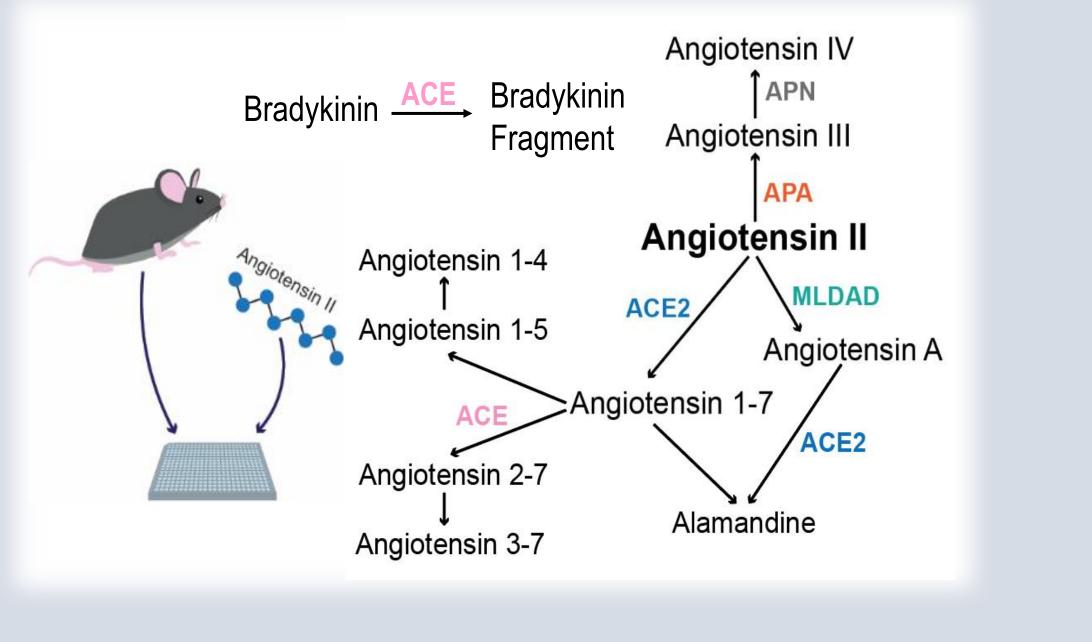
## Introduction:

