

## Additional File 12

**Amino acid sequences and alignment of predicted fungal NOXR partner: Bem1, Cdc24, CBSn-PB1.** To describe species of sequences, we used the following naming:

Mg (*Magnaporthe grisea*), Fg (*Fusarium graminearum*), An (*Aspergillus nidulans*).

Sequences are available from GenBank™ (<http://www.ncbi.nlm.nih.gov/>) by indicated accession numbers. *Gray boxes* indicate predicted characteristic domains. *Underlines* in alignment of Bem1 and Cdc24 protein sequences indicate serine-rich region (SRR) and PRR, respectively.

### Bem1 ortholog

>An-Bem1: GenBank No. XP664634

MKALRRSLKGEKSKPHHHHQHHHLSITPKSAVAI LPPKKV I KALYDYQPEPGNTQELAFSKGDFHVISREDDSDWYEACNPLIPTAR  
GLVPVTFEVIKGTQRDSSGSIDLGKKKEPHDSGFADRATSSGSEFGSGSSKSYQSHPAFPRTSMMGKAGGGAMVYGVVQYDFQAERPDELDAK  
AGEAIIVIAQSNPEWFVAKPIGRGGPGLIPVSFIELRDMQSGQAVADPLEAVRRAGVPKVEEKKMTAEYKNSSISLGKIETTGSMSVTSGM  
ERMSVRQSADHVSHMSQNGHANAYHNRNASKASIA PSTHQPPPHSQQPLVAP IAASIPRYCFDNDKYWYIIEVKMEDGRCWELSRYYHDFYDF  
QIALLTQFEEEAGNRGKPRTPFPMPGPVAHVTD A ISDGRRHNLDEYIKKLLAMPPIHTRCALVRQLFAPRPGDFEIDPSAFGEDARFSGGSQHS  
SGHELSPSASRQSSQQNGPSERSHSHSHSHSHSHQRSQTSSSIPNGKPPMVRQQSSLTQVSTSSGGALKVKVNFQDDLIAIRVPSDINVQQL  
KEKLMDRKINDEIVVQYKDEASGAYVDLISDSDLDTAIQRNSKLTLYVGLA

>Mg-Bem1: GenBank No. XP363776

MKALRRS IKGDKDKPQIS IAPKSAVAI VPPKKV I RALYDYEASTQELSFSRGDFHVI GRENDTDWYEACNPALPDARGLVVPAFFQALGRT  
ERDSAQSDTSVTRTSAPVPSKNPDHDSGYAETSAPVPSTPGFSNRDSKSGKSGAMVYGVIMYDFQAERADELQAQAGEAIIVIAQSNPEWFVAK  
PIGRGGPGLIPVSFIEIRDMASNTVPDPEGAVRRAGIPRVEEKKMAAEYKNSSITLGKFEVGGAPQQQAIEQGMDRMSLQPTDSRSSQGGQL  
NGKLQQAMQPQNA YTPK PSTQLYAPVQASIPRYCF AEEKYWFV IEAILEDGRKYELSRYYEDFYDFQIALLTEFP AEAGNTGTQKRTL PYMPG  
PVNYVTD AITEGRHLNLDAYVKNLLA QPTYISR CNLVKQFFAPREGDYEMDANGE EDEYRMSGGSQQSSPDS PGGISQQSSRNLLSSGGYNNN  
NLAPSQQRGLSAQPPMMRQASSLSQPSQASLSPGIPQAGAFMKV KLSYNGDLIAIRVPSDIQFRELFDKITERLRIQPGEVQLSYKDDITNGK  
LALMNDQDLIYAMQRNEKLLFYHRYSNSFDR

