```
CLUSTAL X (1.8) multiple sequence alignment

MG05280.4           ------------MSLKQEIETWVTALGRYDN--NEFEDALGEFDKISDT-SKILFNMGVI
NCU07850            ------------MSLKQEIETWVSALAQYDN--SEFDAALQEFEKIADT-SKILFNMGVI
EfNoxR              ------------MSLKLEIETWVAALARYDN--NEFDDALGEFDKICDT-SKILFNMGVI
FG04123.1           ------------MSLKQEIETWVAALGRYDN--NEFEEALNEFGKIGDT-SKILFNMGVI
AN6046              ------------MSLKQEIETWVQALEHFDN--QEYDLALRSFAAIADT-SKILFNCGVI
Hs NP_000424        ------------MSLVEAISLWNEGVLAADK--KDWKGALDAFSAVQDPHSRICFNIGCM
Bt AAC82463         ------------MSLAEAISLWNEGVLAADK--KDWKGALDAFTGVQDPHSRICFNVGCI
Mm NP_035007        ------------MSLAEAIRLWNEGVLAADK--KDWKGALEAFSEVQDPHSRICFNIGCV
Gg XP_422288        ------------MSLVETIRLWQEGVCAADG--KEWGAALKAFTAVQNPPAKICFNIGCT
Xt NP_001029119     ------------MALVEIMRLWSEGVAAAEN--EDWNGALKSFTSITDPRSKICFNIGCC
Dr XP_690944        ------------MSFVAPXRQWDEAVACVEQ--RDPDAALRIFLSIEEKNSKIAFNIGCL
Tr BAC79221         ------------MSFLDTLKQWDKASTVADR--QEFSEALEIFLSIEEPNSKIYFNIGCL
Hs AAI10841         -----------MASLGDLVRAWHLGAQAVDR--GDWARALHLFSGVPAPPARLCFNAGCV
Mm AAN75143         -----------MSSLGDQIRDWHRGVLAVAR--EDWDSALCFFSDVREPLARMYFNRGCV
Bt XP_601452        MTESSSTLHTACVPEGPQKKPGSRIVQANGDDYRKQDKRVSLVLSGHISARVLTLNLGQT
Gg XP_415555        ------------MAYRELLRRWHQAALAADG--GDWDAALETLCGIEEPPARICFN----
Xt NP_001005801     ------------MHYKEVVRRWHEGVVAAEG--KDYDAALRSFTAIEDPPSRIWFNVGGI
Dd AAO72634         -------------MLKQTIKKWNQSIERYES--GNVGEALTILTSIEQSTSKINYNIGVM

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NCU07850            HATLGQHEQAVECYQRAIRLDQYLAVAYFQQGVSNFLLGDFEEALANFNDTLLYLRGNQV
EfNoxR              HATLGEHEKAVECYQRAIRLDQYLAVAYFQQGVSNFLLGDFEEALANFNDTLLYLRGNTM
FG04123.1           HATLGEHEKAVESYQRAIRLDQYLAVAYFQQGVSNFLLGDFEEALANFNDTLLYLRGNAM
AN6046              YATLGEHEKAVECYQGAVGLDQYLAIAYFQEGVSNFLLGDFEEALANFNDTLLYLRGNTY
Hs NP_000424        YTILKNMTEAEKAFTRSINRDKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQL
Bt AAC82463         YTILGNLPEAEKAFTKSINRDKHLAVSYFQRGMLYYQMEKYDSAIKDLKEALTQLRGNQL
Mm NP_035007        NTILENLQAAEQAFTKSINRDKHSAVAYFQRGMLYYRMEKYDLAIKDLKEALTQLRGNQL
Gg XP_422288        HLVLGQLAEAEEAFTQSISCDKHLAVAYFQRGTVFYKRHNHEMALKDFKEALAQLRGNQL
Xt NP_001029119     HLVLGDLEKAEKAFTLTIERDMHLAVGYFQRGFVFFQRGKYSLALKDWTRAYTEMRGNQL
Dr XP_690944        CLNNSDLDEAEKAFDGSIGKDEHLAVAFFQRGVTFYKKEKFEESLLDFQQAFKQLRGNQL
Tr BAC79221         HLLNEDLKDAEKAFDSSICKDEHLAVAFFQRAITFYKMTRYEESLADFQQTLKELRGNQL
