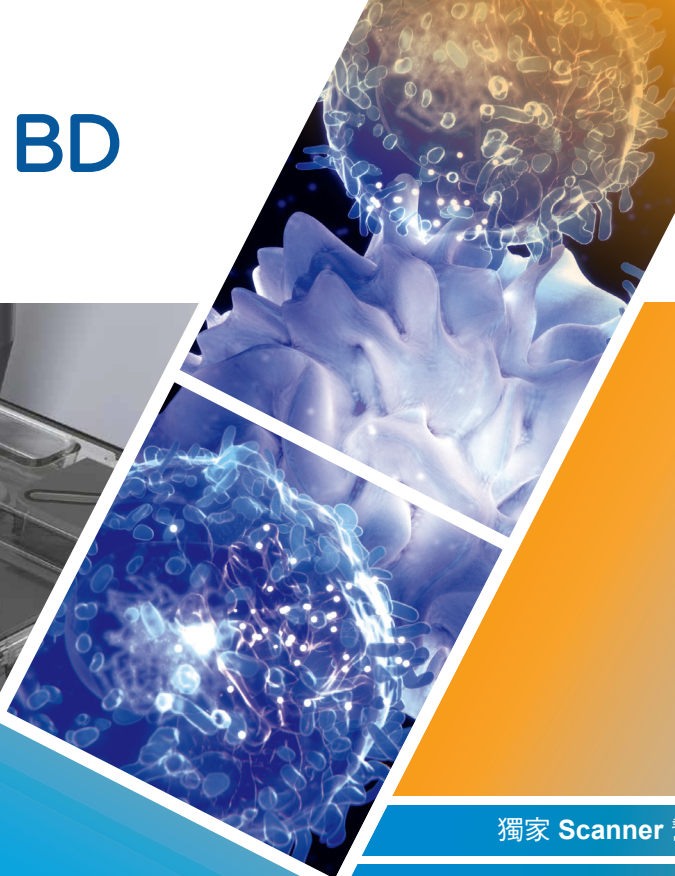
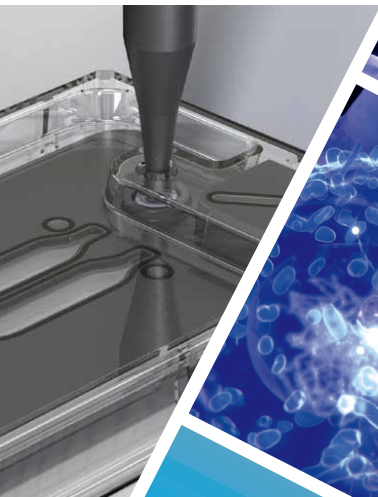




BD Rhapsody™

Single-Cell Analysis System

單細胞基因表現分析系統



獨家 **Scanner** 幫助流程 QC，視覺化確認細胞與磁珠回收數量

支援 **Whole Transcriptome Analysis**，**Targeted Genes** 與 **VDJ** 實驗

Seven Bridges Genomics 雲端及 **SeqGeq** 視覺化分析軟體配套



騰達行

☎ 0800-211-819

BD Rhapsody™ System workflow

BD Rhapsody
cell capture
Beads

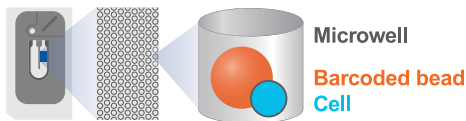
Univ CL UMI Poly-dT

88 萬組獨特 CL 標記單細胞

6 萬組 UMI 真實計算基因表現

20 萬個 micro-wells 與磁珠補獲細胞，
可執行 100-10,000 顆單細胞實驗

1 Load Cells and Beads



Pair ONE cell with ONE barcoded bead in microwell

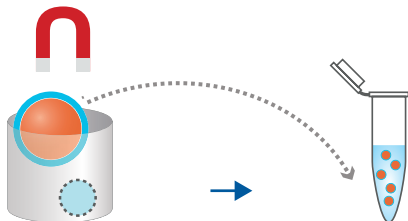
2 Lyse Cells



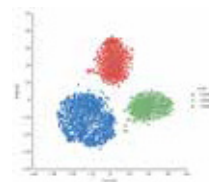
Lyse cell to hybridize mRNA onto barcoded capture oligos on bead

3 Retrieve Beads

4 Synthesize cDNA



5 Analyze Data



Library preparation, sequencing and data analysis

BD Rhapsody Scanner

偵測上機前細胞濃度與存活率
同時提供實驗流程中各步驟效率



Sample QC

- Cell count
- Cell viability

QC Report

- Cell/Bead loading efficiency
- Cell retention rate
- Bead retrieval efficiency
- Number of retrieved beads with viable cells

Jurkat

Date	Sample	Step	Analysis Status
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2018-08-02	Jurkat	Sida A	✓ Completed
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Analysis

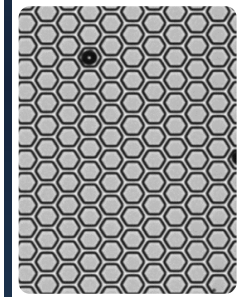
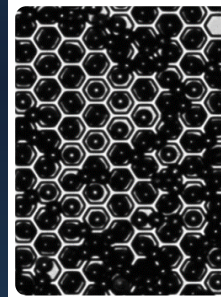
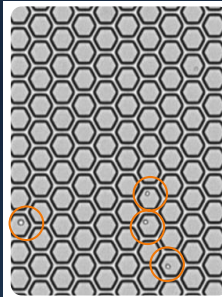
Total cell concentration (live and dead) (cells/ μ l)	165
Cell viability (%)	88.18

