DATA SHEET

Partek™ Flow™ software

User-friendly bioinformatics platform for analyzing multiomics data

- Analyze multiomic data sets easily with an intuitive user interface
- Attain results that you can trust with robust algorithms for data analysis
- Simplify biological interpretation with interactive and customizable visualizations

illumina®

Accelerate insights from multiomics data

Scientists are increasingly adopting multiomic approaches to fuel discovery across multiple levels of biology and better connect genotype to phenotype. By combining genomic data with data from other modalities measuring gene expression, gene regulation, and protein levels, multiomics provides a more holistic view of cellular function and enables deeper biological insights. However, analyzing the large volumes of data generated in multiomic studies typically requires advanced bioinformatics expertise. Additionally, integrating results and visualizing data from multiple assays presents a significant bottleneck for labs.

To help address these challenges, Illumina offers Partek Flow software, a user-friendly bioinformatics platform for analyzing and visualizing single cell, gene expression, chromatin immunoprecipitation sequencing (ChIP-Seq), spatial transcriptomics, and other data used for multiomics research. This intuitive genomic analysis software empowers researchers of all skill levels to maximize insights from data with an easy-to-use interface, robust statistical algorithms, information-rich visualizations, and cutting-edge genomic tools for data analysis.

Integrated solution

Illumina offers a comprehensive suite of genomic tools to enable multiomic analyses with workflows built to support emerging trends and advances in multiomics research. Partek Flow software is compatible with data generated using Illumina NGS workflows (Figure 1) and enables high-resolution multiomic insights. The software accommodates input files from DRAGEN™ secondary analysis or any third-party platform for maximum flexibility.

User-friendly interface

Partek Flow software features an intuitive graphical user interface ideal for individuals with limited bioinformatics experience (Figure 2). Simple point-and-click actions and context-sensitive menus present relevant options that simplify the process of building pipelines. Easy-to-understand dialogs explain the steps in analysis and visualization as they arise, empowering users to perform data analysis with confidence and ease. Additionally, for core laboratories and users with bioinformatics expertise, Partek Flow software provides access to advanced tools, customizable pipelines, and user controls.

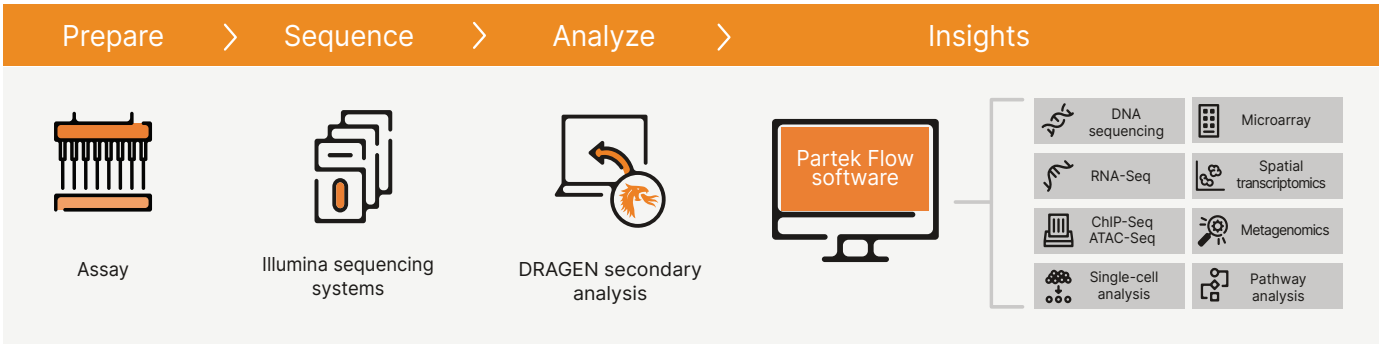


Figure 1: Partek Flow software integrates with Illumina NGS workflows—Partek Flow software accommodates data files generated with DRAGEN secondary analysis and other commercially available platforms for multiomic data analysis, visualization, and biological interpretation.