>Fg-Bem1: GenBank No. XP385437

MKALRRSIKGDKDKGVPVTPKSAVAIVPPKKVIRALYDYEARSSQELFSRGGDFHVI GREND DDWYEACN PALPDARGLVPVTFQALGRTERD  
SAQSDGGQPSPKPNPDHDSGYSESPAMHPAPAVMSPTTNSAPQGHQRNSKSVGKTGAMVYGVIMYDFAAERADELEAKAGEAIIVIAQSNPEW  
FVAKPIGRGGPGLIPVSFVEIRDMSDKAIQNPGD AIKRA GVPKVEEWKMAAEYKNSSITLGKFE GGGPGQPGQIEQGMERMSIQQQHSR  
QPSQNGTQSGYASQPRTSQPQPHQSQVQKPAAPLHAPLEARIPRYCFAEDKYWFVIEAVLEDGRQWELSRYYEDFYDFQIALLTEFP AEAGNT  
GTQKRTL PYMPGPVNYVTDAITEGRHLNLDAYVKMNLNQPPI SRCNLV RQFFAPREGDYEIDPNDNENEYRLSQGSQ LSSMESPAGGSQNNLN  
GSGYGLAPSHPMQTQASSLSQPSQASLGGGMQAPSQPPSAMKIKMYFNGLIAIRVPTDISFQALYDKICDR LKIPANEEIQLFYKDEPTGDK  
PSMISDNDLDFALQRNEKLLLYVEAV

SH3-N

Mg-XP363776 MKALRRSIKGDKDKQP-----ISIAPKSAVAIVPPKKVIRALYDYEAA--ST 46  
Fg-XP385437 MKALRRSIKGDKDKGP-----VTPKSAVAIVPPKKVIRALYDYEAR--SS 43  
An-XP664634 MKALRRSLKGEKDSKPHHHHQHHHQHHHLSITPKSAVAI LPPKKV I KALYDYQPEPGNT 60  
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Mg-XP363776 QELSF SRGDFHVI GREND TDWYEACN PALPDARGLVPVAF FQALGRTERDSAQSDTSVT 106  
Fg-XP385437 QELSF SRGDFHVI GREND DDWYEACN PALPDARGLVPVTF FQALGRTERDSAQSDGGQP 103  
An-XP664634 QELAFSKGDFHVISREDDSDWYEACNPLIPTARGLVPVTF FEVIGKTQRDSSGS----- 115  
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SH3-C

Mg-XP363776 RTSAPVPSKNPDHDSGYAETSAPVPSTPGFS-----NRDSKS--GKSG--AMVYGI 153  
Fg-XP385437 ----PSPKPNPDHDSGYSESPAMHPAPAVMSPTTNSAPQGHQRNSKSVGKTG--AMVYGI 157  
An-XP664634 ---IDLGKKKEPHDSGFADRATSSGSEFGSGSSKSYQSHPAFPRTSM MGKAGGGAMVYGV 172  
\* \*\*\*\* \* \* \* \*\*\*\*\*

Mg-XP363776 VMYDFQAERADELQAQAGEAIIVIAQSNPEWVFAKPIGRGGPGLIPVSFIEIRDMSANT 213  
Fg-XP385437 VMYDFAAERADELEAKAGEAIIVIAQSNPEWVFAKPIGRGGPGLIPVSFVEIRDMSDK 217  
An-XP664634 VQYDFQAERPDELDAKAGEAIIVIAQSNPEWVFAKPIGRGGPGLIPVSFIELRDMQSGQ 232  
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Mg-XP363776 PVPDPEGAVRRAGIPRVEEWKMAAEYKNSSITLGKFEVGGAPQQ--QAIEQGMDRMSLQP 272  
Fg-XP385437 AIQNPGD AIKRA GVPKVEEWKMAAEYKNSSITLGKFE GGGPGQPGQIEQGMERMSIQQ 277  
An-XP664634 AVADPLEAVRRAGVPKVEEWKMTAEYKNSSISLGKIETT GSMQS---VTSGMERMSVRQ 289  
\* \* \*\* \* \*\*\*\*\* \*\*\*\*\* \*\* \* \* \* \*\* \*\*\*

Mg-XP363776 --TDSR--SSQGQLNGKLQQ--AMQPQNA YPTP---KPSTQLYAPVQASIPRYCFAEEK 322  
Fg-XP385437 Q-QHSRQPSQNGTQSGYASQ--PRTSQPQPHQSQVQKPAAPLHAPLEARIPRYCFAEDK 334  
An-XP664634 SADHVS HMQNGHANAYHN RNASKAS IAPSTHQPPPHSQPLVAPIAASIPRYCFDNDK 349  
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PX

