Figure 4

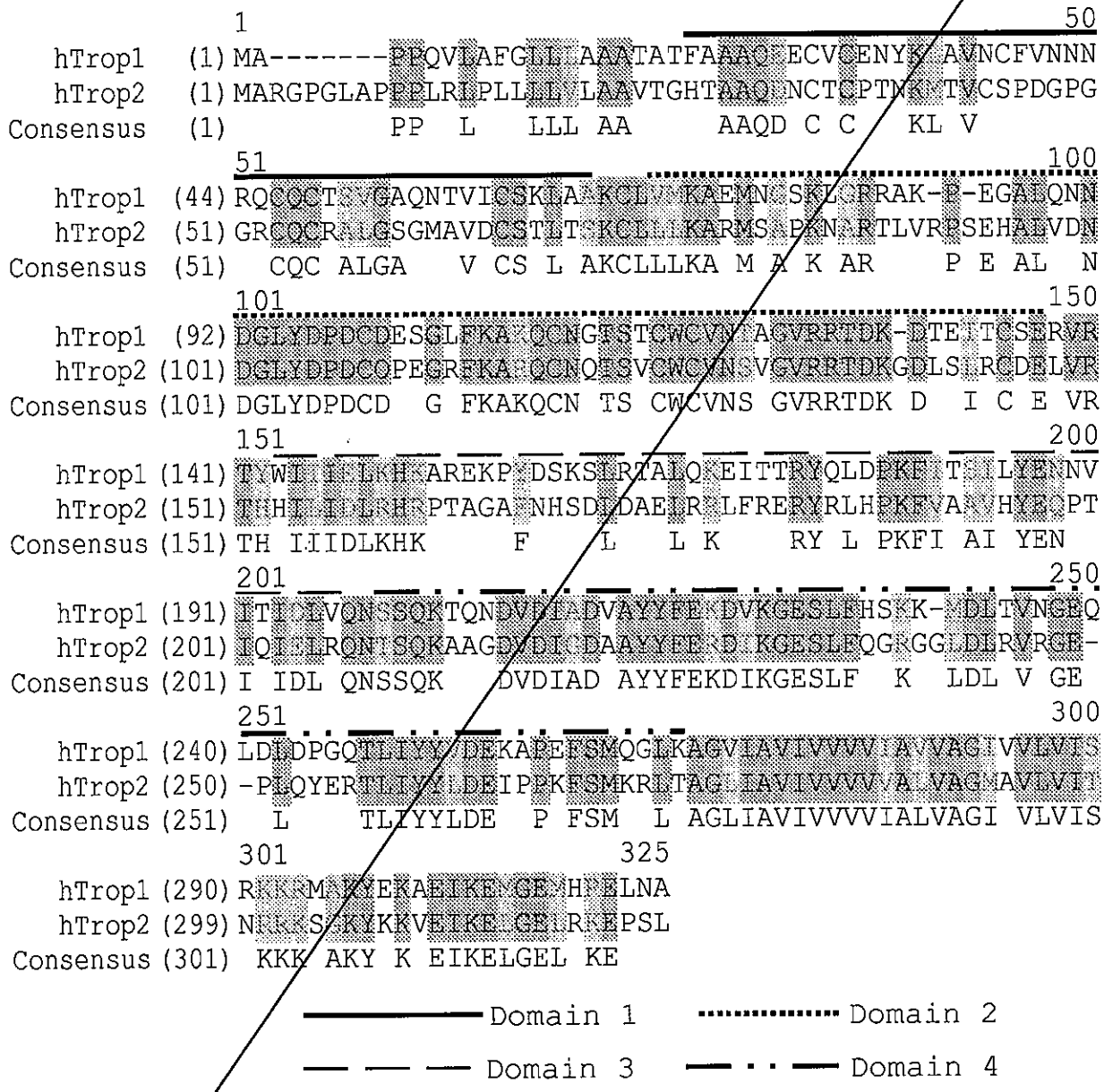

1 50
hTrop1 (1) MA-------PPQVLAFGLL AAATATFAAAQ ECVCENYK AVNCFVNNN
hTrop2 (1) MARGPGLAPPPLRLPLLLL LAAVTGHTAAQ NCTCPTNK TVCSPDGPG
Consensus (1) PP L LLL AA AAQD C C KL V
51 100
hTrop1 (44) RQCQCT GAQNTVICSKLA KCL KAEMN SKL RRAK-P-EGALQNN
hTrop2 (51) GRCQCR LGSGMAVDCSTLT KCLL KARMS PKN RTLVRPSEHALVDN
Consensus (51) CQC ALGA V CS L AKCLLLKA M A K AR P E AL N
101 150
hTrop1 (92) DGLYDPDCDESGLFKA QCNGTSTCWCVV AGVRRTDK-DTEITCSERVR
hTrop2 (101) DGLYDPDCQPEGRFKA QCNQTSVCWCVN VGVRRTDKGDLSLRCDELVR
Consensus (101) DGLYDPDCD G FKAKQCN TS CWCVNS GVRRTDK D I C E VR
151 200
hTrop1 (141) TYWI I LKH AREKP DSKSLRTALQ EITTRYQLDPKF IT ILYENNV
hTrop2 (151) THHT I LRH PTAGA NHSDLDAELR LFREPYRLHPKFVAA VHYEQPT
Consensus (151) TH IIDLKHK F L L K RY L PKFI AI YEN
201 250
hTrop1 (191) ITLELVQN SQKTQNDVDIAD VAYYFEKDVKGESLFHSKK- DLTVNGEQ
hTrop2 (201) IQIILRQN TSQKAAGDVDIC DAAYYFERDIKGESLFQGRGG LDLRVRGE-
