

Synthesis of Novel Pyrimidine Derivatives as Potential Anticancer Agents

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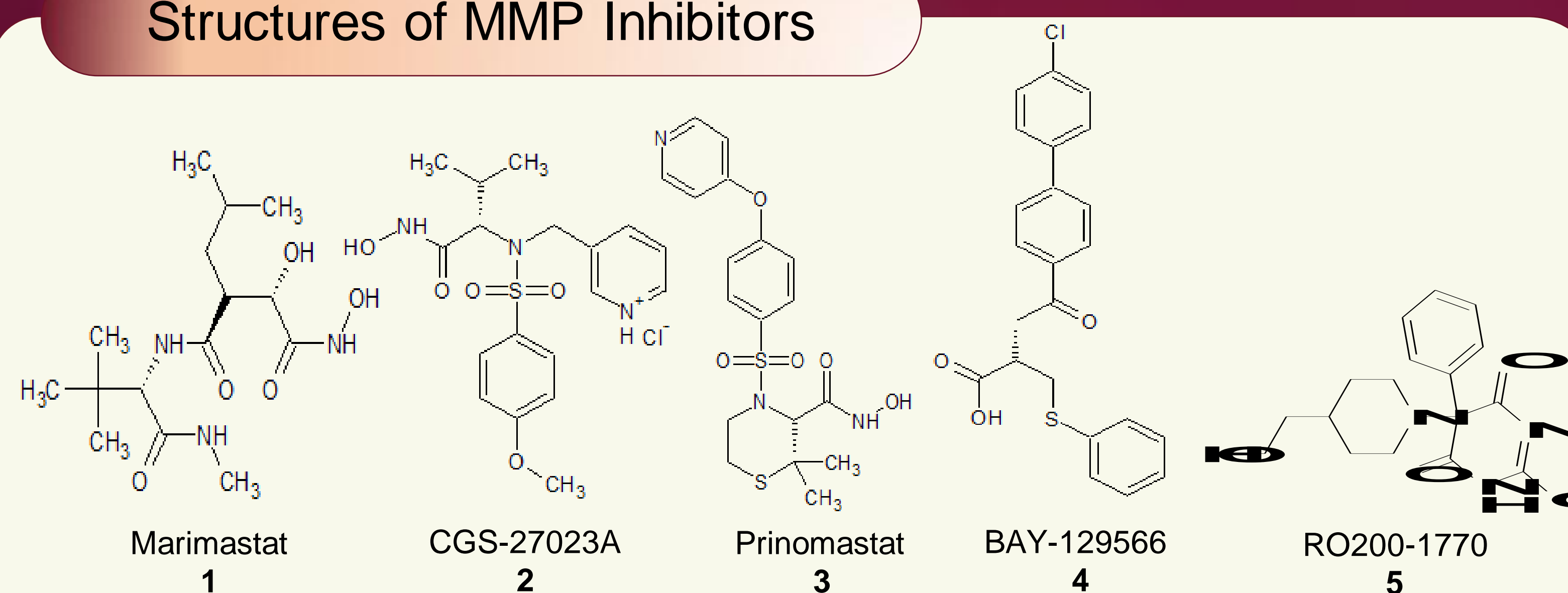
Introduction

Collagenase-II (MMP-8) represent one of the subtypes of Matrix metalloproteinases (MMPs) which are a superfamily of zinc- and calcium-dependent endopeptidases that are responsible for hydrolysis of the peptide bond[1]. Over-regulation of their activity, however, results in uncontrolled degradation of the extracellular matrix in diseases such as cancer[2] (tumor growth, invasion and metastasis), arthritis[3] and multiple sclerosis[4].

Consequently, there has been significant interest in the development of drugs to control the over-regulation of MMP production. Some orally active MMP inhibitors are currently under clinical investigation for the treatment of cancer and/or arthritis. Representative examples include succinamides (Marimastat) **1** [5-7], linear sulfonamides (CGS-27023A) **2** [8], heterocyclic sulfonamides (Prinomastat) **3** [9-10], and biphenylbutanoic acid derivatives (BAY-129566) **4** [11].

Recently, a novel class of barbituric acid derivatives (RO200-1770) **5** was identified as inhibitors of collagenases type 2 (MMP-8) [12].

