

Additional File 3

Alignment of characterized domains of Nox regulatory subunits.

We used the following naming: Hs (*H. sapiens*), Cf (*C. familliaris*), Rn (*R. norvegicus*), Mm (*M. musculus*), Gg (*G. gallus*), Xt (*X. tropicalis*), Dr (*D. rerio*), Tr (*T. rubripes*), Tn (*T. nigroviridis*), Ol (*O. latipes*), Ci (*C. intestinalis*), Sp (*S. purpuratus*), Dd (*D. discoideum*), An (*A. nidulans*), Mg (*M. grisea*), Fg (*F. graminearum*).

PX and tandem SH3 domains of Nox organizers (vertebrate p47phox, vertebrate NOXO1, *C. intestinalis* and *S. purpuratus* p47phox-like proteins).

Gray boxes indicate the amino acid sequences corresponding to the PX (residues 3-132), bis-SH3 (residues 151-285) domains of human p47phox.

	PX-domain	
Hs-p47phox	-----MGDTFIRHIALLGFEKRFVPSQHY-----VYMFLVKWQDLSEKV	39
Cf-p47phox	-----MGDTFIRHIALLGFEKRFVPSQHY-----VYMFLVKWHDLSEKV	39
Mm-p47phox	-----MGDTFIRHIALLGFEKRFVPSQHY-----VYMFLVKWQDLSEKV	39
Rn-p47phox	-----MGDTFIRHIALLGFEKRFVPSQHY-----VYMFLVKWQDLSEKV	39
Gg-p47phox	-----VGDTFIRHIELLRYEKRFVPSQHY-----VYMFLVKWQDLSEKL	39
Xt-p47phox	-----MTEPHIRHIQLLGFEKRFVPSQHY-----VYMFVVKWQDLTEKL	39
Tn-p47phox	-----MADTYVRHVQLLGFEKRFVPSQHY-----VYMLLVKWSDLTEKL	39
Tr-p47phox	-----MAETYVRHVQLLGFEKRFVPSQHY-----VYMLLVKWSDLTEKL	39
Ol-p47phox	-----MEDVYVRHVQLLGFEKRFVPSQHY-----VYMLLVKWSDLTEKL	39
Dr-p47phox	-----MAETYVRHVQLLGFEKRFVPSQHY-----VYMLLVKWSDLTEKL	39
Ci-p47phox	-----MVNRTLKSVKVIDIEKRRLPSKHY-----VYLIEIKWSDGSLCT	39
Sp-p47phox	-----MGKRTVVNANVTDIEKRREPTKHY-----VYIIHVTWSDGSVNV	39
Dr-NOXO1	-----LIKLFIRRVEHRNMDINHSSPPQ-----LYMTTVLWSDGNEIT	39
Ol-NOXO1	-----PADTHMSLSVSAPGSDKLLPSDDRKY-----TFMVSGIWSDGSEII	42
Tn-NOXO1	METQRYPISARLVGVLHKEKSKVGAHKSQVVLFHARFNQQLCPLQMYMTSVLWSDHNEIV	60
Gg-NOXO1	-----YMMFVSWSDQNNIL	14
Xt-NOXO1	-----WSDHNEIL	8
Hs-NOXO1	MAGPRYPVSVQGAALVQIKRLQT-----FAFSVRWSDGSDTF	37
Cf-NOXO1	MAGSRHPVSVRAAALVQTGRLQT-----FAFSVCWSDGSDTF	37
Mm-NOXO1	MASPRHPVSAHAVALVQMDRLQT-----FAFSVCWSDNSDTF	37

Rn-NOX01 MASPRHPVSAHAVALVQMERLQT-----FAFSVCWSDNSDTF 37
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Hs-p47phox VYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAKP-----WFDGQRA---AENRQ 91
 Cf-p47phox VYRRFTEIYEFHKMLKEMFPIEAGDINPENRIIPHLPAPR-----WFDGQRA---AESRQ 91
 Mm-p47phox VYRKFTIYEFHKMLKEMFPIEAGEIHTENRVIIPHLPAPR-----WFDGQRA---AESRQ 91
 Rn-p47phox VYRKFTIYEFHKMLKEMFPIEAGEIHTENRVIIPHLPAPR-----WYDGQRA---AESRQ 91
 Gg-p47phox IYRRFTDIYEFHKALKEMFPIESGDINAENRIIPHLPAKP-----WFDGQRS---TQSRQ 91
 Xt-p47phox VYRKFTIYEFHKSLEKEMFPIEAGDISKEHRTIPHLPAKP-----WFDGLRS---TENRQ 91
 Tn-p47phox IYRTYPEIYTFHKALKEMFPIEAGKIEKRDRIPSLPAPP-----WLDQSKS---TETRQ 91
 Tr-p47phox IYRTYPEIYTFHKSLEKEMFPIEAGKIEKRDRIPSLPAPP-----WLDQSKS---TETRQ 91
 Ol-p47phox IYRSYPEIHTFHKSLKDMFPIEAGQIEAKDRIPKLPAPR-----WLESQKS---RENK 91
 Dr-p47phox VYRRYPEVHTLHKLKEMFPIEAGDIDEKDRIPKLPAPR-----WLDNQKT---TETRQ 91
 Ci-p47phox VGRRFSAFFMMHMTLLEKFPLEGGQKDPSSRRILPFLPGKI-----LFKRSHTRDVTLKRL 94
 Sp-p47phox VYRRYSTFFDFQNKLLSKFPEEAGANNPSSRCIPFLPGKK-----LFGRSHIREVALKRL 94
 Dr-NOX01 VYRSLEDFKKMHRQLKKKFPSPN-PFKRSARIVPEFKGN-----KWSGSK-SVLRM 88
 Ol-NOX01 IYRSFKDFKFFHDQLKKQFPNLT-PFRKEDRMLPKFNGKAR----RSLKQKGSKSVKQM 97
 Tn-NOX01 VYRTFQDFRKMH-KLKRSGKKK-PTR-----SLVRL 90
 Gg-NOX01 IYRTLEEFKRFHKLKRFPIESGSLRRSDRTIPRFKDIING----KQKSGKINRSLERL 70
 Xt-NOX01 IYRTFEDFKLNRQLKKKFPLEAGLFRKSDNLPKLDV-----IFRKNRTNRFIERL 63
 Hs-NOX01 VRRSWDEFRLKKTLEKTFVEAGLLRRSDRVLPKL-----DAPLLGRVGRTRGLARL 92
 Cf-NOX01 VRRSWAEFKELHKLKEAFPVEAGLLRRSDRILPKLP-----DTSLLVRGGRTGRGLARL 92
 Mm-NOX01 VRRSWDEFRLQKTLKTFVEAGLLRRSEQVLPKLP-----DAPLLTRRGHTGRGLVRL 92
 Rn-NOX01 ARRSWEEFRQLQKTLKIFVVEAGLLQRSERVLKLPQACRNAPLLTRRGHTGRGLLRL 97
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Hs-p47phox GTLTEYCGTLMSPKISRCPHLLDFFKVRPDDLKLPD--NQTKKPETYLMPKD-GKS- 147
 Cf-p47phox GTLTEYNTLMGLPVKISRCQQLDFFRVPRPDDLKLPD--SQVKKPETYLVPKD-GKS- 147
 Mm-p47phox GTLTEYFNGLMGLPVKISRCPHLLDFFKVRPDDLKLPD--SQAKKPETYLVPKD-GKN- 147
 Rn-p47phox GTLTEYFNGLMGLPMKISRCPHLLNFFKVRPDDLKLPD--SQVKKPETYLTAKD-GKN- 147
 Gg-p47phox GTLAEYCYTLVNLPHKISRCRHVVSFFEVPRPDDMNPTD--SQIRKPEVFLPKD-AKK- 147
 Xt-p47phox VTLSDYFSSLLSLPPKISRCPHVNLFFQVRSDDVNPVANN-TNGRKPETFLKVDATAK- 149
 Tn-p47phox TSLSDYCALVNLPPHISRCRTHLTSLFKVRPEDENPAAP--NTLKRNETFVVSRLDARG- 148
 Tr-p47phox TTLSDYCHSLVNLPPHISRCRTHLTGFFTVRPEDENPPSP--NILKRNETFVVSRLDARG- 148
 Ol-p47phox TTLVDYCHLLVSLPPHISRCRCKELSNFFKVRPEDENPPAP--NITKRNETFVVSKEPAQG- 148
 Dr-p47phox ATLAEYCRSLLNLPANISRCQLIRDFKMRPEDETPPAP--HPYKRNETFIMSTNRVRSN 149
 Ci-p47phox GSISEYCESLLLLPEHISQCDTILRFFETSSSDIARDTK-----EKT-QSTAVSQ 143
 Sp-p47phox SPIDEYCTALVKLPGKISDSKEVINFFTPPEDVSPSP-----DGGGESTRGRA 144
 Dr-NOX01 KALEEYCGQLLKSDAQVCRSSELIQFLLPKAHDNLADFAKNCIVIMPSDVTLGSSKA--E 146
 Ol-NOX01 EFLESYCDKLLKCDPNVTSSEVTRFFTPKDQDLQPDFTKNSSLLLVYGR-PGALRS--S 154
 Tn-NOX01 KFLQKYNELLSCEPRVQSADLIQFFHPNAQDLEPEFSKNRQEEVKAEGHGSVG---- 146
 Gg-NOX01 KLETYTQELLKVDAKISQGEDVIQFFKAQTQDLDCFPEDSVVIMPSEIGGEKKKEVQQ 130
 Xt-NOX01 RLLEKYSQELLRTDQKISQCDLVLFKFFTPSNNDLNPKEPENSVMMSDSKDKQKQKPL 123
 Hs-NOX01 QLLETYSRRLATAERVARSPITGFFAPQPLDLEPALPPGSRVILPTPEEQPLSRA--- 149
 Cf-NOX01 RLLEDYTRALLAAAEQLRSRAVLTGFFEPQVLDLEPVLPPGSLVILPTPEE-PHRRP--- 148
 Mm-NOX01 RLLEDYVQALLATSEHILRSALHGFFVPKPLDLEPMLPPGSLVILPTPEE-PLSQP--- 148
 Rn-NOX01 RLLETYVRSLLATSQHIVTSSTLNSFFAPKPLDLEPMLPPGSLVILPTPEE-PLSQP--- 153
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bis-SH3 domains

