

New Phytologist Supporting Information

Article title: **A new mode of NPR1 action via an NB-ARC-NPR1 fusion protein negatively regulates defense response to stem rust pathogen in wheat**

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Notes S1: Amino acid sequences and the location of each predicted functional domain of the TaNPR1 proteins in Fig. 1b, c.

NPR1-like proteins on group 3 chromosomes

>G105400_Chr.3AS (400 aa)

MQRHLLDFLDNVEVDNLPLILSVANLNCNKSCVKLFCLEIVVRSNLDMITLEKALPEDVIKQI
IDSRLTLGLASPEDNGFNPKNHVRRI LKALDSDVELVRMLLTEGQTNLDDAFALHYAVEHCDSK
ITTELLDIALADVNLNRNPRGYTVLHIAARRRDPKIVVSLLTGKARPSDITFDGRKAVQIAKRLT
KHGDYFGNTEEGKPS PNDKLCIEILEQAERRDPQLGEASVSLALAGDCLRGKLLYLENRVALAR
IMFPIEARVAMDIAQVDGTLEFTLGPSTNPPLEITTVDLNDTSFKMKEEHLARMRALSKTVEVG
KRFFPRCSNKLDKIMDDEPELASLGRDASSERRRRFHDLQDALLKAFSEDKEEFNKTTTLSSSS
SSTSTVARNLTGRPRR

46-90: DUF3420 unknown domain

89-192: Ankyrin repeats (3 copies)

189-387: NPR1-like-C terminal

>G123800_Chr.3B (633 aa)

MEAPSSHVTASFSDCDDSVSMEDAAPDADVEALRRLSDNLAAAFRSPDDFAFLADALVAVPGAP
DLRVHRCVLSARS PFLRALFKRRAAAAGSSGGVEGNRLELRELLGDEVEVRYEALVLDYLYS
GRVRDLPKSACACVDEGGCAHVGCHPAVSFMAQVLF AASTFQVGE LANLFQESMYSTFPDIIG
KHVHHLSPDNSQHRESATFSIVLLFHVF EKRVLTHVMPFFSMQRHLLDFLDKVEVDNLPLILSV
ANLNCNKSCVKLFCLEMEMVRSNLDMITLEKALPQDVIKQITDLRITLGLASPEDNGFNPKNHVR
RILRALDSDVELVRMLLTEGQTNLDDAFALHYAVEHCDSKITTELLDIALADVNLNRNPRGYTV
LHIAAKRRDPKIVVSLLTGKARPSDITFDGRKAVQISKRLTKHGDYFGNTEEGKPS PNDKLCIE
ILEQAERRDPQLGEASLSLALAGDCLRGKLLYLENRVALARIMFPIEARVAMDIAQVDGTLEFT
LGSSTNPPLEITTVDLNDTSFKMKEEHLARMRALSKTVELGKRFFPRCSNVLDKIMDDEPELAS
LGRDASSERKRRFHDLQDTLLKAFSEDKEEFNRTTTLSSSSSSSTSTVARNLAGRTRR

45-185: BTB domain

279-323: DUF3420 unknown domain

322-411: Ankyrin repeat

422-620: NPR1-like-C

>G107500_Chr.3D-1 (704 aa)

MEAPSSHVTASFSDCDDSVSMGDAAPDADVEALRRLSDNLAAAFRSPDDFAFLADALVAVPGAP
DLRVHRCVLSARSPPFLRALFKRRAAAAAATGSSGGAEGRVELRELLGEEVEVGYEALVLDY
LYSGRVRDLPKSACACVDVDGCAHVGCHPAVSFMAQVLFMASTFQVGEASLQVRLPPPLHH
DAFLVSDIYGACWEYIFARTFLCSDSKESMYSTFPPDTIGKHVHLLSSDNSQHRESATILYRYL
NLCISDAEAGDELRVYHLMITPVGLLLVTVFCRCIDKPVLTGMPFFSMQRHLLDFLDKVEVDN
LPLVLSVANLCNKSCVKLFEFCLEMVVQSDLDMITLEKALPQDVIKQITDSRITLGLASPEDNG
FPNKHVRRILRALDSDDVELVRMLLTEGQTNLDDAFALHYAVEHCDSKITTELLDIALADVNL
NPRGYTVLHIAAKRRDPKIVVSLLTGKARPSDLTFDGRKAVQISKRLTKHGDFGNTTEEGKPS
NDKLCIEILEQAERRDPQFGEASVSLALAGDCLRGMLLYLENRVALARIMFPIEARVAMDIAQV
DGTLEFTLGYGTNPPELITTVDLNDTSFKMKEEHLARMRALSKTVELGKRFFPRCSNVLDKIMD
DEPELASLGTDACSERKRRFHDLQDTLLKAFSEDKKEFNRTTTLSSSSSSTSTVARNLAGRTR

