Discovery of hydrazide based pyridazino[4,5-*b*]indole scaffold as a new phosphoinositide 3-kinase (PI3K) inhibitors for breast cancer therapy

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1.1. Materials and Methods

1.1. General

Melting points are determined using a melting-point apparatus (SMP10) in open capillaries and are uncorrected. The progress of the reactions was monitored by thin layer chromatography (Merck). Detections were achieved by UV light illumination. For flash chromatography commercial silica was used. Nuclear magnetic resonance (¹H NMR, ¹³C NMR and 2D NMR) spectra were determined in DMSO- d_6 and were recorded on Bruker AC 300-500 spectrometers using TMS as an internal standard. Chemical shifts are termed in δ (ppm) and coupling constants are described in Hz. The assignment of exchangeable OH and NH was confirmed by D₂O. CHNS-microanalysis was done using Flash EA-1112 instrument.

1.2. Biological evaluation

1.2.1. Cytotoxic screening using MTT assay

Using the MTT assay [1], cytotoxic efficacy of the tested derivatives was done against breast cancer (MCF-7) and liver cancer (HepG2) cell lines and normal GMSC cell line. Each cell line was cultured in a proper complete medium composed of RPMI-1640 or DMEM, respectively, supplemented with 10% fetal bovine serum, and 1% Antibiotic (Penicillin/Streptomycin (1:1)) according to the standard cell culture work [2]. Cells were treated for 48 h with four working concentrations of compounds (1, 10, 100, and 1000 μ M). The experiment was conducted six times. Data were calculated as percent of cell viability by the following formula: % cell viability = (Mean absorbance in test wells / Mean absorbance in control wells) x 100, then IC₅₀ was calculated were determined using Graph Pad Prism 7.0 [3].

1.2.2. RT-PCR

Based on the significant cytotoxic activity of the studied derivatives, compound 12 ($IC_{50} = 4.25 \mu M$) was thought worthwhile to further investigate its effect on induction of apoptosis in MCF-7 cancer cells. MCF-7 cells were treated with DMSO (control) and compound 12 (5 μ M- treated) for 48 h. Total RNA was extracted from both treated and non-treated cells using Qiagen RNA extraction. The purity of RNA was recorded using nanodrop spectrophotometer. cDNA synthesis was done, then subsequent qPCR test was performed in a single tube [21]. The primers sequence used in the RT-PCR test were provided through the supplementary online material. The results obtained were expressed in cycle threshold (Ct), and relative quantitation of each tested gene was assessed according to the calculation of delta-delta Ct.

1.3. In silico

All molecular modeling studies were conducted on a computational software basis using the Molecular Operating Environment (MOE 2008-10 Chemical Computing Group, Canada). For the docking studies, the crystal structure of phosphoinositide 3-kinase inhibition was obtained from the Protein data bank (PDB code: 1e7V) [18]. Methodology regarding ligand and receptor preparation and optimization was carried out according to Nafie el.al [4]. Each ligand-receptor complex was tested for interaction analysis, 2D images were made using the MOE visualizing tool, and 3D images were taken by Chimera as a visualizing software.

References

- 1. T. Mosmann, Journal of Immunological Methods. 1983, 65, 55–63.
- 2. R. Ian. Freshney, Culture of animal cells: a manual of basic technique and specialized applications, Wiley-Blackwell, Hoboken, N.J., 2010.
- 3. A.I. Khodair, M.A. Alsafi, M.S. Nafie, Carbohydrate Research. 2019, 486, 107832.
- 4. M.S. Nafie, M.A. Tantawy, G.A. Steroids. 2019, 152, 108485.

Table S1: Summarized ligand-receptor interactions for the lead derivatives with 2D and 3D representation					
Compound	Binding affinity (Kcal/mol)	Type of interaction	Bond length (Aº)	Interaction moiety involved	Amino acid
Co-crystallized ligand	-11.76	H-acceptor	1.55	-0-	Val 882
		р=0 Ile963А /r867А			
Compound 2	-13.38	H-acceptor	1.55	C=0	Val 882





* Binding disposition and ligand-receptor interactions of Co-crystallized ligand (Orange) and docked compounds (green).



Supplementary image for the in vivo work (Fig. 6) (Nafie et al 2020)

NMR Spectra



Figure S1: ¹HNMR of 2- DMSO-*d*₆



Figure S2: ¹H NMR of **2** in DMSO- d_6 + D₂O



Figure S3: ¹³CNMR of 2- DMSO-*d*₆



Figure S4: ¹HNMR of **3-** DMSO-*d*₆



Figure S5: ¹³CNMR of 3- DMSO-*d*₆



Figure S6: ¹HNMR of 4- DMSO-*d*₆



Figure S7: ¹³CNMR of 4- DMSO-*d*₆



Figure S8: ¹HNMR of 5- DMSO-*d*₆



Figure S9: ¹³CNMR of 5- DMSO-*d*₆



Figure S10: ¹HNMR of **6-** DMSO- d_6



Figure S11: ¹³CNMR of 6- DMSO-*d*₆



Figure S12: HMQC spectra of 6- DMSO- d_6



Figure S13: COSY spectra of 6- DMSO-*d*₆



Figure S14: ¹HNMR of 7- DMSO-*d*₆



Figure S15: ¹³CNMR of 7- DMSO-*d*₆



Figure S16: ¹HNMR of 8- DMSO-*d*₆



Figure S17: ¹³CNMR of 8- DMSO-*d*₆



Figure S18: ¹HNMR of 9- DMSO-*d*₆



Figure S19: ¹³CNMR of 9- DMSO-*d*₆



Figure S20: ¹HNMR of 10- DMSO-*d*₆



Figure S21: ¹³ CNMR of **10-** DMSO-*d*₆



Figure S22: HMQC of 10- DMSO-d₆



Figure S23: ¹HNMR of **11-** DMSO-*d*₆



Figure S24: ¹³CNMR of 11- DMSO-*d*₆



Figure S25: ¹HNMR of 12- DMSO-*d*₆

Figure S26: ¹HNMR of 12- DMSO- d_6 + D₂O

Figure S27: ¹³CNMR of 12- DMSO-*d*₆

Figure S28: ¹HNMR of 13- DMSO-*d*₆

Figure S29: ¹HNMR of **13-** DMSO- d_6 + D₂O

Figure S30: ¹³CNMR of **13-** DMSO-*d*₆