




ROSALIND®

ACCELERATE YOUR RESEARCH

Exploring data analysis
on the ROSALIND discovery &
collaboration platform.

QUICK START GUIDE

Learn more at www.rosalind.bio



An Interactive Experience for **Analyzing** and **Collaborating** with your Genomic Datasets

Analyze More

Setup experiments across many species and explore interactive results the very same day for RNA, smallRNA, ChIP, nanoString and more

Better Quality Control

Obtain comprehensive Quality Control metrics and graphs with automatic contamination and outlier sample detection

Interpret More

Create comparisons between your samples and obtain deeper insights from over 20 different integrated knowledge bases for pathways, gene ontology, protein interactions and more

Discover More

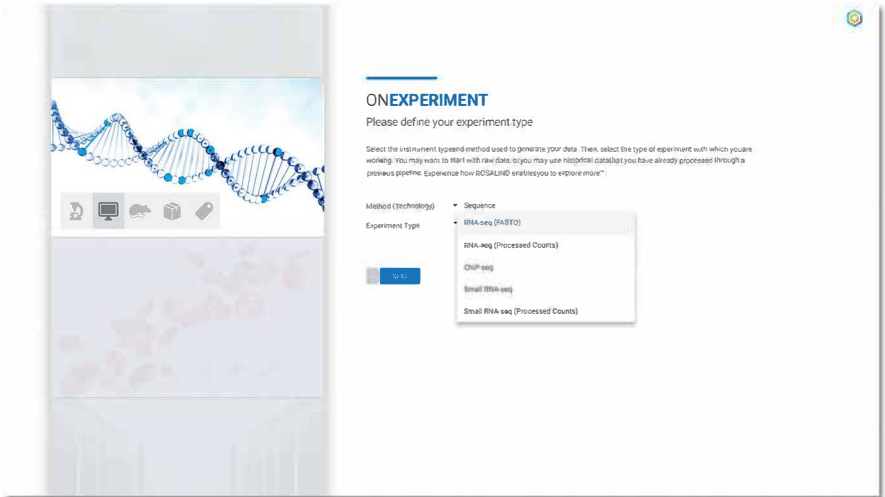
Utilize ROSALIND's artificial intelligence during a Meta-Analysis to identify hidden patterns and interpretations across experiments and comparisons

Collaborate Effortlessly

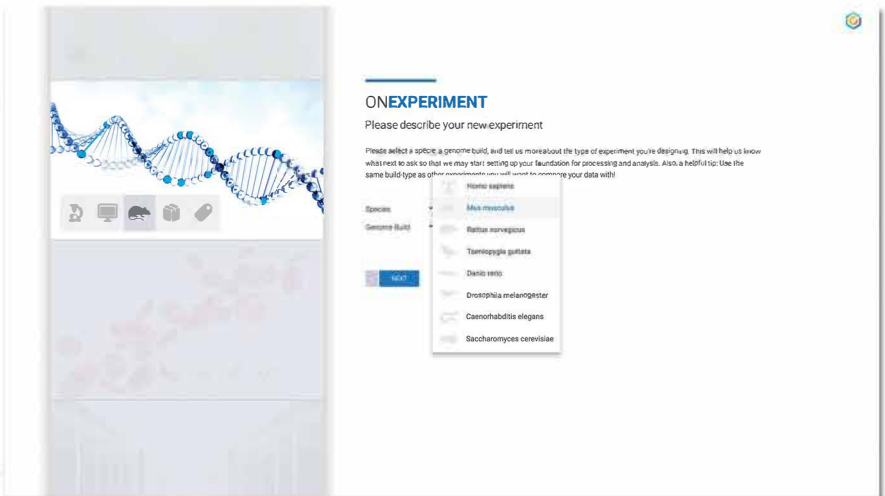
Join a collaboration space to have consistency around your data analyses, where any participant can add or interact with every shared experiment - all without ever transferring or downloading shared data

Analyze More

Setup your experiment in minutes.