Hs AAI10841         HLLAGDPEAALRAFDQAVTKDTCMAVGFFQRGVANFQLARFQEALSDFWLALEQLRGHAA
Mm AAN75143         HLMAGDPEAALRAFDQAVTKDTCMAVGFLQRGVANFQLQRFQEAVSDFQLALAQLRDNAV
Bt XP_601452        QLNK---PPLSQAFDQAVTKDACLAVGFLQRGVANFQLERFMEALSDFQRTLAQLRDNTA
Gg XP_415555        ------------AFDETVMKDNSLAVGYFQRGFVCLQLEMYEEALSDYHMAFSHLRKNPF
Xt NP_001005801     YLLRGDLPRALEAYDKSLAQDPCLAVGYYQRGYLQFKLGRYEKALSDCHLALSNLRNNSF
Dd AAO72634         YIKSNNFRNAIEYFNRSVEQDKYLASSYYMRAIAHHMNGELNHAIVDYDETISKLRGHEY

MG05280.4           IDYAQLGLMFKLYSCEVLFNRGLCYIYLQQKDAGLQDLNYAVKEKVVEDHN-VIDDAIRE
NCU07850            IDYAQLGLLFKLYSCEVLFNRGLCYIYLQQIEAGMQDLSYAAKEKVVEDHN-VIDEAIKE
EfNoxR              IDYAQLGLLFKLYSCEVLFNRGLCYIYLQQQDVGMQDLTYAVKEKVVEDHN-VIDEAIRE
FG04123.1           IDYAQLGLLFKLYSCEVLFNRGLCYIYLQQMDAGMQDFSYAVKEKVVEDHN-VIDDAINE
AN6046              IDYEQLGLKFRLYSCEVLFNRGLCYIYLQQIGPGMQDLEYASKEKVTPDHD-VINDAIRE
Hs NP_000424        IDYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHS-KIDKAMEC
Bt AAC82463         IDYKILGLQFKLFACEVLYNIAFMYAKREEWKKAEEHLALAVSMKSEPRHS-KIDRAMES
Mm NP_035007        IDYKILGLQFKLFACEVLYNIALMHAKKEEWKKAEEQLALATNMKSEPRHS-KIDKAMES
Gg XP_422288        IDYKILGLRYRLFACEILYNIALVYATMENWKKAEEHLTLAMSSKSEPQHN-KIDRAMEA
Xt NP_001029119     IDYKILGLIFKLYSCEILHNIALTHAKEGKWAKAEESILLALSQKVELRHNTKLEKAMED
Dr XP_690944        IDYTPLGLRYKLYACEVLHNIGLAQAQLGKWEKAQENLLTALSLRADAKFS-HIDHALDA
Tr BAC79221         IDYGALGLRYKLNACEVLHNIALTEAQMGHWEKAQESLVKALDYRTESKLG-IIDNALQA
Hs AAI10841         IDYTQLGLRFKLQAWEVLHNVASAQCQLGLWTEAASSLREAMSKWPEGSLN-GLDSALDQ
Mm AAN75143         IDYTQLGLNFKLQAWEVLYNMASAQCQAGLWTKAANTLVEAISKWPEGAQD-ILDIAMDK
Bt XP_601452        IDYTQLGLRFKLQAWEVLFNMAAVQSQLGLWAEAACSLGDAISKGPEGARN-GLDVALGQ
Gg XP_415555        IDYKQLGLRHILYAWEVLYSTAATQCRLQQWQEARDTLEKAVVWRPEGRSA-TLALALER
Xt NP_001005801     IDYKQLGLRHVLFSWEAQYNMAAVLCSLGRWESAEEKLKETLQG--DGRNA-KLDWALDQ
Dd AAO72634         IDYKQLGLDHKLLLAEVLFNKALALGRAGSSVALQATQCFSQPSDSQEFKN-QCKKIQDG

MG05280.4           EAEG--YTVFSIPVGVVYRPNDAKVRNLKTKDYLGKARLVAASDRSNAFTGFAGSEIKNS
NCU07850            NAEG--YTVFSIPVGVVYRPNEAKVRNLKTKDYLGKARLVATSDANNAFTGFAGAEIKNA
EfNoxR              EAEG--YTVFSIPVGVVYRPNEAKVRNLKTKDYLGKARLVAASDRSNAFTGFTGSEIKNA
FG04123.1           QAEG--YTVFSIPVGVVYRPNEAKVRNLKTKDYLGKARLVAASDRANAFTGFAGSEIKNA
AN6046              RAEG--YTVFSIPVGVVYRPNEAKVKNLKTKDYLGKSRVIAANRLS---TPAD-------
Hs NP_000424        VWKQKLYEPVVIPVGRLFRPNERQVAQLAKKDYLGKATVVASVVDQDSFSGFAPLQPQAA
