Identification of a new inhibitor of Ran GTPase with therapeutic value in epithelial ovarian cancer

Zied Boudhraa[δ,1,2], Xiaohong Tian[δ,5], Sabrina Ritch[ξ,1,2], Ryhem Gam[ξ,1,2], Jennifer Kendall-Dupont[1,2], Euridice Carmona[1,2], Diane Provencher[1,2,3], Jian Hui Wu[5], Anne-Marie Mes-Masson[1,2,4*]

[1] Centre de recherche du Centre hospitalier de l'Université de Montréal (CRCHUM), Montreal, Canada.

[2] Institut du cancer de Montréal (ICM), Montreal, Canada.

[3] Division of Gynecologic Oncology, Université de Montréal, Montreal, Canada.

[4] Department of Medicine, Université de Montréal, Montreal, Canada.

[5] Lady Davis Institute, Jewish General Hospital, McGill University, Montreal, Canada

[δ] First Co-authors

[ξ] Second Co-authors

[*] **Corresponding author:** Anne-Marie Mes-Masson, CRCHUM, R10-412, 900 rue St-Denis, Montreal, Quebec, Canada, H2X 0A9. Phone: (514) 890-8000 ext. 25496. E-mail: anne-marie.mes-masson@umontreal.ca

ABSTRACT

Accumulated studies suggest that the small GTPase Ran is critical in cancer initiation and progression. Compounds that block Ran activity would be valuable for cancer treatment. Here, by learning lessons from the discovery of KRAS G12C inhibitors, we generated a structural model of the switch II pocket of GDP-bound Ran to identify potential inhibitors of Ran by virtual screening. After in vitro verification and hit optimization, we identified chemical compound M36 as an efficient inhibitor of Ran with a therapeutic value. Binding of M36 to Ran was confirmed by cellular thermal shift assay. The specificity of M36 towards Ran was demonstrated by the evaluation of the active GTP-bound forms of a range of GTPases including Ran, RhoA, Cdc42 and Rac1; and by the expression of a dominant active mutant of Ran. Remarkably, similar to depletion of Ran by siRNA, M36 exhibits a specific toxicity in aneuploid ovarian cancer cells and represses DNA repair systems. In accordance with this, we established a synergistic relationship between M36 and the FDA approved PARP inhibitor olaparib. *In vivo*, M36 presents acceptable pharmacokinetic properties and, more importantly, inhibits the tumor growth of an aggressive ovarian xenograft model. Clinically relevant, M36 was able to induce cell death in *ex vivo* EOC patient derived micro-dissected tumors. Overall, our study is the first to provide a small-molecule compound inhibitor of Ran with a therapeutic potential.

INTRODUCTION

Ran (Ras related nuclear protein), a member of the RAS superfamily of small GTPases, is unique among other GTPases owing to its subcellular localization. While other GTPases are found in the cytoplasm and associated to subcellular membranes, Ran is found predominately in the nucleus [1]. Ran has been widely studied for its role in mitosis and nucleo-cytoplasmic shuttling of proteins and RNAs [2]. In comparison with normal tissues, Ran was found to be overexpressed in several cancers including breast, renal, gastric, colon, pancreatic, ovarian and lung cancers [3-10]. Furthermore, within the same cancer the expression of Ran has been found to be positively correlated with patient outcomes in myeloma, lymphoma, neuroblastoma, renal cell, ovarian and breast carcinomas [4-6,10-14]. It has been reported that Ran is involved in supporting at least three hallmarks of cancer, namely proliferative signaling, resisting cell death and activating pathways that support invasion and metastasis [7,9,11,15-21]. Interestingly, we and others have been reported that the loss of Ran using specific siRNAs is lethal for cancer cells with no or moderate effect in normal cells [7,18,22-24]. This suggests that targeting Ran could achieve a valuable therapeutic index.

Epithelial ovarian cancer (EOC) is the most common form of all ovarian cancers and is the most fatal of all gynecological malignancies [25,26]. Histologically, EOCs are subdivided into five subtypes where the high grade serous carcinoma (HGSC) is overrepresented and rates among the most aggressive [25,27]. EOCs are characterized by extremely high intratumoral heterogeneity that poses specific challenges for therapeutic strategies [28] (Platinum- and taxane-based chemotherapy are the standard first-line therapies of EOC [27,29]). However, despite this heterogeneity, aneuploidy is a hallmark of EOC, particularly of HGSC [28] where the chromosomal stability control gene, *TP53*, is mutated in >90% of cases [30,31]. Thus, targeting aneuploidy would be an avenue to efficiently treat this cancer.

Recently, we have shown using EOC models, that the differential sensitivity between normal and cancer cells following the loss of Ran is governed by aneuploidy and genomic instability [23]. In particular, we have reported that induction of aneuploidy in rare diploid EOC cell lines or normal cells renders them highly dependent on Ran. We also established an inverse correlation between Ran and the tumor suppressor NR1D1 and reveal the critical role of Ran/NR1D1 axis in aneuploidy-associated endogenous DNA damage repair. We showed that Ran, through the maturation of miR4472, destabilizes the mRNA of NR1D1 impacting several DNA repair pathways [23]. Loss of Ran was then associated with NR1D1 induction, accumulation of DNA damages and lethality of aneuploid EOC cells. Our findings suggest a synthetic lethal strategy targeting aneuploid cells based on their dependency to Ran. We hypothesize that developing small molecules targeting this GTPase is an attractive therapeutic approach for EOC. To date, despite the availability of Ran's crystal structure [32-36], there is no inhibitor proven to be efficient and specific to Ran. The high affinity of Ran to its cognate GTP (pM range) and the high cellular concentration of GTP (millimolar range), makes the identification of an efficient compound with a GTP-competitive mode of action very difficult, if not impossible.

In the present study, inspired by the ground-breaking work of KRAS G12C inhibitors[37,38], we aimed to identify allosteric small molecule inhibitors of Ran. The approach chosen was to target the GDP-bound form of Ran at the switch II pocket, with the hypothesis that this would lock the protein in an inactive state, thereby depleting the active Ran population. To this end, a part of the NCI chemical database (90,000 compounds) was screened virtually. After *in vitro* validation and hit optimization, we identified M36 as a promising inhibitor of Ran. M36 mimics the effect of Ran knock down (KD): specific toxicity in aneuploid cancer cells and significant repression of the DDR process. *In vivo*, M36 is well tolerated by mice at high doses, displays an acceptable

pharmacokinetic (PK) pattern and significantly delays tumor growth of a very aggressive EOC

xenograft model. At the clinical level, M36 was able to induce cell death in *ex vivo* micro-dissected

tumors derived from an EOC patient. Furthermore, owing to its ability to repress DNA repair

systems, we established a synergistic relationship between M36 and the FDA approved PARP

inhibitor olaparib. Overall, our findings suggest a new therapeutic strategy for EOC based on the

modulation of Ran activity.

RESULTS

***In silico* and cell-based screenings identified M26 as hit compound for Ran inhibition**

Inspired by the ground-breaking work of KRAS G12C inhibitors, which bind KRAS G12C mutant

at a pocket nearby switch II (referred to as switch II pocket) [37,38], we aimed to target the GDP-

bound form of Ran (RanGDP) at the switch II pocket to 'arrest' Ran at its inactivated state (**Figure**

1A). However, one key feature of the switch II pocket of KRAS G12C is that it exists only when

it binds with an inhibitor. Our inspection of the crystal structure of RanGDP (pdb: 3ch5) found no

pre-formed switch II pocket. We thus decided to construct a structural model of the switch II

pocket of RanGDP using the crystal structure of KRAS G12C/Inhibitor complex (pdb: 5v6s) as

the template (**Figure 1A**). Next, a part of the NCI chemical database (90,000 compounds) was

screened virtually against the RanGDP switch II pocket. Top-ranking compounds identified in this

in silico screen went through a more in-depth visual inspection for binding modes. A total of 28

compounds were selected for further study as potential Ran inhibitors (**Figures 1B and S1A**).

