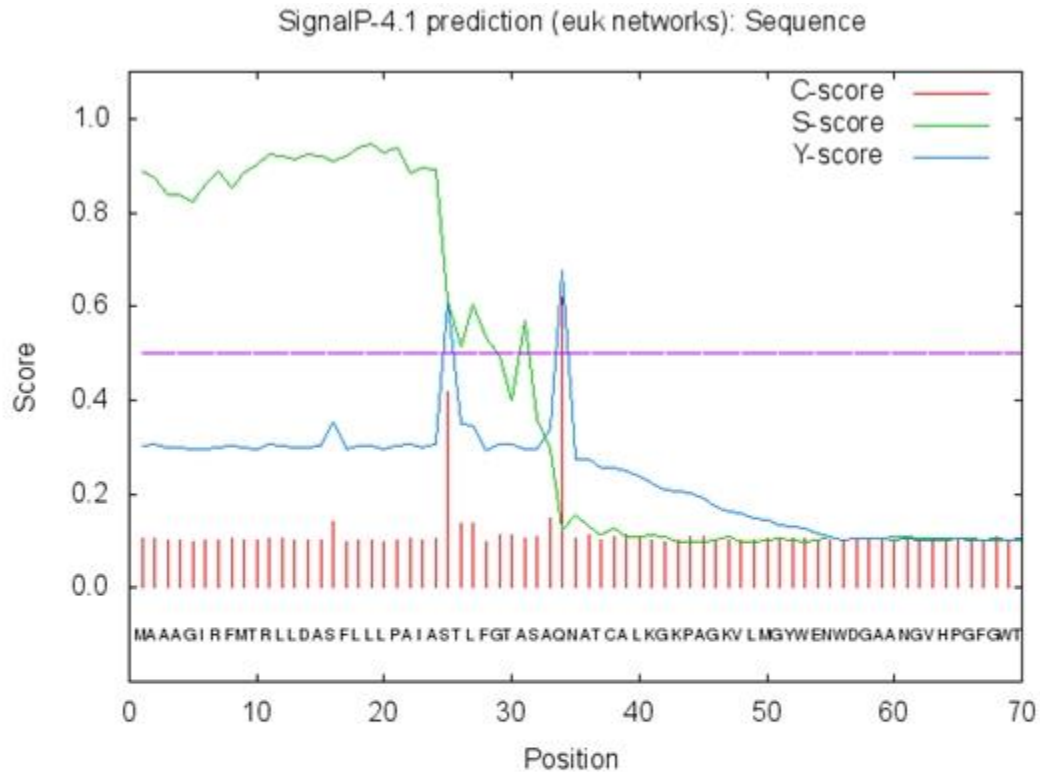


**The isolation and characterization of an endochitinase gene from a Malaysian isolate of *Trichoderma sp.***

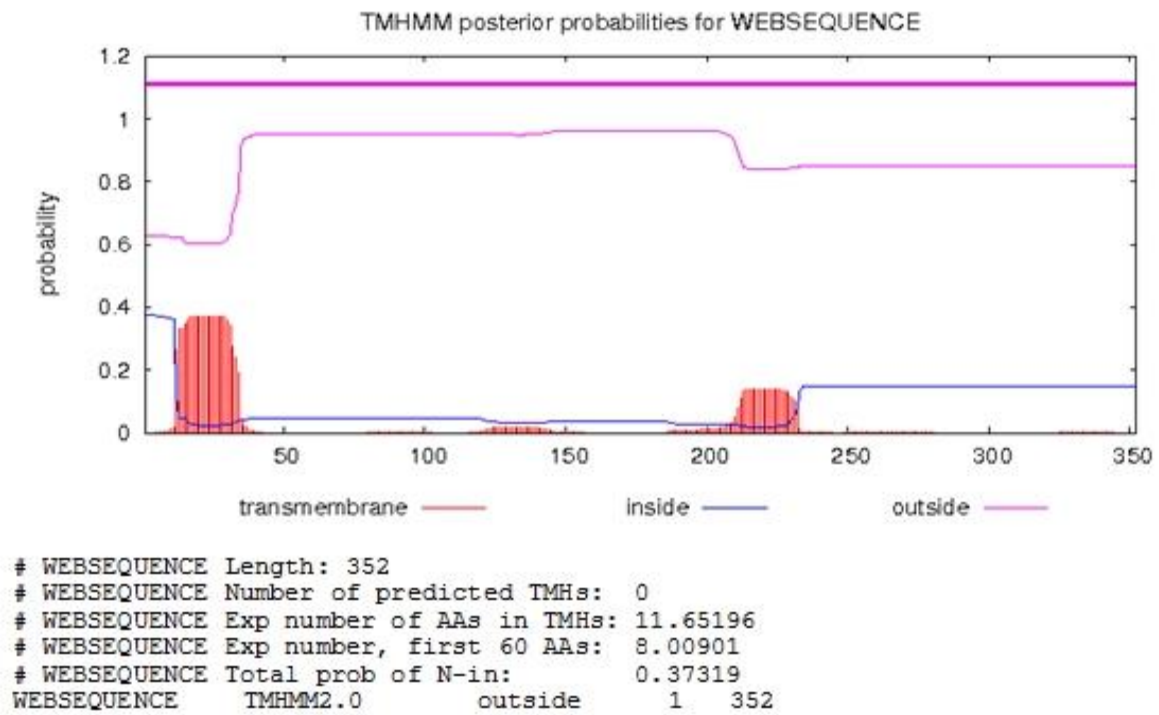
**Kalaivani Nadarajah\*, Hamdia Z. Ali and Nurfarahana Syuhada Omar**