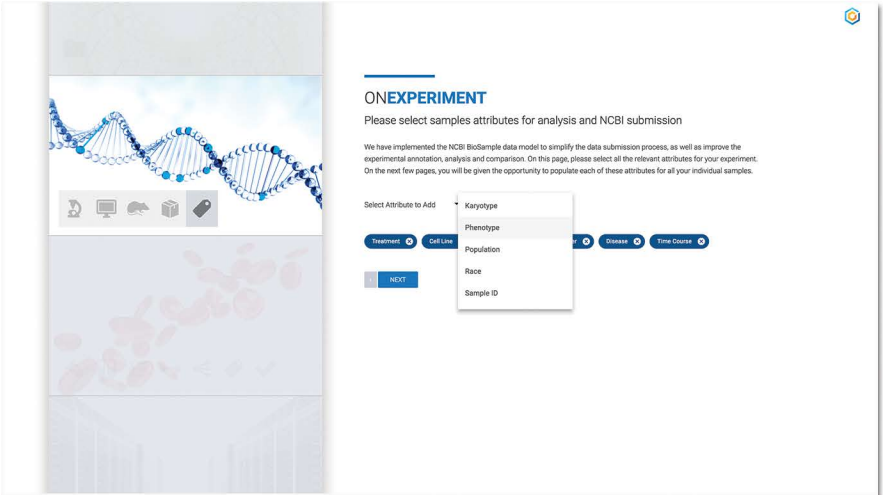


Beginning your experiment design is as easy as selecting a method and choosing an experiment type.



Many species are already included in **ROSALIND** and more can be added upon request.

Analyze More



ONEXPERIMENT

Please select samples attributes for analysis and NCBI submission

We have implemented the NCBI BioSample data model to simplify the data submission process, as well as improve the experimental annotation, analysis and comparison. On this page, please select all the relevant attributes for your experiment. On the next few pages, you will be given the opportunity to populate each of these attributes for all your individual samples.

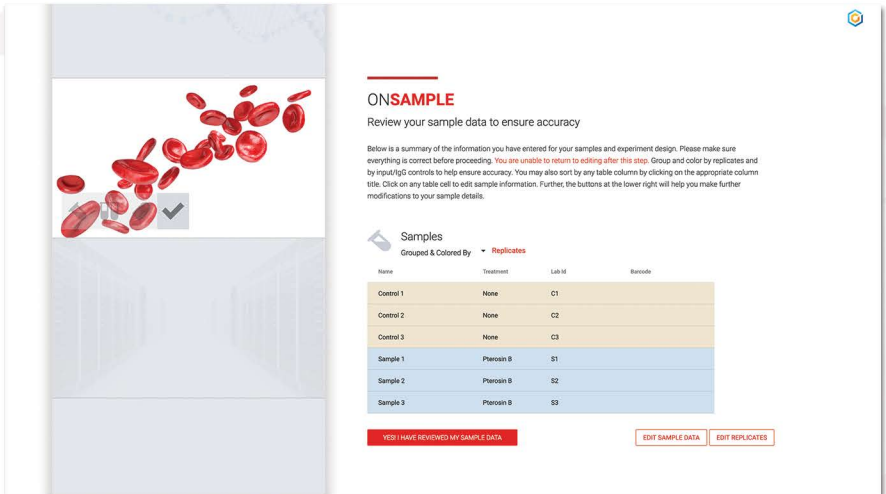
Select Attribute to Add

- Karyotype
- Phenotype
- Population
- Race
- Sample ID

Treatment Cell Line Disease Time Course

NEXT

ROSALIND uses the NCBI BioProject and BioSample data model for annotating samples and to simplify GEO/SRA submissions as well as the automatic importing of public data sets.



ONSAMPLE

Review your sample data to ensure accuracy

Below is a summary of the information you have entered for your samples and experiment design. Please make sure everything is correct before proceeding. You are unable to return to editing after this step. Group and color by replicates and by equal/1g1 controls to help ensure accuracy. You may also sort by any table column by clicking on the appropriate column title. Click on any table cell to edit sample information. Further, the buttons at the lower right will help you make further modifications to your sample details.