Having previously established that aneuploid EOC cells are more sensitive to the loss of Ran than

normal or tumoral diploid cells [23], biological activity was assessed by clonogenic assays (at a single

dose of 10 µM) using one aneuploid EOC cell line (TOV112D) and the diploid normal ARPE

(ARPE-19) cells **(Figures 1C and S1B)**. The criterion for a positive hit was that the compound

did not inhibit the colony formation of the ARPE cells but significantly inhibited the number of

colonies formed by the TOV112D cells. Our results show that one compound from the *in silico*

screening, M26 **(Figure 1B)**, inhibited colony formation of EOC but not the normal cells **(Figure**

1C). Furthermore, by analyzing PARP cleavage by Western blot, we found that M26 treatment

induced apoptosis in TOV112D cells with no notable effect in ARPE cells **(Figure 1D)**, indicating

a differential sensitivity between the diploid and aneuploid cells following M26 treatment. Since

our screening was virtual using Ran crystal structure, it was therefore important to determine

whether our hit compound was able to inhibit Ran in its biological form. For that, the level of

active GTP-bound Ran was evaluated in lysates of EOC cells treated or not with M26 using Ran

pull down assays. Our results showed a marked decrease in Ran-GTP level in TOV112D cells

incubated with this compound compared to DMSO-treated control cells **(Figure 1E)**. Of note,

since the number of cells used in the colony formation assay is lower than that of other cell-based

assays, a lower concentration of M26 (or its derivatives, see below) was used in this assay.

Collectively, our data identified M26 as a potential inhibitor of Ran with an interesting therapeutic

value.

Chemical optimization and cell-based screening identified M36 as a promising inhibitor of

Ran

Plasma esterases are the major drug-metabolizing enzymes in plasma significantly affecting drug

stability *in vivo* [39]. As shown in **Figure 1B**, M26 has three ester groups, which would suggest poor

bioavailability of the drug when injected *in vivo*. To overcome this issue and explore preliminary

structure-activity relationship, a series of M26-derived compounds, in which the ester groups were

replaced by ether groups, were synthetized **(Figures 2A and S2A)**. Our results showed that only

compound M36 and its derivative M98, inhibited colony formation of TOV112D cells without

affecting the ARPE cells **(Figure S2B)**. Interestingly, M36 but not M33 inhibited the activation of

Ran comparably to the parent compound, M26 **(Figure S2C)**. Therefore, for the rest of the study

we selected M36 **(Figure 2A)** for further characterization. Using Ran pull down assays, the effect

of M36 on Ran activation was shown to be dose dependent **(Figure 2B)**. In addition,

immunofluorescence studies using an antibody specific to active Ran-GTP showed no detectable

levels of Ran-GTP in TOV112D cells treated with M36 as compared to the intense staining of the

DMSO-treated cells **(Figure 2C)**. More importantly the direct binding of M36 to RanGTPase was

assessed by CETSA, a widely used technique to verify the interaction of a compound with its target

protein.[40] In this assay, the thermal stability of Ran was investigated at different temperatures in

OV1946 cells treated with M36 or DMSO **(Figure 2D)**. As expected, Ran levels detected by

Western-blot decreased exponentially with increasing temperatures in controls cells treated with

vehicle DMSO. However, a right shift in this thermal stability curve was observed when cells were

treated with 100 μM M36, and significantly higher levels of Ran were observed at temperatures

of 52°C, 55°C and 64.5°C **(Figure 2D)**, indicating M36 engages with Ran and increases its thermal

stability. To test the effect of different concentrations of M36 on CETSA, the temperature of 64°C

was chosen because it is in the exponential phase of the curve. Our results show a concentration-

dependent protection of Ran when cells were treated with M36 **(Figure 2E)**. As negative control,

we show that this protection was not observed when OV1946 cells were treated with increasing

concentrations of the PARP inhibitor Olaparib (**Figure S3A**), a drug known to impact DNA repair

[41]. In all, these results indicate that M36 targets Ran and inhibits Ran-GTP activation.

Regarding its effect on cancer cells, the IC_{50} value of M36 for the TOV112D cell line as determined

by clonogenic assay was found to be 10.02±0.36 μM. Only a minimal effect was observed for the

normal ARPE cell line at high concentrations **(Figure 3A)**. To support our observation regarding

the differential sensitivity between diploid and aneuploid cells with M36 treatment, we expanded

our analysis by using, in addition to ARPE and TOV112D cell lines, five aneuploid HGSC cell

lines [TOV1946, TOV2295(R), OV1946, OV866(2) and OV4485] and one diploid low-grade

serous EOC TOV81D cell line. Proliferation assays were performed on these cell lines after

treatment with M36. As a positive control, the same cell lines were transfected with siRan that we

have previously characterized for its specificity [21,23]. Remarkably, like siRan, M36 demonstrated

a specific toxicity in aneuploid cells with only a moderate effect in normal and EOC diploid cells

(Figure 3B). Similarly, this toxicity was accompanied by the induction of apoptosis specifically

in aneuploid cells **(Figure 3C)**, highlighting the therapeutic potential of M36. Since aneuploidy

and genomic instability are hallmarks of the majority of cancers [42,43], we assessed the toxicity of

M36 in other cancer cell lines derived from prostate, gastrointestinal, breast and skin cancers.

Strikingly, M36 showed a significant toxicity in all the cell lines tested **(Figure S2D)**. These results

suggest that the use of M36 would not be limited to ovarian cancer but could be extended to other

tumors. To investigate the specificity of M36 towards Ran, the effect of M36 on the activation of

other GTPases (RhoA, Cdc42 and Rac1) was assessed. As shown in **Figure 3D**, no significant

effect on the activation of these GTPases was observed when incubated with M36. Furthermore,

overexpression of constitutively active (GTP-bound form) Ran^{Q69L} mutant protein [44] mitigated the

inhibition of TOV112D cell growth by M36 **(Figure 3E)**. Together, these data provide evidence

of the specificity of M36 towards Ran and indicate that this compound acts specifically on the

GDP-bound form of Ran.

M36 mimics the effect of Ran knock down (KD) regarding DDR

We have shown that the differential sensitivity between diploid and aneuploid cells following the

loss of Ran comes from the involvement of the Ran/NR1D1 axis in modulating DNA repair [23]. In

fact, following the loss of Ran, NR1D1 was induced and in turn repressed several DNA repair

pathways including the HR and the NHEJ pathways, leading to the accumulation of DNA

damages. We first assessed the effect of M36 on NR1D1 expression. As observed following Ran

KD, M36 significantly induced the expression of NR1D1 in two aneuploid EOC cell lines

(TOV112D and OV1946) **(Figure 4A-B)**. As negative control, we show that NR1D1 expression

was not affected when cells were treated with the PARP inhibitor Olaparib **(Figure S3B)**,

suggesting that M36 effect on NR1D1 expression is specific. Next, to investigate whether M36

was able to repress the DDR process, TOV112D cells were either transfected with siRan or treated

with M36 and the DDR components were analyzed by immunofluorescence. Remarkably, in

accordance with Ran KD, M36 treatment induced DNA damage accumulation as shown by an

increase of p-ɣH2AX foci number **(Figure 4C)** and an inhibition of the HR and the NHEJ

pathways, which were assessed respectively by the quantification of Rad51 **(Figure 4D)** and

53BP1 **(Figure 4E)** foci formation. Interestingly, since the cytoplasmic staining of 53BP1

following M36 treatment was increased **(Figure 4F)**, the inhibition of 53BP1 foci formation by

M36 can probably be attributed to the inhibition of the Ran-dependent nuclear import of this

protein that has been previously reported [15] and is in accordance with the Ran KD condition

(Figure 4F). Collectively, our data demonstrate that M36 mimics the effect of the loss of Ran

regarding DDR.

Evaluation of the therapeutic potential of M36 *in vivo*

The promising *in vitro* results of M36 led us to initiate *in vivo* analysis of this small molecule

inhibitor of Ran. Pharmacokinetic results showed that after a single IP injection (200 mg/kg),

plasma levels of M36 detected at our first time point of 5 minutes, reached a peak at 30 minutes

(100 μM), remained at around 10 μM after 6 h and is still detectable at 24 h **(Figure 5A)**.

Therefore, M36 displayed an acceptable PK pattern. For the tolerance study, M36 was injected IP.

daily for a period of three weeks. Our results showed that treated mice continued to gain weight

(Figure 5B), suggesting that, even at higher doses (200 mg/kg), M36 was well tolerated. Inhibition

of tumor growth was evaluated in the human chemoresistant ovarian cancer xenograft model,

TOV112D. As we've previously shown, this xenograft model showed resistance to carboplatin

treatment [45]. Furthermore, when mice were treated with the maximum tolerated dose of the PARP

inhibitor Olaparib **(Figure 5C)**, no significant effect was observed regarding tumor growth.