Measure	Position	Value	Cutoff	signal peptide?
max. C	34	0.619		
max. Y	34	0.677		
max. S	19	0.944		
Mean S	1-33	0.784		
D	1-33	0.735	0.450	YES

Name=SequenceSP='YES' Cleavage site between pos. 33 and 34: ASA-QN D=0.735 D-cutoff=0.450 Networks=SignalP-noTM

**Supplementary Fig. 1** SignalP 4.0 Results of ChitT2 protein.



**Supplementary Fig. 2** TMHMM2.0 analysis of the ChitT2 Protein.

>Chitinase Trichoderma T2

SSTILTALITLRRGPTAVISTHSPHPRPTFASIMVFLRLCLPTSALWHLRORTLQAVASRMALFGERTYLSSRNM  
FKTAGCGGTCNITTATCTVALATLTQLALS KDSSLRLTAMQDLPSKAPQSRFRTTCKYQVYLRNQELAVVDMRTG  
KAGRQSLDGLGKLGWSSQRCSFWIWLDTNRKPHHTEWLQCDQRRLPRYSVRWHSVWENDMAPDTQVATPAEMCE  
AKAAGATILLSIGGATAGIDLSSSAVADKFIATIVPILKQYNFDGIDIDIETGLTNSGNINTLSTSQTNLIRIID  
GVLAQMPSNFGLTMAPETAYVTGGSITYGSIWGAYLPPIIQKYVQNGRLWNLNMQYYNGDMYGCSGDSYAAGTVQG  
FIAQTDCLNAGLTVQGTTIKVPYDMQVPLPAQSGAGGGYMNPSLVG

>gi|66844760|gb|EAL85097.1| class III chitinase Chia2 [Aspergillus  
fumigatus Af293]

MYFTTLLSALSILMAAAAALPHQLSSRASGAQNVVYWGQNGGGTVENNDLASYCTSTSGIDIIVLSFLYQ  
YGNGNTIASGTIGQSCYISPSGQPQNC DALASAIKTCQSRGVK VILSLGGAVGAYSLS SQAE AETIGQNL  
WEAYGNTQGNGNVPRPFGSTFVNGWDFDIESYSGNEY YQYLINKLR SNFASDPSNQYYITGAPQCPIPEP  
NMQVIVTKAQFDYLWVQFYNNPGCSVNGP INYDQWVSNLANTPSANAKIFIGVPASPLGATGTSSGAQYY  
LQPSALASLVAEYKDNPAFGGVMWSAGFSDANVNNGCTYAQEAKRILTTGSPC

>gi|70983215|ref|XP\_747135.1| class III chitinase Chia2 [Aspergillus  
fumigatus Af293]

MYFTTLLSALSILMAAAAALPHQLSSRASGAQNVVYWGQNGGGTVENNDLASYCTSTSGIDIIVLSFLYQ  
YGNGNTIASGTIGQSCYISPSGQPQNC DALASAIKTCQSRGVK VILSLGGAVGAYSLS SQAE AETIGQNL  
WEAYGNTQGNGNVPRPFGSTFVNGWDFDIESYSGNEY YQYLINKLR SNFASDPSNQYYITGAPQCPIPEP  
NMQVIVTKAQFDYLWVQFYNNPGCSVNGP INYDQWVSNLANTPSANAKIFIGVPASPLGATGTSSGAQYY  
LQPSALASLVAEYKDNPAFGGVMWSAGFSDANVNNGCTYAQEAKRILTTGSPC

>gi|129558297|gb|EAL92453.2| class V chitinase, putative [Aspergillus fumigatus Af293]

MASNPFNYCLLWLVAFIGLAAPLALSFSSTGNGTGCRTQSNIVAATEHFGEVNMEGGYKSIAYFVNWAIYQ  
RNYHAFDLFPADKLTHVLYAFADVRPDSGEVFLRVAYADVDPKHYPGDTWNEPGNNVYGCIKQLFLLKKQNR  
KLKVLLSIGGWTLNLTQGTSTDAGRNTFAQSAAKLLLDYGFDDGIDIDWEYPQNEVEAQAYVSLQKCR  
EALDRAAGPNRRFLLTIACPAGPNNYSKLLKREMPFLDFYNLMAYDYAGSWDSVAGHQANLFPNSNGNPS  
STPFSTIQAINYYTQVGGVPPSKIILGMPYGRDFLSTNGPGTPYSGNGAGSWEHGVWDYKALPQPGATE  
VFDQQAGASWSYDAGARTMVSYDVTAAEMKVNFIKEQGLGGGMWWEASGDRGGKAANKADGSLIGTFVE  
GVGGVNALEQSQNNLDYHESQFDNLRAGFP

>gi|146323424|ref|XP\_754491.2| class V chitinase [Aspergillus fumigatus Af293]

MASNPFNYCLLWLVAFIGLAAPLALSFSSTGNGTGCRTQSNIVAATEHFGEVNMEGGYKSIAYFVNWAIYQ  
RNYHAFDLFPADKLTHVLYAFADVRPDSGEVFLRVAYADVDPKHYPGDTWNEPGNNVYGCIKQLFLLKKQNR  
KLKVLLSIGGWTLNLTQGTSTDAGRNTFAQSAAKLLLDYGFDDGIDIDWEYPQNEVEAQAYVSLQKCR  
EALDRAAGPNRRFLLTIACPAGPNNYSKLLKREMPFLDFYNLMAYDYAGSWDSVAGHQANLFPNSNGNPS  
STPFSTIQAINYYTQVGGVPPSKIILGMPYGRDFLSTNGPGTPYSGNGAGSWEHGVWDYKALPQPGATE  
VFDQQAGASWSYDAGARTMVSYDVTAAEMKVNFIKEQGLGGGMWWEASGDRGGKAANKADGSLIGTFVE  
GVGGVNALEQSQNNLDYHESQFDNLRAGFP

