

EMPOWER SCIENTISTS TO DISCOVER MORE ON ROSALIND

QUICK START GUIDE

OnRamp.Bio | San Diego, CA WWW.ONRAMP.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

OnRamp.Bio | San Diego, CA

Analyze More

Setup your experiment in minutes.



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

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

Analyze More



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.

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

Analyze More



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

	and the second se	ONLAUNCH Choose your files to uploa Desse select the Single-End or Pared select your FATOL 02, and 02P files. Navigating way from this screen upload files per sample, click the inspirsts But	ad End opsion according to your sequencing data You may also drag. & Grop them in the groy is the upload process may cause your file tran on @ for instructions.	You may use the browse button to neas. Uploads will start automatratify, after to fail. If you have multiple FASTQ	Ø
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		Sample 2	LEFT READ - R1 READ - R2		
		Sample 3	LEFT READ - R1 RIGHT READ - R2		

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.

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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.

DIFFERENTIAL EXPRESSION		6 6 Q	16 11								Ø
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2 Fold Cut Off Filter	贤 581 Genes										
	Name	Description	Fold Change	p-Value	p-Adj	Control 1	Control 2	Control 3	Sample 1	Sample 2	
	Col24a1	collagen_ type XXIV_ alpha 1	-2.12701	1.05e-6	1.68e-5	7.48644	6.74016	6.9024	6.04853	5.88219	
	Col6a5	collagen_ type VI_ alpha 5	3.38297	7.50e-6	0.00010	1.60313	2.64218	0.0	4.25191	4.8592	
• p-A0] < 0.01	Coro1a	coronin_ actin binding protein 1A	-7.05409	3.84e-16	1.75e-14	6.21661	6.52707	5.34136	3.00368	0.975528	
APPLY RESET	Cod1	coactosin-like 1 (Dictyostelium)	-2.24561	3.21e-11	9.31e-10	8.27024	8.58785	7.95058	6.89899	6.96225	
	Cox6a2	cytochrome c oxidase subunit Via polypeptide 2	-2.52664	0.00038	0.00338	4.93315	4.58905	4.26681	2.32529	3.41462	
	Cpa6	carboxypeptidase A6	-2.96315	5.59e-5	0.00062	3.83259	4.76626	4.47846	2.00315	2.28257	
	Cpoom1	carboxypeptidase X 1 (M14 family)	-3.23062	6.31e-32	7.39e-30	8.78532	9.08507	9.03948	7.1022	7.15065	
	Creb3i1	cAMP responsive element binding protein 3-like 1	-2.46923	1.526-33	1.93e-31	11.1635	10.7749	10.9336	9.64082	9.6871	
	Cryab	crystallin_ alpha B	-2.81166	7.27e-28	7.21e-26	9.1641	9.0484	8.85277	7.61151	7.4587	
	Crybb1	crystallin_ beta B1	-2.61458	0.00051	0.00444	3.93225	3.23068	3.47756	1.0021	0.975528	
	Crybg1	NA	2.16834	2.84e-8	5.77e-7	5.95746	5.97417	6.06402	7.03759	7.40213	
	Caffir	colory stimulating factor 1 receptor	-17.0431	2.44e-81	1.48e-78	8.86945	8.73357	8.55903	4.09142	3.65493	
	Csf2/b	colory stimulating factor 2 receptor_ beta_low-affi	-6.97088	2.16e-15	9.27e-14	5.88468	6.33431	5.1893	2.58847	1.96313	
	Csf2rb2	colory stimulating factor 2 receptor, beta 2, low-af	-2.5198	0.00069	0.00575	5.75457	6.38949	5.5741	0.0	1.96313	

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

Interpret More

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LIST TYPE Pathways / WikPathways			Endochondral Ossification								
SORT BY Abs. Fold Change 4	COI Ros	.ORS alind R/B	Term Name		≁ p-Adj	# of Genes in Term	# of Genes in Target	Up	Down		
f Genes in Target 3		7 [†] 21 [↓]	Microglia Pathogen Phagocytosis Pathway	٩	3.5e-12	41	27	0	27		
			TYR08P Causal Network	Q	9.8e-10	58	30	-4	26		
+6	Gene	Fold Change	Adipogenesis genes	Q	1.1e-07	133	46	20	26		
	Cel10a1 Alpi	-3.54043 -3.40947	Endochondral Opsification	Q	2.9e-07	62	28	7	21		
	lbb	-3.16979	XPortNet - numbers contaction interpretinges in the endposte supported by STRING	0,	0.00058	820	155	39	117		
	Ptch1 Pth1r	-3.05585 -2.29712	8 - E Canadian Bathanan	0	0.00005	40			- 22		
	lgf2	2.24162		2	0.0075			*	-		
	Plau Puer2	-2.10517	Myometrial Relaxation and Contraction Pathways	N.	0.00339	156	41	13	-28		
1	Mef2c	-1.60178	Focal Adhesion-PI2K-Akt-mTOR-signaling pathway	Q	0.01002	320	69	22	47		
	Mmp9	1.59525	Focal Adhesion	0	0.03158	182	43	9	34		
	Adamts4	-1.50412	IL-3 Signaling Pathway	Q	0.03638	98	27	6	21		
	Nkx3-2	1,13839	Factors and pathways affecting insulin-like growth factor (IGF1)-Akt	9	0.07559	31	12	4			
11	Bmp6	-1.13602	signaling	0	0.07078			10			
1.0	Fgf2	1.09357	Podivec, prosen-prosen interactions in the podocyse	4	0.07938	312	04	19	63		
	Timp3	0.943244	Spinal Cord Injury	9	0.08759	98	26	- 11	15		
	Plat Tgfb1 Igf1 Scin Igf1r SoxS	-0.922892 -0.911695 -0.850143 -0.808644 -0.797310 -0.775655	C PACE 1 3 Displaying records 1 - 12 of 155								
	Hmgcs1	0.760983									
	Gli3	0.702322									
	G2039	0.646794									

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

SPACES		\otimes		٢
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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, OnRamp.Bio provides ROSALIND[™], 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.rosalind.onramp.bio/register

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