Hs-p47phox TATDITGPIILQTYRAIANYEKTSGSE--MALSTGDVVEVVEKSESGWWFCQMKAKR-GW 204

Cf-p47phox SVTDITGPIILQTYRAIADFEKTSSSQ--MALATGDVVDVVEKSESGWWFCQTKTKR-GW 204
 Mm-p47phox NVADITGPIILQTYRAIADYEKSSGTE--MTVATGDVVDVVEKSESGWWFCQMKTTR-GW 204
 Rn-p47phox NVADITGPIILQTYRAIADYEKSSKTE--MTVATGDVVDVVEKSESGWWFCQMKTTR-GW 204
 Gg-p47phox NTSDITGPIVLQTYRAIADYEKSSKSE--MAVKAGDAVDVVEKSETGWWFCQLKTKR-GW 204
 Xt-p47phox NVSDITGPIILQSYRVIADYEKNSKSE--LAAKNGDVVEIVEKSENGWWFCQLRNKR-GW 206
 Tn-p47phox NASEISGPIILDYRAIADYTKTKYE--INLLAGDQVEIVEKNQNGWWFCQMSKR-GW 205
 Tr-p47phox NVSEISGPIILDYRAIADYTKTKYE--INLHAGDQVEIVEKNQNGWWFCQCDSCR-GW 205
 O1-p47phox TAAEISGPIILDYRVIADFEKTSKHE--LNLHDGDLVEILEKNSNGWWFCQCEAKR-GW 205
 Dr-p47phox TTSEITGPIILETYRVIADYSKSSKYE--LTLKMGDMVDIVEKSPNGWWFCQCESRR-GW 206
 Ci-p47phox IIQDITGPIELETYIAIADYKAEAKTQ--ISLHSGTVEVVEKSESGWWLVCNTYGSNGW 201
 Sp-p47phox DIGNISEPIQAEQYIVVADYKQKQKNE--VELTAGDLVEVFEKNDNGWVFT-VHDQHG 201
 Dr-NOX01 SNSGVTQPFVTETRYCIANYETKDTKNRPFKVEVDETVDVLIKDKGWWLVENESKHLAW 206
 O1-NOX01 GAGNVTHPFVTQTYRCVAPYETRDTKNRPFKVAADKLDVLIKDPAGWWLVESENKRLAW 214
 Tn-NOX01 ---NVTQPFVTVTYRCVSQYETKDTKNRPFKVAADKLDVLIKDKAGWWLVENEKRM 203
 Gg-NOX01 QQLSITYPQVSQSYRCIETFETKDTKNKTFKVAKEIVEVLLKDMTGWWLVENADKQIAW 190
 Xt-NOX01 PEAPAIHPVVSQYICMEDYETKDTKNRPFKVRHELVGVLIKENTGWWLVENEKHLAW 183
 Hs-NOX01 AGRLSIHSLEAQSRLCLQPFCTQDTRDRPFQAQAQESLDVLLRHPSGWWLVENEDRQTAW 209
 Cf-NOX01 PHSPAICSLEAQSRLCLQPFSTQDTGQWPFHARAQEVIDVLLRHPSGWWLVANEEQQMAW 208
 Mm-NOX01 RGSLDIHSLEAQSIPCVQPFHTLDIRDRPFHTKAQEILDILLRHPSGWWLVENKDDQVAW 208
 Rn-NOX01 IGSLAIHSLEAQSMLCLQPFHTLTKDRPFHTKAQEILDILLRHPSGWWLVENKDDQTAW 213