Structures of MMP Inhibitors



Docking Study

All the target compounds were subjected to docking study to explore their affinity and binding mode to MMP-8. The docking study was performed using MOE-2008. The 3D structure of MMP-8 complexed with Compound **5** was obtained from the protein data bank (PDB entry: 1JJ9) [12]. The vicinity where compound **5** is situated was considered as the active site of MMP-8 and compound **1** was considered as lead structure. We performed 30 docking iteration for each ligand, and the top-scoring configuration of each of the ligand-enzyme complexes was selected on energetic grounds. Two important H-bonds between compound **1** and the amino acid residues Ala161 and Leu160, Co-ordinate bond with Zn²⁺ ion and Hydrophobic interactions with aminoacid residues His197, His201 and His207 were observed.

Figures (1-3) showed interaction of Lead compound or Synthesized compounds with active site of MMP-8.

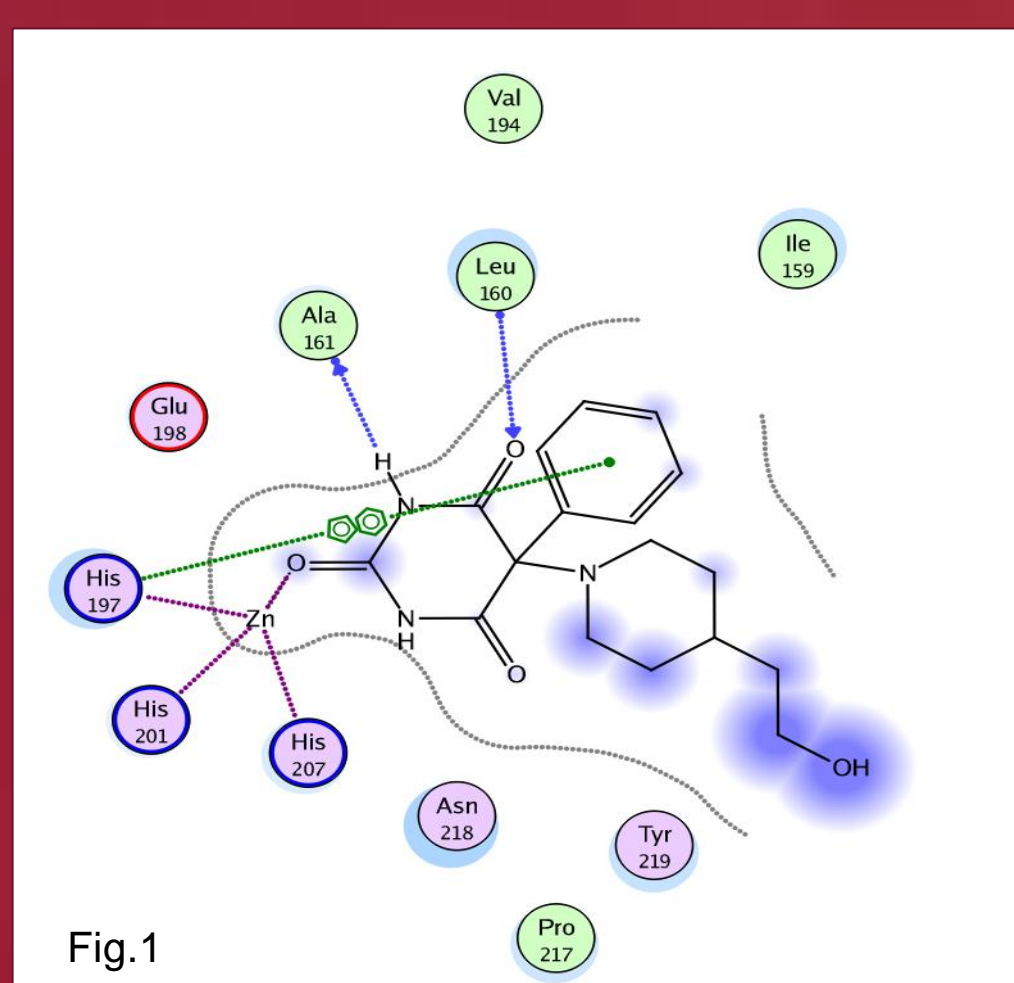


Figure 1. Interaction between The lead compound **5** and binding site of MMP-8 with E-score:-10.4135 (rmsd:1.3486).

