Legend:

- Includes feature (black)
- Partial functionality (blue)
- Uses old or insufficient methods (gray)
- Unique to XPRESSyourself (green)

Column headers (tools):
XPRESSyourself, RiboGalaxy, Riboviz, Ribomap, ORFik, anota2seq, RiboProfiling, Riborex, mQC, riboSeqR, ROSE, RUST, riboStreamR, scikit-ribo, RiboTaper, Plastid, SPECtre, Xtail, RiboDiff, PausePred, Rfeet, Shoelaces, Galaxy, systemPipeR, SuperTranscripts, Deeptools, Picard

Row features by category:

Category	Feature
	Tuned for ribo-seq data
Inputs	Input raw data
Inputs	Input alignment files
Inputs	Input count tables
Curation	Automated reference genome preparation
Curation	Automated CDS reference modification
Processing	Pre-processing
Processing	Alignment to genome
Processing	Alignment to transcriptome
Quantification	Read counts to variable features
Quantification	Isoform quantification
Quantification	Quantify reads on motifs
Quantification	Translation efficiency calculation and analysis
Quantification	Differential Expression Analysis
Discovery	Novel uORF discovery/functional annotation
Discovery	CDS and uORF visualization
Quality Control	General quality control
Quality Control	Read size distribution
Quality Control	Pause prediction
Quality Control	Periodicity
Quality Control	Metagene profile (all genes)
	rRNA probe summary
Other	Other customizable analyses
Other	Flexible organism choice
Other	End-to-end automation