However, M36 treatment significantly delayed tumor growth of this aggressive model **(Figure 5D-**

E) and prolonged mouse survival **(Figure 5F)**, highlighting the promising potential of this

compound for the treatment of EOCs, particularly for those that are difficult to treat.

M36 induces cell death in *ex vivo* ovarian cancer models

To evaluate the clinical relevance of M36 treatment, the viability of microdissected tumor samples

derived from EOC xenografts or patient samples were evaluated *ex vivo* using our microfluidic

methodology [46]. Our results show **(Figure 6)** a significant increase in the intensity of cleaved

caspase 3 (CC3) staining 72 hs after M36 treatment in both the OV1946 xenograft and the

TOV12018G patient tumor models. For the TOV112D xenograft model, this effect was also

observed, but no significance was achieved **(Figure S3B)**, and a 50% decrease in the nuclear Ki-

67 staining was observed in this model 24 hs post-treatment. These results suggest that M36

induces cell death by apoptosis and could decrease cell proliferation in *ex vivo* EOC models,

including patient tumor, further corroborating its therapeutic value.

Combination of M36 and Olaparib triggers synthetic lethality in EOC cells

It is presumed that resistance to PARP inhibitor therapy is closely related to the activation of the

HR pathway of cancer cells [47]. Therefore, combination treatments of PARP inhibitor with drugs

that inhibit the HR pathway would be promising to circumvent this resistance. Based on our finding

that M36 was able to repress the HR pathway, we sought to determine whether M36 was able to

sensitize ovarian cancer cells to Olaparib. First, we investigated the effect of M36 on the activation

of the HR pathway by Olaparib. Our data in two HR proficient BRCA1/2 wild-type (WT) ovarian

cancer cell lines (TOV112D, OV866(2)) showed that M36 efficiently inhibited the induction of

the HR pathway (assessed by Rad51 foci quantification) by Olaparib **(Figure 7A)**, and this

repression was comparable when irradiation was used as an inducer of this DNA repair pathway

(Figure 4E). Next, combination treatments of M36 with Olaparib were undertaken in three

BRCA1/2 WT and Olaparib resistant-cell lines, namely TOV112D, OV866(2) and OV90 cell

lines, together with the normal diploid ARPE cell line. These combinations were performed using

increasing concentrations of both drugs (all concentrations used are below the IC_{50}) and evaluated

using the Bliss independent model [48], in which values below -1 indicate antagonism, values

between -1 and 1 indicate additive effects and values above 1 indicate synergy. Remarkably, in

contrast to ARPE cells that did not respond to any combination condition, M36 displayed a potent

synergistic interaction with Olaparib in all 3 EOC cell lines (Bliss scores ranging from 41.02 to

78.6) **(Figure 7B-D)**. Similarly, while no effect was observed in ARPE cells, M36/Olaparib

combination induced a significant increase of cell death in the EOC cell lines in comparison with

single treatments, as assessed by FACS using DRAQ7 staining **(Figure 7E)** and by Western blot

using cleaved caspase-3 antibody **(Figure 7F)**. Overall, our data indicate that combining M36 with

Olaparib would be an effective combination therapy to counter PARP inhibitor resistance in

ovarian cancer.

DISCUSSION

The involvement of Ran GTPase in cancer initiation and progression has been discussed for more

than a decade [7,8,15-21]. Furthermore, using several *in vitro* and *in vivo* experimental models, Ran

has been proposed as a promising therapeutic target of cancer [8,9,14,19,22,23,49]. Recent reports have

proposed new strategies to target Ran in the context of cancer therapy. One of them relies on

repurposing Pimozide in Ran Targeting [50]. Pimozide was initially identified as a potent antagonist

of dopamine receptor D2 (D2R) and used as an antipsychotic drug for the management of

schizophrenia and other psychotic disorders. It has been shown that Pimozide inhibits the

expression of Ran at the transcriptional level and inhibits breast cancer cell growth *in vitro* and *in*

vivo [50]. Although this molecule displays an interesting cancer therapeutic value, it is likely that this

drug will display severe side effects at the concentrations needed. In fact, it has been shown that

mice lacking D2R had impaired motor activity and movement coordination as well as hyperactivity

[51]. More importantly, the posology of Pimozide for patients with psychotic disorders is about 0.2

mg/Kg/day, however, in the *in vivo* study proposed for breast cancer therapy, mice were treated

daily with Pimozide at 20 mg/Kg/day in order to have a significant effect on tumor growth [50].

These very high doses of Pimozide will inevitably be an issue in the exploration of this drug in the

context of cancer. Another strategy relies on Nano-encapsulation technology (using PLGA-based

nanoparticles) of a shRNA targeting Ran [52] or a peptide inhibiting the activation of this GTPase

by disrupting the interaction between Ran and RCC1 [53,54]. Such an approach presents many

obstacles making its use in clinic very difficult. First, upon entering the circulation, nanoparticles

are often coated with opsonin proteins leading to their clearance by macrophages and affecting

their pharmacokinetic properties [55]. Second, blood vessels are leaky with fenestrations ranging

between 0.2 and 1.2 μm. Since nanoparticles exist in a range of sizes, it is thought that the size of

therapeutic nanoparticles should be well below 200 nm [55,56]. However, the NPs used for Ran

targeting have a mean diameter of 182–277 nm [53].

Here, we aimed to target Ran directly with a new small molecule inhibitor. To date, there

is no available drug specific to Ran. One reason for this is the high intracellular concentration of

GTP as well as the high affinity of GTP to its cognate GTPase, making the development of an

efficient competitor of GTP difficult. Alternatively, it is thought that developing allosteric

compounds able to interact with a given GTPase in its GDP-bound form and to lock it on its

inactive state is more convenient to attenuate GTPase activity. Inspired by the work of KRAS

G12C inhibitors, which bind KRAS G12C mutant at the switch II pocket[37,38], we aimed to target

the RanGDP at the switch II pocket to 'arrest' Ran at its inactivated state. However, our inspection

of the crystal structure of RanGDP (pdb: 3ch5) found no pre-formed switch II pocket. We thus

constructed a structural model of RanGDP switch II pocket by homology modelling and performed

in silico screening against the switch II pocket. Chemical optimization of our initial hit m26 lead

to compound m36 as a novel Ran inhibitor. Importantly, M36 displays, *in vitro,* a very interesting

therapeutic index between normal and cancer cells that is in alignment with our *in vivo* data. In

fact, at higher doses, M36 is well tolerated by mice and exhibits a significant toxicity for one of

the most aggressive xenograft models, TOV112D, that do not respond to conventional treatments

such as Carboplatin and Olaparib therapies. Furthermore, at the clinical level, M36 was able to

induce cell death by apoptosis in *ex vivo* micro-dissected tumors derived from an EOC patient.

Another advantage of allosteric inhibitors is that they bind to less conserved sites across GTPases

and kinases ensuring specificity and avoiding potential severe side effects [57]. In this regard, we

have shown that M36 does not influence the activation of other GTPases such as RhoA, Cdc42

and Rac1. More importantly, overexpression of a dominant active of Ran rescued the toxicity of

M36 highlighting the specificity of our Ran inhibitor.

Olaparib has shown promising results for HGSC treatment and was recently approved by

the FDA as maintenance therapy for patients harboring BRCA1/2 mutations (HR deficient) [58].

This stratification comes from the observation that HR activation is closely linked to non-

responsiveness and resistance to PARP inhibitor therapy [47]. Therefore, combination treatment of a

PARP inhibitor with drugs that inhibit the HR pathway is actively being exploited in the clinical

setting [59,60], and might be effective to induce lethality in HGSC cells. Here, we have shown that

M36 induced HR deficiency and dramatically sensitized three BRCA1/2 WT and Olaparib

resistant cell lines (TOV112D, OV866(2) and OV90 [61]) to PARP inhibitor therapy. This result is

of great interest since it could open new perspectives to circumvent resistance, and possibly to

expand PARP inhibitor therapy to patients that are currently excluded. Many cancers are

characterized by widespread aneuploidy and genomic instability [42,43]. Hence, targeting these

hallmarks would be effective for the development of a new targeted therapy, not only for EOC,

but also for a variety of cancers. In our previous work, we have shown that targeting Ran is an

effective way to eliminate cancer cells with chromosomal and genomic instability [23]. This

prompted us to investigate the therapeutic value of M36 in other cancers. Interestingly, we found

that M36 is also toxic in a range of cancer models including prostate, gastrointestinal, breast and

skin cancers. These results are encouraging and in future studies we plan to investigate the *in vivo*

efficacy of M36 in these models.