Consensus (201) I IDL QNSSQK DVDIAD AYYFEKDIKGESLF K LDL V GE
251 300
hTrop1 (240) LDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAVVAGIVVLVIS
hTrop2 (250) -PLQYERTLIYYIDEIPPKFSMKRLTAGIIAVIVVVVALVAGMAVLVIT
Consensus (251) L TLIYYLDE P FSM L AGLIAVIVVVVIALVAGI VLVIS
301 325
hTrop1 (290) RKKMAKYEKAEIKEMGEMHRELNA
hTrop2 (299) NKKSPKYKKVEIKELGELREPSL
Consensus (301) KKK AKY K EIKELGEL KE
Domain 1
Domain 2
Domain 3
Domain 4

Figure 5

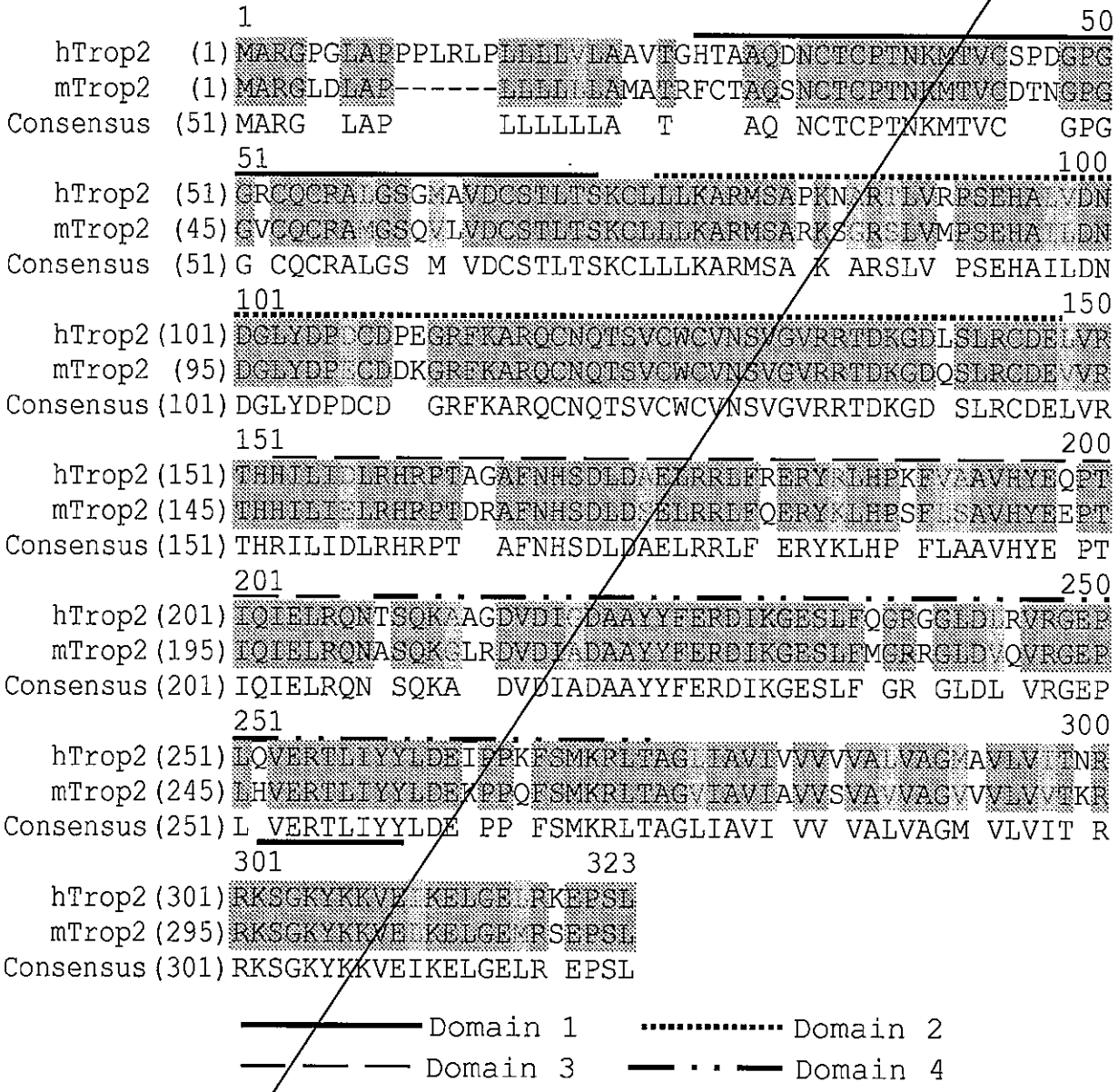

1 50
hTrop2 (1) MARGPGLAPPPLRLPLLLLLLAAAVTGHTAAQDNCTCPTNKMTVCSPDGPG
mTrop2 (1) MARGLDLAP------LLLLLLAMATRFCTAQSNCTCPTNKMTVCDTNGPG
Consensus (51) MARG LAP LLLLLLA T AQ NCTCPTNKMTVC GPG
51 100
hTrop2 (51) GRCQCPALGSGMAVDCSTLTSKCLLLKARMSAPKNVRLVRPSEHAIVDN
mTrop2 (45) GVCQCRAIGSQVLVDCSTLTSKCLLLKARMSARKSVRLVMPSEHAILDN
Consensus (51) G CQCRALGS M VDCSTLTSKCLLLKARMSA K ARSLV PSEHAILDN
101 150
hTrop2 (101) DGLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVR
