

Supplementary Table 2. Tether repeat (TR) motif family

Consensus:

		$\alpha 1$		$\alpha 2$		$\alpha 3$
	TR ¹	xxxx LL xx LL x LL x		xxxxxxxxxxx LL x LL xx LL x		xxxxxxxxxxxx LL x
	ARM ²	GGLPALV x LL		ExxLxx AA x AL xNLS		xxxNxx ALL

¹TR, tether repeat

²ARM, armadillo repeat

p115 (Rab1)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-20 ¹	.. AETIQKLCDRVA ²	(3)	... LLDDRRNAVRALKSLS	(3) RLEVGIQ
TR2	(0) ³	... AMEHLHVLQ T	(3)	...DSEIIGY ALD TLYN II	(18)	...LGSQFTEI FTKQQ
TR3	(1)	... NVTLLSLL	(3)	...DFHVRWP GVKLLTSLKQ	(0)	...LGPQVQ QIILV
TR4	(2)	... MGVSRLLDLLAD	(1)	...REVIRND GVLLQALT	(2)	...NGAIQ KIVAFE
TR5	(0)	... NAFERLLDIITEEG	(5)IVVED CLILLQ NLL	(2)NNSNQ FFKEG
TR6	(1)	... YIQRMKPVFE	(8)	SAQKVTLNLHL MLQLV RVLV	(4)	PPGATSS QKAMFQC
TR7	(0)	... GLLQQLCTILM	(4)	...PADILTE TINTVSEVI	(2)	...CQVNQ DFASV
TR8	(8)	... PAIVVLLMSMVN	(3)	...PFVLRCA VLYCFQCF L	(2)	NQKGQGEI VSTLL
TR9	(11)	... SAGQLLCGG	(6)LSNWC AAVALAHAL	(2)	...NATQ KEQLL
TR10	(13)	... SLLQQCTNI	(5)	...KIQTRV GLMLLCTWL	(2)	...CPIAV THFL
TR11	(4)	... NVPFLTGQIA	(3)	GEEEQLV QGLCALLL GIS IYF	(8)	...MKEK LKQLIEKR
TR12	(1)	GKEN FTIEKLG ISKH	(23)	.HEFTKL VKELEGVITKATYK		

¹N-terminal residue number of tether repeat

²Known GTPase binding regions are highlighted in yellow

³Values in parentheses are number of insertion residues between adjacent helices

Gm130 (Rab1)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-77	GVPSPGAS LT SMA	(2)QNHD ADNVP NLM	(14)	...LSQQ LNG LV CES
TR2	(4)	NGEG PASSANL	(19)TNQ LNI TIEKL	(16)	...ECHQ KGAL REQ
TR3	(0)	LQVHIQ TIG LV	(0)SEK AE LQ TAL	(0)AHTQ HAARQK
TR4	(16)	RVGELER ALS AV	(15)KERD ALR LELY	(14)	...ELEE KLRV L
TR5	(0)	VTEK AGM Q LNL	(4)KKLE MT ELL LLQ Q F	(8)	...ANQQ LQQA MEER
TR6	(2)	LEAH LGQ V MESV	(9)YAEN LK GESAM		
(Gap) ¹						
TR1	N-460	LRKELEGLAGQL	(16)QEER LLE LERAA	(5)	...QAEAR RQIL ETM
TR2	(16)	LKEQLAELQSGF	(3)TNEN ME ITSAL	(2)	...EQHV KREL GK KL
TR3	(2)	LQEKLSLKE TV	(14)RDQ YLGH LQ QYV	(9)	...KEVL HNQL LLQ T
TR4	(8)	QEAQGKVAEMA	(20)LRA QLSL MA HPG	(13)	...EEEE EA VAV PQ
TR5	(9)	ESREAMVAFNSAV	(19)RCR RLA HL LLASA	(0)	...QKE PEAAA P
TR6	(0)	... APGTGGDSVC	(1)E THR AL QQA ME KL	(17)	...VEE LEHR CT QLS
TR7	(0)	GETD TIGEY ITALY				
(Gap)						
TR1	N-869	KLLELQELVLR LV	(5)WHGR FLAAAQ N PA	(14)	...AAN QQGD LC
TR2	(0)	.EV S LAG S VE PA	(13)TAQ QIM QL REM	(23)	...NDE VKIT VI

¹(Gap), a region > 23 amino acids separating the previous TR domain from the subsequent TR domain

