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

Zied Boudhraa[δ,1,2], Xiaohong Tian[δ,5], Ryhem Gam[ε,1,2], Sabrina Ritch[ε,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

[ε] 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

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 different concentrations

of M36 or with DMSO **(Figures 2D-E)**. As expected, Ran levels detected by Western-blot

decreased with increasing temperatures in controls cells treated with vehicle DMSO. However, a

shift in this thermal instability was observed when cells were treated with M36, specially at the

concentrations of 100 and 200 µM. Significantly higher levels of Ran were observed at all M36

concentrations for temperatures of 58°C, 59°C and 60°C **(Figure 2D)**, indicating M36 engages

with Ran and increases its thermal stability. 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 was 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 4D)**. 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 modeling 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/diploid and cancer/aneuploid 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.

ONLINE 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 supplemented with 10% FBS (Wisent), 0.5 μg/mL amphotericin B (Wisent) and 50 μg/mL gentamicin (Life Technologies Inc.).

Small interference RNA (siRNA) treatment

Suspensions of 10^6 cells in 100 μL of nucleofector solution V (Lonza Group Ltd, Basel, Switzerland) were transfected by electroporation with 1.2 nmoles siRNA targeting Ran (J-010353-06, ON-TARGETplus, Dharmacon Thermo Fisher Scientific Inc., Waltham, MA). For each experiment, efficiency of Ran silencing was verified 48 hours after transfection by Western blot analysis. Scramble siRNA (D-001810-02, Dharmacon) was used as a control in all experiments.

Clonogenic survival

Clonogenic assays were performed as previously described [61]. Colonies were counted under a stereo microscope and reported as percent of control. IC_{50} values were determined using Graph Pad Prism 5 software (GraphPad Software Inc., San Diego, CA). Each experiment was performed in duplicate and repeated three times. Sensitivity of the cell lines to small molecule inhibitors of 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

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

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

Germany). Cell lysates were then obtained by three freeze-thaw cycles in liquid nitrogen (1 min

each step of each cycle) followed by centrifugation at 20,000 × g for 20 min at 4°C. The

supernatants were harvested, and SDS-PAGE loading buffer was added before boiling for 5min.

Proteins were migrated and blotted into PVDF membranes. Primary antibodies used were: Ran

(ab53775, Abcam, 1/5000) and β-Actin (ab6276, Abcam, 1/5000). Proteins were detected by

HRP-secondary antibody and the ECL detection kit (Clarity and Clarity Max ECL Western

Blotting Substrates from Biorad). Densitometry analyses were conducted using the UV-VIS

Spectrophotometer (Thermo Fisher Scientific) and relative intensity of Ran protein was obtained

by the ratio over the β-actin band.

Ran, Cdc42, RhoA and Rac1 activation assays

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

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

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

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

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

In vivo **study**

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

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

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

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

Plasma levels of the compound were measured by mass spectrometry. For the tolerance test,

M36 was dissolved 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 inhibited TOV112D without affecting ARPE (blue bar). Bars represent

513   percentage of colonies formed compared to DMSO-treated controls. **(D)** ARPE and TOV112D

514   cells were incubated with M26 (40 µM) to evaluate apoptosis (6 days after treatment) by western

515   blot using the antibody anti-cleaved PARP. **(E)** TOV112D cells were incubated for one hour

516   with M26 (50 µM) before 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 (50,

100, 200 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. Arrows indicate the

temperatures where significant values were obtained with all three M36 concentrations when

compared to control DMSO (as illustrated in the bar graph). *P < 0.05 **P < 0.01 *** P < 0.001

(n = 3, Student's t-test). **(E)** Representative images of the Western Blots; black rectangular box

encompasses the results obtained with the three above-mentioned temperatures.

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 ≥ 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-γH2AX 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 ≥ 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. $*P < 0.05$, $**P < 0.01$.

A

B

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

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).
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).
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).
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).
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).
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).
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).
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).
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).
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).

33   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).

34   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).

35   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).

36   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).

37   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).

38   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).

39   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).

40   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).

41   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).

42   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).

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

44   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).

45   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).

46   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).

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

48   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).

49   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).

50   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).

51   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).