## OHNS HOPKINS **BLOOMBERG~KIMMEL INSTITUTE** FOR CANCER IMMUNOTHERAPY

### INTRODUCTION

Glutamine, the most abundant amino acid in plasma, plays a critical role in cancer metabolism. However, recent studies have challenged the utility of singularly targeting specific enzymes (e.g. glutaminase) for therapeutic gain. Instead, we hypothesized that broadly inhibiting multiple glutamine related pathways would more effectively shut down tumor growth. To test this hypothesis, we employed a novel prodrug of the glutamine antagonist 6-diazo-5-oxo-L-norleucine (DON) in a number of syngeneic mouse models of cancer including MC38 (derived from colon cancer) and B16 (derived from melanoma). In an attempt to explore the anti-tumor mechanisms in each of these models, we applied a MS-based stable isotope tracing strategy to profile [U-<sup>13</sup>C]-glucose/glutamine derived metabolites. Our studies revealed that MC38 was highly sensitive to anti-glutamine treatment when compared to 3LL and B16. Interestingly, [U-13C]glucose tracing study showed that treatment with the glutamine antagonist markedly decreased the flux into "proximal" glycolytic reactions, PPP pathway and serine synthesis pathway.



glucose tracing study Strikingly, our that the flux from succinate to following down glutamine antagonist treatment. This finding implies that the glutamine antagonist used in our study may have direct or indirect succinate dehydrogenase inhibition [U-<sup>13</sup>C]-Furthermore employing bv discovered the plutamine tracing we presence of a rewired Krebs cycle via the aspartate arginosuccinate shunt and GABA shunt in the MC38 model. Overall, our results highlight that broadly targeting tumor glutamine metabolism can markedly affect requiring non-glutamine metabolism essential for tumor growth.



### RESULTS

# resistant to JHU-083



# Targeting glutamine metabolism disables Warburg physiology by inhibiting proximal glycolysis and Krebs cycle rewiring

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## **RESULTS (cont'd)**







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