Bt AAC82463         VWKQKLYEPVVIPVGRLFRPNEKQVAQLVKKDYLGKATVVASVVDQDSFSGFAPLQPQAA
Mm NP_035007        IWKQKLFEPVVIPVGRLFRPNERQVAQLAKKDYLGKATVVASVVHQDNFSGFAPLQPQSA
Gg XP_422288        ILKQKLYEPVAIPTGKLFRPNEKQVAQLEKKDYLGKAMVVASVVDKDSFSGFAPLQPQAS
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Xt NP_001029119       ILKEKVFAAVKIPKGRIFQPNERLVEQLEKKDYLGKALVVASVVDKDSFSGFAPLQPQAS
Dr XP_690944          ILKHKLFPLVEVRARLLFKPNKKYVAELEKRDYLGKAKVVASVVPADEFSGFAPLQPQID
Tr BAC79221           TLKQKLFKLIGFPSKVLFKPNKHYVAELEKKDYLGKAKVVASVVPQDEFSGFAPLMPQVE
Hs AAI10841           VQRRGSLPPRQVPRGEVFRPHRWHLKHLEPVDFLGKAKVVASAIPDDQGWGVRPQQP---
Mm AAN75143           VQKQVPLQLQQVPKGEVFQPPRRYLKHLEPMDFLGKAKVVASVIPDDH--NAQPQQ----
Bt XP_601452          VQKQVPLQPRQVPRGEVFRPHRRHVEHLEPVDFLGKAKVLASALPTDS-HGVAPPQPQAL
Gg XP_415555          VQNHQFLEPMQVPPGEFFRPRKKEVEQLDSKDFLGKPKVISSIIPNDEYIGFEPLRPQKQ
Xt NP_001005801       VQRRSLLQPMSVPEGEFFRPRKQEVEQLNSVDFLGKPTVISSVVPNDQYSGFEPLRPQQP
Dd AAO72634           SQLN--FSTRPIPLSLLFKPPK—VSDAPQKQRSATTSSIQSSSPSTPMSSSPPSYILKG

MG05280.4             GKADVKD-DRPSDNISFAATNLVKPGLQSRARQQSEPPNSRNVFPPTPPPENDKQTMSRG
NCU07850              GKLEVKD-DRPVESLSFAATNLVKPGLQSR-RQQSEPPTNRSMFPPTPPPENEKSQMSRG
EfNoxR                GKMEVKD-DRPADNISFAATNLVKPGIQSR-RQQPEPSANRNVFPPTPPPDNDRP--SRG
FG04123.1             GKLEVKD-DRPADNISFAATNLVKPGLSSR-RQQSEPPNGRNVFPPTPPPENERP--SRA
AN6046                ----TS--QRSVDSVPFATSHLVQKNLTSRSRQQSEPPMHRNLFPPTPPPDADKASLSST
Hs NP_000424          EPPPRPK-TPEIFRALEGEAHRVLFGFVPETKEELQVMPGNIVFVLKKGNDNWATVMFNG
Bt AAC82463           EPPPRPK-TPEIFRALEGEAHRVLFGFVPETPEELQVMPGNIVFVLKKGNDNWATVMFNG
Mm NP_035007          EPPPRPK-TPEIFRALEGEAHRVLFGFVPETPEELQVMPGNIVFVLKKGSDNWATVMFNG
Gg XP_422288          GPPPRPK-TPEILRALEGQPHRVLYEFIPETAEELQVLPGNIVFVLKKEKDNWATVMFNG
Xt NP_001029119       NPPPRPK-TPEILRTLQGEPHRVLFEFNPETAEEMQVLPGNIVFVLKKGDDNWATVVFNG
Dr XP_690944          NVPSIPK-VPEVLRVLEGEPHTVLYEFVPETKEELAVLPGNIVFVLHRGTDNWASVVFNE
Tr BAC79221           SGQTFSKPEPELLRALEGEPHTVLYKFVPETSDELAVVPGNVVFVLQKGADNWASVVFNE
Hs AAI10841           ------Q---GPGANHDARSLIMDSPRAGTHQGPLDAETEVGADRCTSTAY-----QEQR
Mm AAN75143           ----------RSQAEHAG------------HQ-----PSSSMCKRVLSTTG-----GHTS
Bt XP_601452          ----DVR---GEARPRAAARARDTAPGRADTPCSPRTPTDTEMEVSSGQAR-----QHDR
Gg XP_415555          GFYEPSA---DSVRDRESGYYRVLSHYYPEGTEKLAVKASSLVFVLARGANGWATAIHDG
Xt NP_001005801       GFYEPCR---DAMQCREAGYHRVVVHYYPENSNEVAVKANSVLFVLNKDGD-WATAIHDG
Dd AAO72634           PSSPPSSSSPSSSSPSLSSSSSPKLPPTPKPSFGSSPPPSSSSSSSSSSSSSSSSISPLT