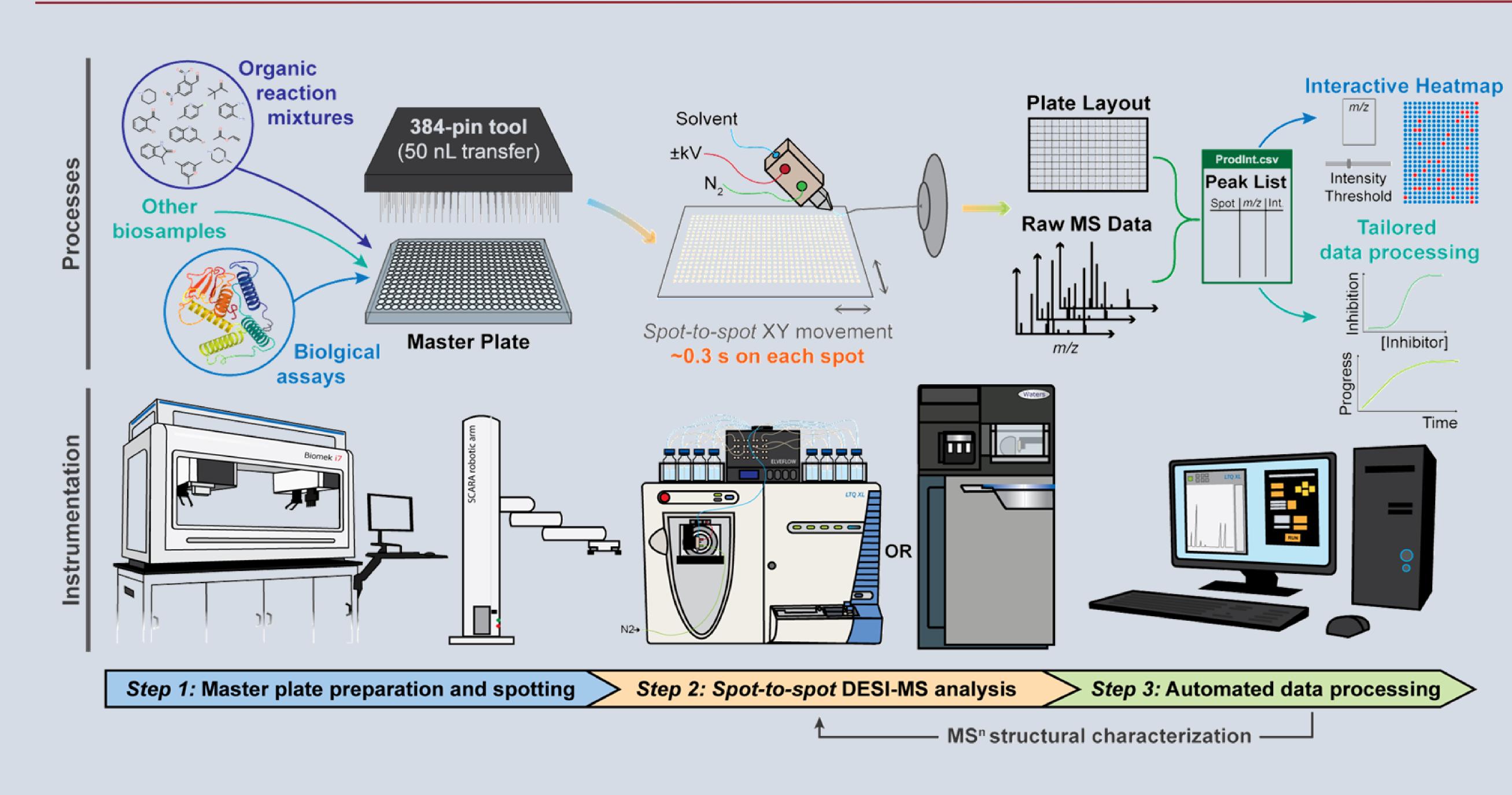
ACE inhibitors target the production of angiotensin II but also affect other angiotensin metabolites. They also inhibit the breakdown of bradykinin, substance P, goralatide, etc.

Metabolic pathways differ between tissue types. Therefore, the introduction of ACE inhibitors may have vastly different effects on different tissues. The effects on other pathways can trigger adverse effects such as a dry cough or angioedema

