

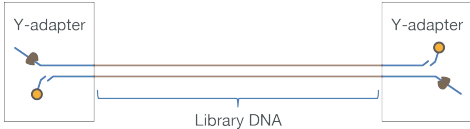
# Ligation Sequencing Kit 1D or Rapid Sequencing Kit

Sequencing is used for a wide range of applications and each has its own requirements for the type of data needed to answer the biological question. Oxford Nanopore offers two ranges of kits: Rapid 1D and Ligation Sequencing Kit 1D, allowing selection of the right tool for the right experiment. Nanopores sequence

any strand of DNA presented to them, independent of the length or source. As a result a user can influence the outcome of their sequencing run by selecting the right kit and protocol for their experimental goals. The table below provides information to guide the selection :

Property	Ligation Sequencing Kit 1D	Rapid Sequencing Kit
	<p><b>SQK-LSK108</b> the simplest method for genomic DNA, amplicon and/or cDNA with control over read length and amounts of input material</p>	<p><b>SQK-RAD002</b> rapid and easy method for genomic DNA</p>
Input sample	gDNA, amplicon, cDNA	gDNA
Yield on R9.4 flow cells	10 GB / run	10 GB / run
Accuracy	<p>R9.4 RNN 450 b/s - 1D</p> 	<p>R9.4 RNN 450 b/s - 1D</p> 
Library prep	50 mins	<10 mins
Protocol overview	<p>A multi-step, 50 minute</p> 	<p>A two-step, 10 minute protocol</p> 
Amount of sample	1000 ng	200 ng
Efficiency of library preparation	<p>*** (All the adapted fragments are available for sequencing)</p>	<p>*** (All the adapted fragments are available for sequencing)</p>

## Ligation Sequencing Kit 1D or Rapid Sequencing Kit (continued)

Property	Ligation Sequencing Kit 1D	Rapid Sequencing Kit								
Protocol / Kit adaptations	Native barcoding PCR barcoding Low input DNA Long reads (>50kb) Read length selection Wash Kit	Wash Kit								
Additional consumables required for library prep	Agencourt AMPure XP beads (A63880) NEBNext End repair / dA-tailing Module (E7546), NEB Blunt/TA Ligase Master Mix (M0367).  Optional Covaris g-TUBE (#520079), NEB FFPE Repair Mix (M6630)	NEB Blunt/TA Ligase Master Mix (M0367)								
Read lengths v fragment length  There are for illustrative purposes only	Read length is the same as fragment length  <table border="1" data-bbox="379 1016 603 1122"> <tr> <td>Read Length</td> <td>8 kb</td> </tr> <tr> <td>Fragment Length</td> <td>8 kb</td> </tr> </table> <p data-bbox="379 1167 778 1193">DNA sheared using Covaris g-TUBE</p> 	Read Length	8 kb	Fragment Length	8 kb	Read length is the same as fragment length  <table border="1" data-bbox="949 1016 1173 1122"> <tr> <td>Read Length</td> <td>4.5 kb</td> </tr> <tr> <td>Fragment Length</td> <td>4.5 kb</td> </tr> </table> <p data-bbox="949 1167 1316 1193">DNA tagmentation by transposase</p> 	Read Length	4.5 kb	Fragment Length	4.5 kb
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