MG05280.4             AS---VRN--GPKPMPAKLNIDKARPNDRYERTTSP-----QEQRSRAPSRAPSNAPSR-
NCU07850              AS---VRN--GPKPMPARLNLDKVRPSDRYEKTSP-------EEPSRRPSRAASATPSR-
EfNoxR                SS---VRN--GSRPMPAKLTIQTQDSNRKYEKAPS-------PEEVRATRSAASSTPSQ-
FG04123.1             AS---VRN---QKPQLAKLNIQQAEPNRRYEKAAS-------PADARRP-MPRSASTTR-
AN6046                GSNGTVRAQPGKAQRPPKLDLDRPGAQPAGRSTTDL-----TAPEKPRLGTIRTASEPR-
Hs NP_000424          QK---GLV---PCNYLEPVELRIHPQQQP--QEE-------SSPQSDIPAPPSSKAPGR-
Bt AAC82463           QK---GLV---PCNYLEPVELRIHPQQQP--QEE-------TSLESDIPAPPSSSAPGR-
Mm NP_035007          QK---GLV---PCNYLEPVELRIHPQSQP--QED-------TSPESDIPPPPNSSPPGR-
Gg XP_422288          KK---GIV---PCNFLEPMEL--QHKLHV--QDE-------APLEPDIPEPPSSTAPRP-
Xt NP_001029119       KK---GIV---PCNYLEPVELRFQSAQQTGVQSEELDSPTNRPQQSDVPAPPDATPPQL-
Dr XP_690944          KR---GLV---PYNFLEPLDIVTMTSKPTEALNE----------NDDIPAPPRRAAPS--
Tr BAC79221           RR---GLV---PYNYLERLEIT-MASKQNNVQSR----------PPSRQPPTRPERKSG-
Hs AAI10841           PQ---VEQ---VGKQA--------------------------PLSPGLPAMGGPGPGP--
Mm AAN75143           P-----------------------------------------GLYDSLLASRRPGPGP--
Bt XP_601452          GT---LVT---HKSAHGEHA-------------G-------QQLPSGLLAAGGPSPGS--
Gg XP_415555          QK---LHI---PTSLLEPAS--KMDKWKI--GDG-------IPLPPAQVPPSRLHVKQ--
Xt NP_001005801       QK---ILI---PTSFLEPTNPPKADIKKM--NNG-------IPLPPMKTPPTRPNVRPGM
Dd AAO72634           NKTLPPKPPPLPSKKLPSRPISCVIQDVKITLKVFYKDR--RLIQIPVPCNLSTFIQKIE

MG05280.4             -----------GFSTRE------------------------------------PPRRRPR
NCU07850              -----------GFSQREQ--P-------------------------------PPPRMRRS
EfNoxR                -----------GFSRRD-----------------------------------HPPIQRRP
FG04123.1             -----------TPLQRE-----------------------------------PPPLQLRP
AN6046                -----------GQSRQPR--G-------------------------------YAPERHVR
Hs NP_000424          ------------PQLSP------------------------------------GQKQKEE
Bt AAC82463           ------------PQLSP------------------------------------GQKGKEE
Mm NP_035007          ------------LQLSP------------------------------------GHKQKE-
Gg XP_422288          ------------RRPAPDCVPV------------------------------TSTQQREA
Xt NP_001029119       ------------LKNTKD-----------------------------------KQDFSAS
Dr XP_690944          ------------RPVAP------------------------------------EGLKTVN