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Hs-p47phox **IPASFLEPLD-SPDETEDPEPNYAG---EPYVAIKAYTAVEGDEVSLLEGEAVEV IHKLL** 260
 Cf-p47phox VPASYLEPLD-SPDEAEDPEPNYEG---EPYVTIKAYTAEMEDEMSELGEAEIV IHKLL 260
 Mm-p47phox VPASYLEPLD-SPDEAEDPDPNYAG---EPYVTIKAYA AVEEDEMSELSEGEAEIV IHKLL 260
 Rn-p47phox VPASYLEPLD-SPDEAEDPDPNYAG---EPYVTIKAYA AVEEDEVSLSEGEAEIV IHKLL 260
 Gg-p47phox VPAAYLEPMD-GPDESEEQEPNYAG---ELYVVQKSYTAVEEDELTLKEGDTIEV IHKLL 260
 Xt-p47phox MPAAYLEPLD-GPDESEEQDPNYEG---DLHITTKDYSGELDDELSQLGEGENVEV IHKLL 262
 Tn-p47phox VPASYLEPLD-GPEESEEAADPDYEGS---ELFITIKAYKAEQEDEISLDLGESIEV IHKLL 262
 Tr-p47phox VPASYLEPLD-GPEESEEAADPDYEGS---ELFITIKAYKAEQEDEITLDELGIESIEV IHKLL 264
 O1-p47phox VPASYLEPLD-GPEEAEAAEPDYEG---ELHVTTNAYKAEQDDEISLDLGETVEV IHKLL 261
 Dr-p47phox VPASYLEPLD-GADESEEPPEPNYAG---ELYKTRRGYKAVEQDEMTLEAGVIEV IHKLL 262
 Ci-p47phox VPGAYLEKED-GSEEDLVTEKA AVGGQ-TWYVATSHYDATSNDEISFPMGAALVQLVNL 259
 Sp-p47phox APGTFQLQNPD-GQEEDE-ETLIPGND-ESYITNNAYQQAQAEDEISFETGVVTVIQKSL 258
 Dr-NOX01 FPAPYLERAEMADDGPDEMDFQSGAVFYVATKAYKATNSDELVELGSLVLEVLQKSD 266
 O1-NOX01 FPAPYLE---VLDGEDEDDEGNL---GSLYCAVRSYSTKKNDEVPLSIGSVVEVLKSD 268
 Tn-NOX01 FPAPYLEK---LEEDGEDDDTGDTR---TLYLTAKNYKASKGDEISVAVGAVVEVLKSD 257
 Gg-NOX01 FPASYLEQ---ISAHKDIQNVESDEEGSLYFVMRAYEAQKADELSLNKGVVVEVRRSD 247
 Xt-NOX01 FPAPYLKD---VDNSED TDSG-TSEDEGLVLYAAKAYEAMNSDEVSI TVGLVVEVIEKSN 239
 Hs-NOX01 FPAPYLEE---AAPGQREGGPSL GSSGPQFCASRAYESSRADEL SVPAGARVRLVLETS 266
 Cf-NOX01 FPAPYLEE---AAP--DREG-TTLRSSGSGFCASQAYESSHADEL SVPAGARVRLVLETS 262
 Mm-NOX01 FPAPYLEE---VATCQQESGLALQGSGRQFCTTQAYEGSRDEL SVPSGARVRLVLETS 265
 Rn-NOX01 FPAPYLEE---IATGQQESGMAVQGSGRQFCATQAYEGSRDEL SVPSGARVRLVLETS 270

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Hs-p47phox **DGWWVIRKDDVTGYFPSMYLQKSGQ** 285
 Cf-p47phox DGWWVVRKDDITGYFPSMYLQKSGQ 285
 Mm-p47phox DGWWVVRKGDITGYFPSMYLQKAGE 285
 Rn-p47phox DGWWVVRKGDITGYFPSMYLQKAGE 285
 Gg-p47phox DGWWVIRKDETTGYFPSMYLQKSGE 285
 Xt-p47phox DGWWVVRKGSITGYFPAMYLQKSGE 287
 Tn-p47phox DGWWVVRKGEFTGYFPSMFLQKASK 287

Tr-p47 <i>phox</i>	DGWWWVRKGEQMGYFPSMFLQKANK	289
O1-p47 <i>phox</i>	DGWWWVRKGETGHFPSMFLTKASK	286
Dr-p47 <i>phox</i>	DGWWWVRKGEETGFYPSMFLCRTGE	287
Ci-p47 <i>phox</i>	EGWWLARYNSNEGWPVGSYLEKSRR	284
Sp-p47 <i>phox</i>	DGWWKVSQGGKQGWAPATFLQIYKG	283
Dr-NOX01	NGWWIVRYNRKAGYVPSMYLQPHNN	291
O1-NOX01	DGWWLIRFNGKVGYPAMYLPYNN	293
Tn-NOX01	SGWWLIRYQGGKVGYPVTLCLQPYNR	282
Gg-NOX01	NGWWLIRYNGRKGYPMSMCLQAYKN	272
Xt-NOX01	NGWWLIR-----	246
Hs-NOX01	RGWWLCRYGDRAGLLPAVLLRPEGL	291
Cf-NOX01	RGWWLCRFRGRSGLLPAVLLQPEGL	287
Mm-NOX01	RGWWLCRYNGRTGLLPAMSLQPEGL	290
Rn-NOX01	RGWWLCRYNGQTGLLPVLLQPEGL	295

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TPR and activation domains of Nox Activators (vertebrate p67*phox*, vertebrate NOXA1, *C. intestinalis* and *S. purpuratus* p67*phox*-like proteins, Dd-p67-like, and fungal NOXR).

Gray boxes indicate the amino acid residues corresponding to the tetratricopeptide repeat (TPR, residues 6-153), activation domain (AD, 196-210 residues) of human p67*phox*.

	TPR region	
Hs-p67 <i>phox</i>	---MSLVEAISLWNEGVLAAADKKDWKGALEAFSAVQDPHSRRCFNIGCMYTIILKNMTEAE	57
Cf-p67 <i>phox</i>	---MSLAEAIISLWNEGVLAAADKKDWKGALEAFSAVQDPHSRRCFNIGCMHTILGNMPEAE	57
Mm-p67 <i>phox</i>	---MSLAEAIRLWNEGVLAAADKKDWKGALEAFSEVQDPHSRRCFNIGCVNTILENLQAAE	57
Rn-p67 <i>phox</i>	---MSLAEAIRLWNEGVAADKKDWKGALEAFSEVQDPHSRRCFNIGCMYTIILDNLQEA	57
Gg-p67 <i>phox</i>	---MSLVEIIRLWQEGVCAADGKEWGAALKAFSTAVQNPAPAKICFNIGCETHLVGLQEA	57
Xt-p67 <i>phox</i>	---MALVEIMRLWSEGVAADGKEWGAALKAFSTAVQNPAPAKICFNIGCETHLVGLQEA	57
Tn-p67 <i>phox</i>	---MSFLDTLRQWDNACTVADGQDFSEALRILLAIPEPNSKICFNIGCETHLVGLQEA	57
Tr-p67 <i>phox</i>	---MSFLDTLRQWDKASTVADRQEFSEALRILLAIPEPNSKICFNIGCETHLVGLQEA	57
O1-p67 <i>phox</i>	---MSFVDTLRQWDDGVTADKQDFSEALRILLAIPEPNSKICFNIGCETHLVGLQEA	57
Dr-p67 <i>phox</i>	---MSFVDTLRQWDEAVACVEQRDPDAALRIFLSIEEKNSKIAFNIGCETHLVGLQEA	57
Hs-NOXA1	---MASLGDVLRVWHLGAQAVDRGDWARALHLFSGVPAPPARLFCFNAGCVHLLAGDPEAAL	58
Cf-NOXA1	---MPSLGDVLRVWHLGAQAVDRGDWARALHLFSGVPAPPARLFCFNAGCVHLLAGDPEAAL	58
Mm-NOXA1	---MSSLGDQIRDWHRGVLAVAREWDSALCFFSDVREPLARMYFNRGCVHLMAGDPEAAL	58
Rn-NOXA1	---MSSLGDQIRDWHRGVLAVAREWDSALCFFSDVREPLAKMYFNRGCVHLMAGDPEAAL	58
Gg-NOXA1	---MAYRELLRRWHQAALADGGDWAALLETLCGIEEPPARICFNIGCMHLAGRRLDAL	57
Dr-NOXA1	---MLYIELIRLWDEAVKAIIDIRWQGALSCLNQTIDHNCRTMFVASTHIALGQVDLAI	57
O1-NOXA1	---MLYAECLKLWDESVQAMDSRDWQGALEKLLQIQEPTSRILFNAATAHLALGHLDMAL	57

