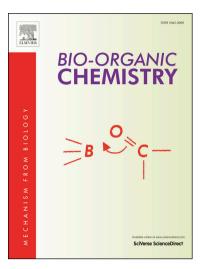
# Journal Pre-proofs

Novel molecular discovery of promising amidine-based thiazole analogues as potent dual Matrix Metalloproteinase-2 and 9 inhibitors: Anticancer activity data with prominent cell cycle Arrest and DNA fragmentation analysis effects

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# Novel molecular discovery of promising amidine-based thiazole analogues as potent dual Matrix Metalloproteinase-2 and 9 inhibitors: Anticancer activity data with prominent cell cycle Arrest and DNA fragmentation analysis effects

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#### Abstract

<sup>b</sup> Ph

Thiazole derivatives are known to possess various biological activities such as antiparasitic, antifungal, antimicrobial and antiproliferative activities. Matrix metalloproteinases (MMPs) are important protease target involved in tumor progression including angiogenesis, tissue invasion, and migration. Therefore, MMPs have also been reported as potential diagnostic and prognostic biomarkers in many types of cancer. Herein, new aryl thiazoles were synthesized and evaluated for their anticancer effects on a panel of cancer cell lines including the invasive MDA-MB-231 line. Some of these compounds showed IC<sub>50</sub> values in the submicromolar range in anti-proliferative assays. In order to examine the relationship between their anticancer activity and MMPs targets, the compounds were evaluated for their inhibitory effects on MMP2 and 9. That data obtained revealed that most of these compounds were potent dual MMP-2/9 inhibitors at nanomolar concentrations. Among these, 2-(1-(2-(2-((*E*)-4-iodobenzylidene)hydrazine-1-carboximidamide (**4a**) was the most potent non-selective dual MMP-2/9 inhibitor with inhibitory concentrations of 56 and 38 nM respectively. When compound **4a** was tested in an MDA-MB-231, HCT-116, MCF-7 model, it effectively inhibited tumor growth, strongly induced cancer cell apoptosis, inhibit cell migration, and suppressed cell cycle progression leading to DNA fragmentation. Taken together, the results of our studies indicate that the newly discovered thiazole-based MMP-2/9 inhibitors have significant potential for anticancer treatment. **Keywords:** Structure-based design; 2-aminothiazole; amidine; MMP-2/9 inhibitor; anticancer activity.

#### 1. Introduction

Cancer is a major medical concern and among the most frequent causes for death worldwide [1, 2] Although the survival rates for certain cancers have increased over the past decades due to early diagnosis and development of innovative treatments, effective therapeutic strategies for the successful treatment of advanced cancers are still lacking [3]. There is clinical evidence that about 80% of cancer-related deaths are due to a lack of early diagnosis [4,5]. For advanced cancers, conventional methods of treatment such as radiotherapy and chemotherapy are no longer efficacious because they destroy normal cells and malignant cells at comparable rates, leading to severe toxicity with only small to moderate therapeutic improvements [6, 7]. On the other hand, progress has been made with targeted therapies such as broad-spectrum kinase inhibition for the treatment of advanced cancers [8]. For targeted anticancer therapies, thiazoles are among the most versatile compound classes. The thiazole heterocycle is found in many anticancer agents and different studies have shown that thiazole based compounds induce a variety of therapeutically relevant pharmacological effects [9-16]. The thiazole nucleus originates from the reaction of the thiosemicarbazone moiety and thiazole-based agents display broad-spectrum antiproliferative effects and

low toxicity in preclinical studies [17,18]. The thiosemicarbazone precursor of the thiazole heterocycle also exhibits anticancer effects. The antitumor activity of thiosemicarbazones appears to be generally due to inhibition of DNA synthesis due to modification of the reductive conversion of ribonucleotides to deoxyribonucleotides [19,20].

Matrix metalloproteinases (MMPs) are a family of extracellular zinc- and calcium-dependent neutral endopeptidases including a number of closely related isoforms playing a crucial role in degradation of extracellular matrix components, tissue remodeling and the pathogenesis of major diseases [21]. MMPs are involved in <u>Journal Pre-proofs</u> sis, cellular variation, and wound healing [22]. Furthermore, they are also implicated in inflammation, tumor cells proliferation, and other diseases [23]. MMPs play a critically important role in the remodeling and repair of physiological tissues, but their overexpression lead to a variety of pathologies including aberrant cell proliferation and cancer [24]. Therefore, inhibiting MMPs is an attractive approach for treating a variety of diseases. For example, many inhibitors of MMP-2 have been proven to prevent tumor growth, some of which have reached clinical trials [25]. Representative examples include compounds 1-4 (**Fig. 1**) that were tested as anticancer agents [26,27]. In drug discovery, a number of MMP isoforms including MMP-2, MMP-3, MMP-8, MMP-9, MMP-12 and MMP-14 are considered as anti-targets whereas MMP-2 and MMP-9 (in the following abbreviated MMP-2/9), the focal points of our study, are regarded as anticancer targets for blocking the proliferation of tumor cells [28,29].

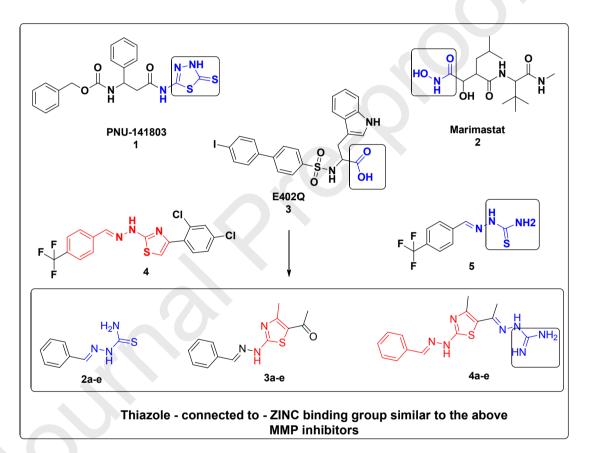


Fig. 1. General strategy for the design of thiazole-based hybrid compounds as MMP-2/9 inhibitors focusing on zinc binding groups (ZBGs) in reference drugs.

Previously, a series of pyrazothiazoles linked to salicylaldehyde were reported as anticancer agents targeting MMP-2/9 [30]. Considering these previous studies, the general anticancer activity of thiazole and thiosemicarbazide moieties, structure-based analyses of the reference compounds in (**Fig. 1**) was carried out as presented below. Our analysis has led to molecular hybridization of the thiazole heterocycle and the hydrophilic metal conjugating guanidine moiety as a zinc binding group in the design of new MMP-2/9 inhibitors targeting their catalytic zinc site in analogy to carbamate- or carboxylate containing clinical inhibitors. Our thiazole/guanidine hybrid design was further extended with different aromatic fragments via a polar linker NH-N=C that contribute to MMP binding of analogues by targeting pockets in the active site region [27]. These newly designed and synthesized compounds with their terminal hydrophilic zinc-chelating substructure were found to be potent MMP-2/9 inhibitors and were also tested for their ability to decrease proliferation of different invasive and non-invasive cancers compared to normal tissues. Antiproliferative activity of our best inhibitors was confirmed for three human cancer cell lines including invasive breast cancer cell line (MDA-MB-231), human colon cancer (HCT-116), and mammary gland breast cancer (MCF-7) compared to two normal cell lines, namely, human keratinocytes cell line (HaCaT) and human diploid fibroblasts (WI-38). In light of recently growing evidence show that MMPs have both proteolytic and non-proteolytic intracellular functions [31], we also examined a

the possible relationship between the combination of internal thiazole with amidine terminus on MMP inhibitory activity of the new compounds and cell apoptosis or cell cycle arrest. Furthermore, SAR features of our inhibitors accentuated the influence of substituents at different positions on the antitumor activity.

