contig39964 Frame-0F

MMKIHNVAAVIAIAIASIGVNADQTSRRLIVGGESVIEGQYNYTVGIRAYANGCTNCVGI

LIHEFLVLTSAACATNVSDEVQPRFAAINQKIVDGTDIETGEVIEVNRVIFHPTYDEKKV

TNDVALLVLKNKSRIKPAKLGCDPEPGSKVWAFGWGKTNSSHDFPSHTLQRVQFEVKTND

FCDMYEMLTPTNLCVGGEEGKDICDNDYGGPLIAEGADKNSNDDDRVIGIIGLGIGNFGE

AC

>contig47712 Frame-2F

MVQPISSLTLVVMAMCLVSVAPLENQLWLSQFKSKINILPKTSGNCFVCFYQQIKYAGPK

FCIGKRIKSCTKANPITAPGTIGSIKFGKGCNLVVNMRVTVVPFEERVDVIFKDVANTGY

NASADQQSTQELYVEEAGRACSLGFPASGEGYGVCYSKNVRAIDLKYLNSITELMLFKSV

AEKFDVILYEHQDYNNCTKSSIRRNGSQAMFHRFSENSKTLETNNFIGKLGMTTSLQNKV

RSVK

>contig51027 Frame-0R|Blast-peptide chain release factor 1 [Phytophthora infestans T30-4](gb|EEY67853.1|) 0.0

MLLRHPRRVLASVLYPWLPRQLDRAQPIANVWKHNQTRGFAMPAVILSQMSLLTRRYDEL

THELSHNDGSYSSEKITNLSIEMAELEPKVMAVQELQRQEKAVKELGGMIAEQLESDEPD

SIELRHMAEEERRELLEATQKLEADVVRLMLPRDEADDKSSILEIRAGSGGDEACLFASD

ILKMYQKVALAKGWKFEIMSISETDLKGVKECVCSLTGRGAYGRMKFESGVHRVQRVPVN

DVRVHTSAVAVVVLPEAEEVEVEIDPKDLRIDVYRSSGAGGQHVNTTESAVRITHIPTGI

VAAVQDERSQHQNKAKALKIMRARVFDGIRRKRDAERQSLRSSQVLSGDRSERVRTYNFP

QSRVSDHRVNVTVYGIERMLNGELLDEIVDTLVVNEQNQLLQQLETSF

>contig24110 Frame-2F

MKIFFTTFAASVALLLNSCSDALNVKLSGVNYGAHPDGTICQSAEQVEQAMVALQKVADT

VRIQSLSNCNQAELVLPAAKKAGLKVQLGVATGPDPSLLNTEKEKLRSLIQSGLVDENVI

GMSVGHNGISRKEVTAAQAIANMNDIRSVFTEVGRNMSLTISDTIESYVDNPIMYRDVDF

MSITYLYNIENTDVDEAVATALDRIYSVRLAAVNKQVEVAEIGWSSGIGVTTGSATPANQ

SKFLSDLVKAFTALRLNLFWSSGFDEPWHSNAIERYFGLHTANGTLKSHIDQLVITFLDP

RVINIHGLFLSVSSFSFGSNKLTMERLTNYLPSRDEQTFFIDYNTNQVRSLSSDRCLTCQ

EPVNGNLPVILTCKTDDNRQKWTYNTRTRQIQLVSNPGICLDVDRNQNNLIQVWDCATDN

PNQMFNLSPPVLRLVWSHQRQNSDTFSSSTYGFSVPLIMIIR

>contig31949 Frame-2R

MRVSKKPRVNFWRWLLQFHIAEASLFHPWGLLAALIRSPSRLLDGVTASHHRFLDRAAAS

VTQNPMLFPNGFFSDGWGDLNTPTRILELVQSRRMSDVVELQEEHLMWDSVQKLSVAKVA

LRVGKFQSTLDNAQQLLPKASLDAFCELVTPLEWEGQAKG

>contig33763 Frame-0F

MVLKSLFVFATSASLALAQGSGSNNLAMAVGTNGDTVQATGGTTVFMDTEYNPNKCVLQF

LSLECDDNCANLNGYELECVSQGRQNGKEKKLCQCKPDEAEMCQNSVSSNVTSGTVAQFG

ECSNENQCADVYGYITTSTEGGPICAEKIHCVQEVNTTATQPASICHTCMSCIAQNDAAE

NQLANVKRFNCSAICPQEILDTVAERNAAGVGIADSYSLTSSDSGSVEPD

>contig34003 Frame-1F|Blast-SCP-like extracellular protein [Phytophthora infestans T30-4](gb|EEY56881.1|) 3e-48 NOT\_ORF

MVFRQSSIALLLLIASSSNDATTAAHVRQRNLQTTLSDVATYTSYEQYASSMLLAVNAQR

ATRGLPPLCLNNKLRIASQSHSDDMATYDYMAHAGSNGSTMSERITEAGYQWTTVAENVA

AGQPTVSAVMEAWINSIEHLKHIMGDYTMFAPTYAFNKNG\*FRHYWTQDFGSSDVESCDH

LVDNIS

>contig35189 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61806.1|) 1e-112

MLCVRALVLRASAVAALPARNQVSRAFSGNWEYPKVEGSVVDVTKALTTIGARLSIPTAP

LYFTRLKVDYIVREMKGKEELQKVHETLLLCDAKMAYPSTLAAGSFISACIKQDAADTAL

NFLRHAENIRCYLKNQSFVRLAEYYAELNDQDTVDEIVNIMAAKGVPLTYKMYTFRVLNA

KKQGKWDEAIALAREAAAELQINSHLIIELLRDQNGNIYKEHVQLAKYLADKGDVFVNER

LADIFAGGDGNLPEVKVEETKQAGKEPEKNERTAKEHKKN

>contig41003 Frame-0R|Blast-hypothetical protein PITG\_18705 [Phytophthora infestans T30-4](gb|EEY68804.1|) 6e-37 NOT\_ORF

MGISFVLRPLTYSSFLSVSCPLAPLLFLLVVEILGIAVQQSPVLTGLLVPGCGTVRHAFS

AFVEDSTIFLEKGRQLGPALYLVSRFGALSGLQAQPAKSKLIFLNSAVRGKDFNGISVLQ

PADTVRYLGYEVGTNN\*QHRNWALRIRKLQRRLFTAVKVSTSVEHRVLILNSIILPSVLF

TAAVFDIPEWARKAIQNLYNQFLWARATSTEASRHKVNPGLLFTPKKAG

>contig47782 Frame-1F

MTRLIILNIQLYRILAKPIQPLGYCEKPRSDGQKRFKCKP

>contig14228 Frame-2F

MQLLLFLLLIIVLTAVYCDYILKERRHLNQNDGHASLRANFANGIEKDKEERGFNIFRKK

NPVDKAARWLLEGYKPLLKQQNPIQRGIEIQTWLSVIETEPIMPKDVITNMESYFNNEES

LELCLWLVHAKNLKLKNWGIHARDKLNAAVIDEESFPTIFKKNPTV

>contig30617 Frame-0R

MKIITIAAILSLAVGSVGAIFGGGVAERDTYTFMGSLRETEAGKTKCSA

>contig32769 Frame-2F|Blast-protein kinase [Phytophthora infestans T30-4](gb|EEY66954.1|) 2e-44

MTCSPKLTLWTFLVVFRARAIGGQTSSPSNAAVSGLTLAESLAQEWFTDNFNDNETQLAV

GVNSALKNLTSKDMICNGSPSIQRRTDKMTPNGGCPAIFTSMNGSCSCLTTGYSDTNTFE

FYVRLRGDEGMEYYPKSLDSSTILAIDSIRTLLVPSDLTTL

>contig51807 Frame-1F

MKFFTTILFTAAIATKYVLANEANTTTSAPATEMMADSPVTTATTDSKHVIGSILDEISQ

TFGSNALAYSSASGSESGSRFGIAYVGDNSTSTNDGASIQMTSLAMLTILATIAADLL

>contig29472 Frame-1R

MSFLFSLTLVSLRVSSSLKPVFGKMCNEALIISSGQNAWSANYFC

>contig42286-0 Frame-2F0

MKDFSPLLTVSTLLRIKLGAQVIDILQI

>contig43968 Frame-0F

MLSCKKTFALCATAALIMSGFSEVESSIASYRRGLREGAVSGEGYSDKMDYKRKHYEHTD

SDGDVGHNGDDTVLYQDSQLHDGLIDIDLVAKLELALGLLREDGVDLLSHHNGALQHQNG

ESPLHLDDLLEIGVGLEIAIDLLREKGVGLLNHHGAEQHQNAETPLHLDNIVDIDADVGV

DLLSV

>contig48882 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY64057.1|) 6e-46

MGRQHISVAVVALSAVTGTTAAAVSMMAYFRFQHPQEFADATIRLSHPELSDDINRKWGL

FGTGIFDSVPQRVNDFFSVPDMAERFELQKKKRDEQIRQTIEDLRPKGK

>contig49162 Frame-2F|Blast-nardilysin-like protein [Phytophthora infestans T30-4](gb|EEY65469.1|) 2e-07 NOT\_ORF

MVPSILLLRLLRGNWSQISKESIGMSP\*PLPNPFMPHDF\*ILPFDPANWPAAL

>contig59318 Frame-2R|Blast-glucose regulated protein /BiP [Phytophthora cinnamomi](emb|CAA53369.1|) 9e-24

MNLSKVILIAAAALATAVVAEDSKGPRGPVIGIDLGTTYSCVGIYKDQKVEIIANDQGNR

IT

>contig15812-0 Frame-2F0

MNLLLGAIGACSVLFVSNGQFLRPDDGALSRPFAASNATGFVPASVDKSATSPRQSDSTV

AEE

>contig17524 Frame-1F|Blast-aspartyl protease family A01B, putative [Phytophthora infestans T30-4](gb|EEY59472.1|) 1e-07

MALIAIVSYGLFSYFARCSECMTTSSLASIQGISASQYTNFQLFKQFNQTRLFSRDKTNE

THAKSHTILVSISKQPTERNFDKKSRKTTFHCGKGHKCGNKQKYLAFAFSDNTTSTSGNS

SMIVPFDKDNAPRVDCLTGK

>contig30615 Frame-1F

MKIISIAAILSLAVGSVGAIFGGGVVERDTYTFMGSLRETEAGKTKCSA

>contig07489 Frame-2R

MKFFFCSAIALAATASAEDTSKPLCIPSETEKGPYYFGNFNPDPPGYSCLSVTSNDSSAI

SWKVDFSFPGVLVDDRYWYDSYLSLNTHTVTMARLHSIPVVFNYISFVNQDLSAIAHITM

HVQPDNIYNLGSMVRLKLCQSGPDPSWLGQYQKEVQVGNVPYSLFQGNIGTMALFTFVPK

KCTTSFEGDMKGFLSPLELQSSYRLLTVRAGFMIRTGVDAVLSVDKQYMTYIAAVDPSP

>contig19297 Frame-1R

MRLSVFLAVGVALVSSRLDTTVQAADAQVKERRLNIVQAAQEAAEKGAASFQWGVNKVLR

KTDDTYGEAIATALAKKKELVDPTNLRAAGGPHVDDIAKNVDGVVPPVNVVNKEVDEVAK

NVDNVAKNDDVVKSLTKKEDEVIPNNKLDDVLNPTPKALPGTLEHVFESVKALANAKAVG

EMPNKFTDEALMKITKKLVKETYKNPSMGAKFKKVLLWLFGGTLVGLGFYGAHQLSQQVF

PSPPEKVTTKVHN

>contig25038 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67964.1|) 2e-22

MSWCGASNRNCSVCLSCSSYLLILLALAELALAVMILI

>contig29232 Frame-2F

MMCWSRAVVARTAWSSSIAAVPRKSIEVRGKIHLKPTIASFVVKSTAISPALPSAATIAC

RSKRGRGSRFRLGASVQLGRHQVDKVLRLKQRN

>contig34270 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY65784.1|) 1e-167

MVDKQLLGLAFVQSLLWEYMCNAEHDDVMQMVANVRDASLALLATRNGARVVNKCLSFGA

AKDRKRVIKALKDKILEACNHPSGYLVIMRILDVVDDSILVQKSVLVEMKDELLSIALHP

SGRKILLQLLSPMNKKYLSADDLELLKPPMLPSSEDSTVLVVNYKKDPESRREELLMGLL

PKLEEMCADNAGDLMRSKEGRDVIVEVAKHSENSKLVRSIVAAVVAQPSEEQEEPLYSDA

NGHYALRRLIKESALVESLLIAVKEQLSKWATSNRGSFVVLAFLEAEHAPKKILDEVKEA

>contig40332 Frame-1F

MVVQASLRLGPRLAMTLLSIALLSAFEEAVLPVPLDAQENQRFEIKSFTQHKAHDNKNDH

VHDGSADEEKI

>contig15814-1 Frame-0R1

MNLLLGAIGACSVLSVSNGQFLRPDDGALSRPFAASNATGFVHAFVDKSVTSPRQSDSTA

AEE

>contig06736 Frame-0R

MTHRAALLRSALCLTTAKPRPSPTLFYFPGLESAPWHDTSKFEWIKHIEANREVITKEFL

ALKAQRANRKSPGTDYNTSDHEHQLHQGQWDWLSYVTQGRRQADFAVYCPKTVELLETIP

GFLSGLPFAYCFFSVLKPKSSIKAHSGPCNIRLRCHFPVFVPKGCGIRVGSESRQWEEGK

ALVFDDAYDHEVWHTGLKKDRVLLLFDIWHPDLIQEERDAIT

>contig26785 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69848.1|) 3e-14

MKTLVSVVLSLVLLLLDAIQGAFEASSATSSSECCHTCIGKASSVPYTYDPGRFCGLHQS

NRRGLLL

>contig54551 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67255.1|) 3e-26

MIFSMLYATGALLILRLNGRKHEHLHGIVMASPLYRRLKLLMLVCAVFTLPYS

>contig18015 Frame-2F|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY58585.1|) 5e-26

MITLRQILLFCVFFSLFPLVALCLCFIENPDPPAIPSAHPSA

>contig25675 Frame-2F

MQPSILLSLAALSAQLTNALDVSVCGDATYALQPVRGAVCSGNGPVPEGTACPLRGDVAV

ADCHFDLSSYQSGRCKAYEDAECRVVTASTWGCVLPSIGCNDTATVPYETDTNCPTWSWN

EATTLANSMDLSVALSSQLEYNASWFVQTTPLAELNHCGEPPPVTPTLTKELPSLAPEKK

TNVPPWELITKAMPSTDSFQSAAPVSAYVPTIPDALATTLEPLESKSATL

>contig38066 Frame-1F

MKFATGLILAAVAVTEATAGNSEYLRSKDSDTLNAGNNFPSSSKNENTTDNDDSNKLPHL

DAAFVDNLSKLNVSEFKHLLTSMIEGDGSGLSDDELLDALKNIYDDEDDGPQTHYSSNRK

VSLTDLNPSSSVSSQYESTTTTKDSSSPIQSNPSYSDADSDEEPSLSKRSTNDVNKNGME

YYNDIDDSEASPGTKSFSKSGKEGIESNSVGSTYNDPMYGTTGEDEDVPSQTSSKAWIDD

SGSEEYPLTTKDNNPSKKYAYSDNPGSLDEVDLTSPLDPTSYPILDDQLPRRDVSPGSHK

FRENLDHATKSIIDSPPTNAAYGSKSWLDDEDDDALTKNGKYDSVDDDDSLDATPYTATK

PVFTKSSKGGIDNNSVGTTYNDTNYGTIGDDDDVATDKTLKAWIDDDASVNSPASPSYGS

KSWLDDEDDDALTKNGKYDSADDDDSLDATPYTATKSAFTKSSKGGIDNNSVGTTYNDTN

YGTIEDDDDVATDKTSKSWINDDAVVDPPNSPSKGFFVSKKSWYEEDDDVLAKNGRHDLN

DDNDSIDVSPHAASKYVDAKASKTGIDNNSAGTSYENFADDKTDDAFASKTKMPKDEILY

LDDNLQMDNKKSDAL

>contig42517 Frame-1R

MILGRYAASALVLVSTAKHVQVEANKCKASDSFFSFLVDDLPTNHGFNTCVANNAGTIAK

ALAKTLFSGCNPSDVYDLVKNEDLRNFYRLFRSIAQTPAAISKLVYKYMAAQTDESVDSL

CDAFGGTLGPCAGHVIPKLLPG

>contig04057 Frame-0F|Blast-hypothetical protein [Monosiga brevicollis MX1]gb|EDQ88626.1| predicted protein [Monosiga brevicollis MX1](ref|XP\_001746730.1|) 5e-08

