SUPPLEMENTARY MATERIAL

Design, Synthesis and Biological Evaluation of new Eugenol derivatives containing 1,3,4-oxadiazole as novel inhibitors of Thymidylate Synthase

¹H NMR spectra of compounds 6-19













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¹H NMR spectrum of compound **11**



¹H NMR spectrum of compound **12**



¹H NMR spectrum of compound **13**



¹H NMR spectrum of compound **14**





¹H NMR spectrum of compound **16**



¹H NMR spectrum of compound **17**



¹H NMR spectrum of compound **18**



¹H NMR spectrum of compound **19**



¹³C NMR spectra of compounds 6-19





¹³C NMR spectrum of compound **8**



¹³C NMR spectrum of compound **9**



¹³C NMR spectrum of compound **10**



¹³C NMR spectrum of compound **11**





¹³C NMR spectrum of compound **13**



¹³C NMR spectrum of compound **14**



¹³C NMR spectrum of compound **15**



¹³C NMR spectrum of compound **16**



¹³C NMR spectrum of compound **17**



¹³C NMR spectrum of compound **19**

Mass spectra of compounds 6-19



Compound 6



Compound 7



Compound 8



Compound 9



Compound 10



Compound 11



Compound 12



Compound 13



Compound 14



Compound 15



Compound 16



Compound 17



Compound 18



Experimental

Ligand preparation:

The DFT Calculations have been performed foremostly using the Jaguar^[1]. DFT simulations have been utilized for geometrical optimizations of studied structures, employing the B3LYP/ 6-311G**(d,p) exchange-correlation functional^[2] with TD-DFT measurements used for the simulations frontier molecular orbital and molecular electrostatic maps.

Protein formulation and active site prediction:

¹Schrödinger Maestro | Schrödinger. Schrödinger Release 2018-1 2018.

²Ha, N. Van; Dat, D.T.; Nguyet, T.T. Stereoelectronic Properties of 1,2,4-Triazole-Derived Nheterocyclic Carbenes - A Theoretical Study. *VNU J. Sci. Nat. Sci. Technol.*2019, 35, doi:10.25073/2588-1140/vnunst.4935.

3D crystal structure of TM protein was obtained from the Protein Data Bank. Charges with bond orders were assigned, H atoms were added to heavy atoms. Then, selenomethionines and selenocysteines transferred to methionines and cysteines. All water molecules were removed. The OPLS force field used for protein minimization to set a maximum heavy atom 0.30 Å RMSD. The binding pockets of protein have been identified using the CASTp package. That applies the modern algorithmic and geometrical analysis for analyzing and validation the binding pockets.

Receptor Grid Generation and Molecular Docking

The Glide software³ was utilized for generation of Receptor grid and Docking simulation process. The created grid was parameterized using default software parameter(1.00 van der Waals, 0.25 cut-off of charge), and submitted to OPLS force field. Then produced and centroid the definite cubic box($12 \text{ Å} \times 12 \text{ Å} \times 12 \text{ Å}$) into active site. This box was used for docking study which were carried out using extra precision and write XP descriptor information. This generates favourable ligand poses which are further screened through filters to examine spatial fit of the ligand in the active site. Ligand poses which pass through initial screening are subjected to evaluation and minimization of grid approximation". Scoring was then carried on energy minimized poses to generate Glide score

³Murphy, R.B.; Repasky, M.P.; Greenwood, J.R.; Tubert-Brohman, I.; Jerome, S.; Annabhimoju, R.; Boyles, N.A.; Schmitz, C.D.; Abel, R.; Farid, R.; et al. WScore: A Flexible and Accurate Treatment of Explicit Water Molecules in Ligand-Receptor Docking. *J. Med. Chem.***2016**, doi:10.1021/acs.jmedchem.6b00131.