

Synthesis and Molecular modeling of some new chalcones derived from coumarine as CDC25 phosphatases inhibitors

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Abstract: New chalcones derived from coumarines were synthesized and tested as CDC25 phosphatase inhibitors. Molecular modeling of these new compounds was also presented in aim to study the mode of compounds orientation within CDC25 A and B. The reversibility of compounds 3, 4 and 5 was confirmed by application of MALDI-TOFMS technique.

Keywords: Chalcones, Coumarines, CDC25 phosphatase, MALDI-TOFMS, Molecular Modeling.

Introduction

CDC25 (Cell Division Cycle) is dual specificity phosphatase that play critical role in the division of eukaryotic cells. Up to date, three CDC25 isoforms were identified: A, B and C ¹⁻⁴. They dephosphorylate CDK/cyclin protein complexes which are key regulator of cell division. Noteworthy, CDC25B is needed for checkpoint recovery to repair DNA before mitosis ^{3,5}.

CDC25A and CDC25B are overexpressed in many different human cancers: (e.g.: breast cancer: 70% and 57%, colorectal cancer: 47-53% esophageal cancer: 46-66% and 48-79% respectively) ¹. Consequently, they appear as potential target in cancer therapy. Wide range of different scaffolds has been reported as CDC25 phosphatase inhibitors including quinoids, dysidiolide and large collection of miscellaneous structures ^{6,7}. Chalcones have numerous biological activities containing antihypertensive, antifungal, anticonvulsant, antiviral, antioxidant, anti-inflammatory, antimalarial, anti-HIV, antiprotozoal, antimicrobial,

antifilarial, ^{8,9} they also proved their antitumor activities through their action against many molecular targets ¹⁰. The substituted chalcones in position 4 of ring (B) was even reported as CDC25 inhibitors with considerable activity (**Figure 1**)¹¹. Coumarines are well known as anticancer ¹² active compounds with many different mechanisms like kinase inhibitors, apoptosis induction, angiogenetic inhibition, HSP90 inhibitors, telomerase inhibitor and antimetabolic. ¹³ Some coumarines have anticoagulant and cardiovascular properties (dicoumarol and warfarin) others have antibiotic activities as novobiocin and clorobiocin which are naturally occurring. ¹⁴ Geiparvarin is another example of coumarine with dual activities: MAO-B inhibitory and antitumor. ¹⁵ Coumarine has been combined with different pharmacophores, and showed antioxidant, anti-inflammatory, anticancer, and antimicrobial activities. ¹⁶ Some of them, hybridized with quinones ^{17,18} or dimerized thanks to a disulfide bond of various lengths (**Figure 1**) ¹⁹ are particularly active.

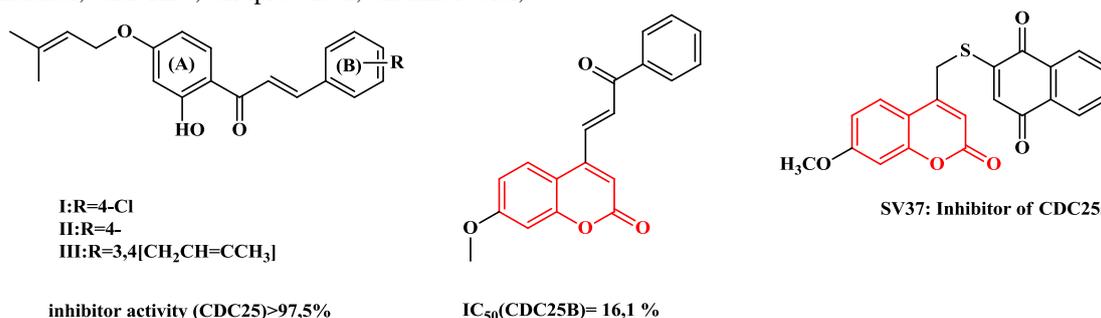


Figure 1. Examples of substituted and coumarines based chalcones inhibitors of CDC25s

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Synergistically, coumarine and chalcones combined structure appeared as promising anticancer molecules. They showed their abilities against number of human cancer cell lines, ²⁰ therefore, series of novel chalcones derived from coumarine were synthesized by aldol condensation. The obtained compounds were investigated by docking simulation and then evaluated *in vitro* on CDC25A and B enzymes.

