

TRIM1 (Q9UJV3)	MGESFASVVLNASGGL-----FSLKMETLESELTPICILELFD-----PILL-PGASISLGFSAHRILVSSC	FQCTCRVYVLSNHRG-LDGLK-RNVTLQNIIDRFQKA--SV
TRIM2 (Q9C040)	MASEG-----TNIPG-----PVVQRIKDKQFLKISICILEYRKN-----PKVL-PGLTFTCEERLQNYIPAHS	LSCFVCRQTSILPEKG-VAALQ-NNFFITNLMQVLRQT--PG
TRIM3 (Q75382)	MAKRE-----DSPG-----FEVQPMKQRFVLSICILDYRQC-----PKVL-PGLTFTCEERLQNYIPAQS	LSCFVCRQTSILPEQG-VSALQ-NNFFISLSMEAMQQA--PD
TRIM4 (Q9C037)	ME-----AEDIQEELTFCPIGLDYFD-----PVSI-EGGNFRCGLLHRNWAFFG	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM5 (Q9C035)	NA-----SGLLVNKRVEVTPICILELLTQ-----PLSL-DGHSFRCAGLNTANHKKSM	SSCFVCRISYQ-----PENIR-PNRIVANIVEKLEVV--KL
TRIM6 (Q9C030)	MT-----SPVLVDIREEVTPICILELLTE-----PLSI-DGHSFRCAGLITPNGRESV	RGCFVQCTSYQ-----PGLNR-PNRHLANIVRRLREVV--VL
TRIM7 (Q9C029)	MAAVGPRTPGGTGAEA-----LALAEALQGEATFCPIGLELFRE-----PVSV-EGHSFRCAGIIGRCMERPG	LPFCQCREPAR-----PSQLR-PNRQLAAGVATLRLRF--SL
TRIM8 (Q9BZ89)	MA-----ENWKNCFEELTFCPIGLHVFVE-----PVQL-PKKNFRCAGIIGEAWAKDS	VRCFEONQAYNQ-----KPGLE-KNKLKTNIVEKFNAL--HV
TRIM9 (Q9C026)	-----MEMEELKFCVPCGSFYRE-----PILL-PGSHNLQAGARNLVQTP	ITCFEHRSLLDLDRG-LRGFF-PNRVLGGVDRYQQS--KA
TRIM10 (Q9UDY6)	MAS-----AASVTLAEAVNFCPIQGTFLRE-----PVTI-DGHNFRCAGLTRVYCEIPG	PTCFPLCKEPPR-----PGSFR-PNWQLANVVENIERL--QL
TRIM11 (Q96F44)	MAA-----PDLSTNLQEEATCAICLDYFTD-----PVMT-DGHNFRCAGLTRVYCEIPG	YACFECRELSLSP-----QRNLR-PNRHLANIVRRLREVV--KL
TRIM13 (Q60858)	-----MELLEEDLTCPICCSLFD-----PVVL-PGSHNFRCAGLTRVYCEIPG	FKCFCTCRKETSATG-----INSLQ-VNYSKLGIVKYEKNI--KI
TRIM15 (Q9C019)	MPA-----TSLKRVHVELPACTICAGPLED-----AVTI-PGHTFRCALIPALSQMGA	LLCFLOQEEEQ-----AETPM-APVPLGAVTETCEE--HG
TRIM17 (Q9Y577)	MEA-----VELARKQGEATFCPIGLDYFD-----PVMT-TGHNFRCAGLTRVYCEIPG	FFCFEHRHPSA-----QRNLR-PNRLLTKVAEMAQOH--PG
TRIM18 (Q15344)	-----METLESELTPICILELFD-----PILL-PGASISLGFSAHRILVSHC	FQCTCRSHVITLSQRG-LDGLK-RNVTLQNIIDRFQKA--SV
TRIM19 (P29590)	-----TER-----APASSEEFQFLRCCQAEARCK-----PKLL-PGLTFTCEERLQNYIPAQS	MCFPTIQAFWF--LGA-DTPAL-DWFFESLQRLRLSVY--KA
TRIM21 (P19474)	MAS-----AARLTMMEEVTPICILEPFVE-----PVSI-EGHSFRCAGLITPNGRESV	SVCFVCRQLF-----LKNLR-PNRQLANVVENIERL--QL