mTrop2 (95) DGLYDPDCDDKGRFKARQCNQTSVCWCVNGVGVRRTDKGDQSLRCDEVVR
Consensus (101) DGLYDPDCD GRFKARQCNQTSVCWCVNSVGVRRTDKGD SLRCDELVR
151 200
hTrop2 (151) THHILIDLRHRPTAGAFNHSDLDAELRRLFERERYKLHPKFVAAVHYEQPT
mTrop2 (145) THHILIDLRHRPTDRAFNHSDLDAELRRLFQERYKLHPSFLSAVHYEEPT
Consensus (151) THRILIDLRHRPT AFNHSDLDAELRRLF ERYKLHP FLAAVHYE PT
201 250
hTrop2 (201) IQIELRQNTSQKAAGDVDIADAAYYFERDIKGESLFQGRGGLDLRVRGEP
mTrop2 (195) IQIELRQNASQKSLRDVDIADAAYYFERDIKGESLFMGRRGLDVQVRGEP
Consensus (201) IQIELRQN SQKA DVDIADAAYYFERDIKGESLF GR GLDL VRGEP
251 300
hTrop2 (251) LQVERTLIYYLDEIPPKFSMKRLTAGLIAVLVVVVVALVAGMAVLVITNR
mTrop2 (245) LHVERTLIYYLDEKPPQFSMKRLTAGVIAVIAVVSVAVVAGVVVLVVTKR
Consensus (251) L VERTLIYYLDE PP FSMKRLTAGLIAVI VV VALVAGM VLVIT R
301 323
hTrop2 (301) RKSGKYKKVEIKELGELRKEPSL
mTrop2 (295) RKSGKYKKVEIKELGELRSEPSL
Consensus (301) RKSGKYKKVEIKELGELR EPSL
Domain 1
Domain 2
Domain 3
Domain 4

Figure 4

