

	XPRESSyourself	Galaxy	RiboGalaxy	PausePred	Rfeet	anota2seq	RiboProfiling	Riborex	mQC	Shoelaces	SuperTranscripts	systemPiper	ORFik	coMET	riboSeqR	Deeptools	Picard	ROSE	RUST	Xtail	RiboDiff	RiboTaper	Ribomap	Plastid	Riboviz
Tuned for ribo-seq data																									
Input raw data																									
Input alignment files																									
Input count tables																									
Automated reference genome preparation																									
Automated recursive CDS reference modification																									
Pre-processing																									
Alignment to genome																									
Alignment to transcriptome																									
Read counts to variable features																									
Isoform quantification																									
Quantify reads on motifs																									
Differential Expression Analysis																									
Read size distribution																									
Pause prediction																									
Periodicity																									
Novel uORF discovery/functional annotation																									
General quality control																									
CDS and uORF visualization																									
Metagene profile (all genes)																									
rRNA probe summary																									
Other customizable analyses																									
Full automation of processing to analysis steps																									

Includes feature  
Partial functionality  
Uses old or insufficient methods  
Unique to XPRESSyourself