TRIM22 (Q81Y49)	ND-----FSVKVDIEKVTFCPIGLELLTE-----PLSL-DGHSFRCAGLITPNGRESV	SSEFVQCTRFQ-----PGLNR-PNRHLANIVRRLREVV--KL
TRIM23 (P36406)	NATLNVNKLGAAGVDSGR-----QSGRTAVVVKLQGVQVDFSLQG--DKVPRLL-DGHSFRCAGLITPNGRESV	IRCFPQVOTLDGDSG-VWGLK-KNFALLELELRLQNG--PI
TRIM24 (Q15164)	SER-----GGEAARLMLLDTCAVQHNIQSR-----APKLL-PGLHSPFCAGLIPAPORYLM	IRCFVCSQEA-----ERHII-DNFFVTKTDEVTST--VE
TRIM25 (Q14258)	MA-----ELCPFAEELSCSICILEPFKE-----PVTT-PGHNFRCAGLTRVYCEIPG	YLCFQRAVYQA-----RQLHL-KNVTLCNVVEQFLQA--DL
TRIM26 (Q12899)	MAT-----SAPLRSLEEVTPICILDYLRD-----PVTI-DGHNFRCAGLTRVYCEIPG	PVCFCKRKFPP-----KRNLR-PNRHLANIVRRLREVV--KL
TRIM27 (P14373)	MAS-----GSVAELQEEVTPICILELQYFAE-----PMML-DGHNFRCAGLTRVYCEIPG	VSCFQCRETFP-----QRHMR-PNRHLANIVRRLREVV--KL
TRIM28 (Q13263)	-----GAELALELHCGVCRELRPE-----REPRLL-PGLHSPFCAGLIPAPORYLM	VDFCFVQKQCF-----SKIDVENYFMR--DS
TRIM31 (Q9BZ79)	MAS-----GQFVNLQEEVTPICILDILQK-----PVTI-DGHNFRCAGLTRVYCEIPG	FKCFPLCKTSVR-----KNAIR-FNSLLRNIVEKIQAL--EA
TRIM32 (Q13049)	MAAAAAS-----HLNLDALREVLKTCPICMESFTEQ-----LRPKLL-HGHTFRCAGLITPNGRESV	VRCFEHRHPSA-----QRNLR-PNRLLTKVAEMAQOH--PG
TRIM33 (Q9UPN9)	-----AGPPGPPASLLDTCVAVCQSLQSR-----EAEPKLL-PGLHSPFCAGLIPAPORYLM	IRCFVCRQCR-----QIDLV-DNYFVKDTEAFSSS--DE
TRIM34 (Q9BY74)	MA-----SKILLNVQEVTPICILELLTE-----PLSL-DGHSFRCAGLITPNGRESV	SSCFVCRISYQ-----PENIR-PNRIVANIVEKLEVV--KL
TRIM35 (Q9DF04)	MERSFDVY-----PQPSRSFKLELLCAVYDFPFD-----AVTL-PGSHNFRCAGLTRVYCEIPG	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM36 (Q9NQ66)	NSESGEMSEFGYIMELIA-----KGVVTIKNIRELTPAKKELFTH-----PILL-PGSHNFRCAGLTRVYCEIPG	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM37 (Q94972)	ND-----EQSVTIAEVRFCPIQEKLRD-----ARLCPHSSKLCQSPKIRWLTQR	AQCFHCRALPQ-----LRELV-NCRWAEVETQOLDL--QL
TRIM38 (Q00635)	MAS-----TSTKMKMEEATFCISLIMNT-----PVSI-NGHSYCHLITDFKFNPS	FCCFQRAFPFH-----MDSLR-PNKGLSGLIEALKET--DA
