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## Synthesis of kinase inhibitors containing a pentafluorosulfanyl moiety†

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A series of 3-methylidene-1*H*-indol-2(3*H*)-ones substituted with a 5- or 6-pentafluorosulfanyl group has been synthesized by a Knoevenagel condensation reaction of SF<sub>5</sub>-substituted oxindoles with a range of aldehydes. The resulting products were characterized by X-ray crystallography studies and were tested for biological activity *versus* a panel of cell lines and protein kinases. Some exhibited single digit nM activity.

### Introduction

The dysregulation of protein phosphorylation mediated by protein kinases is key to the progression of a number of cancers. Unsurprisingly, a number of ATP-competitive kinase inhibitors are in clinical use and development.<sup>1–7</sup> For example, the oxindole-containing antiangiogenic drug Sunitinib **1**, containing a 5-fluorine substituent and a solubilizing side chain on the pyrrole unit, is in clinical use and superseded Semaxanib (**2**, SU5416) (Fig. 1) as well as inspiring a number of other studies on druglike oxindoles.<sup>8–15</sup>

Metal-based analogues such as **3**, **4** have been described by our group and show kinase inhibition down to the nM range and tolerance of a range of substituents at the C-5 position.<sup>16,17</sup>

Meggers's group replaced the sugar unit in staurosporine, a pan-kinase inhibitor with relatively high toxicity and unsuitable for clinical use, by square planar and octahedral transition metal complexes **5–7**, leading to highly potent, selective kinase inhibitors. This was attributed to the novel “imaginary hypervalent carbon” geometry enabled by the metal complexes (Fig. 2, **5–7**).<sup>18–21</sup>

The pentafluorosulfanyl group is attracting increasing interest in medicinal chemistry. Displaying strong polarity, high



Fig. 1 Oxindole-based kinase inhibitors.

lipophilicity and good stability under physiological conditions, an SF<sub>5</sub> substituent has often been shown to behave like a CF<sub>3</sub> group.<sup>22–26</sup> Here we show that a SF<sub>5</sub> group can be incorporated in both classical and metal-based oxindole derivatives, at the 5- or 6-position, leading to analogues displaying kinase inhibition down to the nM range.

### Results and discussion

Microwave-mediated Knoevenagel condensations of the commercially-available 5- or 6-SF<sub>5</sub>-substituted oxindoles **8**<sup>27</sup> with three separate aldehydes led to the products **10–14** (Scheme 1).<sup>28</sup>

The structures of the pyrrole-containing positional isomers **10** and **11** were confirmed by <sup>1</sup>H NMR, <sup>13</sup>C NMR spectroscopy, elemental analysis and mass spectrometry. In their <sup>1</sup>H NMR spectra the most downfield signals were assigned to the pyrrole-NH groups ( $\delta$  11.10–13.40 ppm) due to an intra-

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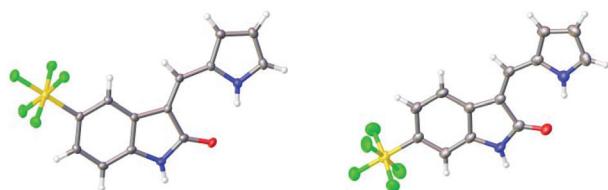
Fig. 2 Staurosporine analogues.



Scheme 1 Microwave-mediated Knoevenagel condensations.

molecular NH...O=C hydrogen bond and further confirmation of their anticipated *Z*-configuration and such a hydrogen bond was provided in the solid state (Fig. 3).<sup>29</sup>

The related reaction with ferrocene carboxaldehyde afforded a mixture of stereoisomers **12a** and **12b**, which were

Fig. 3 Solid state structures of **10** and **11**.Fig. 4 Solid state structures of **12a** and **12b**.

separated by chromatography. Both isomers were characterized in the solid state (Fig. 4).

