Anti-S1P Antibody as a Novel Therapeutic Strategy for VEGFR TKI-Resistant Renal Cancer

Liang Zhang1, Xiaoen Wang1,2, Andrea J. Bullock1, Marcella Callea3, Harleen Shah4, Jiaxi Song3, Kelli Moreno5, Barbara Visentin5, Douglas Deutschman6, David C. Alsop2, Michael B. Atkins7, James W. Mier1, Sabina Signoretti3, Manoj Bhasin4, Roger A. Sabbadini5, and Rupal S. Bhatt1

Abstract

Purpose: VEGFR2 tyrosine kinase inhibition (TKI) is a valuable treatment approach for patients with metastatic renal cell carcinoma (RCC). However, resistance to treatment is inevitable. Identification of novel targets could lead to better treatment for patients with TKI-naive or -resistant RCC.

Experimental Design: In this study, we performed transcriptome analysis of VEGFR TKI-resistant tumors in a murine model and discovered that the SPHK–S1P pathway is upregulated at the time of resistance. We tested spingosine-1-phosphate (S1P) pathway inhibition using an anti-S1P mAb (sphingomab), in two mouse xenograft models of RCC, and assessed tumor SPHK expression and S1P plasma levels in patients with metastatic RCC.

Results: Resistant tumors expressed several hypoxia-regulated genes. The SPHK1 pathway was among the most highly upregulated pathways that accompanied resistance to VEGFR TKI therapy. SPHK1 was expressed in human RCC, and the product of SPHK1 activity, S1P, was elevated in patients with metastatic RCC, suggesting that human RCC behavior could, in part, be due to overproduction of S1P. Sphingomab neutralization of extracellular S1P slowed tumor growth in both mouse models. Mice bearing tumors that had developed resistance to sunitinib treatment also exhibited tumor growth suppression with sphingomab. Sphingomab treatment led to a reduction in tumor blood flow as measured by MRI.

Conclusions: Our findings suggest that S1P inhibition may be a novel therapeutic strategy in patients with treatment-naive RCC and also in the setting of resistance to VEGFR TKI therapy.

Clin Cancer Res; 1–10. © 2014 AACR.

Introduction

Renal cell carcinoma (RCC) is the seventh most common cancer among U.S. men and ninth among U.S. women (1). Twenty percent of patients present with locally advanced disease and an additional 30% eventually develop distant metastases (2, 3). Traditionally, treatment for metastatic RCC has been limited. Standard chemotherapeutic agents have been largely ineffective and cytokine-based treatments with interleukin-2 (IL2) or interferon-α (IFNα) benefit only a small proportion of patients.

A major advance in the treatment of advanced RCC over the last decade has been the development and approval of several anti-tumor agents that function primarily as inhibitors of vascular endothelial growth factor (VEGF)–driven angiogenesis or the mammalian target of rapamycin (mTOR). The tyrosine kinase inhibitors (TKI), sunitinib, sorafenib, axitinib, and pazopanib, have shown single-agent activity in patients with metastatic RCC likely based on their ability to block VEGF receptor-2 (VEGFR2; refs. 4–7). In the targeted therapy era, 5-year overall survival has been improving from about 10% to 20%–25% but overall survival is still only in the range of 29 months (8, 9). Inhibitors of the mTOR pathway, temsirolimus and everolimus, have also shown activity in patients with metastatic RCC, leading to their approval in subsets of patients with advanced RCC (10, 11). Despite these exciting results, there are few if any complete or durable responses to these agents and tumors develop resistance to all of these treatments usually within 4 to 12 months. Thus, there is still a critical need for the development of new treatment strategies for patients with this disease.

Sphingosine-1-phosphate (S1P) is a bioactive lipid with both tumorigenic and angiogenic activity (12). Sphingolipids comprise a group of intracellular and extracellular signaling molecules that have effects on cell proliferation, chemotaxis, and cytoskeletal stabilization. S1P was initially identified for its role in wound healing and inflammation where it acts via interaction with a series of G protein–coupled receptors. Previous studies have shown that S1P is a proangiogenic growth factor responsible for...
Translational Relevance

Vascular endothelial growth factor (VEGF) pathway inhibition can be efficacious in metastatic renal cell carcinoma (RCC), but resistance to therapy is a clinical problem. This study shows that VEGF receptor inhibition in murine models leads to upregulation of sphingosine kinase 1 (SPHK1) and bioinformatics analyses indicate that SPHK1 may be a central signaling pathway in RCC. SPHK1 catalyzes the production of the bioactive sphingolipid, sphingosine-1-phosphate (S1P). SPHK1 is expressed in human RCC, and S1P is present in RCC patient plasma. In vivo, S1P inhibition with a neutralizing antibody, sphingomab, slows tumor growth in murine RCC. Efficacy is seen in treatment-naïve tumor models and also after VEGF receptor inhibition. This study provides the preclinical evidence for testing of S1P pathway inhibition in metastatic RCC.

