

Additional File 4

Alignment of full-length p22phox (vertebrate p22phox and *C. intestinalis* p22phox-like protein).

Gray boxes indicate the amino acid sequences corresponding to the polybasic region (basic, residues 55-61), predicted 1st and 2nd transmembrane segments (TM1-TM2, residues 91-120) and proline-rich region (PRR, residues 151-164) of human p22phox.

Abbreviations: Hs (*H. sapiens*), Cf (*C. familiaris*), Rn (*R. norvegicus*), Mm (*M. musculus*), Gg (*G. gallus*), Xt (*X. tropicalis*), Dr (*D. rerio*), Tr (*T. rubripes*), Tn (*T. nigroviridis*), Ol (*O. latipes*), and Ci (*C. intestinalis*).

Hs-p22phox	-----MGQIEWAMWANEQALASGLILITGGIVATAG----RFTQWY-FGAYSIVAGVF	48
Cf-p22phox	-----MGQIEWAMWANEQALASGLILIMGGIVATAG----QFTKWY-FGAYSIGAGVF	48
Mm-p22phox	-----MGQIEWAMWANEQALASGLILITGGIVATAG----RFTQWY-FGAYSIAAGVL	48
Rn-p22phox	-----MGQIEWAMWANEQALASGLILITGGIVATAG----RFTQWY-FGAYSIVAGVL	48
Xt-p22phox	-----MGQIEWAMWANEQALASGLILLAGGIVAVAG----QFKGWQ-FGAYGVAAGVF	48
Tn-p22phox	-----MGKIEWAMWANEQALASGFILLAGGIVGVAG----RFRGWE-FAAYAVAAGVF	48
Tr-p22phox	-----MGKIEWAMWANEQALASGFILLTGGVVGAVG----QFRGWQ-FAAYAVAAGVL	48
Ol-p22phox	-----MGRIEWAMWANEQALAAGLILLAGGIVGVAG----QFRGWE-FASYAIAAGVF	48
Dr-p22phox	-----MAKIEWAMWANEQALAAGLIYLTGGIVGVAG----QFRGWQ-FAAFGIAAGVF	48
Ci-p22phox	MPSSSSNIRSIQWGMWANETALLGSYVLTGGIIGIVGGLLNKMFWLP IGIYGVVFGIL	60

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	basic		TM1-TM2									
Hs-p22phox	VCLLEY	PRGKRKK	GSTMERW	GGQKYM	TAVVKL	FGPFTR	NYYVRA	VLHLLS	V	PAGFLLAT	I	108
Cf-p22phox	VCLLEY	PRGKRKK	GSTMERC	GGQKYM	TKVVKV	FGPLSR	NYYIRA	FLHLGL	S	PAGFLLAT	I	108
Mm-p22phox	ICLLEY	PRGKRKK	GSTMERC	GGQKYL	TSVVKL	FGPLTR	NYYVRA	ALHFLS	S	PAGFLLAT	I	108
Rn-p22phox	ICLLEY	PRGKRKK	GSTMERC	GGQKYL	TAVVKL	FGPLTR	NYYVRA	VLHLLS	V	PAGFLLAT	I	108
Xt-p22phox	ITLLEY	PRSKRKK	GSTMERC	GGQKYLA	AAVVKL	FGPLTR	NYYVRA	ILHAGL	AV	PGGFILST	I	108
Tn-p22phox	VCLLEY	PRSKRSK	GTSVERP	GGQHCFT	VCVKAF	GPVTK	NYYVRA	VLHAAI	C	VPGGFMLAT	V	108
Tr-p22phox	VCLLEY	PRSKRSK	GTSVERP	GGQRCFT	VCVKAF	GPVTR	NYYVRA	VLHAAI	C	VPGGFMLAT	V	108
Ol-p22phox	VCLLEY	PRSKRAK	GTSVERT	GGQCFT	VCVKAF	GPVTR	NYYVRA	FLHAAI	C	VPGGFMLAT	V	108
Dr-p22phox	VCLLEY	PRSKRK	GTSIERS	GGQCFT	VCVKSF	GPLTR	NYYVRA	FLHAAI	C	VPGGFMLAT	V	108
Ci-p22phox	VGLLEY	PRGKKN	KGNTLL	RSGQSC	FSTMVN	NKL-P	FFSVN	YYFRAI	A	YFIVCIPGI	ISVPTF	119

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	PRR	
Hs-p22 <i>phox</i>	LGTACLAIASGIYLLAAV	RGGEQWPIIEPKPRERQIGGTIKQPPSNPPPRPPAEARKKPS 168
Cf-p22 <i>phox</i>	LGTACLAIASSIYLLAA	YHGEQWPIIEPKKERPVGGTIKQPPSNPPPRPPAEARKKPS 168
Mm-p22 <i>phox</i>	LGTVCLAIASVIYLLAA	IRGEQWPIIEPKKERPVGGTIKQPPTNPPPRPPAEVRKKPS 168
Rn-p22 <i>phox</i>	LGTVCLAIASVIYLLAA	IRGEQWPIIEPKKERPVGGTIKQPPTNPPPRPPAEVRKKPS 168
Xt-p22 <i>phox</i>	LGTVCLGIASIIYFLAA	IRGEWRPIEKQAEPKPRAGETIKRPPNPPPRPPAEVRRK-- 166
Tn-p22 <i>phox</i>	LGCVCLGIASIIYLVAA	IRGEHWEPILPKKEIQKPVAESIKNPPQNPPPRPPAETRKRKV 168
Tr-p22 <i>phox</i>	LGCVCLGIASIIYLVAA	IRGEHWEPILPSKEIRKPVAESIKNPPQNPPPRPPADTRKRKV 168
Ol-p22 <i>phox</i>	LGCVCLGIASLIYLA	AAVIRGEHWEPILPRKDRKPVAESIKSPPQNPPPRPPPEIRRKQA 168
Dr-p22 <i>phox</i>	LGCVCLGMASLIYLSA	PIHGEHWEPILH-IETKKRLGESIKEPPQNPPPRPPPELRRKKA 167
Ci-p22 <i>phox</i>	LGSVCVIVGSGIYLG	AALHKERWNPIESRPQVP-STSNITQPPSQPPRLPQNKQI--- 175
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Hs-p22 <i>phox</i>	EEEEAVAAGPPGGPQVNP	IPVTDEVV 195
Cf-p22 <i>phox</i>	EEEEAAGAVGVSGGPQEN	PVPVIDEVV 195
Mm-p22 <i>phox</i>	EGEEEEASAG---	GPQVNMPVTDEVV 192
Rn-p22 <i>phox</i>	EAEAAAASAG---	GPQVNPIPVTDEVV 192
Xt-p22 <i>phox</i>	--QADEVSVG---	GGHVNPVPTDNDV- 187
Tn-p22 <i>phox</i>	DDLEAAAYDN-----	P----- 179
Tr-p22 <i>phox</i>	EDLEAASYDN-----	PISVTANE- 186
Ol-p22 <i>phox</i>	KDVEGAAYDN-----	PMSVTDDE- 186
Dr-p22 <i>phox</i>	DNLDAAYDN-----	PMSVTINE- 185
Ci-p22 <i>phox</i>	-----	