#### 2. Results and discussion

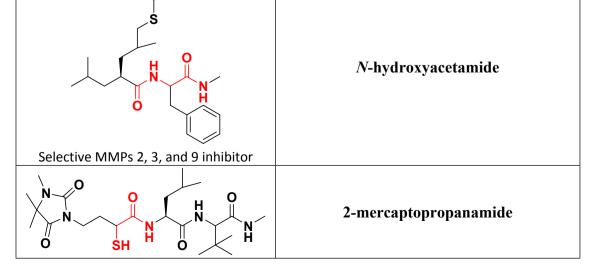
#### 2.1. Structure-based scaffold and compound design

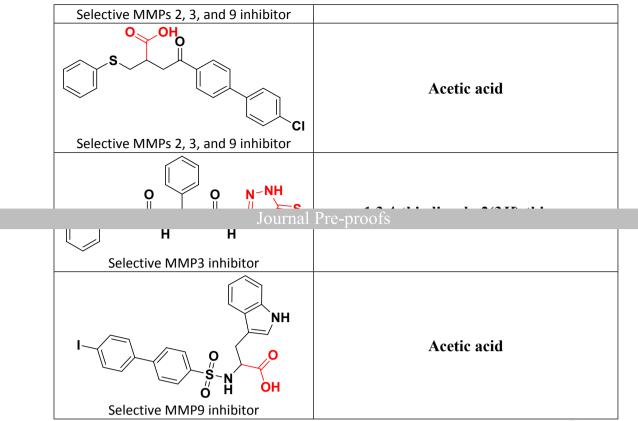
MMP inhibitors (MMPIs) typically act by chelating the catalytic zinc ( $Zp^{2+}$ ) cation, which is a hallmark of MMPIs used as anticancer agents.[32] Some reports indicated that MMPIs act by inhibiting cancer cell growth whereas others reported that MMPIs function by decreasing tumor proliferation through induction of apoptosis via release of TNF $\alpha$  or TRAIL (tumor necrosis factor related apoptosis inducing ligand) from their membrane bound inactive form [32]. MMPs are highly expressed in human cancer and implicated in every stage of cancer development.[32] The cancer cell secrets various agents such as interferon, interleukins and growth factors as well as extracellular MMP inductor which stimulate the surrounding host cell to generate MMPs required for the tumor cell [32].

The structure-based design of our 2-aminothiazole derivative MMP-2/9 dual inhibitors commenced by analyzing a set of different selective MMP inhibitors [33,34] and their binding characteristics in the active sites of MMP-2 (using X-ray structure entry PDB 2SUN) and MMP-9 (PDB 2OW0), respectively. As shown in (**Table 1**), different zinc binding groups (ZBGs) of reference inhibitors were analyzed including hydroxamic acid, thiols, carboxylates and phosphonic acid [21,35]. Among these groups, preference was assigned to the Zn<sup>2+</sup> binding features of hydroxamic acid. In the MMP active site, the NH and deprotonated OH groups of hydroxamic acid form well-defined hydrogen bonds with Ala and Glu residues [35,36].

Table 1. Structural analyses of ZGBs from natural and synthetic MMP-2/9 inhibitors.

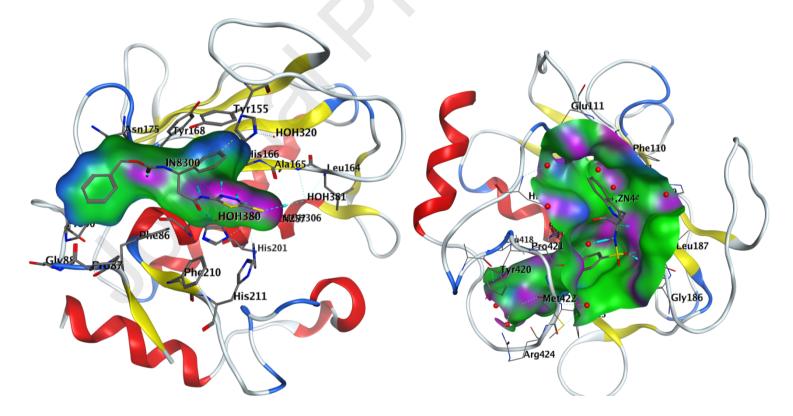
Ligand	ZBG
HO =	<i>N</i> -hydroxyacetamide
HO N	<i>N</i> -hydroxyacetamide
Selective MMPs 2, 3, 9, 13, and 14 inhibitor	<i>N</i> -hydroxythiomorpholine-3-carboxamide
S	





The table lists a variety of MMP reference inhibitors containing different ZGBs (colored in red).

X-ray structures of MP-2/9 are shown in (**Fig. 2**). (**Fig. 2A**) reveal that the thiazolidine-based inhibitor bound to MMP-2 formed a monodentate interaction with the zinc cation in the catalytic site through the sulfhydryl group that was further stabilized by intermolecular H<sub>2</sub>O-mediated hydrogen bonds. In the active site of MMP-2, additional hydrogen bonds were formed through the two imide linkers with involving residue Glu 202, His 205, Ala 167, Tyr 168 and Ala 169. Furthermore, hydrophobic subsites were expected to accommodate terminal lipophilic or aromatic groups of inhibitors. (**Fig. 2B**) shows that hydroxamate-based inhibitor bound to MMP-9 formed a bidentate interaction with the catalytic zinc site and well-defined hydrogen bonds with the active site of MMP-9 involving residues Gly 186, Pro 421, Glu 402, Ala 189, Leu 188 and Tyr 423. This map of interactions are derived from the analyses of both crystal structures was consistent with previous findings [37].



Α

# **Fig. 2.** X-ray structures of **A**) MMP-2 and **B**) MMP-9 with bound inhibitors. Selected amino acids in the active site region and crystallographic water molecules are labeled.

B

On the basis of the observed interaction patterns and bound inhibitors, we carried out a flexible alignment of the MMP-2/9 inhibitors in (Table 1) in the

active sites of MMP-2/9 using the Molecular Operating Environment (MOE) [38] and further refined the alignment though intra- and inter-molecular

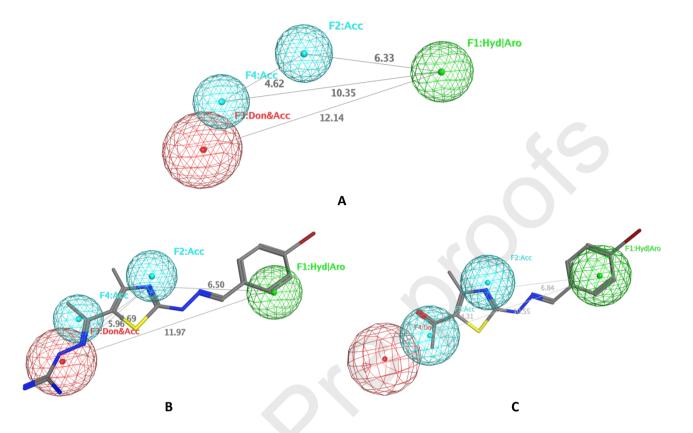
energy minimization. On the basis of these alignments, a 4-point 3D pharmacophore model for inhibitor binding to MMP-2/9 was derived. (Fig. 3A)

shows the pharmacophore model that consisted of a hydrophobic/aromatic feature, two hydrogen bond donor functions and a donor/acceptor function

in a defined spatial arrangement [39]. The model represented substructures of inhibitors that formed characteristic interactions or occupied a hydrophobic pocket within in the active site and were considered important for inhibitory activity.

Guided by our structure-based pharmacophore model, we then designed different thiazole-based compounds and examined their detailed fit to the model, which represented the central part of our structure-based design exercise. Compounds derived on the basis of a newly proposed 2-aminothiazole scaffold yielded an excellent fit to the pharmacophore model, as illustrated in (**Fig. 3B**). In exemplary compounds with and without the amidine group, the amidine moiety consistently mapped to the ZBG site represented by the donor/acceptor feature in strongly active compounds and was absent in case of <u>Journal Pre-proofs</u> low activity compounds. The excellent fit of the newly designed 2-aminothiazole-based compounds to the pharmacophore model motivated us to

synthesize these compounds and test them for MMP-2/9 inhibitory activity.