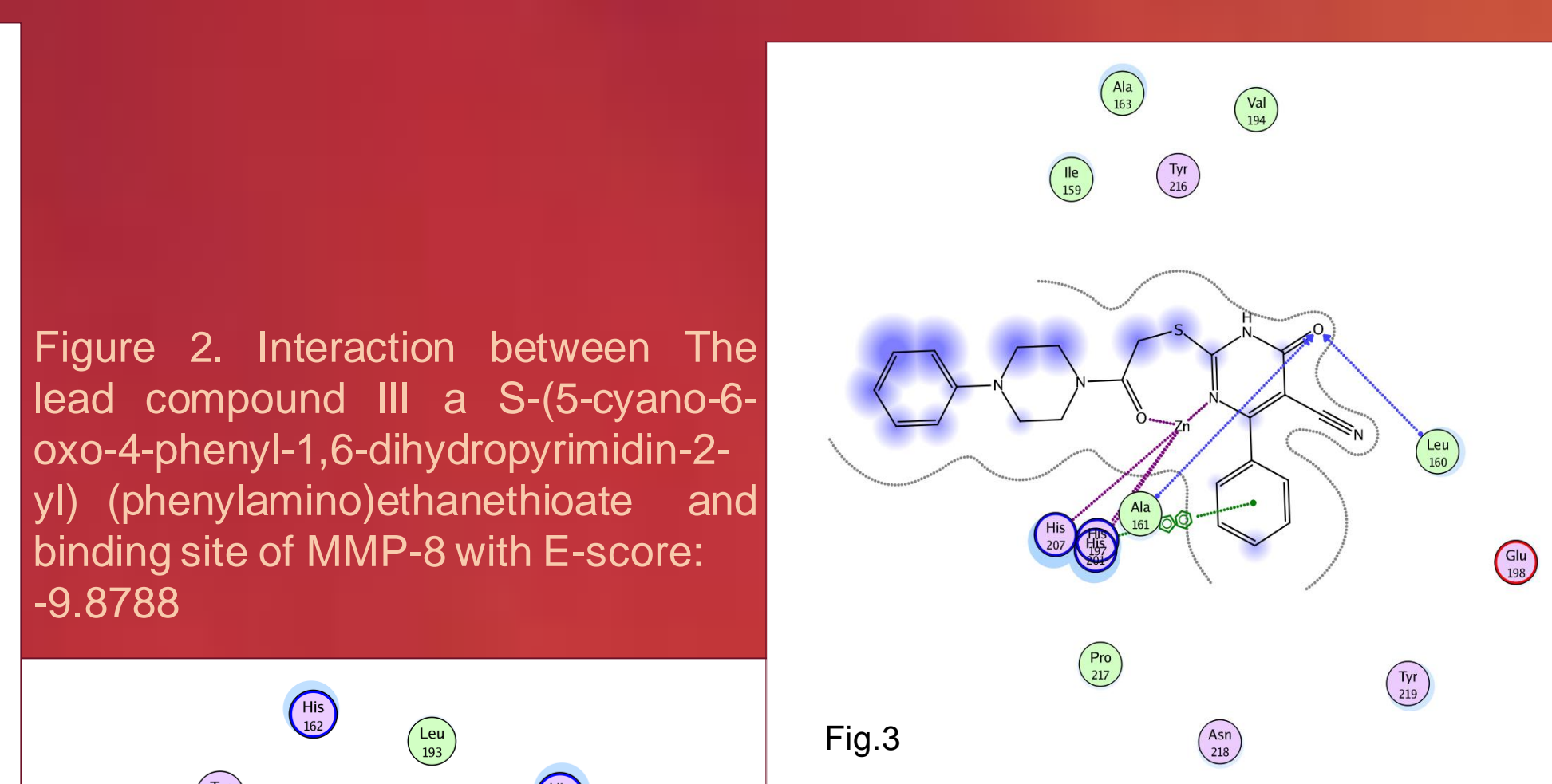


Figure 2. Interaction between The lead compound III a S-(5-cyano-6-oxo-4-phenyl-1,6-dihydropyrimidin-2-yl) (phenylamino)ethanethioate and binding site of MMP-8 with E-score:-9.8788

