2. Materials and Methods

2.1 Chemicals

The following chemicals and material were used: sodium metal (S&C chemicals), 2-methylindoline, Propargyl Bromide (SIGMA-ALDRICH), Piperidine 99% reagent plus (SIGMA), 2-Methylpiperidine 99% (Alfa Aesar), 2,6- Dimethylpiperidine, Pyrrolidine 98%, N-Methylpiprazine 99% (ALDRICH), Hexamethyleneimine 98% (Alfa Aesar), Tetrahydrofuran (ACROS), 1,4- Dioxan (FULLTIME), Diethylether 99%, Perolium ether (AZ Chem. for Chemicals), Benzene (M & B laboratory), chloroform, Acetonitrile (TEDIA), Potassium carbonate anhydrous (SD. FINE-CHEM), ParaFormaldehyde (BDH Chemicals), cuprous Chloride, DMSO, TMS.

2.2 Instrumentation

Infrared spectra (IR) were recorded using a Nicolet Impact 410 FT-IR spectrophotometer. ^{1}H and ^{13}C NMR were acquired with the aid of Varian 300 MHz spectrometer and DMSO-d_6 as solvent, and TMS as standard.

Differential scanning calorimetry were indicated using a Mettler Toledo STAR® System spectrum. The analysis were indicated by elemental analysis apparatus symbols of the elements analyzed; the results obtained had a maximum deviation of ± 0.4% from the theoretical value.

2.3 Methods and Experimental molecular docking

The EGFR kinase domain used in the docking study was downloaded from the protein data bank (PDB: 1XKK) (Wood et al., 2004) then the co-crystallized ligand and all water molecules were removed from the protein structure. Protein atoms were given partial charges using Kollman united atom model in the Autodock Tool program (Sanner 1999, Weiner et al., 1984). The ATP binding site of the EGFR kinase domain was identified by its own co-crystallized ligand (lapatinib) then a grid box of a 60 x