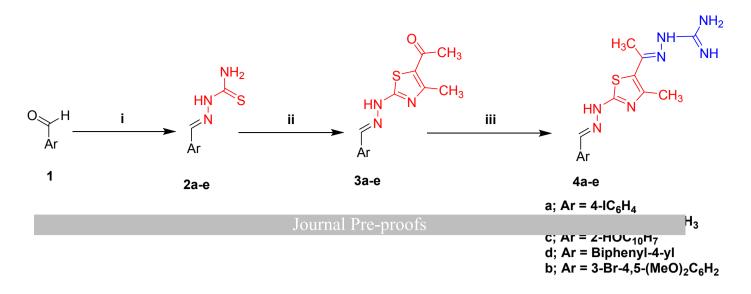


**Fig. 3.** Pharmacophore model and newly designed inhibitors. **A)** Shows the structure-based 3D pharmacophore model for inhibitor binding to MMP-2/9. Distances between pharmacophore features are given in Å. **B**) Shows the fit of an exemplary Amidine thiazole-based compound to the pharmacophore model. **C**) Shows the fit of an exemplary non-amidine thiazole-based compound to the pharmacophore model.

#### 2.2. Chemistry

Condensation of substituted aromatic aldehydes (**1a-e**), namely 4-iodobenzaldehyde, 4-hydroxy-3-methoxybenzaldehyde, 2-hydroxy-1-naphthaldyhde, [1,1'-biphenyl]-4-carbaldehyde and 3-bromo-4,5-dimethoxybenzaldehyde with hydrazinecarbothioamide in ethanol/AcOH solution under reflux afforded the corresponding 2-arylidenehydrazine-1-carbothioamides (**2a-e**). Cyclization of compounds **2a-e** with 3-chloropentane-2,4-dione in absolute ethanol under reflux gave the cycloaddition products, 1-(2-(2-(arylidenehydrazinyl)-4-methylthiazol-5-yl)ethanone (**3a-e**). Interaction of the latercompounds**3a-e**with hydrazinecarboximidamide hydrochloride in absolute ethanol in the presence of a catalytic amount of lithium chloride underreflux for 24 hours resulted in the corresponding <math>2-(1-(2-((E)-2-arylidenehydrazinyl)-4-methylthiazol-5 yl)ethylidene)hydrazinecarboximidamides (**4a**e). These reactions and the newly designed compounds are depicted in**Scheme 1**. The structure and purity of compounds**2-4**were confirmed by the

spectral data as described before [40]. The all characterization data including HNMR, CNMR, LCMS are found in supplementary section in detail.



Scheme 1. Preparation of a series of 4-arylthiazole derivatives (4a-e) as novel MMP-2/9 candidate inhibitors and potential anticancer agents. i) Thiosemicarbazide/EtOH/AcOH/reflux; ii) 3-Chloropentane-2,4-dione/EtOH/reflux; iii) Aminoguanidine hydrochloride/EtOH/LiCl/reflux.

#### 2.3. In vitro MMP-2/9 inhibitory analysis

We first tested our candidate compounds for MMP-2/9 inhibition in comparison to known MMP-2/9 inhibitors such as NNGH and others [41, 42]. The results are summarized in (**Table 2**). We found that compound **4a** strongly inhibited MMP-2/9 activity in the lower nanomolar range, with slightly higher potency against MMP-9 (ca. 40 nM). Moreover, compounds **3b**, **3c**, **4d**, and **4e** showed selective inhibition of MMP-9 over MMP-2, with **3b** and **3c** being potent inhibitors of MMP-9. Compound **2c** was after **4a** the overall second strongest inhibitor of MMP-2/9, with comparable potency against both enzymes (in the range of 70-75 nM). The remaining compounds **2a**, **2b**, **2d**, **2e**, **3a**, **3d**, **3e**, **4c** and **4e** were less potent MMP-2/9 inhibitors with potency in the high nanomolar range.

Cpd.	IC <sub>50</sub> (nM)		
	MMP-2	MMP-9	
2a	99.53±2.12	590.04±12.6	
2b	189.53±4.05	$105.82 \pm 2.26$	
2c	71.38±1.52	76.11±1.62	
2d	215.18±4.60	94.34±2.01	
<b>2</b> e	194.12±4.15	109.17±2.33	
<b>3</b> a	472.17±10.1	358.9±7.67	
<b>3</b> b	352.04±7.53	20.93±0.44	
3c	115.87±2.47	28.77±0.61	
3d	237.24±5.07	138.07±2.95	
<b>3</b> e	$109.82 \pm 2.34$	137.92±2.95	
<b>4</b> a	56.69±1.21	38.60±0.82	
<b>4b</b>	98.15±2.10	62.33±1.33	
<b>4</b> c	105.86±2.26	86.05±1.84	
<b>4</b> d	366.16±7.83	56.87±1.21	
<b>4</b> e	149.6±3.20	64.33±1.37	

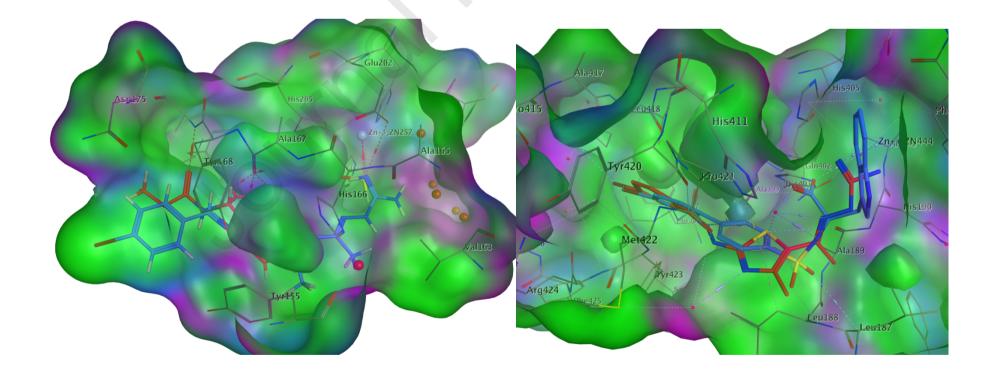
Table 2. In vitro inhibitory MMP-2/9 activity of new candidate compounds.

PNU-141803 <sup>a</sup>	310±1.20	$49500 \pm 0.50$		
E402Q <sup>b</sup>	$9.3 \pm 1.5$	$201.0 \pm 58.6$		
NNGH	39.93±0.85	33.98±0.72		
<sup>a</sup> Data was taken from re	f. [41] and <sup>b</sup> Data	was taken from ref. [42].		
Data are presented as average $IC_{50} \pm SD$ (nM) values for at least three experiments.				

#### 2.4. Molecular docking studies

Having confirmed the MMP-2/9 inhibitory activity of the newly designed compounds, we also investigated putative binding modes of the preferred dual inhibitor **4a** on the basis of docking calculations using MOE [38] and Autodock [43].

From the Protein Data Bank [44] the X-ray structures of MMP-2 in complex with the PNU-141803 inhibitor (PDB entry 2USN) [41] and of MMP-9 in complex with the E402Q inhibitor (PDB entry 20W0) [45] were selected and used as templates for docking. Compound 4a was built using MOE the geometry was optimized by energy minimization with the CHARMm force field and it was then prepared for docking calculations with Python Journal Pre-proofs scripts available in the Autodock package. Prior to docking, bound crystallographic inhibitors were removed from the templates. For re-docking of crystallographic inhibitors and docking of compound 4a, 50 flexible docking runs were performed using Autodock, and the resulting poses were clustered with 1.8 Å tolerance. Lamarckian genetic algorithm was used for the conformational space search with the initial population set to 150. The most populated clusters of low energy conformations were selected for analysis. For both targets, the applied docking protocol closely reproduced the experimental binding modes of re-docked inhibitors. Furthermore, the predicted binding modes of compound 4a corresponded to the proposed fit of 4a to the structure-based pharmacophore model discussed above and to the bound orientation of the crystallographic inhibitors. Specifically, in MMP-2 the guanidine NH of 4a adopted the formed monodentate interaction with S1' pocket zinc cation consistent with the interactions formed by the reference inhibitors. In addition, as expected, the phenyl moiety of compound 4a bound to the S1 where it formed aromatic interactions with residues Tyr155 and Tyr168. Furthermore, thiazole ring was accommodated by aromatic interaction with His166. The 2-aminothiazole fragment bound to the S2 subsite o MMP-2/9 where several hydrogen bonding interactions were possible. Corresponding interaction patterns were observed in the docked complex of compound 4a and MMP-9. The slightly higher potency of 4a against MMP-9 might be attributable to better shape complementarity and further improved hydrophobic/aromatic interactions within the S1 site compared to MMP-2. (Fig. 4) shows the modeled complexes formed by compound 4a with MMP-2 and MMP-9, respectively. Encouragingly, the results of binding mode predictions for 4a were fully consistent with pharmacophore fitting as the underlying structure-based inhibitor design strategy. All putative interactions are provided in Supplementary Table S1, Fig. S1 and Fig. S2.