Gmap-210 (ARF1), (Gmap-210 grab domain: 1774-1823)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-8	LGSG LGQS LG QVG	(5)LTG QISN FT KDML	(13)	...SRTKEI EATHAI
(Gap)						
TR1	N-267	ELEN LLQQG SG GV	(12)KTI QVL Q IEKV	(21)	...SAENDR DLRRE
TR2	(6)	EKRQ IMEECENL	(20)KERI LAQ SAS V	(1)	...EVFRL QQA LS DA
(Gap)						
TR1	N-489	EKET LIAE TEEL	(2)QNQ EAT KH MLI	(6)	...QQNE GDS IT SKL
TR2	(14)	.EDDK M DI T KE L	(8)QSE V AL NDL HL T	(3)	...LEDK VEN LV DQL

(Gap)						
TR1	N-664	.LNENLKKVAFDV	(2)ENEKLVLACEDV	(0)RHQLEBCLAGNN
TR2	(4)	EKNTIVETLKM	(21)KYEKTTEEELSNA	(7)LQLEHEHLTKLN
(Gap)						
TR1	N-1038	.KNISLTKQIDQL	0SKDEVGKLTQII	1QKDLEIQALHAR
(Gap)						
TR1	N-1123	MDIVAAKEAALI	(19)MFRETIQNLSRII	(1)EKDIEIDAL
TR2	(0)	..SQKQTLAVL	(0)QTSSTGNEAGGV	(0)NSHQFEEQLQER
TR3	(12)	WKQQVMTVQNM	(9)ELHQQAQVLV	(7)LQVDYTGTLQSY
TR4	(2)	NETKLKNFGQELA	(11)TKDLLLGKLDII	(17)LRASKSEVLSES
(Gap)						
TR1	N-1435	NENELLRQAVINL	(0)KERILILEMDIG	(14)GKETEYQALQET
TR2	(17)	MKEKALAFEQLL	(9)ELNQLLNAVKSM	(7)QQERDQVMLALK
(Gap)						
TR1	N-1651	QRDETALQLSV	(7)YALS LANLQOMVL	(13)ELEKQKQLTAEW
TR2	(6)	LEGKVISLQECL	(1)EANAALDSASRLT	(15)QNELRQEMLDDV
TR3	(14)	VDKVLMRNLFIG	(7)QRHEVLRLMGSLI	(2)RREEMQLFHDD
TR4	(3)	VTRWMTGWLGGG	(16)VNSSFSELFVKFL	(12)LSVHDMKPLDSP
TR5	(4)	RDTNAPESFKDTA				

Golgin-245 (ARL1), (Golgin-245 grip domain: 2168-2215) (PDB-1R4A)¹

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-57	DTQSFAQKLQL	(0)RVPSVESLFRSPI	(5)RSSSKESLVRTS
(Gap)						
TR1	N-135	NKEQLIQRLRRME	(9)YSELVTAYQML	(2)EKKKLQGILSQS
(Gap)						
TR1	N-267	DGEPVVEDGTSVK	(11)QENLLKRCKETI	(2)HKEQCTLLTSE
TR2	(12)	QELEKIKDLHMA	(5)ITQLRDAKNI	(22)EMKEEIAQLR
TR3	(20)	SERAAFEELKAL				
(Gap)						
TR1	N-658	KDKEIIFQAHIE	(2)NEKTLEKLDVK	(7)SSELSEVLKAR
(Gap)						
TR1	N-834	ERILLTKQVAEVE	(2)KKDVCTELDAH	(0)KIQVQDLMQQL
(Gap)						
TR1	N-909	KENMILQMQREGQ	(0)KKEIEILTQKLS		
(Gap)						
TR1	N-981	LKKELENTALELS	(4)QFNAKMLEMA	(30)SAGISDAVSRL
TR2	(3)	QKEQIESLTVH	(0)RRELNDVISIW	(19)QEKEQEVaelk
(Gap)						
TR1	N-1209	LSEELAIQLDICC	(20)KTNAILSRISHCQ	(3)TKVKEALLIKT
(Gap)						
TR1	N-1536	QKTIEIESLNEVL	(10)HKELVQKLQHFQ	(10)KEAEKILITLE
(Gap)						
TR1	N-1773		YQERLIKLEHAE	(2)QHEDQSMIGHL
TR2	(7)	NKKYSLIVAQHVE	(10)KQNLLENVFDDVQ	(17)KELDSCLVRQK
TR3	(0)	.EVHRVEMEELT	(1)KYEKLQALQQMD	(1)RNKPTELLEEN
TR4	(9)	VQPKLLSNMEAQ	(14)KQKLGKEIVRLQ	(9)HQQELEILKKE
TR5	(18)	KHNSTLKQLMREFN	(6)EQLEMTIKEI	(3)QEVEAEELLES
TR6	(0)	..QEE TNQLLKKIA	(20)EEEMTAKVRDLQ	(13)LEQEENPGNDN
TR7	(5)	LQTQLAQKTTLS	(22)YEKNVYATTVGT	(7)YHTDVS LFGEP
TR8	(0)	TEFEYLRKVLFEYM	(4)TKTMAKVITTVL	(3)DDQTQKILEREDARI