MKSRIILAAATAFASIASAQEQTTQDSSSPAQVTSRSSEMTSSTAELPSSSSENAGSMTD

DTTLNEKNSNNSTSSTSTNSASSPTSNTMTSATPSAVEDVFKDLKTTKTPSDSYHMPAVR

AVHARVQS

>contig30429 Frame-0R

MTRGFGKENRALMLPSITLILEKIEAFGLTLLEPDVEENLRFHKKINNLLITCGTCQLDV

LLLENPGDIEVTLLRRFLTLLCRLFAHPSLLVTEAQILLWLTILKNPRILQYGQPFLPEI

LSQLRHVSFDKYFKLSSPEREPSGSQELACQCSIIEFDDHREYVAFYGNFRGRLYALLRV

LVQFNPTIVLQSLQERLVAVLTHYAAGTDHLKSPHGFCSDLSITYLYHEGMTSLLDCILK

QLPAQALTNSINQQIIQQMVQAILSYASPDPLLKFRQLLVLASFATYYALDTSTLTSVFD

LLFANINYVMPDEEVHGQMSSSTLNVRRRALSSLVSICQAIPAHILPVLPVLCAKAQELF

AADRVTDTEGVMLYEMLVLVSNSMETQDERVQFIQLIVQDPLTQWTSPDMTALVSSPETI

VVAIEAANTDEKAKKLLGMVLKSLTTLYSIAKRAGATFSSKKIHATDAFEGAWPHVLPNL

LALVRSLHGLHRPAIKDQILKSSTACWVLSVSMDEVAQLLGGKNELEDHQVAQLPVASKW

SKWHKNVRDIAYHLLGVAVGRSHFYQNSQVLSVLENSLLSDLDLMEHRHLKGALAYVFLP

LLKKCPTELYASLLDPVLTTLLTHFAQRAKSMFNPATEGTTRWSALIVGVDNAKQEVARE

KMVMELTRQVMDFLEYAVDPKTVIGVDTDHPKHVTKPADAYQRDYMLIHSATLPLAIGAV

VMEVIRWKDTLSCRKAVLLGDILVNVLHENTRYHLLLGRDLFTAALEGILKEHIGHVKDD

GLKWEIINLLRNIYCRLTLGLSPVEECIGIDPCHQPLRPTSSLCSIPRELLLSLPNVTLG

EIEALETLLREKHSVKTQKNAFKELLEVPILAIRSQQPLVSGSALPATGNALKKTSIVGK

GIADLPEPLQLSSKDDSKRKMWKEAQNLALDTQFLFQ

>contig43449 Frame-0R

MIGNFKKGLFVAAVAVALATSVEGYTGAASYESKRMLRQQTQAIAEESVADDPECGSLEM

AEIDDPECGSLEMAEENNDNNDNNDNTNDNNNNYSSGNNGNNGNFWTPPDNGNNGNSGNY

WTPPDGKKNLHTGQEGTPSGQDTKGNTVIQTD

>contig12503 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57791.1|) 1e-16

MKLQLLLALATLYHAANAVDDIGCKSWGSEERTRVSTAYGGNGGTAYNDISLVAPGQRMK

SVTINSGDRINGVTFNVQLPSGATAAFKHGGDGGSKKEISFSEDEYIISFVLQTGEKDGK

SRIRYLKFVTSKNQIIEGGTIGN

>contig21471 Frame-0F|Blast-serine protease family S33, putative [Phytophthora infestans T30-4](gb|EEY57809.1|) 1e-122 NOT\_ORF

MVFLLTLVFDTIRFVSGFSAKNASVDKYTWSYIERKGKDKKDADVVVFLHGFSSTKEAWV

RVARGIDKRYKIIIPDLPGQGRTTPVDTLTDYSMPNQAKRLHDFLEQEVPADKNIHLVGC

SMGGMLAGVYTGLYPERVKSLTMVCPAGISMPSKSTLLKMLEETGRNLLLAHTVEDLGEM

NSYLSYEPLKVPYVILKILALERTKQLPVLQKIIHDSLQNPTVLEDLLPQIRQKMLVMWG

KSDQILDVSSVDVLKSKWSFEAQGQILLFDQCGHTLHHEKYVECTAAINKFLLEL\*IKVK

SQG

>contig33902 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66138.1|) 9e-70

MKQNVMIAPTAAVCTAAQLQGAITIGNNCAVHPGASVRSPGGIIVMGERCLVEDGTILAN

DTLNVMEIGSNNLFESGCEVRSHSVGNGNWFEPKSLALEGSIIGNNCIIGSGVVVAAGEL

VPDNSILVAVQTPGGDMRRIVREQKDYFVKAHSTMIQKYVDIFSRGSKSIYALEKHHDMR

ELSEQ

>contig45428 Frame-1F

MLRPSSSPSLITDTLLIVSQLARASKSNYDLILKANLLPHFCDLVQHPEATVRAKALNCI

GNLCRHAATFYSHFATPWDGQIAHTIVAGMIFGLRDNDQYVRRFACFAVGNAAFHSGELY

DALRPAIPPLIQNLGNDDEKTRSNAGGALGNLVRNSDELCRELCAHAAPWALFKLAMTET

SVACRCVVLFSLGNFCTYEECFNHLVEAESDFISELETLYNEAADDVSRRNIRRIFAKCE

ALGNEEDHDTR

>contig50211 Frame-2R

MQNHQATSMMATLMLAGATQATTCGQHKKLSWLLSSKGAAEEFRQMQPKSEASLKCCGIC

ERKFGILSSVASCNLCLVSICSRCRISRDLCFVKRPSNITQHRNQSEDQDATIQVQRRVA

VFCKNCKVTASNLDARVMVRRQVEAGKKQRDDNSKVCRISGGKTTFLDTPGDLKLESSDP

LIALSLSSFQDRDSINEETRLELTSYKHRLQHQHQYAGEEPELSCIRLSAPDMESSQAEL

VR

>contig52716 Frame-2F|Blast-ATP-dependent helicase, putative [Phytophthora infestans T30-4](gb|EEY61840.1|) 3e-55

MGLGKTVQTIAFLLLLKSLEQSGKSAVGPHLVVVPASVLNNWTREFAWIAPKLRLVTYHG

SKNHRREM

>contig42336 Frame-0F

MTMSNILLPIFVGFLVESFVSNAKTVESATSYVNSAHEMAVNDEEDRMTLLETRQLQEED

DLESASVALASTAKRVPPSPCSVSSSSASEVHFKYKRRGSGVHDQMFDAVKLSDVSRLTL

QVEQKEEELAQQDMEIRKLESNVLSMKNRLKQSQHVILAYESKMEELSRALRVAQDRQLE

IETGHPSSFQQSNSENSLSSHNRTRRDRSSSWKIWTAHV

>contig49751 Frame-0F

MQWELTSKAQLAHLLVVELLAYQFASPVQWIKTQALLFSEGGARRFVEIGPAPTLTNMAI

RTLQVGDFPNVSREILWYQRDREAVHFEEETSNISASEYARGLAAEAEAAVANAFAPKMS

AAPLKPTASTPAQILATPVQYTQAAPVASAPAVAVADAPVSPLHILRVLLAVKLNKDLGE

IKEDTDVKALCAGKSAVQNEILGDLEKEFGGGVPDGAGEIPLKELAAKFSGYTTLGKVTN

GLINKVVASKMPGGFTMSSVKEYLGVDKGLGAGRTESILAHSLLLAPQARLKSDTDARKW

LDESLSGYASFAGISLDRPSINAASGSAGMAFNSASFSVPTVVDKPVEAKHALLVMLAVK

LGKIFSEISETTTIKELAAGKSAVQNEIVGDLEKEFGSGPDDAAEMKLSELANKFSNYAS

PGKVTSALIAKLLASKMPGGFTLSVIKEYLSSERCLPRSRTESVLLHALTQNPQHRLSDD

TSAKQWLDGVVDDYAKYAAIDIPYLSKLGGVTTGSSIGQQAMLSSALPSDFEKRLKSMIA

DQVEALNSYLGDDQLDWHRKIETEVDMREDLESSVSQWVTEHGEFYGAGIAGKFDAKKER

QYDSYWNWAKQDAMELYYRTAAAASGLAISPKLTVNKGLSAHFEAMTRFINKNVDTITDE

LALPPLEWFKPYLCNRATPELLRCTQFFVSRALKESSPELAQAVQLLVEQIEEWLNTNPV

NMQIFKPTQPLLRILDNGVLEYAEVPRDGVTDSINYVDEVARGLEYNDAIETGKVAGSDV

TAGMTSAVGFETTLNDNGSMNSDEVDSYDEEDYKDEKSAITNKQTSNTSEASKAKGAKLN

ALRDSLRKRSKRETEKSLVARSSSLRFGLNENLKKIVLPHVHIRKPSNVDPTIRLYDVES

TCVLLSCMREMASTGISFTGKVALLTGCGKNSIGAEIVKALLEGGATVFVTTSSFSMKTA

GLFREIYEQHGSRGSRLFVLPFNQASKVDVHSLVAHIYNVHKLDLDFVIPFAALSEVGRT

ITDIDSRSELAHRIMLTNTVRLLGEVVVAKKSRDITTRPALVILPMSPNHGNFGGDGLYA

ESKLGVESLMRKWYSEGWDDQVSIVGAIIGWTRGTGLMSGNNMVAAGVEKMGMRTFSTTE

MGFNLSALMHPSIVDRAAESPIFADLTGGMAQISDLKDQVDAIRADINKKSKVQASIYAA

QENDKKMSVLPLFKQVAAFNSKTFAPRANISSYYCNGFPKLSGVTGLSASTEQALLRGML

DMRQIVVVTGFGEVSPWGNSRTRWEMESYGEFSLEGCIELAWLTGRIVFDKGNWVDAETK

EIVPDHQVKSRYEEDILKHSGIRIVEPELFDGYDPKNKMVLHQVAIDKKMSPIEVADRDE

AFQFRKELGKENVDIFQHSSGAWMIRLRKGSVLNIPRALNFDRFVAGQIPTGWSAERLGL

SKDLAASVDPVTLYALAATMDTFVAAGVTDPYEFYQYVHVSEVGNTSGGGMGGMRGFSQI

YKYRLLGKAAPSDALQECFINTPPAWVNMLLLSSSGPIKTPVGACATAAESVDIGAETIK

SGKARVCIVGGYDDFGEEGAYEFAQMKATSDSVKEVGMGREPKEMCRPCSTTRGGFMESH

GAGMQLLMDAQLALEMGLPIYGIVALTNTATDKNGRSVPAPGQGILTTARETSSDTSKPS

PLLDVMYRRRQFDDELDSIEKWFAREKALNNEDESRVAFLDEMKARKVQSAQAMWGDSFY

HGRIDIAPLRGALSVWNLSIDDLGAASFHGTGTTANDKNESEVTHKQMAHLGRSLGNPLP

VICQKHLTGHPKGAAAAWMLNGLLQVLNTGLIPGNRQLDNTCETLRKYDHLMYPNRSFQT

VGVKAVLMKSFGFGQAGGEVLLVHPDYLLSTLPADDFQQYSARRTQRMVKMNLHSQNVIT

GKLLHIQVKNEAPYSSAQESNVYLDPTARAEYDVTSKTWRFGGADSLTANENRRLRAEKR

AKKAKAAAEIASLSRKTSNAPFEDSSSTLLTAINQAALDLGLLSKNMGMGVDVEPVATFK

NLNGREDFIRRNFTDKEMAYCYSSPYPAASFAGRWAAKEAVIKAISSSAPTEPNLWKGAG

APLREIEIYMTASGAPSVLLSGYPLQVYNRLGLSKLSVSMSHSGDFAVSQAVALFQQE

>contig16134 Frame-1R

MTRKHKRLASLCCLVLLSCYHIAICVQNVALTEAPVLNKSRRLRSGVGLEERVVPTSEGL

TNSFGTLSQGLTHFFRTLTPRMKDYVASWKWIIKYFPHLHVRFAKDKVAAAARVFPDDLA

NSMTKNLFEVNAFIEWDKLIRRSIKRTTEEVDAIITAALVAKFGNARAIQLFTEATFEAG

LVNAKWLPLLHNHYVQAKADLYELFKDILKIKNLNGVDQKSVEFFIKVGSVKQNNEDDAF

EVMNRVLIENEEVLVDMHKLGGDVAAYRDKWHLLKFAYYTIVFDSIPNADAIPIKRLKNL

ADKRKYGSNTAASWIADSYAQSAEGFNVLRIAKQTLQKEDGLNSIFDKAFAKKILKQIGL

KWDRNNYDIGNVLKHFVAEKGIADNFLQSPEGLAVLHAVTASMEVKAKGTEEVVLVFRKA

FGDDLVAKMIRNADQKDLNLVKFKSVFEKMVVVA

>contig44021 Frame-0R

MSAVRRFEGGAIIKSVNVGSLMLLLGGIAAVLSALLARHGFTGRDHVVGIDLGTTYSVVA

ILQKNEITPIADKDGHVLVPSTVAFLPDGGLLVGREARAYRTTDPQHTIFNAKRFIGQSY

TDVMGSEANESGVVPYEFSVKKLENNDHDGVCFKLNLHNQPECVAPLEIGTAIVRHLRSM

ACQFVGHEQITKAVIAVPVDFNAKQRNATKAAFEAAGLVVSRILEEPTAAAIAYGLHQDP

NVSFLLVFDFGGGTLDVSLLFARNDAITVLDTVGDNHLGGEDLDVQLSAWLVQQFEAQIG

TAITSRGGTETYRTELAHGLNEPPCTLAGVRQVAELAKRQLSDETVTTAACAWSDRGQVV

RPVVEITRSQFESLCLPLLERTMIPVLDILEA

>contig57991 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67964.1|) 3e-23

MSWCGASNRNCSVCLSCSSYLLILLALAELALAVVILT

>contig18220 Frame-0R|Blast-putative GPI-anchored serine-threonine rich hypothetical protein [Phytophthora infestans T30-4](gb|EEY58896.1|) 2e-06