45-185:BTB domain
350-394:DUF3420 unknown domain
395-481:Ankyrin repeat
691-727:NPR1-like C

>G117002LC_Chr.3D-2 (902aa)
MVATRPLAERDAMFVAIDAAAEELDNETEDVISSTSAIPPPFAPLRHDEDTASMYTAVYNE
EKYNIGGTPPLEFQEGHHQRLAGPHSRYAGMIWMAGSRIIVCGDYHGSSQLDWHTCYKIEGI
CNGLHYLHEQIDKSVLHLDLKPANVLLDNNLAPKLTDFGLSKLLDQYQTMFTPNRFGTLGYMA
PEYIDEGTITPKTDIFSGFVIIMELITGHRDYPVAGTSSDGFIELALKKWRNTLEKAQGYTK
IEVDCQQIKRCIQIGLICVNPECSKRPTTAKIIKMLKGLEISDCRISNEATSSAHQTSNGVSE
QGKPHPKNTLCIEISEEADRQDLALVSLAIAGDCLCGNLKLLYLKNGEHI SPQASIVRIVVPG
SPAGTELHVDPYMLSMRSPYLRAIFARHNNHYGASGSSAEGNRMDLQEFGLGKEVKVEYDALL
VLLYLYSGRVGDLPEPAYICADENGCAHLGCHPTVSFKVQVLFVAFTFQVPELTSLFQVCISL
SLLPMRDLFDVLHKVEVDNLPLILSVANLCKKSCRKLLERCLEMVVQSNLDMITLEKVLPPDV
VKQITDLRLSFGLASSEDMGFNPKHVRRILRALDSNDVELVRILIKKGQTNLDDAFALHYAVE
HCDSKITTELLDIALADVSLRNPRGYTVLHIAARRKDPKIVVSLLTGKARPSDFTLDGRKAVQ
ISKRLTKHGDFGSTEAGKPSPKDKLCIKILEQAERRDPQLGEASVSLALAGDCLLGKLLYLE
NRVALARIMFPIEARVAMDIAQVDGTLEFTLGSSTNPPELITTVDLNDTSFKMKEEHLARMRA
LSKTDKLNANVSSRAVQLYWTSSWMMNLSWLHSEEMHLPRFHDLQDTLLKVFSEDKKEEFART
TALSSSSSSTSLSKEFDRSA

1-290: Protein Kinase domain
370-451: BTB domain
620-695: Ankyrin repeat
654-679: Ankyrin repeat
696-891: NPR1-like_C

>G158300LC_Chr.3B 96831605-96839117 (932 aa)
MPAMASSSKALWGSLSSTEQKLACRVALQDADELAPPPLPVDITLGQARAHYTDMRGKSRRRHS
GRRHRTKGTTYGSSTSTDSRRKKSQSLRDPVRMVATRPLAERDAMFVAIDAAAEELDNETED
VISSTSAIPPPFAPLRHDEDTASMYTAVYNEEKYNIGGTPPLEFQEGHHQRLAGPHSRYAG
MIWMAGSRIIVCGDYHGSSQLDWHTCYKIEGICNGLHYLHEQIDKSVLHLDLKPANVLLDNN
LAPKLTDFGLSKLLDQYQTMFTPNRFGTLGYMAPEYIDEGTITPKTDIFSGFVIIMELITGHR
DYPVAGTSSDGFIELALKKWRNTLEKAQGYTKIEVDCQQIKRCIQIGLICVNPECSKRPTTA
KIIKMLKGLEISDCRISNEATSSAHQTSNGVSEQGKPHPKNTLCIEISEEADRQDLALVSLAI