Table 3 (to be continued)

¹See Fig.8A

Giantin (Rab1)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-155	EKEELISTLQA	(12)SSTEMEEFVMM	(10)QLQEKEEFISTL
TR2	(4)	SQTQAEQAAQVV	(13)HEDELLQLVTQA	(4)EMQQKLRVLQRK
TR3	(3)	HEESLVGRAQVV				
(Gap)						
TR1	N-316	ESKILLEKMEEL	(11)LQEEEMHLLLEQF	(8)ELESRYSALEQK

TR2	(7)	KTSH ILSLQK TG	(0)QE LQSACDAL	(0)KDQNSK LLQD
TR3	(0)	KNEQ AVQSAQTI	(9)KSKE ISQFLNRL	(5)ETASQ TSFP
TR4	(0)	..D VYNEGTQAV	(15)ENEK GALLSSI	(10)KLSSQ ITLLEAQ
TR5	(5)	ADRE VSEISIV	(20)KHKE LSVLLLEM	(1)EAQEE IAFLKLQ
TR6	(19)	KQME GEGIAP I	(0)KMKV FLEDTGQDFP	(3)NEESS LP AVEKE
TR7	(12)	EEIS LNDAGVEL	(6)GDKS LSAVPDIG	(6)LERLK SQILE
TR8	(0)	LELN FHKAQE IY	(9)EISN LNQLIEEF	(5)NNSSA FTALSE
TR9	(0)	ERDQ LLSQVKEL				
(Gap)						
TR1	N-843	KESE VLEGAERV	(2)ISSK VEELSQAL	(5)EITKM DQLLE
TR2	(0)	KKRD VE TLQQTI	(9)ISFS MTEK MVQL	(0)NEEK FSLGVEI
TR3	(4)	EQLN LLSRAEEA	(17)NYDE MSPAGQ I	(3)ELQH EFDLLKKE
TR4	(13)	NRKE LLQRVSRL				
(Gap)						
TR1	N-1054	KCQE IEIY LKQTI	(19)AEEQ FQALVKQM	(5)DKT NQIDLLQAE
TR2	(1)	.SEN QAI IQKLI	(9)DSVA LVKETVVI	(11)KPE LEBKILALE
(Gap)						
TR1	N-1378	LQIA GLEHLREL	(0)QPK LDELQKLI	(12)QLS EKEAALTKI
(Gap)						
TR1	N-1502	LQEE LSLARGTI	(19)EKDT VLGRLLALL	(7)IT EMDRS LLENQ
TR2	(4)	SCES LKLAL EGLT	(1)DKEK LVKEIESL	(17)LQK EYBIL LQSY
TR3	(5)	EAER IQHVVEAV				
(Gap)						
TR1	N-1814	SVPS AKSANPAV	(8)EINN YLQO IDQL	(20)LENE KNTLLSQI
TR2	(9)	LQEE VTKMNL L	(6)ELSR VTKLKE TA	(3)KDD LEERLMNQL
TR3	(2)	LNGS IGNYCQDVT	(11)EMKN LKCVSEL	(0)EE EKQQLVKEK
TR4	(6)	IRKE YLEKIQGA	(5)NKSH AKELQELL	(6)VK QLQKDC TRYQ
TR5	(0)	EKIS ALERTVKAL				
(Gap)						
TR1	N-2155	LEET IGEIQVTL	(16)TVT QLAAFTKSM	(2)LQD DRDRVIDEA
(Gap)						
TR1	N-2390	GKEE AIQVAIAEL	(3)HDKE TKELENLL	(1)QEE EENI VLEEE
TR2	(6)	KTNQ LMETL KTI	(9)QLDS FVKSMSSL	(14)EER HL SILEKD
(Gap)						
TR1	N-2621	LQEE GTLGLYHA	(4)KEEE VHRLSALF	(6)IAE LEEE LV CVQ
(Gap)						
TR1	N-2731	QIQS FGRSMSSL	(17)YDAS LKELAQ L	(5)LNR ERDALLSET
(Gap)						
TR1	N-2830	QVQS FSKAMASL	(2)ERDH LWNELEKF	(3)EEG KQRSAAQPS
TR2	(4)	EVQS LKKAMSSL	(2)DRDR LLKE LKNL	(22)EYQ DKTKAFQIM
(Gap)						
TR1	N-3146	TRQE VNELRKLL	(4)DQR VAAENALSVA	(22)CGT QEQALLIDL