**Hypothesis:** High throughput DESI-MS can be used to track angiotensin metabolism in mouse tissue



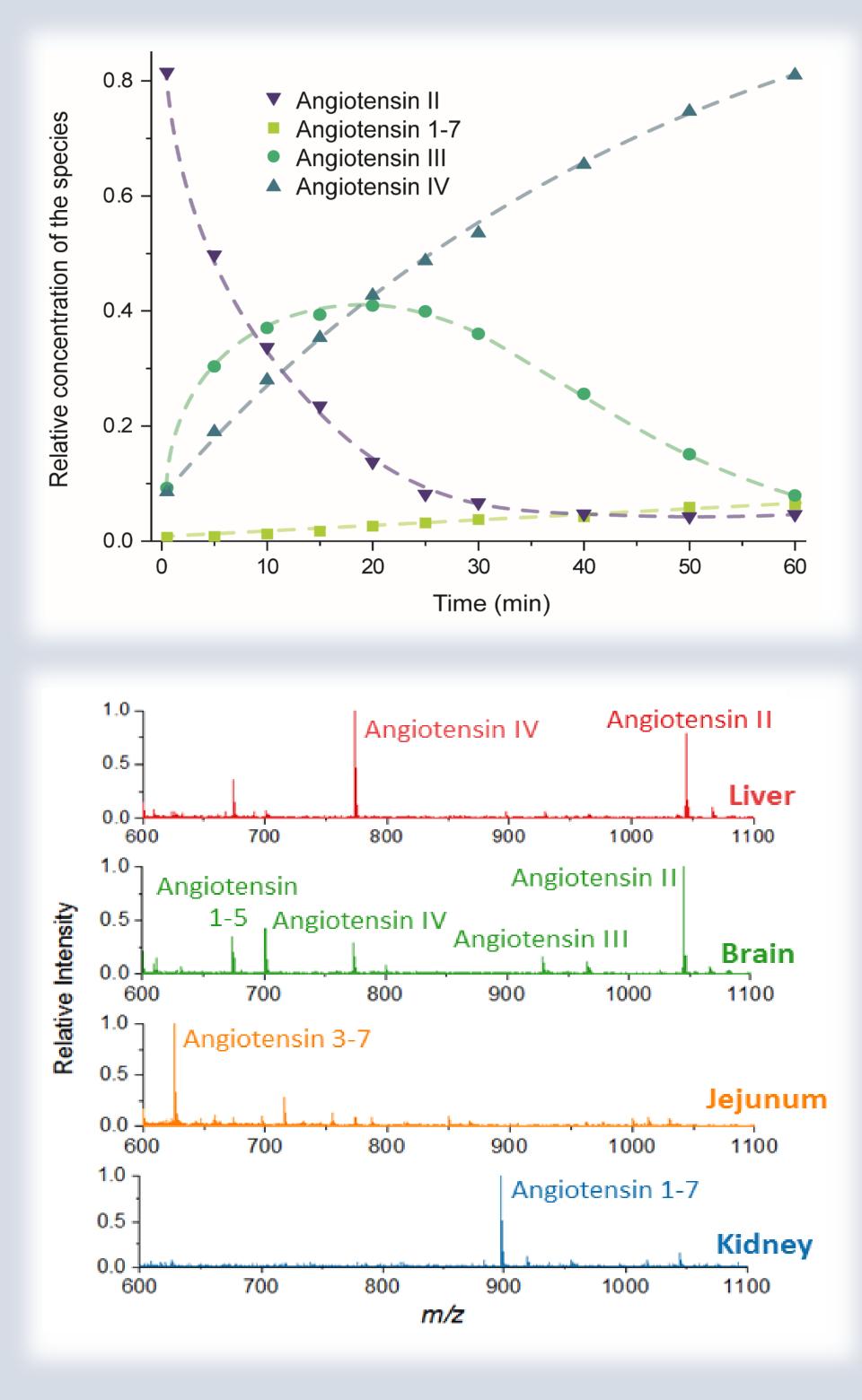
### Method:



