Supplementary Figure S1  Stereo-view of the simulated-annealing omit map of the αCter helix of ArfBD at the interface with ARF1. The colour code is as in Figure 1. The simulated annealing omit map is contoured at the 2 sigma level and shown in black.
Supplementary Figure S2 Surface representation of the hydrophobic pocket (grey) and the triad patch (red) of ARF1 bound to GTP (A; PDB code 1O3Y) and bound to GDP (B; PDB code 1RRF).
Supplementary Figure S3 Cdc42 GTPase activity in presence and absence of ArfBD/RhoGAP domains (P48) of ARHGAP21 and Δ17-ARF1GTP-Q71L.
Supplementary Figure S4 Arf:effector complex structures. The five known Arf:effector complex structures are shown: ARF1:GGA-NGAT domain (PDB code 1J2J; blue (Shiba et al., 2003)); ARL1:Golgin245-GRIP domain (PDB codes 1UPT and 1R4A; green (Panic et al., 2003) and (Wu et al., 2004)); ARF1:ARHGAP21-ArfBD (yellow; this study); ARF6:CTA1 (cholera toxin A-subunit, PDB code 2A5D; red (O’Neal et al., 2005)), and ARL2:PDEδ (PDB code 1KSH; pink (Hanzel-Bayer et al., 2002)). The orientation of the Arf proteins is the same in each structure. Despite variations in the effector structures, all bind a common area on the Arf protein: the switch-interswitch region shown in dark grey. This is true even for the interspecies complex of ARF6:CTA1.