

# Introducing REM-I

A benchtop single-cell imaging and sorting instrument for high-dimensional morphology analysis

## Highlights

- Obtain high-dimensional single-cell morphology analysis with the REM-I instrument
- A fast workflow to go from sample to publishable figure in a few hours
- Part of the REM-I platform, which also includes Deepcell's Human Foundation Model (HFM) and Axon data suite

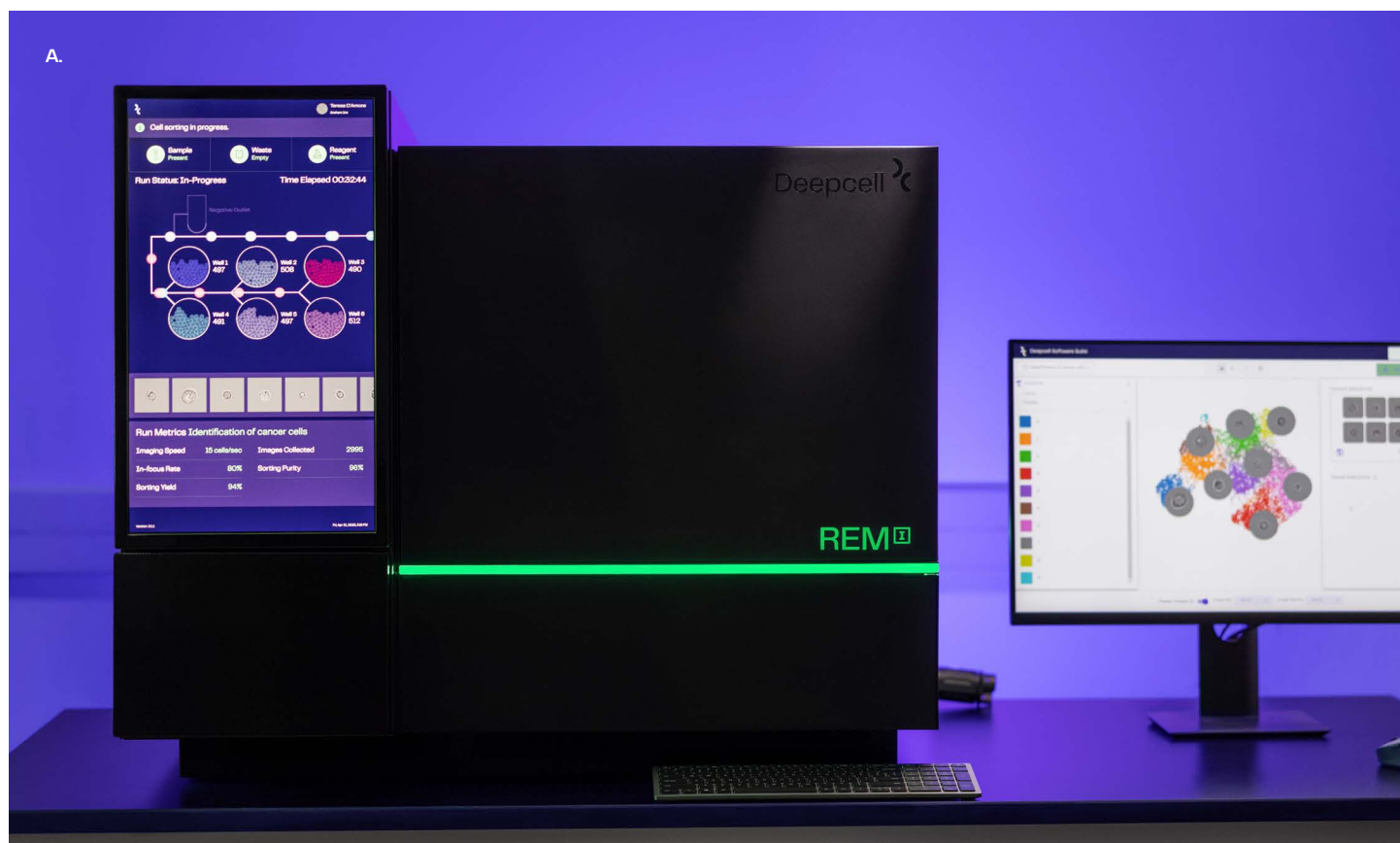
Cell morphology can be highly indicative of a cell's phenotype and function, but it is also highly dynamic and complex, and analyzing morphology by eye can only tell us so much.

A more quantitative, high-dimensional, unbiased approach to assessing cell morphology would magnify the insights into a cell's phenotype and function. Methodologies to assess and characterize cell morphology have been limited to either imaging or sorting with labels—until now.

