## **Supplementary information**



Fig. S1: Sequence alignment of kinase domain of all classes of PI3K showing important regions.



Fig.S2: RMSD profiles of top 5 poses of (a) PI-701 in complex with PI3KC2 $\alpha$  (b) PI-702 in complex with PI3KC2 $\alpha$  (c) PI-701 in complex with PI3KC2 $\gamma$  and (d) PI-702 in complex with PI3KC2 $\gamma$ .



Fig.S3: RMSD of Ca and selected pose of (a) PI3KC2 $\alpha$ -PI-701 complex (b) PI3KC2 $\alpha$ -PI-702 complex (c) PI3KC2 $\gamma$ -PI-701 complex (d) PI3KC2 $\gamma$ -PI-702 complex (e) PI3K $\gamma$ -PI-701 complex and (f) PI3K $\gamma$ -PI-702 complex.



Fig.S4: (a) Binding mode of PI-701 in PI3K $\gamma$  (b) residue wise decomposition of binding free energy of PI3K $\gamma$ -PI-701 complex (c) binding mode of PI-702 in PI3K $\gamma$  and (d) residue wise decomposition of binding free energy of PI3K $\gamma$ -PI-702 complex. In case of PI3K $\gamma$ -PI-702 complex, interaction analysis was carried out on frame obtained at 8.5ns and residue wise free energy decomposition was carried out on frame obtained between 8 and 8.5ns of MD simulation.



Fig.S5: RMSD of C $\alpha$  and selected pose of (a) PI3KC2 $\alpha$ -Freitag26 complex (b) PI3KC2 $\beta$ -Freitag26 complex (c) PI3KC2 $\alpha$ -Freitag30 complex and (d) PI3KC2 $\gamma$ -Freitag30 complex.



Fig.S6: (a) Binding mode of Freitag26 in PI3KC2 $\alpha$  (b) residue wise decomposition of binding free energy of PI3KC2 $\alpha$ -Freitag26 complex (c) binding mode of Freitag30 in PI3KC2 $\alpha$  and (d) residue wise decomposition of binding free energy of PI3KC2 $\alpha$ -Freitag30 complex (e) binding mode of Freitag30 in PI3KC2 $\gamma$  and (f) residue wise free energy decomposition of PI3KC2 $\gamma$ -Freitag30 complex.