50 x 60 Å size was created using the Autogrid module (Morris et al., 1998, Morris et .al., 2009) with a grid spacing of 0.375 Å

Ligand 3D structures were built then were energy minimized using the Maestro program (Maestro 2011) and the OPLS force field (Jorgensen and Tirado-Rives 1988) respectively. Atomic partial charges were given for all ligands by Gasteiger-Marsili model (tertiary amine groups were assigned as protonated) (Gasteiger and Marsili .(1980

Next, ligands were docked into the ATP binding site using the Autodock software (version 4.2) (Morris et al., 1998, Morris et al., 2009) where the Lamarckian Genetic Algorithm (Morris et al., 1998) was employed for the conformational sampling process. Subsequently, docked poses were scored via the Autodock scoring function which includes terms for van der Waals, hydrogen bond, electrostatic interactions, and .the ligand internal energy.

The 3D structures of COX-1 and COX-2 were downloaded from the protein data bank (RCSB Protein Data Bank) (PDB, ID: 3N8Z) (Sidhu et al., 2010) and 3NT (Duggan et al., 2010) and then all water molecules were removed. Partial charges were assigned to all atoms using Kollman united atom model that exists in the Autodock Tool software (Sanner 1999, Weiner et al., 1984). Preparations of the COX-1 and COX-2 active site were completed by creating a grid box of a 50 x 50 x 50 Å size with a grid spacing of 0.375 Å using Autogrid (part of the Autodock software package (Morris et al., 1998, Morris et al., 2009). The active site was identified using the COX1 and COX2 co-crystallized ligands. After preparing the protein structures, the ligand preparation process was initiated by building their own 3D structures using the Maestro software (Maestro 2011). A minimization process was carried out on each ligand structure using OPLS force field (Jorgensen and Tirado-Rives 1988).