Results and Discussion

Chemistry

All compounds were synthesized by well-known base-catalyzed aldol condensation ²¹ between 3-acetyl coumarines and cinnamaldehyde. Previously, in our laboratory, substituted 3-acetyl coumarines were prepared starting from salicylaldehyde ²² and ethylacetoacetate ^{23,24}. Commercially available

cinnamaldehyde and other synthesized derivatives were introduced as condensed partner. In addition cinnamaldehydes compounds were synthesized with two different methods:

Method A consisted of the reduction of cinnamic acid using $\text{LiAlH}(\text{OtBu})_4$ ²⁵ **Method B** was done by Wittig reaction ²⁶ between a benzaldehyde and an acetal ²⁷. All prepared compounds were purified by column chromatography (cyclohexane: ethyl acetate 9:1).

Biological evaluation

Fluorimetric analysis

Compounds **1** to **8** were evaluated *in-vitro* against recombinant human CDC25 phosphatases by fluorimetric method. (**Table 1**)

Table 1. Inhibitory activity of product **1-8** with CDC25A and B (concentration of compounds 20 μM)

compounds	CDC25A	CDC25B
DMSO	0 ± 3.81	0 ± 1.25
1	24.02 ± 3.98	30.42 ± 2.66
2	16.59 ± 5.59	28.32 ± 3.95
3	28.65 ± 3.23	18.39 ± 1.29
4	35.95 ± 1.29	16.42 ± 1.13
5	40.64 ± 0.92	54.94 ± 1.13
6	32.72 ± 3.97	34.63 ± 2.31
7	28.56 ± 2.38	32.89 ± 1.09
8	7.34 ± 1.77	28.94 ± 3.43
Naphtoquinone	99.68 ± 4.52	99.41 ± 3.12

The electrophilic substitution: Cl and Br on position 6 of the coumarine part led to inhibit CDC25A in higher extent than methoxy substituted analogue. The order of activity of these compounds was **4**>**3**>**2**. This order was inverted in the case of CDC25B. Introduction of methoxy group on the phenyl moiety increased the activity of compound **4** toward CDC25B but it diminished with CDC25A (from 35.95% to 7.34%). Furthermore, comparing the activities of compounds **1**, **6** and **7**; it showed that the methoxy group substitution on the phenyl ring increased the activity against both isoforms. The substitution on position 7 of coumarine with N, N-diethylamino group (compound **5**) increased the inhibitory activity on CDC25A: $40.64 \pm 0.92\%$ and CDC25B: $54.94 \pm 1.13\%$). This compound was

finally the most potent candidate among all tested structures (Table 1).

MALDI-TOFMS

Matrix-assisted laser desorption/ionization-time-of-flight mass spectrometry (MALDI-TOFMS) was applied to check if the synthesized structures may be a candidate to CDC25 inhibition. In case of inhibition, the applied procedure is also able to inform about its reversibility or irreversibility. ²⁸ Compounds with the highest values in biological analysis as inhibitor (**3**, **4** and **5**) gave a positive results in MALDI-TOFMS. Their protonated molecular ion directly appeared in the mass spectrum meaning that they behaves as reversible inhibitors as described by *Sibille et al.* ²⁹ and *Bana et al.* ¹⁷.