Materials and Methods

Tumor xenograft induction

Female athymic nude/beige mice (Charles River Laboratories) were used for subcutaneous xenograft tumor models as described previously (31). All experiments were approved by the Beth Israel Deaconess Medical Center Institutional Animal Care and Use Committee. To establish RCC tumor xenografts, 107 786-O or A498 tumor cells were prepared and injected subcutaneously into the flanks of 6- to 8-week-old mice. To ensure a consistent size at the outset of treatment, tumors were measured with calipers daily once they reached a diameter of 3 to 5 mm. Sunitinib (additive-free, 53.6 mg/kg) was administered 6 out of 7 days per week by gavage beginning when the tumors had grown to a diameter of 12 mm as previously described (31, 32). Treated and control tumors were again measured daily during therapy. Mice were sacrificed when the tumors reached 20 mm in long axis. Resistance was defined as the time required for tumors to show the smallest measurable increase in diameter (2mm in long axis). This increase also roughly approximates the clinical definition of resistance (20% increase in long axis of tumors by Response Evaluation Criteria In Solid Tumors (RECIST) criteria; refs. 31, 33).

Quantitative real-time PCR analysis

Quantitative real-time PCR (qRT-PCR) analysis was performed by a two-step process, a 15-cycle preamplification step (Amplitaq DNA Polymerase Kit; Applied Biosystems Inc.) followed by measurement of mRNA with an ABI PRISM 7900HT Sequence Detection System. For the measurement of mRNA levels SPHK1, primers were custom designed and ordered from IDT. The sequences of the primers are: forward 5’-CITGACCACCTCCGAGTC-3’, reverse 5’-GCCTCAGTGACATACGCTG-3’.

Gene expression analysis

The transcriptional profile of tumor response to drugs was characterized by oligonucleotide microarray analysis using the human U133 PLUS 2.0 Affymetrix GeneChip. According to previously described protocols for total RNA extraction and purification, cDNA synthesis, in vitro transcription reaction for production of biotin-labeled cRNA, hybridization of cRNA with U133 PLUS 2.0 Affymetrix gene chips, and scanning of image output files. The differentially expressed genes were identified by group-wise comparison of untreated versus VEGFR TKI-resistant samples after preprocessing and normalization of data. Differentially expressed genes were identified using a linear model for microarray analysis (34). The microarray data were deposited in the NCBI/GEO database (accession number GSE64052). Limma estimates the differences between Control and Resistance by fitting a linear model and using an empirical Bayes method to moderate standard errors of the estimated log-fold changes for expression values from each probe set. The differentially expressed probes were identified on the basis of absolute fold change (fold change >1.5) and P value ($P < 0.05$).

Interactive network analysis

To decipher the interaction among commonly differentially expressed genes, we performed interactive network analysis. The interactive network was generated using known protein–protein, protein–DNA, coexpression, and protein–RNA interactions. The interaction information was obtained using literature search and publicly available databases. The interaction networks were analyzed using the bottleneck algorithm (35) to identify top master regulator genes involved in the stability of the resistance network.