Mg-XP363776 YWFVIEAILEDGRKYELSRYYEDFYDFQIALLTEFP AEAGNTGTQKRTL PYMPGPVNYVT 382  
Fg-XP385437 YWFVIEAVLEDGRQWELSRYYEDFYDFQIALLTEFP AEAGNTGTQKRTL PYMPGPVNYVT 394  
An-XP664634 YWYIEVKMEDGRCWELSRYYHDFYDFQIALLTFE EAGNRG--KPRTL PFMPGPVAHV T 408  
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SRR

Mg-XP363776 DAITEGRHLNLDAYVKNLLAQPTYISRCNLVKQFFAPREGDYEMDANGE EDEYRMSGGSQ 442  
Fg-XP385437 DAITEGRHLNLDAYVKMNLNQPPI SRCNLV RQFFAPREGDYEIDPNDNENEYRLSQGSQ 454  
An-XP664634 DAISDGRRHNLDEYIKKLLAMPPI TRCALVRQLFAPRPGDFEIDPSAFGEDARFSGGSQ 468  
\*\*\* \*\* \*\*\*\*\* \* \* \* \* \* \*\* \* \* \*\*\*\*\* \* \* \* \* \* \*\* \* \*\* \*

Mg-XP363776 QSS--PDSPNGGISQSSRNLSGGYNNLAPSQQRGLSAQPPMRQASSLSQPSQAS 500  
Fg-XP385437 LSS--MESPAGG-----SQNNLNGSGYG---LAPS-----HPDMQTQASSLSQPSQAS 497  
An-XP664634 HSSGHELSPASRQSSQQNGPSESSSHSHSHSHSHQRSQTSSSIPNGKPPMVRQQSS 528

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PB1

Mg-XP363776 LSPGIPQAG---AFMKVKLSYNGDLIAIRVPSDIQFRELFDKITERLRIQPGEEVQLSYK 557  
Fg-XP385437 LGGGMQAPSQPPSAMKIKMYFNGDLIAIRVPTDISFQALYDKICDRLKIPANEEIQLFYK 557  
An-XP664634 LTQVSTSSG---GALKVKVNFQDDLIAIRVPSDINVQQLKEKLMDRLKIN--DEIVVQYK 583

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Mg-XP363776 DDITNGKLALMNDQDLIYAMQRNEKLLFYHRYNSNSFDR 595  
Fg-XP385437 DEPTGDKPSMISDNDLDFALQRNEKLLLYVEAV----- 590  
An-XP664634 DEASGAYVDLISDSLDLTAIQRNSKLTLYVGLA----- 616