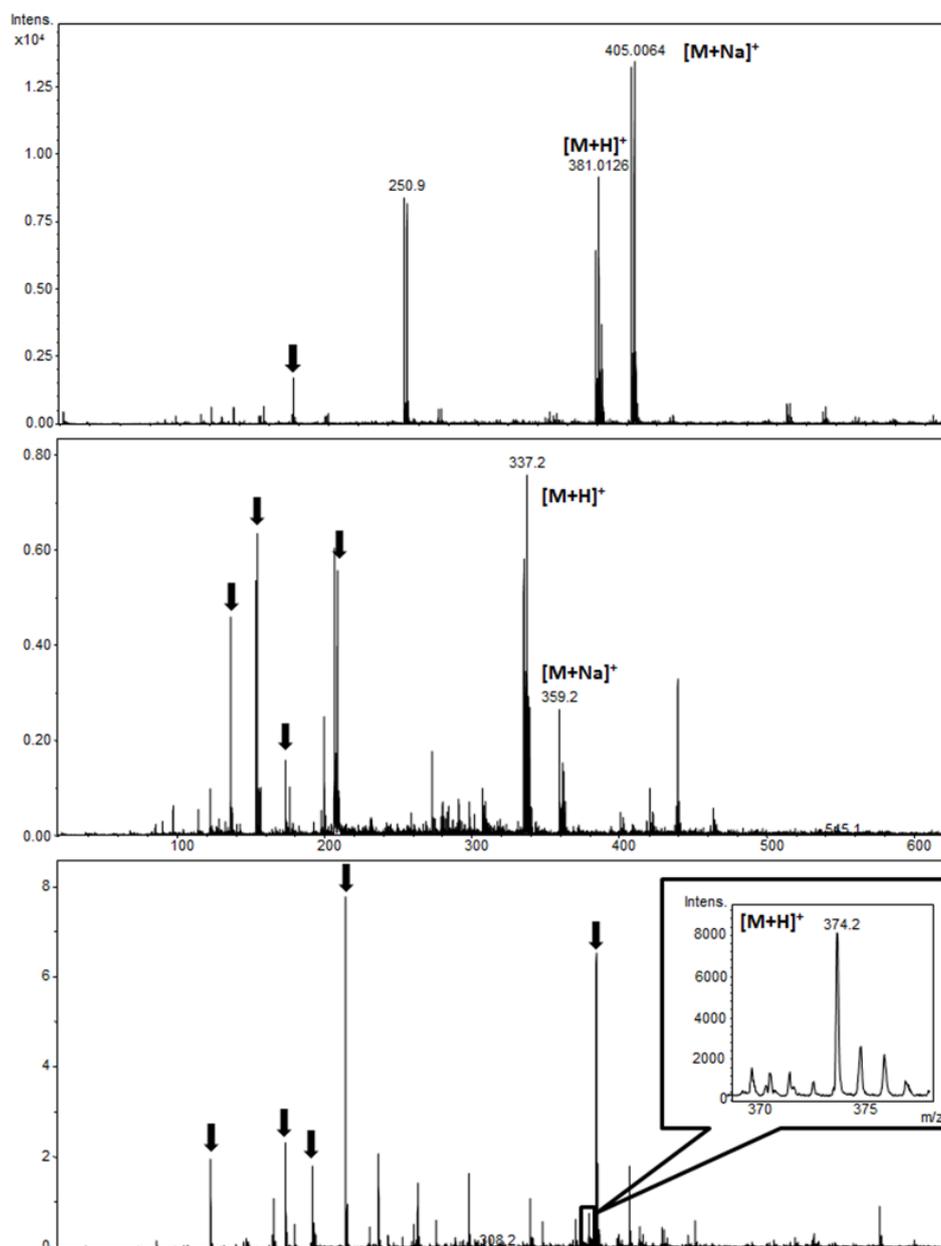


Figure 2. MALDI-TOF mass spectra (reflectron mode) of compounds **3**, **4** and **5** from up chart to down (DHB matrix for compound **3** and HCCA matrix for compounds **4** and **5**, $C = 2 \times 10^{-4}$ M) and CDC25A incubated with them. The ion $m/z=381.01$, $m/z=337.2$ and $m/z=374.2$ corresponding to $[M+H]^+$ of **3**, **4** and **5** respectively.