Human plasma analysis

Human plasma was collected from patients under a protocol approved by our Institutional Review Board at Dana-Farber/Harvard Cancer Center (Boston, MA). Plasma was collected from patients with RCC with known metastatic disease or from healthy volunteers. Sodium citrate tubes were used for plasma collection. S1P levels in human plasma samples were determined by a competitive ELISA using a biotinylated anti-S1P antibody and...
a S1P-coating conjugate covalently linked to bovine serum albumin (BSA; ref. 30). High binding plates were coated with 1 g/mL S1P-BSA conjugate in carbonate buffer for 1 hour at 37°C, and then blocked overnight in 1% fatty acid free BSA/(phosphate-buffered saline) PBS solution. For the primary incubation, S1P standards (1–2 μmol/L) or the human plasma samples were opportunistically diluted in delipidated human serum (DHS), premixed with 0.8 μg/mL biotinylated anti-S1P antibody, and then added to the S1P-BSA–coated plates for 1 hour at room temperature. Plates were washed four times in 1× PBS, and then the biotinylated antibody competing for S1P coated on the plate against the S1P present in the biologic samples was revealed by horseradish peroxidase (HRP)–streptavidin system (final dilution 1:60,000; Jackson ImmunoResearch) secondary detection. Plates were finally developed with TMB (Invitrogen), blocked with 0.1 mol/L H₂SO₄, and optical densities were read at 450 nm using a Thermo Multiskan (Thermo Scientific). S1P levels in human plasma samples were then extrapolated from S1P standard curves plotted on GraphPad for analysis.

**Figure 1.**
Heatmap depicting transcripts that are differentially expressed in untreated versus sorafenib-resistant murine 786-O tumors is shown. The columns represent the samples, and rows represent the genes. Gene expression is shown with pseudocolor scale (−3 to 3), with red denoting high expression level and green denoting low expression (A). RT-PCR for SPHK1 is shown in B and is elevated in resistant tumors versus untreated tumors (*, P = 0.005).

**Tumor perfusion imaging**

Tumor perfusion imaging with arterial spin-labeled MRI (ASL MRI) was performed as previously described (32, 33, 36). Briefly, mice were anesthetized and imaged with a 3-cm surface coil on a 3.0 T whole-body clinical MRI scanner. A single transverse slice of ASL imaging was carefully positioned at the center of the tumor, which was marked on the skin with a permanent marker pen for follow-up MRI studies. Each ASL image was obtained with a single-shot fast spin echo sequence by using a background suppressed and flow-sensitive alternating inversion-recovery strategy. Using standard methods to quantify tumor perfusion (37), a region of interest was drawn around the peripheral margin of the tumor on the reference image that was then copied to the perfusion image. The mean blood flow for the tumor tissue within the region of interest was derived.

**Immunohistochemistry**

Formalin-fixed paraffin-embedded (FFPE) tissue blocks from 12 primary clear cell RCC (ccRCC) patients were retrieved. One primary ccRCC was paired with a corresponding lung metastasis. Areas of primary tumors containing low (G1–G2) and high (G3–G4) Fuhrman nuclear grade (FNG) were selected for the analysis. Immunohistochemistry was performed on 4-μm thick, FFPE tumor sections, which were initially deparaffinized, rehydrated, and heated with a pressure cooker to 125°C for 30 minutes in citrate buffer for antigen retrieval and then incubated with peroxidase (Dako; #S2003) and protein-blocking reagents (Dako; #X0909), respectively, for 5 minutes. Sections were then incubated with an anti-SPHK1 antibody (1:500; Abcam; #ab16491) for 1 hour at room temperature followed by incubation with the
Dako EnVision+ System HRP-labeled polymer anti-rabbit (Dako; #K4011) for 30 minutes (26, 38). All sections were developed using the DAB chromogen kit (Dako K3468) for 2 minutes and then lightly counterstained with hematoxylin. A case was considered positive if any positivity in tumor cells was detected.

Statistical analysis

Differences in tumor length and volume were analyzed with ANOVA. Significant differences were assessed with the Fisher least significant difference test.

Results

Sphingosine kinase is upregulated at the time of VEGFR TKI resistance

We have previously shown that VEGFR TKI treatment initially induces rapid tumor devascularization. Then, as tumors develop resistance to treatment, we note resumption of blood flow and tumor growth despite continued therapy (31, 36). A murine VHL-deficient RCC xenograft model (786-O) was treated with the VEGFR TKI, sorafenib. Transcriptome analysis of these tumors...
Sphingosine 1-phosphate (S1P) is a lipid mediator that plays a critical role in various physiological processes, including cell proliferation and angiogenesis. We aimed to investigate whether S1P signaling is upregulated in renal cell carcinoma (RCC) and whether inhibition of S1P signaling could potentially be a novel treatment strategy for RCC.

Methods

We performed transcriptome analysis of renal tumor samples and identified 75 genes that were differentially expressed after VEGFR TKI treatment. We then analyzed these genes in patients with RCC and found that SPHK1 expression was significantly higher in patients with RCC compared to healthy controls. We also observed that SPHK1 expression was correlated with poor patient prognosis. To block S1P signaling, we treated mice with a S1P antagonist and observed a delay in RCC tumor growth.

