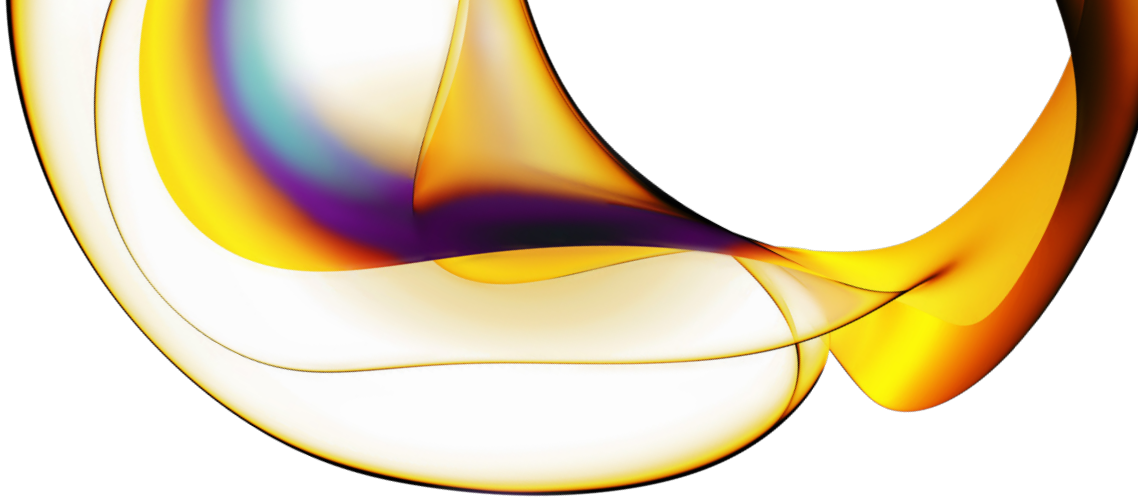


revvity

Complement your screening with scalable transcriptomics.

The challenge:

Phenotypic screens show what happened, but not always why.

MoA blind spot

Phenotypic readouts rank hits by severity but often provide limited insight into mechanism

Hit prioritization cap

Without transcriptional context, morphological hits advance with similar confidence, increasing risk of pursuing off-target or low-value compounds.

Off-target risk undetected

Imaging and viability may not capture pathway-level off-target activity. Gene-expression signatures reveal unintended biology before *in vivo* studies.

The solution:

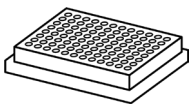
Alithea´s MERCURIUS™ DRUG-seq & Total DRUG-seq
Built for scale.

Revvity is an authorized distributor of:

ALITHEA GENOMICS

Extraction-free

Direct from cells. Eliminates the need for RNA isolation.



Early multiplexing

Sample barcoding enables pooling of up to 1,000+ conditions in a single tube.

Genome-wide coverage

Gene-expression signatures across the genome.

Ultra low-cost

Significantly cheaper than conventional alternatives.

Two use cases in screening workflows

Compound screening

- **MoA assignment:** cluster compounds by transcriptional signature to support MoA inference
- **Hit prioritization:** rank hits by pathway activity alongside phenotypic severity
- **Off-target insight:** flag potential unintended pathway activity before *in vivo* studies

Morphology + transcriptomics = higher-confidence MoA, smarter hit triage.

CRISPR & siRNA screens

- 384-well arrayed CRISPR/siRNA screens with transcriptional readout.
- On-target confirmation: assess expected pathway-level transcriptional responses
- Off-target identification: detect potential unintended pathway activation or silencing
- Pair with imaging for dual phenotypic plus transcriptional annotation of every perturbation

From genetic perturbation to pathway hypothesis in a single workflow

Selection guide

Available in 96-, 384-, and 1,536-well formats to match screening workflows.

	DRUG-seq	Total DRUG-seq
Data output	Gene-level expression signatures	Full transcriptome resolution
RNA captured	Poly(A) RNA (mRNA only)	Total RNA (mRNA + non-coding)
Transcript coverage	3′ gene-level counting	Full-length transcript coverage
Reads/sample	~1–2M	~2–5M

- **DRUG-seq** enables high-throughput profiling with efficient gene-expression signatures for large-scale screens.
- **Total DRUG-seq** extends this approach to full transcriptome resolution, capturing isoforms and non-coding RNA for deeper biological insight.

Did you know?

Revvity provides an end-to-end screening workflow of instruments and reagents to support MoA analysis, hit prioritization, and off-target assessment.

See beyond the phenotype

Contact your Revvity representative to integrate DRUG-seq into your screening workflow.

Learn more

www.revvity.com

For research use only. Not for use in diagnostic procedures.

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