Comparing CodePlex Highly Multiplexed Walk-Away Immunoassays with Traditional Multiplexed Bulk ELISA

IsoPlexis' highly multiplexed walk-away immunoassays save time with automated workflows, need 10x lower sample volume, and provide best in class quantitation

In this Technical Note we outline:

- Isoplexis' highly multiplexed walk-away proteomics

- How CodePlex offers highly multiplexed insights in 10x less sample volume in a modular fashion

- How CodePlex provides sensitive ELISA readouts with fully quantitative analysis

- IsoSpeak software's automated analysis and data visualizations for push-button publication ready figures

Highly Multiplexed Walk-Away Proteomics

The CodePlex family of solutions enables you to automate your entire workflow with one system, giving you the ability to run an entire highly multiplexed ELISA workflow in a completely automated and hands-off manner. This walk-away automation saves time and resources, allowing researchers to gain insights into their samples much faster compared to status quo and bead-based technologies.

CodePlex Provides Sensitive ELISA Readouts with Fully Quantitative Analysis

Quantitative antibody-based detection on the Codeplex chip enables the quantitative detection of protein at concentrations of 2-2000 pg/mL. At a sensitivity level of 6.8 pg/mL, the CodePlex chips are comparable in sensitivity to traditional multiplexed ELISA (Figure 1a). Side-by-side comparison shows high quantitative sensitivity (Figure 1b). The IsoSpeak advanced bioinformatics suite allows for fully quantitative analysis of the CodePlex chips with powerful end-to-end integration.

With a 32 sample or 64 sample run with replicates, the Codeplex walk-away proteomics workflow saves 3-4 hours of time that would normally be spent on many tedious manual steps (Figure 2) .With CodePlex, you can add your sample and walk away, achieving fully analyzed data on the same day. No additional equipment is needed. A fully automated workflow means no washing and incubation stations, no centrifuge, no vortexer, and no plate reader. You can unlock your data immediately, lowering costs per run and total instrumentation requirements.

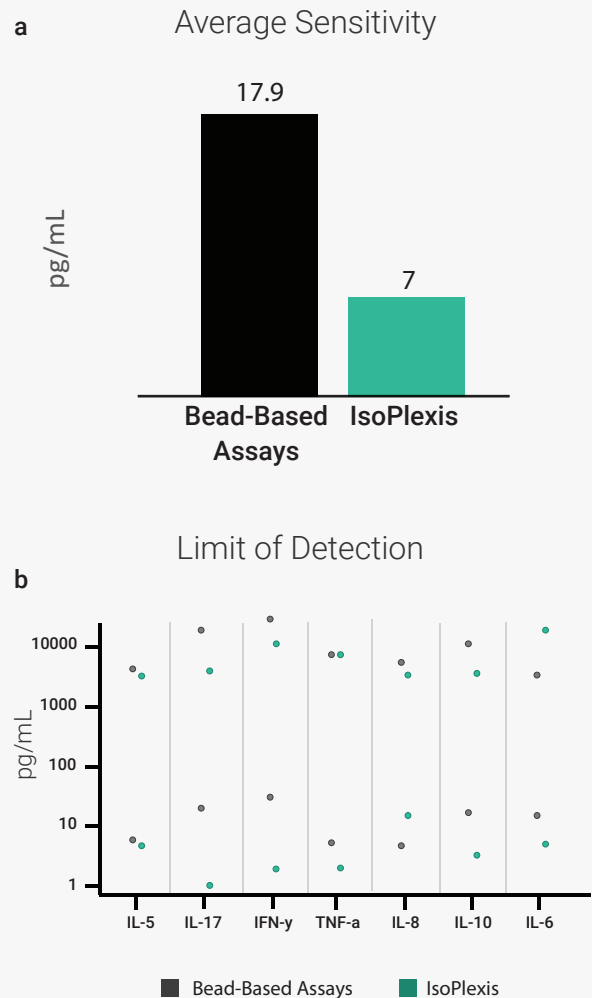### IsoPlexis' High Quantitative Sensitivity Side-by-Side vs Bead-Based Assays

Figure 1 | a) IsoPlexis provides sensitive and quantitative protein readouts comparable to or more sensitive than traditional multiplexed bulk ELISA. b) Limit of detection across 6 relevant cytokines.