In conclusion, though further medicinal chemistry optimization is required, our study is the

first to provide the generation of a first-in-class compound inhibitor of Ran with a therapeutic

potential for cancer in general and EOC in particular.

MATERIALS AND METHODS

Computational modeling and in silico screening

The structural model of RanGDP with switch II pocket was built using crystal structure of RanGDP
(pdb: 3ch5) and crystal structure of KRAS G12C in complex with an inhibitor at switch II pocket
(pdb: 5v6s) as the templates, by software Modeller (UCSF, CA, USA). Among the 200 models
generated, the model with lowest objective function was selected for further work. 90,000
compounds from NCI-open database were virtually screened against the switch II pocket of the
RanGDP model, using software GOLD (The Cambridge Crystallographic Data Centre,
Cambridge, UK).

Medicinal chemistry

28 top-ranking candidate compounds were kindly provided, as a gift, by the Drug Synthesis and
Chemistry Branch, Developmental Therapeutics Program, NCI, Bethesda, MD, USA. Initial hit
M26 was re-synthesized and characterized by NMR analysis. Chemical optimization of M26,
leading to compound M36, is described in the supplemental information.

Cell lines and cell culture

The human EOC cell lines used [TOV81D, TOV112D, OV90, OV866(2), TOV1946, OV1946,
TOV2295(R), OV4485] were derived in our laboratory from patients' tumors (TOV) or ascites
(OV) [62-65]. All EOC cell lines were maintained in low oxygen at 7% O_2 and 5% CO_2 and grown in
OSE medium (Wisent, Montreal, QC) supplemented with 10% FBS (Wisent), 0.5 μg/mL
amphotericin B (Wisent) and 50 μg/mL gentamicin (Life Technologies Inc., Burlington, ON). The
human retinal epithelial cell line ARPE (ARPE-19) was purchased from American Type Culture
Collection (ATCC, Manassas, VA) and maintained in DMEM-F12 (Wisent) medium

318   supplemented with 10% FBS (Wisent), 0.5 μg/mL amphotericin B (Wisent) and 50 μg/mL

319   gentamicin (Life Technologies Inc.).

Small interference RNA (siRNA) treatment

321   Suspensions of 10^6 cells in 100 μL of nucleofector solution V (Lonza Group Ltd, Basel,

322   Switzerland) were transfected by electroporation with 1.2 nmoles siRNA targeting Ran (J-010353-

323   06, ON-TARGETplus, Dharmacon Thermo Fisher Scientific Inc., Waltham, MA). For each

324   experiment, efficiency of Ran silencing was verified 48 hours after transfection by Western blot

325   analysis. Scramble siRNA (D-001810-02, Dharmacon) was used as a control in all experiments.

Clonogenic survival

327   Clonogenic assays were performed as previously described [61]. Colonies were counted under a

328   stereo microscope and reported as percent of control. IC_{50} values were determined using Graph

329   Pad Prism 5 software (GraphPad Software Inc., San Diego, CA). Each experiment was performed

330   in duplicate and repeated three times. Sensitivity of the cell lines to small molecule inhibitors of

331   Ran was assessed using a concentration range of 0–40 μM.

IncuCyte cell proliferation phase-contrast imaging assay

Cells (2,000 cells/well) were plated in a 96-well plate. The next day, compounds were added at

the indicated concentrations. Following treatment, cell confluence was imaged by phase contrast

using the IncuCyte live cell monitoring system (Essen BioScience, Ann Arbor, MI). Frames were

captured at day 0 (immediately after treatment) and at the end of the experiment using a 10X

objective. For Ran KD experiments, cells were seeded in a 96-well plate (4,000 cells/well) directly

after transfection. Cell confluence monitoring started the next day as described above.

Protein preparation and western blot analysis

Cells were lysed with RIPA buffer containing protease inhibitors. Whole cell lysates were run

through a Bradford assay (Thermo Fisher Scientific) for protein quantification. Around 25–50 μg

of protein was separated by 12.5% SDS-PAGE and transferred onto nitrocellulose membranes.

The resultant blots were probed with Ran (1:10 000, sc-271376 Santa Cruz Biotechnology, Dallas,

TX), cleaved PARP (1:1000, #9541, Cell Signaling Technology Inc., Danvers, MA), cleaved

caspase 3 (1:1000, #9661, Cell Signaling Technology Inc.), GAPDH (1:2500, #2118, Cell

Signaling Technology Inc.) or beta-actin (1:50 000, ab6276, Abcam Inc., Toronto, ON, Canada)

primary antibodies overnight at 4°C then with peroxidase-conjugated secondary antibodies for 2

hours at room temperature. Proteins were detected using enhanced chemiluminescence (Thermo

Fisher Scientific).

RT-PCR

The total RNA from TOV-112D or OV1946 cells was isolated using RNeasy Kit (Qiagen®). The

total RNA concentration and purity were measured on a NanoDrop™ spectrophotometer. RNA

was reverse transcribed using the QuantiTect Reverse Transcription Kit (Qiagen®) according to

the manufacturer's protocol. cDNA amplification was performed with SYBR Green PCR master

mix (Applied Biosystems®) using the StepOnePlus Real-Time PCR system (Applied

Biosystem®). Negative controls were included in all experiments, and actin served as the

housekeeping gene. Primers were ordered from Integrated DNA Technologies, Inc:

NR1D1:
Forward primer: TGGACTCCAACAACAACACAG
Reverse primer: GATGGTGGGAAGTAGGTGGG
β-actin:
Forward primer: CATGTACGTTGCTATCCAGGC
Reverse primer: CTCCTTAATGTCACGCACGAT

Cell death analysis by flow cytometry

Cells were treated with M36. Six days after treatment, adherent and floating cells were mixed and

incubated 5 minutes at room temperature with DRAQ 7 (ab109202, Abcam Inc). A maximum of

30,000 events were counted per condition using the Fortessa flow cytometer (BD Biosciences,

Mississauga, ON) and analyzed with the FlowJo software.

Immunofluorescence

M36-treated and control cells grown on coverslips were washed with 1X PBS, fixed in 4%

paraformaldehyde and permeabilized with 0.25% Triton X-100 (Sigma-Aldrich Inc.). After

blocking (4% BSA and 4% FBS in PBS), coverslips were incubated with anti–RanGTP (26915,

NewEastBioscences, diluted 1:100), anti p-γ-H2AX (Ser139) (05-636, EMD Millipore, diluted

1:2000), anti-Rad51 (ab213, Abcam, diluted 1:750), anti 53BP1 (NB100-305, Novus Biologicals,

diluted 1:2500) and anti-Geminin (10802-1-AP, Proteintech, diluted 1:1000) antibodies in

blocking buffer for 2 hours at room temperature. Subsequently, samples were incubated with Cy-

5 (1:500, Life Technologies Inc.) and Alexa Fluor 488 (for Geminin) secondary antibodies for 1

hour. Coverslips were mounted onto slides using Prolong® Gold anti-fade reagent with DAPI

(Life Technologies Inc.). Images were obtained using a Zeiss microscope (Zeiss observer Z1) with

a 20X objective. For Rad51 and 53BP1 analysis, cells were transfected with siRan or treated with

M36 for 48 hours then gamma-irradiated at 10 Gy and fixed one hour after irradiation. Automated

analysis software from Zeiss (AxioVision™, Carl Zeiss) was used for foci counting. In each

condition, γ-H2AX, Rad51 and 53BP1 foci were quantified in roughly 400 nuclei.