AGDCLCGNLKLLYLKNGEHISPOASIVRIVVPGSPAGTELHVDPYMLSMRSPYLRAIFARHNN
HYGASGGSAEGNRMDLQEFGLGKEVKVEYDALLVLLLYLYSGRVGDLPEAYICADENGCAHLG
CHPTVSFKVQVLFVAFVTFQVPELTSLFQVCISLSLLPMRDLFDVLHKVEVDNLPLILSVANLC
KKSCRKLLERCLEMVVQSNLDMITLKVLPDVKQITDLRLSFGGLASSEDMGFPNKHVRRIL
RALDSNDVELVRILIKKGQTNLDDAFALHYAVEHCDSKITTELLDIALADVSLRNPRGYTVLH
IAARRKDPKIIIVSLLTKGARPSDFTLTGDKAVQISKRLTKHGDFGSTEAGKPSPKDKLCIKI
LEQAERRDPQLGEASVSLALAGDCLLGKLLYLENRVALARIMFPIEARVAMDIAQVDGTLEFT
LGSSTNPPLEITTVDLNDTSFKMKEEHLARMRALSKTDKVEILDFIFPSC

197-384: Protein Kinase

649-692: Unknown function domain DUF3420

693-781: Ankyrin repeat

792-924: NPR1-like C termina

>Chr.3A 69307893-69310005 (the gene has not been predicted by
IWGSC) (125 aa) (The DNA sequence corresponding to the Kinase
region of the 3B and 3D Kinase fused NPR1 gene was used to as a
query to search the IWGSC, and no homologs found on 3A)

MRGLRLIFGWAGVSEFYVADV RTPAKPPRLLLFCGTS DIRAHLRTNGYRIGWHNASGQLV
ASARILFPIEARIAMNIAQVDGALEFTLGSSTNPPPAITTVDLNYTPFKLKDVLHARMRA
LSQNI

1-132: NPR1-like C termina

NPR1-like proteins on group 7 and 4A chromosomes

>G023600LC+G023700LC+G021800_Chr.7A (1,437 aa)

MGRSPSSSTGVAGVKKGPWTVEEDILLINYFQRHGNNGNWRTL PQCAGLNRS GKSCRLRWTNYL
RPNIKRGTFTDDEEKTIIHLHSIHGNKWSAIAATHLPGRGTGNFIKNYWNTNLRKLLQMGINPV
THRHTDLSMLKGLPGLHAAAPGNSLSGVSMTGTRAQPHTNAASFAGSSSDMNTLG IKDKAASF
AGSSSDMTTLGVKDEAASFTGSHSDMKPPRIKDKAASFTGNYSKMKPFRIKDEALSFTGSYS
DMNSLR IKDEATSFTGSYS DIKSVSLQDETTSFTGSYSATGTGWD MNALSGLQADPKFQLLQ
DHCWVISASLGAMRALVEKLDMLLLAYSSPQECSSKRVKDGMHLLKDDLEEISSYLDELLEVE
DPPPMAMCWMNEARELSYDMEDIIDSLLLCVPPDHFNKNKKRKNKKKI IKKRLKWHRQITYI
AQVSEHGVRTSKRIHVTVVPLPKKSKIAETISEFRIYVQEAIERH DRYLIVIDDLWDASAWD
IIKCAFPKGS HGSRIIITQIEDVALTCCCDHWEHVFEMKPLDDDH SRKLFNFRLFGSESDCP
EEFKQVSNEIVDICGGLPLATINIASHLANQQTGLALDLLAYMCD SLRSHSWSSSTLERTRKV
LNLSYNNLPQHLKTCLLYFHMYPEGSI IWKDDLKQVVAEGFVATGKGKEQDKETTEKTAGIY
FDALVDRRFIQPLYINYNNKVRRLSLIFGDAKYAKTPENITR SQVRS LRFFGLFKMPCVRDF
KVLRLVNLQLSGHCGAHPIDLTGISELFQLRYLKITS DICIKLPNSIRGLQCLKTLDLMDAT
RVTAVPWDIIHLPHLLHLLTPVDTNLLDWIGSMTDSVISLWLSGLKLN YLQDLHLNMSCIPSLL
GVEALAHLIGGHGNLKTIVMSHGSSVIPGASKAII SWDDLEPLPLLQRFECSPHSCITFSRIP
KWIKELSHLCILKIAVVELQISWVDILRGLPALTALS LYVRRAPIERII FNKADGFSVLKYFK
LTCTSGIACLKFEAQAMPNLWKLKLGFNATPRMDQHQLIRIEHMPNLKGISVKFGGVA AHIEY
ARSVVTSHPRNPTINMQLVNFC SNCDGSTKQNLLTNWAVKSRAAASAPMEDPPSHFTTTTFSSS
DGIFMADMNLEALCRLSDNLAAVFRSPDVFAFLVDMHIVVPDAPDLPVLF AASTFQIAKLTNL
FQEKGWRLLDVLDVDDVEVDNLPLILSLVANL CNKSCMKLLERCLEMVVR SNLDMITLKEALPP
DIIKQIADSRSLGLVSAEDKGFNKHVRRILQALDSNDAEVATILHQEGQTNLDDAFALHYA