Golgin-84 (Rab1)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-3	WFVD LAGKAEDLL	(0)NRVD QGAATAL	(18)LHQ QNTDLIYQT
TR2	(1)	PKST YISSAADNI	(1)NQKA TILAGTANV	(18)VPR PSSH FVRRK
TR3	(15)	SQKE PTGRVEI	(20)VNPS VTTIKTI	(4)FGS QTHEAASNS
(Gap)						
TR1	N-275	KSDR MTRGLRA	(0)QVDD LTEAVAA	(10)RLQ EADQLLSTR
(Gap)						
TR1	N-350	LQER LHEADATL	(9)MQSE FAARLNKV	(5)NLAE AITLAERK
(Gap)						
TR1	N-611	EKNS LVFQLERL	(16)INMS GIDN GEGT	(0)RLR NVPLFNDT
TR2	(2)	NLAG MYGKVRKAA	(1)SIDQ FSIRLGI	(0)FLR RYPIAR

Bicaudal D1 (Rab6), Bicaudal D1 rab6a binding domain: 663-803)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-30	EKI QAAEYGLVVL	(19)LKQE LEQLKEAF	(10)GET REETLLQES
TR2	(2)	KEAY YLKILLEM	(16)ENER LTAVVQDL	(20)YKF REARLLQDY

TR3	(4)	EENI TLQKLVSTL	(23) LNSQLEDAIRL	(3)	... AEHQLEEALETL
TR4	(9)	LRKE LSQYISL	(6) ISVDGLKFAEDG	(9)	... NGHIHGPLVKLN
TR5	(9)	KGES LNPVSDLF	(16) EREKAILLANL	(5)	... QLEHTKGALTEQ
(Gap)						
TR1	N-483	MEKE LQKMTSIA	(16) FSEELAQLYHHVC	(3)	... NETPNRVMLDYY
(Gap)						
TR1	N-621	EPMN IYNLNAII	(0) RDQIKHLQKAV	(8)	... QRAAARELAPMI
TR2	(2)	DKEALMEEILKL	(8) EQIATLRAVLKA	(1)	... KQTAEVALANLK
TR3	(4)	NEKAMVTETMTKL	(8) EDAATFSSLRTMF	(10)	... LDEMQRQLAAAE
TR4	(0)	DEKKTLNTLLRMA	(2) QKLALTQRLEDL	(6)	... SRRSKGKLGKSK

Iporin(Rab1), (Iporin run domain: 1031-1175)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-1032	VGHLVLKYLCPAV	(3) LEDGLKAFVLDVI	(3)	... RKNMPWSVVEAS
TR2	(4)	PSTKVLHGLYNKV	(8) HTMRFNAFILGLL	(10)	... HLNHEDIIQTH
TR3	(0)	YQPWGFLSAAHTV	(3) LFEELLLLLQPLA	(0)	... LLPFSLDLLFQ

MICAL-1(Rab1), (MICAL-1 rab1 binding domain: 1029-1067)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-1029	AEDQVLRKLVDLV	(10) EERRLSELALGTG		

Rabenosyn-5(Rab4, 5 & 22), (Rabenosyn-5 rab4 binding domain: 440-503) (PDB-1ZOK)¹

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-456	SDPLLQQIHNITSFIRQA KA	(3)	MDEVRTLQENLRQLQDEYDQQQT EKA		

¹See Fig.7B

Rabenosyn-5(Rab4, 5 & 22), (Rabenosyn-5 rab5 & rab22 binding domain: 728-784) (PDB-1ZOJ)¹

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-736	EELLLQQIDNIKAYIFDA KQ	(3)	LDEVEVLTENLRELKHTLAKQKG GTD		

¹See Fig.7B

Rabaptin5(Rab5), (Rabaptin5 rab5 binding domain: 789-862) (PDB-1TU3)¹

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-803			KNKAQRLQTELDVSEQVQRDFVK LSQTLQVQLERIRQ	(3)	... LERIRAILND

¹See Fig.7B

EEA1(rab5), (EEA1 rab5 binding domain: 38-63)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-38	SEGFICPQCMKSLG	(0) SADELFKHYEAV		

Rim3(Rab3A)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-217	TCDP LYQQALLF	(20) DHKCFMGMAQIML	(0)	... DELDLSAAVTGW

Noc2(Rab3A)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-169	LFHE VVQAFRAAV	(17) TDSAAFNALVTFCI	(2)	... LIGCLQKLLFGK

Rabphilin-3A rab3A binding domain: (40-170)

		$\alpha 1$		$\alpha 2$		$\alpha 3$
TR1	N-50			EKEIINRVIARAEKMETMEQERI GRLVDRLETMRKN	(64)	... SGAWFF