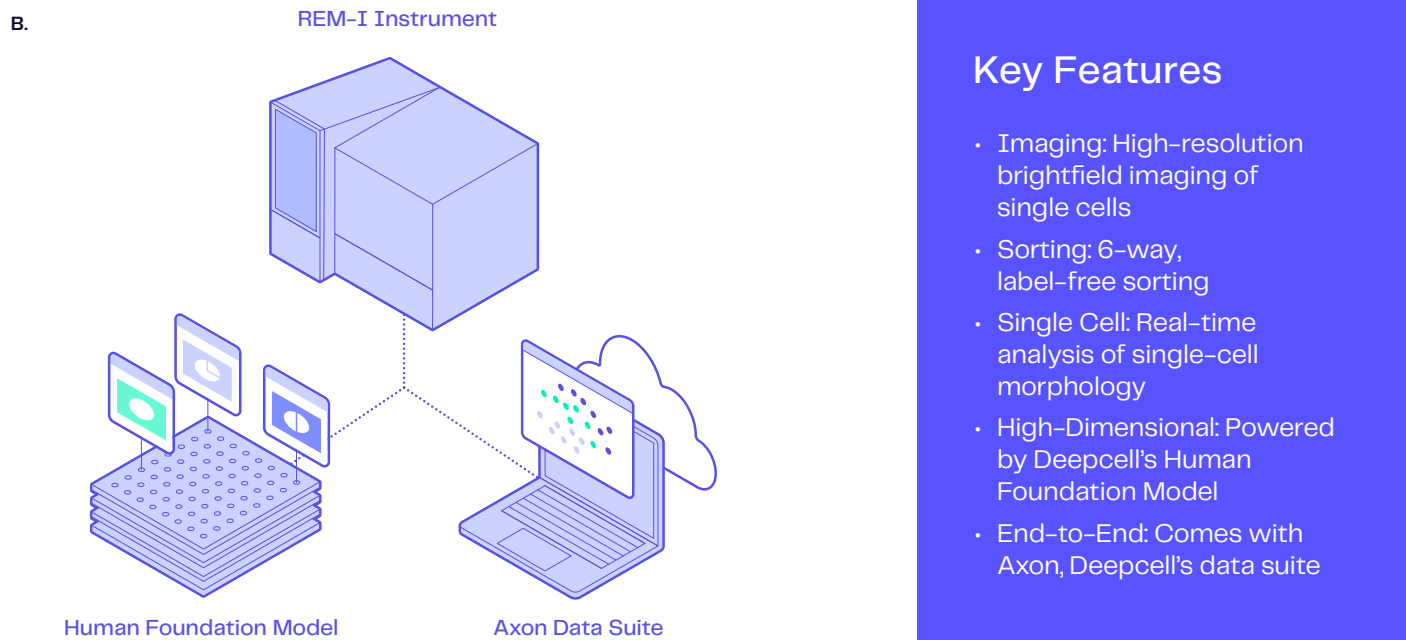
Deepcell's REM-I instrument takes the best of these worlds and builds upon them to provide imaging of single cells and label-free sorting in one platform (Figure 1A). REM-I directly takes real, high-resolution brightfield images of each individual cell. REM-I also has the ability to sort cells 6 ways based on their morphology without the need for any labels. Furthermore, you can collect these viable, minimally perturbed cells for downstream analysis such as single-cell RNA sequencing (scRNAseq).

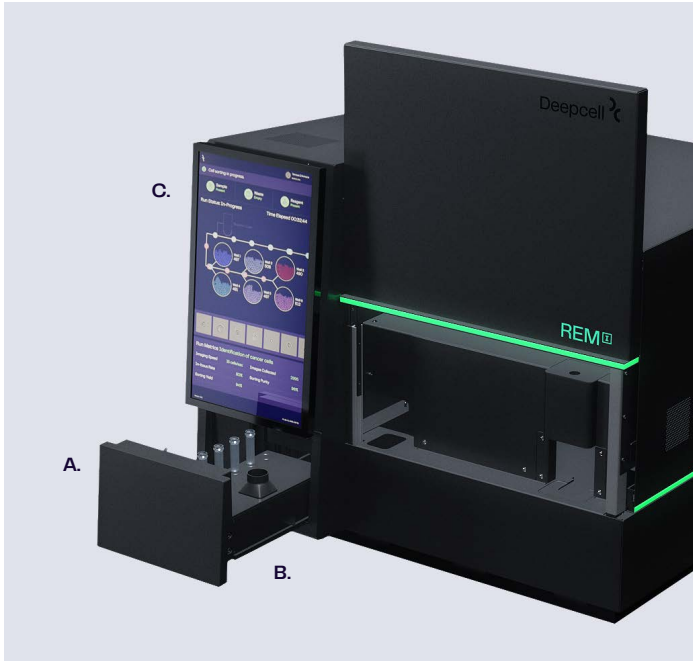
The REM-I instrument is part of the REM-I platform, which also consists of Deepcell's Human Foundation Model (HFM) for high-dimensional morphological feature analysis and Axon data suite, where you can store, visualize, and analyze images and high-dimensional data (Figure 1B).





