



Supplementary Figure 2: Stereo representation of the nucleotide binding site and catalytic loop region in IpgB2/RhoA crystals of complex A, B and C, respectively. Similar orientations as in Figure 3 A-C are shown. IpgB2 is blue, with the catalytic loop marked in red. Switch I, switch II and other regions of RhoA are shown in yellow, green and brown, respectively. GDP is shown as orange sticks, the Mg ion and water molecules as yellow and red spheres, respectively. (A): GDP-binding pocket and interaction of IpgB2 residue Gln116 in complex A. The SigmaA-weighted [2F_o-F_c] electron density map contoured at 1σ for GDP, Mg²⁺, the Mg²⁺ coordination sphere and Gln116 is colored as blue mesh. (B,C): Similar representation as in (A) for complex B and C, respectively.