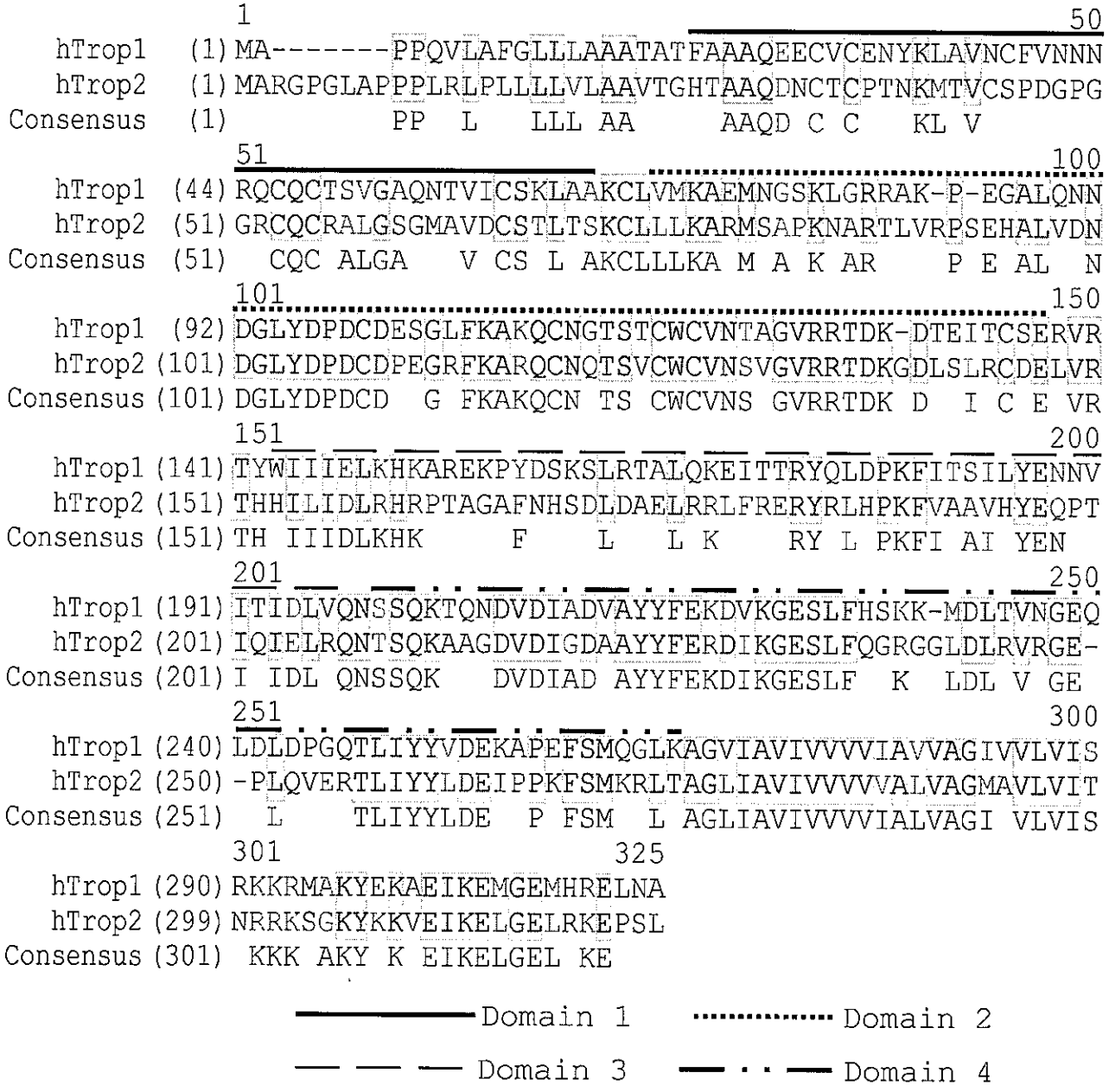
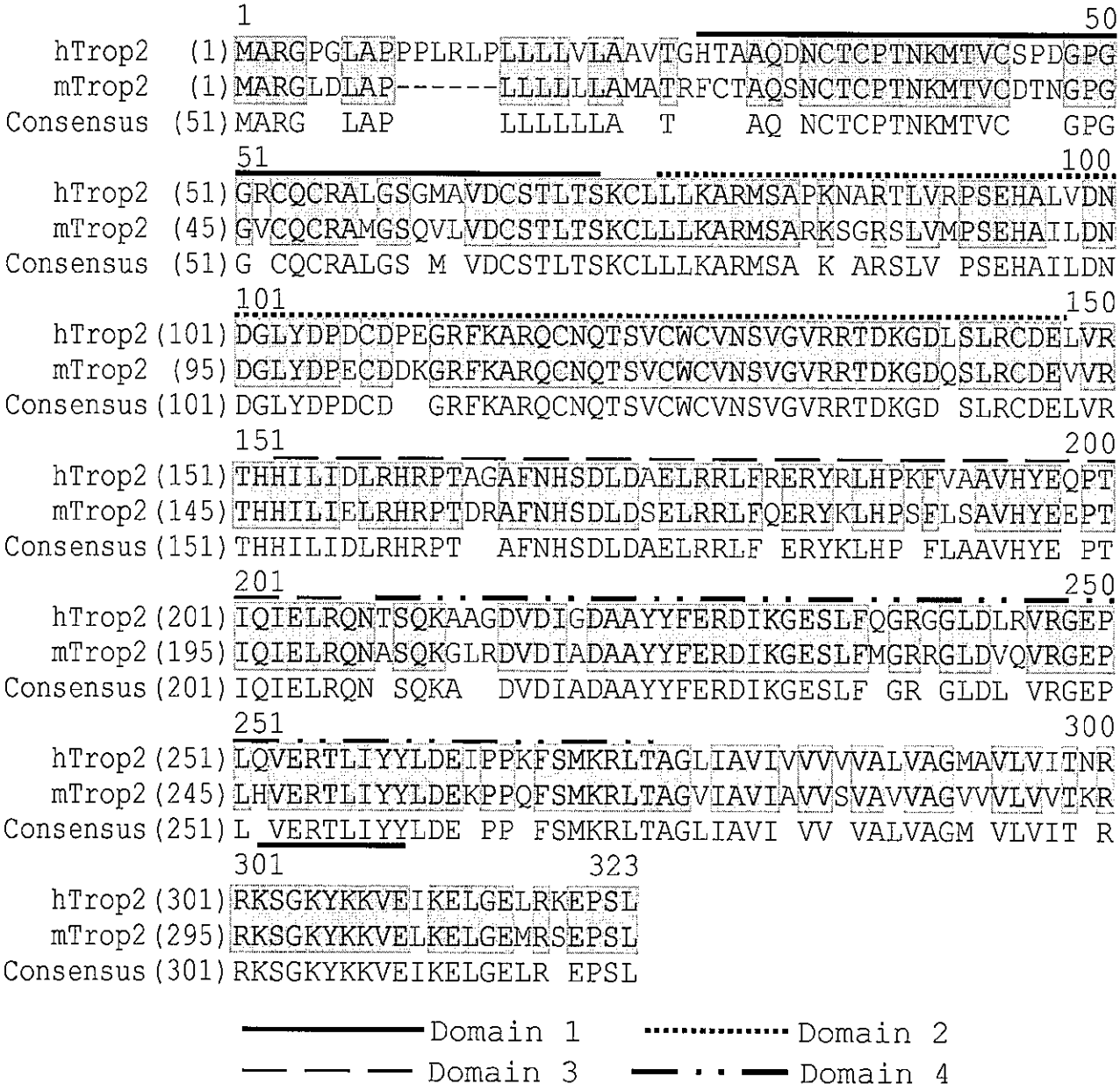

1 50
hTrop1 (1) MA-------PPQVLAFGLLLAAATATFAAAQEECVCENYKLAVNCFVNNN
hTrop2 (1) MARGPGLAPPPLRLPLLLLVLAAVTGHTAAQDNCTCPTNKMTVCSPDGPG
Consensus (1) PP L LLL AA AAQD C C KL V
51 100
hTrop1 (44) RQCQCTSVGAQNTVICSKLAAKCLVMKAEMNGSKLGRRAK-P-EGALQNN
hTrop2 (51) GRCQCRALGSGMAVDCSTLTSKCLLLKARMSAPKNARTLVRPSEHALVDN
Consensus (51) CQC ALGA V CS L AKCLLLKA M A K AR P E AL N
101 150
hTrop1 (92) DGLYDPDCDESGLFKAKQCNGTSTCWCVNTAGVRRTDK-DTEITCSERVR
hTrop2 (101) DGLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVR
Consensus (101) DGLYDPDCD G FKAKQCN TS CWCVNS GVRRTDK D I C E VR
151 200
hTrop1 (141) TYWIIIELKHKAREKPYDSKSLRTALQKEITTRYQLDPKFITSILYENNV
hTrop2 (151) THHILIDLRHRPTAGAFNHSDLDAELRRLFRERYRLHPKFVAAVHYEQPT
Consensus (151) TH IIIDLKHK F L L K RY L PKFI AI YEN
201 250
hTrop1 (191) ITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKK-MDLTVNGEQ