Molecular modelling

The molecular surface scanning of CDC25B reveals that its 3D structure exhibits a large groove just close to active cysteine³⁰. Thus, this site called swimming pool also appears as an interesting target for inhibiting CDC25 by the binding of small molecules.³¹

Hence, the binding inside this catalytic site cannot only be taken into account as a dependable mode of inhibition. We suggested designing of chalcones derived from coumarine and investigating the designed products by docking simulation to test the mode of orientation of each moiety in relation to active and inhibitory sites. Possibility of formyl pyranone ring to surrogate the phosphate group of the native substrate was presumed⁶.

The surface structure of the CDC25B catalytic domain (1QB0)³², indicated that the distance between the shallow active site and the large groove is ~ 7.3 Å. This distance must correspond to the linker length between the position 3 of the coumarine and the position 1 of the ring (B) of the chalcone-like moiety for inhibitor in 3D model.

Using CDC25B as key model, we found that conjugating ketone-diene chain ($n=2$) provided a better linker length than a single double bond ($n=1$) for our approach. Coumarine was one of the counterparts of choice while the other was substituted aromatic ring, and they were intended to be hybridized.

Table 2. Synthesized derivatives and their molecular modeling interaction scores with CDC25 phosphatase A and B indicating hydrogen bonds (number and length) and energy.

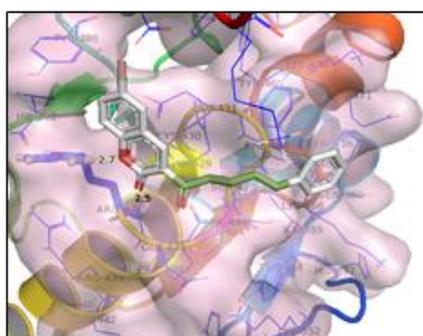
Compounds	R1	R2	CDC25A Energy (Kcal/mol)	HB		CDC25B Energy (Kcal/mol)	HB	
				no°	Length (Å°)		no°	Length (Å°)
1	H	H	-4.5	3	2.4; 2.6	-6.9	1	2.8
2	6-OMe	H	-5.6	1	2	-7.3	1	2.6
3	6-Br	H	-5.4	2	2; 2.5	-6.5	1	2.7
4	6-Cl	H	-5.6	2	2.5; 2.6	-7.5	1	2.7
5	7-N(C ₂ H ₅) ₂	H	-3.9	2	2.7	-7.7	2	2.5; 2.6
6	H	2,4-OMe	-6.2	1	2.9	-7.6	2	2; 2.7
7	H	2,5-OMe	-6.1	2	2.6; 2.9	-7.8	2	2.3; 2.7
8	6-Cl	2,4-OMe	-5.9	2	2.7; 2.9	-7.4	1	2.2

The docking study was achieved using AUTODOCK Vina³³. We assumed that the coumarin compound is able to bind the cysteine of the catalytic site of CDC25B. Our docking study showed that, for the half of the structures tested, the coumarin part rather fitted inside the swimming pool of CDC25B, while the chalcone part entered the active site. This is observed for compounds **1**, **4**, **5** (**Figure 3**) and **6** blocked whereas it is the contrary for compounds **2**, **3**, **7** and **8**.

The docking with CDC25A was more challenging as the catalytic cysteine is located inside

very shallow groove, with a very small cavity appearing unsuitable for fitting neither coumarin nor phenyl moiety of the compounds series. The docking results showed that the most of molecular poses are oriented in a way that the coumarin was toward the catalytic cysteine (cys430) which complying with phosphates group simulation assumption (**1**, **2**, **3** (**Figure 4**), **4**, **5**, **6**). (**Table 1**).

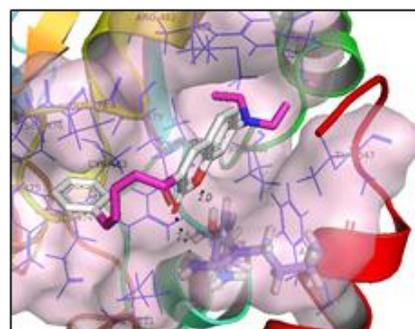
This orientations similar to phosphate cradling model of the native substrate³⁴. Compounds **7** and **8** had their binding mode in the opposite direction.