Prep, Run, Analyze

IsoPlexis Saves Critical Resources with Walk-Away workflow

a

Hand On Time

CodePlex Offers Highly Multiplexed Insights in 10x Less Sample Volume in a Modular Fashion

CodePlex chips measure up to 30+ cytokines in bulk, automated on the IsoLight system, and can selectively run eight conditions per chip in "MacroChambers" across eight chips on a single run. The CodePlex solution only requires a sample volume of 11uL for replicates (Figure 3a) in contrast to the 100ul or more sample volume needed on traditional technologies, allowing for the analysis of precious patient samples or *in vivo* mouse model samples.

b

Total Time

IsoPlexis Requires 10x Less Sample Volume and Allows for Flexible Sample Numbers

a

Sample volume needed for replicates on **CodePlex Secretome** — 11 uL

Sample volume needed for replicates on **Status Quo Instrumentation** — 100 uL
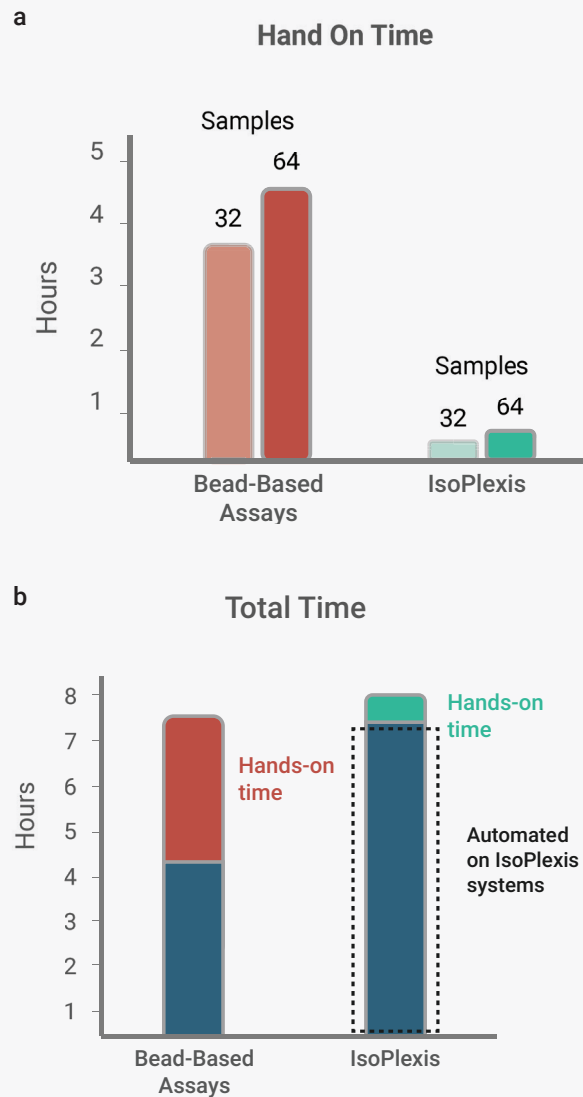
b

Figure 2 | Hands on time comparisons. a) IsoPlexis saves hours of hands on time compared to traditional multiplexed ELISA b) Total time for 32 samples. IsoPlexis allows for completely walk-away analysis, providing researchers the freedom to work on other critical experiments.
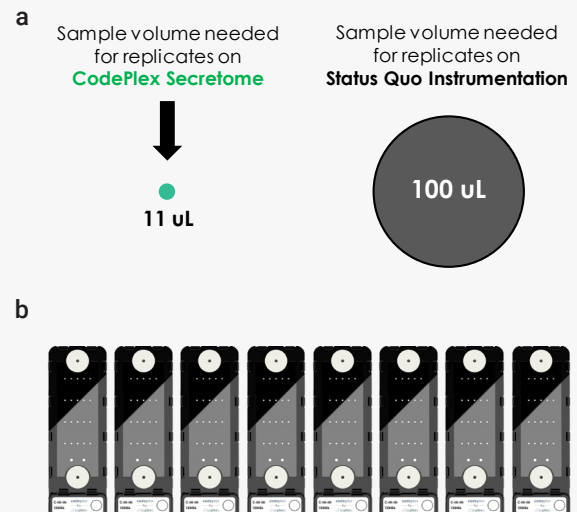
Figure 3 | Low sample volume and modular sample loading. a) IsoPlexis requires 10x less sample volume, allowing for the analysis of rare and precious samples, as well as *in vivo* mouse model samples. b) IsoPlexis' modular chip capability allows for sample runs as few as 8 samples and upwards of 64 samples.