Xt-NOXA1 ---MHYKEVRRWHEGVVAEGKDYDAALRSFTAIEDPPSRIWFNVGGIYLLRGDLPRAL 57
 Ci-p67phox ---MASKHAALLQQEGVEASEENDWFKALSIFQQVNPSSVIWFNIGCCHLQVQQYLKAE 57
 Sp-p67phox-N MDKQTHKDI IQVWHEGVQTFDKGNVDAALQAFLGIGDPSAKILFNIGHLEMSQYRFGE 60
 Sp-p67phox-C ---MTHKDTIATWYEGVLAFERGESSEALNQLNSIVDPSAKILYNIGILQKSLGQLEDAN 316
 Fg-NOXR ---MSLKQEIETWVAALGRYDNNEFEEALNEFGKIGD-TSKILFNMGVTHATLGEHEKAV 56
 An-NOXR ---MSLKQEIETWVALEHFDNQEYDLALRSFAAIAD-TSKILFNCVGIYATLGEHEKAV 56
 Mg-NOXR ---MSLKAELETWAAALKAYDEEDFEKSLDLFSRIAD-SSKILTNIGLIYATLGEHEAAV 56
 Dd-p67-like ----MLKQTIKKWNQSIERYESGNVGEALTILTSIEQSTSKINYNIGVMYIKSNFRNAI 56

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Hs-p67phox **KAFTRSINRDKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFK** 117
 Cf-p67phox KAFTRSINRDKHLAVAYFQRGMLYYHMEKYDAAIKDLKEALTQLRGNQLIDYKILGLQFK 117
 Mm-p67phox QAFTKSINRDKHSAVAYFQRGMLYYRMEKYDLAIKDLKEALTQLRGNQLIDYKILGLQFK 117
 Rn-p67phox QAFTKSINRDKHLAVAYFQRGMLYYSMKEYLLCVYCLREALVTFRKKQVLSPKPEGLQFL 117
 Gg-p67phox EAFTQISCDKHLAVAYFQRGTVFYKRHNHEMALKDFKEALQLRGNQLIDYKILGLRGR 117
 Xt-p67phox KAFTLTIERDMHLAVGYFQRGFVFFQRGKYSALQDWTRAYTEMRGNQLIDYKILGLIFK 117
 Tn-p67phox KAFDSSISKDEHLAVAFFQRAITFYKMSRQTHRPCHFQQTFKELRGNQLIDYGALGLRYK 117
 Tr-p67phox KAFDSSICKDEHLAVAFFQRAITFYKMTRQEYSLADFQQTLELRLGNQLIDYGALGLRYK 117
 Ol-p67phox KAFDCSIRKDEHLAVAFFQRGITFYKMRYEESIGDFQRAFKTLRGNQLIDYKALGLRYI 117
 Dr-p67phox KAFDGSIGKDEHLAVAFFQRGVTFYKKEKFEESLDFQQAQFQLRGNQLIDYTPLGLRYK 117
 Hs-NOXA1 RAFDQAVTKDTCMAVGFFQRGVANFQLARFQEALSDFWLALQLRGHAAIDYTQLGLRFB 118
 Cf-NOXA1 RAFDQAVTKDTCMAVGFFQRGVANFQLERFQEALSDFRLALQLRGNAAIDYTQLGLRFB 118
 Mm-NOXA1 RAFDQAVTKDTCMAVGFLQRGVANFQLQRFQEAVSDFQLALQLRDNAVIDYTQLGLNFB 118
 Rn-NOXA1 RAFDQAVTKDTCMAVGFLQRGVANFQLQRLQEAVSDFQLALQLRGNAAIDYTQLGLDFK 118
 Gg-NOXA1 RAFDETVMKDNSLAVGYFQRGFVCLQLEMYEEALS DYHMAFSLRKNPFI DYKQLGLRHI 117
 Dr-NOXA1 KALDRVIAKDSLAVGFFQRGSVAVHMMANRLEEALSDCIWAQKYMRENPI DYKQLGLRYK 117
 Ol-NOXA1 KCLDLTISKDEHLAVGFFQRAAVNMQLERLEDALSDCIWAQKHMKNTPV IDYKQLGLRFB 117
 Xt-NOXA1 EAYDKSLAQDPCLAVGYFQRYGLQFKLGRYKALSCHLALSNLRNNSFI DYKQLGLRHV 117
 Ci-p67phox NAFSQAIAKDKYLAVGYFQLAVSQTHLGNVYAEIDNFSSALSSLRGNPFI DYKQLNMLCK 117
 Sp-p67phox-N VNFTAAVEKDPHMAHAHFQGMVYFHLHRYNESRNSYKAKVCLRGNRFIDYRQLGFVHK 120
 Sp-p67phox-C SILKEVVSRRPHLAIGHFQSGVVLGGLGRGDDAWHAFEKARETLRG-KMINYKPLGLQYK 375
 Fg-NOXR ESYQRAIRLDQYLAVAYFQQGVSNFLGDFEELANFNNTLLYLGRNAMIDYQALGLLFB 116
 An-NOXR EYQAGVGLDQYLAIAFYQEGVSNFLGDFEELANFNNTLLYLGRNTYIDYEQALGLKFR 116
 Mg-NOXR QRFIEATNFDQYLAVAYFQCGVSNFLARYELAYKDFEELLYLRGNQAINYEQLGLKFR 116
 Dd-p67-like EYFNRSVEQDKYLASSYMRVIAAHMNGELNHAIVDYDETI SKLRGHEYIDYKQLGLDHK 116

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Hs-p67phox **LFACEVLYNIAFMYAKKEE-WKAEELALATSMKSEPRH-SKIDKAMECVWKQ**----- 169
 Cf-p67phox LFACEVLYNIAFMYAKNEE-WKAEHLALAMSMKSEPRH-TKIDKAMECVWKQ----- 169
 Mm-p67phox LFACEVLYNIALMHAKKEE-WKAEELALATNMKSEPRH-SKIDKAMESIWKQ----- 169
 Rn-p67phox LQRSPVLYNIALMHAKKEE-WKAEELALATNMKSEPRH-SKIDKAMESIWVS----- 169
 Gg-p67phox LFACEILYNIALVYATMEN-WKAEHLTLAMSSKSEPH-NKIDRAMEAILKQ----- 169
 Xt-p67phox LYSCEILHNIALTHAKEGK-WAKAEESILLALSQKVELRHNTKLEKAMEDILKE----- 170
 Tn-p67phox LTACEVLHNMALAEALGR-WEKAQESLVKALDYSSDSKL-GAIDKALQATLQK----- 169
 Tr-p67phox LNACEVLHNLALTEAQMGH-WEKAQESLVKALDYRTESKL-GIIDNALQATLQK----- 169
 Ol-p67phox LYACEVLHNMALAEALGN-WEKAQENLRKALDYKTDACL-SVIEKAQQAVLKE----- 169
 Dr-p67phox LYACEVLHNLGLAQAQLGK-WEKAQENLLTALSLRADAKF-SHIDHALDAILKH----- 169
 Hs-NOXA1 LQAWEVLNVAQAQQLGL-WTEAASSLREAMSKWPEGSL-NGLDSALDQVQRR----- 170
 Cf-NOXA1 LKTWEVLFNVGAAQCALGL-WAEAGSLEEALCKGPEGAG-EDLHAALAQVQKQ----- 170
 Mm-NOXA1 LQAWEVLYNMAQAQAGL-WTKAANTLVEAISKWPEGAQ-DILDIAQVQKQ----- 170
 rat-NOXA1 LQAWEVLYNMAVQQAQAGL-WTKAANTLVEAISKRPEGAQ-DTLEAAMDQVQKQ----- 170
 Gg-NOXA1 LYAWEVLYSTAATQCRLQQ-WQEARDTLEKAVVWRPEGRS-ATLALALERVQNH----- 169

