Electronic Supplementary Material (ESI) for New Journal of Chemistry. This journal is © The Royal Society of Chemistry and the Centre National de la Recherche Scientifique 2022

## **Supporting Information**

## Design and synthesis of potent benzimidazole derivatives via scaffold hybridization and evaluating their antiproliferative and proapoptotic activity against breast and lung cancer cell lines

# Mohamed Saleh Elgawish<sup>1,2,\*</sup>, Mohamed S. Nafie<sup>3</sup>, Asmaa S. A. Yassen<sup>4</sup>, Koji Yamada<sup>5</sup>, Nagat Ghareb<sup>4</sup>

<sup>1</sup> Medicinal Chemistry Department, Faculty of Pharmacy, Suez Canal University, Ismailia 41522, Egypt,

<sup>2</sup> Chemistry Department, Korea University, Seoul 02841, Republic of Korea

<sup>3</sup> Chemistry Department, Faculty of Science, Suez Canal University, Ismailia 41522, Egypt

<sup>4</sup> Pharmaceutical Organic Chemistry Department, Faculty of Pharmacy, Suez Canal University, Ismailia 41522, Egypt

<sup>5</sup> Graduate School of Biomedical Sciences, Nagasaki University, 1-14 Bunkyo-machi, Nagasaki 852-8521, Japan

#### \*Corresponding Authors

#### E-mail: mohamed\_elgawish@pharm.suez.edu.eg

Phone:+82109893-8184;

Fax: +20643230741

ORCID ID: orcid.org/0000-0002-0910-2893





**Figure S1. (A)** Alignment of the crystallographic bound Lenvatinib (green) and re-docked ligand (grey), (B) the catalytic domain of VEGFR2 shown the distribution of the main regions.



**Figure S2.** two-dimensional-binding modes of sunitinib in DFG-In conformation of the catalytic domain of VEGFR2 (PDB: 3WZD)



**Figure S3** (**A**)Three-dimensional-binding modes of lenvatinib in DFG-In conformation of the catalytic domain of VEGFR2 (PDB 3WZD). (**B**) 2D of Lenvatinib in VEGFR2 catalytic domain, (**C**) Three-dimensional-binding modes of sorafenib in DFG-out conformation of the catalytic domain of VEGFR2 (PDB 3WZE) (**D**) 2D of sorafenib in VEGFR2 catalytic domain.



Figure S4. (A)Three-dimensional-binding modes of Compound 17 in DFG-In conformation of the catalytic domain of VEGFR2 (PDB 3WZD) shown the hydrophilic-hydrophobic interaction. (B), (C), (D) 2D of compounds 8, 12, and 19, respectively in VEGFR2 catalytic domain.



**Figure S5.** (A)Three-dimensional-binding modes of Compound 24 in DFG-In conformation of the catalytic domain of VEGFR2 (PDB: 3WZD) shown close-up view of piperidine ring and Phe-1047, distance and angle of interaction. (B)Three-dimensional-binding modes of Lenvatinib in DFG-In conformation of the catalytic domain of VEGFR2 (PDB: 3WZD) shown close-up view of cyclopropyl ring and Phe-1047, distance and angle of interaction.

## IC<sub>50</sub> graph of VEGFR2 inhibitory assay



IC<sub>50</sub> values were calculated according to non-linear regression curve fit of log(inhibitor) vs. response (three parameters); https://www.graphpad.com/guides/prism/7/curve-fitting/REG DR inhibit.htm

### <sup>1</sup>HNMR and <sup>13</sup>CNMR of the designed molecules





























#### The purity of compounds (17)

The purity of the designed compounds was checked by liquid chromatography using the following condition:

HPLC separation and quantitation were made on a 150 x 4.6 mm (i.d.) Phenomenex® (5  $\mu$ m particle size) reversed phase C18 analytical column. The best composition of the mobile phase through isocratic elution was prepared, the mobile phase was 0.1% orthophosphoric acid: acetonitrile: methanol in ratio 60:20:20 The flow rate was 0.2 ml min<sup>-1</sup>. Quantitation was achieved with PDA detector. All determinations were performed at 25 °C. The injection volume was 20  $\mu$ l.