MKLLSTLVFAAAPTAYSTAEFSVSSCTSEASRTSINHLSFIEHVIFKSSGGAIFQNVQMV

TAAEFNSDDPSQFFMQNASSKHTFTCSFAYDESNVPACESARVSSDFLDSSPSDALSAGT

PVSDFEGGDATEAPDKILISDGSSKSLFQGFAAVAAAVMVTATAALL

>contig28850 Frame-0F

MYHMFSFSSLFCFVKTMFCGEKTSSYSKVSIRSY

>contig36196 Frame-1R

MLLKYFIAILAVQHSAGAALDPNEQKLIDPIRRRLEPLLSFPANQLVDESHGALRTSRGL

AQDDDNETRMISTAAIKPPILKSLANSQTGGMRNAVSKIVAEKANQVEHFLADKDTVAAI

AAKGAKDLPDAETSSTARTSRIAERSSDAKASNFVAETSDAVNAKPVVLLLDEVEKKKLT

TTYGTDFAEVLASHLPAAKKLMEKSERYAFEYKVYLDLIDHVPHKQFIVKSLDDYDPEEI

YGFLPHFASMDMRNELAWSNAVLKAKDKPVLFNPIEAFKNVASIDGETKINGIVRKLRFL

VLAKNKHALTNPLVKHVLNNVLRDFEMDTNSLRVILQSFPDFNELLKDFNSLFKKEAKAA

NAKLKKATGISRNGVFHILSLRRLSDNNNCFLL

>contig44153 Frame-1R

MKIFTPIVAASMAVAGVASDVASPSRQLIVGGRNALPGEHDFVVSVRAVVDEITYCQGCL

ISPNIVVTTQFCGMTEPAEYKLDYAVVGAYNSLGSTNDGKPDGEAFKIIEHIIHPKFSDP

IRSVNLAVLVLDGESKATPMSLPQSSEINLETPLRGFGYGTIYHHDDPDNARQSETLQTS

LLNPISHEDCVKKNKDENITTAFFCATGENNGGFCFGDSGGTVIDEKNELPSAYIAMERV

ATITLSPIWPLR

>contig16131 Frame-2F

MKFVFVFGALFALFIRLNCAALVAREANSLELSHDRANFRTITRRLRIDTLNASEERNIF

NFWRRKKHANWEGLLNVDDVPQFTPRQIQENIKWSKKDLKEVLTALNFRKVTSPEVTRQK

MFQLDEYLDSLDLKTEVKTMDEIVAKRLKVLGMLKGNDWEHTKELKRHLAHVWVIKRIPV

RNVYRGLKMNEEESLENLFSIRSGEETLDFFLDFFYATRKYHNDKEELAELFLETYDVAT

VLHLINVGSRLDSAQVFVAQLEHSLHRKWSSMSHNKVFFDILHLDKKGSQVFNTFEMQTW

YRFIKGTDPDEAEAKTLIFLIHSYGTAFLSDELIRGQGQSISSLRPIFRKALLDHWAKQK

TGS

>contig17293 Frame-0F

MFMRAGRHLVALLAIAVVALAIDIEEEDDVIVLTESNFAEAVSTYDALLVEFYAPWCGHC

KSLAPEYATAAKNLKEMDSSTRLGKVDATVETKLAEQFAVRGFPTLKLFKGGVEAVKEYD

GGRTSSEIETWVVKKSGPAVTIIGTIDELEEIKEANDVVVFVVVDSKEGNARSMLEKLAD

DDARAVYVATTNTNVTEDANAVNTVVLYKKFDEGKVIYDGDFDKDALGEFIKGNSLPLVI

TFQQDIAPTIFGGDMTEHVLAFADTSEDYVSGIETALRSPAKLNKGKLLHVIMPSTEKRI

VEYFGLTDEDMPTIMIVNMSGSMKKYVFDHKADDLIAKVTDGLADDLIAFETSYLNGNLT

PQLKSAEPEDDSDEAVKVIVGKDFQKRVIDNDKDILLEFYAPWCGHCKSLAPKYEELAEN

FADVDSIIIAKMDATANEIDHAGVNVRGFPTILFFPAKDKHNPVVYEGPRDVEGLTQFLK

TNAQKFVLDGFEHGAELDQDEDEGEDEEKKEVEHEEL

>contig35745 Frame-0F

MNLHFLLLSLLLTTANAALNKNASENSAQPPSSLPEHSRPFLPKSPNKDLAIQGPRFNDA

HDMTGSQATSIEERNLLDSIKHTTLDAVYKLAAKLRASPRFMFYAMGIFISRLTKKLHKK

INLYQWLLYVDKHMFQPCKSHDELLAASSTFFSFFQRKFTDVQLAGFFRSLRTYPGLSNL

GDWMQTYMATNVATSSAMREAWSWYGDTIDVVFKTLRVENEADLVGSRVVTAWLEYCHAR

>contig50216 Frame-0R

MQVCFHVTALVMINALSISSLTSAKFSLGTAAFALEPSHMESHEAMRSLRAQQTSTLDVD

EERLRFKLTRLVGNICEKIVDAFYRVKNRTKVFQGEFFPPDP

>contig18684 Frame-1F

MFSTVLFLVAACAKSSYGHSVSIFTRDSTKYIASNFDEYSTIPEDIDAKRRLREAVGVDG

IARDAEKTFADIRHSLDRLNKDFVRSNSFKNINPLITAEALVKQPSFYQEAFLPLITARG

IKCSKDFEFATMALLGVSPGTLRQKIQVAAQQPSNIWSYQTSEYNEHFVASYKKYLDVVF

MAPTISESSAFVKKHISMSIPEPSEMTYKLLNAAVIQLLQLAIRNVDDVNELAKLATSVT

FKYALEHDEEFSTIMMFGNLEAWISNPVLNKLLMVHQVLLKS

>contig35498 Frame-2R

MLTSLELDLLLALLAQDDSQVLQCIYDYKTRTQESAVMLRDSLVAIVDELTLEVGDDEKA

AAAFGHGMDDAVREEDNGPLDGCHDDERDWLGWQRHLTFLLRQWQRQAELSPIAATTLHK

MVAQRHNLLESAYEVFARDADATELLDTLQRVAKLQRQMEQQGARNECPPITTKHLSLEN

VVRQMQRSGTLEDEDAAGLLELFHGGNEALQAANEAFQADRDVRELEETLLLVVKHARFG

KDTVGDAETDEFQVKARLLRTLGQTGRLDIWQVQLLVSLLKSRDSRVLAAVDVYDEENEI

EDFVETLEILAELAAWECHGHAIVQDWIAPLARSNKLPRGGAERLVQLVKSRDDRVVAAL

VVFLSDNNQDDFVDTLVRIACLEAMKLKGMQSDEAREGHVALAMLQELTDYRVVSREERA

QVKALVCAGEARMLAALDVLAATHDAEDFADTARRILALLEVKAVLKDDAAQQLLDISGK

DPTTGRCSIEREHKKSLDETRKKGKEICLCEVTDVTMDLAETIKIDAFEKKQENQAEEGA

KGDN

>contig45264 Frame-2F

MTVKSFLPALMSVTSAATTSHVFDTRVTALQPRVFDMYILAQSWQPTFCLGKENLYPGCE

TPQMYWRTHLTLHGLWPELSGSAPPSFCSDEAFDADKIERELGIATLHQYWPDVKFKDAS

PRYAEFWKHEWTRHGTCSGLTQIDYFTHAIDLERNETLAPTPEIIQNHVGGQVDVQKLRT

VFQDAALKCQHVHGQTVVFAQVFTCWQKDAKNVPIRRCACPAHIHAEDTCGHGVVTIPAF

PRDA

>contig47244 Frame-0R

MLASAVGASLISGLQLRCPMCGTSNDLACVSRCDVCNSRLTIAEELSTTTPRSESSTYSY

SSVSPTRGSFSVAENGRTVIYNGYFSCTMHGTQAVMTADGSTCQVFVLCCTWQPKGLERQ

QTYATWYVSQRFSQFEKLHKALKKKLAHSSMLSLPPFPAKYYLKNRNSKRQQGLGMYMPR

LLEMSTQIPNAQPVPELDEFLDIAHQVQIFQSRLISVADPP

>contig50217 Frame-0R|Blast-putative chitin synthase (Chitin-UDP-GlcNac-transferase) [Phytophthora infestans T30-4](gb|EEY61714.1|) 3e-13

MFRPSCTQLLRLGSLSWVSTAWRTSSHSYCVTQNNLSWSTKGLHCYPLVIASLENSGMGA

CKGGVAMHCAIEKSCREEIELLEIRKDSFEAFRLGIFLSISCRLCGVFLLFVRV

>contig53850 Frame-0R

MRILSLLASYLVKASIVIFLCESRALLLAGEVSSSVPSCTFRIDNTTKIKDIFECSRIHF

IGSFNEYYVACDLKLPTQPDIALLEIVNVTLDGSVLSPHNGVHVELIIQLNTSLATVSIR

NSQVQASAVHIRAANVSIDEPSSVNVTARGLKFGPGYNSWTSMGGSYGG

>contig59517-0 Frame-2F0

MLCIALICFMAVDGTQERTFIEIVTKDVRTADIFTFMQ

>contig21931 Frame-0F

MNVRLFALVGATALAVRTASAVTTCPVSVQSRTTSTLLKPITKVVSSIPATIDSSDSTSS

DVSDPSTPSTDEGSQGLQPDVGSLMNSSLPITSGSADKNNGSGSPSDANTGSDDTGDSGT

TTSTTTPSSPSAPSSSPSSPSSPSSPSSPSSPSSTLTPATPTTDSHITDAPSTTTNSPS

>contig25386 Frame-2F

MIFRSCRVCLLFSLFQCLPCISYQIKDSHISILIFYSACCPYA

>contig32971 Frame-0F

MANELAEMTWLSAACAAAVTIIASLLLHRICFCDTMPIDNSSGTCSLDEYMIEHSTDELD

AKFQVAVDFISARGQDKLTNEQKLVLYALYKQAKFGSCNVEKPSAIDMVGLAKWESWKAL

GAVNQDVAKQHYLEWVQDSFEEFDVRAPIVGRSLSKAAKMSMSLKGSMGMAGAVSIPKVD

MSTEEWKVKEDVFHYASTGDVDKILAALNQGENVNVQDLEGRTMLHWAVGREHTTVVEEL

LRREASPNIQDSDGMTPLHYAASCEHEALARL

>contig44488 Frame-1F

MTASPQLHSAIATFCPMIVLDSTISLNLQCYLLHELYFTKRFCSEC

>contig59020 Frame-0F

MFIVACIGLCVNLVLMQILGHGHSHGGGGHGHSHG

>contig07000 Frame-2R

MWAVQLSMMSIIFRPATLLQTTWAIPKKILCAVFAAKIVAVDVFEAAWIKELPDYPQGQI

IRATAIAADDGSKAFLALLPSLRLHCRQRVDRMNFPKSGFMFEVRKNS

>contig23150 Frame-1F

MRFAFSCLVVLIAASVVASETTDFTRKALATDEASTILVPKFSAQRRRLKGSLYKVIVGV

GSKVLTNPKVQKFIDLYRRLKKPKRATTATFMPNAKPAATATFKPVF

>contig28744 Frame-2R

MRQTLILAMAIVSCRHPCSAIELGHEGALVYEVCVGLKNLPASKRDKSSGMKTKREAHAI

NRLSAAQPLLFAQQVRQITLYKGEPRSKQRLEC

>contig36549 Frame-2F

MLRQLITSWLASLLMLWHSHEQYNLFRPLKNLAKR

>contig50721 Frame-2F

MAIVATSLRALGLFDLSTTCNSVLSYTLS

>contig56236 Frame-0F

MRFVTRVSGLLMMLVFALAVVYTYWNELPLVRKTLQLSYEHHVLSPEREALSKNVTVYRN

GYSTGGVEIQLSAQVLASRTKKGELAAYLSQFVEVEGLDETMNDSEEEMERVVFTVVADR

VYNGQGALVHGYTDLQFGDRLYLVAPNLHFMWPFVKLGHRVLVTSTFSPIKEPVIIESMS

ESPRTFRLHNFFTHEEADTLIKQTLLIDDPYDRLQPSSVGATMDRQITSKHRTSENAFDT

MSTTAMSIRKRVFDVLSLGTYQDDMCDGLQLLRYHQKQAYIPHYDYFPINLTENFNFNPH

RGGSNRFATVVLYLSNVPLGGQTV

>contig35494 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66604.1|) 2e-40

MLPNAFFTAIVVPLVFAIRTQSDGQILANEMTLNWPTLAFHFEIKRSSMAIHGYANFSVL

AFPVLSRTYKGIDSIMYDTVATFTEGSTLSRYMVVEGKAYASHVSLRDNGLNAGVECDDT

GVTPPINAIINAINQAEPVSSNSSNSSGTIECSSETALMISIDGIELGLCFAESSGFTLY

GS

>contig38884 Frame-2F

MVIIPSLTDFYIIFICSVHSSTSAAQNDTVVQIFGHIHPQLQ

>contig39160 Frame-1R

MLLRASTLAFVLAVVLVAAGFVDDTDARPMHAAIVSKYNNYLEEKETIILELNNWLDSYG

TQGLKYGYIPSRDSRNSADELEDLLQRFYLTKEQISEARIANPMAEFSTDGPLTLMTMDE

FKEFLLNKHVSDSKGNNGTSKKPIHSFEKENSTLSSGELKDYDPAPAHQHVEKKKILAPS

QEHTKAKPIVRRLEDGGSVASAHSQGDHTSNSELEQFSKPTYQTNSAASANTDGYTRKGW

NFKDLLTDENTYDVKAPNVDNGLSWKRQGVNNWARDYIQVSGNDEWGSGSNVGSQSISKD

LQSDHRFIPAKRHSIASSTMENTHAPGANFPPTFKEEQTTSTQEALDAVIFAARTSAKER

LVNKEPDSAIDIISKDIPGLTDSTTLSVTATKDSKSVDWSLSACVNPPGLQGDQCSSCWA

FASLGALE

>contig40083 Frame-2F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY67267.1|) 4e-51

MGLFSVVMYTLLLSSLCLNFVDSHEAYATKVPNGRNVKGVDAIGHTDPAGGGIRNAFGRD

FRDSGHTWTEALCQKDSDRDGQTNGEELGDPCCEWKPESAQDPLWSTGVSNPGDDASTSM

KSLWPTYECLTTTKGSENSDSGSIGIGNRTIDSDSLTSSASLAWSRLTVATMTTLLILLA

TFAS

>contig52660 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60396.1|) 4e-13

MAVVGKLLIAVGALLLVHAGYYSVQYEFYVKLTETVDAPMPPYEV

>contig56967 Frame-1F|Blast-glucanase inhibitor protein 2 [Phytophthora sojae](gb|AAL11721.1|AF406608\_1) 7e-12

MMNVVATIIAAATTFAGVTGNTVHTSRQLILGGHPVTDSSHQYVAGLRDSPYENTFCGGV

LITKLHILTTQTCVEHIQDGMSMYAAIGARYIMGLNFPNGTQEANALKSRRSRSTQSIIT

T

>contig23155 Frame-2R

MPVPFKLITAVAIAFLLIGSSTSLPMAKTSLTSTTNQGRHYESREEDGRLLRGAERALSV

EQEERGRFNLLNIFRKLFKGKPKTKRTPAFKKIV

>contig50690 Frame-0F|Blast-hypothetical protein PITG\_05283 [Phytophthora infestans T30-4](gb|EEY69099.1|) 5e-14