Cellular Thermal Shift Assay (CETSA)

OV1946 cells (10^7 cells/petri) were seeded in 100 mm × 15 mm petri dish and allowed to attach

for 24 h. Then, cells were treated with DMSO or M36 at concentrations from 50 to 200 μM and

incubated for 1 h at 37 °C. After incubation, cells were washed, trypsinized and centrifuged for 5

388 minutes at 1200 rpm. Cells were resuspended in HBSS, divided into different aliquots and heated

389 for three minutes at different temperatures using the Biometra TOne PCR (Analytikjena, Jena,

390 Germany). Cell lysates were then obtained by one freeze-thaw cycle in liquid nitrogen (1 min each

391 step) followed by centrifugation at $20,000 \times$ g for 20 min at 4°C. The supernatants were harvested,

392 and SDS-PAGE loading buffer was added before boiling for 5min. Proteins were migrated and

393 blotted into PVDF membranes. Primary antibodies used were: Ran (ab53775, Abcam, 1/5000) and

394 β-Actin (ab6276, Abcam, 1/5000). Proteins were detected by HRP-secondary antibody and the

395 ECL detection kit (Clarity and Clarity Max ECL Western Blotting Substrates from Biorad).

396 Densitometry analyses were conducted using the UV-VIS Spectrophotometer (Thermo Fisher

397 Scientific) and relative intensity of Ran protein was obtained by the ratio over the β-actin band.

398 **Ran, Cdc42, RhoA and Rac1 activation assays**

399 Cells were seeded onto 6-well tissue culture plates in such a way that cell confluence reached

400 approximately 70% the day of the experiment. The day of the experiment cells were treated for 1

401 hour with the indicated compounds prior to protein extraction and quantification. Assays were

402 performed using the Ran, Rac1 activation assay kits (Cell Biolabs) and the RhoA and Cdc42 G-

403 LISA activation assay kits (Cytoskeleton®) according to the manufacturer recommendations.

404 ***In vivo* study**

405 For the PK studies, 6-week-old female CD1 mice (Charles River laboratories, Senneville, QC,

406 Canada) received a single intraperitoneal injection of M36 (200 mg/kg), dissolved in DMSO 10%,

407 Kolliphor® EL 10%, PEG-400 20% and PBS 60%. For each time point (5, 30, 120, 240, 360 and

408 1440 minutes), 3 mice were sacrificed and blood was collected by cardiac puncture. Plasma levels

409 of the compound were measured by mass spectrometry. For the tolerance test, M36 was dissolved

410 as described above and injected intraperitoneally into 6-week-old female NOD.Cg-

Rag1^{tm1Mom}Il2rg^{tm1Wjl}/SzJ (NRG) female mice (The Jackson laboratory, Bar Harbor, ME) every

day (except on weekends) at 200 mg/kg. During this study, mice were monitored for survival and

weight loss/gain. For the tumor xenograft experiment, NRG mice were injected with 10^6

TOV112D cells suspended in a mix of 1:1 PBS and matrigel (BD Biosciences) at subcutaneous

sites. Treatments with M36 started the following day. Measurements of tumor size were collected

at least twice a week until tumors reached limit points (2000 mm3). All animal procedures were

performed in accordance with the guidelines for the Care and Use of Laboratory Animals of the

CRCHUM and were approved by the Comité institutionnel de protection des animaux (CIPA)

(Protocols #C18009AMMs and C22014AMMs).

Micro-dissected tissue (MDT) production, culture and treatment

MDTs were obtained from both ovarian cancer cell xenografts or patient tissue samples. For the

xenografts, cell suspensions containing $1x10^6$ cells for TOV112D or $5x10^6$ cells for OV1946 in

PBS-Matrigel were injected subcutaneously in NRG female mice. Solid tumours were harvested

at volumes between 800 and 1500 mm^3. For patient tissue, samples were collected from patients

following informed consent from the Centre hospitalier de l'Université de Montréal (CHUM),

Division of Gynecologic Oncology. Samples were processed immediately upon retrieval. The use

of human samples was approved by the Comité d'éthique de la recherche du CHUM (CÉR-CHUM,

Protocol #BD 04.002).

The micro-dissection and loading procedures were adapted from previously published work [46,66].

Briefly, both xenograft and patient tumours were sliced into 1cm slices using a scalpel and

processed into 350μm slices using a McIlwain™ tissue chopper (Ted Pella©). Tissue slices were

kept in Hank's balanced salt solution (HBSS, Wisent) supplemented with 10% FBS, 55 μg/mL of

gentamicin and 0.6 μg/mL of amphotericin B. A 500 μm biopsy punch (PUN0500, Zivic

instruments) was then used to produce MDTs, spheroidal tissue of approximately 300 μm in

diameter. The loading and trapping of MDTs in microfluidic devices were performed as previously

described [46]. MDTs were cultured in OSE (xenografts) or Ovarian TumorMACS™ (MILTENYI

BIOTEC; patient samples) media supplemented with 10% FBS, 55 ug/mL of gentamicin and 0.6

ug/mL of amphotericin B.

MDTs were treated with either 100 or 200 μM of M36 in 1% DMSO (Sigma) for 24 or 72hrs

continuously. MDTs were then fixed with 10% formalin (Chaptec) and processed following a

previously published paraffin-embedding lithography procedure to create micro-dissected tissue

microarray (MDTMA) blocks [46].

MDT Immunofluorescence staining and quantification

MDTMA blocks were cut into 4μm sections and put on Matsunami TOMO® hydrophilic adhesion

slides (VWR). Slides were stained for KI67 and cleaved-caspase 3 (CC3) to assess proliferation

and cell death, respectively, using the *Discovery Ultra* automated stainer (Ventana Medical System

inc. (VMSI)). A pan-cytokeratin (CK) antibody was also used to identify the tumour epithelium

of the MDTs. Slides were heated at 60˚C for 20 min before staining. Antigen retrieval was carried

out with Cell Conditioning 1 solution (VMSI) for 90 min. Mouse anti-KI67 (1:500) (9449S, Cell

Signaling), rabbit anti-CC3 (1:200) (9661S, Cell Signaling) and guinea pig anti-pan-CK (1:200)

(BP5069, Cedarlane) antibodies were dispensed automatically and slides were incubated for 60

minutes at 37˚C. Secondary antibodies, including anti-mouse Alexa 488 (1:250) (A-11001, Life

Technologies), anti-rabbit Alexa 750 (1:200) (A-21039, Life Technologies) and anti-guinea pig

Alexa 647 (1:200) (706-605-148, Cedarlane) were also dispensed automatically and slides were

incubated for 60 minutes at 37˚C. A mounting medium with DAPI (MJS Biolynx inc) was used to

stain the nuclei. Slides were scanned at 20x with either an Olympus BX61 (Olympus) or an Aperio

Versa 200 (Leica) microscope. IF filters used for DAPI, KI67, CC3 and tumour epithelium were

DAPI, Alexa-488, Cy7 and Cy5, respectively. Stained MDTs were quantified using the

VisiomorphDP software (VisioPharm, Denmark, http://visiopharm.com). Percent of CC3 staining

or nuclear K-67 staining in the cytokeratin positive area were quantified and plotted as bar graphs.

Statistical analysis

Data from at least three independent experiments are presented as the means ± SD. Statistical

analyses were done using GraphPad Prism version 10 (GraphPad Sofware Inc., http://

graphpad.com). Comparisons were carried out using Student's t-test. Analysis of MDTs was done

using Two-way ANOVA followed by Tukey's test. Comparisons of survival curves were

performed using log-rank test. A p-value of less than 0.05 was considered statistically significant.

ACKNOWLEDGMENTS

We thank Kim Leclerc Désaulniers and Lise Portelance for technical assistances with the animal

experiments and biobank specimen procurement, respectively. We acknowledge the CRCHUM

animal facility, the ICM Imaging/Live Imaging platform, the Molecular Pathology core facility of

the CRCHUM and the CRCHUM Microfluidic platform. A-MM-M and DP are researchers of the

CRCHUM/ICM, which receive support from the Fonds de recherche du Québec – Santé (FRQS).

ZB was supported by a MITACS fellowship and by the ICM NathalieMoreau Bursary. SR was

supported by a studentship from the Canderel Fund of the Institut du cancer de Montréal (ICM).

FUNDING

This work was supported by the Canadian Institute for Health Research (CIHR MOP142724 and

PJT148642), the Oncopole in collaboration with the FRQS, the Cancer Research Society, Génome

Québec and IRICoR (#265877), and the ICM (Fonds Défi Spyder and Anne-Marie Chagnon). Cell

lines as well as patient tissue samples used in this study were provided by the CRCHUM ovarian

tumor bank, which is supported by Ovarian Cancer Canada (OCC) and by the Banque de tissus et

de données of the Réseau de recherche sur le cancer (RRCancer) of the FRQS affiliated with the

Canadian Tumor Repository Network (CTRNet).