Dr-NOXA1	LYSWQVLYNAAA VHSRLQQ-WDKARDILLAASQERGAGRS-NLIDTALEAISRK-----	169
O1-NOXA1	LYSWQVLYNAAAAYCRMGG-WEQATEVLLQGG---GAG----HLEAALDSIERR-----	163
Xt-NOXA1	LFSWEAQYNMAAVLCSLGR-WESAEEKLKETLQ--GDGRN-AKLDWALDQVQRR-----	167
Ci-p67phox	ISACDIRLNLALLHIFSGD-VPKAREILNEAMSPHDEDKMKNCKSALDALVNENWVYFG	176
Sp-p67phox-N	LYECEVLNLYALTYATMMNNSEYALELLEDEAKKVSVEARHGPLIEKAQKRLLLY-----	174
Sp-p67phox-C	LHKCEVLHNQAWAYN-ELDQRDWARNQLEEARECKADPRHE--KIEDSYRAFTSGRSFK-	431
Fg-NOXR	LYSCEVLNRLGLCYIYLQQ-MDAGMQDFSYAVKEKVVEDHNVIDDAINEQAEGYT-----	170
An-NOXR	LYSCEVLNRLGLCYIYLQQ-IGPGMQDLEYASKEKYSRSR-----LTPQGYT-----	162
Mg-NOXR	LFSAEVLNKLGLAQIYMGR-AQEGGLADMEEARREKATDEHNVIDDAIQERGEGYT-----	170
Dd-p67-like	LLLAEVLNKLALGRAGS--SVALQATQCFSQPSDSQEFKNQCKKIQDGSQLN-----	168
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Hs-p67phox	--KLYE-PVVIPVGKLFPRNERQVAQLAKKDYLGKATVVASVVDQD-----	212
Cf-p67phox	--KLYE-PVVIPMGRLFRPNERQVAQLAKKDYLGKATVVASVVDQD-----	212
Mm-p67phox	--KLFE-PVVIPVGRLFRPNERQVAQLAKKDYLGKATVVASVVDQD-----	212
Rn-p67phox	--VVVDGPCCLAQYHVQRASHKQVPVLS-KDLLGEETVVASVVDQD-----	212
Gg-p67phox	--KLYE-PVAIPTGKLFPRNEKQVAQLEKDYLGKAMVVASVVDKD-----	212
Xt-p67phox	--KVFA-AVKIPKGRIFQPNRERLVEQLEKDYLGKALVVASVVDKD-----	213
Tn-p67phox	--KLFK-LTGFPSKVLFPKNRYVAELEKDYLGKAKVVASVVPQD-----	212
Tr-p67phox	--KLFK-LIGFPSKVLFPKNHYVAELEKDYLGKAKVVASVVPQD-----	212
O1-p67phox	--KLFK-LVEFPSKMMFKPNKHYVAELEKDYLGKAKVVASVNPQD-----	212
Dr-p67phox	--KLFK-LVEVRAGLLFKPNKHYVAELEKDYLGKAKVVASVVPAD-----	212
Hs-NOXA1	--GSLP-PRQVPRGEVFRPHRHLKHELPVDFLGKAKVVASAIPDD-----	213
Cf-NOXA1	--ATLQ-LRQVPRGEVFRPHRRHVEHLEPVDLFGKAKVVASAIPDD-----	213
Mm-NOXA1	--VPLQ-LQQVPKGEVFPVPRRYLKHLEPMDFLGKAKVVASVIPDD-----	213
Rn-NOXA1	--VPLQ-LRQVPKGEVFPVPRRYLKHLEPMDFLGKAKVVASVIPDD-----	213
Gg-NOXA1	--QFLE-PMQVPPGEFFRPRKKEVEQLDSKDFLGKPKVISSIPND-----	212
Dr-NOXA1	--DVLE-PLLLPEGEVFRPRKLEVDQLKPRDFLGEAKVITSMIPND-----	212
O1-NOXA1	--ELPT-PLTVPELVFRPRKQVEVEQLKQKDFLGKAKVISSIPND-----	206
Xt-NOXA1	--SLLQ-PMSVPEGEFFRPRKQVEVEQLNSVDFLGKPTVISSVVPND-----	210
Ci-p67phox	ESALERLVRLSSSCLFRPSKTKMEGLKSGTKFMNTATVVSATNDEY-----	222
Sp-p67phox-N	-----EPVVLPSNQLFRPPKSKVGLKNVDYLGKPKVSELPESS-----	214
Sp-p67phox-C	-----LYELPKPLLFKPPKSKIDNDR-KDYLGKAKIVAKLPTVR-----	470
Fg-NOXR	-----VFSIPVGVVYRPNKAVRNKTKDYLGKARLVAASDRAN-----	209
An-NOXR	-----VFSIPVGVVYRPNKAVRNKTKDYLGKSRVIAANRLSTPAD-----	204
Mg-NOXR	-----VFSIPVGVLYRPESEKLNKSMQKDYMGKAKLVAASDPNDIFT-----	212
Dd-p67-like	-----FSTRPIPLSLLFKPPK--VSDAPQKQRSATTSSIQSSSPSTPMSSSPSY	216
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The N-terminal SH3 domain of Nox Activators (vertebrate p67phox)

The amino acid sequences corresponding to the N-terminal SH3 (SH3-A) domain (residues 240-299) of human p67phox were aligned.

Hs-p67phox	LEGEAHRVLFVGFVPETKEELQVMPGNIVFVLKKGNDNWATVMFNGQKGLVPCNYLEPVEL	299
Cf-p67phox	LEGEAHRVLFVGFVPETPEELQVMPGNIVFVLKKGNDNWATVMFNGQKGLVPCNYLEPVEL	299

Rn-p67 <i>phox</i>	LEGEAHRVLFQFVPEPEELQVMPGNIVFVFLKKGSDNWATVMFNGQKGLVPCNYLEPVEL	299
Mm-p67 <i>phox</i>	LEGEAHRVLFQFVPEPEELQVMPGNIVFVFLKKGSDNWATVMFNGQKGLVPCNYLEPVEL	299
Gg-p67 <i>phox</i>	LEGQPHRVLYEYFIPETAEEELQVLPGNIVFVFLKKEKDNWATVMFNGKGI VPCNFLEPMEL	299
Xt-p67 <i>phox</i>	LQGEPHRVLFQFNPETAEEELQVLPGNIVFVFLKKGDDNWATVVFNGKGI VPCNYLEPVEL	300
Tr-p67 <i>phox</i>	LEGEPTHVLYKQFVPETSDELAVVPGNVVFLVQKGDNDWASVVFNEERRGLVPYNYLERLEI	300
Tn-p67 <i>phox</i>	LEGEPTHVLYEYFVPETSDELAVVPGNVVFLVQKGDNDWASVVFNEERRGLVPYNYLERLEI	306
Dr-p67 <i>phox</i>	LEGEPTHVLYEYFVPETKEELAVLPGNIVFVFLHRGTDNDWASVVFNEKRGLVPYNFLEPLDI	299
Ol-p67 <i>phox</i>	LEGEPTHVLFQFVPETCDELAVKPGNMVFLVQKGDNDWAYVIFNGRTGLVPYNYLERQEI	299

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PB1 domain of Nox Activators (vertebrate p67*phox*, vertebrate NOXA1, fungal NOXR and Dd-p67-like).