Samples
Grouped & Colored By: Replicates

Name	Treatment	Lab ID	Barcode
Control 1	None	C1	
Control 2	None	C2	
Control 3	None	C3	
Sample 1	Paclitaxel B	S1	
Sample 2	Paclitaxel B	S2	
Sample 3	Paclitaxel B	S3	

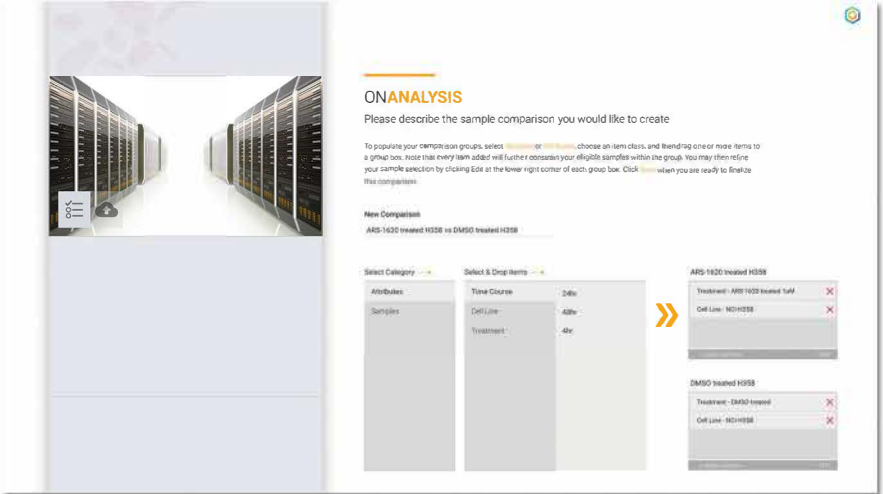
YES! I HAVE REVIEWED MY SAMPLE DATA

EDIT SAMPLE DATA

EDIT REPLICATES

ROSALIND provides a sample sheet with color-coded replicates for easy review of your experiment design before you upload your data.

Analyze More



ONANALYSIS

Please describe the sample comparison you would like to create

To populate your comparison groups, select **Attributes** or **Time Course**, choose an item class, and then drag one or more items to a group box. Note that every item added will further decrease your eligible samples within the group. You may refine your sample selection by clicking Edit at the lower right corner of each group box. Click **Done** when you are ready to finalize this comparison.

New Comparison
ARS-1630 treated H526 vs DAMSO treated H526

Select Category	Select & Drop Items	Table
Attributes		
Samples	Cell Line	AR16
	Treatment	4hr

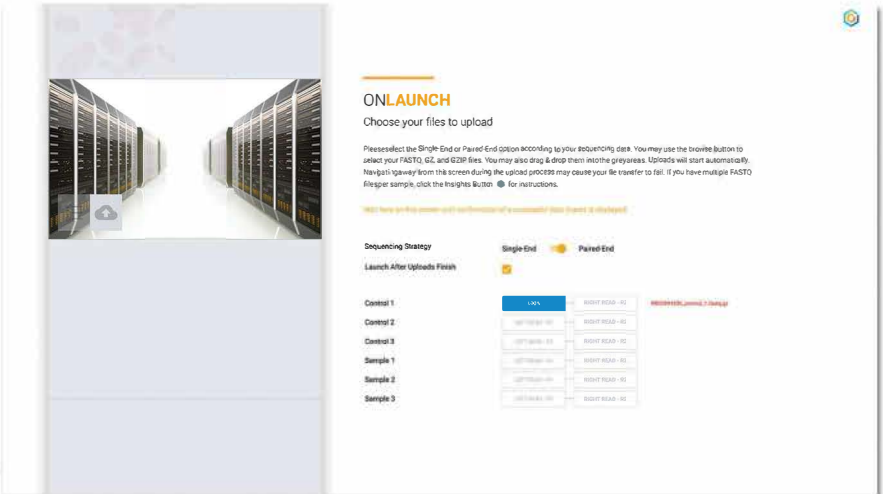
ARS-1630 treated H526

Treatment: ARS-1630 treated 4hr	X
Cell Line: AR16H526	X

DMSO treated H526


Treatment: DMSO treated	X
Cell Line: AR16H526	X

Comparisons may be setup during the initial experiment design or at any time after the experiment has completed processing.