**Figure 1.** The REM-I platform. (A) The REM-I instrument is a benchtop microfluidics instrument that captures high-resolution brightfield images of single cells and can sort cells 6 ways in a label-free manner. (B) The REM-I instrument is part of a fully integrated platform, compatible with Deepcell's Human Foundation Model (HFM) and Axon data suite.





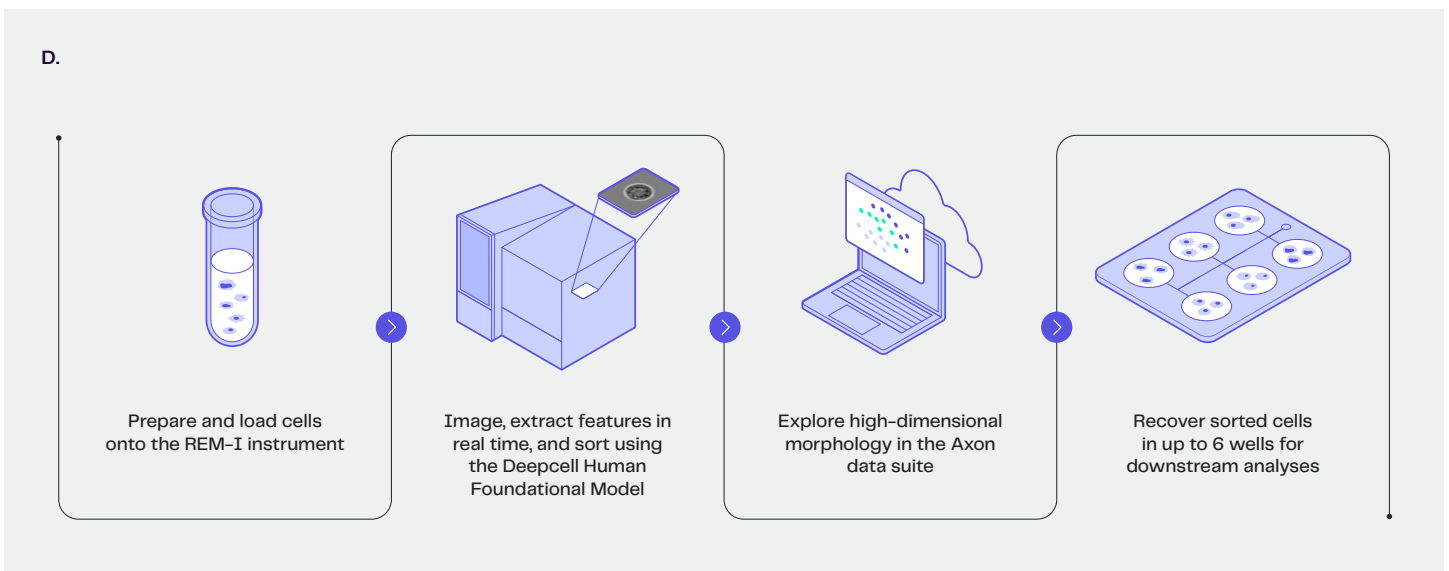
**Figure 2.** How the REM-I instrument works. The REM-I instrument uses a set of reagents and chips provided by Deepcell. Reagents are placed in the reagent drawer (A) and chips are loaded onto the stage. (B) The REM-I instrument is controlled by the REM-I controller software while the REM-I on-instrument display (C) shows real-time run status. (D) The workflow is simple and streamlined, starting with dissociation of cells into a single-cell suspension, followed by loading of the suspension onto the instrument. The cells are imaged and characterized in real-time with the Deepcell HFM as they flow through the microfluidic chip. Axon, Deepcell's data suite, pairs with the REM-I instrument for in-depth data analysis, including the ability to select cell populations of interest to sort on the REM-I instrument. Sorted cells can be used for further downstream analyses such as scRNAseq.