AUTHOR CONTRIBUTIONS

ZB, XT, EC, JHW and A-MM-M designed the study. ZB, XT, SR, RG and JK-D performed the

experiments. ZB, XT, EC, SR, RG and JK-D analyzed the data. ZB and XT wrote the manuscript.

EC, JHW, DP, and A-MM-M supervised the study, provided guidance, and edited the manuscript.

FIGURES

Figure 1: *In silico* **and cell-based screenings identified M26 as a hit compound for Ran**

inhibition.

(A) Left side: Crystal structure of RanGDP (pdb: 3ch5) was aligned to RanGTP (pdb: 3nc1),

showing different conformations of Switch I at the activated and inactivated states; Right side:

Structural model of the switch II pocket of RanGDP was built by homology modeling and the

predicted binding mode of M26 (green sticks with blue surface) at the switch II pocket of RanGDP

was showed. **(B)** Chemical structure of M26. **(C)** Colony formation inhibition by selected M

compounds at 10 μM in normal ARPE and EOC TOV112D cells. Only the compound M26

503   inhibited TOV112D without affecting ARPE (blue bar). Bars represent percentage of colonies

504   formed compared to DMSO-treated controls. **(D)** ARPE and TOV112D cells were incubated with

505   M26 (40 µM) to evaluate apoptosis (6 days after treatment) by western blot using the antibody

506   anti-cleaved PARP. **(E)** TOV112D cells were incubated for one hour with M26 (50 µM) before

507   performing RanGTP Pull-down assay on the resultant cell extract.

Figure 2: M36, a derivative of M26, binds and impacts Ran activation in EOC cells

(A) Chemical structure of M36. (B) TOV112D cells were treated for one hour with increasing

concentrations of M36. Subsequently, RanGTP pull-down assay was performed to assess Ran

activation. **(C)** TOV112D cells were treated with M36 (100 µM) for one hour. After cell fixation

and permeabilization, RanGTP was revealed by immunofluorescence using a specific antibody

(pink). Nuclei are shown by Dapi staining (blue). **(D)** OV1946 cells were treated with M36 (100

µM) or DMSO for one hour. CETSA was performed after heating the cell suspensions at different

temperatures for three minutes. Cell lysates were subjected to Western blot for evaluation of Ran

levels. Data points are densitometry values relative to ß-actin control and normalized to the levels

obtained at the lowest temperature used. **(E)** OV1946 cells were treated for one hour with DMSO

or increasing concentrations of M36 and CETSA was performed at 64 °C for three minutes and

Ran levels were measured by Western blot. Bar graphs represent densitometry values relative to

ß-actin control and normalized to the levels obtained for the untreated cells. *$P < 0.05$ (n = 3,

Student's t-test).

Figure 3: M36 shows selectivity for aneuploid cells and does not interferes with the activation of other GTPases.

(A) Clonogenic assay using different concentrations of M36 in ARPE and TOV112D cells. IC$_{50}$ value was calculated for the TOV112D cells. Bars and curve points represent percentage of colonies formed compared to DMSO-treated controls. **(B)** different EOC cell lines and the normal

ARPE cells were transfected with a siRNA targeting Ran or with M36 (40 µM) before assessing

cell proliferation using the live cell imaging IncuCyte system. Data are expressed as the percentage

of control cells at the end of experiment (96 h) and are representative of at least three independent

experiments. **(C)** ARPE and EOC cells were treated with M36 (40 µM) for 6 days and then cell

death was assessed by FACS using DRAQ7 staining. **(D)** TOV112D cells were treated for one

hour with M36 (50 µM) in order to evaluate RhoA (left), Cdc42 (right) and Rac1 (bottom)

activities. **(E)** Immunoblots showing successful overexpression in TOV112D cells of dominant

active Ran^{Q69L} and dominant negative Ran^{T24N} (left panel). These cells were treated with M36 and

cell proliferation was assessed using the live cell imaging IncuCyte system (right panel). Data are

expressed as the percentage of DMSO treated cells. *$P < 0.05$ (n $\geq$ 3, Student's t-test).

Figure 4: M36 mimics the effect of Ran KD regarding DDR

(A) The expression of NR1D1 was evaluated by qRT-PCR in TOV112D cells transfected with

siRan or treated with M36 (40 µM). **(B)** OV1946 cells were treated with M36 (50 µM) and

expression of NR1D1 was evaluated by qRT-PCR. **(C-E)** TOV112D cells were treated with siRan

or M36 (20 µM) and allowed to grow for 72 hours. For p-ɣH2AX staining **(C)**, cells were fixed

and stained. For Rad51 **(D)** and 53BP1 **(E)** staining, cells were gamma-irradiated at 10 Gy and

fixed 1 hour after irradiation. Representative images after irradiation **(upper panel)** and

quantitative analyses of foci formation **(lower panel)** are presented. For Rad51 and 53BP1 foci,

data are expressed as the ratio between foci number after and before irradiation. **(F)** Images

obtained from **(E)** were used to quantify cells presenting cytoplasmic staining of 53BP1. *$P < 0.05$

**$P < 0.01$ ($n \geq 3$, Student's t-test).

Figure 5: Evaluation of the therapeutic potential of M36 *in vivo*

(A) Measurements of plasma levels of M36 compound after a single intraperitoneal injection (200

mg/kg) in CD1 mice. **(B)** M36 (200 mg/kg) was injected IP daily in NRG mice for 3 weeks. Mouse

weight was measured at the indicated time points and expressed as the percentage of their weight

on the day of the first injection. **(C-D)** TOV112D cells were subcutaneously injected in NRG mice

and treatments with Olaparib (75 mg/kg, daily) **(C)**, and M36 (200 mg/kg, daily) **(D)** were

performed. Data are normalized with the mean of tumor size at the first day of injection. **(E)** Tumor

growth in individual mice treated with M36 is shown. **(F)** Kaplan-Meier survival curve of mice

from **(E)**. In **(D)** and **(E)** data were analyzed using the two-tail Student's t test. In **(F)**, data were

analyzed using the Log rank test. $*P < 0.05$, $**P < 0.01$.

Figure 6: M36 induces cell death of *ex vivo* micro-dissected tumors from xenografts and

patients

Samples from OV1946 xenografts **(A)** or TOV12018G patient tumor **(B)** were processed as micro-dissected tissues (MDTs) and cultured in microfluidic devices as described in Methods. MDTs were treated with M36 at different concentrations for 24 or 72 h and then formalin-fixed, paraffin embedded. Sections (6μ) were stained for KI67 (green), cleaved-caspase 3 (red), a cytokeratin cocktail (yellow) and DAPI (blue). Bar graphs represent the expression of nuclear KI67 (left panels) or CC3 (right panels) within the tumour epithelium (CK positive cells) of each MDT. Data shown represents mean ± SEM of three separate experiments, normalized to Ctrl 24hrs. Statistical analysis was done using Two-way ANOVA followed by Tukey's test. *P < 0.05. Scale bars of representative images are 200 μm.

Figure 7: Combination of M36 and Olaparib triggers synthetic lethality in EOC cells

(A) TOV112D and OV866(2) cells were treated with M36 (20 µM) for 48 hours then with Olaparib

(10 µM) for 24 hours. After fixation, cells were immunostained with Rad51 antibody. Quantitative

analyses of foci formation are presented. **(B)** Cells were treated with increasing concentrations of

M36 and/or Olaparib. The heat map shows Bliss scores calculated for each combination at day 6.

(C) For each cell line, an example of proliferation profile following Olaparib and M36 combination

treatment is presented. **(D)** At the end of the experiment presented in **(C)**, dead cells were removed

by PBS washes and cell confluence was measured using the live cell imaging IncuCyte system.

Data are expressed as the percentage of control cells. **(E, F)** ARPE and EOC cells were treated as

in **(C)** and apoptosis was assessed by flow cytometry **(E)** and western blot **(F)** using DRAQ7 dye

and cleaved caspase 3 antibody, respectively. $*P < 0.05$ $**P < 0.01$ $*** P < 0.001$ (n = 3. Student's

t-test).

