



About our guest
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SPEAKING OF **MOL BIO**

High-throughput transcriptomics and AI for drug discovery

Season 2, Episode 1

Episode notes

Doing something complex and meaningful in a new way requires thinking and acting a bit differently. This is the case with how Dr. Joey Azofeifa, from Arpeggio Bio, is using systems biology to discover new drug candidates.

Join us in this Season 2 kickoff episode where we dive headlong into transcriptomics, systems biology, machine learning, and learn how they're being used to innovate drug discovery. We learn about 3'-end mRNA barcoding and in-cell reverse transcription methods that allow pooling of up to 1,536 samples so that only a single library preparation is required while still allowing deconvolution of RNAseq results. This reduces their RNAseq costs by up to 400-fold, which enables them to generate enormous transcriptomic data sets. We also learn about how they're using generative adversarial AI networks to use this transcriptomics data to design potential drug candidates. We even hear how one of their drug candidates, which targets iron homeostasis pathways, has progress to successful testing in mice.

Join us for some great conversation on molecular biology, AI and machine learning methods, and entrepreneurial life too.

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Joey's recent publications

1. Read, T., Simpson, D., Rimel, J., Rhine, C., Pham, C., Liechty, C., Martin, E., Azofeifa, J., [Enhancer RNA Profiles Predict Sensitivity to a Novel GPX4 Inhibitor](#). *Cancer Res* (2003) (7_Supplement): 4913.
2. Read, T., Winograd, Z., Goliaei, A., Liechty, C., Grachala, C., Damon, L., Dickson, J., Harris, J., Pham, C., Rimel, J., Rhine, C., Simpson, D., Martin, E., Azofeifa, J., [Identification of Novel GPX4 Inhibitors Using Global Transcriptional Reporters](#). *Cancer Res* (2023) 83 (Supplement): 2755.

“... We would love to say boil everything down to like transcriptomics is the answer, and that's the only thing that we have to do to like to make billion-dollar drugs. But it's definitely not the case. The value in transcriptomics is that it's extremely multivariate.”