MDMSTVKVLLALAATWGVPAKLFISRQLSWTESSYNPLHRPQ

>contig09679 Frame-1R

MWLLVMLLLGGCNGEKSFLDFSVPDLQGHPVSMREFNAFPVILVVNVASECGYTDRNYLE

LQELYEKYHDEGLMVLGFPCNQFGGQEPGTAEDILKFTKEKYHVTFPLFSKLDVNGESAH

PLFVYLKKKLSGFVTDDIKWNFTKFLVVNHKPFKRYGTTTSPLEIENDVMQALHNSRHVD

EFDDGGAADGDDDGRDEL

>contig19106 Frame-0F

MKIFVPSFIASVALVLFPSAGALNVQLPGVNYEMMYGDNKCKSAAEVEADMMLIKKVADK

IRIHSLIPCQHGEVVLPAAKKVGLKVELGIQTCSNYYQEKKLLSRLVEVGLFDSNIVTFH

VGSNEVSNGEVQPDVALTHLIEIQSIIRSCGKSTAVTVSDSIDTYMQNPSIFEKVDFVSI

SSMPIRNGIAISDAVSITLEQVQKLLKKATELDKKVAFSEVGWSSDAVGSDQALYMKRVF

QMAKAYDFEFYWFTAFDSKGGNGNQLAANFGIFDKNNKMKAHLQELKIELLEPRILQNLG

TKLVLAESKSAVVMHKHEAAEGANAV

>contig22870 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60284.1|) 7e-28

MRRHASKERLFFLLVLTGALLLLSVTMLRNSNAIPATRTFRDGFTVAEDMVRRTQTLNST

DRSPKKAVLPEESTLNHSENSVRMTTIKTEDGDEITIKRAATSKGNNIMTISRDDRGKLT

IEDTTTTNEKTLTGFPNITFYEGEKVKAFINLETTEDDEGFGSNSGKVAVVRMGPVISRD

AGT

>contig28858 Frame-1R

MVSMTRIQNSVLVVAAAVSHGCSYALALEDYHFAMLAAVNHERAKEGVPPLCMNNKLQQA

AQAHSDNMARNNYMGHEDVDGSTLVDRVTRAGYSFDAIAENVAIDSSDVAAVMIAWMKSE

NHHLNIMNTEYTMIGIGYTSSQESMVKIYWTQDFGTGTTEVCDNTSPTLGNGNVTNPGLV

PTMAPTLVPTSVAPMATPVPATIPPIPEVPETLAPLATLYPTTSGPTEAPVQTTLAPSAP

PTAETPTLTPPMPTTLAPSAPPTPKTPTTPKTPILVPPFVPTTR

>contig58916 Frame-2R

MTGMDKSNGMCYRVALIFLATSSFMETYAYSKPHAW

>contig28097 Frame-0F

MRRSLRRHVGHMALFVLLLERSVRAQVLLTDACEKPAPTLATLRRSETIPSNAEVVYENC

TVVQITSTSSNGSTAVDASNLGIAVISSFPDVTTVILSGNQVTTIYEDSDATVKMLDLSA

NGLSALDALSIPSSVNK

>contig36656 Frame-2R

MTFLLFLIRAAMMNYAVGKPSRFFGFKDQGDRILRVSDMRHERMGFMFQLNEDLPSEFLN

APHT

>contig44099 Frame-2R

MTWLHSLLVMAACAASTAATEISVCRDATYNISVDAASLCAGTGAAPAGWSCPKAGEVAV

ADCVSTLATYTSDHCVTYEDAVCQVIHNNTWGCVLPSVGCNVNAPREVESVCKTWDYSDN

DLIDSSTLFNTKEKYNTSWFMPLTKVRPLYECGRTPTPAPSTTLFEASSIASKTTTTTEQ

LATTSTLNSTNTSSNPLADVSQSEALPTKS

>contig57121 Frame-2F

MPVCWIFSKLFLAVCVCTSPLRPRSFRECSTLWLALIRADCLNVLATAYTSTQLISVIAC

LDRLKYLLYRLLAGNLVNESKPFCERSLLRLLHLQESDTTAYFHGNCVEK

>contig59052 Frame-2R

MMFNKPIIALCIASVALFGSTVDASTEVAEAVALRNPTNDNAVYRDGDADGYNDRDGYDD

DDRDDSNDDGNGRRLTGRRSYDRSRYVSSERYNNRYRSRYGGDGYSNRDNRYRSSYRHSY

NSYDRSD

>contig08574 Frame-2R

MARLVPLFLVWAAIFAVNLRSIRATWPPVSTNAVAPERNVAPTRRNSTRDNSISRRQRAF

EERSKISRYVSKLKQMFGVKKQLGLPFDLVAMLKTYHLPTMTPTEVIKKQKLFRNPRNSE

QTRLEVELYDAYVEVWNKHAAYHQSGNAISKCNVLSGLREVVG

>contig16959 Frame-1R

MGACAGFALRKVSKLGAVAIGALFVLLQCASYSGYVHVDYQKMEHDVKKYLNRHKDETKD

DDSIFTSLMEVLEFNLPAGSGFAIGWIVGFRAG

>contig30638 Frame-0F

MKSYNAFAASAFIVAATIDSGVAMESYLEKLPNGAKFAKELGHVGGDSSKLTDFASNFLA

KSLTWDKSFCGETFPGSTMTNGEAFGDPCCMWTPGGPKTPDFAVAAFTTTPGEPTVCANA

GSSESPPDEKTSASDESAGNNPTQFDPAVPDTTDSTTTESTSYGAPSPDVSTPPAPETID

PLPTSGGGCAVKGARKLRQ

>contig38285 Frame-1R

MPPNRILNLYKSLYVALVFPILRCRILSAHDGKHLTQNLQ

>contig51688 Frame-2F

MPQIVQLPCLYIAVAGCFKTLAAFLFITPISQSVARPFLWKPACRDRIHEPLCVQPSSHE

P

>contig15832 Frame-0R

MHPHRVVAMATLFACITSGSPVASEPYVPGLAPVDMAAPKLRGKNAATTNGDTENRINWF

FWKTTDERLKSKIKQQIGLMDQLKLRPYDKKIIQALEKLDPKIEKLLKKYRKKLNEVRE

>contig38284 Frame-1F

MRGFLSLTVALILLPGAYASRFQFTLTSRAEECFMEAVHARASDNKVLFRFGILEPKSYD

LVDVVVKNPSQREVMMWKGEQTNFETAKVRESGLYHLCFRKRKGASSTITLFYSFDFISA

GSRSLTLVPHLAVTISKDAPTVSAYSQMALTTVKGQPVRMGIIEFDLVAVSRSILRDSTR

VKLLLTVDRITDGEYVNIALALLPKAVHPVTWEKLEDFATGGYRDYVIDDAITELGSHVA

FDVTELFEEKLNNNEETITFLIFTPGDRDAIVFGTHHVAADYFPQIIVEG

>contig39243 Frame-0F

MIKRAFATAIYAVLVACTSASSPHDEIRPFPQPKPTKASEEVALKFKPQLFTSRVVCVPY

PAVDASGTVSGGLKASNGNEDCKFAEKGSQVYGRAMWYQNLYAIMYSWYFPKRFWLGFPT

KRHDWKSVVVWIKDPSEKTRKIVGVSMSKSLDLYNTKTELYPNNFARIQVSASSIVASNT

SLRFEYYEFGMRASYLKLTGHDGQYQDLILWEQLTPAARKALNNDANFYDAIVPFSDKHF

KAQIVAAYPLALESNT

>contig43325 Frame-1F

MNFRALFVATVAALMSPTYADLPSLDLCPVTKQIDALASLSSLSEDSYNQCEFDSEFVLR

KAKSLPSPAQYKRMCNSIACQTLMVNIKLLSLPNCVLKLPFSGLKINLFSYAEDFPGNCL

VLQEKESAGSFQHTFSEILQ

>contig53768 Frame-0F|Blast-ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4](gb|EEY70130.1|) 1e-43

MTWSMLLLVLIDFAASSASISFLTASATCDPLYEKRNSITGQCDCREGFSGFGCRMCATS

AELTSTSDSDVCSATFGDDYSCVTGLNYDDHAAFKTYGCTLSSDLQTLFPDGAMDVHCDR

DERGIANCSAVVFKATESVRSVHTIECNITHCAFATGNASGECAQ

>contig14083 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55062.1|) 9e-55

MFFFLGAMALILVPIGAKADNFFFAAGAPDHNNKIVGNLLARVSSIRKNGEAYAVFDWDN

TCMFGDISYTSVLYQVENLNFRLNPDNFESFFSLGYNASSSDICLPHGTNSVLGQDVNDN

DVTLAKVLASTAEDYKVLYSAYIAPTYIFKDAT

>contig27148-0 Frame-1R0

MAVLSVYIVLCTSAVFRFSPGDVE

>contig29793 Frame-0F|Blast-vacuolar protein sorting-associated protein, putative [Phytophthora infestans T30-4](gb|EEY62207.1|) 3e-70

MKWTDELRLLCVFASGSCVAFSMMGDEEARFSLLPPGGKDKIATFEAWGGGLVALTEKMA

LVQVLEIDSVRPKVSLLPDCGLSETNPPTCMAVLNPKFLKSSYPEVLLGTSSKSLMIVSK

EGGAQD

>contig40381 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62938.1|) 1e-31

MMPSVYMAVETMLATMLSEAVRSANLEHVFRWQELRNMLVLELAQTNMTKVFEAKFKDML

WKRVASDPDYLLEKDSKRYRNIRKTFSAVKS

>contig30747 Frame-2F

MRCAALVHSTTILATSVWAYPNDAIRRLICRLKKQFLSFSQSEQFKDAHFSLNLT

>contig41484 Frame-0F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY66740.1|) 9e-17 NOT\_ORF

MMSTIIMVMMMAQLLTAADQEDMIAGHSRFIILLDFCKDYDTVDR\*ILYETLLQFGFNKC

FGDLIRHFHNGTTASFVVNGCESSAMLVTSNIRQGCPLAPLRFC

>contig26398 Frame-0F

MRLLLLALLGAGLHTAAFVEAIVAGVDFGGEFFKIALVKPGTPFEIVTNVHSKRKTETMV

AFDGDERLYGADAATVGVRRPQTAYLQIRRLLGTKLSDPQVSALLEEEYLPYELLQNTTR

GGTISLKHGKEHVFHAEELVAMVFTHARQITDTFAEAPVKDWVVTVPTYFSQAQRQAMLD

AAEISGVRVLSLINENTAAALQLAVHSSYDPDEKPKKILFYNMGSTSLQVSIAEFSSQVV

PDGFKKNKTVSTFQIISNAWDATLGGAKFDLRLAEYLATEFSEKVGEDIRKVPRPMAKIR

AQAKKTKTVLSANEEIPVVMQSLYNDIDFFTSITRSKLEALSSDLFERTLKPVEVALEKA

GLTVADIDEIELVGGGVRMPKIQQQLAEFFGGKDLGVHLNGDEAMALGAAFRAANLSNSF

RVRQVGMTDIATYPIGVRLMDLSAIELAGSNTADIDGETKQWVKRASLFTEAHRLGLRKS

VSFVHSSDLSCTFRYDKPSMLPAGVSVQIATFNITGVDKFVARMAKKDLGEPKITLSFEL

DSNGIARIVKAEATIEEEVEVEVVVKKKKAKKEDASAESSQAGDDVAVEEEEKPETRIEK

QTKTHRERLIVVHAFGTREPEEGYSVLLMSEAIKKDSMRMLKEMELADNKRREDLEAKNS

LETFIYTSHDALLAQKEQIELVTIPEQVESLQTKLSETEEWLYEDGEKVEAAEYKKKMDA

LDSELSAILFRVAELTELPIALNTGKAYAVNTRELMEEWSTSKPQVMEAERNDVLEKLTD

LEAWLTESELSQKATQKHEKPVVTSADVAKKVQSVKKFVSVLAKRPKPQPVKVGENHT

>contig27821 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55361.1|) 7e-53

MLTRRSCLVLQSTALRAMQTTTSVAVSKKFQYESLAIHNDTLLPAHKVMRRVLKYLLVDP

KFLKGSILTEEARSLPYKTIFTPQQVMKLTSLVRWGFQQLEGDSLAADAVFKALEPHANM

TRGTVWRQYFQRQFFISNAPLWTYLRVYKTHLDALAAAKDQATAENRKAEVGEDENKEVN

KAAFFTTVQKYTSRREKVFSGKKREVTILDENKNWDWVPLPVAFSIVKEFCFRGRFAEAI

EAYVLLPMTDSMSRDVVAILQAYEQYSSVLCLYEVHRALGSAGNSLDVAPELDALNKVGR

TEEVKMRFQKLSIIEQSRSDIQKIIGN

>contig40596 Frame-0R

MSLRFGTFFISICSGDCLPKSDLLGL

>contig42543 Frame-0F

MLRMLRPAVSLQVRAFAQPLLLYNGARSLRTARGGTRRQKDHIARIAKLEAMAQEREYAQ

QEQRRRVLEARSRPPVIPGFIRVRDLAKALRQPFKDVLKRTVTKAHRRFSLKTKTHPPAE

FRSVKQIVLPYRVAQEVANSFNIQTAYDDVEPRLSDVEADLSKERIGQRQPVIAVMGHVD

HGKTTLMDTLRKQMRMELKLIAPYEKHGITQKINVCEAALTPNVKVTFLDTPGHFHFFRM

RTNAAQVADAVLLIVAADEGVLLQTEESIGALEEAGLPAIICINKVDLLDNKDEQVENII

QELRSFVALQDSPVVRISGKTGAGLDELKHTVSMLVTSLTDNHQLNALAGPDTLAEGLVL

ETVAIKGRGAVLRVLIKNGELVGKQHFVAGMIHGVVREMHDAEGRDVKRALPGTVVDITY

TNKSRNVDAPNEHGFFVLSEDRAKQVIEQRELALEFKDCLVPNEGDLYTHPNAELVTSDK

EVTIKSAQVSPDDAKEPCDRDIIDERELIETKSIIVKADGAGALTSIQDTVDDMAGISTV

RLGIGNISTKDIDVAINGECPIFGFNVKLRNREAKSAAKRGVRVILRATVHELIEEISAF

EELNDKDRKIASE

>contig48912 Frame-0F|Blast-elicitin-like protein INL3B [Phytophthora infestans]gb|EEY69856.1| elicitin-like protein INL3B [Phytophthora infestans T30-4](gb|ABB55937.1|) 8e-30

MNFSTTLVIGILTFVATAYAEECSTTQFLTIAGSVHLEGCTSDIGFRGFEAMSTLSEDQI

VAVCVSPQCLKLMDEMRSMNLGDCIIQGTNVALDKDFLDPFKKRCGGGDVANSSSTDGIG

SSVITSSSVTIKAALELVGLTLLTVLLLSF

>contig49429 Frame-1R

MPAGTATITIMWCLFFLLSVASCVKHGPRDATAVNPQNRRHLSMTNNSKLVHESDSSEER

VLPVHRPFSNSMEDSLKTTVAAILKQVDFANPHKTLPFKDYFLTQYRADPKFRHQSLNQL

YEVLKMKLGPNYLLMAGLHFFNSD

>contig36714 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY63941.1|) 6e-75