>gi|432580|gb|AAB28479.1| acidic class III chitinase SE2 [Beta vulgaris]

MAAKIVSVLFLISLLIFASFESSHGSQIVIIYWGQNGDEGLADTCNSGNYGTVILAFVATFGNGQTPALN  
LAGHCDPATNCNSLSSDIKTCQQAGIKVLLSIGGGAGGYSLSSTDDANTFADYLWNTYLGGQSSTRPLGD  
AVLDGIDFDIESGDGRFWDDLARALAGHNNGQKTVYLSAAPQCPLPDASLSTAIATGLFDYVWVQFYNNP  
PCQYDTSADNLLSSWNQWTTVQANQIFLGLPASTDAAGSGFIPADALTSQVLPTIKGSAKYGGVMLWSKA  
YDSGYSSAIKSSV

>gi|472236402|gb|EMR81338.1| putative class iii protein [Botryotinia fuckeliana BcDW1]

MYSTKSLIGFASMLAALPSAIAGFSSSSNSVAIYWGQPNQGTIASYCSNAGFDIIPIAFLISLNKLTV  
NVGNADPAQVAKDIVTCQGLGKTILLSIGGATYTENELASADAATTAAKNVWAAFPGKTSSTTRPFGDA  
VVDGFDIETQGLTNLDVFAQELRTLSDAETSCKKYLLTAAPQCPYPDQADKSFLOGAVSFDAVVFVQFYN  
NNCGLNKFVKGSTTQSEFNMATWDKWASTTSKNKNVKVFVGI PGSTSAATTGYIDQATLTDLITYSKTFK  
SFGGIMSWDMVTIIGNSGYLANINKALGGVPASGSTGSSKTSAAATTAKATAAPTLLTKVKSTVVSSKV  
VATTTAKAAATTTAKAADDQTTVSSAVASATAASGAVPQWSQCGGEGYTGSTVCASGFKCVKTDWWSAC  
E

>gi|472237083|gb|EMR81997.1| putative class iii protein [Botryotinia fuckeliana BcDW1]

MPSLSALAPLAGIIASIPSVMAGFDPTSQSNVAVYWGQNSYGQSGAYVQQRLSYYCQNTTEINIPLAFL  
SSINTPVLNLFANQGDPCVTVISGSTLFYCSELEADITTCQKTYGKTIMLSVGGATYTEGGFTSTQAATTAA  
NNLWSWFGPDTSGDIRPFGSAVIDGFDFDFESTVSNMPTFANQLRSLMDTDTTKTWLLSAAPQCPYPDAA  
DGPMLDGTVAFDIVVWQFYNNYCGVQSFVSSASIQNNFNFDWTDNNAKTVSLNPNVKVMLGIPSN TGAGA  
GYTSGAALASVIAYS KSFSSFGGIMMWDMSQLYANPGFLDAVNADLGKPAVTVPVTTTTITSTVTSTTTT  
TTTSTTTTSATTTSPGSTLTTITTTTSASPTSTGGSLVNEWNQCGGQGWNGGTVCVAGTSCVAYS IWYSQCN  
PN

>gi|21264396|sp|P46876.2|CHI1\_CANAX RecName: Full=Chitinase 1; Flags:

Precursor

MILNLIILLAISIVASASNIAAYWGQONAGGDQOTLGDYCSSSPASIIILSFLDGFNLSLNFANQCSGTF  
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GFDFDIENKDQTGYAALATQLRKYFSTGTKSYLSAAPQCPYPDESVDLMSQVDLDFAFIQFYNNYCSL  
NQQFNWNSWSNYARGKSIKLYLGLPGSSSSAGSGFVGLSTVQRVVASIKGDSSFFGGISIWDISSAENGGY  
LNQLYQALSGSGSPAAPSNSYQPNTPLTRTYGGSTATASAYISVGFTAGATHGSTTTNDLLAWIDSLFGS  
SQSSVQQYATPVQSVTATPQPVAATTTAPKPTASAFNWFQWFDGTTTSTTLQTVYSTVPADQTVYVTLT  
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>gi|1168933|sp|P40954.2|CHI3\_CANAL RecName: Full=Chitinase 3; Flags:

Precursor

MLYLLTIFSLLLPALAINARSNSNVAVYWGQNSGGSQRLSYCYCSDAVIDIVILSFMHQFPSPFIQLNFAN  
ACEGTYTANGILQCQTI AEDIKYCQNKGKTILLSLGGAGSYGFSDDATAKQFAHTLWDLFGNSKNLATN  
DRPFYDAVLDGDFDIENNWSTGYPALATELRTLFQKDTSKNYLGAAPQCPYPDASVGPLLKQSEIDFV  
FIQFYNNYCNLSSSFNWDTWLNYAETDSPNKNIKLFVGVPPASSRAAGSGYNDPSAVSQYLTSIDILNSKY  
FGGISMWDVSAWNSNTNSNGNFVENMKAIKKASPEETTSSSTTTTTTTTTSTTISSSSSSSKTSKTSTT  
STSSSISSTTSSTTSSTSSSSSTSSSTSSSTSSSTSSSTSSQISTTSTAPTSSSTSLSSSTISTSASTSDTTSV  
TSSETTPVVTPLSSSLSAITIPGDSTTTGISKSSSTKPATSTTSALSSSTTTVATIPDDKEIINTPTDTET  
TSKPPAIITESDATTITQNLTPSTTTKNVKTSTNIVTEWVWAPTTLRLTLTTYQILTTRTHIETVFAEP  
STVVIYN