Prep, Run, Analyze

Save Time With Accelerated Insights Enabled by Automated Software Analysis

a

IsoPlexis Push-Button Data Analysis Workflow

PROJECT INFO · BIOMARKER ANALYSIS · EXPORT · *Publication Ready*

b

Status Quo Multiplexed Bulk ELISA

Read sample · Import data · Enter batch properties · Enter run properties · Enter analyte properties · Create curve · Perform data QC · Create data figures · Compile data report · *3+ hours*

c

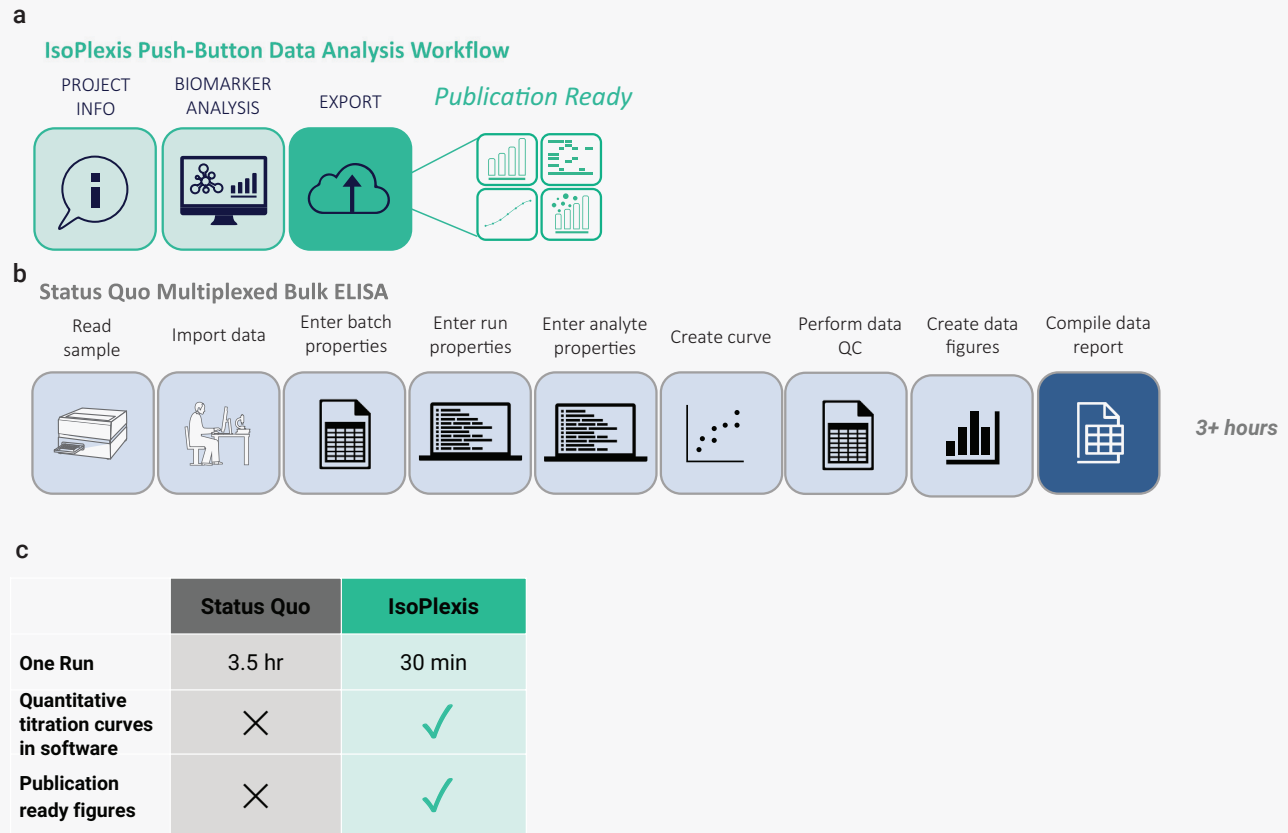|	Status Quo	IsoPlexis
One Run	3.5 hr	30 min
Quantitative titration curves in software	✕	✓
Publication ready figures	✕	✓

Figure 4 | Comparison of data analysis workflows. a,c) IsoSpeak provides fully quantitative analysis with push button visualizations and generation of publication ready figures. b,c) traditional proteomic analysis workflows require longer analysis times and manual data visualization methods.