MVSILFVCLGNICRSPAAEAVLKGIVARNAGNEVGSYRIDSCGTGGGSSSWYKAGGWSYH

EGDASDSRMIKEAKKRGYIMTSRSRPLTKQDIYDFDYIVCMDNANKVAVFEAAEAWGGVS

CLDVAKSKISMMTDYCITCKGATRVPDPWYEGGFDRVLDLLEDACQGLYNHLSKK

>contig40522 Frame-0R

MPWSLVMLLLLSLTTFVWANKVLHEAYPDPDYNLTVTEIINARGYDVEVHKVTTVDGYIL

TMYRLPKSYQECQRNTAVVAKKPAVYLIHGLLDSSYTFVCNFRNQSLAYVLADAGYDVWL

GNNRGTTWSNHHVTYTTDNYEYWDFSWQEMALYDMPAMLHYVLNETQHATLSYVGHSEGT

MQAFAGFSINQNLAKKVSFLGALAPVASVGHVSSPIFKLMSIFGVDVIYAILGIHAFGSR

NWLLEQLMGWYKCSTPHECISIVNLITGPSNGINMTRVPVYVSQTPAGTSVKNMAHFAQG

MRANTFRYYDYGCMCLEYLGLAHCPTFMCPNKQIYGTFKPPAFDLSAVQYPRMGFYTGTD

DWLATDADILQIRAGLKNATIVSNLSVKYSHIDFTWGYTANELVYQDLLSQIAKFDSIG

>contig54326 Frame-0F

MLKFRIYLSSLSHSLALVMKATSGSLYGALSPPEKKTRSISFRDEFAALFFSAAHSAISA

IKLHRSSPLPRPIHYELRRECWICSERSADLVEAHNVVLSAT

>contig08573 Frame-1R

MARLVPLFLVWAAIFAVILRSIRATWPPVSTNAVAPERNVAPTRRNSTRDNSISRRQRAF

EERSTISRYFSKLKQMFGVKKQLGLPFHPVAMLETYHLPTMTPTEVIKKQKLFRNPRNSE

QTRLEVELYDAYVEVWNKRTAYHQSGNAVSKCNVLSGLREVVE

>contig11306 Frame-0R

MQVTQFAAVYSFACSMAIVAALKTMTYPTKSGIGPWIDVDTPSDKYVYQTSRGRRWDLVM

SDEFNVPNRSFRAGDDHMWTSLEKPDGVNGALEVYSHNMTSTACSKDGTCYFYIKTIDEV

TKVQVYNMYTHPPSFEEVKFWYRGAMVQSWNKFCYQGGMLEVRAQLPGAVSAESGNPDRA

RGPSGKTTATRYYPTWPGIWMLGNP

>contig17447 Frame-0R

MWRHVRVLCFLVGIPLSAATSAAHLSLKVSKESTDATSLTDSNSSSTSPGTVSAAPTDGS

LSTSAFVNSDTLTASNSSVWHMKPVTSIQARVQGDAPVWNKDAKMWLSMYGKTLNETYES

SLDTANTATVEGVLMYVQAEGINVNEHSVKCERKNKMQYIVFYEITIVQPSYGIKFYEKH

NPPEYGEFVAMDGGKCTDVGDALSEDCKVYYGLDDAMYIGPMVGCGLQTLDPRAPYPGNY

WFSYPGACAQELREDKTEESRALYPSGLCAMGKEPDGETCSFSYKILGYLDLDNLVGITQ

LGYKNYTDFCQDGGVEFKAKNTGSGFTVEESIDFWKNPSDQEANANRTSAMVKMYNDLVI

SGNNSNMEPLPDIKDLTSTNPNCYENSEACATTSYGCNRTLYSQICTVCMSNAKGCVAAP

TSFSFPKLTAVRPASSDSSLNSTETSDSSQLSCLMPMLVGIVAAFVGGVL

>contig24324 Frame-1F

MLLIILLSTCHRTHLGVKNVRHRDVKSTPALNTSATSVAAFLRHLGQLFPHDEIGALIKL

ARNN

>contig52167 Frame-1F

MNCQFGAHVLHVLFTPFGVVSALFDEGTLLREVENTRWKAGDTAYVTSKSWWTQWLLYVQ

SCHYNPDNLHNQSNSNLLGGQETGKQQVHENDLARQQQLPHLVVCHPRP

>contig03092 Frame-2F|Blast-demethylmenaquinone methyltransferase, putative [Phytophthora infestans T30-4](gb|EEY56017.1|) 7e-55

MGQVVVISAPTGITSAVFGGLLATAAKARNVAGIVTDGRVRDVQALCRLNFPAFASGTSV

HGEWGSTAIGEVNCPIVVAGCVVRQNDIIRGDVNGVIVIPAERAQEIVMRAEVIEDQDHE

IVQALNEGLPLQRSLYRVRSSRDI

>contig13871 Frame-1R

MVYSPRFSLISAAVAVASLKMQQASAGSMYYGAHTVSDATNSIGPNFPGRGGEVDEKYTA

VEVTIDSTLPVLANIPSVPILYPELLSNVTAPPKEPVSNVVGNPVVAEKPEKTPDEYVYT

GSPPVVLGEHASKDCATGWENPLAYPPKHEKSGLTQSRGVSQDRRLNTYSNRDILSLEWY

LQRKLELNWKNLPTEGVMVKAPWPGPYWPDFQDSINVEWARGQPSAAAKYAMAFNYDVPQ

FTDGISRVHGIKSEGFTKQCTRNSDCLSISNRTFCGVPKMETSGWCIDSWLGICHAWAAA

AIAEPEPNCPVTHNGVEFRALDIKGLLSILYADTAVGTVFTGVRFKHGTNSTDTYGRGVD

PIFRDLNPGFFHLAMTNVLGIDKKSFIVDVSADLEVWNQPVRGYKVYEQTEMSLQEAAQT

FYGLKEYPWNVEAKSIVFVTARLSWVDSTYDDGNLVDTGIVDRFTKGEWYYYLLEIDASG

LIIGGEWLFVSNVKHPDFLWLVASKPAPNAVTRTGISYKEVSMLLQKSVECSG

>contig46873 Frame-0F

MKYFSLGLVIWGAILSLTAAKSYYSHLDCLTQGCVGPRIYCDSSTGVCRAATSDTECYNA

TVARFQDECDKGYKCVDKLCRVAAQPVDNRKCKTSCAAGLLCENGHTTCRGPSYKNECFN

LSTGFFQDGCTKGFYCSFNKCVDISLNKERKKHAFR

>contig48013 Frame-1R

MVRSTSKGLTSCTVRRLMLLAVFALSACVATLSTSPNTMTLSSYRHLKELPDTRRALRFP

KTGSIRTTTCSKQWLNSWKLAF

>contig52890 Frame-1R

MSIVAIAATSAWYVALDWIRSTRSAFLPLVRRPNLRQISVSSFTRRFERFIGVGFYCKYR

T

>contig23820 Frame-0F

MKSFNLATAIAIVIASVGVKADQTSRRLIVGGETVEEGQFKYTVGVRATANGCTNCGGTL

IHERLVLTSARCATRDSDDFDPKFAAIGQHLNIGTDIDAGEVIKIEKVAFFPGYNNETNL

NDVALLFLEKKSHQARKIWRRSTAGLKSMGLWLG

>contig49451 Frame-2R

MLVLFLTRFSLSSSTESLVPTIEMIIALQTAIRVDKEATVTTKTLQILDALVSGVHGDIL

PIGRVILHCYLPG

>contig56052 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY54793.1|) 1e-105

MAAVWRRPGVLLSGAALYAGVAFTTYVVLYDPRKREGDGATATVDDARRRKIFDTNAAKY

DKEIDWDERLTGISLMRRFLLRKAHGHVLEVAAGTGRNLAYYSPTSHATLIDFSREMLNQ

ASISQQQRLASCDLQVMKAENLVFNDDQFDTVVDTFGLCSMDDPVRALKEMQRVCKKTSG

RILLLEHGQSSFAWLSGILDKFADLHAQKWGCHWNRDIVALLDQAGLEVETMHRFHFGTT

YFIVAKPQAAGAH

>contig04605 Frame-2F

MPSLKLLVVALAAMQLTFVNATYLAGNRKSSVDAFYSNPNGRRLVEVKPVSWFGTYASNS

GNRRLDQTEEERLFGLGSSKALTHLVET

>contig56053 Frame-1F

MSFVTLKPATGRCRTVLLVALVLKGCIESSSVIATVSDNETTLSIGSGLGTNEDRSIKIG

HVVPAVLSSNPFAAVYKRYAQMYSAYHKKLNQDEEFEELVRRYTLPHIALMVASAHIYPD

LNTLVLRPLLFKKWGRGNFEGAFKDLNLNDASEALLARWQIWAEFGEWHGRIPIRSSHMD

QVNSAYDA

>contig23825 Frame-1R

MRNYLFKAIALGSLAFVSAQEINIDEIEPLPGLEPNSTMNKIILQFQPQLHVSSGCQPYP

AVDSAGHTSSGLGLWKMGTKCNGSPLGSQVYARTDKFNGYTAIMYAWYFPRDYVVRPTGH

RHGWEHAIVWLGGYG

>contig56771 Frame-2F

MPRTAHNYSMFLLYSALTLQVAPLFVDAAGTSMQNESLTVL

>contig51685 Frame-0R

MLSKIDQERGILSLELLIAVLSFSEARSVNTAACHLFLEKKGLSVLADALTCMDAPSFQQ

MLQNKELFDSSNRNMARM

>contig52033-0 Frame-0R0

MIVLLRRIIIVCAASVLCVRQCRSLCRKVYFTSHILTLTKK

>contig52118 Frame-0F

MGLGKTICCLALICESLRQVRAADVLARSKTGSSIPTLTSPTLIVTPLSILSQWEQEIRA

KTNLSVVTYQGASRQSFQTATQFMGADIVLSTYDTLRLSECKVRDNSNEENDYRHGLGNE

WYEAPRLAPQSKRSVVTSKLHQLKWFRVILDESHLIANANCARARAAFTLSSRRRWCVTG

TPIQNRTADLAALLQFVGLGSRAHALSERELSALVPRVVMRRLKSTIDARSRAP

>contig57698 Frame-2R

MTTRMLVLRVLANLFLYDKARAVLVAHKTDVLKALPSFLTYPHKLVALSFSTVLLNFARA

IWTCKEAFTIADSIVVMSLAADLLNGSYTVEELGNDTLLRLLVTIGTL

>contig08929 Frame-2F|Blast-chaperone protein dnaJ, putative [Phytophthora infestans T30-4](gb|EEY57996.1|) 0.0

MTMRLVLLRSATLRALGAPKLKPATLMYGATALLQQCATFHSTRTTMEPSKRDYYDILGI

SRDASKNDIKKKYYQLAKKYHPDANKADVNAAKKFAEATEAWEVLGDDKKRQKYDNYGHA

GVDEQAGFNGPEGFQGQGFEDIFGEFFSGQGFGGRSNRSSATQPQRGSDIQVDITLSFME

AVKGTTRDLNITANVECDTCDGSGAKPGTKAKTCPTCNGSGVQVMQQGFFAVESPCRRCR

GQGTMIESPCSTCRGQGMVQKPRAVEVKIPEGVDQGMNLRLAHQGEPGQRGGPAGHLYVG

IHVLPDPFFKRRKADVLVDVPISVAQAVLGGAVVVPTLTGEVEMKIPRGTQPDTVLQMRG

KGIKELNSNRRGSQLVNLQVCVPTNLSTRQEELMKEFLKEETDRAEKGEDPDSKPHTFTK

SVRNTVDRIKSFIKGYKSEDS

>contig39684 Frame-0F

MQPSLRFLAAVSTLAPYSLAMASQCSNIDTCYEGGATATPCSVSSRGCPPCVTFANDGCY

VLVNGSCPFGVDCSSVWSGASTPSIGDGSLSTTTSSPTDSTPTTPPSTLAPAPSTNTATS

PSTGGTSKSLTSPSTT

>contig46714 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY55494.1|) 7e-72

MFTKTSIKTMNKLLAPRARRSVTALALLSAGTYAVDEANANILSRSLRVLVTGGQVLWDY

QIHFKGTSRDDANYRLKLQSLNQRIAQRIYRVCYENGGIYTKVGQQLATFNHGIPKEYTE

TLARLQDQAKPIPFKKIKMSLEAELKQPWRVFFKEFDEKPIASASLAQVHHAVDHQGREV

AVKIQYPHLELQMNTD

>contig52940 Frame-2F

MANWPVQRWPICSWKPLIPRTGLILCFLRTLHLLQLSIHSLRMKSMWWQRRQSYFRRCRQ

RIRRQIQ

>contig54537 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67166.1|) 1e-21

MQTLEALALVARLHVVAARSSFPELHSNTQTTKEQVLNMTQELKQLAGDWGDRELLASTP

MASARQQFEEMIK

>contig03095-1 Frame-1R1

MKTFLFVLGSIIFTWVESAQLPSHGMQIKSFDGKNRALFGYGNGDGNGNGDGNGDGDGDD

DMDNGDADDMDEHVVGNLVAGKFSNPENVP

>contig08667 Frame-1F

MSLRALVIYFHLSTLVVVVISNLETLSSPATILSKAELCALDVDRSRIALNL

>contig20364 Frame-2F

MKVAFIILLAMTSTVFFSGVWPINTGPTNGVVSHGSRILSPYVDWASTPHYSHPALSMFT

TKVTLAKYAKRIGLDLAHYEAAGMAAVENDSALKQLFDRYSAYHNLLLDIERNEHLPDKT

RERAKKLRTK

>contig27970 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY60307.1|) 4e-90

MAGTRLQIVGAFVLFVLLAAPVAWHLTLVKRVDLPYLRIQQLSWDASCFGVPDKFEVDVY

SLGSEASLSALSSSASTIVYVPRSIQLNAEQEHLLQEAYKSGLQATDDVLKTLVTRDSKR

FSLVLVCNENAAISASVLAVGKYRHAWSPQCQVSEGDGVHLAMERLLQRYVYPAKDTQNY

NSSTGVKLARRALHYRLQFSLLKENPVTEWKEDLPTLVTQYLGQFIRKVGVLAKFTIETQ

VIQYAKVANEVTPNANETEFYIHADDLKH

>contig33690 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY55495.1|) 1e-14

MRSFIALTLVAAPALVSVSATLAPCQTNSAHMCPGFYNCNATTISPAIQAAECSHNTRTH

>contig39731 Frame-1R

MLSGPCYTSIHAAFLIFFKVCHACVSSRSIAATILAWLIMIRSCVADDANIPFACFCHCI

LVQLLTAIRINEFLSSERCFINNRF

>contig54910 Frame-1F

MIIFDVCLFALATCFLRCRSHCPYRPTLLRIILIALGQRSVESTA

>contig56022 Frame-1F

MSLRKSSTAAALAGILAASLVSANVDVSVNRDATYTLSESCGLPCSGNGLHPAGNACPKA

GDVATAECTPSMMSYNGKDCVAPVDAQCVLMSHKVWGCEFPMSETPLGVNCEVVDAPSEH

MGGKEESGHYYSAQESTPSVEYTHPYSEKHPGEYKSTMHFDSVATGKTEGDFTHYGTPSM

THESKHGHSMGHDYGTTKSALKKYHHSHGYDEHLTMYAPKELQQTNAYHSPMYHGYEAAA

PYGNSVPSAYHNNYDSVYSTPHSSKMESVYTTEKPCDTDVPVYSTLDPISTLPFPITLPP

ITLPPISVPILP

>contig14113 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY69767.1|) 0.0

MEQSVIFWQTLVADCLVFIVSSSLTLATEVPKLARLLKTLCGRLKPAVAKVSPHIVNLSS

FAQLFEGGSLAGTSPEGGVRQVSCMLQTITAIQVALFIVLLQKNRKMDRETGDMGNEAAL

SRREHASIVKELHCLFFEEEWEQKGLQSVAMLAWAGFLASNNDGNNNNQNVTFAEVEATT

NVVKKAIEGRAFHTLVEVQLKYLPDRKRDLRLYNIYEQNFELLFQTYSSKMMVDVPTIAD

KAAISAMQSESDDDAAAWNGDCLENIIDFATALGARNATFCSSFWYGTDEELDVHDSDGS

TEPREDDSTRQRNSLLHSANGASCHDFLIACRDAAYKNPGCITAYMRLVGAAASGPGCAP

QAFHHIKKNPQQLSWDQFFAVMAKYQRLLTEAEKPSGYSSLMSGGVPQAIGINGSSFNGN

ISAANPGPRFIRPKELEALEAIQKLIQAVISDPQLALIFFHNHDWSPIPTFVAFLQCRIP

SSLKGSIMKTLAAFARVPDIAPFVWRQVDALQ

>contig18935 Frame-2F

MPLLLFLLSFLVKSPQLITLHDWLIPKLISLNSVSYDADVKKRVDMLI

>contig28943 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67876.1|) 7e-47