**Figure 3.** Compound **5** docking orientation with CDC25B interacting by two hydrogen bonds with Tyr428 and Arg544

Docking could not give the explanation of the inhibitory activity^{29,35-47}, so it was necessary to synthesize these molecules and evaluated their biological activities with CDC25A and B then verification of their reversibility.

The CDC25s have two interesting sites: the active site and the swimming pool which can play an

important role, so it would be efficient if both of them are tested in same time.

**Figure 4.** Docking of compound **3** with CDC25A forming two Hydrogen bonds with Arg436

It has been suggested that the hybrid structure may be more efficient at inhibiting CDC25s. Indeed, the first moiety of the inhibitor could fit the binding pocket (i.e. the swimming pool) while the other part could bind to the active cysteine⁴⁸.

Conclusion

The antitumor characteristics of both coumarin and chalcones inspired our approach to design hybrid structures could block both grooves of the protein

(active and inhibitory) highlighting the lack of toxicity in the same time.

Several chalcones derived from coumarine were synthesized, the binding modes of them were tested by molecular modelling simulation, the probability of phosphate surrogating by coumarine ring has been shown by certain derivatives. Biological evaluation revealed some activity of the compounds. *N, N*-diethylamino substitution on position 7 of coumarine (compound **5**) increasing the inhibitory activity on both isoforms of CDC25. The derivatives proved to perform reversible inhibition by MALDI-TOF analysis (compounds **3**, **4** and **5**). The designed scaffold could be considered as a basis of further lead optimization in order to obtain better inhibition.

Experimental Section

Chemistry

All solvents were used as purchased unless otherwise noted.

Melting points were determined on a Buchi 530 digital melting point apparatus. ¹H and ¹³C NMR spectra were recorded at 400 MHz and 100 MHz, respectively, using Me₄Si as the internal standard. Hydrogen coupling patterns are described as singlet (s), doublet (d), triplet (t), quartet (q), multiplet (m). High resolution mass spectra were measured using a MicroTof-Q98 instrument in ESI mode. Column chromatography was performed using silica gel (60M, 0.04-0.063 mm). Thin layer chromatography (TLC) was performed using silica gel plates (POLYGRAM SIL G/UV₂₅₄, 0,20mm). For the visualization, TLC plates were placed under UV light.

General procedure for synthesis of compounds 1 to 8

In round bottom flask, 1.1 mmole of cinnamaldehydes and 1 mmole of substituted 3-acetyl coumarine were mixed in ethanol, and stirred under reflux till dissolving of coumarine derivatives. Afterward, 5% mole of piperidine was added and the reaction retained under reflux for 24 h. When the reaction completed, the solution allowed to be cooled, and the product started to precipitate. The obtained solid was filtered and recrystallized using ethanol.

3-(1-Oxo-5-phenyl-2Z, 4Z-pentadien-1-yl)-2H-1-benzopyran-2-one (1)

Yellow powder; Yield: 52%; Mp: 184°C.⁴⁹

¹H NMR (400 MHz, CDCl₃): δ(ppm)=7.07 (d, 1H, J=6Hz); 7.08 (d, 1H, J=8Hz); 7.35- 7.42 (m, 5H); 7.68-7.70 (d, 1H, J=8Hz); 7.67-7.69(dd, 1H, J=8Hz, J=1.6Hz);7.52-7.54(dd, 1H, J=8.4Hz; J=1.6 Hz);7.51-7.34(d,1H, J=9.6Hz); 7.49-7.52 (d, 1H, J=10Hz); 7.72 (d,1H, J=2.4Hz); 8.60 (s,1H); ¹³C NMR (100 MHz, CDCl₃): δ(ppm)=116.7, 118.6, 124.9, 125.39, 127.3, 127.4, 128.9, 129.3, 130, 134.1, 136.1, 142.7, 145.2, 147.8, 155.2, 186.3.