Tr BAC79221           ------------LPPCA------------------------------------DDRRNTQ
Hs AAI10841           ------------CEDPAG----------------------------------AGGAGAGG
Mm AAN75143           ------------SEVSSG----------------------------------SEGAATKD
Bt XP_601452          ------------SSEAAS----------------------------------TGGAAPGR
Gg XP_415555          ------------TPDSPG----------------------------------EENVSAND
Xt NP_001005801       EPLTGVQAGAPVPPQPAGGAAEPYKIKALPVGMEPIVEVAVPVQRSVPTHKETGNVPLGN
Dd AAO72634           LKFEITISDKFSLSFQLD-----------------------------------GEENEIN

MG05280.4             SQ------------------------EEEEGYL--------------DDVYDNYGGGIGG
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NCU07850            QQ------------------------EEEDSYP--------------SELYDMYGG--PG
EfNoxR              TRR---------------------IDEMEEADA--------------GDLYDMYQGS-GS
FG04123.1           KQ-----------------------IPEETGSP--------------EDVYAMYSAT--D
AN6046              SSD---------------------GYGHRRGAS--------------DHGFGVSNGHSDD
Hs NP_000424        PK------------------------EVKLSVP-------------MPYTLKVHYKYTVV
Bt AAC82463         PKQ-----------------------EIKLSVP-------------KSYTLKVHYKYTVV
Mm NP_035007        PK------------------------ELKLSVP-------------MPYMLKVHYKYTVV
Gg XP_422288        SKPNSLCCE----SREKPDTPIHHLQESEPDIP-------------KPYVLKVHYKYTVA
Xt NP_001029119     SKQ---------------K-----LQETEAVAV-------------ASYLVKVYYKYTVA
Dr XP_690944        AK------------------------VQEFSG----------------CVVKVHFQFTIA
Tr BAC79221         MK------------------------ESELADD-------------S-CVVKVRYTFTFA
Hs AAI10841         SEP--------------------------------------------LVTVTVQCAFTVA
Mm AAN75143         PES--------------------------------------------LVTVTVQCHFTVP
Bt XP_601452        SES--------------------------------------------LATVTVQCALTLS
Gg XP_415555        SGSQVDFES---------------PLTHREASS----------STDRPAVLRVRCECTVV
Xt NP_001005801     DASLVEDAGRTIIKPKGESAPEPGPFPTRQTGPDNGPMATPVPTDDDKLVLSVHAEFTVN
Dd AAO72634         SQVQLDKMICMEINEINVKDIIPSPSPSPSPSPDKTN-------NSTSSYSSSSSSSSSS

MG05280.4           GGGSIRGSR------SQRRAPQQRYIEEEDE---GSDFDDGSFDEGDFEMVSNRRPGTNS
NCU07850            PNRNSRGQR------SNRSAP--RYIQEEDD---ESDYD-VSFDEAEFEMVSGRRPSLST
EfNoxR              NRRTSRDSRRP----SVRSRTQPRYYDD-DD---GSDYDDGSLDGAEFEMVSNNRRRQGS
FG04123.1           GYRNSRGSAG-----SRRLRPQ-QYSEE-ED---ASDYE-GTINENDFEMIGQRR-GPGS
AN6046              AYGMYGEARAMTLANGGRPFQQQGYIDEEEEYG-SSPCDEDLVPDASFELMGSRP-RARS