MVLRHSLLSLSLLLLPIILGQQCAYFSKEDLFSRLEMHIKTCIDPIPSTPALSTLTERFI

ANEFDGRQPLALVFFSNSSHMLRSLAGALASSLFGSSRSPQTVQSVDFQALLEPSPRLSN

YDIKQRLRAAIAAPLNACPERSL

>contig40787 Frame-0R

MTYRFAGSVSFFRCSIAWSALCNVQIIGDER

>contig45942 Frame-1R

MYVVLASVAVTISCVCVLIWWHKTKKSIKELQKEANHASGYSSTRQATMHSTNSMGGPTL

AVTSPPEGFYVATVLTPRRASNRSGRSRSLTSHTSTVSSSSKSRKAKPVEIPIMAEQKYP

SMSSPRSPMSDTSSIALLSEYASSRGSIDSWRPNAKPADLKDWGPSLKENEF

>contig49722 Frame-0F

MPLIQTMRVCHFALLAAAIFITNMLASTADEVISHNEGTNSVTRLRVPSDKSIANYEEER

LLSRVKG

>contig49797 Frame-0F|Blast-putative GPI-anchored serine-threonine rich hypothetical protein [Phytophthora infestans T30-4](gb|EEY58896.1|) 1e-10

MNLAATLLFAACTAATVNARFTVTSGTTETNTNSSMNSADYVRQWTINSAATGDAVNSID

L

>contig59077 Frame-1R

MPSVCLLSAINKSARKYVMIQFILMLALALMAAHPFVGVVAGTINEKHQAASFSEARWFP

LETFMELFTRSKKT

>contig36606 Frame-1F

MFRVTIFAAIALIATNGVPFVQAGGGPTQQISCDDTSGQLKVGDYFKPATSQTSLELNNV

APNSRSPCPGFNSLANGGYLPRDGKNVNKDMIRTAFMNVFNIAEDWINAQFSRLPDVFSL

DFLSTLDRHASFVRDDINLNPNAVEVNTTLAKDFLSRADADGKISLAAVAKARVDRENQC

KAINPVCNYTAPVEMTAFRQAALLLHIMGQIDFITAAHAESFLVQEKIPVDFVKSGVPIT

VAALNMTYTKLVEAAPK

>contig43585 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY57766.1|) 1e-12

MSRAWHAFCMLLSITFLVNAAFTHDSIVRDDDVASSKTAPLSAKTLTTSTQLPVHADTNA

TSSHKPHDSFFSYTKVPLISLNFSLNGSIPPNWVGPSIGDYVDTACYRKQLPLNSHGHCP

QGYRASHNRCWAQCPMAYPVQCFSQCIPH

>contig52770 Frame-1F

MAAIWFRRVRVAHLSQLLASSSISGDAGKLAFLLICSRSVCKEVDDAFIDKDAMEMHLNA

LSGEMVALIGKIVLTKINQNARVASLHGKASMSLK

>contig56257-0 Frame-0F0

MRFAFVWLVVMIAASVAANDTTDSTRKALATKEIATSVVAKPSA

>contig07991 Frame-0R

MINIKNSQFLLVIALLASVSAVTPISKIKSFAGPEEETSDLTRQLRASRPVSSKSVPNLL

RSLSSIDSKGVSAGAIVEERNPGIRHSMAWAFSEPINTVLRLKGLTAEEAEAKLRAGKFY

RKFLYGTYPNHFRDYQNNLHPRNRKIGRKPKIVPTNYPQPI

>contig17738 Frame-2R

MLLRAFLGSLCVYSLSWRYTVDAFEVITTTEELAAVERSAKVYALLIFGTEAKAQDMSLK

ELALTAYPELSDFETELEGLVTFGVLDIAPHRKDSIGNKWNLKKLPALVIYKGRPKENPY

TGKYYRESKAMDVDVLTNPRKLKKMLKQAILPDYVQELQDDQATLTSVQELISTTAKDES

IALLVSKQKHASPMYRALAAEFYGQGLTFVFLNNDQDGAEEIINRLKIEVLPSFAVLKSL

TDYEVLKAENLDSYAELKKFVEPFAVQKDNAMKNEAVKGTTHSEAVKFFTEKDFDDLVLR

SNVIWIIEFMDAEREETLVEEEWKALLTELHRKAGIVSIGAVSCEKEAELCERHGGPGVR

IYSQGLAESKAPKRGDIATFATLDEAKEAAIAAIPDVTTEVKSAAELNIFVSRAREQRCL

PILFFTAKTSAPPMIKAMVLSVRTQRVMLAVIHDADENLKKQFMIKPSTSTSLIILVPTN

EVSEDGRSAPFGVVAYEKKKMGAYNYPNIMQFLLQVLAQYPHPQTDELDSEELDFSSPEK

SAQSLVPYMTKENMADLCSGNKICAIGFFEDHIETLRDSESRLTKWYTTLVHVAAQSKKK

RNLSISCGLMESVKWLLLKHLALVFIKCRRLLCTLLQSIAMQRT

>contig21267 Frame-0F|Blast-beta-mannosidase, putative [Phytophthora infestans T30-4](gb|EEY61220.1|) 1e-111

MRSSFIVMTSLVSSNALVIPLKQWSFSSINGSVYADNVSIPGTSHIHLLEAGIIDDPYYR

FNEREYQWIAYEHWVYKTHVTLSYEEANSDAVLVFENLDGVASVRVNGEKVMTTSNSFVP

YRINATAVLRTGLNQIQVDFPSILQYARHEAVNYPYSVPVSENYNTWSEPTRRSFVRKAG

SDFGWDWGPAFITSGIAGAAFIELNKLAIKVKDLHVVQNFTNGKDDLSKVDVIVRVTLDG

RRINHENVSFNLYVNEKKEFAITRTIPEDWSENGTIDLTFHLKNPKLWWPFGYGKPYLYH

VRVDVSDSSFSSSLSHKFGIRHVELIQEDTNAGNVDGKTFYFKVNNVPIFIKGANWIPTE

SFPTRTKESMVRYLLESIRAANMN

>contig23715 Frame-2F

MSNDAVLVVVIISVFLPSPATETTPASTPSTKTSPPVSAERSSPNPELLLVAITNVSGSS

SCLSWRSCRTQSRLVGSSNICGRNGSSNSKNSGLHNLAFLTDSRPNVVFGLFERS

>contig27597 Frame-0R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62524.1|) 2e-35

MMFFFRALTASIVPLVSTALQATITSGTSECFYVDVESYKHGISLNYEALRGVADELETE

LMVDRDQILYTHKGTSGRYVSPIEKSGIYSACFKNDHSPVGDVVIGFSFHADDPNHEVLS

NADATKI

>contig40819 Frame-0R|Blast-pentulose/hexulose kinase [Brachybacterium faecium DSM 4810]gb|ACU86862.1| pentulose/hexulose kinase [Brachybacterium faecium DSM 4810](ref|YP\_003156452.1|) 2e-06

MNSFVPLLAASLAAGAWLYNYHIQQRKKIFLGFAKLKYYQGLPIVIIFDVGSSSIRASCF

ALVSKAQWVFIDESLQQQHLSSIDDNGEADIVKIEALVEKLMDQMMDFLRATGLSQKVMG

VGFSTFAMNVIGLDAKGNAVTPVYTYAGKRKATAKWSKVLRERLAECGEL

>contig57943 Frame-0R|Blast-transmembrane protein, putative [Phytophthora infestans T30-4](gb|EEY70002.1|) 3e-31

MHVLSIVAFKWSWVVVVGLAGISGIEYVLAFFFLTFECSAFTELLNEVQLQLHLQEHRMA

RD

>contig26924 Frame-0F

MKCVSCTASVGLVSILLGTFVQPSTSVETPAVSCLSGELKNLARLFNKDRFHEMFPEALE

LYSFDGLISAANKFSAFANSGNNSTNTLELAAFLAQIAHETDSLKAAEEYARDDFSVWQY

CDNTTVPCAPGRRYHGRGAIQISWNFNYNAAGKALGLDLLNNPDIVITNSTVAWMTALWY

WMTPQKNGCVIHDVVTGVDGFALSTNIINGEFECGPEAINKENDLNRVVLFNGMCQELGV

EALGKISCNA

>contig43587 Frame-1F

MAASKITLRINTLFSMLVASRVVVASCRCTLRTQAAEFVVVRSLF

>contig45400 Frame-1F

MNEKQRFEVLVFAAVVLASHVDGLGGVAFPTFLGRLLYELGMKSQDVKIDFPVGFETRGN

WVVPFLSPPNVKWPAWLLNDELKLDNFVQIANSETIDFRIDSGLISGECNDEEQPLSLET

IRKILSRVPAESKVHLVLTRGLQKEYFTREETHAAFVREHNL

>contig53182 Frame-1R

MKVLHLLLCTALAISRVSGATIRATASSPAAASPTTLTETSTAPLTATSTETVTT

>contig58257 Frame-0R

MFMCFKVSLLAFVANVYRIAWSNGFSALEFAVKSEHTKLREQCLSKGANLNAPTLNGKIS

LHLAATLSNSETIL

>contig21214 Frame-1R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY68778.1|) 2e-16

MLISAILQVLIVELIYCNSDRWHAQALVMIVPQHMPLYTILLQAQLYYM

>contig40668 Frame-2R|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY67169.1|) 3e-07

MTLMIWTLINLTSVLLSNIASMLIAYKFYRDWDFRVSSVR

>contig40736 Frame-2F

MRGVHRNSAMLCKISLLTTILLLNTLTTAVTSTDDQSKKSVDVEVTEVEPNGNDKPVPEF

VATNEWQDLLPGQGVPRGLHMRLNLETGKREAKLVDRSDTDAEEFTRLLVTGSDSQETTV

TVLTDYAGDAATDFENGETLSVTDDRLGNYALKEDAEHDEAPRAEPKWNHEKIYEVLQAL

PEPPEVDGMNIHEAHEKLSPAEFRRQVVYLWKKRQAELKEALESLQDDAKYLGKLLKQFK

EAEENGDMNGQISVLEVLEWEVQDLDKTHVFNFIGGFSIMADYLNSTSLPVRASAAWVIG

SAAKNYKDGQDWAIDAGVIPKLLDSIALDIPNKNDVAKDVHEVKKKSIYALSSIVRSNAR

GQRLFLLQNGPEQLAGLFDNAHSAKLHLKVLLFMYDLMIEEPNLELAPEAESTASSLVHL

KKIFQAPKWCERLLTTFVE

>contig13320 Frame-2F

MWNFIFAVAILAMESAAFFSARPTALETTLNEHLKNNVIPFLSPADNTLSSNNLKTVKTE

LLESLKRFKEECETTKKKAGAYENWAMNHVTQIRDDASIQKLFDTLVLAKSINPKSKYLK

EVIKAVFEPKSHLNPEDAQGWFKFSRDPKNTPEEAAEKLFTSSNLAMLTWFVTYKRIDRP

NLYLATALLLPFGDSLKPMLDFAMKKGYSDLAGKIMNGLEHSIPDVVDFLLFSRELGNPI

FSKKMEIAVAYAEQSGDEGLQSLVVKLRQLYENSLTKYIMWALDVDENDAMALKIQKWAT

VDKPSVPSTTLTNHASPVVVDLTPPNVEDPIPMLTEKTDTVSAQKKISKTIARCFPASKT

RKVTTSTNLPSIEATKIENP

>contig28058 Frame-1F|Blast-C2 domain-containing protein, putative [Phytophthora infestans T30-4](gb|EEY63881.1|) 1e-112

MPQLLVTLLRANSLPVADTYVQGNASDPFVTFQLDDEYMRSSCITKALDPVWQPAETFVF

ELPHPSQATERHLLVQVSDNDRWKLDDLLGELSIPLSSFERRPNEAVIGTYELIVPETLK

AAMKTIETKASIQLDICYLQETDGQQTLCVWENEDYVDGHWTPSHNKERRHWSSFDLQTS

SDNFEQVVPDVPEGLEASGWAYSNKRGDDHGWIYASTYTGPWSSMPSALCYARRRLWQNH

CRPAVACE

>contig50813 Frame-1R

MDREAARTRMLNLWLMLSTTSAANISVHTNQGTVMHVDNLISNAGQTLLACINLATPVGT

YTHAVLRDHEVAQIEWNLSKTELKTLVYDDLIEMP

>contig58251 Frame-2F

MWFLSRFLLPSIFSRAKLLAPAKLLRVATQAMTITATRLPKRIIRFQL

>contig08055 Frame-2F

MRLLLCLLAFIFLSAIYFKHVLKGKSQHPRPNASTVESLRGNVANTSMATQEERAFLEQF

FLKRRIDNVTSAILKQYKKILKLQTMADRGKTLDEWLHRKSGKLFHPMEALQNLRGQLKV

FEWVELLVHFAESKNKNVLSWTSHAKEQLSSICNEPNLLPTIFQDYPKLSLSVLQIVDRI

KGNDALFQKWFLSVSTNTQFSPEALYELLNLSATKTLSILKLFTELQTFEATRKGAEEML

TFMSSNKAISQKLLSEWQKENKHENLVTFWRILPLSQTAGFTSSIFTLWLEAYGKFSRKT

NFLAQDMCFHQLLEEAHFYPVDHGQAVTNPAATSPLFPRNRR

>contig24509 Frame-0R

MKLMWLVSLSLVALVSRLSEGQTCGPRLRKDWNALTEAEKTTYRGAIAAAMDSGEYAKFI

EMHTEMMSEREAHRQCMFIYWHRYILTAFENMLRGQGGDFACVTVPYFNWITGSARFTAG

SCSSFGDCLSIATELGGWTSGVTRTLSINGVSNTGRCVNLPPLDHFCQLTSSAPSACARC

VPRSNWGTVRLPASTSYAAIRNQVLSGRNIGEMSSSVEQGCHNNIHANMGSTMGTFAAPA

DPLFWSHHAMVDNLHVIFHRCRVGTARMTFAQKAANPVAWQSCARRNSNVNFEPTDVVMI

RTGLRGNNPIPASTDPVVGRYFAGLPNQYAGLMDTRDLGVHSYGYEISGQLASLFTQCDA

SPTSRRMEETNASTPHANCGAGPDYAALNNFPETDFNGQEDDHQDVVVIDNLGNPVSPDT

PKDDYISDDSAKKVVSWYDQTLDAMGGDSPENMVDLERQACMFEHICLGGTQDFSPEFKE

LWKVKEPRCKTIVDAISNGSQTIQYEAWREDMELAFGCPEPTNDMSSNSGSDGSSQSSKC

GFLHANNTIQLDEPEVNILG

>contig28516 Frame-0F

MAFEFRLLPFLAIVLTCFISSKGNFHTAVRLVTIHPHNTSAFTEGLVFDDGALIESTGLN

GKSFI

>contig33974 Frame-1F|Blast-serine protease family S10, putative [Phytophthora infestans T30-4](gb|EEY61195.1|) 0.0

