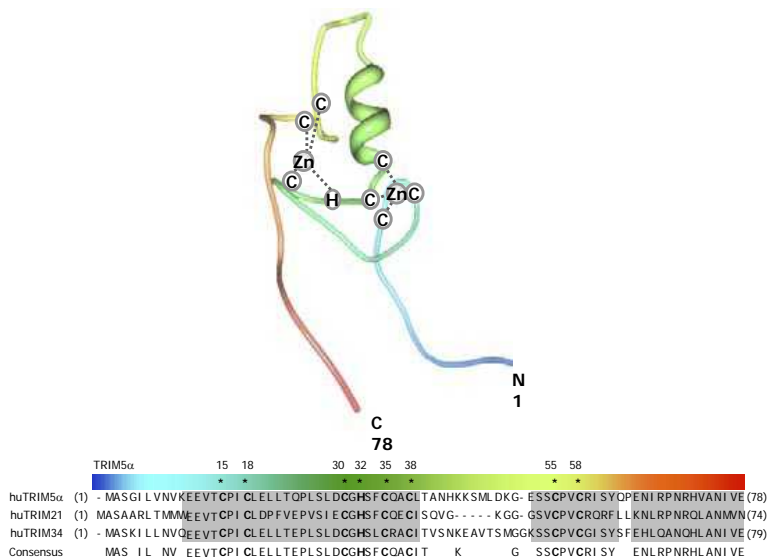
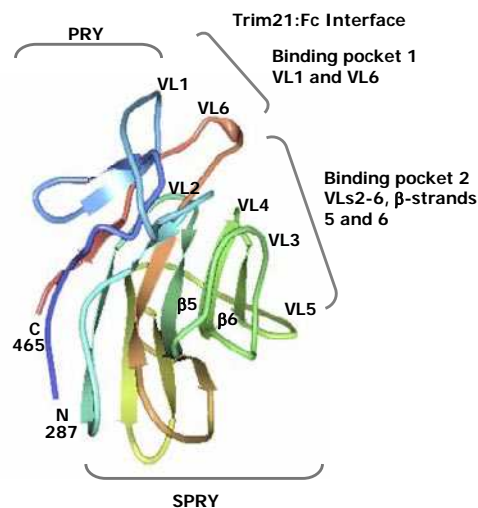


S2 Figure

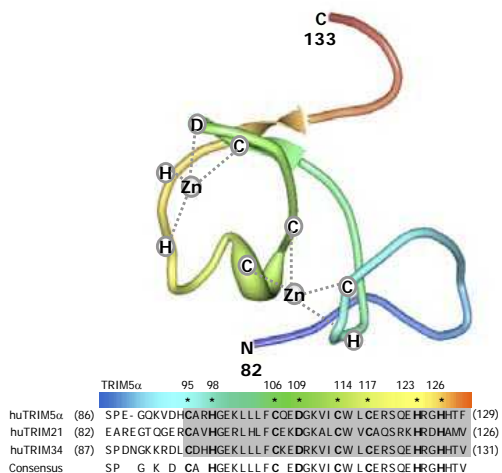
A Human TRIM5 α RING



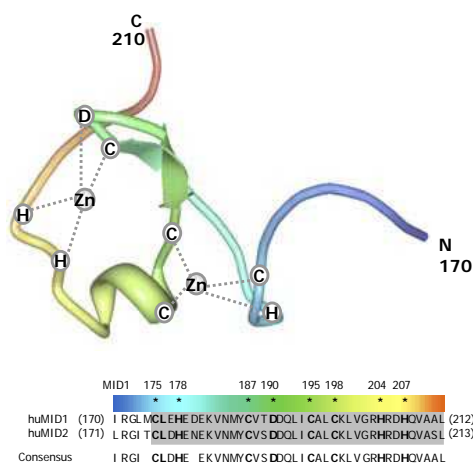
D Human TRIM21 PRYSPRY



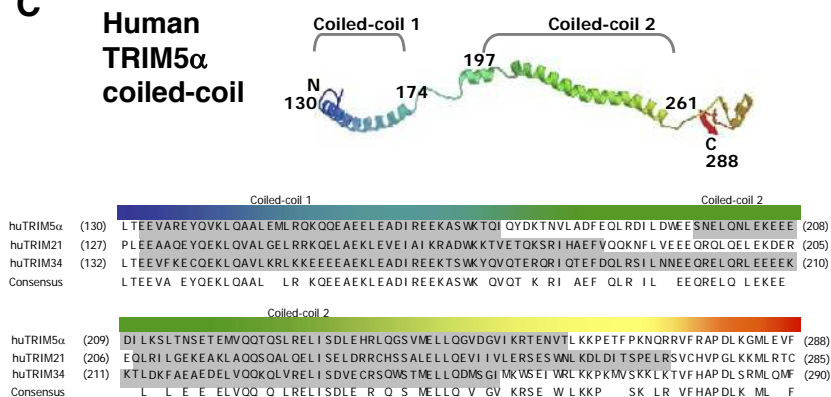
B Human TRIM5 α B-Box2



Human MID1 B-Box2



C Human TRIM5 α coiled-coil



3D structures of TRIM domains

(A) The RING domain. Nuclear magnetic resonance (NMR) analysis of tripartite motif-containing 5 α (TRIM5 α), deposited by Abe, H. *et al.* (PDB ID: [2ECV](#) in the [RCSB Protein Data Bank](#)). The RING-finger motif (from C15 to C58) coordinates two zinc atoms. Comparison of the RING domain amino-acid sequences in three TRIM members with the cysteine (C) and histidine (H) residues involved in zinc-binding are marked with asterisks (*). The grey blocks indicate the conserved regions that contain identical and related amino acids. The rainbow colour represents the N-terminal to C-terminal orientation.

(B) The B-Box domain (B-BOX 2 motif). NMR analysis of TRIM5 α , deposited by Qin, X. R., Hayashi, F. & Yokoyama, S. (PDB ID: [2YRG](#)). The MID1 B-Box is from Massiah, M. *et al.*¹ (PDB ID: [2DQ5](#)). This domain also has a zinc coordinating motif with cysteine (C) and aspartic acid (D) or histidine (H) marked by asterisks.

(C) The coiled-coil domain. Predictions by the [\(PS\)²: protein structure prediction server](#) for the indicated TRIM members. Grey blocks indicate predicted coiled-coil structures.

(D) The PRYSPRY (also known as B30.2) domain. Crystal structure analysis of TRIM21 is by James, L. C. *et al.*² (PDB ID: [2IWG](#)). These domains of TRIM21 interact with the Fc domain of IgG. The PRY and SPRY subdomains are indicated by lines.

1. Massiah, M. A. *et al.* Solution structure of the MID1 B-box2 CHC(D/C)₂H₂ zinc-binding domain: insights into an evolutionarily conserved RING fold. *J. Mol. Biol.* **369**, 1–10 (2007).
2. James, L. C., Keeble, A. H., Khan, Z., Rhodes, D. A. & Trowsdale, J. Structural basis for PRYSPRY-mediated tripartite motif (TRIM) protein function. *Proc. Natl Acad. Sci. USA* **104**, 6200–6205 (2007).