Jurkat	38.1 μ l
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Buffer volume	589.1 μ l
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Loading cell concentration	19.9 μ l
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Estimated cell double rate	2.4%
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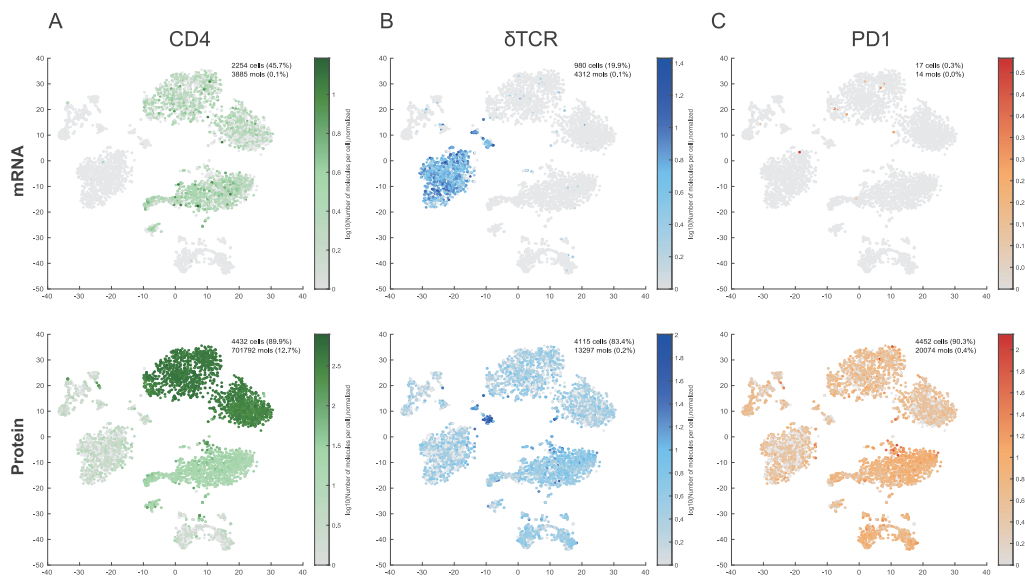


BD AbSeq™

同時分析單細胞基因與表面蛋白

- 獨特 **DNA barcode** 序列結合抗體
- 不需考慮螢光補償

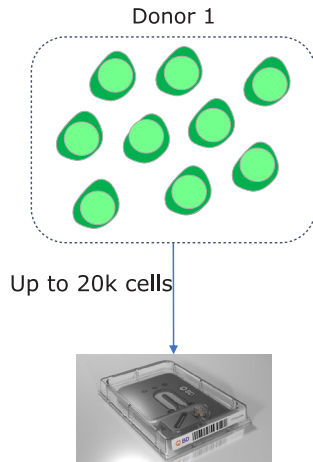
- 更簡單的抗體 **panel** 設計
- 支援複雜的多隻抗體實驗 (**1-40 plex**)



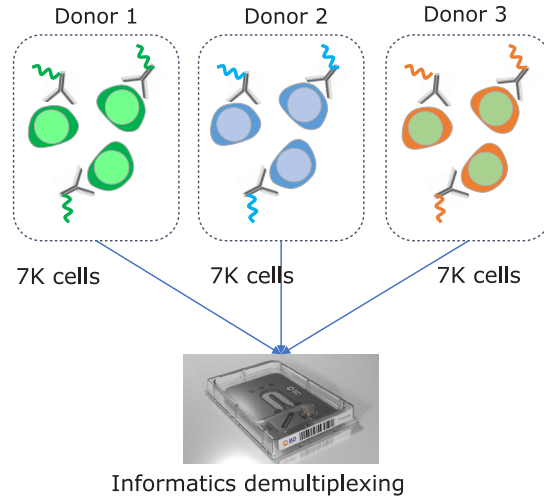
Detection of protein targets associated with low mRNA expression.

BD Sample Multiplexing kit™ (SMK)

BD Rhapsody



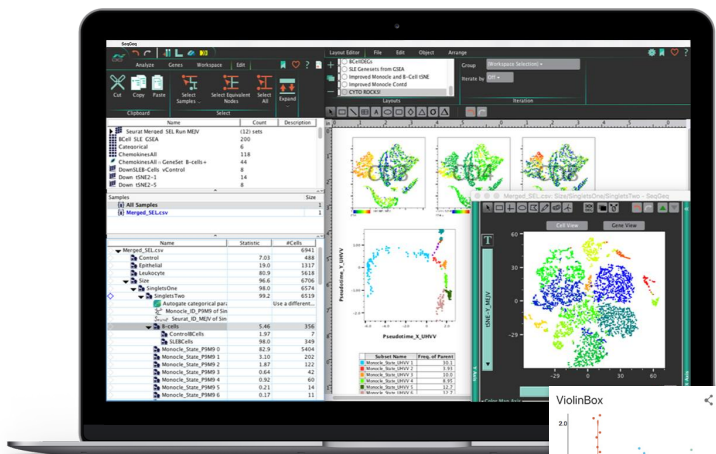
BD Rhapsody with sample multiplexing



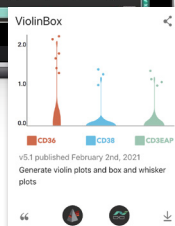
提供混樣上機，增加實驗彈性
降低試劑成本減少 technical errors 產生

633781 Human Single Cell Sample Multiplexing Kit (12 samples)
633793 Mouse Immune Single-Cell Multiplexing Kit (12 samples)

SeqGeq™ is a desktop bioinformatics platform that makes complex scRNA-seq analysis accessible with an intuitive interface.



These tools allow for the direct use of third party algorithms in the form of R scripts, or for very quick implementation of features once a requirement has been identified.



Quality Control

Dimensionality Reduction

Clustering

Differential Gene Expression

Gene Set Enrichment

FlowJo Exchange Plugins