MLKLLLSLALLARTAAASPFSGTNYSLTMNTVDEDFCDSTKQLSGYFKISGSKSKNYFYW

FFESRGGPSTDPLIIWLTGGPGCSSILALLMENGPCSVNDDLTLKRNPSSWTERANVMWI

DQPVGVGFSYGDRSEYDTSEKEVGDDMFHFLQEFFVAKPEYQKLPFYVFGESYAGHYVPA

IAHRIFRGNQQMEGSVKINLAGFGIGNGLTDPEVQYKYYPDMAYNNTYGVKAVSYPVYMA

MKAAVSPCRNMIRSCQTTKVACLAAQTFCNAALVAPYSASGLNVYDVRSKCEHFPMCYDF

SHVEAFLNLESTLKKLHISPKSAKWKSCNMEVHAGFTFDWMKNFQQLVPPMLEAGIRGLV

YAGDADFIVNWMGCKAWTLELPWSQHLEFLAAEDKAWTVEGKKAGRIRQVGPLAFQQVFE

AGHMVPMNQPKNALAMLKAFTLREDQIKDIVGDAKQHDFDVEAKIKEDSVMSVM

>contig36854 Frame-0R

MLVSIRFAATIAVAILGQATVVKCWDSTQLKVMSFNLRTSLANDPCPSGCWALRKFRAEQ

LVERYEPDFIGTQEGAPDQIDFFIQQLGFTSTGECAGNCDGNERNSIFYKTERWDLLESS

TFALSDTPNVIPSNSWNLQYLRAAVIARFRDKATHQVVCMLNTHFDISRGHDQSSSLVAK

LLSEHCDVADTIILTGDLNTGPESPAIKYLSNQDSLNGSCTPVPMYDTLAAAGVGGPTWV

GSSFGNITVDYKFDYIFLRPDDHTCLLNSLILVDLFDGFSSSDHAVVQSEFSLGKGCTSD

FQKAEPLVSVSCHAYDTTARFL

>contig53213 Frame-2F

MSPKSMLHLLLRDFVSLLSILALLGCSETTAVVASAGANQANRGLRLPHIRNSAYISADV

EERTRPPPSLVNSLLTDAIHSSQHFIDPIINAVNRQKNEPSVKVQKALAKHIETILTTDS

GKKFVAKCKEISANANLAWPPTSAVSQTLDPFVTVAQLVSVVDERIPNLIKRFAAMDNNV

ERLAASAQMFIDELFDHDQVVNAAVMTDLETQRTGYWIFNVNSNAAG

>contig58252 Frame-1R

MRLGSLVAVIVIACVATRSSFAGAKSSALENNDYGKRKRLRSHILPSFGKTDA

>contig04036 Frame-2R

MKFISILFLSSLLSQANAIPTSNEVLAGINAYRTSIGFPRACRNDIVANGAQGAVEAQFI

KFYGGNFDIAQQIDINLSGLDVVTSTINYYSDPESAGAVVKEWLLTNNATILETEVLFGF

GTVTPDNQAYKLLEREKKNGGTASLSSFRSLFSVLLVSSRNAQCP

>contig21914 Frame-2R

MKFFPIFAVASLFTLASAQLDNDAVLDVINRNRFQKGFSFACNNEHVARATQDYAEAVVK

HLAVTGSVPPNGLTPFLLNKTENVISSSPASFYGNYNAESLVKEWAELRGEFISSTEILF

GLGHVDTKSQVYKDALARSDIRGASELRFPHLYVIGLADIKDVKC

>contig25334 Frame-1F|Blast-mannose-1-phosphate guanyltransferase beta, putative [Phytophthora infestans T30-4](gb|EEY62296.1|) 1e-141

MKALILVGGFGTRLRPLTLSCPKPLVEFCNKSIVMHQIEALVAVGVTEVILAVNYQPQVM

LAALESMEKKYHIKISCSHETEPLGTAGPLALARDLLDDGDPFFVFNSDVICEYRLQELL

EYHQQHGAEGTILVTRVDEPSKYGVVLSKNDGQIERFVEKPRDYVGNKINAGIYIFHPNV

LDRIQLRPTSIENEIFPQMAAEHNLYSMVLPGYWMDIGQPKDFLAGMCLHLEYLERTNPE

MLSTGPTFLGNVLVDSSATIGDKCLLGPNVVIGPKCVIED

>contig30549 Frame-2F|Blast-peptidase, putative [Phytophthora infestans T30-4](gb|EEY58883.1|) 1e-172

MKLFHPSYCFAAVAFVLTSWPQNQVDACTAIGVTKGASVDGSTLIAHTDDAGDGAADLRL

VRVPAQDHALGSKRAIYNFNGGYPRVVARDRGIQYQPVIDLESGKSQEYSKPMGFIPQVE

HTYAYFDQDYGMMNEEQLSIGESTCGAKTVGWPLDVPEGNNLFGIAELTKIALERCATAR

CAIDMMGSLSEEFGFFSEDSGDMASPDFGDSAEALLIGDKLGEVWVFHVMTGKDHSGAVW

VAQRVPDGHVTVVANAFTIREIDLSQPDWYMASSNVISLAEEMNWWNRTSGQAFDFTAAY

GFADKDAVGPLYTGRRVWRVFDVLAPSLHLDARLGSFSQFATYPFSVKPDHVIETFEIMD

LLRDHYEDTR

>contig47738 Frame-0F|Blast-protein kinase, putative [Phytophthora infestans T30-4](gb|EEY66702.1|) 1e-28

MSLRRCLYTSALMLVMPSLARSLATEEIYSVSHCAGTPNIIKMVETDNCVPQACTQNDLG

GYNLFVAATCNVKDRFQYSNERLHGFDYVMMEEYKGDGC

>contig50965 Frame-0F

MKRCWQWQLQCLSIAVFLQLCVGMFSTDLTLGACEFASESYYIMSTNDSHSPTSVGYLEC

AKATKTDADICKICSCREKKVGVVNGVIVAWAVCVELG

>contig09911 Frame-0F

MKVAQFLTLASAFTTVAHAYAASDTPNALIRSFGTKEPHVYDKRRMLTRSESSSNIRLRR

LSLAELDLAEKNVLQDQEAIKTAKHLENEALKKLKKDVMSNNDKDLDKDIAAKLAAEEVE

EEAEEVEKMDEEIEENEVEKELESLFDSVDEDSEDKKDETKKEKDDATPKKKTTPKSSTS

KKEQGSKEIQDSDDDSEEEEVARRRHRLLLALVDLKVTEDAIRKDKKLEKEAKKVENEAL

EKLKADIMASNEKDIDEDMVVKMVAEEVEEEAEEAEKADEDNAETQVEHDLETLLEVEDD

DDSVDEETESSTSKVKQVAEEKTDESDDEDEEEGGRIRFRRRLTQEELKLAEQNIRDDKK

LKKEAKILAAEAKKLLQIDATGSNDEAIDDDIAIKLVAKEMEVKAKEAEELDKGIAEYQM

ENELEELYDAENDDVSDDSETKGSKDSLKQTKITSDVAVSKKKVPTHTDEVQEKDDDDDE

DEDEDEEEDEDDEARRHLRRLSVVDEADVEKEIGEAEAAMKVAEGEDAKASVELVEALKD

SDESEIEDAIKAELAAKEEKAEAEIEEEIGEDLELLDLEKELEVGDAEDGEAEEEEEEDT

SDKAAKKPAKSSKKSKAAGESDKKGKEQSSSDKKTSKTSKQSQTGDSSDQGTKSEDEAEV

PSKKISKKAKTEEVPDEEDDTVPAKKLKKSSKTVQVEEDDDSDDDGN

>contig23528 Frame-2R

MNDLSEALWTFLFGASCVAGLILARRRKLHRFHLQILNAKSADCGRLFGLDIGGTLTKLV

YFQSVDGAAVAQQTQLENLSDLVAHSERQKVKGSLPLIDDFIMRLDTTEEAQREDRLKMV

VPELGGTIHFVNFPTIKMDDITEFVRRRFFHRYIKKIACTGGGAFKFSQLFQSRLGIELV

KTDEMDALIQGLNYVLQYARGECYRFVNVIPDTHGLGRATKEIVPTPEKCNLYPFLLVNI

GSGVSIIKITGKLQYERVSGSSLGGGTFLGLCRALSKLRTFDEAMDASVQGDSNEVDMTV

GDIYGSAGYEHFQLKPETVASSFGKAGSRQLSHPLRDADLARSLLFMITQNLGQLAFLNA

RRANVKQIYFSGNFLRHNEVACRQLAYAINFWSKNEMQAQFFHHEGYFGALGTFLQRFNS

NETEFAESENNAG

>contig33301 Frame-0R

MIIAIATFSLILGLLTLVANLVPQVSNIAFAARSATSSFRTQTLIIAVHH

>contig44178 Frame-1F|Blast-acyltransferase, putative [Phytophthora infestans T30-4](gb|EEY65844.1|) 1e-69

MLSTLWWITLALAVLVTQCYKIIVRFLQLLLHTYFRKIVINGLNNFPREGPVILCPNHPN

MLVDAILVMTEAASYGRSTYVWAKGSLFKNPFAAFILKKLGAVPVYRPRRKDASLADEDS

QKTPQELDAANRVMFEQTWRVLSEGNVMVLFPEGTSYTAPK

>contig57949 Frame-1F

MIITIFLLLVVQVSSRALGIRRLGVHICCWLCLKSYYV

>contig27503 Frame-1R

MYEQYLLNCLLQLMQTTAARNLGLLNFKCIVIKWPCQPLVLKRGS

>contig31193 Frame-1R

MALMLSTSRSPARVTTFLLVQASSLVQYLQNSTRCNLILPIKHF

>contig44544 Frame-0F

MKSAVISPALSIWWKLGALSGASGVLL

>contig55230 Frame-2F

MQRLGVAIATIPALLHNYVASGISDLPAPVRSRDMIDYLQCQVCQTPELTGSVQDS

>contig56680 Frame-2F|Blast-PREDICTED: hypothetical protein [Mus musculus](ref|XP\_001478231.1|) 5e-06 NOT\_ORF

MVRCGTGTIS\*LSVFFSRFAALTALRASSSSVSTRVK\*LSASRSRRRRSQRFMSASSGQF

PSLTSNRRYSLASSHDKSFTESSSTAVST\*NVVNIYWTSTFVAKLSTTELTATPRS\*RIS

\*TSSKLFGIFITFPTPSSFHTTIK\*STTALPTV\*NSG\*ASASTAHRARSDTGCSRCSTFT

I\*RGQFFISVCWAYSTNHTAL\*RKKGFSTISSAL\*SVAYKSRNGSGLGSLILRRDCKISD

L\*TESVFGSGRPFKSSSTNKCNTNSSSSTSKTDFHEEGSMYRAYSIQIKNTGSVRK\*FSN

FASCRPSSENILAASKVCFHFSNNGSLKSIPPSEAAWSISANSALL

>contig34584 Frame-0F

MTHKFHGCFWSVVAVAGTVTAAVVFYKYASRRNRESEESELHTATEMQIATECQECEECI

TDDESEEKEDLDNSQK

>contig37453 Frame-1R

MVSPPLASVNPSLPAMLSLLSFVRSYVAEVRQSPG

>contig47238 Frame-1R

MLSSKKMLAICAAAAIAMASMTEATSYAAPDSNDTPGSDPYGNPTEPSTSPT

>contig50436 Frame-2F

MVFSSSIVGIVALASAYFAASTAAQDMPIPWDGTGKGLDVATLNKKFMIHILTMRNGAEN

GNVTKYVAIEENGRAPAYNGDSSVIEIGVDAEAIFQQQKTFRRS

>contig54007 Frame-2F|Blast-cyst germination specific acidic repeat protein precursor [Phytophthora infestans](gb|AAC72309.1|) 1e-10

MSLRKSSTAAALAGILAASLVSANVDVSVNRDATYTLSESCGLPCSGNGLHP

>contig56683 Frame-2R|Blast-endomembrane protein 70-like protein, putative [Phytophthora infestans T30-4](gb|EEY69817.1|) 4e-31

MLYFGYMAIISGALALLTGAVGVGASLWFTRKIYASIKVD

>contig10231 Frame-2R

MCDVGLLVFFLFLVRLKSKVPCLFKGPTVVTHMTIRSERNRSCLATSAQRGKKENVARKA

RKCILKERTV

>contig18150 Frame-1R

MRLRDRFVAFLVAIVALCPHVEPLRIPKGSKQPLKHEGMITQTDPSFNEITLQRDEPT

>contig30545 Frame-0F

MRSSKLLPTFAFIKLQRLSTARTVSSETTGSDAFTFSGAAAKAQPSN

>contig36947 Frame-1R

MRNHMGLSCFTLAFLASLHSVTASTLTTAAQDAYQVDLPIGSRSASRTLMPEPPLPKLTS

WAIRILKTTPASFEWTVSKKIEPSAFYLMRVPTDTTKWHVSDHVARFKHLLAQLANAFGE

IEASELLARALSAKLGEHKLAMLVENAENELDPTVLAIEKGIYAAW

>contig40810 Frame-2R

MALAVLFTLVIAGCTLATVLSAEALLSKAALCEVDVDKSRPVINMLQVSEEPANQYPRVL

CFAVTYSSQHHTRVQAVAETWGQRCDKLLFFSNMSDTIIVGANTSRERHFDIVHFDIIAD

HKHLWLRTRAALKYLYDHFRHEFDWFYKCDDDTYVIVENLRSYLKRPEILQRVNRAPMQI

GHRFSMPTQVLDYYIKNSTLRAEWHIHWDRMIYNSGGSGYVMNRLYLDTFVKSLPETTCL

SDTASSTMPEDAAVAFCMIWNDVYPWDTRDHHGRDRWHALNPRLISRTWRNRNDWYERYH

IGLGGLRSSNECAAPDSVAFHYVKPVLMYHLERSLYFCRSKYNDIAAFNEHNGLAIGDKV

MVV

>contig52611 Frame-1R

MGVLWNFVLTSLLLTNAVCILHEKRFLRSHGWHKVDSSQGMTIKNQIVGFLIAVQYLR

>contig56682 Frame-2R|Blast-endomembrane protein 70-like protein, putative [Phytophthora infestans T30-4](gb|EEY69817.1|) 4e-31

MLYFGYMAIISGALALLTGAVGVGASLWFTRKIYASIKVD

>contig57142 Frame-1F|Blast-phospholipase A2, putative [Phytophthora infestans T30-4](gb|EEY63036.1|) 5e-09