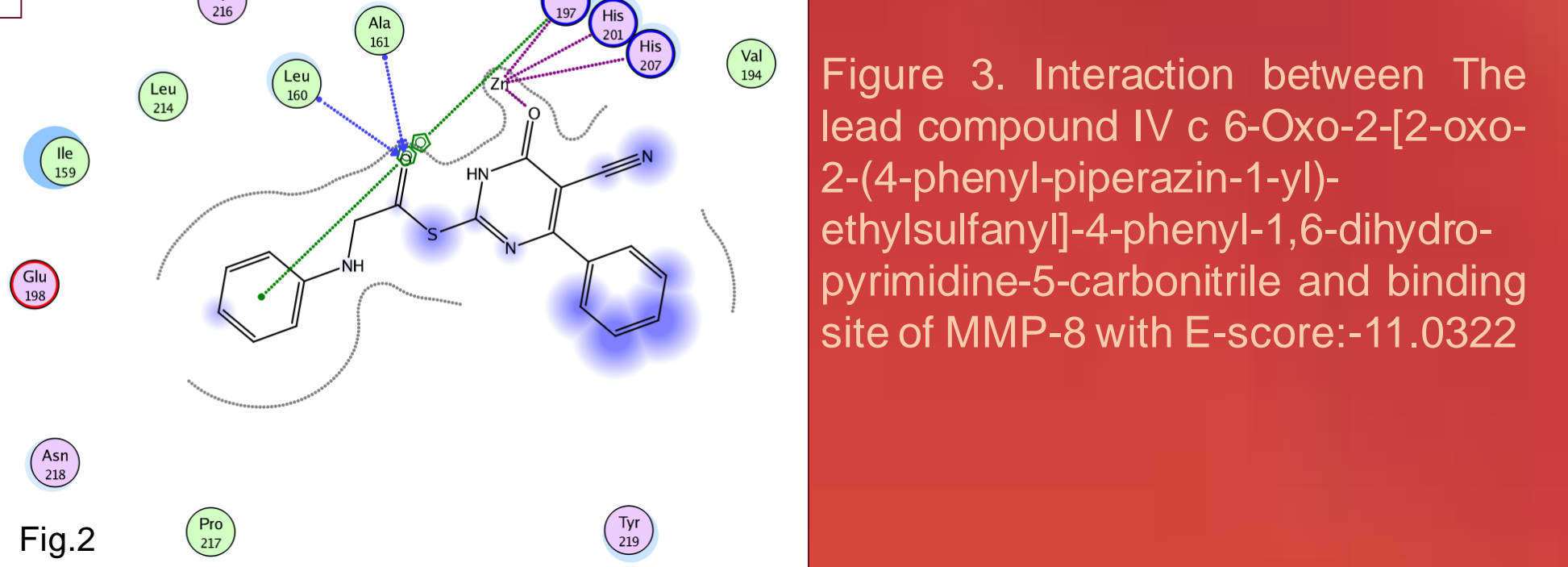


Figure 3. Interaction between The lead compound IV c 6-Oxo-2-[2-oxo-2-(4-phenyl-piperazin-1-yl)-ethylsulfanyl]-4-phenyl-1,6-dihydropyrimidine-5-carbonitrile and binding site of MMP-8 with E-score:-11.0322