We tested all synthetic compounds against a panel of kinases in a biochemical assay. Each data point was measured in duplicate (technical replicates). The potencies of compounds that showed appreciable (approx. 50%) inhibition at 1 μM concentration were established by testing them over a dose range to determine their IC<sub>50</sub> values. Additional kinase binding studies were performed *vs.* a select group of functionally and structurally divergent kinases including AAK1 (Adaptor-associated protein kinase 1), BMP2K (BMP-2-inducible protein kinase, where BMP is bone morphogenic protein), GAK (Cyclin G-associated kinase) and STK16 (Serine/threonine-protein kinase 16) (Table 1). In all assays a control of staurosporine, a known promiscuous kinase inhibitor, was used.

In the case of a number of kinases, *e.g.* VEGFR2 (vascular endothelial growth factor receptor 2) and DYRK2 (Dual-specificity tyrosine phosphorylation-regulated kinase 2), no appreciable inhibition was observed for any of our synthesized compounds, suggesting that we might observe differences in their selectivity, *i.e.* no promiscuity, towards this panel of kinases. Compound **10** bound to BMP2K with an IC<sub>50</sub> of 452 nM whereas **11** displayed nM potency *vs.* PDGFR2 (98 nM) and submicromolar potency *vs.* VEGFR3 (230 nM). Stereoisomeric **12a** and **12b** only inhibited DYRK3 in the low micromolar range. The positional isomers **13** and **14** both inhibited VEGFR3 with IC<sub>50</sub>s of 530 and 18 nM respectively whereas the latter displayed an excellent 3.1 nM IC<sub>50</sub> *vs.* PDGFRα.

The synthesized compounds were next tested in breast cancer and non-transformed breast cell lines. Compounds **10** and **11** potently inhibited MCF7 and T47D breast cancer cell proliferation with GC<sub>50</sub> values ranging from 0.35 to 3.8 μM with compound **11** proving superior to compound **10**.

MCF7 and T47D cells are luminal A ER<sup>+</sup>/PR<sup>+</sup>/HER2<sup>-</sup> cells that would normally be responsive to estrogen and progesterone receptor (ER/PR) antagonists such as tamoxifen and megestrol respectively, but not to human epidermal growth factor receptor 2 (HER2) inhibitors. MDA-MB-231 (abbreviated as MM231) cells are triple negative (ER<sup>-</sup>/PR<sup>-</sup>/HER2<sup>-</sup>) and cannot be treated with hormone receptor and EGFR (HER2) inhibitors, making cancer cells such as these refractory to most treatment strategies. Compounds **10** and **11** may offer advantages for the treatment of ER<sup>+</sup>/PR<sup>+</sup> cancer cells by poly-



Table 1 Biochemical kinase assays

	Kinase <sup>a</sup>	10	11	12a	12b	13	14	Staurosporine <sup>c</sup>
1	IC <sub>50</sub> (M)	STK16 <sup>b</sup>	1.76 × 10 <sup>-5</sup>	1.35 × 10 <sup>-4</sup>	nt	nt	—	1.14 × 10 <sup>-7</sup>
2		GAK <sup>b</sup>	3.42 × 10 <sup>-5</sup>	4.76 × 10 <sup>-7</sup>	nt	nt	—	1.89 × 10 <sup>-8</sup>
3		BMP2K <sup>b</sup>	4.52 × 10 <sup>-7</sup>	1.87 × 10 <sup>-4</sup>	nt	nt	—	3.17 × 10 <sup>-9</sup>
4		AAK1 <sup>b</sup>	1.0 × 10 <sup>-6</sup>	1.0 × 10 <sup>-3</sup>	nt	nt	—	2.47 × 10 <sup>-9</sup>
5 <sup>d</sup>		DYRK3 (h)	—	—	1.7 × 10 <sup>-6</sup>	2.4 × 10 <sup>-6</sup>	—	4.5 × 10 <sup>-8</sup>
6		PDGFRα (h)	—	9.8 × 10 <sup>-8</sup>	—	—	3.1 × 10 <sup>-9</sup>	1.2 × 10 <sup>-9</sup>
7		FLT-4 (h) (VEGFR3)	—	2.3 × 10 <sup>-7</sup>	—	—	5.3 × 10 <sup>-7</sup>	1.8 × 10 <sup>-8</sup>

