ROSALIND Powered by ONRAMP

SHARE AND COLLABORATE ON EXPERIMENTS WITH COLLEAGUES SEAMLESSLY

With Spaces, ROSALIND gives you the ability to share your experiment with colleagues and collaborators without sending a single file.

Now everybody can work in real time on the same experiment and results.





COMPARE MULTIPLE EXPERIMENTS WITH META-ANALYSIS

Exploring insights across your experiments is easy with Meta-Analysis: ROSALIND can identify hidden patterns and visualize your results with interactive heat maps, gene lists and pathways.

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ROSALIND works for all types of transcriptomics and epigenomics analysis: Analyze your RNA-seq from FASTQ, raw or normalized counts, smallRNA-seq, ChIP-seq and even nanoString gene expression, proteomics and miRNA panels!

Single-Cell, Exome/Whole Genome, Multi-omics Meta-Analyses and Methylation coming soon.



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Looking to develop a custom analysis? Our talented bioinformatics team can help. Email us for an affordable consulting quote: support@onramp.bio

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ChIP-SEQ The bioinformatics expert you always wanted



SET-UP YOUR EXPERIMENT IN MINUTES

ROSALIND will guide you through experiment design: Describe your samples and inputs using the NCBI BioSample Data Model, enter the antibodies used, identify your kits and drag-and-drop your FASTQ files.

GET YOUR QC FOR FREE!

ROSALIND provides access to all the QC metrics and graphs you need to assess the quality of your experiment and each of your samples. All this is for free, so you do not have to pay for when a sample fails!

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For additional information about this page	D01-H0023ve3	3000000	2822795 (94%)	0 (2%)	2.21#=06 (1%)	m	-	36479		
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	DR01-Input	3008000	2851136 (854)	364 (2%)	1.64e-06 [PN)	975	55		N	
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	HETT10-Input	23682102	333609 T3 (MA)	4000 (PN)	3.50w=07 (2N)	175	27%		N	
	HETTIG-ROBANIC	19013125	16222230 (88%)	112877 (1%)	1.16+08 (175)	82%	35%	25772		
	HETT10-R06Arms3 Rep2	44047058	58733969 (K7%)	08022 (5%)	1.42x=00 (7%)	85	15%	34445		

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	Peak Results Chit peaks identified in your company Tracks Plot page to further explore pe			orted by best score	Cick on any	revita learch the				
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\$! \$	ele1131633049-131605060	38,7799		promotae TSL	-961	MAD	regulatory subunit of t			
***	Known Motif Enrichment	Result			Med	"Looks with mett"	alkiller			
	AGTTTCASTTIC				1973(89)	12.225 (1.425)	0.31008	00		
	AGGTCAAGGICA			8.48	R00(940).245	7.00% (0.00%)	0.31008			
	RETGASTCAIRS				ur-AP1(52P)	7.095 (0.055)	0.31008			
	IGQTGASTCA				0+(2)(29)	7.005 (0.075)	0.31008			

EXPLORE YOUR RESULTS WITHIN HOURS!

In addition of the list of peaks identified in each sample, ROSALIND enables you to perform unlimited differential binding comparisons and look for known or de novo motif enrichment.

ROSALIND provides functional enrichment analysis using over 20 knowledgebases like GO, KEGG, WikiPathways, MSigDB, Pfam, Interpro, and more.

All the tables and graphs are downloadable for your publication, and an embedded genome browser is provided to compare the peaks in your samples.



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