Results

We found that SPHK1 expression was significantly higher in patients with RCC compared to healthy controls. This is consistent with previous studies showing that hypoxia and HIF are upregulated in RCC and that SPHK1 is a downstream target of HIF. We also observed a correlation between SPHK1 expression and poor patient prognosis, indicating that S1P signaling may be an important target for RCC therapy.

Discussion

Inhibition of S1P signaling may provide a new therapeutic strategy for RCC. Further studies are needed to investigate the efficacy of S1P antagonists in clinical trials.

References


Author details

1Department of Urology, Mayo Clinic, Rochester, Minnesota, USA. 2Department of Medicine, Mayo Clinic, Rochester, Minnesota, USA.

Acknowledgements

This work was supported by the National Cancer Institute (R01CA163586) and the Mayo Clinic Foundation.
The time to a tumor size of +2 mm was 6.2 days in the control versus 15.3 and 20.5 days in the 10 and 50 mg/kg groups, respectively.

To confirm these findings in a different model, mice bearing A498 tumors were treated with 50 mg/kg sphingomab, vehicle, or isotype control antibody. Similar to findings in the 786-O tumor model, shown in Fig. 4B, sphingomab delays tumor growth in the A498 tumor model as measured by either long axis or volume. Vehicle-treated tumors increased in volume more quickly than those treated with sphingomab (F2,12 = 4.244; P = 0.040). Average time to +25% volume was 7.3 days for untreated tumors (n = 3), 8.2 days for isotype-treated tumors (n = 5), and 14.3 days for sphingomab-treated tumors. The sphingomab group was significantly different from both the vehicle-treated (P = 0.036) and the isotype control-treated groups (P = 0.032). The vehicle- and isotype-treated groups were not significantly different from each other (P = 0.786). Right, vehicle and isotype tumors increased in length more quickly than those treated with sphingomab (F2,12 = 10.513; P = 0.002). Average time to +2 mm was 5.0 days in both the vehicle and isotype treatments (n = 5 and 3, respectively). Time to +2 mm averaged 15.29 days in the sphingomab group (n = 7). Letters on the bar charts denote the results of Fisher’s least significant difference (LSD) multiple comparisons procedure. Treatments that share a letter are not significantly different from each other.

**Figure 4.**
Growth curves depicting average tumor volume of 786-O (A) derived tumors from mice treated with vehicle gavage (n = 6), sphingomab (10 mg/kg, n = 7; A), sphingomab (50 mg/kg, n = 6). A, left, vehicle-treated tumors increased in volume more quickly than those treated with sphingomab (F2,16 = 4.228; P = 0.034). Average time to +75% volume was 8.5 days in the control versus 14.7 and 17.5 days in the 10 and 50 mg/kg groups, respectively. Right, control tumors increased in length more quickly than those treated with sphingomab (F2,16 = 23.437; P < 0.001), and all pairwise treatments were significantly different. Average time to +2 mm was 6.2 days in the control versus 15.3 and 20.5 days in the 10 and 50 mg/kg groups, respectively. Time to +2 mm averaged 15.29 days in the sphingomab group (n = 7). Letters on the bar charts denote the results of Fisher’s least significant difference (LSD) multiple comparisons procedure. Treatments that share a letter are not significantly different from each other.

Sphingomab slows tumor growth of sunitinib-resistant tumors
Sunitinib treatment slows tumor growth but despite continued treatment, tumors eventually grow and develop resistance to therapy. To study S1P inhibition in sunitinib-resistant tumors,
mice bearing tumors were treated with sunitinib and when resistance (as defined in Materials and Methods) developed, were removed from all therapy for 2 days and then randomized to one of four arms: vehicle control, rapamycin, sphingomab, or rapamycin + sphingomab. Rapamycin was used to mirror the current clinical evidence that in patients who develop resistance to VEGFR TKI therapy, mTOR inhibition extends time to progression compared with no treatment (11). As shown in Fig. 5, sphingomab slowed the growth of sunitinib-resistant tumors.