Α

В

Fig. 4. Docking modes of active compound 4a. Shown are predicted complexes of 4a with A) MMP-2 and B) MMP-9. For comparison, the bound crystallographic inhibitors are shown. Carbon atoms of 4a and crystallographic reference inhibitors are colored red and blue, respectively. Possible hydrogen bonding interactions between compound 4a and MMP-2/9 are indicated by dashed lines.

#### 2.5. Computational estimation of pharmacokinetic properties

The pkCSM ADMET descriptors algorithm protocol [46-48] was used for calculation of pharmacokinetic (PK) properties such as absorption, distribution, metabolism, excretion and toxicity (ADMET) profiles of compound **4a** and MMP reference inhibitors. (**Table 3**) summarizes the predicted (computationally estimated) PK profiles of compound **4a** and the reference inhibitors.

Duonouty	Madal Nama		Predicted Value	
Property	Model Name	40	PNII_141803	F402Q
	Journal Pre-proofs	<del>44</del> 1.J	414.3	J40.4
	LogP	2.7	3.8	4.4
Molecular	Rotatable Bonds	5	7	7
properties	Acceptors	6	7	3
	Donors	4	3	3
	Surface Area	151.3	171.1	193.1
	Water solubility	-3.05	-3.53	-4.08
	Caco2 permeability	-0.35	0.262	-0.02
	Intestinal absorption (human)	71.5	81.1	69.8
Absorption	Skin Permeability	-2.73	-2.75	-2.73
	P-glycoprotein substrate	Yes	Yes	Yes
	P-glycoprotein I inhibitor	No	Yes	No
	P-glycoprotein II inhibitor	No	Yes	Yes
	VDss (human)	0.37	0.197	-0.933
Distribution	Fraction unbound (human)	0.32	0	0
Distribution	BBB permeability	-1.49	-1.23	-1.31
	CNS permeability	-3.72	-2.56	-2.25
	CYP2D6 substrate	Yes	No	No
	CYP3A4 substrate	Yes	Yes	Yes
Metabolism	CYP1A2 inhibitor	No	No	Yes
	CYP2C19 inhibitor	No	Yes	No
	CYP2C9 inhibitor	No	Yes	Yes
	CYP2D6 inhibitor	No	No	No
	CYP3A4 inhibitor	No	Yes	No
Examplian	Total Clearance	0.273	0.064	-0.39
Excretion	Renal OCT2 substrate	Yes	No	No
	AMES toxicity	Yes	No	Yes
	Max. tolerated dose (human)	0.15	-0.17	0.22
	hERG I inhibitor	No	No	No
	hERG II inhibitor	Yes	No	Yes
	Oral Rat Acute Toxicity (LD50	) 2.4	2.4	2.2
Toxicity	Oral Rat Chronic Toxicity (LOAEL)	1.63	2.25	1.15
	Hepatotoxicity	No	Yes	Yes
	Skin Sensitization	No	No	No
	<i>T.Pyriformis</i> toxicity	0.27	0.43	0.28
	Minnow toxicity	4.59	1.73	0.79

Table 3. Predicted ADMET properties of compound 4a compared to MMP-29 reference inhibitors.

The water/octanol partition coefficient (P) is an important parameter for assessing the hydrophobicity of a compound. The calculated LogP value of **4a** was smaller than for PNU-141803 and E402Q with values of 2.7, 3.8, and 4.4, respectively, indicating that **4a** was less hydrophobic, consistent with the presence of multiple hydrogen bonding donor or acceptor groups. The results for the penetration potential of the blood–brain barrier indicated that compound 4a and the reference inhibitors had only low potential to cross the barrier, and cause side effects in the central nervous system [48]. The

calculated values of the permeability through human skin were -2.73 cm/h 4a, -2.75 cm/h (PNU-141803), and -2.73 cm/h (E402Q); therefore, the compounds cannot be absorbed through human skin. In the analysis of human intestinal absorption, one of the main parameters for new drug candidates, the analyzed alkaloids had values of 71.5% **4a**, 81.1% (PNU-141803), and 69.8% (E402Q). Some studies [49] have shown that values between 70% and 100% indicate good intestinal absorption. The recommended parameters for the prediction of oral absorption of drugs use Caco-2 permeability models. Calculated values–were 0.35 nm/s **4a**, 0.26 nm/s (PNU-141803), and -0.02 nm/s (E402Q). Furthermore, only PNU-141803 was expected to inhibit P-glycoprotein I, while compounds **4a** was not expected to inhibit P-glycoprotein II a protein responsible for ADME characteristics of different drugs. Cytochrome P450 (CYP) profiling calculations indicated that **4a** was unable to inhibit CYP 2C19, CYP 2D6, and CYP 3A4, increasing the ability

#### 2.6. Anticancer assay

Anti-proliferative activity of the synthesized compounds **2a-e**, **3a-e** and **4a-e** was examined on three human cancer cell lines, namely, invasive breast cancer cell line (MDA-MB-231), human colon cancer (HCT-116) and mammary gland breast cancer (MCF-7). In addition, the two normal cell lineshuman keratinocytes cell line (HaCaT) and human diploid fibroblasts (WI-38) were investigated as controls. *In-vitro* cytotoxicity evaluation using a viability assay [50,51] was performed with staurosporine as a cytotoxic reference compound. The results were expressed as growth inhibitory concentration (IC<sub>50</sub>) values which represent the compound concentrations required to produce a 50% inhibition of cell growth after 24 h of incubation as shown in (**Fig. 5**) and (**Table 4**).

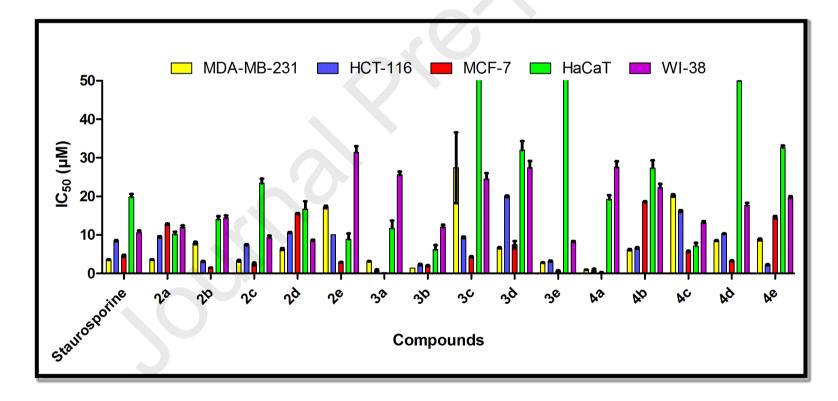
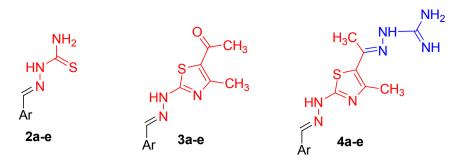


Fig. 5. IC<sub>50</sub> (µM) of the target compounds against MDA-MB-231, HCT-116, MCF-7 tumor cells and HaCaT, WI-38 normal cell lines.

Table 4. Cytotoxic activity of the target compounds against different cell lines.



