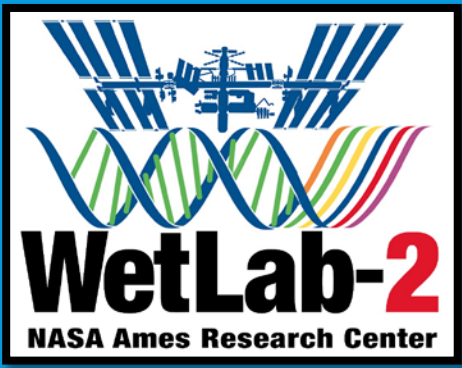




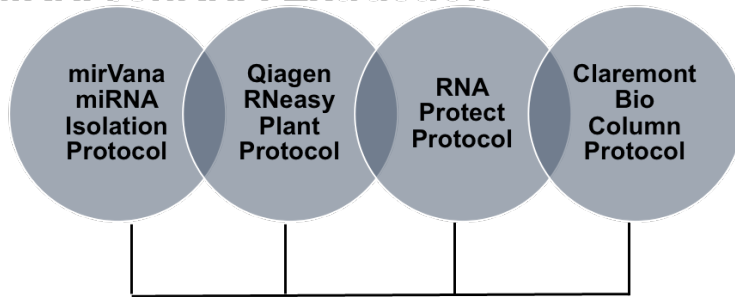
IN FLIGHT miRNA ISOLATION AND RECOVERY ON THE ISS USING THE WETLAB-2 SYSTEM

Emily Johnson (NASA SLSTP) & Wetlab2 team

Current Wetlab-2 system: “end-to-end” (tissue to gene expression) capability on the ISS, for mRNA

Goal of this project: to extend the Wetlab-2 capability to snRNAs (including miRNA)

From benchtop to SPM (sample prep module)



Bioanalyzer

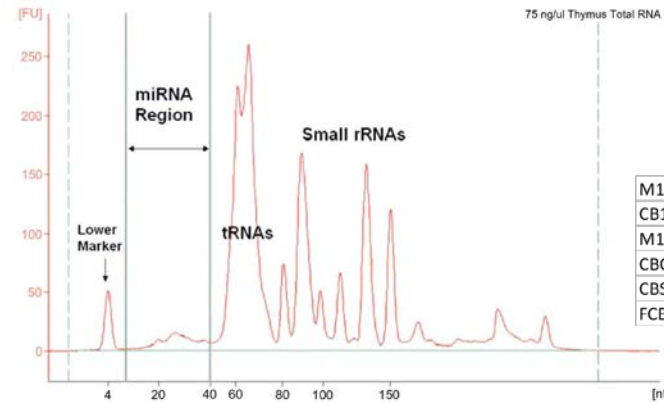
Extracted samples are analyzed on small RNA chip
miRNAs: ~20-40 nt; snRNAs: ~80-150 nt

qPCR

To confirm extractions are miRNA, qPCR analysis with endogenous miRNA primers

SPM

ClaremontBio protocol will be optimized to isolate miRNA



The CB column retains snRNA with higher yields than the benchtop MirVANA kit.

M1= Mirvana isolation
CB1= Standard CB with fresh tissue
M1CB= M1 sample run through a CB column
CBO= CB isolation with fresh sample in omnilyse
CBS= CB isolation with fresh sample in syringe
FCB= Frozen syringe CB

Relative Total Amount (pg)

	M1CB	CBO	CBS	FCB
Ave miRNA	17890	18450	22410	10770
Ave tRNA	4810	6020	5410	3830
Ave total snRNA	47530	50990	54170	32700



Stop by the Space Biosciences booth to see the Wetlab-2 system in person.