REFERENCES

1   Matchett, K. B. *et al.* Ran GTPase in nuclear envelope formation and cancer metastasis. *Adv Exp*
Med Biol **773**, 323-351, doi:10.1007/978-1-4899-8032-8_15 (2014).
2   Cavazza, T. & Vernos, I. The RanGTP Pathway: From Nucleo-Cytoplasmic Transport to Spindle
Assembly and Beyond. *Front Cell Dev Biol* **3**, 82, doi:10.3389/fcell.2015.00082 (2015).
3   Azuma, K. *et al.* Ran, a small GTPase gene, encodes cytotoxic T lymphocyte (CTL) epitopes
capable of inducing HLA-A33-restricted and tumor-reactive CTLs in cancer patients. *Clin Cancer*
Res **10**, 6695-6702, doi:10.1158/1078-0432.CCR-04-0818 (2004).
4   Ouellet, V. *et al.* Tissue array analysis of expression microarray candidates identifies markers
associated with tumor grade and outcome in serous epithelial ovarian cancer. *Int J Cancer* **119**,
599-607, doi:10.1002/ijc.21902 (2006).
5   Ouellet, V. *et al.* Discrimination between serous low malignant potential and invasive epithelial
ovarian tumors using molecular profiling. *Oncogene* **24**, 4672-4687, doi:10.1038/sj.onc.1208214
(2005).
6   Abe, H. *et al.* High expression of Ran GTPase is associated with local invasion and metastasis of
human clear cell renal cell carcinoma. *Int J Cancer* **122**, 2391-2397, doi:10.1002/ijc.23400 (2008).
7   Xia, F., Lee, C. W. & Altieri, D. C. Tumor cell dependence on Ran-GTP-directed mitosis. *Cancer*
Res **68**, 1826-1833, doi:10.1158/0008-5472.CAN-07-5279 (2008).
8   Yuen, H. F. *et al.* Ran is a potential therapeutic target for cancer cells with molecular changes
associated with activation of the PI3K/Akt/mTORC1 and Ras/MEK/ERK pathways. *Clin Cancer*
Res **18**, 380-391, doi:10.1158/1078-0432.CCR-11-2035 (2012).
9   Deng, L. *et al.* Ran GTPase protein promotes metastasis and invasion in pancreatic cancer by
deregulating the expression of AR and CXCR4. *Cancer Biol Ther* **15**, 1087-1093,
doi:10.4161/cbt.29217 (2014).
10   Sheng, C. *et al.* Knockdown of Ran GTPase expression inhibits the proliferation and migration of
breast cancer cells. *Mol Med Rep* **18**, 157-168, doi:10.3892/mmr.2018.8952 (2018).

11   Boudhraa, Z., Carmona, E., Provencher, D. & Mes-Masson, A. M. Ran GTPase: A Key Player in
Tumor Progression and Metastasis. *Front Cell Dev Biol* **8**, 345, doi:10.3389/fcell.2020.00345
(2020).
12   Harousseau, J. L., Shaughnessy, J., Jr. & Richardson, P. Multiple myeloma. *Hematology Am Soc*
Hematol Educ Program, 237-256, doi:10.1182/asheducation-2004.1.237 (2004).
13   Hartmann, E. *et al.* Five-gene model to predict survival in mantle-cell lymphoma using frozen or
formalin-fixed,   paraffin-embedded   tissue.   *J   Clin   Oncol*   **26**,   4966-4972,
doi:10.1200/JCO.2007.12.0410 (2008).
14   Schnepp, R. W. *et al.* A LIN28B-RAN-AURKA Signaling Network Promotes Neuroblastoma
Tumorigenesis. *Cancer Cell* **28**, 599-609, doi:10.1016/j.ccell.2015.09.012 (2015).
15   Cekan, P. *et al.* RCC1-dependent activation of Ran accelerates cell cycle and DNA repair,
inhibiting   DNA   damage-induced   cell   senescence.   *Mol   Biol   Cell*   **27**,   1346-1357,
doi:10.1091/mbc.E16-01-0025 (2016).
16   Kurisetty, V. V. *et al.* RAN GTPase is an effector of the invasive/metastatic phenotype induced by
osteopontin. *Oncogene* **27**, 7139-7149, doi:10.1038/onc.2008.325 (2008).
17   Ly, T. K. *et al.* Activation of the Ran GTPase is subject to growth factor regulation and can give
rise to cellular transformation. *J Biol Chem* **285**, 5815-5826, doi:10.1074/jbc.M109.071886 (2010).
18   Xia, F., Canovas, P. M., Guadagno, T. M. & Altieri, D. C. A survivin-ran complex regulates spindle
formation in tumor cells. *Mol Cell Biol* **28**, 5299-5311, doi:10.1128/MCB.02039-07 (2008).
19   Yuen, H. F. *et al.* Ran GTPase promotes cancer progression via Met recepto-rmediated downstream
signaling. *Oncotarget* **7**, 75854-75864, doi:10.18632/oncotarget.12420 (2016).
20   Yuen, H. F. *et al.* RanGTPase: a candidate for Myc-mediated cancer progression. *J Natl Cancer*
Inst **105**, 475-488, doi:10.1093/jnci/djt028 (2013).
21   Zaoui, K. *et al.* Ran promotes membrane targeting and stabilization of RhoA to orchestrate ovarian
cancer cell invasion. *Nat Commun* **10**, 2666, doi:10.1038/s41467-019-10570-w (2019).
22   Barres, V. *et al.* An essential role for Ran GTPase in epithelial ovarian cancer cell survival. *Mol*
Cancer **9**, 272, doi:10.1186/1476-4598-9-272 (2010).
23   Boudhraa, Z. *et al.* NR1D1 regulation by Ran GTPase via miR4472 identifies an essential
vulnerability linked to aneuploidy in ovarian cancer. *Oncogene* **41**, 309-320, doi:10.1038/s41388-
021-02082-z (2022).
24   Deng, L. *et al.* Ran GTPase protein promotes human pancreatic cancer proliferation by deregulating
the expression of Survivin and cell cycle proteins. *Biochem Biophys Res Commun* **440**, 322-329,
doi:10.1016/j.bbrc.2013.09.079 (2013).
25   Torre, L. A. *et al.* Ovarian cancer statistics, 2018. *CA Cancer J Clin* **68**, 284-296,
doi:10.3322/caac.21456 (2018).
26   Siegel, R. L., Miller, K. D., Fuchs, H. E. & Jemal, A. Cancer Statistics, 2021. *CA Cancer J Clin*
71, 7-33, doi:10.3322/caac.21654 (2021).
27   Lheureux, S., Gourley, C., Vergote, I. & Oza, A. M. Epithelial ovarian cancer. *Lancet* **393**, 1240-
1253, doi:10.1016/S0140-6736(18)32552-2 (2019).
28   Bashashati, A. *et al.* Distinct evolutionary trajectories of primary high-grade serous ovarian cancers
revealed through spatial mutational profiling. *J Pathol* **231**, 21-34, doi:10.1002/path.4230 (2013).
29   Lheureux, S., Braunstein, M. & Oza, A. M. Epithelial ovarian cancer: Evolution of management in
the era of precision medicine. *CA Cancer J Clin* **69**, 280-304, doi:10.3322/caac.21559 (2019).
30   Cancer Genome Atlas Research, N. Integrated genomic analyses of ovarian carcinoma. *Nature* **474**,
609-615, doi:10.1038/nature10166 (2011).
31   Patch, A. M. *et al.* Whole-genome characterization of chemoresistant ovarian cancer. *Nature* **521**,
489-494, doi:10.1038/nature14410 (2015).
32   Scheffzek, K., Klebe, C., Fritz-Wolf, K., Kabsch, W. & Wittinghofer, A. Crystal structure of the
nuclear   Ras-related   protein   Ran   in   its   GDP-bound   form.   *Nature*   **374**,   378-381,
doi:10.1038/374378a0 (1995).

Stewart, M., Kent, H. M. & McCoy, A. J. Structural basis for molecular recognition between nuclear transport factor 2 (NTF2) and the GDP-bound form of the Ras-family GTPase Ran. *J Mol Biol* **277**, 635-646, doi:10.1006/jmbi.1997.1602 (1998).