ONLAUNCH

Choose your files to upload

Please select the Single-End or Paired-End option according to your sequencing data. You may use the **treeview** button to select your FASTQ, GZ, and BZIP files. You may also drag & drop them into the grey areas. Uploads will start automatically. If you log away from the screen during the upload process, you may see your file transfer to fail. If you have multiple FASTQ files per sample, click the **treeview** button  for instructions.

Sequencing Strategy
Single-End Paired-End

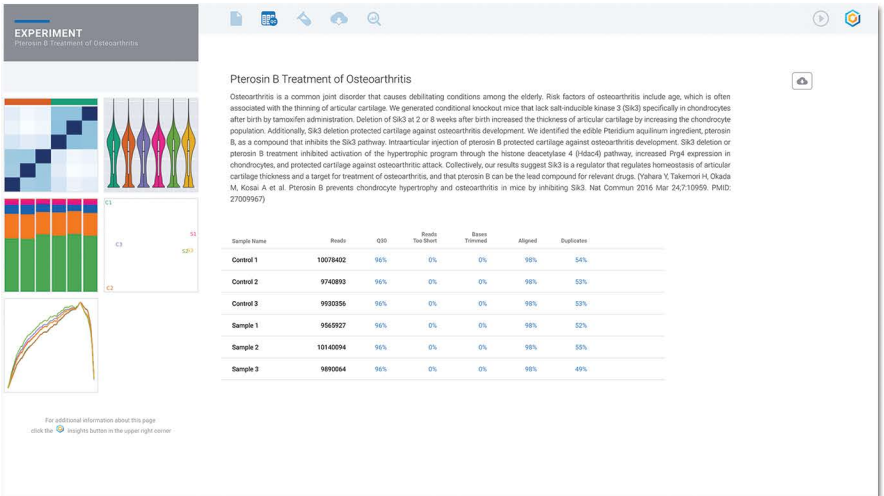
Launch After Uploads Finish

Control 1	FASTQ	RIGHT READ	REDUNDANT
Control 2	FASTQ	RIGHT READ	
Control 3	FASTQ	RIGHT READ	
Sample 1	FASTQ	RIGHT READ	
Sample 2	FASTQ	RIGHT READ	
Sample 3	FASTQ	RIGHT READ	

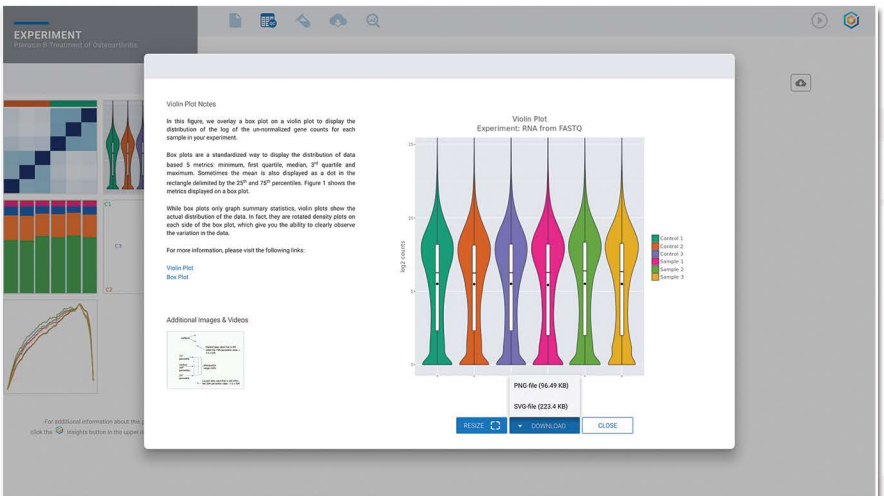
Easily import FASTQ, SRA and Counts data files. **ROSALIND** supports paired and single-end files, as well as multi-lane and multi-run files.

Better Quality Control

Comprehensive QC is provided specific to the experiment type.



Quality Control plots on ROSALIND summarize pertinent aspects to verify the experiment and each sample before you begin your interpretation.