Cn		Journal Pre-proofs				
Cpu.	Ar	Cancerotoxicity		Normotoxicity		
		<b>MDA-MB-231</b>	HCT-116	MCF-7	HaCaT	WI-38
2a	$4-IC_6H_4$	$3.06 \pm 0.09$	9.5±0.12	12.82±2.1	10.20±0.66	11.94±0.74
2b	4-HO-3-MeOC <sub>6</sub> H <sub>3</sub>	7.89±0.31	3.12±0.16	1.46±1.6	$14.06 \pm 0.81$	14.42±1.03
2c	$2-HOC_{10}H_7$	3.30±0.13	7.48±2.30	$2.46\pm0.44$	23.39±0.78	9.30±0.44
2d	Biphenyl-4-yl	6.35±0.33	10.61±0.11	15.56±1.5	16.72±0.71	8.43±0.43
2e	3-Br-4,5-(MeO) <sub>2</sub> C <sub>6</sub> H <sub>2</sub>	17.26±0.82	10.02±0.23	2.92±1.3	8.86±0.39	31.43±1.87
3a	$4-IC_6H_4$	3.18±0.22	$0.84{\pm}1.4$	0.23±1.5	11.71±1.37	25.55±1.46
3b	4-HO-3-MeOC <sub>6</sub> H <sub>3</sub>	$1.35 \pm 0.04$	2.26±2.5	2.01±2.1	6.24±043	12.04±0.81
3c	$2-HOC_{10}H_7$	27.44±9.76	9.38±11.2	4.31±10.2	69.98±2.22	24.54±1.62
3d	Biphenyl-4-yl	6.65±0.24	26.06±1.3	7.49±3.1	32.04±1.91	27.38±1.55
3e	3-Br-4,5-(MeO) <sub>2</sub> C <sub>6</sub> H <sub>2</sub>	2.83±0.09	3.26±2.1	0.66±1.4	61.14±2.69	8.11±0.33
4a	$4-IC_6H_4$	$0.97{\pm}0.03$	0.77±0.05	0.02±2.2	19.21±0.88	27.61±1.62
4b	4-HO-3-MeOC <sub>6</sub> H <sub>3</sub>	6.16±0.51	6.62±0.32	18.62±3.1	27.34±1.14	22.23±1.08
4c	$2-HOC_{10}H_7$	20.28±1.31	16.19±2.1	5.75±14.2	7.15±0.34	13.16±0.76
4d	Biphenyl-4-yl	8.53±0.41	10.33±4.2	3.29±2.1	49.97±2.17	17.70±0.64
4e	3-Br-4,5-(MeO) <sub>2</sub> C <sub>6</sub> H <sub>2</sub>	8.80±0.26	2.25±10.2	14.60±4.1	32.69±1.79	19.60±0.69
aurosporir	ne -	3.57±0.07	8.5±0.11	4.6±0.21	19.85±0.75	10.63±0.47

<sup>a</sup> IC<sub>50</sub> values expressed in  $\mu$ M as the mean values of triplicate wells from at least three experiments and are reported as the mean  $\pm$  standard error.

From Table 1, it was noticeable that staurosporine had an IC<sub>50</sub> of  $3.57-8.50 \,\mu$ M and  $10.63-19.85 \,\mu$ M against all the cell lines that were investigated with a differentiation between cancer and normal cells. In addition, some of the new compounds displayed an excellent to modest growth inhibitory activity against the tested cancer cell lines and were active or inactive against normal cell lines, HaCaT and WI-38. Compounds **2a** and **2c** were the most potent derivatives against cancer cell lines such as MDA-MB-231 with IC<sub>50</sub>  $3.06\pm.0.09$  and  $3.30\pm0.13\mu$ M, respectively, as compared to the standard staurosporine (IC<sub>50</sub>,  $3.57\pm0.07 \,\mu$ M) Compounds **2b** and **2c** also showed cytotoxic activity against cancer cell lines HCT-116 and MCF-7 with IC<sub>50</sub>  $(3.12\pm0.16, 1.46\pm1.6 \,\text{and} 7.48\pm2.30, 2.46\pm0.44 \,\mu$ M), respectively, as compared to staurosporine (IC<sub>50</sub>,  $8.5\pm0.11$  and  $4.6\pm0.21 \,\mu$ M) Compound **2e** possessed excellent antiproliferative activity against MCF-7 with IC<sub>50</sub>  $2.92\pm1.3 \,\mu$ M. Compounds **2a-e** were moderately active or nearly inactive against the cell lines HaCaT and WI-38 with IC<sub>50</sub> ranging from  $8.43-31.43 \,\mu$ M compared to Staurosporine (IC<sub>50</sub>,  $19.85\pm0.75$  and  $10.63\pm0.47 \,\mu$ M, respectively. Additionally, compounds **3a,b,e** with IC<sub>50</sub> = 1.35-3.8, 0.84-3.26 and  $0.23-2.01 \,\mu$ M, respectively, possessed excellent antiproliferative activities against

all cancer cell lines MDA-MB-231, HCT-116, and MCF-7, which was superior to Staurosporine with IC<sub>50</sub>, 3.57±0.07, 8.5±0.11 and

4.6±0.21µM, respectively. Compounds 3a-e displayed a growth inhibitory activity against normal cell lines HaCaT and WI-38 with IC<sub>50</sub> ranging from

8.11-69.98 μM. Furthermore, compounds 4a had superior potency against all the cancer cell lines MDA-MB-231 HCT-116 and MCF-7 with IC<sub>50</sub>

0.97±0.03, 0.77±0.05 and 0.02±2.2 µM, respectively, compared to Staurosporine. Compounds 4e,b also exhibited strong cytotoxic activity against the

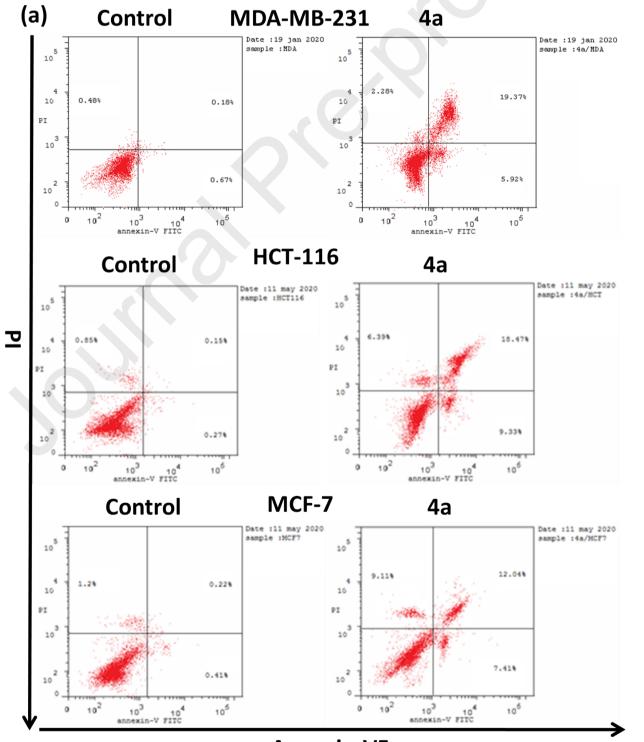
cancer cell line HCT-116 with IC<sub>50</sub> 2.25 $\pm$ 10.2 and 6.62 $\pm$ 0.32  $\mu$ M, respectively, while compounds 4d,c displayed less anti-proliferative activities than

Staurosporine with IC<sub>50</sub> values of 3.29±2.1 and 5.75±14.2 µM, respectively. Finally, compounds 4a-e had growth inhibitory activity against HaCaT and

WI-38 with  $IC_{50}$  ranging from 7.15-49.97µM. In particular, **4a** was only weakly active against these control cell lines, with strong selectivity in antiproliferative effects for the cancer lines.

#### 2.7. Cell apoptosis

Annexin V binding to phosphatidylserine (PS) exposed on the external leaflet of the plasma membrane during apoptosis is widely accepted as an indicator of apoptotic <u>Journal Pre-proofs</u> induced by compound **4a** treatment was related to apoptosis, we determined apoptosis using the Annexin/PI double staining flow cytometric assay (**Fig. 6a**). The percentage of total apoptotic cells (early and late apoptotic cells) increased from about 2% for the control to about 30% in the case of all tested cancer cells treated with compound **4a**. These results showed that compound **4a** induced apoptosis at a similarly higher rate in MDA-MB-231, HCT-116, and MCF-7 cancer cells (**Fig. 6b**). Necrosis cell death leads to the release of the intracellular contents that affects neighboring cells and triggers an inflammatory reaction [53]. However, we did not observe cells undergoing necrosis upon treatment with compound **4a**, indicating that cell death occurred primarily through apoptosis. In cancer therapy, most efficient and safe anticancer agents typically interfere with the balance between cell proliferation and apoptosis and shift cells toward the induction of apoptosis [54]. Our findings are consistent with other studies showing that MMPIs inhibit tumor proliferation by inducing apoptosis [55,56], as clearly detected for compound **4a**.