Additionally, CodePlex offers a modular solution to analyze as few as eight small volume samples at a time (Figure 3b), and up to 64 samples, instead of requiring a full 96 samples before generating multiplexed bulk cytokine data.

IsoPlexis' CodePlex solution is helping researchers accelerate insights by providing a faster and more streamlined approach to generating highly multiplexed bulk cytokine data via a fully automated end-to-end workflow.

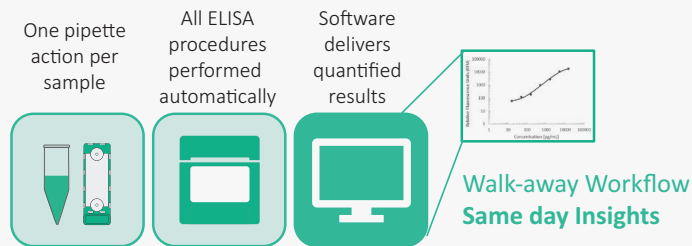## IsoSpeak Software Automates Analysis and Data Visualizations for Push-Button Publication Ready Figures

A key unique end-to-end feature of IsoSpeak data analysis software is the ability to organize and annotate data, prepare the data for visualization, and to enable collaboration. IsoSpeak allows for the organization of the datasets such that you can immediately dive into the data

Prep, Run, Analyze

IsoPlexis Walk-Away Proteomic Workflow vs. Status Quo

a

IsoPlexis High-Plex Automated Immunoassay Workflow

One pipette action per sample

All ELISA procedures performed automatically

Software delivers quantified results

Walk-away Workflow
Same day Insights

b

Status Quo Multiplexed Proteomics

Additional 3+ hours for data analysis

Capture antibody binding

Adding sample

Washing microplate

Adding detection antibody

Washing microplate

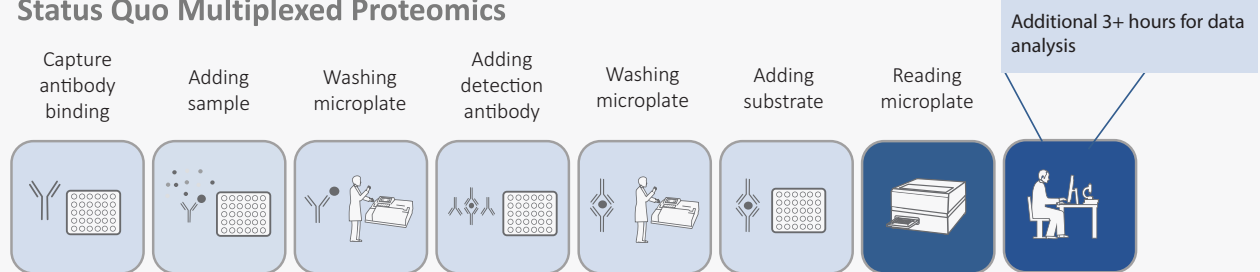Adding substrate

Reading microplate

Figure 5 | Workflow Comparison. a) IsoPlexis' walk-away automation saves time by performing all assay procedures and data analysis. b) Traditional workflows are laborious with many hands on steps and lengthy data analysis procedures.

to explore differences with push-button visualizations. IsoSpeak's graphical user interface enables a more intuitive and faster understanding of functional proteomic data so that any user can focus on the core biology driving their therapeutic, rather than focusing on underlying code, validating software, or putting together spreadsheets. Compared to status quo technologies, IsoSpeak saves a user over three hours of data analysis and figure generation time (Figure 4a). The analysis and visualization of data generated via a status quo multiplexed ELISA workflow often requires multiple steps such as manual export and data aggregation, and may require specialized training (Figure 4b). IsoSpeak software is fully quantitative, enabling the generation of publication-ready figures with one click, saving upwards of three hours of valuable time (Figure 4c).

IsoSpeak creates advanced visualizations and figures that can be exported and shared to enable collaboration, analytics, and conclusions directly – communicating knowledge across your organization in a visual manner. Decisions can be made in an expedient fashion to match the accelerated timelines necessary for the development of breakthrough medicines.

With CodePlex, you can add your sample and walk away, achieving fully analyzed data saving hours of manual workflow steps (Figure 5a). Traditional multiplexed bulk ELISA platforms require multiple instruments and multiple personnel, in addition to long wait times for data analysis (Figure 5b).