>gi|23499324|gb|AAN37391.1|AF435028\_1 class III chitinase [Capsicum annum]

MTINLLLPSILFLALIQTISIARSGIAYWGQNGNEATLNDTCASGNAYVNL SFLNKFGNGQTPEINLAG  
HCNPAVNGCTILGPQIKFCQKLGKVMVLSMGGGVGNYSLSKDKDAKDVARLYNNFLGGRSSFRPLGNAR  
LDGIDFDIELGSSLYEDLAQYLKRYSKLGRKMYLTAAPQCPFPDRLLGTALNTGLFDNVWIIQFYNNPSC  
QYTTNNVDDLKNSWTRWTTSVNARRIFLGLPAAPQAAGSGFIPA EVLTGGILPVIKSRKYGGVMLWSKF  
WDEQTYGYSASIVKSV

>gi|307159110|gb|ADN39439.1| class I chitinase isoform 2, partial [Castanea sativa]

EQCGRQAGGAACANNLCCSQFGWCGNTAEYCGAGCQSQCSSPTTTTSSPTASGGGGGDVGSLSIASLFDQ  
MLKYRNDPRCKSNNGFYTYNAFIAAARSFNGFGTTGDVTTTRKRELAQTSHEHETGGWATAPDGPYAWG  
YCFIMENNKQTYCTSKSWPCVFGKQYYGRGPIQLTHNYNYGOAGKAIGADLINNPDLVATNPTISFKTAI  
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LGVSYGNLDCYNQKPPA

>gi|115502371|sp|P54197.2|CHI2\_COCP7 RecName: Full=Endochitinase 2; Flags:  
Precursor

MGPTNILAAFIASLFIQSLALNPYAKSNLAVYWGQAGQNRLSYFCEKTSFDIIIVVGFINVFDPDQGPA  
GWPGSNFGNQCADSYYYTKNGTKKLLDGCYQIKEDLPKCKALGKTILLSLGGGAVHDFYEVKSEESALN  
FADFLWGAFGPLTPDWTGPRPFGEASVDGDFDIEKGSNFGYSIMVRRRELFLQDPLNRYIISAAPQCI  
MPDKYLSHAISNSAFDFIFIQFYNNPSCSAKRWTNPKSVTYTVDDWVKYIRKSGNPLAKLFIGLPASKS  
AAAKEDYLTPGEATKIVSTYMAKYPSTFGGMMVWEATASENNKLGGLPYADIMKEVLLRCDPDPPTSTVT  
STTSASTSTQTSSTMETKLSASTPSSPSTVSPSSTMQTTSTGSTSIEVTTTRSQEPPTTISTR  
ASTEPVTTTRSQEPPTTISTRASSTETVTTTRSQEPPTTISTWSASTETSTSSQDSPSTTISTKSAPTGT  
VTTRSQDLPTTISTRSPETETETATTKSQGSPSITLSTRSSAETVSTRSQHSSSTTISTKSAPTETGT  
TSEHSTSMFPVSTRASSTETVITRSQNSDSQSMVSTRSPSTESITTRSQGSPSETFSTKSVPVDTISTEL  
PSQTPTTIITGTPSDPVSAPTPTTVPPNPTLTLAPSSSTTEDRTTITTIITTSYVTVCPGTFTVITYTT  
TYCPETASLTPTPPIPGAPAPPDGTIIVTVCPQCAPPTTVTLVPTRSAFLPARTETRPVVTVPV  
PENPIKVKPSESGDFVTVTTAAPATVTKTLEYNNPVDSDVNVQPTGGSSPVEFEGSAMTVRSMDDVAKA  
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>gi|263413885|sp|P0CB51.1|CHI1\_COCP5 RecName: Full=Endochitinase 1;  
AltName: Full=CiX1; AltName: Full=Complement-fixation antigen; Short=CF-AG;  
Short=CF-antigen; Flags: Precursor

MRFLIGALLTLQTLVQASSMSPNYYPVPEAPAEAGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYA  
FANIRPSGEVYLSDTWADTDKHYPGDKWDEPGNNVYGCIKQMYLLKKNRNLKTLSSIGGWYTPNFKTP  
ASTEGRKKFADTSLKLMKDLGFDGIDIDWEYPEDEKQANDFVLLKACREALDAYSARKHPNGKFLLLTI  
ASPAGPQNYNKLKLAEMDKYLDLFWNLMAFDYDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKAVKDYIKAG  
VPANKIVLGMPLYGRAFASTDGIGTSFNGVGGGSWENGVWDYKDMPPQGAQVTELEDIAASYSYDKNKRY  
LISYDVKIAGKKAEYITKNGMGGGMWESSDKTGNESLVGTVVNGLGGTGKLEQRENELSYPEVSYDN  
LKNGMPS

>gi|118200080|emb|CAJ43737.1| class III chitinase [Coffea arabica]

MTACLRLPLFLAIIISLMISSLRSSEGAGIAVYWGQNGNEGSLEEACRSGYYDYVNIAFLVDFGSGQTPE  
LNLAGHCIPSPCTFLSSQIEVCQSLGKIVLLSLGGGGAGAGRGPILASPEDARGVAAYLWNNYLGGQSDS  
RPLGAAVLDGIDFDIEYGSNLYWDDLARALSGYSTAERKYLSAAPQCFPDYLDVAIRTLGLDFVWVQ  
FYNNPPCQYGTSTGNADNLLNSWSNDWAPHPGVNKLFLGLPAAPEAAPSAGGYIPPEVLINQILPVVQSY  
KYGGVMLWSRFYDRNYSPAIRPYVNGDPLTYTTKSVKSHAVA