Annexin-V5

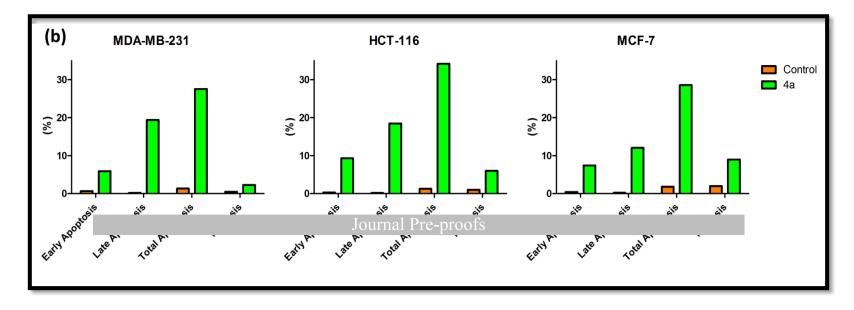


Figure 6: (a) Dot plot of Annexin V/PI double staining of control and treated cells. (b) Statistical analysis of the apoptosis percentage of MDA-MB-231, HCT-116, and MCF-7 cells after incubation with compound 4a for 24 h (IC<sub>50</sub> value). The data are reported as the mean  $\pm$  SD of three independent experiments in triplicate.

#### 2.8. DNA fragmentation

DNA fragmentation is the characteristic event common to all processes of apoptosis [57]. Diphenylamine assay was used to determine the percentage of fragmented DNA released from apoptotic nuclei into the cytoplasm. The relative quantity of DNA fragments in the MDA-MB-231, HCT-116, and MCF-7 cells treated with compound **4a** is shown in (**Fig. 7**). The percentage of DNA fragmentation increased significantly in all cells treated with compound **4a** (about 30%) compared to untreated control (about 5%), without significant differences observed between tested cells. These results were consistent with the apoptosis results discussed above suggesting that treatment of MDA-MB-231, HCT-116, and MCF-7 cells with compound **4a** induced cell membrane disruption followed by fragmentation of chromosomal DNA.

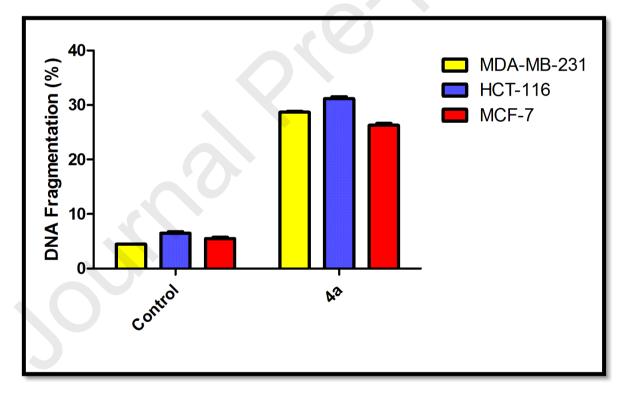
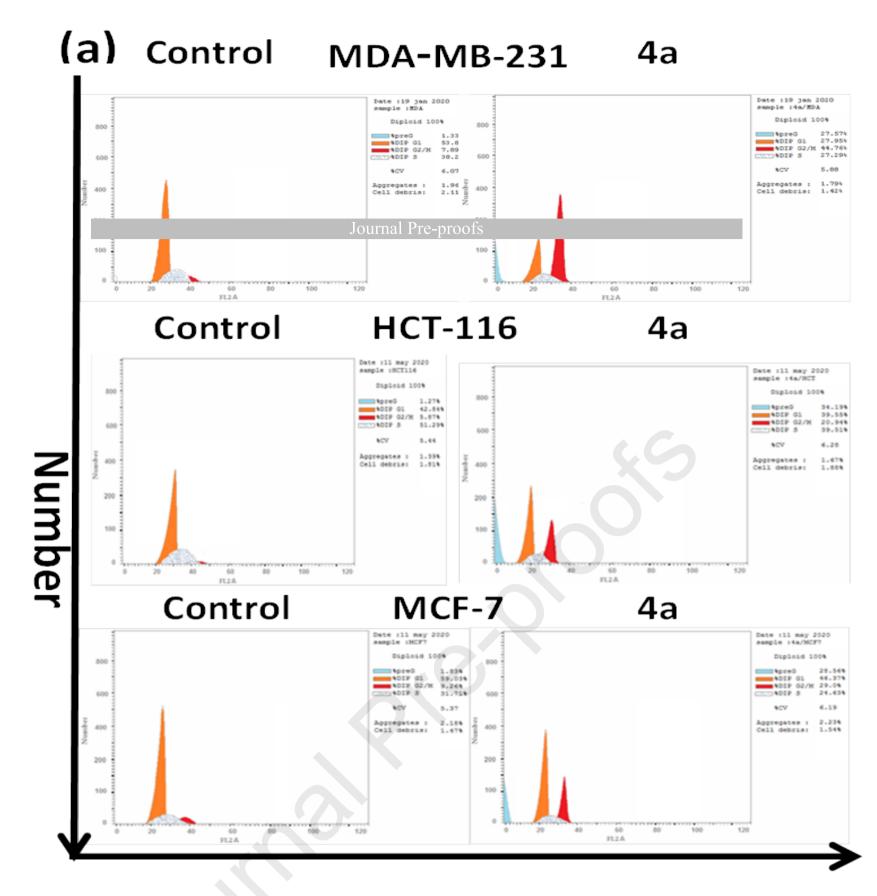


Fig. 7: Statistical analysis of the DNA fragmentation percentage of MDA-MB-231, HCT-116, and MCF-7 cells after incubation with compound 4a for 24 h (IC<sub>50</sub> value). The data are reported as the mean  $\pm$  SD of three independent experiments in triplicate.

#### 2.9. Cell cycle analysis

For the reduction of possible nonspecific drug effects in cancer treatment, the design and synthesis of novel chemotherapeutic agents that can regulate

cell cycle progression and apoptosis is an attractive approach [58]. Therefore, further effects of compound **4a** on regulating cell cycle progression were explored using the Propidium Iodide Flow Cytometry Kit assay (**Fig. 8a**). The percentages of compound **4a** treated MDA-MB-231, HCT-116, and MCF-7 cells in the G2/M phase were significantly higher than those in the control group. Moreover, the distribution of cells in the G1 and S phases was notably decreased in all tested cells compared to the control (**Fig. 8b**). Previous studies showed that MMPs aligned along the microtubular network within the cells during the mitotic phase. In addition, intracellular MMP-2/9 inhibitors have been associated with antimitotic action [59,60]. This might provide a possible explanation of cell cycle arrest observed at G2/M phase in cells treated with compound **4a**.