Chook, Y. M. & Blobel, G. Structure of the nuclear transport complex karyopherin-beta2-Ran x GppNHp. *Nature* **399**, 230-237, doi:10.1038/20375 (1999).

Vetter, I. R., Arndt, A., Kutay, U., Gorlich, D. & Wittinghofer, A. Structural view of the Ran-Importin beta interaction at 2.3 A resolution. *Cell* **97**, 635-646, doi:10.1016/s0092-8674(00)80774-6 (1999).

Vetter, I. R., Nowak, C., Nishimoto, T., Kuhlmann, J. & Wittinghofer, A. Structure of a Ran-binding domain complexed with Ran bound to a GTP analogue: implications for nuclear transport. *Nature* **398**, 39-46, doi:10.1038/17969 (1999).

Ostrem, J. M., Peters, U., Sos, M. L., Wells, J. A. & Shokat, K. M. K-Ras(G12C) inhibitors allosterically control GTP affinity and effector interactions. *Nature* **503**, 548-551, doi:10.1038/nature12796 (2013).

McGregor, L. M., Jenkins, M. L., Kerwin, C., Burke, J. E. & Shokat, K. M. Expanding the Scope of Electrophiles Capable of Targeting K-Ras Oncogenes. *Biochemistry* **56**, 3178-3183, doi:10.1021/acs.biochem.7b00271 (2017).

Li, B. *et al.* Butyrylcholinesterase, paraoxonase, and albumin esterase, but not carboxylesterase, are present in human plasma. *Biochem Pharmacol* **70**, 1673-1684, doi:10.1016/j.bcp.2005.09.002 (2005).

Martinez Molina, D. *et al.* Monitoring drug target engagement in cells and tissues using the cellular thermal shift assay. *Science* **341**, 84-87, doi:10.1126/science.1233606 (2013).

Zeng, Y., Arisa, O., Peer, C. J., Fojo, A. & Figg, W. D. PARP inhibitors: A review of the pharmacology, pharmacokinetics, and pharmacogenetics. *Semin Oncol* **51**, 19-24, doi:10.1053/j.seminoncol.2023.09.005 (2024).

Levine, M. S. *et al.* Centrosome Amplification Is Sufficient to Promote Spontaneous Tumorigenesis in Mammals. *Dev Cell* **40**, 313-322 e315, doi:10.1016/j.devcel.2016.12.022 (2017).

Charames, G. S. & Bapat, B. Genomic instability and cancer. *Curr Mol Med* **3**, 589-596, doi:10.2174/1566524033479456 (2003).

Clarke, P. R., Klebe, C., Wittinghofer, A. & Karsenti, E. Regulation of Cdc2/cyclin B activation by Ran, a Ras-related GTPase. *J Cell Sci* **108 (Pt 3)**, 1217-1225, doi:10.1242/jcs.108.3.1217 (1995).

Brodeur, M. N. *et al.* Carboplatin response in preclinical models for ovarian cancer: comparison of 2D monolayers, spheroids, ex vivo tumors and in vivo models. *Sci Rep* **11**, 18183, doi:10.1038/s41598-021-97434-w (2021).

Simeone, K. *et al.* Paraffin-embedding lithography and micro-dissected tissue micro-arrays: tools for biological and pharmacological analysis of ex vivo solid tumors. *Lab Chip* **19**, 693-705, doi:10.1039/c8lc00982a (2019).

Lord, C. J. & Ashworth, A. BRCAness revisited. *Nat Rev Cancer* **16**, 110-120, doi:10.1038/nrc.2015.21 (2016).

Bansal, M. *et al.* A community computational challenge to predict the activity of pairs of compounds. *Nat Biotechnol* **32**, 1213-1222, doi:10.1038/nbt.3052 (2014).

Xia, Y. *et al.* Increased miR-203-3p and reduced miR-21-5p synergistically inhibit proliferation, migration, and invasion in esophageal cancer cells. *Anticancer Drugs* **30**, 38-45, doi:10.1097/CAD.0000000000000687 (2019).

Dakir, E. H. *et al.* The anti-psychotic drug pimozide is a novel chemotherapeutic for breast cancer. *Oncotarget* **9**, 34889-34910, doi:10.18632/oncotarget.26175 (2018).

Anzalone, A. *et al.* Dual control of dopamine synthesis and release by presynaptic and postsynaptic dopamine D2 receptors. *J Neurosci* **32**, 9023-9034, doi:10.1523/JNEUROSCI.0918-12.2012 (2012).

52 Sharma, A., McCarron, P., Matchett, K., Hawthorne, S. & El-Tanani, M. Anti-Invasive and Anti-
Proliferative Effects of shRNA-Loaded Poly(Lactide-Co-Glycolide) Nanoparticles Following
RAN Silencing in MDA-MB231 Breast Cancer Cells. *Pharm Res* **36**, 26, doi:10.1007/s11095-018-
2555-6 (2018).
53 Haggag, Y. A. *et al.* Nano-encapsulation of a novel anti-Ran-GTPase peptide for blockade of
regulator of chromosome condensation 1 (RCC1) function in MDA-MB-231 breast cancer cells.
Int J Pharm **521**, 40-53, doi:10.1016/j.ijpharm.2017.02.006 (2017).
54 Haggag, Y. A. *et al.* Novel Ran-RCC1 Inhibitory Peptide-Loaded Nanoparticles Have Anti-Cancer
Efficacy In Vitro and In Vivo. *Cancers (Basel)* **11**, doi:10.3390/cancers11020222 (2019).
55 Desai, N. Challenges in development of nanoparticle-based therapeutics. *AAPS J* **14**, 282-295,
doi:10.1208/s12248-012-9339-4 (2012).
56 Haley, B. & Frenkel, E. Nanoparticles for drug delivery in cancer treatment. *Urol Oncol* **26**, 57-64,
doi:10.1016/j.urolonc.2007.03.015 (2008).
57 Fang, Z., Grutter, C. & Rauh, D. Strategies for the selective regulation of kinases with allosteric
modulators: exploiting exclusive structural features. *ACS Chem Biol* **8**, 58-70,
doi:10.1021/cb300663j (2013).
58 Kim, G. *et al.* FDA Approval Summary: Olaparib Monotherapy in Patients with Deleterious
Germline BRCA-Mutated Advanced Ovarian Cancer Treated with Three or More Lines of
Chemotherapy. *Clin Cancer Res* **21**, 4257-4261, doi:10.1158/1078-0432.CCR-15-0887 (2015).
59 Drean, A., Lord, C. J. & Ashworth, A. PARP inhibitor combination therapy. *Crit Rev Oncol
Hematol* **108**, 73-85, doi:10.1016/j.critrevonc.2016.10.010 (2016).
60 O'Sullivan Coyne, G., Chen, A. P., Meehan, R. & Doroshow, J. H. PARP Inhibitors in Reproductive
System Cancers: Current Use and Developments. *Drugs* **77**, 113-130, doi:10.1007/s40265-016-
0688-7 (2017).
61 Fleury, H. *et al.* Cumulative defects in DNA repair pathways drive the PARP inhibitor response in
high-grade serous epithelial ovarian cancer cell lines. *Oncotarget* **8**, 40152-40168,
doi:10.18632/oncotarget.10308 (2017).
62 Ouellet, V. *et al.* Characterization of three new serous epithelial ovarian cancer cell lines. *BMC
Cancer* **8**, 152, doi:10.1186/1471-2407-8-152 (2008).
63 Fleury, H. *et al.* Novel high-grade serous epithelial ovarian cancer cell lines that reflect the
molecular diversity of both the sporadic and hereditary disease. *Genes Cancer* **6**, 378-398 (2015).
64 Letourneau, I. J. *et al.* Derivation and characterization of matched cell lines from primary and
recurrent serous ovarian cancer. *BMC Cancer* **12**, 379, doi:10.1186/1471-2407-12-379 (2012).
65 Provencher, D. M. *et al.* Characterization of four novel epithelial ovarian cancer cell lines. *In Vitro
Cell Dev Biol Anim* **36**, 357-361, doi:10.1290/1071-2690(2000)036<0357:COFNEO>2.0.CO;2
(2000).
66 Astolfi, M. *et al.* Micro-dissected tumor tissues on chip: an ex vivo method for drug testing and
personalized therapy. *Lab Chip* **16**, 312-325, doi:10.1039/c5lc01108f (2016).