VEHCDSKIITEILDITLADVNRNPRGSLMKILFPIEATVAMEIPQVNVQLGKRFFPCCSNVL
KKIMDDESELDSIGRDTSTERKRRFHELQDLLQKAFSEDKESSSLTSLRFI

15-63:HTH myb-type DNA binding motif
69-114:HTH myb-type DNA binding motif
525-814:NB-ARC domain
1085-1154:BTB domain
1248-1292: DUF3420 unknown domain
1315-1390:Ankyrin repeats

Green-color letters are the locations of the mutations in the mutants of Cd^{A529E}, Cd^{M357I}, and Cd^{L1224R}. Red-color letters are the locations of the mutations in Al^{S736L} and Al^{R805Q}

>G703400LC+G470500_Chr.4A (1,314 aa)
MGRSPSCGSEAPVKKGPWTEEEEDRLLDVYIKLHGTGGNWRTIPKRAGLNRCGKSCRLRWTNYL
HPDIKRGPFDDDEEKTTHLHSM LGNKYVYCSLLLLLYTIYLS TIFFSNSGASYSVAADDLSL
KQVVGDCNPSAGKDRQFYQELLEHEPAQEATPHGHRPHHAQPARRPQPAYRAPQSPRHRRRPQ
MGRSPSCGSEAPVKKGPWTEEEEDRLLDVYIKLHGTGGNWRTIPKRAGLNRCGKSCRLRWTNYL
HPDIKRGPFDDDEEKTTHLHSM LGNKYVYCSLLLLLYTIYLS TIFFSNSGASYSVAADDLSL
KQVVGDCNPSAGKDRQFYQELLEHEPAQEATPHGHRPHHAQPARRPQPAYRAPQSPRHRRRPQ
MKPLDEDHSRKLFFNRLFGSGSDCPEEFKQVSNEIVDVC GGLPLATINIATHLANQQKAVSLD
FLTYIRDSLRSQSWSSSASERTRQVLNLSYNDLPHHLKTCLLYLHMYPEGSIVWKDDLKQVW
AEAFINTRKKGKGDQNWMEKAAGIYFDELVDRRFIQPLNINYNKVL SCTVHEVVRDLLAHKS
VVVDYNRKNISLSHKARRLSLLFANASYAKTPVNITKAQVRS LN FVGLFECMPCIGEFKVLRV
LNLQLSGHCGDHPIDLTGISEL FQLRYLKITS DVCIKLPNQMRKLQCLETLDIIDAPRVTAI
PWDI IYLP HLLH LTL PVD TNLL DWIGSMTGSI ISLWSLGNLNYLQDLYLTISSTHPSGHPEKN
MEALGSLGGHGNLKIIVVSHGPLVMRAYRSM LSVQSPFLDAVFARRAAEGEDDPLDLRELLG
EEVEVGYEALQLVLEYLYTGRI RDLPKSACVCADVDGCAHVGCLPAISFMAQVIFAASIFEVA
VLTNH FQVRL FLLLSVAMISSYHLFIMPAGMHIGKRKGNC SKHGNDVLPVLFNKNLFEAVWRG
ADMRLLLDVLDDVEVDNLPLILSVANLCNKSCMHLLERCLEMVVRSNLDMITLEKALPPDVIK
QITDSRISLGLISPKDNGFPNKHVRRIFGALDSYDVELVRL LLYEGQTNLDDAFALHYAVEHC
DPKITTELLDLELADVNRNRNQRGYTVLHIAARRRNPKILVSVLTKGARPSDLTFDGRKAIQIS
KRLTKHGDYFGITEEGKPSPEYSLCIEILEQAERRGPQLGEASVSLAIAGDCQRGTLHLLENR
VTLMRIMFPTEARVAMDIAQVDCTLELTL DSEAKPPSEKEVATIDLNETRFQMND EHLARMSA
LFKTDKIMNDEPELASLQRDTSTERNRRFRGDMHDTLQKAFSEDKGSSSFDKSGS