Conclusion

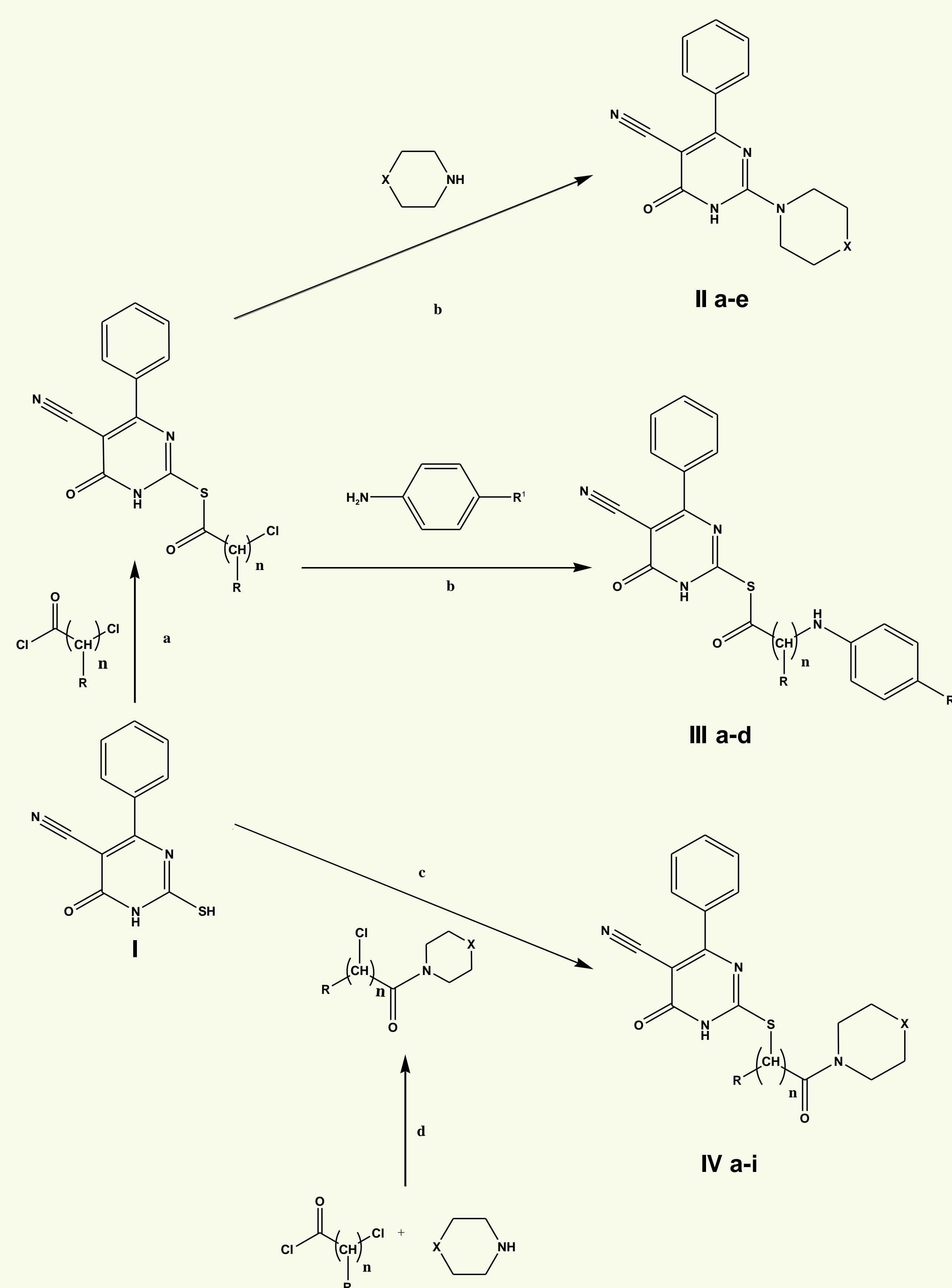
The docking study revealed that almost all of the proposed target compounds bind to Zn²⁺ ion, Ala161, and Leu160 in MMP-8 with higher or comparable binding energy score than the lead compound **1** and thus showed promising activity as MMP-8 inhibitors. Accordingly, these compounds were synthesized hoping that they have potential anticancer activity.

Research Objectives

We were encouraged to prepare a novel series of S-acylated **III a-d** and S-alkylated **IV a-i** pyrimidine derivatives as inhibitors of MMP-8. All the target compounds were subjected to docking study to explore their affinity and binding mode to MMP-8. We also aim to study the effect of the length of spacer and the bulkiness of aryl groups on the anticancer activity.

The synthesis of the target compounds is outlined in **Scheme 1**

Scheme I



Scheme 1. Reagents: a) dry benzene, dry DMF, anhydrous K₂CO₃
b) dry benzene, dry DMF, TMA
c) dry benzene
d) dry DMF, anhydrous K₂CO₃

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