**DNA Content** 

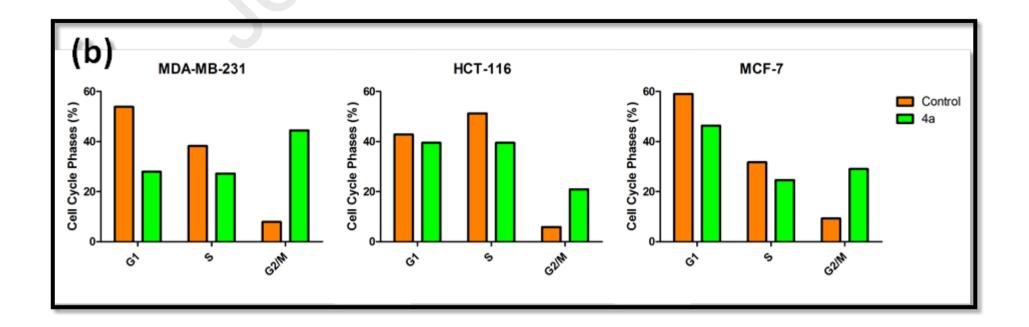
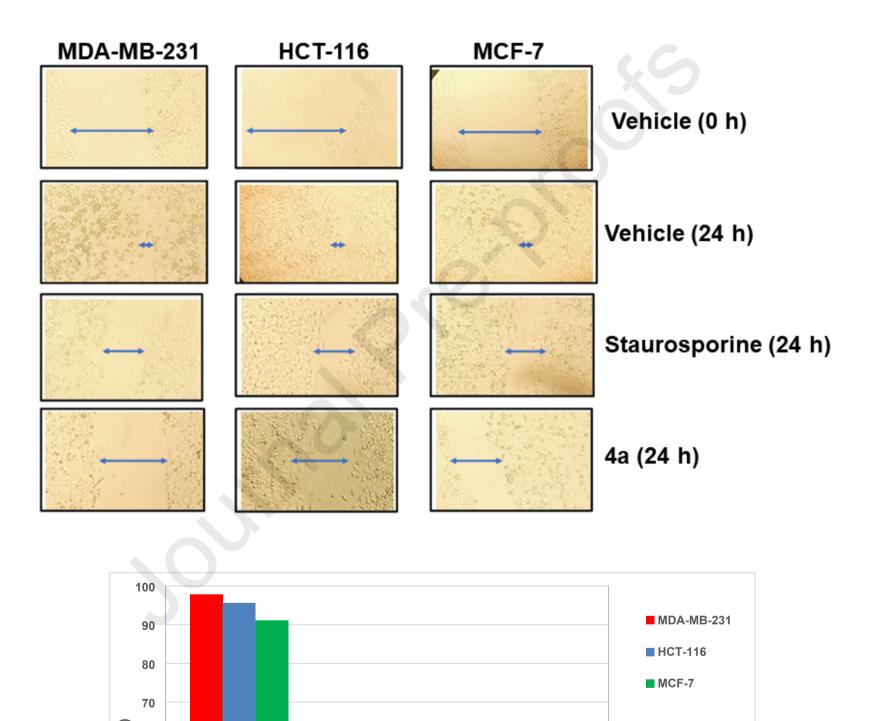


Fig. 8: (a) DNA content distribution histograms of control and treated cells. (b) Statistical analysis of cell cycle phases percentage of MDA-MB-231, HCT-116, and MCF-7 cells after incubation with compounds 4a for 24 h (IC<sub>50</sub> value). The data are reported as the mean  $\pm$  SD of three independent experiments in triplicate.

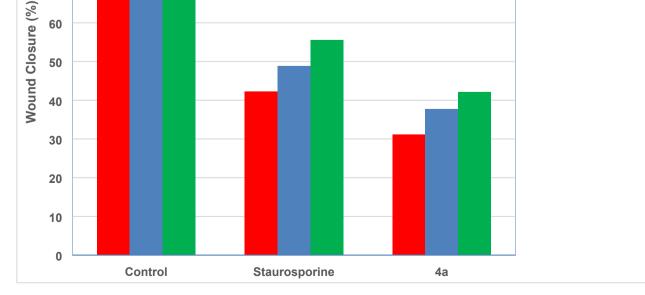
#### 2.10. Wound healing assay

Controlled proteolysis is required for cell migration across and through tissues in wound healing, tumor growth, and metastasis. Several MMPs were prominently expressed in wound healing and migration of tumor cells within the surrounding matrix environment [61]. Furthermore, in a culture-dependent gelatinase secretion profile, higher expression levels of MMP-2 and MMP-9 were observed in both spheroids and monolayer cultures of MDA-MB-231 cells [62]. In this study, the observed cell cycle arrest at the G2/M phases raised the possibility that compound **4a** might manipulate cell migration. Therefore, a wound healing assay (see Experimental Section) was used to determine possible effects of compound **4a** on the migratory **100** and **100** MDA-MB-231, HCT-116, and MCF-7 cells (**Fig. 9a**). Compound **4a** induced a substantial decrease in the wound closure percentage in all the tested cells compared to untreated control cells (**Fig. 9b**). This result is consistent with another study also showing the inhibitory effect of triazole derivatives on metastatic cancer cell migration and invasion [63]. Indeed, the inhibitory effect of compound **4a** on MMP-2/9 reduced the migration potential of the MDA-MB-231, HCT-116, and MCF-7 cancer cell lines.

a)



b)



**Fig. 9:** (a) MDA-MB-231, HCT-116, and MCF-7 cultured cells confluence in 24-well culture plates containing an insert that forms a 0.9 mm gap on the monolayer (Vehicle control at 0 h.). After the insert was removed, untreated cells (Vehicle control at 24 h) and cells treated with staurosporine or compound **4a** for 24 h were imaged under an inverted light microscope. Arrows are pointing toward wound edges. (b) Statistical analysis of wound closure percentage of MDA-MB-231, HCT-116, and MCF-7 cells after incubation with compound **4a** for 24 h (IC<sub>50</sub> value).

#### 2.11. Structure-activity relationship studies

The structure-activity relationship (SAR) study revealed that the antitumor activity of the three series 2a-e, 3a-e and 4a-e was significantly affected by

the hydrophobic vs. hy

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ng. In a comparison of the

cytotoxic activities of the three series (2a-e, 3a-e and 4a-e) against invasive breast, colon and breast cancer, we found that varying the substitution patterns of the phenyl, naphthyl, and biphenyl rings at the 2-position of the hydrazine carbothioamide moiety, compounds 2a and 2c (first series) revealed significant impact on the activities against the MDA-MB-231 cell line compared to staurosporine where the activities were decreased in the order of  $4-I > 2-OH > Ph-4-Ph > 4-HO-3-MeO > 3-Br-4,5-(MeO)_2$ . These observations suggested that modifying the phenyl or naphthyl ring with small hydrophobic (iodo atom) or hydrophilic (hydroxyl group) substituents was more beneficial than other substitutions. With respect to the activity against the HCT-116 and in particular MCF-7 cell line, molecules 2b, 2c and 2e were the most effective analogues generated in this study compared to staurosporine. These findings also indicated that the combination of hydrophilic and hydrophobic (hydroxyl and methoxy groups) or hydrophilic (hydroxyl group) and hydrophobic (bromo atom and two methoxy groups) substituents resulted in excellent antiproliferative activities. Further investigation of the impact of the substitution pattern of the aryl moiety in the thiazole derivatives **3a-e** (second series) against the cancer cell lines MDA-MB-231, HCT-116 and MCF-7 was carried out. Incorporation of iodo atom, hydroxyl and methoxy groups or bromo atom and two methoxy groups on the phenyl moiety rendered compounds 3a, 3b and 3e highly cytotoxic against the three tumor cell types, implying that the presence of small hydrophobic or hydrophilic (iodo, bromo atoms or methoxy and hydroxyl groups) substituent was indispensable for the activities against cancer cell lines. Furthermore, the assessment of the substitutions at the previous positions of the aryl group on the thiazolyl hydrazinecarboximidamide system (4a-e) (third series) for activity against the cancer cell lines MDA-MB-231, HCT-116 and MCF-7 revealed that that compounds 4a showed high activity against all cancer cell lines. These findings suggested that grafting of a hydrophobic substituent such as the iodo atom on the phenyl ring was more favorable than the other the substituents, while introduction of a hydroxyl and methoxy group or bromo atom and two methoxy groups on the phenyl moiety of compounds 4b and 4e and hydroxyl or biphenyl groups for compounds 4c and 4d resulted in an increase in activity against cancer cell lines, HCT-116 and MCF-7, respectively,. It follows that the substitution pattern on the aryl moiety was a crucial element of the antitumor activity. The incorporation of hydrophobic and/or hydrophilic groups greatly enhanced the activity. Finally, the order of anticancer activities of the three series was decreased in the order of 4a - e > 3a - e > 2a - e.