15-63:HTH myb-type DNA binding motif
204-252: HTH myb-type DNA binding motif
369-514:NB-ARC
768-841:BTB domain
992-1036:DUF3420 unknown function domain
1035-1123:Ankyrin repeats
1135-1314:NPR1-like-C

>G023000LC+G019000_Chr.7D (1,351 aa)
MGRSPSCSSEPPKKGPWTEEEEDRLLDVYIKLHGTGGNWRTIPKRAGLNRCGKSCRLRWTNYL
HPDIKRGPFDDDEEKTTHLHSM LGNKWSAIATHLPGRTGNFIKNYWN TNLRKKLLHMGIDPI

THNPRTDLSQLTGLPSLPATAAAPMREFLACRYLIIIDDLWDASAWDI IKYAFPNGNRGSR I
ITTQIEDVALTCCCDHSEHVMMKPLDDDDHSRKLFFNRLFSGSDCPEEFKQVSNEIVDVCGG
LPLAMINIASHLANQQTAVSLDFLTYIRDSLRSQSWSSSTSERTRQVLNLSYNNLPHHLKTCL
LYLHMYPEGSIVWKDDLKQWVAEAFINTRKGKEKDQNWMEKAAGIYFDELI DRRFIQPLNIN
YNNKVLSTVHEVVRDLLAHKSAEENFIVVVDYNRKNI SLSHKARRLSLLFATARYAKTPVNI
TKPQVRS LN FVGLFECMPCIGEFKVLRLVNLQLSGHCGDHDPI DLTGISELFQLRYLKITS DV
CIKLPNQMRKLQCLETLDIIDAPRVTAI PWDIIYLPHLLHLTLPVDTNLLDWIGSMTDSI ISL
WSLGNLNYLQDLYLTISSTHPSGHPEKNMEALGSLGHHGNLKIIVVSHGPSVKDIVVPGASK
VIISWDELEPLPLLRQFECSPHSCVIFSRIPKWKKLGNLCLIKIAVVELQMSCVDILRGLPA
LTALS LYVRCAPAQRILFDKMAGFSVLKYFKLRFTSGIPWLKFEADAMPNLWKLKLGFNAI PR
MDQHQLIRIEHMPDLKEISVKFGGIAALIEYAVKTVISNHLRNPRVHVCLVTSTSYGDESTKE
KPPTNSAVEMRAYRSVLSVRS PFLDAIFARRAAE GEGNPLDLRELLGEEVEVGYEALQLVLEY
LYTGCIRDLPKSACVCAVDGCAHVGC LPAISFMAQVIFAASIFQVAVLTNHFQVRLFLLSV
AMISSYHLFIMPAGMHIGILVLT FHDDL CVYHLRIILVESLLRLLLDVLDDEVDNLPLILSV
ANLCNKSCMHLLERCLEMVVRSNLDMITLEKALPSDIEEQITDSRLSLGLVSPEDKGF PNKHV
RRILRALDSDDVCLVRMLLKEGRTNLDGAFALHHA VEHCDSKVTMELLDIGLADVNRNPRGY
TVLHVAARRRDPKILVSVLTKGARHSDLTFDGRKAVQISKRLTKHGDYFGITEEGKPSREDRL
CIKILEQAERRDPQLGEASVSLAIAGDRQRGKLLYLENRVALMRIMFPTEARIAMDIAQV DCT
LKLTLD SGAKPPPEKELATIDLNETPFHMNEEHLARMSTLSKTDKIMDDEPELAPLQRDASTE
RTRRFGLQDAVQKALSEDKASF DKS GS