Figure 2: Partek Flow software user interface—The graphical interface allows users to perform analyses with simple point-and-click gestures. Partek Flow software can be installed on a server, cluster, and cloud and accessed from any browser on your preferred device.

With Partek Flow software, researchers can produce publication-ready visualizations, share customized analysis pipelines with collaborators, aggregate multiomic and phenotypic data, augment cohorts to include curated public data sets for well-powered studies, and perform statistical analyses, all on a single platform.

Powerful multiomic analysis tools

Integrating findings from complementary modalities, including genomics, transcriptomics, epigenomics, and proteomics, into multiomic data sets provides a more comprehensive picture of cellular function and helps extract more high-quality information from every sample. Partek Flow software offers comprehensive support for multiomics applications and is compatible with a broad range of inputs (Table 1). The software includes analysis tools built using publicly available, industry-standard statistical algorithms so researchers can be confident in their results (Table 2).

At each step in the process, from raw data to variant calls, Partek Flow software provides comprehensive QA/QC reports to check data quality and tools for removing low-quality data.

The software enables simultaneous high-resolution profiling of the genome, transcriptome, epigenome, and proteome. Users can explore multiomic data in the following ways:

- Assess relationships between different omics layers (Figure 3)
- Separate and combine various modalities to uncover hidden relationships (Figure 4)
- Retain relevant information for each omics layer then merge matrices to explore both individual and combined data (Figure 5)

Analysis and visualization tools included in Partek Flow software support a range of applications, including DNA sequencing, RNA-Seq, ChIP-Seq/ATAC-Seq, and more (Table 3). Add-ons for single-cell and spatial analysis and pathway analysis can be purchased as needed.

Table 1: Supported input file formats

Application	Input file format[a]
DNA sequencing	BAM, BCF, BCL, CBCL, FASTA, FASTA.GZ, FASTQ, FASTQ.GZ, SAM, SRA, VCF, VCF.GZ
RNA-Seq	BAM, BCL, CBCL, count matrix (CSV, TSV, TXT), FASTA, FASTA.GZ, FASTQ, FASTQ.GZ, SAM, SRA.
Single-cell analysis	Count matrix (CSV, TSV, TXT), H5, H5AD, sparse matrix (MTX), Seurat objects (RDS, QS), BED
Spatial analysis	10x Space Ranger, NanoString CosMx
ChIP-Seq/ATAC-Seq	BAM, CBCL, count matrix (CSV, TSV, TXT), FASTA, FASTA.GZ, FASTQ, FASTQ.GZ, SAM, SRA
Metagenomics	CBCL, FASTA, FASTA.GZ, FASTQ, FASTQ.GZ, SRA
Microarray analysis	CEL, intensity matrix (CSV, TSV, TXT)
Proteomics	Olink (TXT), SomaLogic (ADAT), Akoya (CSV, TXT)

a. List is not exhaustive.

Table 2: Statistical analyses included in Partek Flow software

Application	Statistical analysis
Normalization and scaling	RPKM, TMM, scTransform, Scran deconvolution, TF-IDF normalization, and more
Dimensionality reduction	PCA, t-SNE, UMAP, SVD
Batch effect removal	General linear model, Harmony, Seurat3 integration
Clustering	K-means, graph-based and hierarchical clustering analysis
Differential analysis	DESeq2, GSA, Hurdle model, LIMMA-trend, LIMMA-voom, negative binomial regression, Poisson regression, one-way ANOVA, nonparametric ANOVA (Kruskal-Wallis and Dunn tests), Welch's ANOVA, multifactor ANOVA, and alt-splicing ANOVA
Others	Survival analysis (Kaplan-Meier and Cox regression), correlation analysis, biomarker computation, descriptive statistics

Alt-splicing, alternative splicing; ANOVA, analysis of variance; GSA, gene-specific analysis; LIMMA, linear models for microarray data; PCA, principal component analysis; RPKM, reads per kilobase per million mapped reads; SVD, singular value decomposition; TF-IDF, term frequency-inverse document frequency; TMM, trimmed mean of M-values; t-SNE, t-distributed stochastic neighbor embedding; UMAP, uniform manifold approximation and projection.