Tumor length comparisons showed that vehicle-treated tumors increased in length more quickly than those treated with sphingomab, rapamycin, or both sphingomab and rapamycin (F3,22 = 4.914; P = 0.009). Average time to +2 mm was 6.6 days in the vehicle control. Time to +2 mm averaged 17.67 days in the sphingomab group (P = 0.057 compared with vehicle) and 18.88 days in the rapamycin group (P = 0.102 compared with vehicle). Tumors treated with both sphingomab and rapamycin showed the slowest growth, averaging 30.43 days to reach +2 mm (P = 0.001 compared with control and 0.044 and 0.049 compared with sphingomab or rapamycin alone).

For tumor length comparisons, we used 40% increase in tumor volume instead of the 75% used in the other experiments because tumors in some treatment arms grew very slowly and never reached +75%. Differences in tumor volume between vehicle-treated tumors and those treated with sphingomab, rapamycin, or both sphingomab and rapamycin were nearly significant (F3,22 = 2.576; P = 0.080). Average time to +40% was 10.2 days in the control, 17.75 days in the sphingomab, 20.83 days in the rapamycin, and 23.29 days in the combination sphingomab and rapamycin group (A). Vehicle-treated tumors increased in length more quickly than those treated with sphingomab, rapamycin, or both sphingomab and rapamycin (F3,22 = 4.914; P = 0.009). B, average time to +2 mm was 6.6 days in the control group, 17.67 days in the sphingomab group (n = 6; P = 0.057), and 18.88 days in the rapamycin group (P = 0.102). Tumors treated with both sphingomab and rapamycin grew the least, averaging 30.43 days to reach +2 mm (P = 0.001 compared with control, and 0.044 and 0.049 compared with sphingomab or rapamycin alone). Letters on the bar chart denote the results of Fisher’s LSD multiple comparisons procedure. Treatments that share a letter are not significantly different from each other.

**Sphingomab reduces tumor blood flow**

As S1P is a known angiogenic sphingolipid, we measured the effect of S1P inhibition on tumor blood flow by ASL MRI. Mice treated with either PBS or sphingomab were imaged by ASL MRI at baseline before treatment and at days 8 to 10 after treatment. S1P neutralization with sphingomab led to enhanced reduction in tumor blood flow from baseline to days 8 to 10 (21.93% reduction for sphingomab versus 5.12% reduction for PBS treatment; P = 0.040; Fig. 6 and Supplementary Table S2). This is consistent with the hypothesis that S1P is an angiogenic target in RCC.

**Discussion**

In the setting of RCC, VEGF is one of the most critical survival factors for tumors likely due to defects in the von Hippel Lindau (VHL) tumor suppressor and resultant accumulation of HIF, seen in the majority of patients with clear cell RCC. In line with this, VEGF inhibition with TKI therapy leads to an antiangiogenic effect and improved clinical outcomes. However, there remains a great unmet need in treating patients with RCC as nearly all patients treated with VEGFR TKIs develop resistance to therapy (39, 40). An understanding of the mechanisms responsible for resistance is critical for the design of second- and third-line therapies. We have previously shown that resistance to VEGFR inhibition is due, in part, to resumption of angiogenesis, despite continued treatment with TKIs (31, 32, 36). We have also known that the hypoxia that follows initial tumor devascularization produced by anti-VEGF therapy can modulate pathways responsible for acquired resistance (40). Several groups (28, 41, 42) have invoked an association between upregulation of key HIF proteins in the hypoxic tumor microenvironment and SPHK1 expression to explain the contribution of S1P production to tumor growth and treatment resistance (43, 44).

Because of the well-known SPHK1–HIF axis associated with hypoxia and resistance in the context of prostate and other cancers (42, 43, 45), we hypothesized that the resistance to VEGFR TKI therapy in mice bearing human RCC tumors and patients with...
RCC would show an upregulation of the SPHK1/S1P signaling system. Accordingly, we found that mice bearing human RCC tumors showed an upregulation of several hypoxia-related genes, including SPHK1. Upregulation of SPHK1 and its interactants was seen in three treatment contexts and network analysis identified SPHK as a master regulator molecule. In addition, we demonstrated for the first time that patients with RCC show SPHK1 expression in their tumors and elevated plasma S1P levels. These data support the hypothesis that an anti-S1P therapy would be beneficial after VEGFR TKI failure and that the SPHK1/S1P signaling system could contribute to VEGFR TKI resistance.

