

A

zP75 : -----MFTVT---VVELLVCEALS-SRDTCPSCAFITTRGECCKCQCEGEMVVKPCGANQTVCEPCLDSFTFSENFSHKDKLIPCTCCSEIMRML : 85
 hp75 : MG-AGATGRAMDGR--LLLILLVSLGGAKEACPTGLYTHSGECCKRACNLGEGVAQPCGANQTVCEPCLDSVFFSDVVSATEFGKPCTECVGLQSMS : 96
 mp75 : MRRAGAACSAMDRLRLLLLLLVSVFGGAKETCTGMYTHSGECCKRACNLGEGVAQPCGANQTVCEPCLDSVFFSDVVSATEFGKPCTECVGLQSMS : 99

Signal peptide **CRD 1** **CRD 2**

zP75 : TPCITANDALCVQYGFNQLSGRCEACTVCPVGCQVQVCFNFERDTVCKECEDITYSDQDTSFDPCPLCTVGDQPEMEVKSCTFVSDAVCQDFLAPN : 184
 hp75 : APCVEADAVCRCAQYGYQDETTGRCEACRVCVCEAGSGLVFSQDQKQNTVCEPCPDGTYSEANHVDPCLPCTVCEEDTQRQLRCECTRWALCAECEIIPGRW : 195
 mp75 : APCVEADAVCRCAQYGYQDETTGRCEACRVCVCEAGSGLVFSQDQKQNTVCEPCPECTYSIEANHVDPCLPCTVCEEDTQRQLRCECTRWALCAECEIIPGRW : 198

CRD 2 **CRD 3** **CRD 4**

zP75 : SSPSPSAPPEPTPYFTFSPSIHKFSSHPGSVVSYTEKLLPDNPEESVTTTDEGQRRLHGLSDNLIPIYTSILAAVLLGLVAFIIFKRWNSCKQNKCANNR : 283
 hp75 : ITRS---TPEEGSDTAPSTQPEAF--PEQDLIASTVAGVVTVMGSSQFVVTR--GTDNLIPIYVCSILAAVVVGLVAVIAFKRWNSCKQNKCGAN-- : 286
 mp75 : ITRS---TPEEGSDVTTPESTQPEAF--PERDLIASTVADVTVMGSSQFVVTR--GTDNLIPIYVCSILAAVVVGLVAVIAFKRWNSCKQNKCGAN-- : 289

transmembrane domain

zP75 : ACSANPSQTFSPPEGEKLSHSDSGISVDSQSLHDCGPPHTV----VKIDGGSALSLELHTREEVEKLLNRTEGEEESAANEETDWCSLAGLGLYKEEHIA : 378
 hp75 : --SRPVNQTFFPEGEKLSHSDSGISVDSQSLHDCGPPHTQTAGGQALKGDGGLYSSLEFARREEVEKLLNGS-----AGDTRHRLAGLGLYQPEHID : 374
 mp75 : --SRPVNQTFFPEGEKLSHSDSGISVDSQSLHDCGPPHTQTAGGQALKGDGGLYSSLELHTREEVEKLLN-----GDTWRHLAGLGLYQPEHID : 374

death domain

zP75 : NFKQDERFICALLSHWASQDSANITLCTALKINREDAQSIIIVKFTATSAV : 431 Identity Similarity
 hp75 : SETHACFVRALLASWATQDSATLQALLAALRRICRADLVESLCSESTATSEV : 427 45% 61%
 mp75 : SETHACFVRALLASWAGQDSATLQALLAALRRICRADLVESLCSESTATSEV : 427 45% 61%

B

zLINGO-1 : MTFLLQVTIKMVAR-EASGHSYLVACQPIILITMLGTVLSSGATGCFPSRCECSAQCFRSVVCHRRKRLITPEGIEIDTRLLDLISKNRIL : 85
 hLINGO-1 : ---MQVSKRMLAGGVRSMSEFLLACQPIILITMLGTVLSSGATGCFPSRCECSAQCFRAVLCHRKRFRVAVPEGIETETRLLDLIGKNRI : 83
 mLINGO-1 : ---MIAGGRSMSEFLLACQPIILITMLGTVLSSGATGCFPSRCECSAQCFRAVLCHRKRFRVAVPEGIETETRLLDLIGKNRI : 77