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## Cdc24 ortholog

>Mg-Cdc24 :GenBank No. XP364852

MNQASRRQPLNAPRDTKLAGSVQSNQVQPLLPAPKPPDQSLPGPSRRSASENIGVGHPTCPVAFTPPNALAMAYAPLLRTNTTPIFPSS  
TGGVARLQGTMGSTGPAVGIPPLRASQLSGTTLHNSTTSLSSLASASTVVPANQGGQVAVTSNIINQKADASRSLYQICMSLKQRLAQPFGFEE  
YMSLMDQWEAEDPEGGIVESVWKLRLMGTPLIVIFNLLKPENPMSFDPDPAKAKMYIYKFAEQCKNELGIEDIFTISDLLKNDTTFVVKVTT  
VVNQVLDIAQTRGMLIQQQYPEDDMPDGSKMSYRDYIVRELVDTERKYVDLENLHDLKALTERGIVTGDVAYQIFGNDAILDQRRFL  
IRVETTSMPGEVQQWGSPPVAMEASFDPIYTPFIANQRKAALIAQSEFDKIKSIEHPVACDFNTLDGFLKPMQRLVKYPLLLKDLKKSSED  
KVKDDLSLGLIAAERTLQKANEAVDRDLDDALEDLKTRVDDWKNHQVDQFGLLHGVTVLTKSESERDYEYILFECILLCKEISSTKSK  
DKKDKTKSTGPKIRNKGAKLQKGRIFMTNVTEVLSFAKPGSYTVQIWWKGDPGVENFIKFKQNEEMKKWAAGLDQQRKASGSQSATSPDQPT  
AEFAWMRSQSAVENPYAQTQPEEEEEYFGAIPQSSQYQAMAGTMRPNSTASIRGRSQTGESSQSIASIARGPPRFPPLPQPPLSVQTLQ  
QGGNSPGFRPGDSYFSPIGESPVSSRTSTASNVFPGSAGYGSFKGVTGQPYPMWMDGPIVDQNRYTAPAMPAPRSRDPSPVNAYGMSGANGRN  
PRGSPMPVMASHAQASQSRSSYSTPDIQGGPPGMRRTPGGSQSNVPAVPGIPAHLHAAHERHDSNIPRSNTGSPALSLRNDLPMRSNTQ  
SPGVQRDRMLQGGGGYSGGTLAQFPMQPVYPRGGTPNPPGSGHTPAPLNLSDMGRTVSPPLGTGTPPPNTAGLMSPDQGGGIMPTQLKVKVN  
YDTSNYMTLVAAYNITYRSLVDRIDAKLARFTNSSISRGNLRVYRDEESDFVIVCEDEVQMAFTDGRNGDRDMYNGGVGEVELFCVGI

>Fg-Cdc24 :GenBank No. XP390087

MNHAPRASQLSGSTAYTGSSASLSSLATATTITPTNGGPVHATANIINQKADASRSLYQICISLKQRLAQPFGFVYLDLDELPTDVPDPLWNL  
RSGYPLLLIYNALRPNEELKVDDSSANEAKSKIAIFKVFQACMKELEIPSTQSFVITDLMGTDTSGFVKVTQVVNYVLDRAEERGYLMAQAP  
DVESNEPTGGQMYRDIHIRELVDTERKYVDLENLHDLKKTLEQQEIPGDTLHQIFFNINAILDQRRFLIRVETTSMPALNQRWGAPFVH  
YEDALIDIYQPFIANQRKAAQVANQVFDKIQRSSHPVAADYNTLDGFLKPMQRLVKYPLLLKDLNKKTEDDEVKMDLTTGCEAAERVLKANE  
AVNRDLLDEAVEDLTSRVEDWKSHEVQFGKLLHGVYVITGKTDQEKDYEYILFESILLCKEISSKSKDKKDKLRSGGPKARNKSAKLQL  
KGRIFMTNVTDIVSFTKPGSHSVQIWWKGDPGVENFIKFLNEETLKKWVNTLETQRKHNVPQRSTNSDTLSTDFAWTRDQVAGLENPYLKEND  
DEDEDIGPATAPAGFPVTHPMSLGPRTASSNNLRARAGTGESSASLAGMVRAPPPRFPPLPAPPGLSLQTQPNGAHSASAWAGDSYFSPVTE  
SPASTRTSTTSGMFSTPQYGFPKSATPNPQQWEDANGNRYTAPAMPAPRSRDPSPNPARNPRGPSLPAMSSSSQAALAAQQRNRSYSTPDING  
PGMPRTRQPSHGNIAPVPGIPQHLHPGHNPNSRDQTSRPNQDPTRAQTNSPGAQRERMHKPTGVSVGGSMNHFAQPVHPRSITPGGGNQILR  
VDAANAANSRTVSPALGTATMPPSANPLSPEIPLPTQLKVRVNCESGNYVTLVAFNITYQSLVDRIDAKLARFTTSSISKSMKLRYRDEDGD