>gi|380484068|emb|CCF40231.1| endochitinase [Colletotrichum higginsianum]  
MLFKKSFLAAAAAISPALAHSSSQPQSKAPSSFGGLSLYWGOYGDPSDRLSSYCDAPGVTSTVAVSFVTYS  
PKNSGGYPGTNFGAGHCGGEVIFYKNPKTGEDTKLIMNCDYIKQDIKHCQSKGIKVLLAIGGYCPTDGPCSY  
DISSEDEGHQFAELLHKTFGPYDPTWSGPRPFDISATEHVSVDGFDLDFKYPNQKQWIRWVEKLRVSG  
IYYISAAPQCPTSDTYFQLKELIYNAQFDSLFIQFYNNPGCQASDTPNYDDWENVISQTSKSKDARLYIG  
VLASPGAGWNGYVPPSRVKELICKFKSRPHFGGVSIWDATRGAMNQIDGQAFHEAVADALKYGCPIPPK  
TSTTSVSTSTPTSSLVSSTATSSTAVSTTSSASSSVSSESVSSSHSASASASSSGSASVSASVSASASAS  
QTGTESVSTSTASVSASASASASVSDSATHTSTITSLSSASVSASASASASASVSDSATHTSTITSLS  
SSASVSASSXAXRSAPTSARYH

>gi|477532312|gb|ENH83952.1| class III chitinase [Colletotrichum orbiculare  
MAFF 240422]  
MLGRTRPHFLMRLFVVLALLGVAVSRCSGFDPTSKNNVVVYGGQPNQGD LINQCQQPEIDVIVLSFVH  
LFPAQANGYPGTNFGNRCGGQVYPGPGFNGVNDPSRDQLQSNCP SLNAQIPVCQQQYGGKILLSLGGGVT  
TYQLTGRNEGELLATYLWHMFGPKSPDWTGPRPFNDNDNSEGYIALVRLRLRSLFQSASKPYYL TGAPQCIV  
PDANMAAMISATQFDMIFVQFYNTPSCSAATWAAANPSYAAGQPYQEAGFTYDAWAQWLSNTPSRDAKIY  
LTLPASPDAASDGNYYITPEQTKSLVGAFYCRPSFGGI AVWEATRGDNNPYNGKSFQAVMKDLLVAAAATG  
CEVEFRAESRSFYESRNEP

>gi|442564139|gb|AET86622.2| class III endochitinase [Dactylis glomerata]  
MALAHSRSASLLFLLAVTTFLAGPAAATGKTGQVAVFWGRNKNEGLREACDSGTYTIAIISFLDGFHGH  
NHHLDLSGHDISRVDGIKHCQSKSILVFLSTGGFGGKYFMPSPRAVEAVADYLWNAFMLGTRKGVYRPF  
GDAYVDGIDFFVENGSPDNYDELARRLWNYNKGFRARTPVQLTATPRCGFPDRHVERALATGLFTRIFVR  
FYDDPHCAADWQQEWDRTAAFGTSAQIYFGLPASEKKVGYVYPKNLYYGIIPVVQKAANYGGIMVWERF  
DDKQGTGYSSYAIQWA



>gi|442564141|gb|AET86623.2| class IV endochitinase [Dactylis glomerata]  
MARSPMAVFVALGLAAALLSAAGPAAAQNCGCQADFCCSKFGFCGKTDDYCGDGCQSGPCKSGGGSSGGG  
GDVGSIVTDDFFNGIKSQSGSGCAGQSFYTRQAFLSAVGSPSGSGFGSGSSDAAKREIAAFFAHVTHETG  
HFCYIEEINGASQNYCDTGFPQWPCSSGAKYYGRGPLQLTWNYNYGAAAGKAIGFDGLNPNQIQAQDNVVA  
FKTALWYWMTNVHGVLPQGFATIRAINGAVECDGKNTAQMNARVGYQAYCROFGIDAGGSLTC

>gi|74621315|sp|Q8SSI7.1|CHS1\_ENCCU RecName: Full=Chitin synthase 1;  
AltName: Full=Chitin-UDP acetyl-glucosaminyl transferase 1; AltName:  
Full=Class-IV chitin synthase 1

MLSQGEILRNPSRTRLQRPPKRSERKGGWYRVTFITCLIPNFMRLRCFGMTTPEVQHAWREKVALCICI  
FFCWIILGFTTYGMNTIICKGSNQYVASRLKRDAFDGNTVIANGGIYYTDDEYAFGENHTYAFEEKSGAC  
KLAFGRQLPSGDEDIDDLERINDIYWDWGDIMSKGMIVVGNKVYDPSYCTEPLFEEFNRYAGTEGKPDF  
DTDEWRCYEDMFYAGKVATKTPGCLLADTMFWITTSIFGLIITKFLGFFYSWYAKRRPKPSKITPCI  
LLVTCYSEKGDGIKNTLDSLCKQDYGDYKLIIVVICDGNITGSGNSMSTPDIVLGLSDVDRRAEPKGYIS  
LTHGTRKRYNRAKVHAGYYHVREKKSRRYRCWPCFGRQADSSEVENYKTRILVINKCGNPSETFKAGNRG  
KRDSQVILMSFFSKLIYGDRMTELD FEIYQKMKFLMPHIEPEDFECILMVDADTIVKPDALSIMVNVFET  
DQKVI GMCGETMILNKFESWVTMIQVFEYYISHHLSKAFESVFGGVTCLPGCFCMYRIKIVTNQQQLLS  
GPSKSRASVPRFSSMKSISSSLEKSLCLPILANPAIINAYSVLEVKTLLHQLNLLHLGEDRYLTLLLLKT  
FYRRKLVFIPAAKCETYVPGEFVLLSQRRRWINSTIHNL FELVQVNNLCGAFCFMSQLVVMELFGTLV  
LPAAIIFTFVMIAVSILIEPAWVPLIMLVGIFGLPAVLILITMEIQYVFWCLVYILSIPIWNFVLPTYA  
FWHFDNFSWGDTRKVDGEGKEDEEGFDHTKIRIRELEEFLLSEANK