hTrop2 (201) IQIELRQNTSQKAAGDVDIGDAAYYFERDIKGESLFQGRGGLDLRVRGE-
Consensus (201) I IDL QNSSQK DVDIAD AYYFEKDIKGESLF K LDL V GE
251 300
hTrop1 (240) LDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAVVAGIVVLVIS
hTrop2 (250) -PLQVERTLIYYLDEIPPKFSMKRLTAGLIAVIVVVVVALVAGMAVLVIT
Consensus (251) L TLIYYLDE P FSM L AGLIAVIVVVVIALVAGI VLVIS
301 325
hTrop1 (290) RKKRMAKYEKAEIKEMGEMHRELNA
hTrop2 (299) NRRKSGKYKKVEIKELGELRKEPSL
Consensus (301) KKK AKY K EIKELGEL KE
Domain 1
Domain 2
Domain 3
Domain 4

Figure 5


1 50
hTrop2 (1) MARGPGLAPPPLRLPLLLLLVLAAVTGHTAAQDNCTCPTNKMTVCSPDGPG
mTrop2 (1) MARGLDLAP------LLLLLLAMATRFCTAQSNCTCPTNKMTVCDTNGPG
Consensus (51) MARG LAP LLLLLLA T AQ NCTCPTNKMTVC GPG
51 100
hTrop2 (51) GRCQCRALGSGMAVDCSTLTSKCLLLKARMSAPKNARTLVRPSEHALVDN
mTrop2 (45) GVCQCRAMGSQVLVDCSTLTSKCLLLKARMSARKSGRSLVMPSEHAILDN
Consensus (51) G CQCRALGS M VDCSTLTSKCLLLKARMSA K ARSLV PSEHAILDN
101 150