The amino acid residues corresponding to the Phox/Bem1 (PB1) domain (residues 352-429) of human p67*phox* were aligned. *Red* and *blue* letters indicate the amino acid residues corresponding to the positions of two basic amino acid residues (K355 and K382) of PB1 domains of human p67*phox* and four acidic amino acid residues (D289, D291, D293 and D302) of OPCA motif of human p40*phox* PB1 domain, respectively.

Hs-p67 <i>phox</i>	--YTLK V HY---KYTVVMTQPGLPYSQVRDMVSK K LELRL E HTKLSYRPR D SN-EL-VPLS	406
Cf-p67 <i>phox</i>	--YTV K VHY---KYTVVMEIQAGLPYSQRLRDMVAK K LELLPEHTKLSYRPP D SH-EL-EPLS	408
Rn-p67 <i>phox</i>	--YML K VHY---KYTVVMTQLGLPYSQRLRDMVSK K LELLPEHTKLSYQRR D SP-EL-LLLS	406
Mm-p67 <i>phox</i>	--YML K VHY---KYTVVMETRLGLPYSQRLRDMVSK K LALSPEHTKLSYRRR D SH-EL-LLLS	405
Gg-p67 <i>phox</i>	--YVL K VHY---KYTVAMQVKPDLSEKLLGLVCD K LELQPEHTMLRYKSAASG-EL-VPLS	408
Xt-p67 <i>phox</i>	--YLV K VY---KYTVAIQISSKLPFADLLTLISS K LQLLPSRMKLSFK-- E D Q - D D-VLLN	402
Tr-p67 <i>phox</i>	--CV V KVRY---TFTFAVLVPRGSSYATLAEKISE K LSVPANAI VLSLSSEATE-QN-VIDG	404
Tn-p67 <i>phox</i>	--YVV K VRF---TFTFAVIVPRGSSYATLAQKVGE K LSVPADAVILSLSEAAE- E D-VING	411
Dr-p67 <i>phox</i>	--CV V KVHF---QFTIAIAIAHQGPYGVILQMISS K LKLPASTLTTRYAKEGSA-ER-VIIE	411
Ol-p67 <i>phox</i>	--YIV K VHF---TFTFAVSI PRESSYEVLRKISK V KLPSDNISLSFSLDSSG-QR-AIDA	396
Hs-NOXA1	--VTVT V QC---AFTVALRRARGADLSLRALLGQALPHQAQLGQLSYLAPGED-GHWVPI	369
Cf-NOXA1	--VTVT V QC---AFTLALKVPWGAGLPHRLTLLSQALPLQAQHGQLSYR D PSHE-ARWVALP	347
Rn-NOXA1	--VTVT V QC---HFTVPLKVPRTGLSSFRLLSQALLQQTQKGQFSYKARGED-RAWVPIS	339
Mm-NOXA1	--VTVT V QC---HFTVPLKVPRTGLSSFRLLSQALLHQTQTGQLSYKAPGEE-RSWIPIS	341
Gg-NOXA1	RPAVL R VRC---ECTVVVRAGEVPSVPALRALLRER F GQAERGRLSYRH L DGK--ELGAVS	410
Xt-NOXA1	--LVLSVHA---EFTVNMTVSKAITYPELQCALREELRKHGEMANHLSYR D PESRGLTPVT	489
Dr-NOXA1	--VV V KVHY---TYTVALRPAETPFRLDQEKIA Q KLGGPAMNIRLRHRRPGTR-VL-TPLN	400
Ol-NOXA1	--VV V KVHY---TYTVAVTPLNTPYHELKQRI A Q K LGHPA SELCLRHKQGGSH-LL-SPLS	416
An-NOXR	--RR F R V KVHSFEDTRYILIPPTIEFAEFETRIRE K FGFQMA-LKIKM Q DE---GDMITMV	481
Fg-NOXR	--TKI R VK V HA---DEVKLIMITPDTRFETLSDKVRD K FNKR--FKIK V K D DDMPNGDMITV	486

Mg-NOXR --TLIRVKLHYQDDTRGMLTPDTPFADFMDKVTA~~K~~FGKQINGLGLKFK~~DE~~D---GGKVTLR 515
Dd-p67-like --ITL~~K~~VFYK---DRRLIQIPVPCNLSTFIQKIEL~~K~~FEITISDKFSLSFQ~~L~~D---GEENEIN 363

Hs-p67phox -EDSMKDAWGQV-----KNYCLTLWCENT--- 429
Cf-p67phox -EDNMKAAWGQV-----RNYCLTLWCENT--- 431
Rn-p67phox -EESMKDAWAQV-----KNYCLTLWCEHT--- 429
Mm-p67phox -EESMKDAWGQV-----KNYCLTLWCEHT--- 428
Gg-p67phox -AQNLEEAWSHS-----KDQCLTVWCDCCT--- 431
Xt-p67phox -EENTEKAWSLA-----TDNCLKCLKCT----- 423
Tr-p67phox -G~~T~~DMEGVWSRV-----SGRCITLWCR----- 425
Tn-p67phox -S~~T~~DMEAVWGRA-----SGRCITLWCR----- 432
Dr-p67phox -DSEMEAVWNSA-----KDGRITLWCS----- 432
Ol-p67phox -NTDMETVWSQV-----RAGRITLWCKEK--- 419
Hs-NOXA1 EEESLQRAWQDA-----AACPRGLQLQ----- 391
Cf-NOXA1 GEEALQGAWRDT-----AASPRGLQLQ----- 369
Rn-NOXA1 TEDSLQSVWRNV-----PVSPRGLQLQ----- 363
Mm-NOXA1 TEESLQSIWRNV-----PVGPGGLQLQ----- 361
Gg-NOXA1 GEE~~D~~LEKMWQQL-----TDGRITLCCQ----- 432
Xt-NOXA1 GSK~~D~~WQEVKLKLS-----RANQVTLCK----- 511
Dr-NOXA1 GDDGLDCLEGVA-----ESGRAQIWCQ----- 422
Ol-NOXA1 GEPG-GTVQDLA-----VAGRATLWCQRF--- 439
An-NOXR DQ~~E~~DLDLLMASREIARREGSEMGMKIWVEERPMI 517
Fg-NOXR DQ~~D~~DL~~E~~MVIDSVKDEARKQRTETGKMEIWILQL--- 509
Mg-NOXR DES~~D~~YELAIETARESAK--GKPEGRL~~E~~LWCMDL--- 546
Dd-p67-like SQVQLDKMICMEINEINVKDIIPSPSPSPSPSP--- 390

The C-terminal SH3 domain of Nox Activators (vertebrate p67phox, vertebrate NOXA1 and *S. purpuratus* p67phox-like protein).

The amino acid residues corresponding to the C-terminal SH3 (SH3-B) domain (residues 457-526) of human p67phox were aligned.