<sup>a</sup> Unless stated otherwise, performed in the presence of 10 μM ATP. <sup>b</sup> Binding displacement assays have no ATP present. <sup>c</sup> No activity was observed for **10–14** vs. KDR kinase (h) (VEGFR2), PDGFRβ kinase (h); DYRK1a (h); DYRK2a (h); FLT-1 kinase (h) (VEGFR1), where staurosporine positive controls gave IC<sub>50</sub>s of 2.3 × 10<sup>-9</sup>; 2.5 × 10<sup>-9</sup>; 3.2 × 10<sup>-8</sup>; 8.3 × 10<sup>-7</sup>; 2.8 × 10<sup>-8</sup> respectively. <sup>d</sup> Entries 5–7 performed by CEREP (France; <http://www.cerep.fr>). nt – not tested. — insufficiently active for an IC<sub>50</sub> determination.

pharmacologically targeting multiple kinases such as the receptor tyrosine kinases and other serine/threonine kinases. Lastly, it is encouraging that normal MCF10A cells were resistant to all inhibitor treatments suggesting these compounds would have a large therapeutic window (Table 2).

Compound **11**, which bears a methylidene indolinone scaffold (Fig. 1), demonstrated its greatest potency against the receptor tyrosine kinase PDGFRα, which adopts an inactive conformation according to X-ray crystallographic analysis (Fig. S1B†); however, an X-ray co-crystal structure containing a methylidene indolinone-based inhibitor (**15**, Fig S1†) bound to the RET kinase domain reveals a type 1 inhibitor binding-mode, or binding to an active kinase conformation (Fig. S1B†). Alignment of **15**-bound RET with the PDGFRα structure reveals gross structural shifts between analogous β-hairpins and α-helices, which is not surprising as the active conformation is generally rigid and condensed and the inactive conformation is generally more open.<sup>30</sup> Alignment of the Dasatinib-bound co-crystal structure of Protein-tyrosine kinase 6 (PTK6), a non-receptor tyrosine kinase, with the **15**-bound RET reveals that they share a similar, active conformation (Fig. S1C†). Based on this analysis, it makes sense to use an active kinase conformation, as the above elements (β-hairpin and α-helix) are proximal to the ATP-binding pocket and likely to have an impact on binding mode. However, rather than performing docking studies with RET, we decided that PTK6 would be superior as this kinase has a threonine gatekeeper residue, similar to that of PDGFRα, whereas RET has a valine at the same position. Valine is slightly bigger and more hydrophobic than threonine, lacking a hydroxyl group compared to threo-

nine, and could drastically perturb interactions necessary for **10** and **11**-binding. Furthermore, based on the similarity of **10** and **11** with other type 1 methylidene indolinone inhibitors, we predicted that docking these compounds to an active PTK6 kinase conformation would yield improved binding energies; a result confirmed by docking **10** and **11** to the inactive kinase conformation of PDGFRα (PDB: 5K5X), which reported higher binding energies, and thus less avid binding, for both **10** and **11**.

Against PTK6, both compounds bind in a very similar manner as seen in Fig. 5 (top panel). We found the SF<sub>5</sub> moiety of **10** and **11** to bind deeply in a predominantly hydrophobic

Table 2 Cellular activity of **10** and **11**

Compound	MCF7	GC <sub>50</sub> <sup>a</sup> , μM T47D	MDA-MB-231	MCF10A
<b>10</b>	4.8 ± 1	0.49 ± 0.4	na	na
<b>11</b>	0.69 ± 0.4	0.35 ± 0.1	na	na

<sup>a</sup> The GC<sub>50</sub> value was defined as the amount of compound that caused 50% reduction in cellular proliferation in comparison with DMSO-treated control and was calculated using GraphPad Prism version 6 software; na = not applicable.



Fig. 5 Docking poses of **10** and **11**. Docking was performed using AutoDock 4.2.6.; Lamarckian Genetic Algorithm empirical free energy scoring function. PDB format files for the ligand and kinase domain were pre-processed using AutoDock Tools 1.5.6.







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