# 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.

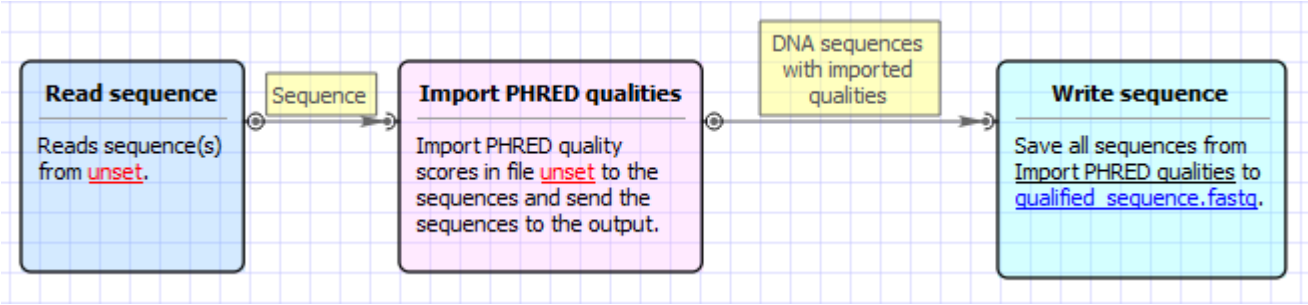
> **How to Use This Sample**
>
> If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

## Workflow Sample Location

The workflow sample "Convert "seq/qual" Pair to FASTQ" can be found in the "Conversions" section of the Workflow Designer samples.

## Workflow Image

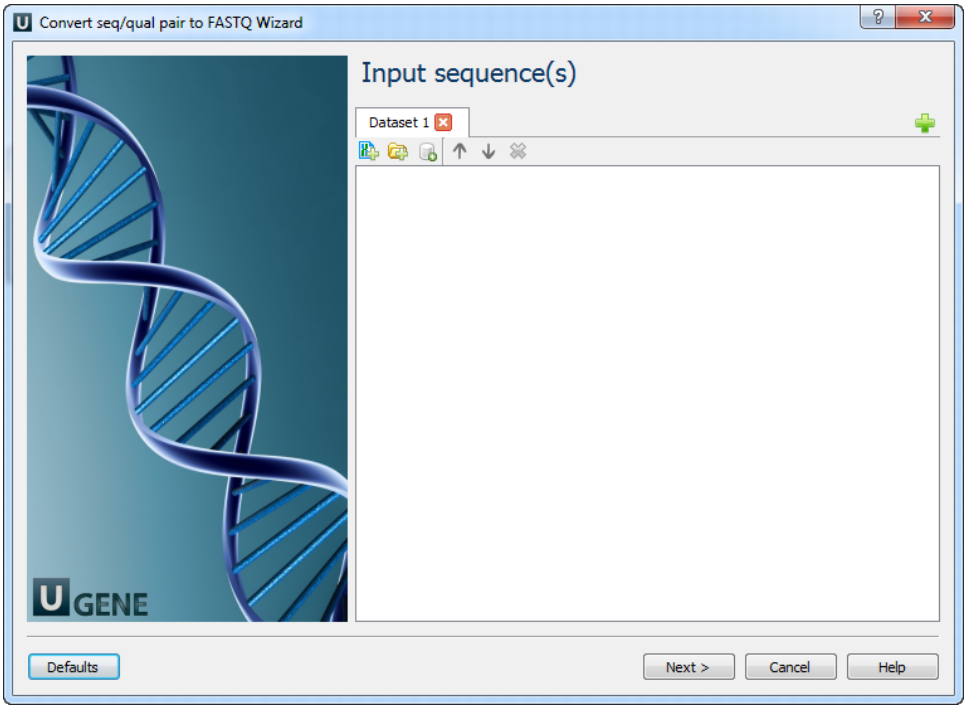
The workflow looks as follows:



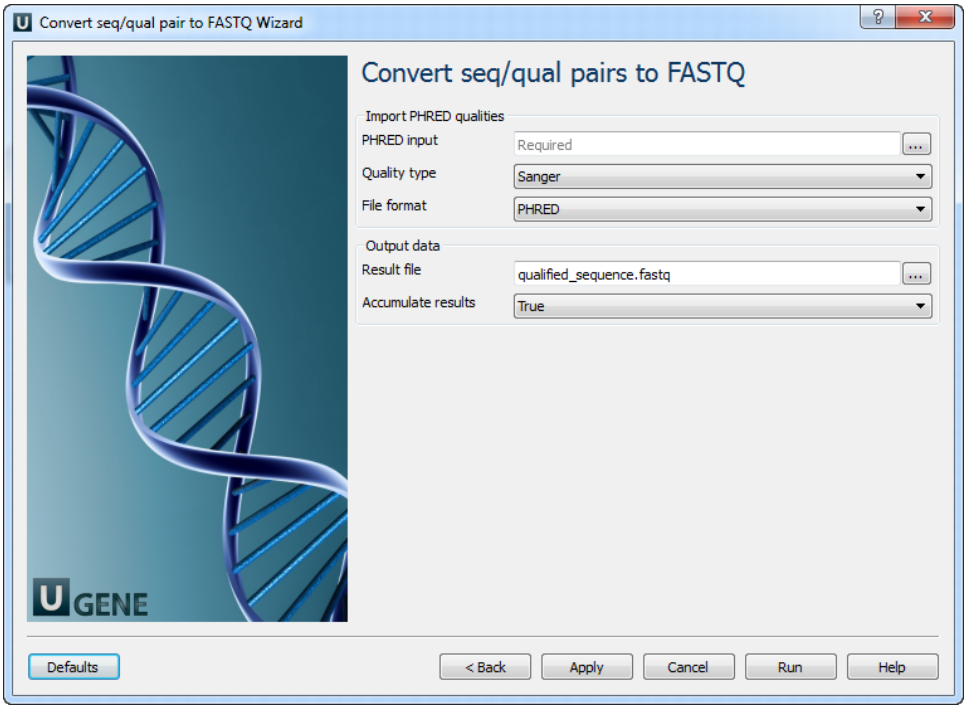

## Workflow Wizard

The wizard has 2 pages.

1. Input Sequence(s): On this page you must input sequences(s).




2. Convert "seq/qual" Pair to FASTQ: On this page you can modify converting and output settings.




The following parameters are available:

| | |
|---|---|
| PHRED input | Path to file with PHRED quality scores. |
| Quality type | Choose method to encode quality scores. |
| File format | Quality values can be in specialized FASTA-like PHRED qual format or encoded similar as in FASTQ files. |
| Result file | Location of output data file. If this attribute is set, slot "Location" in port will not be used. |
| Accumulate results | Accumulate all incoming data in one file or create separate files for each input.In the latter case, an incremental numerical suffix is added to the file name. |