### **3.** Concluding remarks

Many of pathological disorders like cancer invasion, metastasis, and angiogenesis, as well as cardiovascular, neurologic and inflammatory diseases are linked to expressing a lot of metalloproteinases like MMP2/9 [64-66]. Accordingly, MMP expression is tied to tumor progression, stages, and patient prognosis [67]. These MMPs are also involved in processes and signaling pathways implicated in angiogenesis, cell migration and invasion, and other

cellular functions such as proliferation, apoptosis, and differentiation [68]. Accordingly, MMP-2/9 is attractive targets for cancer therapy development. In this study, a series of 4-aminothiazole compounds containing lipophilic aromatic and guanidine termini have been designed, synthesized and evaluated for dual MMP-2/9 inhibitory activity. Most of the synthesized derivatives had comparable of higher activity than reference inhibitors. Compound **4a** was the most potent MMP-2/9 inhibitor with IC<sub>50</sub> values of 56 nM and 38 nM, respectively. We also evaluated anti-proliferative activities of the news compounds against MDA-MB-231, HCT-116, and MCF-7 cells compared to two normal cell lines HaCaT and WI-38. Most of the compounds exhibited higher antiproliferative activities than a positive control drug. In addition, compound **4a** promoted apoptosis of MDA-MB-231, HCT-116, and MCF-7 cells, induced cell cycle arrest at the G2/M phase, inhibited the invasion and migration and induced DNA fragmentation in MDA-MB-231, HCT-116,

and MCF-7 cancer cells. Based on our results, compound **4a** is indicated to have considerable potential as a new amidine-based lead compound for the discovery of new anticancer agents targeting MMP-2/9 enzymes. We plan on continuing optimize efforts on this compound to obtain chemical entities with highly anticancer activity.

#### 4. Experimental section

#### 4.1. General chemistry

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The starting reagents and solvents were purchased from the Aldrich Company and were used as received. Melting points (Mp) were determined in open capillary tubes using electrothermal apparatus (Stuart, UK) and are uncorrected. The IR spectra were recorded on a KBr disc on a Schimadzu 8201 PC, FTIR spectrophotometer ( $\nu$  max in cm<sup>-1</sup>). All the new compounds were characterized by the <sup>1</sup>H-NMR and <sup>13</sup>C-NMR, using a <sup>1</sup>H-NMR (400 MHz) and <sup>13</sup>C-NMR (100 MHz) spectra, and were measured in DMSO at room temperature. The chemical shifts ( $\delta$ ) were reported in ppm to a scale calibrated for tetramethylsilane (TMS), which is used as an internal standard. HPLC-Mass Spectrometry was performed on Agilent 1100 / ZQ MSD including C18 column and diod-array UV detector. The mobile phase (containing 0.01 M ammonium acetate) was gradient starting from 20% acetonitrile/80% water to 80% acetonitrile/20% water. Purities are reported according to percentage of Peak Areas at wavelength 254 nm. Biological activities were carried out at the Regional Centre for Mycology & Biotechnology, Al-Azhar University, Cairo, Egypt. The follow up of the reactions and the check of the purity of the compounds were made by the TLC on silica gel-protected aluminum sheets (Type 60 GF<sub>254</sub>, Merck), and the spots were detected by exposure to a UV-lamp at  $\lambda$  254 nm for a few seconds.

#### 4.1.1. General procedure for the synthesis of substituted 2-arylidenehydrazine-1-carbothioamides (2a-e)

2-Arylidenehydrazine-1-carbothioamides were prepared according to previous reported procedure [40].

#### 4.1.2. General procedure for the synthesis of substituted 1-(2-(2-arylidenehydrazineyl)-4-methylthiazol-5-yl)ethanones (3a-e)

1-(2-(Arylidenehydrazinyl)-4-methylthiazol-5-yl)ethanone (3a-e) were prepared according to previous reported procedure [40].

# 4.1.3. General procedure for the synthesis of substituted 2-(1-(2-(-2-(4-benzylidene)hydrazinyl)-4-methylthiazol-5-yl)ethylidene)-

## hydrazinecarboximidamides (4a-e)

2-(1-(2-(-2-(4-arylidene)hydrazinyl)-4-methylthiazol-5-yl)ethylidene)hydrazinecarboximidamides (4a-e) were prepared according to previous reported procedure [40].

#### 4.2. MMP Enzyme inhibition assay

Screening for MMP-2 (EC 3.4.24.35) inhibitors was performed using the MMP-2 Inhibitor Screening Kit (Fluorometric) (BioVision, Milpitas, CA 95035 USA, Catalog # K2017-100, https://www.biovision.com/ ) and MMP-9 assay was performed using abcam139448 kit MMP9 Inhibitor Screening Assay Kit (Colorimetric) (abcam, Catalog # ab139448, https://www.abcam.com/) according to the manufacturer's guidelines.

## 4.3. Cytotoxicity evaluation using a viability assay

The cytotoxic activity was assessed using the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide (MTT) colorimetric assay as reported previously [50,51].

## 4.4. Quantification of apoptosis by flow cytometry

Annexin V-FITC apoptosis assay was performed by using Annexin V-FITC/PI double staining detection kit (BD Pharmingen, USA).[69, 70] Flow cytometric analysis was performed on FACS Calibur flow cytometer (BD Biosciences, Franklin Lakes, NJ, USA). Annexin V-FITC was detected

through (FL1) channel while PI was detected through the (FL2) channel. Finally, a minimum of 10,000 cells per sample were acquired and analyzed using Cell Quest Pro software (BD Biosciences).

#### **4.5. DNA fragmentation**

DNA fragmentation was quantitatively determined using diphenylamine (DPA) reagent according to the method of Boraschi and Maurizi.[71-73]

### 4.6. Cell cycle analysis

Cell cycle arrest and

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lowed by flow cytometry

analysis. The DNA content in each cell nucleus was determined by a FACS Calibur flow cytometer (BD Biosciences, Franklin Lakes, NJ, USA). Finally, cell cycle phase distribution was analyzed using Cell Quest Pro software (BD Biosciences) showing collected propidium iodide fluorescence intensity on FL2 [74].

#### 4.7. Wound healing assay

Cancer cell migration was assessed using a wound healing assay (CytoSelectTM Wound Healing Assay Ki. Cell Biolabs, Inc. San Jose) as previously reported [75,76]. Cells were imaged under an inverted light microscope (Nikon Eclipse Ti and NIS-Elements software).

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#### **Declaration of interests**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

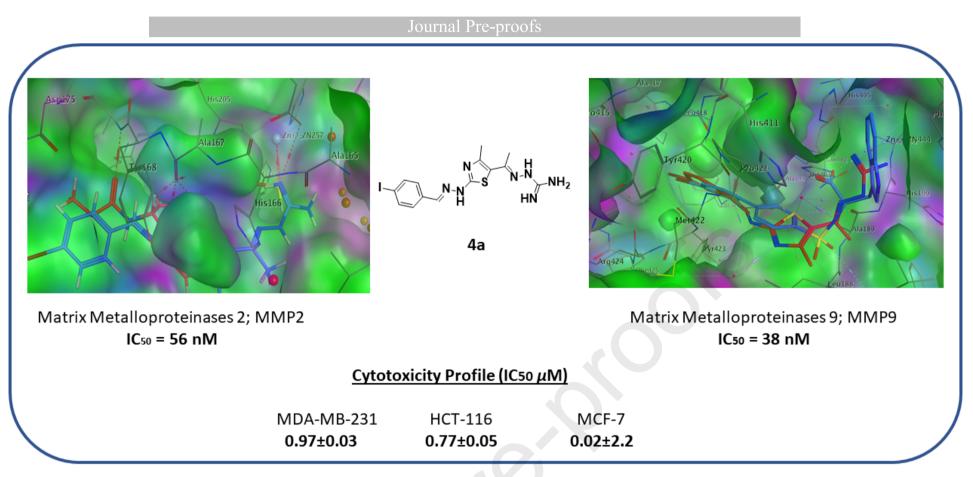
The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:



Journal Prevention

## **Graphical abstract**

Novel Molecular Discovery of Promising Amidine-based thiazole analogues as Potent Dual Matrix Metalloproteinase-2 and 9 Inhibitors: Anticancer Activity Data with Prominent Cell Cycle Arrest and DNA Fragmentation Analysis Effects



## Highlights

- 2-Aminothiazoles, linked amidine moieties were synthesized as potential anticancer agents.
- The cytotoxic activity was tested against (MDA-MB-231), (HCT-116) and (MCF-7) cell lines.
- The thiazole-based MMP-2/9 inhibitors have significant potential for anticancer treatment.
- Compounds 4a were able to induce cell cycle arrest at G2/M phase, cause intrinsic and extrinsic apoptotic cell death.

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