TRIM39 (Q9HCM9)	MAETSLLEAGASAAT-----AAALENLQVEASCSVGLVYLKE-----PVII-EGGNFRCAGLITPNGRESV	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM40 (Q6P9F5)	MI-----PLQKDNQEGVCPICIQESLKE-----AVST-NGHLLFRVGLTQHVKEAS	FCCFPLCKPCS-----EVLGL-TGICENHQRVCRCF--CE
TRIM41 (Q8WV44)	MAAVAMT-----PNPVQTLQEEAVCAICLDYFTD-----PVSI-DGHNFRCAGLTRVYCEIPG	FTCFQCRKSPF-----RSLFR-PNRQLANVVENIERL--QL
TRIM42 (Q81W25)	-----PANSHLVNHLNCPVMSRLRLH-----PMLP-PGNLSLCKKLRQLQKHAQ	LICFVCRSHSCPMYSN-KMQLP-ENYHLGRITKRYMQE--HG
TRIM43 (Q96B03)	ND-----SDFSHAFQKELSCVILNLYVD-----PVTI-CGHSFRCAGLITPNGRESV	ANCFAPREPSF-----KMDFK-TNILLKNIITAKRA--SL
TRIM45 (Q9H8W5)	MSENKFLPLGFPVSKLT-----SGTALNSGKTHCPILGLFKA-----PILL-PGLTFTCEERLQNYIPAQS	ILCFVDAQVQLPMPG-VKAIT-IDHILVNDVMSLSR--GS
TRIM46 (Q724K8)	MAEGEDMQFTSMDALV-----RISTSMRMEKELLPVQCEMYKQ-----PVLV-PHTNVQAGARVGLQGG	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM47 (Q96L04)	-----MDSGSFFSFCPIGLELRE-----PVTL-PGSHNFRCAGLTRVYCEIPG	ARCFLQCFPPD-----GLQLR-KNHLSELGLRQGS--GP
TRIM48 (Q81W24)	NN-----SGISQVQRELTFCPIQMNFFD-----PVTI-DGHSFRCAGLITPNGRESV	TQCFEIKTQ-----QNLK-TNHLKMASLARKA--SL
TRIM49 (P0C125)	NN-----SGIIQVQFQELTFCPIQMNFFD-----PVTI-DGHSFRCAGLITPNGRESV	VQCFSEKTSKTE-----QNLK-TNHLKMASLARKA--SL
TRIM50 (Q8X6T4)	MAM-----QVSLLELEDLTCPIGLEVFKE-----PMLQ-QGHSYCKGGLVLSLCHLD	LRCFVQRAVD-----GSSSL-PNVSLARVIEALRLP--GD
TRIM51 (Q9BSJ1)	MN-----SGIIQVQFQELTFCPIQMNFFD-----PVTI-DGHSFRCAGLITPNGRESV	AQCFSEKTSKTE-----QNLK-TNHLKMASLARKA--SL
TRIM54 (Q9BYV2)	MNFTVGF--KPLLDG-----AHSMDNLEKGLTCPICLEMFSK-----PVVILP-QGNLRCAGLITPNGRESV	FRCPSCRHVEVLDHRG-VYGLQ-RNLLVNIIDYKQE--SS
TRIM55 (Q9BYV6)	MSASLNY--KSFSSK-----QOTMDNLEKGLTCPICLEMFSK-----PVVILP-QGNLRCAGLITPNGRESV	FRCPSCRHVEVLDHRG-VYGLQ-RNLLVNIIDYKQE--SS
TRIM56 (Q9BRZ2)	MVSHG-----SSP-----SILLEALSDFLACKTCLEQLRA-----PKTL-PGLTFTCEERLQNYIPAQS	VRCFEONQAYNQ-----KPGLE-KNKLKTNIVEKFNAL--HV
TRIM57/59 (Q81WR1)	-----MHNFEELTFCPIQYIFED-----PVVL-PGSHNFRCAGLTRVYCEIPG	LKCFNORSITVEIAPFG-IESLP-PNWFALRAIIEYKQP--AC
TRIM58 (Q8NG06)	MAM-----APPGERLREARCPVLDLQK-----PVSV-DGHSFRCAGLITPNGRESV	YACFECRELSLSP-----QRNLR-PNRHLANIVRRLREVV--KL