- 15-63: HTH Myb-like DNA binding domain
- 69-114: HTH Myb-like DNA binding domain
- 146-347:NB-ARC domain
- 828-886:BTB domain
- 1031-1075:DUF3420 unknown domain
- 1098-1173:Ankyrin repeats
- 1174-1351:NPR1-like domain

>G021700_Chr.7A (1,107 aa)
MEAAAATAFVVGRIAPKLEFLAANHKLRQNLEHDITYIQREFALISA AIQQDDDCRWRSGDHV
KRAWIQIIRDLAHAIEDCIDRFMHRVTISGASTWIRQAVHRVQTVTVRKEFAKAIRELKKISQ
ESSKLRETYYSANIGAGTSSSSVASSVMACETATQMVIDD TLSAGQPVGMDAPWEELELIQQ
QQQLKVISIVGFDGIGKTL LARCVYDTIENQYEARAWVSAAEQGVPTNVIKEILQQFAIPTN
GGNLSKLCAILRLYLGT KRFFIVIDDMRTEFWHDIKDAFVGLSGRVLVTTAIHVSANACSSS
AAHDHVYAMKTLADEHSRLLFFKEAFQDDNPPIDKEDQLGSEALKKCDGLPLALVTTARYLQS
TGNPHTGNWATLCHNLGAHLETKEMLARMKRVLVHSYTSLVKHDVKTCLLYLGIYRSGRTVRR
GSLIRKWCAEGFIQGDYMCNALDAAKANFKELLNRSIIKHTDASSKNNKDQVKTYH THGMMLE
FILHMSKCDNFITLLYDQMAPPPPSKIRWLSLHDASARVVNDLSLVRSLTVFGKAHDSVLDL
SKYELLRVLDLEEC SNHLEDKHLREICSNLLLLRYLSLGA AHKVAVLPKEIKKLQ LLETLDVR
KTKIEVLPTQVMELPCLIH LFGKFKLQQGVGGRKM HKLQIWFSENSKLETVAGFVVDSNKSQG
FAQFMEHMKHLTKVKIWCEQSSNNSRDPTASGSSSNTN NYTHVSKAIKGFIKRSTDVKKAHSL
SLHCNDKWFQDLLVNLSLEKEEASSCYLSS LKLGGNICSLPPFVTMLGGLTKLCLSSPHHQ L
GGDILVALSRVRCLAYLKMIASQLDNLVIVEGALGNLRQLCIVVEVMTELEVQEGALPLLES L
QLLCKDLNGFCSKMIQSLRRIKEVTLHDGVNGETKQKWKEAAKKHPRRPNLLFVKTAEDADMG
SEPADNSESPVAQTTATTVSVIT TQDAISTGQSVQVDGADLQQGDEKEHAYKIDILEDFASKT

CLDPPMNTESFEQMEGMVGLERMEDVTHSTDQADQNVVLSVVGENRRKRARLDIGEDNSM
DKVVDRVKRKKPEDVQEPRLKARPRGRQVAVGAEDL

6-119:Rx-CC-like domain

176-458:NB-ARC domain

>G018900_Ch1.7D (1,103 aa)