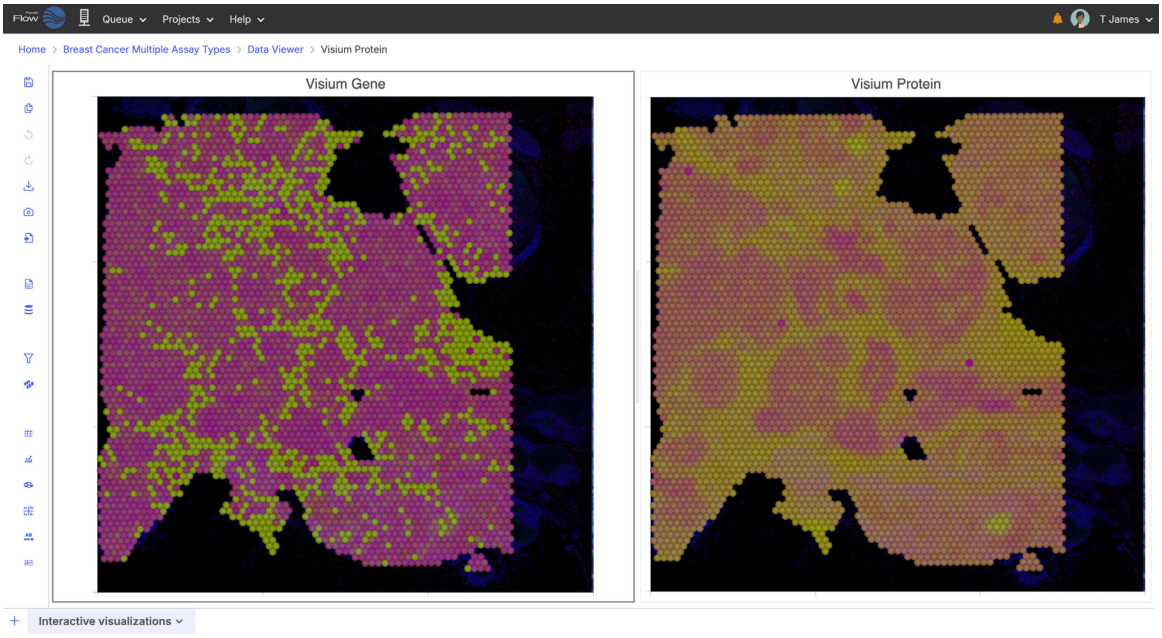
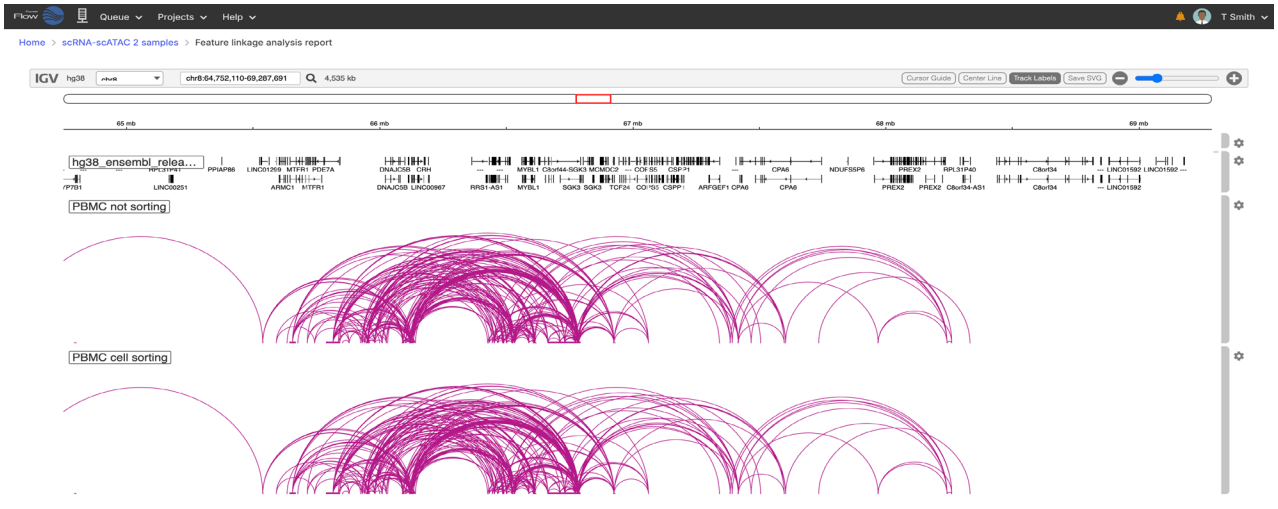