YVAIEGDDDIQIAFMEWREGVRNMYSGGVGEIELFCVGDTA

>An-Cdc24: GenBank No. XP663196

MADTAGLNPGGPVAEDNIINRRGNEG IYQSCVNLKKRLAEVPGFEPYLREMEEDLAQGNSDPVASLWNYLRHGYPLLA IYNASDPGAPLEIDT
SKVPEARRPKAATFKFLQAAIQEMAFPPQECFLITDLYGENTIGFTKVIKMNVRVLDILEIQGQLKKPSDTAMAAPAAGRKLTKEHILKELLE
TERDYVHHLQNLQALKKELEDTGALTGDASHQIFLNLNLLDFSQRFLIRLEQHYPARPEEQNWGELFIQHEEAFRQYEPFIANQMRCDKTCQK
EWDKIQAAPRSPDLQMQVAQPATLNGFFVKPFQRLTKYPLMLSELRKQIEDPDLQADISRAIDS IQSVLDAANDAIDKEQLAAAFVELDERVDD
WKALKIETFGELLRFGTFTVIKNDNNKDSEREYHIYLFERILLCKDINPNKQKSRLVGGSKDKPNTSKGKPRVLKGRIMANVTDIVWLQKP
GSYRIQIFWKGDPGVVDNFIIRYQNETMRKWKYKDINTQREIQAEQRSARNTGTSDEFTYMKSLSNIPNPYQQEYDVEEQSTKEAAFFSEFPM
SRNASSTSLRTRSATGGSGSSGPPSTSRPRYPAMPDSTLSVHTQFPGGSMSPGERNGNSYFSPTESARSSSQSAGYPYNRQVTPVTPWGDNN
RYTAPALSRATSRDGSNSGYFNGAPPNGRSAQRPSLPPMSGNSQSSNASQMRMSASSPDIIHHNPESRRYMGVHTMQTVDNVPPPIPAHMAN
MKAPVNRSQNNSPTNQLSPLIRTNTSHAFHEPQYSDGRAAAPLSDQPTSPLSHEPEEPPMPTQLKAKVNFDENYVTLVISSNIGFRTLDRVDA
KLARFTNRSIGSKTVRLRYQDEDGDFVTIDSDEAVQLAFVEWKEQHREELARGQVGEIQLFCQPIEN

Mg-XP364852 MNQASRRQPGLNAPRDTKLAGSVQSNVDVQQLLPTPAPKPPDQSLPGPSRRSASENIGV 60
Fg-XP390087 -----
An-XP663196 -----

Mg-XP364852 GHPTCPVAFTPPNALAMAYAPLLRTNTPIFPSSTGGVARLQGTMGSTGPAVGIPPLRAS 120
Fg-XP390087 -----MNHAP-----RAS 8
An-XP663196 -----

Mg-XP364852 QLSGTTLHN-STTSLSSLASASTVPPAQNGGQVATSNIINQKADASRSLYQICMSLKQR 179
Fg-XP390087 QLSGSTAYTGSSASLSSLATATTITPT-NGGPVHATANIINQKADASRSLYQICISLKQR 67
An-XP663196 -----MADTAGLNP-----GPVAEDNIINRRGNEG--IYQSCVNLKKR 37
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CDC24

Mg-XP364852 LAQVPGFEEYMSLMDQWEAEDPEGGIVESVWKLRLMGTPLIVIFNLLKPENPMSFDPTP- 238
Fg-XP390087 LAQVPGFGPYLDELDPDVPD-----LWNLFRSGYPLLLIYNALRPNEELKVDSSS 120
An-XP663196 LAEVPGFEPYLREMEEDLAQGNSDPVASLWNYLRHGYPLLA IYNASDPGAPLEIDTSKV 97
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Mg-XP364852 --DAKKAKMYIYKFAEQCKNELGIED--IFTISDLLKNDTTGFVKVTTVVNQVLDIAQTR 294
Fg-XP390087 ANEAKKSKIAIFKQVQACMKELEIPSTQSFVITDLMGTDTSGFVKVTVVNYVLDRAEER 180
An-XP663196 P-EARRPKAATFKFLQAAIQEMAFPPQECFLITDLYGENTIGFTKVIKMNVRVLDILEIQ 156
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RhoGEF

