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Title of Thesis: Synthesis, biological evaluation and docking studies of some novel heterocyclic compounds.

**Keywords:** Diketo acids, Amino acid-triazole hybrids, 1,3-thiazoles, 1,2,3-triazole-quinazolinone conjugates, Biological studies, Cytotoxicity, Molecular docking, ADME prediction.

## ABSTRACT

The present research work deals with the synthesis, biological evaluation and docking studies of some novel heterocyclic compounds. The thesis comprises of five chapters.

**Chapter-1** deals with the general introduction, literature reviews of heterocyclic compounds. The biological importance of heterocyclic compounds has been discussed.

**Chapter-2** deals with the designing and synthesis of diketo esters, diketo acids, and their amino acid/dipeptidic analogues. Thirty-two compounds were synthesized and characterized by various spectroscopic techniques. The results of *in vitro* antibacterial screening of synthesized compounds revealed fifteen compounds (**1a–c**, **1e–h**, **1j**, **1l**, **2a–c**, **3d**, **5c** and **5e**) as potent against different bacterial strains. By using the MTT assay on human cell line (HepG2), the viability of cell proliferation was evaluated and nine compounds (**1c**, **1e**, **1j**, **1l**, **2a**, **2b**, **3d**, **5c** and **5e**) showed no cytotoxic effect at the concentration range of 50–450 µg/mL. In the biochemical evaluation against purified methionine aminopeptidase (MetAPs) from *Streptococcus pneumonia* (*Sp*MetAP), *Mycobacterium tuberculosis* (*Mt*MetAP), *Enterococcus faecalis* (*Ef*MetAP) and human (*Hs*MetAP), compounds displayed differential behavior against these four enzymes.

**Chapter-3** deals with designing and synthesis of amino acid-triazole hybrids as anti-leishmanial agents. The synthesized compounds were screened *in vitro* against the promastigote form of *Leishmania donovani* (Dd8 strain). Among the eighteen synthesized compounds, three compounds **6d**, **6g** and **6q** were found to be most potent growth inhibitors with  $IC_{50} = 88.83 \pm 2.93$ ,  $96.88 \pm 12.88$ ,

and  $94.45 \pm 6.51 \mu$ M respectively and displayed no cytotoxicity towards macrophage cells. Supported by docking studies, the lead inhibitors (**6d**, **6g** and **6q**) showed interactions with key residues in the catalytic site of trypanothione reductase.

**Chapter-4** deals with the synthesis, characterization and antimicrobial evaluation of 2,4-disubstituted thiazoles. The structure of the compounds was established using various spectroscopic techniques and X-ray crystallography was performed for compound **1**. The synthesized compounds were screened for their *in vitro* antimicrobial activity. Out of twenty-three compounds, nine compounds (**2a**, **2b**, **2f**, **4a**, **4c**, **4d**, **4e** and **4f**) showed comparatively lower IC<sub>50</sub> values against the tested microbial strains. The three compounds (**2f**, **4c** and **4e**) were selected as promising inhibitors among the synthesized compounds and hemolysis as well as *in vitro* cytotoxicity results of the lead compounds revealed their non-toxic nature. The docking studies of lead inhibitors (**2f**, **4c** and **4e**) showed good binding interactions with bacterial methionine aminopeptidase (MetAP). The significant antimicrobial activity of some of the synthesized compounds and good *in silico* ADME properties highlights them as promising molecules for further synthetic and biological exploration.

**Chapter-5** deals with the synthesis of thirty-four 1,2,3-triazole-quinazolinone conjugates. The structural analysis was further confirmed by X-ray crystallographic studies for compounds **2** and **5c**. Compounds, **5g**, **5n** and **6e** show activity against all the three strains of Candida, viz. *C. albicans, C. glabrata* and *C. tropicalis* with IC<sub>50</sub> values in the range  $8.36 \pm 1.31 \,\mu$ g/mL to  $65.58 \pm 3.20 \,\mu$ g/mL. The compound **5n** emerged as a most potent inhibitor among compounds (**5a–5q**) and **6e** among compounds (**6a–6q**). The hemolysis results of compounds **5e**, **5g**, **5n**, **6c**, **6e** and **6n** revealed non-toxic nature of these compounds. The docking studies of compounds (**5e**, **5n** and **6e**) with lanosterol 14 $\alpha$ -demethylase (CYP51) of *C. glabrata* (PDB ID: 5JLC) showed good binding interactions. Further, *in silico* ADME prediction of synthesized compounds indicated that compounds have a potential to develop as good oral drug candidate.