>gi|2934696|dbj|BAA25015.1| class III acidic endochitinase [Glycine max]  
MASERQALMLILLTFFFTIKPSQASTTGGITIIYWGQNIDDGTLTSTCDTGNFEIVNLAFLNAFGCGITP  
SWNFAGHCGDWNPCSIQEQIQYCCQKGVKVFSLGGAAGTYSLSLCPEDAKEVANYLYQNFLSGKPGPLG  
SVTLEGIDFDIELGSNLYWGDALAKELDALRHQNDHYFYLSAAPQCFMPDYHLDNAIKTGLFDHVNVOFYN  
NPPCQYSPGNTQLLFNSWDDWTSNVLNNSVFFGLPASPDAAAPSGGYIPQVLISEVLPYVKQASNYGGV  
MLWDRYHDVNLNYHSDQIKDYVPKYAMRFVTAVSDAIYESVRSARTHRILOKPKY

>gi|12698917|gb|AAK01734.1|AF335589\_1 chitinase class I [Glycine max]  
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TPTTPSSGGDISRLISSSLFDQMLKYRNDGRCSGHGFYRYDAFIAAAGSFNGFGTTGDDNTRKKEIAAFL  
AQTSHETTGGWASAPDGPYAWGYCFINEQNQATYCDGGNWPCAAGKKYYGRGPIQLTHNYNYGQAGKALG  
LDLNNPDLVATDATVSKTALWFWMTAQGNKPSHDVITGRWTPSSADSSAGRAPGYGVITNIINGGLE  
CGHGQDNRVQDRIGFYRRYQMMGISPGDNLDCNNQRPFA

>gi|351726922|ref|NP\_001236631.1| class III acidic endochitinase precursor  
[Glycine max]  
MASERQALMLILLTFFFTIKPSQASTTGGITIIYWGQNIDDGTLTSTCDTGNFEIVNLAFLNAFGCGITP  
SWNFAGHCGDWNPCSIQEQIQYCCQKGVKVFSLGGAAGTYSLSLCPEDAKEVANYLYQNFLSGKPGPLG  
SVTLEGIDFDIELGSNLYWGDALAKELDALRHQNDHYFYLSAAPQCFMPDYHLDNAIKTGLFDHVNVOFYN  
NPPCQYSPGNTQLLFNSWDDWTSNVLNNSVFFGLPASPDAAAPSGGYIPQVLISEVLPYVKQASNYGGV  
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>gi|1469788|gb|AAB67842.1| class I chitinase [Gossypium hirsutum]  
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PGGLTNLISRETFNQMLLHRNDGACPARGFYTYDAFIAAARSFPAPFATTGDQATRKREIAAFLAQTSHET  
TGGAGWAAPDGPYAWGYCYNRELNPPSSYCASDPNYPCAPGKQYFGRGPMQLSWNYNYQCGRRAIGVDLL  
NNPDLLSSDPTISFKSAFWFWMTPQSPKPSCHNVIIGAWSPSSSDRAAGRVPYGVITNIINGGLECGKG  
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>gi|1791007|gb|AAB68047.1| class I endochitinase [Gossypium hirsutum]  
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GACPARGFYTYDAFIAAARSFPAPFATTGDQATRKREIAAFLAQTSHETTGGAGWAAPDGPYAWGYCYNRE  
LNPPSSYCASDPNYPCAPGKQYFGRGPMQLSWNYNYQCGRRAIGVDLLNNPDLLSSDPTISFKSAFWFWM  
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>gi|3334147|sp|Q39799.1|CHI1\_GOSHI RecName: Full=Endochitinase 1; Flags:  
Precursor  
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TGGAGWAAPDGPYAWGYCYNRELNPPSSYCASDPNYPCAPGKQYFGRGPMQLSWNYNYQCGRRAIGVDLL  
NNPDLLSSDPTISFKSAFWFWMTPQSPKPSCHNVIIGAWSPSSSDRAAGRVPYGVITNIINGGLECGKG  
WNAQVEDRIGFYKRYCDILGVSYGNNLDCYNQSPFGNGVSVDSM