MEAAAATAFACRIAPKLLAFLATNHKLRQNLEHDITYIRNEFALISAAIQDDHRWRSRPSR
DHMQRAWVKIIRDLAHAVEDCIDRFMHRVTISGTSTWLRQAVHRVQTVTVRKEFAKAIREIKK
ISQESSKLRETYYSASIAAGTSSCSAASSSVASETTTQMAIDDTLSAGRSVGM DAPQDELLEL
IQQQQQQLKVISIVGFHGIGKTL LARRVYHRMENQYEARAWVSAAKQGVPTNVLKQILQQLGI
PTNGGGNFNKLCAVLRRLYLGSKRFFIVIDD MQTEFWHDIKDI FVGLSGRVLVTTAIQSVANAC
SSSAAHDHVYAMKTLADEHSRLLFFKEAFQDDNPPVNKEDQLGSEALKKCDGLPLALVTTARY
LQSTGNPTRENWATLCHNLGVHLETKEMLARMKCALVHSYTSLVKHDVKTCLLYLGIYHTGRT
VRRGNLIRKWCAEGFIQGDYMCNALDAAVANFRELVNRSIIQRTDASSKNIKDQVKTYRTHGM
MLEFILHMSKCDNFITLLYDQLAPPPPPSKVRWLSLHDASARVANDLSLVRSLTVFGKAHESV
LYFSKYELLRVL DLEECGNHLEDKHLREICNNLLLLRYLSLGAALTVTVLPKEIKKLQLLET
DVRRTRIEILPTQVMELPCLIH LFGKFKLQQGVGGRKMLKLQTWCSENSKLETVAGFVVDNNK
SQGFAQLMEHMKHLTKVKIWCQQSTNNSMDPISSGSSSSSKYTHLSEAIKGFIKRSTDKKAHS
LSLSFNDRWCQDLLVNLSLEKEQASSCYLSSLKVQGGNICSLPPFVTMLGGLTSLCLSSPHHQ
LSGDILAALS RVRCLAYLR LIASQLGKLVIVRGALGSLRRLCIVVEVMTELEVQEGALPLLES
LQLLCKDLNGFCSIMI QSLGRIKEVT LHDGVNDETRQKWKEAAKNHPRRPKLLFVKTAEDVDM
GSEPADNSESP TVPTNDTTL PVTAPHDAI STGQSVQVDGDDLQQDDDEKEDTDKIDMLVDFVS
KTCLGTMNKESFEQMEGMVVG ENRRKRARTV GEGNSMDKVFDRVKRKNPEDI PVKLGSRLE
VIFWSWALKFTGDVRNLVAVGDVALIWTIWR C

6-119:Rx-CC-like domain

179-461: NB-ARC domain

>G470600_Ch1.4A (1,057 aa)

MEAAAATAFACRIAPKLLAFLAANHKLRQNLEHDITYIRNEFALISAAIQDDHRWRSRPSR
DYMQRRAWVKIIRDLAHAVEDCIDRFMHRVTISGTSTWLRQAVHRVQTVTVRKEFAKTIRELKK
ISQESSKLRETYYSASIAAGTSSYSAASSSVASETMTQMAKDDTLSAGRSVGM DAPQDELLEL
IQQQQQQLKVISIVGFHGIGKTL LARRVYHTIENQYQARAWVSAAEQGFPTNVLKQILQQLGI
PSNGGGNFNKLCTVLRRLYLRSKRFFIVIDD MQTEFWHDIKDI FVGLSGRILVTTAIQSVANAC
SSSAAHDHVYAMKTLADEHSRLLFFKEAFQDDNPPVNKEDQLGSEALKKCDGLPLALVTTARY
LQSTGIYPTGRTVRRGNLIRKWCAEGFIQGDYMCNALDTAVANFKELVNRSIIQRTDASSKNI
KDQVKTYHTHGM MLEFILHMSKCDNFITLLYDQLAPPPPPSKIRWLSLHDASARVANDLSLVR
SLTVFGKAHESVLYFSKYELLRVL DLEECGNHLEDKHLREICNNLLLLRYLSL GATLTVTVLP
KEIKKLQLLETLDVRRTRIEILPTQVMELPCLIH LFGKFKLQQGVGGRKMHKLQTWSSKNSKL
ETVAGFVVDNNKSQGFAQLMEHMKHLTKVKIWCQQSTNNSMDPISSGSSSSSKYTHLSEAIKG
FIKRSTDKKAHSLSLNFNDRWCQDLLVNLSLEKEEASSCYLSSLKVQGGNICSLPPFVTMLGG
LTSLCLSSPHHQ LSGDILAALS RVRCLAYLKL IASQLGKLVIVKGALGSLRRLCIVVEVMTEL
EVQEGALPLLES LQLLCKDLNGFCSMMIQSLGRIKEVT LHDGVNDETKQKWKEAAKHP RYPK
LLFVKTTEDVDMGSEPADNSESP TVPTNGRTL PMTAPHDAI STGQSVQVDGDDLQQDDDEKED
TDKIDMLADFASKTCLGTMNKESFEQMEGMVGLDDQQMEDVTPSTQADQSLVLLLVG ENR
RKRARTV GEGNSMDKVFDRVKRKNLEDPETRP TKQTAPGLAVAI SDGN

6-119:Rx-CC-like domain
179-383:NB-ARC domain