HRMS (ESI): m/z [M+Na]⁺ calculated for C₂₀H₁₄O₂: 302,32; found : 325,085

6-Methoxy- 3-(1-oxo-5-phenyl-2E,4E-pentadien-1-yl)-2H-1-benzopyran-2-one (2)

Yellow powder; Yield: 24%; Mp: 190°C.

¹H NMR (400 MHz, CDCl₃): δ(ppm)= 3.89 (s, 3H, OCH₃); 7.07 (s, 1H); 7.09 (dd, 2H, J=5.6Hz and J=2.5Hz); 7.24 (d, 1H, J=6Hz); 7.32-7.35 (d, 1H, J=14.4Hz); 7.33-7.38(dd, 1H, J=18Hz); 7.36-7.40 (d, 1H, J=14.4Hz); 7.50 (d, 1H, J=6.8Hz); 7.53 (dd,2H, J=8Hz); 7.60 (t,1H); 7.68 (dd, 1H, J=18Hz); 8.50 (s,1H) ; ¹³C NMR (100 MHz, CDCl₃): δ(ppm)= 55.9, 111.0, 117.8, 118.9, 122.6, 125.5, 127.3, 127.4, 127.5, 128.9, 129.3, 136.1, 142.7, 145.1, 147.7, 149.9, 156.4, 159.4, 186.4.

HRMS (ESI): m/z [M+Na]⁺ calculated for C₂₁H₁₆O₄: 332.35; found 355.095

6-Bromo-3-(1-oxo-5-phenyl-2E,4E-pentadien-1-yl)-2H-1-benzopyran-2-one (3)

Yellow-orange powder; Yield: 54%; Mp: 237°C.⁵⁰

¹H NMR (400 MHz, CDCl₃): δ(ppm)= 7.08 (d, 1H, J=6Hz); 7.30 (d, 1H, J=16Hz); 7.38 (m, 3H); 7.46 (d, H, J=16Hz); 7.53 (d, 2H, J=9.2Hz); 7.68 (dd, 1H, J=16.8Hz); 7.71 (dd,1H,J=16.8Hz); 7.73 (dd, 1H, J=2.4 Hz and J=8Hz); 7.81 (d, 1H, J=2.4Hz); 8.48 (s,1H); 8.47 (s,1H); ¹³C NMR (100 MHz, CDCl₃): δ(ppm)=117.5, 118.4, 119.7, 125.5, 127.5, 128.9, 132.2, 137, 145.9, 154.1, 158.5, 194.9.

HRMS (ESI): m/z [M+Na]⁺ calculated for C₂₀H₁₃BrO₃: 380,9; found: 402,994

6-Chloro-3-(1-oxo-5-phenyl-2E,4E-pentadien-1-yl)-2H-1-benzopyran-2-one (4)

Yellow-orange powder; Yield: 70%; Mp: 244°C⁵⁰

¹H NMR (400 MHz, CDCl₃): δ(ppm)= 7.08 (d, 2H, J=6Hz); 7.34 (d, 1H, 14Hz); 7.36 (d, 1H, J=8.8Hz); 7.41 (m,2H); 7.46 (d, H, J=14.4Hz); 7.53 (d,1H, J=6.8Hz); 7.61(dd, 1H, J=14Hz); 7.55 (d, 1H, J=1.2Hz); 7.7 (dd, 1H, J=14Hz); 8.50 (s,1H); 8.47(s,1H); ¹³C NMR (100 MHz, CDCl₃): δ(ppm)= 118.1; 119.2; 125.5; 127.1; 127.2; 127.5; 128.9; 129.1; 129.5; 130.3; 133.9; 134.2; 143.1; 145.6; 146; 158.6; 195.