Hs NP_000424        MKTQPGLPYS-----QVRDMVSKKLELRLEHTK--LSYRPRDSNE--LVPLSEDSMKDAW
Bt AAC82463         METQFRLPYS-----QVRDMVAKKLDLLPEHTK--LSYRRQDSNE--LVPLSEFSMKDAW
Mm NP_035007        METRLGLPYS-----QLRNMVSKKLALSPEHTK--LSYRRRDSHE--LLLLSEESMKDAW
Gg XP_422288        MQVKPDLSYK-----ELLGLVCDKLELQPEHTM--LRYKSAASGE--LVPLSAQNLEEAW
Xt NP_001029119     IQISSKLPFA-----DLLTLISSKLQLLPSRMK--LSFKEDQDD----VLLNEENTEKAW
Dr XP_690944        IAIAHGQPYG-----VILQMISSKLKLPASTLT--LRYAKEGSAE--RVIIEDSEMEAVW
Tr BAC79221         ILVPRGSSYA-----TLAEKISEKLSVPANAIV--LSLSSEATEQ--NVIDGGTDMEGVW
Hs AAI10841         LRARRGADLS-----SLRALLGQALPHQAQLGQ--LSYLAPGEDGHWVPIPEEESLQRAW
Mm AAN75143         LKVPRGTGLS-----SFQTLLAQALLHQTQTGQ--LSYKAPGEERSWIPISTEESLQSIW
Bt XP_601452        LTAPRGADLS-----SLRALMSQALPPHAQRAQ--LSYQDPSEDGRWVPLSGEEALQRAW
Gg XP_415555        VRAGEVPSVP-----ALRALLRERFGQQAERGR--LSYRHL-DGKELGAVSGEEDLEKMW
Xt NP_001005801     MTVSKAITYP-----ELQGALREELRKHGEQMANHLSYRDP-ESRGLTPVTGSKDWQEVL
Dd AAO72634         SSSSSSSSYDNKPKSSFIPKTTTRPILPPTTTTTTSTSNNFNRNATLPKKFGSTPSSPSF

MG05280.4           MSSSS-RG---------QSRRPDIRNIKVKVHYT--------A-TDDTRMILIG------
NCU07850            VRSSGGRG---------SSRRPELRSIRVKVH------------AGDVRYIMVG------
EfNoxR              RSES--RA---------TSRRPEIRKIRVKVH------------AGDVRYIMIG------
FG04123.1           VSGS--R----------NSRRTEVTKIRVKVH------------ADEVKLIMIT------
AN6046              CSRGPARG---------YSRRPEVRRFRVKVHS-----------FEDTRYILIP------
Hs NP_000424        GQVKN--------------YCLTLWCENTVGDQGFPDEPKESEKADANNQTTEPQLKKGS
Bt AAC82463         AQVKN--------------YCLTLWCENTVGDQGFPDEPEESKKSDANNQTTEPELKEGS
Mm NP_035007        GQVKN--------------YCLTLWCEHTVGDQGLIDEPIQRENSDASKQTTEPQPKEGT
Gg XP_422288        SHSKD--------------QCLTVWCDCTEGE-GFLPDSKPEEPQQAAAETG-P-----T
Xt NP_001029119     SLATD--------------NCLKLKCTEVQVEEPIIKVEEVQVQQEIPASDK-----AET
Dr XP_690944        NSAKD--------------GRLTLWCSVTEG--------------KSASHAK--------
Tr BAC79221         SRVSG--------------RCITLWCRLAQTN-----E-------RVQKESS--------
Hs AAI10841         QDAAACP------------RGLQLQCRG-----------------AGGRPVLYQ------
Mm AAN75143         RNVPVGP------------GGLQLQCQG-----------------VWGRPVLYQ------
Bt XP_601452        RDAAG-P------------GGLQLQCRG-----------------VGGRPVLYQ------
Gg XP_415555        QQLTD--------------GRITLCCQDSDS--------------HSGRPILYR------
Xt NP_001005801     KLSRA--------------NQVTLCCKETTL--------------CAGRPVLYR------
