

FAQ CircAID-p-Seq

How much RNA input amounts can be used?

At least 50 ng of starting RNA material.

What sequencing platform is suitable for CircAID-p-Seq?

It's suitable for Oxford Nanopore Technology (MinION, GridION, PromethION).

Which kits from Oxford Nanopore are compatible with CircAID-p-Seq?

It is compatible with direct cDNA sequencing (SQK-DCS-109), ligation sequencing kit (SQK-LSK-109)

Is it compatible with Flonge Flow Cell?

No, it is not compatible.

What pipeline should be used to analyse the data?

We developed together with [Genexa](#) the [CircAidMe](#) pipeline which is publicly-available on our website ([link](#)). The output of this pipeline is a fast a file containing consensus sequences, suitable for downstream data analysis.