HRMS (ESI): m/z [M+Na]⁺ calculated for C₂₀H₁₃ClO₃: 336,06; found: 359,045

7-N,N-diethylamino-3-(1-oxo-5-phenyl-2Z,4Z-pentadien-1-yl)-2H-1-benzopyran-2-one (5)

Orange powder; Yield: 33%; Mp: 166°C⁵¹

¹H RMN (400 MHz, CDCl₃): δ(ppm)=1.17 (t,6H); 3.38 (q,4H); 6.40 (d, 1H, J=1.6Hz); 6.54 (dd, 1H, J=2.5Hz and 9.2Hz); 6.98 (d,1H, J= 10Hz); 7.08 (dd,1H, J= 10Hz and 10.8Hz); 7.23 (d,1H); 7.31 (m,5 H); 7.33 (d, H,J=9.2Hz); 7.57 (d,1H, J= 9.6Hz); 7.60 (dd,1H ,J= 9.6Hz);8.45 (s:1H) ; ¹³C RMN (100 MHz, CDCl₃): δ(ppm)= 12.5; 30.6; 96.7; 108.7; 109.8; 116.8; 127.3; 127.8; 128.8;

131.8 ; 136.4 ; 141.2 ; 143.5 ; 148.6 ; 153.0 ; 158.6 ; 160.9 ; 186.4.

HRMS (ESI): m/z $[M+Na]^+$ calculated for $C_{24}H_{23}NO_3$: 373,17; found: 396,158

3-[1-Oxo-5-(2,4-diméthoxyphenyl)-2E,4E-pentadien-1-yl]-2H-1-benzopyran-2-one (6)

Red Powder; Yield: 31%; Mp: 195°C

1H NMR (400 MHz, $CDCl_3$): δ (ppm)= 3.88 (s, 3H); 3.92 (s, 3H); 6.54-6.56 (2d, 2H, $J=2.4$ Hz and $J=8$ Hz), 6.48 (d, 1H, $J=2$ Hz), 7.34-7.43 (m, 3H), 7.63 (s, 1H), 7.66- 7.69 (dd, 2H, $J=18$ Hz), 7.89 (d, 1H, $J=16$ Hz), 8.17 (d, 1H, $J=16$ Hz), 8.56 (s, 1H); ^{13}C NMR (100 MHz, $CDCl_3$): δ (ppm)= 55.5, 98.4, 105.6, 116.6, 117.2, 118.7, 122, 124.8, 126.1, 129.8, 131.1, 133.8, 140.7, 147.3, 155.1, 159.3, 160.7, 163.5, 186.8.

HRMS (ESI): m/z $[M+Na]^+$ calculated for $C_{22}H_{18}O_5$: 362.12; found 385.015

3-[1-Oxo-5-(2,5-diméthoxyphenyl)-2E,4E-pentadien-1-yl]-2H-1-benzopyran-2-one (7)

Yellow powder; Yield: 36%; Mp: 132°C.

1H RMN (400 MHz, $CDCl_3$): δ (ppm)= 3.75 (s, 3H, OMe), 3.81 (s, 3H, OMe), 6.48 (d, 1H, $J=8$ Hz); 6.79(d, 1H, $J=8.8$ Hz); 6.88 (dd, 1H, $J_1=6$ Hz, $J_2=2.4$ Hz), 7.14 (d, 1H, $J=3.2$ Hz), 7.36 (dd, 1H, $J=14.4$ Hz); 7.38(dd, 1H, $J=14.4$ Hz); 7.58 (m, 2H); 7.86 (d, 1H, $J=16$ Hz), 8.10 (d, 1H, $J=16$ Hz); 8.17(d, 1H, $J=7.2$ Hz); 8.48 (s, 1H). ^{13}C RMN (100 MHz, $CDCl_3$): δ (ppm)= 55.9, 56.2, 112.6, 113.4, 116.7, 118.2, 118.6, 124.4, 124.6, 124.9, 125.7, 129.9, 134.0, 140, 147.7, 153.6, 153.7, 155.2, 159.3.