Signal peptide **LRR N-cap** **LRR**

zLINGO-1 : KAINPEEELNYFQLEDLQLNENIISVIEPGAISNLLGLRITLGLRNNLKLKILGVFTGLSNLTRLDISENKIVILLDYMFOQLYNI : 171
 hLINGO-1 : KTLNQDEEASFFLEELLENENIVSAVEPGAENNLFNRLTGLRNNLKLKILGVFTGLSNLTKLDISENKIVILLDYMFOQLYNI : 169
 mLINGO-1 : KTLNQDEEASFFLEELLENENIVSAVEPGAENNLFNRLTGLRNNLKLKILGVFTGLSNLTKLDISENKIVILLDYMFOQLYNI : 163

LRR

zLINGO-1 : KLELVGNDLVYIISHRAFSGINSLEQLTLEKCNLTSIPEALSHLHGLIVLRLRHLNINAIIRDYSEFRRLYRLVLEISHWYFLDTM : 257
 hLINGO-1 : KLELVGNDLVYIISHRAFSGINSLEQLTLEKCNLTSIPEALSHLHGLIVLRLRHLNINAIIRDYSEFRRLYRLVLEISHWYFLDTM : 255
 mLINGO-1 : KLELVGNDLVYIISHRAFSGINSLEQLTLEKCNLTSIPEALSHLHGLIVLRLRHLNINAIIRDYSEFRRLYRLVLEISHWYFLDTM : 249

LRR

zLINGO-1 : TAKSLHGLNITLSTITNCNLTAVPYVAIQHLVYLRFNLSFNPTIEVVEGKMHNLRLQAFHLVGGRTVSIIEPYSFKGLNYLRVNL : 343
 hLINGO-1 : TPNCLYGLNLTSLSTITNCNLTAVPYLAVRHLVYLRFNLSYNPTIEGSMLEHLRLQEIQLVGGQAVVEPYAFRGLNYLRVNL : 341
 mLINGO-1 : TPNCLYGLNLTSLSTITNCNLTAVPYLAVRHLVYLRFNLSYNPTIEGSMLEHLRLQEIQLVGGQAVVEPYAFRGLNYLRVNL : 335

LRR

zLINGO-1 : VSNSTLSTLEESA FHSVGNLETLITLDSNPLACDCRLLWVFRWRRLNFRNQPFQATPEFVQGEKFKDFPDVILPNYFTCQKSKTR : 429
 hLINGO-1 : VSGNQLTLEESA FHSVGNLETLITLDSNPLACDCRLLWVFRWRRLNFRNQPFQATPEFVQGEKFKDFPDVILPNYFTCRRRARTR : 427
 mLINGO-1 : VSNQLTLEESA FHSVGNLETLITLDSNPLACDCRLLWVFRWRRLNFRNQPFQATPEFVQGEKFKDFPDVILPNYFTCRRRARTR : 421

LRR **LRR C-cap**

zLINGO-1 : EKAIHRFVDEGTVQVFCRAGDGEFEAILNLSPKHLVSAKSNGLRITVFDGTELVRYACVQDNGTYLCLIAANAGGNSMPFAHLH : 515
 hLINGO-1 : EKAAQVVFVDEGTVQVFCRAGDGEFEAILNLSPKHLVSAKSNGLRITVFDGTELVRYACVQDNGTYLCLIAANAGGNSMPFAHLH : 513
 mLINGO-1 : EKAAQVVFVDEGTVQVFCRAGDGEFEAILNLSPKHLVSAKSNGLRITVFDGTELVRYACVQDNGTYLCLIAANAGGNSMPFAHLH : 507