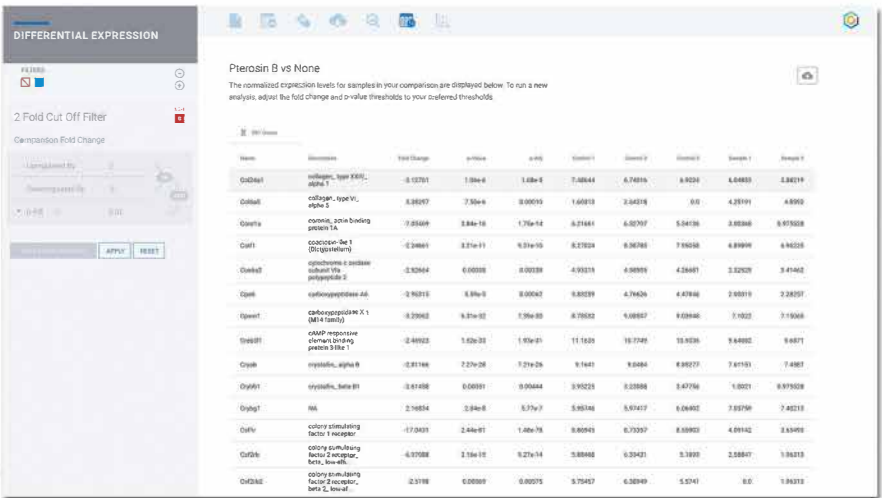
Each Quality Control plot includes an explanation with links to additional references and the ability to download CSV, SVG, and PNG file formats.

Interpret More

Interactive experiences allow deeper exploration of your data.

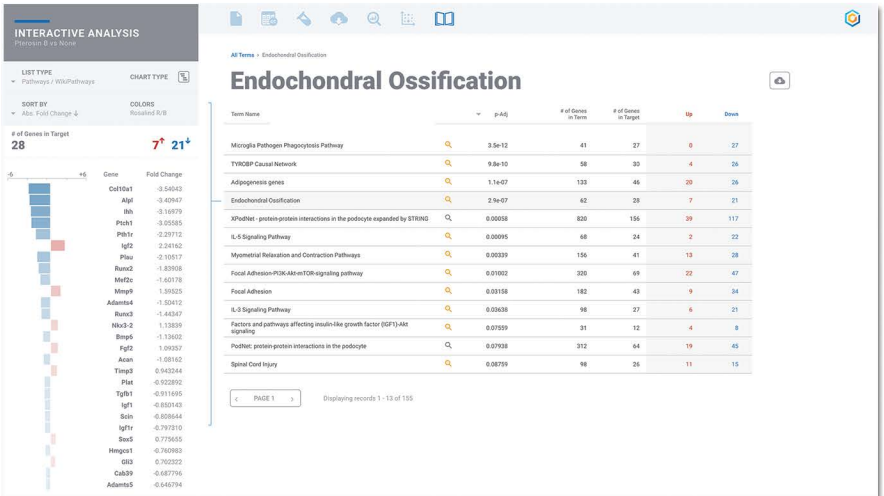


Interactive charts enable rapid exploration of differentially expressed genes with full pathway, gene ontology and protein interpretations.

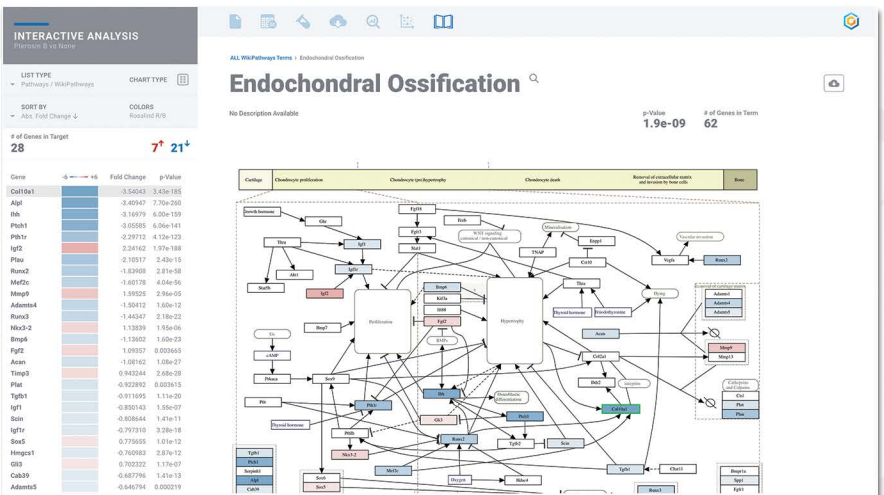


Adjust cut-offs by creating new filters at any time and produce new Interactive Graphs and pathway interpretation.