Dd AAO72634         SSPSSSSSGGGGGPPIPTRGSPSISLLKQQNQTQSIN--IPPKVPTSSRPKMTQS-----

MG05280.4           MACEYSDFVEKIRNKFKIASRRSVRIKVRDDED-GGTMITMGDQDDLDMAIMASKSMARR
NCU07850            TAIEFPDFEEKIRSKFGIRRR--IKIKIKDDDSPDGDMITVGDQDDLDMLIQTVKQNARK
EfNoxR              AAIEYPDFVDRIKDKFGMKRR--FKIKIPDEDMPDGDMITVGDQDDLEMAIQSSTSLAKR
FG04123.1           PDTRFETLSDKVRDKFNIKRR--FKIKVKDDDMPNGDMITVGDQDDLEMVIDSVKDEARK
AN6046              PTIEFAEFETRIREKFGFQMA--LKIKMQDE----GDMITMVDQEDLDLLLMASREIARR
Hs NP_000424        QVEALFSYEATQPEDLEFQEGDIILVLSKVN----EEWLEGECKGKVGIFPKVFVEDCAT
Bt AAC82463         KVVALFSYEATQPEDLEFLEGDVILVISTVN----EQWLEGECKGKVGIFPKAFVEQHPT
Mm NP_035007        QVVAIFSYEAAQPEDLEFVEGDVILVLSHVN----EEWLEGECKGKVGIFPKAFVEGCAA
Gg XP_422288        QVVAQYSYEATQPEDLEFQAGDVILVLSKG----------GKRAEKVCIECKGFTPVR--
Xt NP_001029119     YVTALFEYEATQPEDLPFCKGDIIKILSHVS----EDWWEGECQGRMGIFPKVFTEEIQ-
Dr XP_690944        -VVALYSYESSTPEDLEFKQGNVITVLSKVN----DEWLEGQCNGKIGIFPSSFVEPLNG
Tr BAC79221         -LLALHSYDSSNPEDLSFHQGDRITLLSKVN----QDWLEGEFNGNTGIFPAAFVEEVPA
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Hs AAI10841         -VVAQHSYSAQGPEDLGFRQGDTVDVLCEVD----QAWLEGHRDGRIGIFPKCFVVPAGP
Mm AAN75143         -VVAQYNYRAQRPEDLDFHQGDTVDVLCEVD----EAWLEGHRDGCVGIFPKCFVVPAGA
Bt XP_601452        -VVAQHVYSAQRPEDLALQPGDTVDVLCEVD----QAWLEGHCDGHIGIFPKSFTVPAAR
Gg XP_415555        -MLAQHSYSAQGPGDLEFSKGDVLDILSEVN----EDWLEGHCNGKTGIFPKCFATQTSC
Xt NP_001005801     -MRAQYDYLAQGPADLSFQQGDLISILSEVN----GEWLEGHCHRGIGIFPKCFAQRAEG
Dd AAO72634         HSPPSSSPLSSYSTSFQSVSSPSLSSSYNGSTSSYGGFSSSRPPPTPYPYQVLYTDSNEK

MG05280.4           ERSDNGKMEVWIQDA---
NCU07850            QRLETGKMEVWVQEI---
EfNoxR              QRQDVAKMEIWIFEL---
FG04123.1           QRTETGKMEIWILQL---
AN6046              EGSEMGKMEIWVEERRMI
Hs NP_000424        TDLESTRREV--------
Bt AAC82463         TDLESTPGRV--------
Mm NP_035007        KNLEGIPREV--------
Gg XP_422288        ------------------
Xt NP_001029119     ------------------
Dr XP_690944        DPHTSAE-----------
Tr BAC79221         NG----------------
Hs AAI10841         RMSGAPGRLPRSQQGDQP
Mm AAN75143         YVEAMLVLGP--QPGDQN
Bt XP_601452        RA----------------
Gg XP_415555        AAFP--------------
Xt NP_001005801     I-----------------
Dd AAO72634         YYLNTETNETFWELP---
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Supplemental Figure 3. Alignment of vertebrate p67^{phox} and Nox activator 1 (NOXA1), and fungal NoxR proteins used for phylogenetic analysis (Figure 1C).