Convert "seq/qual" Pair to FASTQ

This workflow allows to add PHRED quality scores to the sequence and save output to Fastq. For example, one can read a Fasta file, import PHRED quality values from corresponding qualities file and export the result to Fastq.

To execute the workflow do the following:

- 1. Select "Sequence Reader" task and specify source file(s) at "URL" field in the Property Editor.
- 2. Select "Import PHRED qualities" task and specify URL to the quality file. Usually such files have .qual extension.
- 3. Launch the schema with pressing Ctrl+R shrotcut.

After running the workflow, target fastq file will appear in the same folder as the source file, with the same name but diffrent extension.



How to Use This Sample

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If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.