Mg-XP364852 GMLIQQPYPEDDMPDSGKSKMSYRDYIVRELVDTERKYVQDLENLHDLKALKALTEGIVT 354
Fg-XP390087 GYLMQAQPDVESNEPTGG--QMTYRDHI IRELVDTERKYVQDLENLHDLKKTLEQQGEIP 238
An-XP663196 GQLKKP-SDTAMAAPAAG-RKLTKEHILKELLETERDYVHHLQNLQALKKELEDTGALT 214
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Mg-XP364852 GDVAYQIFGNIDAILDFQRRFLIRVETNSMPGEVQQWGSFPVAMEASFDPIYTPFIANQ 414
Fg-XP390087 GDTLHQIFFNINAAILDFQRRFLIRVETNSMPALNQRWGAPFVHYEDALIDIYQPFIANQ 298
An-XP663196 GDASHQIFLNLNLLDFSQRFLIRLEQHYPARPEEQNWGELFIQHEEAFR-QYEPFIANQ 273
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Mg-XP364852 RKAALIAQSEFDKIKSIE-----HPVACDFNTLDGFLLKPMQRLVKYPLLLKDLLKXSED 469  
Fg-XP390087 RKAQVANQVFDKIQRSS-----HPVAADYNTLDGFLLKPMQRLVKYPLLLKDLNKKTED 353  
An-XP663196 MRCDKTCQKEWDKIQAAAPRSPDLQQMVAQPATLNGFFVKPFQRLTKYPLMLSELRKQIED 333

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Mg-XP364852 DKVKDDLSLGIAAAERTLQKANEAVDRDLLDDALEDLKTRVDDWKNHQVDQFGSLLHGV 529  
Fg-XP390087 DEVKMDLTTGCEAAERVLKANEAVNRDLLDEAVEDLTSRVEDWKSHEQVQFGKLLHGV 413  
An-XP663196 PDLQADISRAIDSIQSVLDAANDAIDKEQLAAAFVELDERVDDWKALKIETFGELLRFGT 393

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Mg-XP364852 HTVLTG--KSESERDYEIYLFECILLCCKEISSSTKSKDKKDKTKSTGPKIRNKGAQLQK 587  
Fg-XP390087 YGVITG--KTDQEKDYEIYLFESILLCCKEISSSKSKDKKDKLRSRGGPKARNKSAKLQK 471  
An-XP663196 FTVIKNDNNKDSEREYHIYLFERILLCCCKDINPNKQKSRLVGGSKDKPNTSKGKPRVLK 453

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Mg-XP364852 GRIFMTNVTEVLSFAKPGSYTVQIWWKGDGP-VENFIIKFQNEEMKKWAAGLDQQRKAS 646  
Fg-XP390087 GRIFMTNVTDIVSFTKPGSHSVQIWWKGDGP-VENFIIKFLNEETLKKWNTLETQRKHN 530  
An-XP663196 GRIYMANVTDIVWLQKPGSYRIQIFWKGDGPVVDNFIIRYQNE<sup>DMRKWKDINTQREIQ</sup> 513

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Mg-XP364852 G-SQSATSPDQPTAEFAWMRSQSA-VENPYAQTQPEEEEE-YEFGAIPQQSQYQAMAGT 703  
Fg-XP390087 V-PRQSTNSD<sup>LSTDFAWTRDQVAGLE</sup>NPYLKENDEDEDIGPATAPAGFPVTHPMSL 589  
An-XP663196 AEQRSARNTGTSDEFTYMKSLSN-IPNPYQQEYDVEEQS-TKEAAFFSEFP----- 563

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Mg-XP364852 MPRMNSTASIRGRSQTGESSQSIASIARGPPPRFPLPQPPLSVQTQLQGG-NSPGFRP 762  
Fg-XP390087 GPRTASSNLRARAGTGESSASLAGMVRAPPRFPLPAPPGSLSLQTQPNGA-HSPSAWA 648  
An-XP663196 MSRNASTSLRTRSATGSGSSGPPLSTSRP-RYP-AMPDSTLSVHTQFPGGSMSPGERN 621