Interpret More



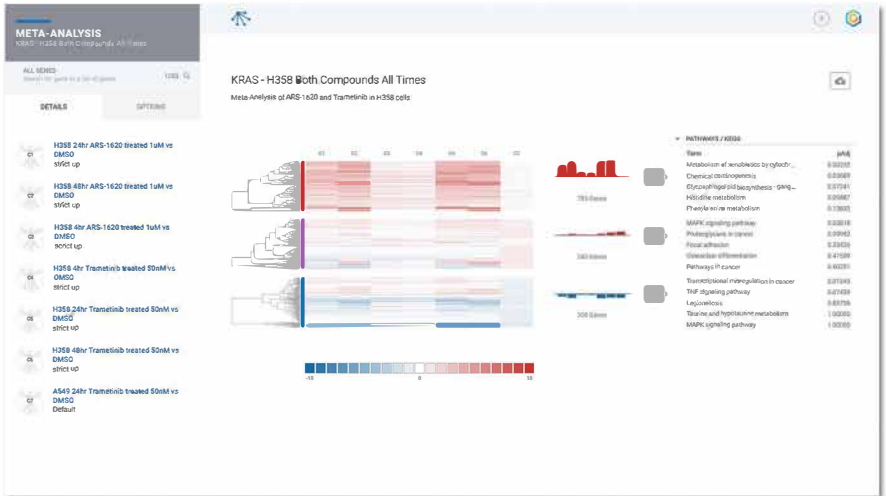
Seamlessly explore the relationships between differentially expressed genes and each associated pathway, gene ontology, and protein interaction.



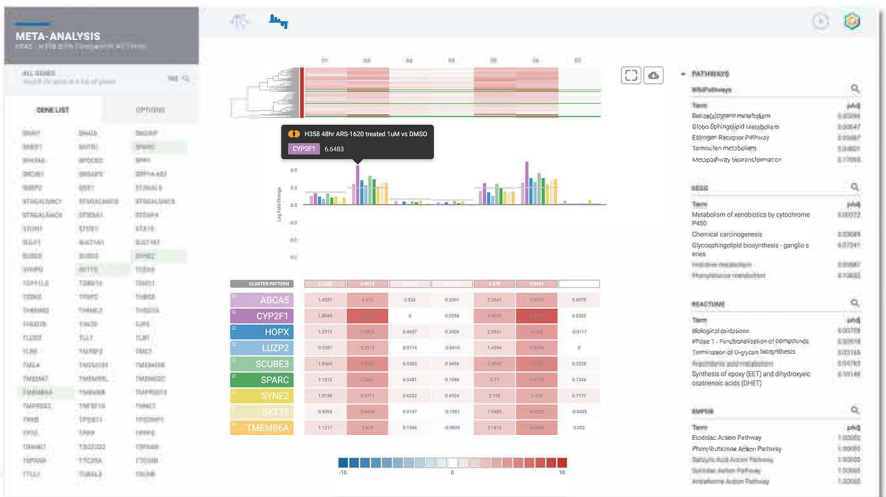
Fully interactive pathway diagrams and heatmaps enable rapid observation of gene expression and gene regulation effects.

Discover More

A.I. unlocks hidden patterns in your data with Meta-Analysis.



Meta-analysis finds all the possible patterns in between your comparisons and experiments.



Explore each pattern, see the enriched terms and even change colors before downloading the graphs.

Collaborate Effortlessly

Share experiments without transferring or downloading data.