# High Throughput DESI Analysis of Angiotensin

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**Results:** 



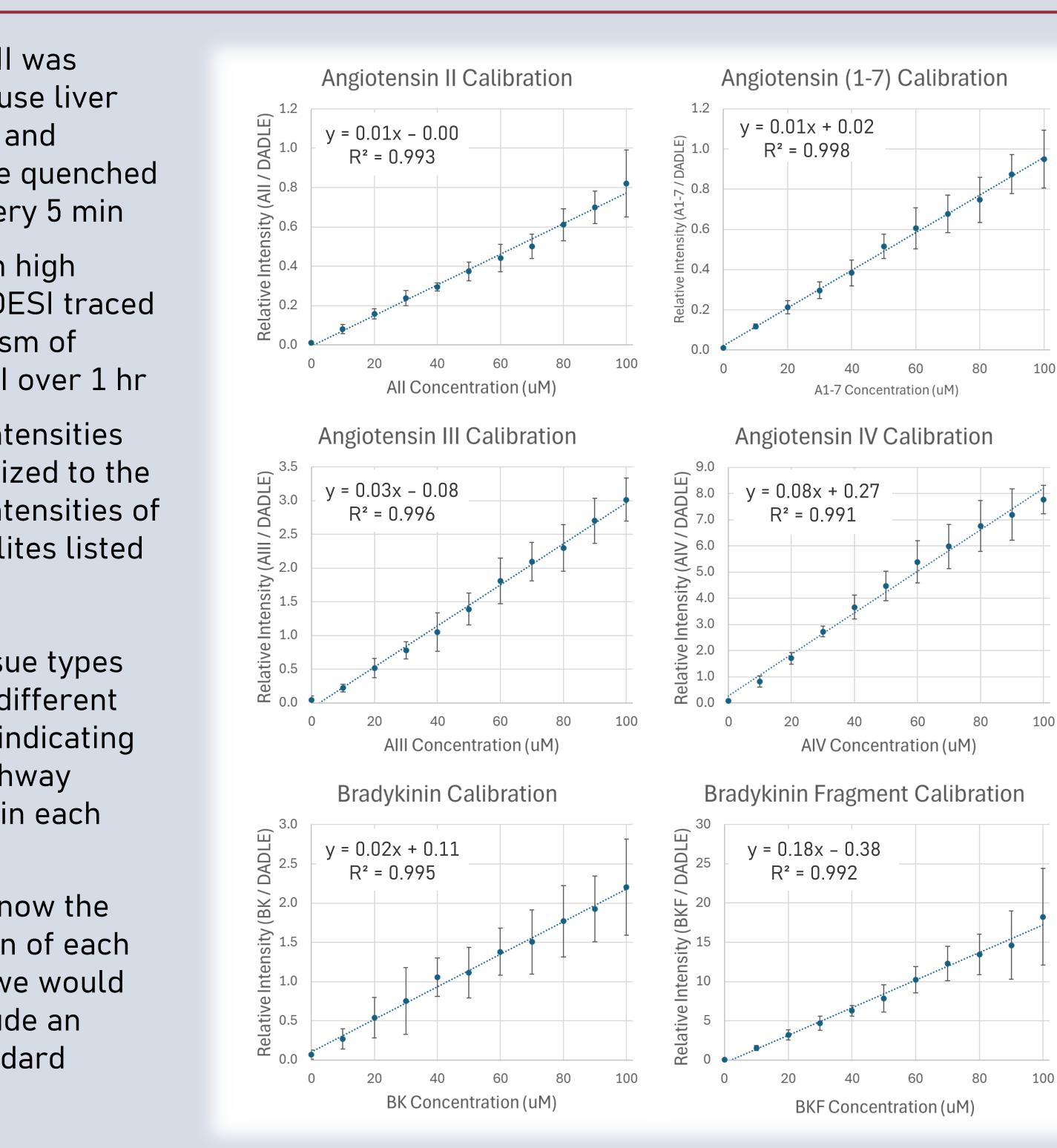
Angiotensin II was added to mouse liver homogenate and aliquots were quenched with heat every 5 min

Analysis with high throughput DESI traced the metabolism of angiotensin II over 1 hr

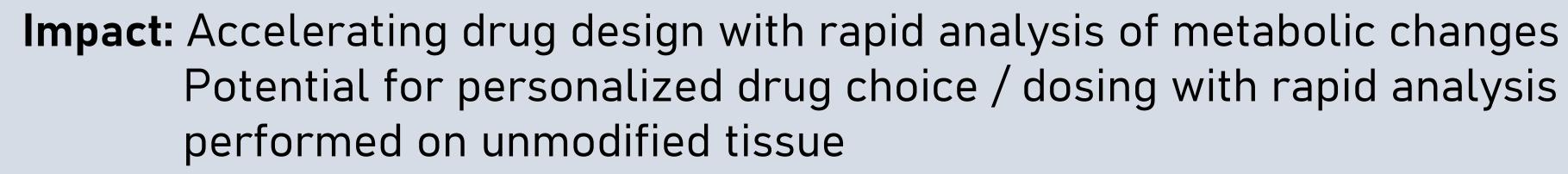
Metabolite intensities were normalized to the sum of the intensities of all 4 metabolites listed