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Mg-XP364852 GDSYFSPIGESPVSRTSTASNVFPGSAGYGSFKGVTGQPYPGMWDGPIVDQNRYTAPAM 822  
Fg-XP390087 GDSYFSPVTESPASTRTSTTSGMFS-TPQYGFPKSAT--PNPQQWED--ANGNRYTAPAM 703  
An-XP663196 GNSYFSPT----ESARSSQS-----AGYPYNRQVT---PVTWGD---DNNRYTAPAL 665

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Mg-XP364852 PRAPSRDGPSPVNAYGMSGANGRNPRGSPVMASHSAQGASQSRSRSYSTPDIQGGP 882  
Fg-XP390087 PRAPSRDGPSPN-----PARNPRGSLPAMSSSSQAALAAQQRNRSYSTPDING--- 752  
An-XP663196 SRATSRDGSNSGYFNG-APPNGRSAQRPSLPPMSGNSQSSNSASQRMRSASSPDIHHNP 724

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Mg-XP364852 PGMRRTPGGSQSNVPAVPGIPAHLHAAHERHDSNIPRSNTGSPALSRLNDLPMRSNTQSP 942  
Fg-XP390087 PGMPTRQPSHGNIPAVPGIPQLHHPGHN---PNLSRDQTGSP----RNDQPTRAQTNSP 805  
An-XP663196 ESRRYMGVHTMQTVDNVPPIPAHMANMK--APVNRSQNSP---TNQSLPIRTNTS-- 777

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Mg-XP364852 GVQRDRMQGGGYSGGTQAQFPMQPVYPRGGTPNPPGSGHTPAPLNLSDMGRTVSPPL 1002  
Fg-XP390087 GAQRERMHKPTG-SVGGSMNHFAQPVHPRSITP---GGNQILRVDA<sup>AAAANSRTVSPAL</sup> 861  
An-XP663196 -----HAFHEPQYSDGRAAAPLSDQPTSPLSHEP----- 806

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PB1

Mg-XP364852 GTGTQPNTAGLMSPDQGGGIMPTQLKVKNYDTSNYMTLVAAYNITYRSLVDRIDAKL 1062  
Fg-XP390087 GTATMPPP-SANPLSPEIP---LPTQLKVRVNCESGNYVTLVVAFNITYQSLVDRIDAKL 917  
An-XP663196 ---EEEP-----FMPTQLKKAVNFD-ENYVTLVISSNIGFRTLDRVDAKL 848



MG-XP361856 -----  
Fg-XP386485 MSGSHNTHRSTPNKGRGAVPFANSPSGGGGSSNI PRPVLEP-----TPPAET 50  
An-XP663320 MS--STPTFRGTTSHR--TVGRGRLPDFEGGSSASHIPRPRPESSTITSHNPHTPSSDI 56