## How it works

The REM-I instrument uses high-throughput imaging to characterize, classify, and sort cells based on morphological analyses (Figure 2).

The benchtop instrument uses a microfluidic chip, which allows for the input and flow of cells in suspension. The high-speed system collects brightfield images of cells (up to 1,000 events per second) as they flow through a microfluidic chip. High-resolution images capture subcellular and subnuclear features of the cells in high contrast. The HFM classifies cells, allowing them to be sorted in up to 6 collection wells. A laser-based system tracks cells in real-time to assist with imaging and sorting, and to report on the purity and yield of the run.

The REM-I workflow is simple and streamlined, starting with preparation of a single-cell suspension, followed by loading of the cells onto the instrument. The cells are imaged and features are extracted in real-time and sorted using the HFM. Axon, Deepcell's data suite, pairs with the REM-I instrument for in-depth data analysis, including the ability to select cell populations of interest to sort on the REM-I instrument. Sorted cells can be recovered in up to 6 wells and used for further downstream analyses such as scRNAseq.



## Key research areas

- Cancer Research
- Developmental Biology
- Cell & Gene Therapy
- Drug & Functional Screening

## Applications

- Discovery
  - Morphology as a novel biomarker
  - Drug and CRISPR perturbation screening
- Sample-Level Profiling
  - Heterogeneous sample evaluation and characterization
  - Disease detection and enrichment
  - Sample clean up
- Cell-Level Phenotyping
  - Cell health status
  - Cell state characterization
  - Multi-omic integration

**Table 1.** REM-I Instrument Key Parameters and Specifications  
*\*Denotes specification is dependent on sample characteristics and/or sorting configurations*

Category	Parameter	Specification
Facilities	Instrument dimensions	H: 29.5 in / 75 cm W: 35.5 in / 90 cm D: 29.5 in / 75 cm
	Included ancillary equipment	Computer tower Monitor Keyboard Mouse
	Electrical	3x 100–240 V surge-protected outlets
	Network connection	1 Gbps ethernet with >150 Mbps upload bandwidth
	Clean dry air connection	0.55–0.72 MPa / 80–105 psi
	Temperature operation ranges	59–86 °F / 15–30 °C
	Operating relative humidity (%)	15–70, non-condensing
Instrument	Input cell size (µm)	6 – 25
	Output cell viability (% of input viability)	≥95*
	Output collection	6x positive outlet wells 1x negative outlet tube 1x waste bottle

Table 1. (Continued from previous page)

Instrument	Positive outlet capacity (cells/well)	Up to 3,000
	Recommended run time (min)	Live cells: Up to 180
		Fixed cells: Up to 600
	Image resolution (pixels/μm)	6.3
	Image size (pixels)	256 x 256
	Imaging throughput (events/s)	Up to 1,000
	Sorting throughput (cells/s)	Up to 30

Table 2. REM-I Platform Components

Name	Description
REM-I Instrument	Microfluidic instrument
REM-I Imaging Kit	Reagents and consumables for imaging workflow
REM-I Sorting Kit	Reagents and consumables for imaging plus sorting workflow
Human Foundation Model (HFM)	Deepcell's AI model for high-dimensional single-cell morphology analysis
Axon data suite	Deepcell's data suite for visualizing, analyzing, and storing data



## References

1. Salek M. et al. Realtime morphological characterization and sorting of unlabeled viable cells using deep learning. bioRxiv, 2022. DOI: 10.1101/2022.02.28.482368.
2. Mavropoulos A. et al. Artificial intelligence-driven morphology-based enrichment of malignant cells from body fluid. Mod Pathol, 2023. DOI: 10.1016/j.modpat.2023.100195.
3. Masaeli M. et al. Multiparameter mechanical and morphometric screening of cells, Scientific Reports, 2016. DOI: 10.1038/srep37863.
4. Bagheri N. et al. The new era of quantitative cell imaging—challenges and opportunities. Mol. Cell, 2022. DOI: 10.1016/j.molcel.2021.12.024.
5. Way G. P. et al. Predicting cell health phenotypes using image-based morphology profiling. Mol. Biol. Cell, 2021. DOI: 10.1091/mbc.E20-12-0784.
6. Walter T. et al. Visualization of image data from cells to organisms. Nat. Methods, 2010. DOI: 10.1038/nmeth.1431.

## Resources

- [REM-I Platform Brochure](#)
- [Human Foundation Model Panel Sheet](#)
- [Public Datasets and Axon Demo](#)
- [Oncology Application Note](#)
- [Other Resources](#)

## Contact us

INFO@DEEPCELLBIO.COM • DEEPCELL.COM