Hs-p67phox KKG~~S~~QVEALFSYEATQPEDLEFQEGDIIILVLSKV-----NEEWLEGECKGKVGIF 506
Cf-p67phox KEGGHVVALFTYEATQPEDLEFQ~~Q~~GDIIQIISMV-----NEDWLEGECKGKIGIF 508
Rn-p67phox KEGTQVVAIFSYDATQPEDLEFVEGDVILVLSHV-----NEEWLEGECKGKIGIF 506
Mm-p67phox KEGTQVVAIFSYEAAQPEDLEFVEGDVILVLSHV-----NEEWLEGECKGKVGIF 505
Xt-p67phox A~~Q~~GKYPIALFEYEATQPEDLPFCKGDIIKILSHV-----SEDWLEGECKG~~R~~MGIF 493
Gg-p67phox ---TQVVAQYSYEATQPEDLEFQAGDVILVLSKV-----NEDWLEGCNGKIGIF 501
Tr-p67phox -KESLLALHSYDSSNPEDLSFHQGDRI~~T~~LLSKV-----NQDWLEGEFNGTGIF 483
Tn-p67phox RRETFLALHTYDSPNPEDLTFQ~~Q~~GDKILLLSKV-----NQDWLEGC~~H~~QNGTGIF 492

Dr-p67 <i>phox</i>	---AKVVALYSYESSTPEDLEFKQGNVITVLSKV-----NDEWLEGQCNGKIGIF	488
O1-p67 <i>phox</i>	GEETHKVALHSYQSANPEDLNFKEGDEITVLARI-----NQDWLEGRNGSTGIF	493
Hs-NOXA1	PVLYQVVAQHNSYSAQGPEDLGRFGDVTVDLCEE--PDVPL-AVDQAWLEGHCDGRIGIF	455
Cf-NOXA1	PVLYQVVAQHNSYSAQGPEDLGRFGDVTVDLCEE--PDVPL-AVDQAWLEGHCDGRIGIF	436
Rn-NOXA1	PVLYQVVAQYDYRAQRPELDLFRQGDVTVDLCEV-----DEAWLEGHRDGRVGIF	420
Mm-NOXA1	PVLYQVVAQYNYRAQRPELDLFRQGDVTVDLCEV-----DEAWLEGHRDGCVGIF	418
Gg-NOXA1	PILYRMLAQHSYSAQPGDLEFSKGDVLDILSEV-----NEDWLEGHCNGKTGIF	490
Xt-NOXA1	PVLYRMRQAQYDYLQGPADLSFQQGDLISILSEV-----NGEWLEGHCHRGIGIF	569
Dr-NOXA1	TILYQMVALYDYNAQGPEDLEFSEGDTIDILSEV-----NEEWLEGHVAGNIGIF	480
O1-NOXA1	HILYQMVALYNYDAQGPEDLEFSEGDTIDILSEV-----NEEWLEGHCAGNVGIF	514
Sp-67 <i>phox</i>	GQRKTALVIASHETDVEGEVSVSEGDILITITGEV-----GDWLEVEVKGRKGRV	1094
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Hs-p67 <i>phox</i>	PKVFVEDCATTDLESTRREV-----	526
Cf-p67 <i>phox</i>	PKAFVEEHATTDLESSPRGV-----	528
Rn-p67 <i>phox</i>	PKAFVEGCAAKNLEGTPREV-----	526
Mm-p67 <i>phox</i>	PKAFVEGCAAKNLEGIPREV-----	525
Gg-p67 <i>phox</i>	PSAFVRDGNTKDP-----	518
Xt-p67 <i>phox</i>	PKVFTEE-----	500
Tr-p67 <i>phox</i>	PAAFVEEVPANG-----	495
Tn-p67 <i>phox</i>	PAAFVEEVSVE-----	504
Dr-p67 <i>phox</i>	PSSFVEPLNGDPH-----	501
O1-p67 <i>phox</i>	PASFVNFCSPRQL-----	505
Hs-NOXA1	PKCFVVPAGPRMSGAPGRLPRSQQGDQP	483
Cf-NOXA1	PKCFVVPAG-----	445
Rn-NOXA1	PKCFVVPAATCVEALP--VPEPQPGEQH	446
Mm-NOXA1	PKCFVVPAGAYVEAML--VLGPQPGDQN	444
Gg-NOXA1	PKCFATQTSAAFP-----	504
Xt-NOXA1	PKCFAQR-AEGI-----	580
Dr-NOXA1	PQSFAHRDTSISGASTD-----	498
O1-NOXA1	PSCFAYRENSSLYP-----	528
Sp-67 <i>phox</i>	PRSCVKDFSKPRV-----	1106
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PX domain of p40*phox* (vertebrate p40*phox*).

The amino acid sequences corresponding to the PX domain (residues 19-140 of human p40*phox*) were aligned.

Hs-p40 <i>phox</i>	DVAISANIADIEEKRGFTSHFVFVIEVKTGGGSKYLIYRRYRQFHALQSKLEERFGPDSK	78
Cf-p40 <i>phox</i>	NIAISANIADIEEKRGFTSYFVFVIEVKTGGGSKYLIYRRYRQFHALQSKLEERFGPENK	78
Mm-p40 <i>phox</i>	DVAISANIADIEEKRGFTSHFVFVIEVKTGGGSKYLIYRRYRQFYALQSKLEERFGPESK	78
Rn-p40 <i>phox</i>	DVAISANIADIEEKRGFTSHFVFVIEVKTGGGSKYLIYRRYRQFYALQSKLEERFGPESK	78
Gg-p40 <i>phox</i>	DVPVSANIADIEEKKGFTNYYMFVIEVKIKSGGRYLIFRRYREFYALHTKLEERYGGESK	78
Xt-p40 <i>phox</i>	DVPVFAHIADVEERRGFSLYYTFVIEVKTGGGSKYFIYRRYSQFFTLHAKLEENYGP--D	76
Tr-p40 <i>phox</i>	NVAVTATIADIEEKKGFIDHYRFVIEVKTGGGSKYFIYRRYREFFTLHQTLKESKYSPEES	77
Tn-p40 <i>phox</i>	NVPVTATIADIEEKKGFIDHYRFVIEVKTGGGSKYFIYRRYREFFTLHQNLKESKYPEDA	68

O1-p40phox	NIPVSATIADTEEKRGFIDYFRFVIEVKTKGGSKYLIYRRYKEFFNLHQTLQLEAKYSPGDL	78
Dr-p40phox	NIPVTATIADIEEKKGFIVYFSFVIEVKTEGNSKYLIYRRYREFFALHQSELEKYTAEAQ	78
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Hs-p40phox	S--SALACTLPTLPAKVYVGVKQEI AEMRIPALNAYMK-----	114
Cf-p40phox	S--NPFTCSLPTLPAKVYVGVKQEI AEMRIPALNAYMK-----	114
Mm-p40phox	N--SPFTCNLPTLPAKVYMGAKQEI AETRIPALNAYMK-----	114
Rn-p40phox	N--SPFTCSLPTLPAKVYMGVQKQEI AETRIPALNAYMK-----	114
Gg-p40phox	N--SAFTCTLPVLPQKIVYVGVKQEI AENRIPILNIYMK-----	114
Xt-p40phox	NGIAPYICTLPELPPKIFVGNKQEI AETRIPLLNGYMK-----	114
Tr-p40phox	DRQGQNTCLPPLPGKIVLGNKQEI AEGRIPELNTYMK-----	115
Tn-p40phox	EKPGPNTCLPPLPGKIFVGNKQEI AEGRIPELNTYMKVISAGWALRMDGCRMARSDSPT	128
O1-p40phox	ERPGPNTCVLPSLPGKIYVGNKQEI AESRIPELNTYMK-----	116
Dr-p40phox	S--GYNCQLPTLPGKIVFMGNKQEI AESRIPELNMYMK-----	114
	* *	
Hs-p40phox	-----SLLSLPVWVLMDEDVRIFFYQSPYDS	140
Cf-p40phox	-----SLLSLPIWVLMDEDVRIFFYQSPYDS	140
Mm-p40phox	-----NLLSLPVCVLMDDVRIFFYQSAYDA	140
Rn-p40phox	-----NLLSLPVCVLMDDVRIFFYQSAYDA	140
Gg-p40phox	-----NLLCLPVWVLMDEEVRLFFYHSNFDS	140
Xt-p40phox	-----GLLNSPTWLLDDEDLRMFFYQTLSDS	140
Tr-p40phox	-----RLLGLPAWFLDDTLRMFFYQTDQDS	141
Tn-p40phox	TFHQSPPTIPSPRLLGLPVWFLDDTLRMFFYQTDQDS	166
O1-p40phox	-----RLLHLPWVLLDDETLRIFFYQTDSDS	142
Dr-p40phox	-----RLLCLPTWVLLDDLIQCFSTRLSPTA	140
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Proline (P)-basic, SH3 and PB1 domains of p40phox (vertebrate p40phox).