>gi|298106229|gb|ADI56257.1| class I chitinase [Gossypium hirsutum]  
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PGGLTNLISRETFNQMLLHRNDGACPARGFYTYDAFIAAARSFPAPFATTGDQATRKREIAAFLAQTSHET  
TGGAGWAAPDGPYAWGYCYNRELNPPSSYCASDPNYPCAPGKQYFGRGPMQLSWNYNYQCGRRAIGVDLL  
NNPDLLSSDPTISFKSAFWFWMTPQSPKPSCHNVIIGAWSPSSSDRAAGRVPYGVITNIINGGLECGKG  
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>gi|2506281|sp|P11955.4|CHI1\_HORVU RecName: Full=26 kDa endochitinase 1;  
Flags: Precursor  
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HETTGGWATAPDGAFAWGYCFKQERGATSNYCTPSAQWPCAPGKSYGRGPIQLSHNYNYGPAGRAIGVD  
LLRNPDLVATDPTVSFKTAMWFWMTAQAPKPSHAVITGQWSPSGTDRAAGRVPFGFVITNIVNGGIECG  
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>gi|45934508|gb|AAS79333.1| endochitinase class III PR3 [Malus x domestica]  
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QNIKVLLSIGGAVGSYNLTSADDARQVADYIWNFLGGQSASRPLGDAVLDGVDFAIVIGGGQFYDELAR  
LLNGHNROAKTVYLAAPQCPIPDALDGAIQTGLFDYVWVQFYNNPPCNRI PAA

>gi|485920234|gb|EOD46321.1| putative class iii protein [Neofusicoccum parvum UCRNP2]

MPSTSTLASVVVGLSALRVVQAGFDNTSSSNIAVYWGQNSYQGTGDLAQORLAYCANDDIDVIPMAFM  
TVITDTTGHPQLNFANQGDKCTTFDGTSLFNCTELATDIPICQEQYNKTITLSIGGATYTEGGFSNETEA  
QAAADMIWATFGPNQNDSSVLRPFGDAALDGFDFDFESTVSNMAPFAQRLRDLMDASEAADGKHRILTAA  
PQCPFPDAADDQFLSGPAGDGAGAVPMDAVLVQFYNNYCGQQSYVAGAADQWNFNFATWDNWKATLSANA  
GVRVLLGVPASATAAGSGYKSAADMAPIIDYVENFTSFGGVMMWDVVSQAYANTGFLDGVKGELEDAAAEE  
PEYCG

>gi|11558417|emb|CAC17793.1| endochitinase [Nicotiana sylvestris]

MRLREFTALSSLLFSLLLLASAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQSQCPGGPTPP  
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TTGGWATAPDGPYAWGYCWLREQSPGDYCTSSGQWPCAPGRKYFGRGPIQISHNYNYGPCGRAIGVDLL  
NNPDLVATDPVISFKSALWFWMT PQSPKPSCHDVII GRWQPSSADRAANRLPGFGVITNI INGGLECGRG  
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>gi|19843|emb|CAA45821.1| chitinase C class I [Nicotiana tabacum]

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AAFFAQTSHETTGGWDTAPDGRYAWGYCYLREQNPPSYCVQSSQWPCAPGQKYYGRGPIQISYNYNYGP  
CGRAIGQNLNPNPDLVATNAVVSFKSAIWFWMTAQSPKPSCHDVITGRWTPSAADRAANRLPGYGVITNI  
INGGLECGHGS DARVQDRIGFYRRYCSILGVSPGDNIDCGNQKSFNSGLLLETM

>gi|19847|emb|CAA45822.1| chitinase B class I [Nicotiana tabacum]

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TTGGWATAPDGPYAWGYCWLREQSPGDYCTPSGQWPCAPGRKYFGRGPIQISHNYNYGPCGRAIGVDLL  
NNPDLVATDPVISFKSALWFWMT PQSPKPSCHDVII GRWQPSSADRAANRLPGFGVITNI INGGLECGRG  
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CGRAIGQNLNPNPDLVATNAVVSFKSAIWFWMTAQSPKPSCHDVITGRWTPSAADRAANRLPGYGVITNI  
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>gi|2425170|dbj|BAA22266.1| basic class III chitinase OsChib3b [Oryza sativa Japonica Group]  
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LAQTSHETTGGWATAPDGPYAWGYCFKEENGGAAGPDYCOQSAQWPCAAGKKYYGRGPIQLSYNFNYGPA  
GQAIGADLLGDPDLVASDATVSDTAFFWMT PQSPKPSCHAVATGQWTPSADDQAAGRVPYGVITNII  
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>gi|425772463|gb|EKV10864.1| Class III chitinase, putative [Penicillium digitatum PHI26]  
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GARLMWETFGPKKEGSKAFRPFQDVALDGFDFDFEANVQHMAPFANELRSIMKADESKQQFYLTAAPOCP  
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TSASTDSTKTTEPTKTTEPTKTTEQTKPKTTTTSSSSNVPDSSSSSSSSSASASHKGVEETTTATNE  
QKTTITATITATITDHKPQSTEAEPPTGTSAETTATPTSTASSHDESSTDDSQSSDDGSDGSDGS  
DSNALSSILGNDLLTLLSGLRQANNIASGVTHGPSNNLRRARNT

>gi|28848952|gb|AAO47731.1| acidic class III chitinase [Rehmannia glutinosa]

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AGHCDPTITNGCTHLSSQIKSCQAKGIKVMLSIGGGAGSYLSSSQDAKQVATYLFNNFLSGKSSPRPLG  
DAILDGIDLDIEGGTDLYWDDLARYLSNYGKRGRKVYLTAAPQCFFPDYIIGNALQTGLFDYVWVQFYNN  
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>gi|116319|sp|P29027.1|CHI2\_RHIOL RecName: Full=Chitinase 2; Flags:  
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SFDYVNVQFYNNYCSATGSSFNFDTWDNWAKTTSFNKNVKIMFTVPGSSSTAAGSGYVPMSTLQTIIVPSLA  
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TPGSCPVANQPCSTQNYACTADGKYAVCDHGKQWVASSCPSNTVCIPTTDGASICYGYATGSGSTCPSVS  
ALEITAASLGSKNGFVPRPYKASKVAAQLAVTSTDKNSFEAVINARRTTLTPFEKSVTIEFTTPSNIKFT  
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>gi|171334|gb|AAA34539.1| endochitinase [Saccharomyces cerevisiae]  
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FANACSDTFSDGLLHCTQIAEDIETCQSLGKKVLLSLGGASGSYLFSDDSQAETFAQTLWDTFGEETGAS  
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GIALWDASQAFSNEINGEPYVEILKNLLTSASQTATTTVATSKTSAASTSSASTSSASTSQKKTQSTTS  
TQSKSKVTLSPASSAIKTSITQTTKTLTSSTKTKSSLGTTTTTESTLNSVAITSMKTLSSQITSAALVT  
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YF