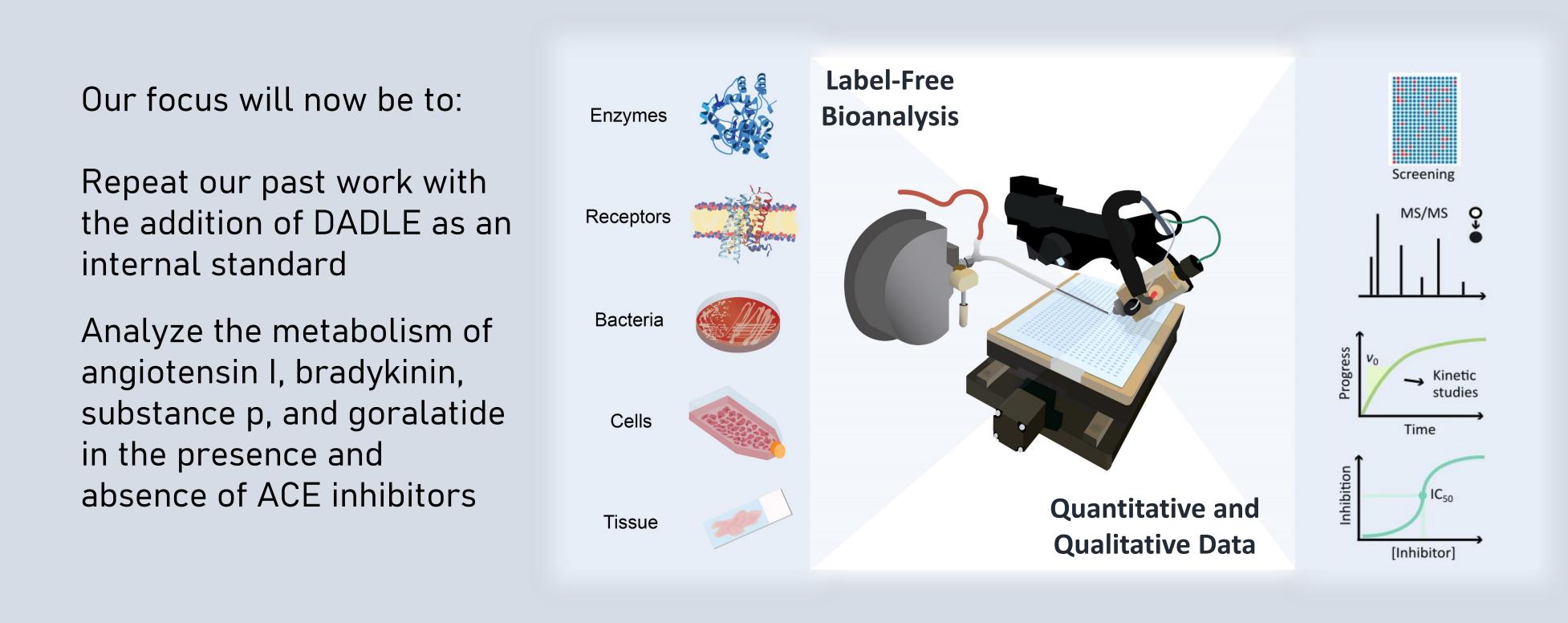
Different tissue types gave rise to different metabolites indicating different pathway preferences in each tissue type

In order to know the concentration of each metabolite, we would need to include an internal standard



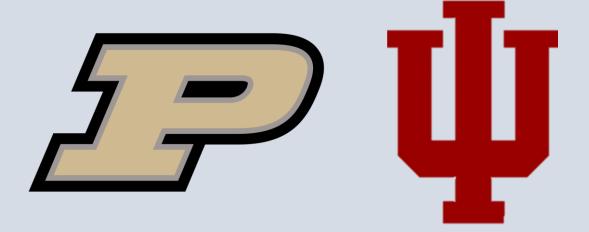
### Impact and Future Direction:





\*This presentation could not have been done without the generous funding and support from CTSI UL1TR002529 from NIH





### Introducing DADLE as an internal standard demonstrated good linearity in a range of 0-100 uM

Samples were analyzed at a rate of ~3000 samples per hour; a rate of >6000 samples per hour is possible on the same system

**Conclusion:** High throughput DESI can track angiotensin metabolism and identify differences in its metabolism between tissue types. With high throughput DESI, the exact concentrations can likely be quantified using an internal standard

Potential for personalized drug choice / dosing with rapid analysis