SPACES
Collaboration Space for Customer Demos

Participants: 7
Experiments: 3

ACTIVITY

- Tim Westelman removed experiment: numofung18:Brain vs U480 - Histone (Feb 21, 2019)
- Tim Westelman removed experiment: HNSC Counts (Feb 21, 2019)
- Tim Westelman removed experiment: small RNA: Brain vs U480 (Feb 21, 2019)
- Jean Loesch removed experiment: Targeting KRAS Mutant Cancers with a Covalent G12C-Spice (Feb 21, 2019)
- Sarah Douglas left this Space (Dec 19, 2018)
- Conelia Zindro joined this Space (Dec 5, 2018)
- John Burill joined this Space (Oct 22, 2018)
- Tim Westelman added experiment: numofung18:Brain vs U480 - Histone (Oct 17, 2018)
- Tim Westelman added experiment: HNSC Counts (Oct 17, 2018)

Collaboration Space for Customer Demos
Demonstrating the power of ROSALIND SPACES. It's much more than SHARING. Any participant can explore, or add experiments, run new filters and comparisons.

Experiments | Meta-Analyses | **Participants**

	Company/Institute	Title	Team	Email	Phone
1	Tim Westelman	Onkang Bioinformatics	CTO	-	tim@onkang.bio (948) 705-1256
2	Jean Loesch	Onkang Bio	CTO	Exec Team	jean@onkang.bio (615) 269-4900
3	Cassandra Wisniewski	Onkang	Marketing	Staff	cassandra@onkangbio.com (941) 803-2449
4	Jeremy Deane-Turk	Onkang Bioinformatics	VP Bioinformatics	-	jeremy@onkang.bio -
5	Scott McIntire	Onkang Bioinformatics	-	-	scott@onkang.bio (948) 213-1278
6	John Burill	ThermoFisher Scientific	-	-	john.burill@thermofisher.com -
7	Conelia Zindro	Adasta Bio	-	-	conelia@adastabio.com -
8	-	-	-	-	quillanne.dumas@genentix.fr -

ADD PARTICIPANTS

Easily create a space and invite colleagues or collaborators to work alongside you on your experiments.

SPACES
Collaboration Space for Customer Demos

Participants: 7
Experiments: 3

ACTIVITY

- Tim Westelman removed experiment: numofung18:Brain vs U480 - Histone (Feb 21, 2019)
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Experiments | Meta-Analyses | **Participants**

Effects of the loss of DNA Methylation on Cancer Epigenome
The effects of the global loss of DNA methylation on the functional cancer epigenome, using 8 samples, 4 antibodies and 2 attributes. We compare the global histone modification patterns of HCT116 colon cancer cells with its genetic derivatives DKO1 cells which lack DNMT3B and DNMT1 activity Comparison of histone marks in two cell types.
13 1 Feb 2, 2018

Brain vs Universal RNA - Qiagen Kit
Comparisons of Human brain and universal RNA using 4 different mixtures
12 2 1 1 1 Jean Loesch

nCounter assay 20130226_GX (from nSolver 4.0 normalized data)
GX Train RCC File Annotations Lanes 1-3: 100ng Human Reference RNA Lanes 4-6: 70ng Human Reference RNA / 30ng Human Brain RNA Lanes 7-9: 30ng Human Reference RNA / 70ng Human Brain RNA Lanes 10-12: 100ng Human Brain RNA
12 1 1 1 1 Jean Loesch

Collaborate, explore and analyze the same data simultaneously without having to download, transfer or install anything.

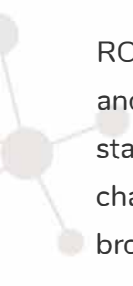
About ROSALIND



Based in the Genomics Capital of San Diego, ROSALIND is the first-ever genomics analysis platform specifically designed for life science researchers to analyze and interpret datasets, without any prior bioinformatics skills.

Named in honor of pioneering researcher Rosalind Franklin, who made a major contribution to the discovery of the double-helix structure of DNA with her famous photograph 51, the ROSALIND platform aims to simplify the practice of genomic data interpretation, so biologists, researchers and drug developers can harness the potential of genomic information from DNA sequencing to microarrays and mass spec, while reducing costs and increasing productivity.

ROSALIND puts the researcher in the driver's seat of data analysis, and helps to free up valuable time for Bioinformatics Cores to offload standard analyses and focus precious resources on more complex challenges. ROSALIND brings bioinformatics analyses to the bench by broadly expanding access to genomic and proteomic technologies for cancer research and precision medicine.



Register for Free: www.app.rosalind.bio/register

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www.rosalind.bio



Learn More: www.rosalind.bio



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