TRIM60 (Q495X7)	MEF-----VTALVNLQEESSFCPIGLEYLKQ-----PVTI-NGGNFRCAGLITPNGRESV	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM61 (Q5EBN2)	MEF-----VTALADLRAEASFCPIGLDYLD-----PVTI-SGHNFRCAGLTRVYCEIPG	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM62 (Q9BV03)	NA-----CSLDELLTSCISLQYQD-----PVSL-EGHSFRCAGLITPNGRESV	RDCEFRRTFA-----EALA-PSLKLANIVRRLREVV--KL
TRIM63 (Q96901)	NDYKS-----SLIQD-----GNPMENLEKGLTCPICLEMFSK-----PVVILP-QGNLRCAGLITPNGRESV	FRCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM64 (A6NGJ6)	ND-----SDDIQVQFQELTFCPIQMNFFD-----PVTI-DGHSFRCAGLITPNGRESV	MRCFSPKRISE-----KPNFN-TNVLKMASLARKA--SL
TRIM65 (Q6PJ69)	MA-----AQLLEKLTCAICLGLYQD-----PVTL-PGSHNFRCAGLTRVYCEIPG	KACFECREPPD-----GAELR-RNVSLGVLEVVRAG--PA
TRIM68 (Q6AZ21)	MDP-----TALVEAIVVEVAFICMTFLRE-----PMSI-DGHSFRCAGLITPNGRESV	YTCFQRAVYQA-----RQLHL-KNVTLCNVVEQFLQA--DL
TRIM69 (Q86W76)	MEVSTNPSNIDPGDYVEMNDSITHLPSKVVIQDIIMELHCPICNDWFRD-----PMLL-SGHNFRCAGLTRVYCEIPG	ITCFEHRSLLDLDRG-LRGFF-PNRVLGGVDRYQQS--KA
TRIM71 (Q2Q1W2)	M-----ASFPEFDQFLCILEKEMCGSPAGAAARRLHLV-PGLHSPFCAGLIPAPORYLM	LRCFVQRAVYQA-----RQLHL-KNVTLCNVVEQFLQA--DL
TRIM72 (Q6PM05)	MS-----AAPGLLHQLSCLPILQLLFD-----PMLL-SGHNFRCAGLTRVYCEIPG	YLCFQRAVYQA-----RQLHL-KNVTLCNVVEQFLQA--DL
TRIM73 (Q86VU7)	MAM-----QVSLLELEDLTCPIGLEVFKE-----PMLQ-QGHSYCKGGLVLSLCHLD	VRCFEONQAYNQ-----KPGLE-KNKLKTNIVEKFNAL--HV
TRIM74 (Q86U6V)	MAM-----QVSLLELEDLTCPIGLEVFKE-----PMLQ-QGHSYCKGGLVLSLCHLD	VRCFEONQAYNQ-----KPGLE-KNKLKTNIVEKFNAL--HV
TRIM75 (A6NK02)	MAM-----AAALTLQAEAKSICILDYLD-----PVTI-EGGNFRCAGLITPNGRESV	FFCFEHRHPSA-----PAAIR-PHWALARITEKTRR--RL
TRIM77 (I1YAF6)	MA-----SAITQCSTSELTSIGTDYLD-----PVTI-CGHSFRCAGLITPNGRESV	NCFVCRISYQ-----PENIR-PNRIVANIVEKLEVV--KL

[...]

Figure S1. Alignment of TRIM family RING domains

TRIM family RING domain alignment based on secondary structure prediction and available structural coordinates performed by PROMALS3D (52). Residues coloured in red and blue represents amino acids either observed in, or with a propensity to form, α -helical and β -strand conformations, respectively.