>gi|1144307|gb|AAB08443.1| chitinase, class II [Solanum lycopersicum]  
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NTRNKEIAAFLAQTSHETTGGWATAPDGPYSWGYCYKQEQSGPDY CASSQQWPCAPGKKYFGRGPIQIS  
YNYNYGAAGSAIGVNLLNPN DLVANDAVVSFKTALWFWMTAQQPKPSAHDVITGRWSPSVADSAAGRVP  
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>gi|1705805|sp|P52403.1|CHI1\_SOLTU RecName: Full=Endochitinase 1; Flags:  
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TAPDGPYAWGYCFLREQSGPDYCTPSSQWPCAPGRKYFGRGPIQISHNYNYGPCGRAIGVDLNNPDLV  
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TSHETTGGWPTAPDGPYAWGYCFLREQSGPDYCTPSGQWPCAPGRKYFGRGPIQISHNYNYGPCGRAIG  
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>gi|308212836|gb|ADO21646.1| class III chitinase [Tamarindus indica]  
YWGQNGNEASLAEACATGKYSYVNIAFLNKFNGQAPEIFIAGHCPPFSNNCSLVGSDIKKCQNQGIKV  
MLSIGGASGSSSYSLASSGDAKNVSDYLWNNFLGGESSRPLGDAVLDGIDFEILNNSTRYHEDLAGHLKS  
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>gi|924951|gb|AAA80656.1| class I chitinase [Theobroma cacao]  
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DLLATDPTISFKSAFWFWMT PQSPKPSCHDVIIGAWSPSGSDQAAGRVP GFGLITNIINGGLECGQGWNA  
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>gi|133753040|gb|ABO38127.1| endochitinase [Trichoderma atroviride]

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TNFANAGDRCTPFSDNPWLLSCPEIEADIKTCQANGKTI LLSLGGDSY TQGGWSSASAAQAAANQVWAMF  
GPVQSGSSAERPFGSAIVDGFDFDFEATTNNLAAF GAQLKSLSNAAGGKKYFSAAPQCF PDAAVGALI  
NAVPMDWIQIQFYNNPCGVSGYTPGTSSQNNYNYQTWDTWAKTSPNP NVKLLVGIPAGPGAGRGYVSGSQ  
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>gi|19073001|gb|AAL84697.1|AF395758\_1 endochitinase class V precursor  
[Trichoderma virens]

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RKNVVYFTDWSIYGAGFLPQNL PADDITHLLYAFAGIAADG SVVVYDPWADEQKLLGKRNTQGESVHGAV  
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DAQNFVLLLQECRRALDEYAGRNGQNYHYLLTVATPAGPEHYSLLDMRAMDQYVDAWHLMAYDYAGSWDT  
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GPVQSGSSAERPFGSAIVDGFDFDFEATNNLAAF GAQIKLSLSNAAGGK KYFSAAPQCFPPDAAVGALI  
NAVPMDWIQIQFYNNPCGVSGYTPGTSSQNNYNYQTWDTWAKTSPNPV KLLVGI PAGPGAGRGYVSGSQ  
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>gi|19073001|gb|AAL84697.1|AF395758\_1 endochitinase class V precursor  
[Trichoderma virens]

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>gi|19073005|gb|AAL84699.1|AF395760\_1 endochitinase class V precursor  
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AGSWDQTSGHQANLHPSHDNPTSTPFSTDAADIFYTRNGVAPSKIVLGMPIYGRAFENTDGPGRPYNGIG  
EGSWENGI FDYKVLPLQGSQEIYDQATGSSYCYNPQTRKLVSYDTPHASRVKAGYI KEWGLGGGMWWESS  
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>gi|210161999|gb|ACJ09604.1| endochitinase [Trichoderma virens]

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NGVAPSKIVLGMPIYGRAFENTDGPGRPYNGIGEGSWENGI FDYKVLPLQGSQEIYDQATGSSYCYNPQT  
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>gi|416029|emb|CAA53626.1| endochitinase [Triticum aestivum]

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TSHETTGGWPTAPDGPYSWGYCFNQERGAASDYCSPNSQWPCAPGKKYFGRGPIQISYNYNYGPAGRAIG  
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>gi|2306811|gb|AAB65776.1| class IV endochitinase [Vitis vinifera]

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GIISQAASSCAGKNFYTRAAFLSALNSYSFGNDGST DANKREIAAFFAHVTHETGHFCYIEEINGASHN  
YCDSSNTQYPCVSGQNY YGRGPLQLTWN YNYGAAGNSIGFNGLSNPGIVATDVVTSFKTALWFWMNNVHS  
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>gi|2306813|gb|AAB65777.1| class IV endochitinase [Vitis vinifera]

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SHNYCDSSNTQYPCVSGQNY YGRGPLQLTWN YNYGAAGNSIGFNGLSNPGIVATDVVTSFKTALWFWMNN  
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**Supplementary Fig. 3** Protein sequences used for phylogenetics analysis.