HRMS (ESI): m/z $[M+Na]^+$ calculated for $C_{22}H_{18}O_5$: 362.12; found 385.015

6-Chloro-3-[1-oxo-5-(2,4-diméthoxyphenyl)-2E,4E-pentadien-1-yl]-2H-1-benzopyran-2-one (8)

Colorless solid, Yield: 20%; Mp: 80°C

1H RMN (400 MHz, $CDCl_3$): δ (ppm)= 3.77 (s, 3H); 3.88 (s, 3H), 6.34(s, 1H); 6.38(dd, 2H, $J=8$ Hz); 6.4(dd, 1H, $J=16$ Hz); 6.7(d, 1H, $J=15.5$ Hz); 7.36(d, 1H, $J=16$ Hz); 7.43 (dd, 2H, $J=8.4$ Hz); 7.57 (dd, 1H, $J=15.5$ Hz); 7.24 (d, H); 7.99 (s, 1H); 8.47 (s, 1H); ^{13}C RMN (100 MHz, $CDCl_3$): δ (ppm)= 55.4, 60.1, 98.5, 105.2, 116.2, 116.7, 130.4, 139.9, 145, 153, 159.8, 162.6, 167.9, 182.49, 199.13.

HRMS (ESI): m/z $[M+Na]^+$ calculated for $C_{22}H_{17}ClO_5$: 396.08; found 418.9755

Docking simulation

3D structures of all compounds were designed and the best conformer picked by VEGA ZZ 2.3.1 software⁵². It was also used for adjusting the force field of the molecule as AMBER, and atomic charge which applied as Gasteiger, products was energetically minimized using MOPAC and finally introduced as PDB format.

CDC25B (1QB0) and CDC25A (1C25)⁵³ phosphatase catalytic domain was obtained from the Protein Data Bank. AutoDock Tools was employed to remove unwanted elements and water. It

transformed to PDBQT file format, to make them ready for docking which was processed using AUTODOCK Vina. Docking parameters was adjusted as the following

CDC25B: Grid box centered in X= 18.3, Y= 4.6, Z= 16.3, Volume = 23*23*23 Å

CDC25A: Grid box center: X= 11.6, Y= 40.2, Z= 69.3, Volume = 16*16*18 Å

Pymol software⁵⁴ was used for visualization and determination of the interaction of compounds with enzyme.

Biological evaluation

Recombinant human CDC25 phosphatases were prepared by previously described method¹⁹. Assay took place in 96-well plates; buffer solution was adjusted in the following quantities: 50 mM Tris-HCl, 50 mM NaCl, 1 mM EDTA, and 0.1% Bovine Serum Albumine, pH 8.1. Incubation period of substrate 3-O-methylfluorescein phosphate with enzyme was 2 h in 30°C. Enzyme was exposed to the inhibitors for 20 min and the residual activity of the enzyme has been determined by fluorimetric method.

MALDI/TOFMS

All compounds were dissolved in ethanol at a concentration of 10^{-2} M. The solution were then further diluted to 2.10^{-3} M with ultrapure water. Phosphatases CDC25A was solubilized in Tris A buffer (50 mM Tris, 50 mM NaCl, 1 mM EDTA and 1 mM dithiothreitol [DTT], pH 8.0) at a concentration of 8.10^{-5} M. One hundred and fifty μ l of CDC25A was incubated with 40 μ l of compounds for 1 h. Solution was ultracentrifugated on Microcon filter unit with a mass cutoff of 30 kDa (Millipore). The unbound material was eliminated by centrifugation during 10 min at 12,000 rpm and washed three times by 100 μ L of ultrapure water. The retentate was then dissolved in 20 μ L of ultrapure water. Two μ l of the retentate was spotted on the MALDI plate (2 spot for sample in two line), evaporated to dryness at room temperature. Then one μ l of saturated solution of DHB (dihydroxybenzoic acid) was deposited for one of spot and HCCA (α -hydroxycyanocinnamic acid) was deposited for the second spot of each sample on the plate to evaluate the response of each compound with both of matrix, and conserved the spectrum which had the intense response.

The presence of the protonated molecular ion in the MS spectrum is corresponding to a reversible inhibitor activity.

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