The amino acid sequences corresponding to region from proline-basic (P-basic) region to PB1 domain (residues 144-339 of human p40phox) were aligned. *Gray boxes* indicate the amino acid sequences corresponding to the P-basic region (residues 144-158), SH3 domain (residues 170-229), and PB1 domain (residues 237-339) of human p40phox.

	P-basic region	SH3 domain	
Hs-p40phox	PQALRRRLRPTRKVKVSPQGNVSDR	MAAPRAEALFDFGTGNSKLELNFKAGDVI	204
Cf-p40phox	PQALRRRLRPTRKVKNESPQDAIFDR	MAAPRAEALFDFGTGNSKLELNFKAGDVI	204
Mm-p40phox	PQALRRRLRPTRKIKGVSPQGAIMDR	MEAPRAEALFDFGTGNSKLELSFKAGDVI	204
Rn-p40phox	PQALRRRLRPTRKIKGVTPQGPSMDR	MEAPRAEALFDFGTGNSKLELSFKAGDVI	204
Gg-p40phox	PRRLRRRLRPTRRVKSISSQLPVLDR	VAAAPRAEALFDFSGTNSKLELSFKKGDLI	204
Tr-p40phox	PRALRRRLRPQTRKVKTIKP---	KMDLFSSPRAEVMFDFRNGNGEELNKKGEVI	202

Tn-p40phox PRALRRLRPQTRKVKTKVP---KMDLFSSPRAEVMFDFRNGKEELNLKKEVIFLLQRVN 227
 O1-p40phox PRALRRLRPPTRKVKTVPEPQ---KMDLFSSPRAEAMFDFRNGSKAELNLKKEVIFLLRRVN 204
 Dr-p40phox PRALRRLRPPTRKVKTKVP---KTDLLSAPRAEAVFDFSGSRELSLKAGDVIFLLRRVN 201
 Xt-p40phox PRALRRLRPQTRKLLKDSQ---PISDVDRPRAEALFDFKGNAPMELNLKCGDLIYLLSWVN 201

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PB1 domain

Hs-p40phox **KDWLEGTVRGATGIFPLSFVKILKDFP**-----EEDD-----**PTNWLRCYIYEDTI** 249
 Cf-p40phox FFLPQGTVRGATGIFPQSFVKILKDFP-----EEED-----PTNWLRCYIYEDTI 249
 Mm-p40phox KDWLEGTSGATGIFPGSFVKILKDFP-----EDED-----TTNWLRCYFYEDTG 249
 Rn-p40phox KDWLEVRQRGRAEVSSTLVFPLGAST-----EPG-----HRNHIGCPMALEA 248
 Gg-p40phox KDWLEGTVNDATGIFPSAFVKI IKDLP-----QQED-----TVNKIRCYYDET V 249
 Tr-p40phox ADWLEGTVNNQGTGIFPQSFVKI IKPLPDSNTEGEGEG-----HTYSLRCFLLTPSG 254
 Tn-p40phox ADWLEGTVNNQGTGIFPQSFVKI IKPLPDVSAEGEDEG-----HTYSLRCFLLSPAG 279
 O1-p40phox ADWLEGTVNNQGTGIFPESYVKI IKALPESDSESNGGG-----HTYSLRCFLLTPSG 256
 Dr-p40phox NADWLEGTVRDRGTGIFPESFVKI IKALPENESDEEGGASRNSRAQGSYSCLHCYFLQPEG 261
 Xt-p40phox REWLEGTVGNRTGIFPASFVRI IKNLPELLYQ-----VSLLRICYFHDHDR 246

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Hs-p40phox **STIKDIAVEEDLSSTPLL-KDLEL**TRREFQREDIALNYRDAEGDLVRLSDEDVALMVR 308
 Cf-p40phox STTKDIAVEEELSSSTPLF-KDLMQMRREFQREDIALNYRDAQGDLVRLSDEDVGLMVK 308
 Mm-p40phox KTIKIDIAVEEDLSSTPLF-KDLLALMRREFQREDIALSYQDAEGDLVRLSDEDVGLMVK 308
 Rn-p40phox TVVTTTVIRGSVDHCPVFWKVLSSMSREFQREDIALNYQDAEGDLVRLSDEDVGLMVK 308
 Gg-p40phox STIRDISVEENLSSIPLF-KDLMELIKQEFDQHDIVLNYRDLGDGDLIRLLSDQDVLMVS 308
 Tr-p40phox VDTRDVCVEEELTTQPTY-KDLFHMNRNVFKVNDIALNYRDMEGDLIRVVDDEDIQLMIK 313
 Tn-p40phox VDTRDVCVEEELTTQPTH-KDLLTLMRNVFKVNDIALNYRDPEGDLIRVLDDEDIQLMVK 338
 O1-p40phox VETRDVCVEDLSIQPTY-NELLSMRNVFKVEDIALNYRDLEGDLIRILDNEDVQLMIE 315
 Dr-p40phox IETRDICVEDLSIQPSY-EELLSMRDVFHVDDIALNYRDAEGDLIRILDDEDVVLVQ 320
 Xt-p40phox CLIRDISLEEDVGKCPYSY-KELLDLIRNQFPDAEVALNMRDKDGELIRLLDNSDMEFLIT 305

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Hs-p40phox **QARGLPSQ**---KRLFPWKLH---ITQKD---NYRVYNTMP----- 339
 Cf-p40phox QAQGLPSQ---KHLFPWKLH---ITQKD---DYRVYNTVP----- 339
 Mm-p40phox QARGLPSQ---KRLFPWKLH---VTQKD---NYSVYNTVP----- 339
 Rn-p40phox QAQGLPSQ---KRLFPWKLH---VTQKD---NYGVYNTVP----- 339
 Gg-p40phox QSRKRSSE---KHFFPWKLH---ITHKD---DFSVYSTSPGIGDTQTVRAT----- 350
 Tr-p40phox ESRGQESKIKRPVNQFPWELY---VTLAS---DFSVYNTTEL----- 348
 Tn-p40phox ESRDQQGKVKRPVNQFPWELHFASVTYSSPTRGDTSAVLSPLTPERRQMVGVLVSVTQR 398
 O1-p40phox EGKRQKGGKVKRPVNQFSWELH---VTKAF---DLSVYNFEA----- 350
 Dr-p40phox ESKRTEKVKRPVNQFPWELL---VTHAK---DLTVYNTTEY----- 355
 Xt-p40phox RGKRPP---RAKNYFPWELH---VTHED---DLEAYKTEA----- 336

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