Figure 3: Combine feature expression data with histology for spatial transcriptomics—Sample output from the Partek Flow data viewer shows spatial transcriptomics data colored based on *BCL2* expression for (left) gene and (right) protein expression.



Sample name	Chromosome 1	Start 1	End 1	Chromosome 2	Start 2	End 2	Name	Score	Strand 1	Strand 2	Significance (-log10 pvalue)	Distance	Linkage type
PBMC not sorting	chr1	267,553	268,447	chr1	817,370	817,371	<AP006222.2_distal><FAM87B>	0.45	.	.	6.03	549,370	peak-gene
PBMC not sorting	chr1	1,032,751	1,033,633	chr1	1,137,016	1,137,017	<AGRN_distal><LINC01342>	0.44	.	.	6.33	103,824	peak-gene
PBMC not sorting	chr1	1,136,303	1,136,894	chr1	1,137,016	1,137,017	<LINC01342_promoter><LINC01342>	0.54	.	.	8.50	418	peak-gene

Figure 4: Explore multiomic layers of data simultaneously—Sample output from Partek Flow software showing feature linkage results for single-cell RNA-Seq and ATAC-Seq data sets to study gene expression and potential regulators together.

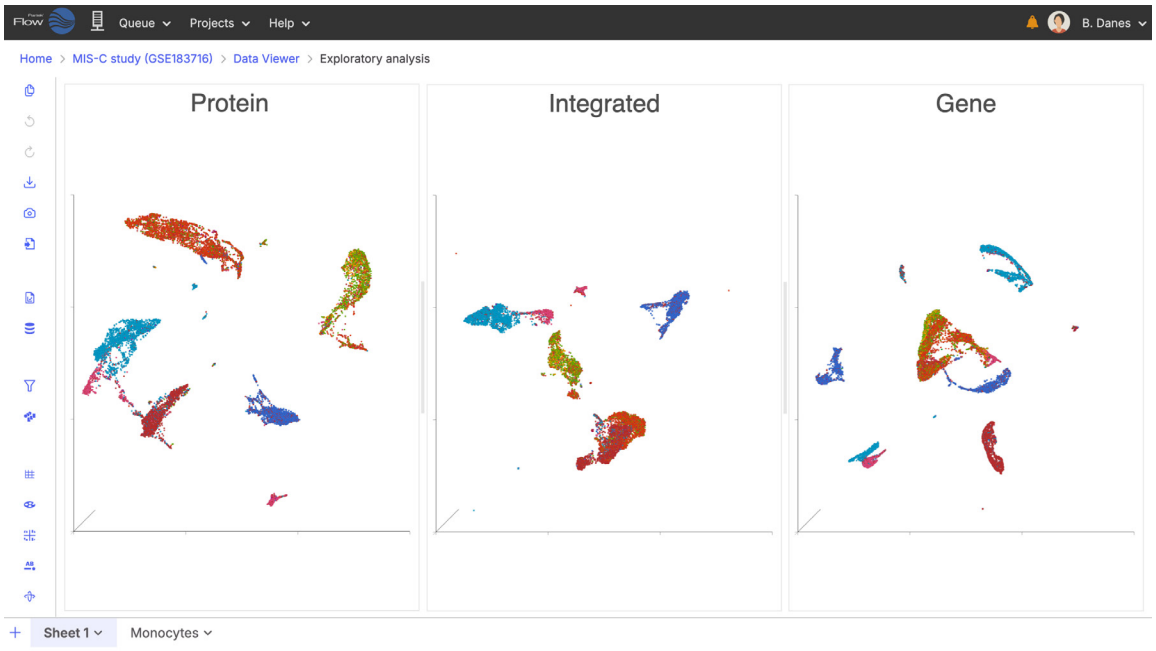


Figure 5: Gain a holistic view of cellular function with integrated RNA-Seq and CITE-Seq data—Sample output generated using uniform manifold approximation and projection (UMAP) for dimension reduction is used to profile both transcriptomic and proteomic data simultaneously, providing a dual view of cell states. CITE-Seq, cellular indexing of transcriptomes and epitopes by sequencing.

Table 3: Application support available in Partek Flow software

Application	Description
DNA sequencing	Call germline and somatic variants, detect SNPs, indels, and CNVs, annotate and classify variants, detect known and novel variants, and predict the impact of variants on biological function
RNA-Seq	Identify differentially expressed genes and alternative splicing and visualize isoform expression results with the integrated genome browser
ChIP-Seq/ATAC-Seq	Explore gene regulation and chromatin accessibility, integrate results of ChIP-Seq or ATAC-Seq with RNA-Seq data, and visualize aligned reads and detected peak regions with the chromosome view
Metagenomics	Access ultrafast metagenomic classification with Kraken2 and powerful statistical tools for accurate taxonomic identification of sequencing reads to uncover meaningful changes in microbial diversity
Microarray	Import microarray data, align to reference genome or quantify against transcriptome, analyze results with powerful multivariate statistical algorithms, compare results with NGS data sets, and visualize findings