Ig domain

zLINGO-1 : VHSYSEWPHQPNKTFAFILNQFSDNSANGTCAMDFPFDMKPLTIATTMGFISFLGVVLFCLVLLFLWSRGKGNTRKNIEIEYVE : 601
 hLINGO-1 : VRSYSEWPHQPNKTFAFISNOFGEGEANSRATVPPFFDIKTLTIATTMGFISFLGVVLFCLVLLFLWSRGKGNTRKNIEIEYVE : 599
 mLINGO-1 : VRSYSEWPHQPNKTFAFISNOFGEGEANSRATVPPFFDIKTLTIATTMGFISFLGVVLFCLVLLFLWSRGKGNTRKNIEIEYVE : 593

transmembrane domain

zLINGO-1 : RRVDGENSPNEGSHKISMKMI : 622 Identity Similarity
 hLINGO-1 : RRS DAGTSSADAPRKFNMKMI : 620 72% 86%
 mLINGO-1 : RRS DAGTSSADAPRKFNMKMI : 614 71% 85%

C

zTROY : MPQAQILSRFPQLRILILEL CVLFAVMAFERDCRREOEYKDFKFSGIFCRQDAGCELSKECGFGYGEDAQCVECRASRFKEERSLQKC : 89
 hTROY : MALKVLLLEQKTFFTLLVLLGYLSCKVTCBSGDCRQOEFRRDRSGNCVPCNQGGFVELSKECGFGYGEDAQCVECTRLHRFKEDWGFQKC : 89
 mTROY : MALKVLP LHRTVLAAILLHLACKVSCBTGDCRQOEFRRDRSGNCVPCNQGGFVELSKECGFGYGEDAQCVECRPRFKEDWGFQKC : 89

Signal peptide **CRD 1** **CRD 2**

zTROY : KPCIDCSLNNRFCKGNCSTNNNAVCGDCLPGFYRKTKLIGFQDMECI PCGDP PPPPYE FHCASKVNLVKIASTASSPRDTALAAVICSAL : 178
 hTROY : KPCIDCAVNNRFCKANCSATSDAICGDCLPGFYRKTKLIGFQDMECI PCGDP PPPPYE FHCASKVNLVKIASTASSPRDTALAAVICSAL : 178
 mTROY : KPGADCALVNNRFCKANCSATSDAVCGDCLPGFYRKTKLIGFQDMECI PCGDP PPPPYE FHCASKVNLVKIASTASSPRDTALAAVICSAL : 178

CRD 2 **CRD 3**

zTROY : ATVLLALFILCVIYCKRQLLEKKE--VSMRAHEGPFILGSELSCLDR-RVLELSQRFCCCHCTHSEEQTCGGVQLVSSVCCEDVWSQNRNRD : 265
 hTROY : ATVLLALFILCVIYCKRQFMKKPSWLSRSQDIQYNGSELSCLDFRQPLRHCARACQYHRD SAPMYGPFVHLIFSLCCEEARSSARAVL : 267
 mTROY : ATVLLALFILCVIYCKRQFMKKPSWLSRSQDIQYNGSELSCLDFRQPLRHCARACQYHRD SAPMYGPFVHLIFSLCCEEARSSARAVL : 267

transmembrane domain

zTROY : APAFHSHCRISDN----GRLTNESVGSQTDMACAP-DEVWPLVC-----SRRTDLSIQTNQRCSCEEEDEEVQIS : 331
 hTROY : GCGVHSAASLQARNAGPAGEMVPTFFGSLTQSIICGFSDAWPI MGNPMGGDNISFCDSYPELTGEDHISINPELESSTSLDSNSSQDLV : 356
 mTROY : GCGLRSPTTLQERNPASVGDTMPAFFGVSRSICAEFSDAWPI MGNPLGGD-SSLDSYPELTGEDHISINPENESAASLDSSSGGQDLA : 355

zTROY : D-----QRTAEPEPDAASHKPE-----LIQTTDTEG----- : 356 Identity Similarity
 hTROY : GGAVPVQSHSENTFAATDLSTRYNT--LVESASTQDALTRMSQLDQESGAVIHPATQTSLQEA : 417 43% 56%
 mTROY : G--TAALESSGNVSESTDSFRHGDGTGVWEQTLAQDAQRTPSQGGWEDRENINLAMPTAFQDA : 416 42% 56%

Figure S1