

4.2 Conclusion

Following the docking experiments for our compounds into the COX-1 and COX-2 active sites, the best docked pose of each compound was studied. Whereas Am6 seems to have the best affinity towards the COX-1 enzyme, (Am4) possesses the best fit in the COX-2 catalytic pocket. Their binding modes appear to be familiar and similar to those shown by different NSAIDS; apart from the unusual hydrogen bonding made by (Am4) with the backbone amide chain of Leu352 and Ser353.

The amino group and the cyclic carbonyl group are the key functional groups and have a direct role in binding with the COX enzymes, whereas the acetylenic group appears to the anchor role; probably by rigidifying the compound structure and hence forcing it to adopt the active conformation. To sum up, the *in silico* findings presented in this work indicate that the synthesized compounds have the required complementary shape and electrostatics interaction needed for COX inhibition. This is strongly supported by the *in vitro* results presented in the previous work for structurally similar synthetic compounds (*i.e.* Aminoacetylenic Isoindoline 1,3-Diones) which were proven to have an inhibition activity against both COX-1 and COX-2 enzymes.