Single-cell and Spatial analysis[a]	Classify single cells automatically, overlay gene expression data to visualize spatial relationships, analyze data to identify patterns in gene or protein expression, compare cell type populations between samples, analyze and visualize multiple samples together or independently, and explore clusters in their spatial context
Partek Pathway[a]	Calculate pathway enrichment, detect disrupted or influential pathways, search for specific pathways and genes, and color code genes based on p-values and fold changes to visualize gene relationships

a. Can be purchased separately as an add-on to Partek Flow software.

Flexible, scalable workflows

Partek Flow software offers the advanced tools, user administration controls, and flexible scaling abilities that core labs and enterprise organizations need to enhance operational efficiency. Labs can create custom analysis pipelines to standardize and automate the most frequently used tasks, then easily share workflows and data with collaborators without transferring data. Partek Flow software can be installed at a centralized location, allowing labs to manage user access, review audit trails, re-prioritize tasks when needed, and set up automated control through REST API in a secure environment. Additionally, Partek Flow software offers the enterprise tools for storing, managing, and collaboratively analyzing large genomic data sets. Whether using a cloud, cluster, or server deployment, Partek Flow software provides elastic computing resources and the flexibility to scale workflows to meet everchanging needs.

Summary

Partek Flow software is an easy-to-use bioinformatics platform that enables simplified analysis of next-generation sequencing and large-scale multiomics data in a visual user interface. The software supports multiple applications, including DNA sequencing, bulk RNA-Seq, ChIP-Seq/ ATAC-Seq, single-cell analysis, spatial transcriptomics, pathway analysis, microarray analysis, and metagenomics. Robust statistical algorithms, information-rich visualizations, an interactive interface, and cutting-edge genomic tools empower researchers to analyze their data confidently, without the need for advanced bioinformatics expertise. Partek Flow software offers flexible installation options and tools to accommodate individual users, core laboratories, and large enterprise organizations.

Learn more

Partek Flow software

Multiomics methods

Ordering information

For qualified inquiries, Illumina offers a free 14-day trial for Partek Flow software, allowing users to work with publically available data or upload their own data. Lab or enterprise editions are available. Contact an Illumina sales representative for more information.

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