(CBS)n

MG-XP361856 ----MSAS----RQKQTKRDEAIRK MENDLAKKKHVTGRARHSRKAPPGTVLALKPSQA 52  
Fg-XP386485 G-SSFSAS----RQKQSKRDEAIRK KLENDLSKKKHLTSRARHSRKAPPGTVLALKPSQA 105  
An-XP663320 GSSTMSAASSRQRQNSKRDEAIRK LEADLNKKRSNPARANRTRKAPPGTVLALKPSSA 116  
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MG-XP361856 LQIKPGTTVAEAAQLMAAKREDCVLVTD DDDRIAGIFTAKDLAFRVVGAGLKATNVITAE 112  
Fg-XP386485 LQIKPNTTVSEAAQLMAAKREDCVLVTD DDDRIAGIFTAKDLAFRVVGAGAKASAVITAE 165  
An-XP663320 LQIKPSTTIAEAAQLMAAKREDCVLVTD DDDRIAGIFTAKDLAFRVVGAGLKARDITVSE 176  
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MG-XP361856 IMTKNPLCARDTDSATDALDMVRKGRHL PVDENQDISGILDITKCFYDAMEKLERAY 172  
Fg-XP386485 IMTKNPLCARDTDSATDALDMVRKGRHL PVDENQDISGVLDTKCFYDAMEKLERAY 225  
An-XP663320 IMTKNPLCARDTDSATDALDMVRKGRHL PVDENQDISGVLDTKCFYDAMEKLERAY 236  
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MG-XP361856 SSSRKL YDALEGVQSELGASQPQQI IQYVEALRTKMSGPTLESVLNGMPPTTVGVKTSVK 232  
Fg-XP386485 SSSRKL YDALEGVQSELGSTQPQQI IQYVEALRSKMSGPTLETVLNGVPPTTVSVRTSVR 285  
An-XP663320 SSSRKL YDALEGVQSELGSSQPQQI IQYVEALRSKMSGPTLESVLDGMPPTTVSVRTTVK 296  
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MG-XP361856 EAAQMMKENHTTAVLVQDQGQITGIFT SKDVVLRV IAPGLDPGNCVVVRVMT PHPDFAPM 292  
Fg-XP386485 EAAQLMKENRTTAVLVQDQGAIITGIFT SKDVVLRV IAPGLDPANCSVVVRVMT PHPDFAPM 345  
An-XP663320 EAAALMKEHHTALLVQDQGSITGIFT SKDIVLRV IAPGLDPATCSVVVRVMT PHPDFAPS 356  
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MG-XP361856 DMSIQ AALRKMHDGHYLNLPVMNDSGEI VGMVDVLKLT YATLEQINTMSSGDNEGPAWNK 352  
Fg-XP386485 DMTLQAALRKMHDGHYLNLPVMNDGGEI VGMVDVLKLT YATLDQINAMSNNDGPAWNK 405  
An-XP663320 DMSIQ AALRKMHDGHYLNLPVMNEGGEI VGMVDVLKLT YATLEQINSMSTQDDEGPAWNK 416  
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MG-XP361856 FWLSLDNETESMVSGDGHSHSHSHI HRSVMSPDLTRERL-D SVAPGDSASHAGVESPG 411  
Fg-XP386485 FWLSLDAETESMMSGEGSQAQ-HTNLGSR-LTSPDMVRDLN DTVAPGDSASHVGMESPP 463  
An-XP663320 FWLSMDHESMSVSGSHQPHRSIVNPE---SPKASF DAR-DSVLPNESASHHGGD--- 469  
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PB1

MG-XP361856 HSIVQHSPELPV-SEIPFPFKFKAPSGRVHRL QVIASHGVAA FITNVT SKLGGIEAVGG 470  
Fg-XP386485 RSILPDVLEHQLPPELPPFKFKAPSGRVHRM KIVATDGEAFVEA IASKLGAEADNIGG 523  
An-XP663320 ----EHSEFHGELSPFPFKFKAPSGRVH RVNILPAAGIAELVAQVTAKLGPEVEAVGG 524  
\* \*

MG-XP361856 APEVTE DQVRGGFALS YLDNEGDSV SITADQLLEAILL ARQSGRDKVDFVH DPEKPP 530  
Fg-XP386485 VPDVEDGKIVGSGFALSFLDDEGDS ISITADHDL LEAVILARQAHHDKVDFVH DPEKPP 583  
An-XP663320 AASCADGVLSNTGYALSYVDNEGDTVSI ITDQDLVD AVYIARHARRDKVDFVH DPAQPP 584  
\* \*

MG-XP361856 VAVAAPA AVPPAPSEPVSVPIPTPP ASSVARERRRRKS-PASDESDEEESEDDGSGSTLR 589  
Fg-XP386485 VSAADPRHP-----ATPSVSTGAGLRRERK WWPPEEEEEEDDDSEDEHPARR 631  
An-XP663320 VIPAP-----VEPAPVPEVKT-----PASDDQLSEE-----SPIP 616  
\* \*

MG-XP361856 RPRRHQRA-AAAQQEPLIAGVPNELLLPGAIIVTLAVVIVGVFTISRISNNR 640  
Fg-XP386485 KSRAATH-AHAHEEQIIAGVPNELILPGAIIVTLAVAIIVGVFTIARLTSR-- 680  
An-XP663320 KPRATQAYPAHPPEEQLIAGVPNDLLLPGAIIVTLAAVIAGVFILSRATSR-- 666  
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