

Interactive V(D)J analysis

User-friendly data analysis tools from Partek™ Flow™ software enable deeper insights into the immune repertoire

V(D)J sequencing is a powerful approach to assess the diversity and frequency of T- and B-cell receptor clonotypes. Combining single-cell RNA-Seq with immune repertoire profiling provides a high-resolution view of variation, expansion, and diversity within the adaptive immune system. Partek Flow software offers a user-friendly bioinformatics solution to analyze and visualize spatial transcriptomics data, empowering researchers of all skill levels to maximize insights from multiomic studies.



Point-and-click analysis
Analyze data easily with an intuitive, context-sensitive interface



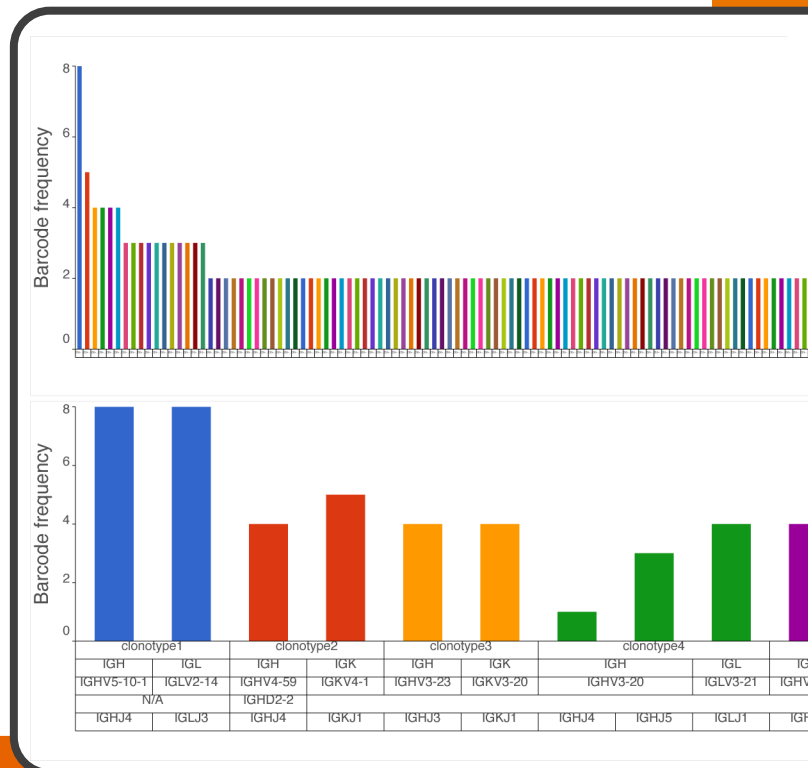
Advanced visualization tools
Create informative, publication-ready visualizations with just a few clicks



Powerful statistics
Access industry-standard statistical algorithms for results you can trust



Customizable workflows
Build custom analysis pipelines visually and share with collaborators



Powerful analysis and visualization tools

Whether you are studying immune cell development, mapping the immune repertoire in response to infection or vaccination, or identifying T- or B-cell clonal evolution in cancers, Partek Flow software has the tools to help you analyze and visualize your V(D)J sequencing data easily.

Many ways to explore data

Transform V(D)J sequencing data into interactive figures and maximize biological insights from your immune repertoire studies. The data viewer in Partek Flow software makes visualizing immune cell types and differential expression fast and easy.

What can you do with Partek Flow software?

- Detect V(D)J variation using V(D)J contig annotation files (CSV)
- Determine T- and B-cell receptor chains that make up clonotypes in samples
- Quantify clonal diversity and use histograms to visualize frequency
- Compare the immune repertoire between samples
- Visualize clonotypes and gene expression data together in interactive plots

Learn more

Partek Flow software

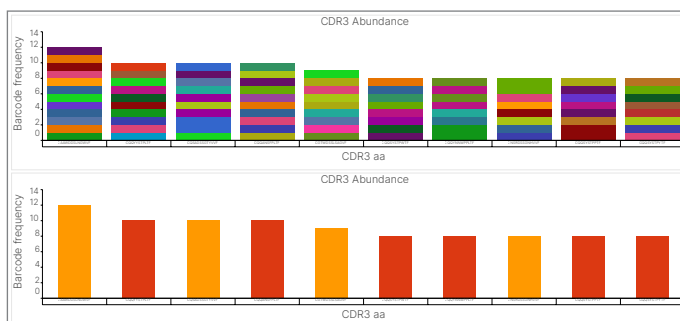
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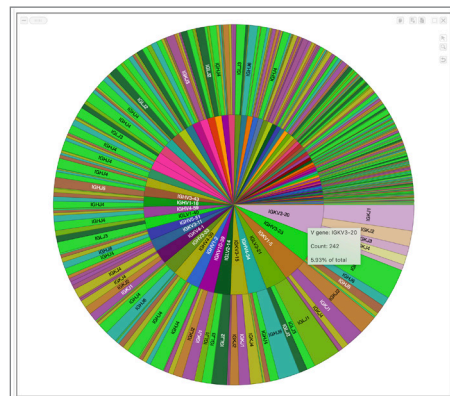
1.800.809.4566 toll-free (US) | +1.858.202.4566 tel
techsupport@illumina.com | www.illumina.com

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Predict CDR3 amino acid sequence by barcode frequency and color by the (top) clonotype ID or (bottom) chain. Visualize the predicted CDR3 nucleotide sequence (cdr3_nt) or information for other complementarity-determining regions.



Split V genes and J genes by chain and filter to only the heavy chain (IGH) or sort content to quickly determine abundance using interactive pie charts. Hover over the chart to see content, count, and percent of total.

Abbreviations: CDR3, complementarity-determining region 3; IGH, immunoglobulin heavy chain; RNA-Seq, RNA sequencing; V(D)J, variable, diversity, and joining gene segments; UMAP, uniform manifold approximation and projection for dimension reduction

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