



Comparison of the crystal structures of the ternary complexes

Superposition of the ternary complexes (1:1:1) (comprising wildtype BMP-2:BMPR-IA_{ECD}:ActR-IIB_{ECD}) and (1:2:2) (comprising BMP-2L100K/N102D:(BMPR-IA_{ECD})₂:(ActR-IIB_{ECD})₂). Fitting was performed using the positions of the C α atoms of BMP-2 involved in ligand-receptor contacts and the receptor ectodomains. The overlay shows that the structures of both crystal forms are basically identical for the ligand-receptor interacting parts. Only the conformations of some loops in the BMP-2 monomer of the ternary complex (1:1:1) that are not involved in receptor interactions, namely the pre-helix loop in the wrist epitope, differ to the conformations of the respective regions in their bound state.