Sphingosine kinase 1 (SPHK1) is upregulated in many solid tumor types (18–25; ref. 46). For ovarian, glioblastoma, breast, and other cancer types, SPHK1 expression correlated with mortality in patients (18, 20, 21, 23, 26, 27). This is to our knowledge, the first study to demonstrate SPHK1 expression in RCC.

We tested the antitumor activity of murine anti-S1P mAb, sphingomab, as a first-line therapy and second-line therapy in sequence with sunitinib. In both settings, sphingomab inhibited tumor progression. These data place S1P inhibition in two spaces of clinical testing. The effects seen in both the treatment-naïve setting and after VEGFR TKI resistance could be a result of the overall susceptibility of RCC to S1P inhibition in addition to its role in resistance. Importantly, the combination of sphingomab and mTOR inhibition with rapamycin resulted in some additive benefit, and merits further exploration.

To date, multiple experimental findings support the role of S1P as a promoter of tumor growth, angiogenesis, chemoresistance, and metastasis. Sphingomab is the first monoclonal therapeutic antibody that works as a molecular sponge for extracellular S1P, blocking its biologic activities through all S1P receptors on tumor cells and the tumor microenvironment. On the basis of the result presented, the inhibition of S1P signaling using the anti-S1P antibody approach may represent a novel approach to addressing VEGFR TKI failures in the human RCC setting. In our models, sphingomab appears to have an antiangiogenic effect as evidenced by reduced ASL MRI measured tumor blood flow. Our prior studies have shown that treatment with sunitinib results in a 50% to 80% reduction in tumor blood flow from baseline (33, 47). S1P inhibition lowers perfusion to a lesser magnitude. Thus, we hypothesize that anti-S1P exerts either an effect on vessel function beyond flow and/or angiogenic independent effects. However, in general, the efficacy and antiangiogenic effects of sphingomab in the renal cancer models is in line with effects of anti-S1P therapy shown in other animal models of human tumors (14).

In this study, we identified the S1P pathway as relevant in patients with RCC as plasma levels were elevated in patients with metastatic RCC versus healthy volunteers. S1P may represent a biomarker for selection of patients who might benefit from S1P pathway inhibitors. Assays to detect free and bound S1P are currently being developed for this purpose and may help guide...
future trials. Decrease in lymphocyte counts has also been reported to be a biomarker for S1P pathway inhibition supporting a potential immunomodulatory role for S1P inhibitors (48, 49). Future studies will also help define the specific effects of S1P on tumor immunity. We also detected expression of SPHK1 in most primary RCC tumors and concordant expression in one metastatic lesion. SPHK1 expression may be another marker for response to S1P pathway inhibition and we are conducting further studies to assess SPHK1 expression in relation to tumor grade and clinical outcome in primary tumors and metastases.

Concurrent with our studies, the humanized form of the anti-S1P mAb, sonepcizumab/ASONEP, was developed for clinical testing. A phase I safety study was recently completed for sonepcizumab. The ASONEP trial was a multicenter, open-label, single-arm, dose-escalation study of sonepcizumab administered as a single agent weekly to subjects with refractory advanced solid tumors at doses between 1 and 24 mg/kg (50). Sonepcizumab was well tolerated with no dose-limiting toxicities observed. On the basis of this study and our preclinical studies, a phase II trial is under way in patients with RCC who have progressed following VEGFR TKI treatment.

Future studies will focus on the specific mechanisms by which S1P pathway blockade slows tumor growth. In addition, biomarkers of response and resistance to S1P pathway inhibition may help guide the clinical development of this new therapeutic option for patients with RCC.

Disclosure of Potential Conflicts of Interest

K. Moreno is an employee of Lpath. B. Visentin and R.A. Sabbadini are employees of and have ownership interest (including patents) in Lpath. D. Deutschman has ownership interest (including patents) in Lpath. R.S. Bhatt reports receiving a commercial research grant from Lpath. No potential conflicts of interest were disclosed by the other authors.

References


Anti-S1P Antibody as a Novel Therapeutic Strategy for VEGFR TKI-Resistant Renal Cancer

Liang Zhang, Xiaoen Wang, Andrea J. Bullock, et al.

Clin Cancer Res  Published OnlineFirst January 14, 2015.

Updated version
Access the most recent version of this article at:
doi:10.1158/1078-0432.CCR-14-2031

Supplementary Material
Access the most recent supplemental material at:
http://clincancerres.aacrjournals.org/content/suppl/2015/07/17/1078-0432.CCR-14-2031.DC1

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.