hTrop2 (101) DGLYDPDCDPEGRFKARQCNQTSVCWCVNSVGVRRTDKGDLSLRCDELVR
mTrop2 (95) DGLYDPECDDKGRFKARQCNQTSVCWCVNSVGVRRTDKGDQSLRCDEVVR
Consensus (101) DGLYDPDCD GRFKARQCNQTSVCWCVNSVGVRRTDKGD SLRCDELVR
151 200
hTrop2 (151) THHILIDLRHRPTAGAFNHSDLDAELRRLFRERYRLHPKFVAAVHYEQPT
mTrop2 (145) THHILIELRHRPTDRAFNHSDLDSELRRLFQERYKLHPSFLSAVHYEEPT
Consensus (151) THHILIDLRHRPT AFNHSDLDAELRRLF ERYKLHP FLAAVHYE PT
201 250
hTrop2 (201) IQIELRQNTSQKAAGDVDIGDAAYYFERDIKGESLFQGRGGLDLRVRGEP
mTrop2 (195) IQIELRQNASQKGLRDVDIADAAYYFERDIKGESLFMGRRGLDVQVRGEP
Consensus (201) IQIELRQN SQKA DVDIADAAYYFERDIKGESLF GR GLDL VRGEP
251 300
hTrop2 (251) LQVERTLIYYLDEIPPKFSMKRLTAGLIAVIVVVVVALVAGMAVLVITNR
mTrop2 (245) LHVERTLIYYLDEKPPQFSMKRLTAGVIAVIAVVSVAVVAGVVVLVVTKR
Consensus (251) L VERTLIYYLDE PP FSMKRLTAGLIAVI VV VALVAGM VLVIT R
301 323
hTrop2 (301) RKSGKYKKVEIKELGELRKEPSL
mTrop2 (295) RKSGKYKKVELKELGEMRSEPSL
Consensus (301) RKSGKYKKVEIKELGELR EPSL
Domain 1
Domain 2
Domain 3
Domain 4