Submit Tracefiles

On the BOLD website: http://v4.boldsystems.org

Left side menu, go to **Projects** > **View All Projects** On main page: select project **ARIQ**

For each of your specimens:

Find the specimen listing on the Record List page Click on the "Sequence Page" entry for the specimen (something like *ARIQ00x–17*) On the resulting window, click *Upload Trace* Fill in the form this way:

A Upload Trace Activity Rep Specimen Details Laragen Specimen Details Select My institution or type in the name of your institution and select it from the drop-down list of matches	
Or type in the name of your institution and select it from the drop-down list of matches	
Sample ID LA Process ID AF Process ID AF Propet AF Promer: Tax Names Ar Rank Name ge Sampling Protocol V & BIN URI N BIN URI N BIN URI N	
Kingdom Ar Sequencing Primer Forward Reverse Pick the correct direction for this tracefile: Sample Report From LIMS Sequencing Primer: Select Sequencing Primer Junction: Sample Report From LIMS Upload up to 4 trace files and phred files. (Phred files are not required or trace upload) Pired 1: Choose File no file selected	feedback
Trace 2: Choose File no file selected Phred 2: Choose File no file selected Trace 3: Choose File no file selected Phred 3: Choose File no file selected Trace 4: Choose File no file selected Phred 4: Choose File no file selected	
Upload	

Use **Choose File** to select the correct tracefile, then click **Upload**

Repeat for each tracefile (normally, each sequence has one forward and one reverse)

Submit Sequences

On the BOLD website: http://v4.boldsystems.org Left side menu, go to Projects > View All Projects On main page: select project ARIQ On the left side menu: select **Uploads > Sequences** For each of your sequences, fill in the form this way:

В	B Sequence Submission			
	Required fields for sub Select ID:	equired fields for submission are marked in red. Select ID: Sampleid Must change to Sampleid		
	Markers: COI-SP + Run site: Laragen Select the institution responsible for generating the sequences listed by beginning to type in the name. BOLD will return matches in a drop			
	Paste sequences in fasta format:		Start line with a greater-than symbol, then the BOLD sample ID for the specimen (replace the "0000" with the DISCO specimen ID). Then a linebreak. Then the sequence.	
			Submit	
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Then click **Submit**