FAST AND EASY ANALYSIS OF
Lexogen QuantSeq Data
USING PARTEK® FLOW® SOFTWARE

Find the biological meaning in your Lexogen QuantSeq 3' mRNA-Seq data using the Partek® Flow® QuantSeq analysis pipeline built by Lexogen and Partek scientists. Partek Flow guides you from data to discovery with an intuitive user interface, powerful statistics, and interactive visualizations; no bioinformatics experience needed. Designed for the way biologists think, Partek Flow is accessible without sacrificing flexibility.

QuantSeq Data Analysis with Partek Flow

- Partek Flow is an all-in-one solution that takes you from raw data to biological insights

- The Partek Flow QuantSeq pipeline automates QuantSeq data processing from FASTQ files to gene counts for fast and easy analysis

- Quickly analyze your gene count data in the easy-to-use point-and-click graphical interface

- Find new patterns in your data using t-SNE, PCA, and clustering tools enabled by powerful statistics and interactive visualizations

- Identify differentially expressed genes with award-winning Partek gene specific analysis algorithm

- Discover biological insights with GO and pathway enrichment

- Quickly and easily access your results - download your data at any step and save visualizations as publication-quality images

- Work from anywhere using a web browser on any connected device

- Cloud, cluster, and laptop deployment options

- Try it yourself with a free trial at www.partek.com

Partek®
turning data into discovery®

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QuantSeq Analysis with Partek Flow

Features

Seamless integration with Lexogen QuantSeq data	✓
Easy-to-use graphical interface	✓
Customizable and shareable pipelines	✓
Deployment on public/private cloud, cluster, or desktop	✓
Multi-core computing and scalable power	✓
Accessible through a web browser on any connected device	✓
Flexible user and group management options	✓
Strong data security	✓
Audit trail for every analysis	✓

QuantSeq Pipeline

Starts with unaligned reads in FASTQ format or quantified data	✓
Removes poly-A tails and sequencing adaptors	✓
Trims reads based on quality	✓
Aligns reads to any reference genome using the STAR aligner with Lexogen parameters	✓
Maps aligned reads to any public or custom transcriptome database	✓

Data Analysis and Visualization

QA/QC reports for each step of the QuantSeq pipeline	✓
Multiple options for data normalization	✓
t-SNE and Principal Components Analysis	✓
Differential expression analysis with gene specific analysis (GSA) and ANOVA	✓
Hierarchical and K-means clustering	✓
Interactive visualizations including dot plots, volcano plots, heat maps, scatter plots, Venn diagrams, and chromosome viewer	✓
Gene Ontology and pathway enrichment	✓
Download data at any step of analysis	✓
Save visualizations as publication-quality images	✓

LEXOGEN

Enabling complete transcriptome sequencing