MLLPSVLWLSCALISYSEGAPIDFPDLTKFKQECEPFRCRPKRTPAPVK

>contig21377 Frame-1F

MNGRVTTVTYFVFFCFWEFLPTVLLLCLVSSKAGGVGAPKHGSASQKLPDYGIFHIINTN

EGKLLTASSLGTSASSSYGTRPVGDPERGRPRWTHGGDLFQDPLRYDSDDGPVPSLPHHY

LNNYHGEVSNNSTHYYE

>contig24503 Frame-0R

MLLHQWGTLLLVVLATHTNATVEGNELQQQQEKISTTQWPSLLFVIKTERSFINGHTDFS

IVANPIVSADESTVAYDIFATFTVGTNLYNYTRVGSAAYLETMMVDSSTSLIQCLQSELD

DLPPIDAIIAAVNQATPVSNQLKVCTSKDVYQVTVGTLTFALCASSNSGFEMFAHDLKIA

VSYLDEPVNIIPPNYLEECITEVKPSQVSSIGRSLLTGEQVVTDESRSLFSFAFAEDACS

CKSKPRPCVFIHGFGVKEEFPVLRSSLRYWGNFIADRAPCCTVMKFAQLNTVNYTWTNAT

QQQKVCDRALAVSHTSSGRLIKDTIIVSHSMGSLILAGAIANGTCKLDASTTWVSTGAPM

FGTMASDFAQKVCTEDTNLLAEELAVIKHQCPVKKALKSLVYQNGLYITPSLREAYAAAQ

GAYRKNVDAAMCSEGYSGILSSHQVQFWLLAKLIPHKSHKNDGTVEFQSCVKGLNISRFH

NTYKSRFYRTKLNHFDMQFRTGDSIWNEAKMPLKWFECLL

>contig35817 Frame-0R

MRERKFLIIVGALVVCAPAHSAAEKHRIGLRQETTSSKTKLPSASIEDRAMSDWIKIFRG

AANVDPTDVAVPKSSVISKVQQALQNAADGAKLAEDLDTYSIFTLLLSGLPTSWFKSLYG

KAFTFNPEKATTVLQRVFAEVGKLPSRSEDVDIQSALLFTTTQVSISLAKTLVGKYASFI

PHLATLMDRSFGNPTAPAIEKLAKDVGKFALMDAGSWVLSKFINPLTEKKLWISYGSTTA

GTSRGGHFSIDMQQGRVKISMNALDETLIPNAGINTNRARAPRLRLNQPTSVARPDPTIN

RLGSATVNFDHVEP

>contig55987 Frame-1R

MAAILTAASIMALGCFAVWLGGGWKVAKWRVFETFAVTSAMRRNIGILRYDGRVKDCKLR

LRPFSSQIPVYLAEKSVLAGPLAIFWPYPQT

>contig56803 Frame-1R

MQLRYIFTIVMATLAAPHSSAFVATGVNPSLRRLAT

>contig27598 Frame-2R

MAFIKACVSLTVSRFTLSSYTKSSSSCTCSAASIKLNHAIRHRLSISFRQYST

>contig49284 Frame-0F

MRHHARSAQLKPSVMLFHVVLLLSSHWIAGLRLVAFNDSFVPGDNSPGKLRQSSHLVASR

LDEDSDDSIQQVSGVVEDRMDLDSKKNAILAKETAVAESSWTAP

>contig06620 Frame-0F

MKIGVLAGLVAACITVTQSATTLAQHHEERNIEVVRSDTLRRRLQNAKETNKTSKAAANS

ESRSMNPVQELSSSDSVNGPVEFTESFGSPVGKEFSDASSVIPGQIVSSISIWANTRITG

VNIQISAPQEQSFEHGEREGIPITLALTLGEYIVSMEAHWGIYNGVTLIYYVCFTTNLQA

TIQGGTKTKNRRTVLMPENYQLAGLFGHSDGDITQLGAIMTTAPMLAYLPNVPTTPMNTG

STQNNLPPASLSSQPGNSPSQLGNPPMT

>contig09980 Frame-0F|Blast-glycoside hydrolase, putative [Phytophthora infestans T30-4](gb|EEY65895.1|) 0.0

MSVLFAMLAIIALLQSTATAAPVDSVIIVRGNKLYNAKTGERFFMKGLTYEYAVSDEYYD

KYSKAVIEENLAGLEFNTLRLYNIHPGSSYKKFMDDMAKLGVYVMVSASPDNDEYYGKYR

YSTITKKLSCTGKVSTSGGAKTVDQTETCYPALLLEYGKKIIQNFAQYDNTLGVVVANEI

MQEDLTSASCVKAYVADLKKWMAVNGKKLRILPLAYAAADSSNDKVSNADDYHVIKVQGL

LCGDKMINGMMAESIDIYLINEYRWCPDSTFAEAFQRYINMAQGIPIVVAFGEYGCKLSK

STPRDWTMVPYLYEEPSKTKEFSAVWSGGLAYSYGEAKLSKDSLFPMFTGGSIDFLSTPS

SKPTTVTRI

>contig14869-1 Frame-2F1

MWFSAWRQKLQLLIIVFFIFVAFAASNAAWIP

>contig30878 Frame-1R

MLVILVIAVALALIILRTYYKHKCAGTNAQNNDTTATLMSKGEVDTGKGSFISNDDLLRN

FRLPQSDVSTVKSWGSGRLWLCEYRGKKVMVKRVESEVTDSYVTKALIVEARTLSTISHP

NITNLLGVTWLAGTDFAVVTEFMAKGDLKTVLTSAEVDLDISAKLSMCFDVASALAYLHE

TERILSVKQLSSRKVLINEALDCKLSLFECVPSTDNSRGPITYGLDKIVWLPPEIITRSS

PMDARKHNIYAFGVLASEILTRTAPYKSLIDKLGNTMSDIELVSRVRRQDPLRPHENRQE

FSSVPAIVRQLIEQCLSYAPMSRPTARDLVKVLSFAKNEVTTISL

>contig49210 Frame-1F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY62254.1|) 6e-64

MRLNFRSFSDMMVVLLVFVSGIVLHKALAQLDTHESSARVNVWERSFSAFRDTPASIVES

MSFEVLQYNLFGRPYEVSKDGQRERLLRVPESLHRISETIDIVTFAEADIQTQRDEMLTE

FQQFGFHFWTTILHDPDPFTSLLNGGVMVVSKWPIIREAQHVYRDACHYSDCLAAKGVKY

ARVLKTVNDTSKVFNVFAT

>contig36024 Frame-0R

MGPSKIIFWCWCLQVFLADADSPDCITCKKILPDTKIKGRMNEPADDYVNLPT

>contig43024 Frame-1F

MKGLILLGLVVAAASADEIDPLEAKFASPSLSANTSMLANSSLPTFSSQSEFASTSVSFA

GSNAFGSGSASSNVDTTILDEEDTSDSAASNSTDNVMVGDSESGSNGSVEIIIESDKSTD

SEFSSSESATGVPPFNSYTDSSSGPSYNSSSSSEAVSIQLATLQASTFIFVAISVLM

>contig22655 Frame-0R

MQPFVSLMSLFAAIMQAITVPENIKCKLQFQRGGGH

>contig35893 Frame-2F

MRMSGFIAMVLFASIANCSSFSNVKNVAQVSGQDQYKHHLKGHHDTWAASKTDVVVEERI

FSDFSNLMRRINEHVASRLESIRNSHYWDIFKTGIVEGIGHGIGFMLVSLCLHY

>contig44978 Frame-1R

MHSRHSFVASALACALLSSHDSLVAADYTVKAAASPNENTWQGYGTSLCWWANVFGERAD

VADALFTLKPSVTLEGATGEIPGLGFNIARYNVGGSSKGVVNVSGTDVAMKMSSKMPDFK

FMESFMVGLETNDLSSPIWNWEADSKQRAMMKLAVDRGVDQIEAFSNSPPWWMNKNLATA

GGDDGTVDNLKTENHEAFALYLASVVKKARNDWGIEMNYVELFNEPSETWWQFPGGQEGC

HFSFEAQQAILPLLRKQLDAMDLQDVAIAAADENSPTRALENLKSLSANPNAVDTVEKWN

THGYEGLKAYRGPDRHGLNEPISQLGMDLWNSELGEEDGTGLTMAETIGLDINEMGVSGI

VYWQALDSGGWGLIQSNPGDNWIGEANPKYYVMAQYSRHIRPGMKIL

>contig53471-0 Frame-1F0

MKTLVISSTIALMLLALPTSVNAHGQLILPVPRLITQQYRAKCGALDGAGDQELQYAPV

>contig57156 Frame-2F

MRLFQISATILAGAKGLNANAAPRCFPSDFMFGSATAAYQVEGAWNEGGRTPSIWDDFCR

SNHSNVACANVADDFYHRYRQDVNLMVKTGLESSRFSISWSRVMNWEPATKRMRPNPEGL

AFYHALVDELHAHKIAPILTLYHWDLPLELHTELSPQGWLNPCIVDHFVDFATLMYHELG

KKVNIWTTFNEPLTFTIAGYASGTGAPGFKDSDTLAYIVAHNVLRSHAAAVKVFRELKTV

SPPVLHPNARIGIVLNSDAAYPLDKHNPLDVAAAERKMQFELGWFLSPLVTGDYPAIMRE

RVGDRLPKFTQEETAYLSNRMTCTCLITIRRN

>contig08041 Frame-2F

MKLSVCLAFMAVARETAFAWTFDASEVNHHEGIDGEHQPLQRTWTITSTAQLEQLYLAVP

GRVFVELDPSLLPMTKNPEEKAPSKELPNVPVKVNSATERPGVLPGVTPGVRPGFIPGVV

PGFVPGENPAEHNEGPRWKKNESSLVDKTVEVPSKATSTKIPVTSSPDTIATEVPGVLPG

VTPGVRPGVIPGVEPGFVPGENPAGQKAGSGLADKSSETPRL

>contig11858 Frame-1F

MVKACWGSVILMCTLALHPYNEIAQAREESVLRAVNASTKGEVLQSHFEERAPSYTDLAR

MAAGFAEKIHNYISS

>contig12240 Frame-0R|Blast-protein phosphatase 2C, putative [Phytophthora infestans T30-4](gb|EEY56002.1|) 6e-67

MAASLDLASLHAMAQTLQSSFLSQVIVLLLFVLVLRYVAASWRNSFTPYEVQTCPPINPH

VHYRYGVSQMQGRRPYMEDRFTAIADLNGDPTQSFYGIFDGHGGDGAAEYCVQAMCQNII

RDPLISKEPIEALKNGFLRTDH

>contig24432 Frame-1F|Blast-cysteine protease family C01A, putative [Phytophthora infestans T30-4](gb|EEY59924.1|) 0.0

MIFPVVMLAVFAFLPTSAQSDTRNHPIVYSVSEEGSCHGSSTEDVCLKNHCAWCECAAVP

SSCYTIAEAEKLPSAIFKCKKVELYSSWDLTTVPSTSAELSRLFESWKFHHAKSYDSAMQ

NELRRGIFEINARSVAMHNTKADKKFTMELNEFADLTWDEFQSWYLGAPQQCSATESNGV

EYGDVPAQKDWRADEAVSPVKNQGKCGSCWTFSTTGCLESHVKLKHGKFTILSEQNLLDC

AQNFDNHGCNGGLPSHAFEFIKYNQGLDTEETYPYEAKEGKCKFNTHHVGVKVNQVMNIT

TRDEEELKAAVGSAGPVSIAFQVVSDFRFYKSGVYESTECHSGEKDVNHAVLAVGYGVED

GKNHWIVKNSWGTKWGMDGFFQIKRGVNMCGVADCASYPIVA

>contig45129 Frame-0R

MRNTTTKHLIIILSFARTVLHRTSLTSATAIYPSECNKIGRSFIDELILVELPILRIKCG

RAGIVYSLHVHRHGEALNGRALQL

>contig47941 Frame-0F

MASDGSMSVMLPMVSMMLLLVFAGGLWFLLTRNQLRGTSHSFLARVLLQDQDTITRLDIE

RGEAQAERWRCLVCEFSNAMDRPTCVLCGTKNSKREEPSRLKHSIAGREERVSSTSSITM

LTRPSLAASVVSTNSRPSLRPLRLSTLNPRQKYARRRKEWVRCVGE

>contig54703 Frame-0R|Blast-ATPase [Phytophthora infestans T30-4](gb|EEY56694.1|) 1e-30

MHLTLTMMLMNLQARANLPLLFLACTTSSCDTQDLPDDLLALFNENPTVSLTS

>contig42444 Frame-1F

MNAIVQALAALPEFVTAVLDEGNLLRAIQMHLNRNSKGKTMEQVKTVFNKWRTSGDAKQL

PLQYTLSQMLQRVANGSETPINPEPLKNVMGKKNSIFATHFQQDAHEFLLNLVSEYEQEL

VQMVHDVTAKIQEEATTSSTAQNSSLVHFFRNDLKTKSAAQEKSDRSVDAKLDLICRLTP

AKSFRAEFNRTLTCRKCGYSRKQPETFYDFSLDLPCKSFSEPQCIAEQEPQAQPSPEKQC

FCDLTAVSAREGYYCCPKASCSYQQKIENGVEPAKSPAKPTIAVMKSTVSPLMSTGDCAS

RPQHIELGSLIRKQFDIEVLQVNCEQCKEGREAQSAYEIQSLPSVLVFHLKRFEVNPHTG

DLYKRCDPIVPPAKIDLANFINLASSTGGETRYAL

>contig51949 Frame-0F

MKVVVIFLLVVFTLQDSKRFQGAIACSTSSECAWGHSCVAGESHNAVQACVPHTVCGGPS

MGNCPRKNERLA

>contig52690-1 Frame-2R1

MTPLRVGDGALFTAASDANFVSLWIFFLLISARSEKTGSKVLRPLSRFSPSSSVSERLGV

AVLSMSSSDGKFRNSSSPLSISAPCSLSSSSTSSSTPPNTNRLISAELWSSIIPKGEETP

ST

>contig00029 Frame-0F

MWTALGLCAGGFLASRAYATEPQLRYGFGDCVDEKRTLYYYIKGDGTCSANSTGQVLAKP

PVHGLRCDVHCARGFYLGANFSGPTPVSSCERCPQGKYSLGGGKLFSQRTNAWTSPLPVE

LETDCMTQDMFTGEWKHNCNPWSASKDGSLISSGENSGVLENFGGTKLYSTLRIGATFVR

DGYVTFKYRVDAELPYDGLLFQVDDTAGAESVSQSDGWKEKVVPVTMGAHVLAWHYRKDY

TGDVGEDKAFLKVIEVVGTAYSDLHCHTCGGDMTNSGGSLCAFCDVDEYAAAKSNSELEF

TCYTCPDNTHAPKGSIGISSCVEQRPCSLDDVNATYTPCTNGLRNVTYSWRQPQTCELQQ

TSSIQLPKAEQGVECASCARGYQLGKGDECEPCGTNQVRSVTGQCTICRAGTVVVKTLEF

GVGTPDGWEEWPSIVDATAATKAGWKLTKSGVLLAQHTSPDDESGRWKRPSRTVLLFHVL

FEHSGSLTITYNLSGVPTFEDIGSRAWVELEIRDVGANSIKIKREMNITGSSYDVASSSS

TSDVTDEFTATHLLHGSENGEYSQVIPINVTTAVLKEIALVVRATSAEAKRAMEVRVMFL

GLVGTRDGAGVTCENCPMGYAPFESEGTGCHVCPAGTFADTEDPSGIVACVKCPLNTYSK

EGASTCTPCGANTYSEVGAITCAAPQALTVKASPTASLSSSSEVVSSALGGLQVTYNLSL

LEALVWGNASLFLDDTVYGNATSLLSTTRVHASIPFEADGQSFWFSGLFRPLGTGWKEKV

PGQIVDEQVDTNKDVAHVVIASITNPREAGHFFQQNSGLYGNVLCSAPP

>contig14792 Frame-2F

MLQHFFCALCVVALIACLHFVAAAAAANQPLLKMQQNRSLASSVKGVKGLVDVFGSTLPK

STVVRSDLLKIEGDVKNSVKNAVESWSTISSNFLKITLDEEN

>contig29558-0 Frame-0F0

MKIVAIGTWLMEVFAHVLLRKECIELMNDFIVLI

>contig30840 Frame-1F

MFFFRCDSILLSSSVGAFCKQVTTHDVGNYNFLSTHGKRIEENTVAPYGGQSMNIIDGCD

>contig51715 Frame-0F

MKLLIVLRSASSSLNLSLGSSVSHQVETLTIPITRSPNVGIKKLRLVGHFPDPLAFLNPN

QKIAKSNKSDR

>contig06510 Frame-2F|Blast-conserved hypothetical protein [Phytophthora infestans T30-4](gb|EEY61223.1|) 5e-06 NOT\_ORF

MGWLLFL\*FASQLAKKAELRAERFGLNGETKKRLDRAKRFGMENSKFVRSLLVGSLSYSA

F