

GridION Q IT requirements

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GridION Q IT Requirements Checklist

This checklist represents the minimal requirements for installing the GridION Q in your institution. For a full explanation of requirements, please continue to the document.

Item/setup required	Reason	Provided?
1x 1 Gbp/s RJ45 port with DHCP service running	Connection to IT infrastructure and internet	
1x 1 Gbp/s Ethernet cable	Connection to IT infrastructure and internet	
HTTPS/port 443 to 52.17.110.146, 52.31.111.95, 79.125.100.3 (outbound-only access) or DNS rule for ping.oxfordnanoportal.com	Telemetry feedback	
HTTPS/port 443 to 178.79.175.200 and 96.126.99.215 (outbound-only access) or DNS rule for cdn.oxfordnanoportal.com	Software updates	
USB mouse	Device control	
USB keyboard	Device control	
HDMI- or DisplayPort-compatible monitor	Device control	
Power supply capable of delivering 650 W	GridION power	
Storage: Sufficient infrastructure for required storage option*	Long-term data storage	

**Size of storage required will depend on use case. Refer to the information below for storage guidelines.*

GridION Q device

Overview

The GridION™ Q is a benchtop device for nanopore sequencing designed to run and analyse data from up to five flow cells. It enables labs operating under regulatory requirements to access the benefits of nanopore sequencing:

- Simple library preparation
- Real-time analysis
- Biological insights from long reads

In addition, the GridION Q also allows users to offer nanopore sequencing as a service when certified.

The GridION Q benefits from the inclusion of on-board compute which permits data acquisition, analysis and feedback, basecalling, data streaming and device control, all without placing any additional burden on existing IT infrastructure.

All device control, basecalling, analysis and orchestration on the GridION Q is carried out by pre-installed custom software created by Oxford Nanopore Technologies.

Specifications

The GridION Q is designed around a simple user interface on top of cutting-edge custom electronics providing real-time analysis solutions:

Component	Specification
Operating system	Ubuntu 22.04 running off Intel CPU You are advised to keep up to date with all software and security patches
Storage	7 TB internal SSD
Memory	64 GB RAM
Size and weight	H220 x W365 x D370 mm Weight 14.4 kg
Environmental ranges	System functional range +5°C to +40°C Designed to sequence at +18°C to +25°C

Site requirements

Installing the GridION Q is similar to installing any new computer. Requirements for the device are as follows:

Component	Requirements
1x RJ45 port	IP address via either DHCP service or statically assigned TCP running on port 443 HTTPS Requires perimeter firewall permissions: - To access HTTPS/port 443 to 52.17.110.146, 52.31.111.95, 79.125.100.3 (outbound-only access) or DNS rule for ping.oxfordnanoportal.com for telemetry feedback - HTTPS/port 443 to 178.79.175.200 and 96.126.99.215 (outbound-only access) or DNS rule for cdn.oxfordnanoportal.com for critical software updates (these are available on an opt-in basis) Connected to local storage infrastructure
1x power supply	5x country-specific C13 cables included with device - Maximum power draw 650 W - Maximum current 6 A - Supply voltage 100–240 VAC (50/60 Hz)
1x monitor	Compatible with HDMI or DisplayPort connection (a DisplayPort to HDMI adapter is included in the GridION shipment)
1x keyboard	Compatible with USB connection
1x mouse	Compatible with USB connection

Telemetry

The sequencing software collects telemetry information if the GridION Q is connected to the internet. This allows monitoring of device performance and enables remote troubleshooting. Some of this information comes from free-form text entry fields, therefore no personally-identifiable information should be included. We do not collect any sequence data. If you are running the GridION Q offline and require troubleshooting, you will be able to send telemetry to Oxford Nanopore Technologies via a different route.

Storage

File types

Nanopore sequencing data is stored in two file types: FASTQ and BAM. Basecalling summary information is stored in a sequencing_summary.txt file:

- FASTQ is a text-based sequence storage format, containing both the sequence of DNA/RNA and its quality scores. By default, nanopore sequencing experiments save up to 4000 DNA sequences in one FASTQ file. File size can vary from <1 Mb to tens of Mb depending on the number and length of sequences.
- BAM files are output if you perform alignment or modified base calling on the basecalled dataset.
- sequencing_summary.txt contains metadata about all basecalled reads from an individual run. Information includes read ID, sequence length, per-read q-score, duration etc. The size of a sequence summary file will depend on the number of reads sequenced.

In addition, sequencing data is available in two other optional file types:

- POD5 is an Oxford Nanopore-developed file format which stores nanopore data in an accessible way. This output also reads and writes data faster, uses less compute and has smaller raw data file size than .fast5.
- .fast5 is a file format based upon the .hdf5 file type, which contains all information needed for analysing nanopore sequencing data and tracking it back to its source. A .fast5 file contains data from multiple reads (4000 reads as default), and is several hundred Mb in size.

Example file sizes below are based on different throughputs from an individual flow cell, with a run saving POD5, FASTQ, and BAM files with a read N50 of 23 kb.

Flow cell output (Gbases)	FASTQ.gz storage (Gbytes)	Unaligned BAM with modifications (Gbytes)	POD5 storage (Gbytes)	.fast5 storage (Gbytes)
10	6.5	6	70	90
15	9.75	9	105	135
30	19.5	18	210	270

As an experiment progresses, POD5 files are produced for all reads. If you choose to basecall your data, these reads are used by the sequencing software to generate sequence data which is then stored in FASTQ files and/or BAM files.

Long-term storage

The GridION Q has sufficient SSD disk space for multiple runs to be carried out, storing both FASTQ and BAM to prevent successive runs from terminating due to lack of storage space. For this, a site must provide storage to transfer data off the device.

The GridION runs on Ubuntu and can mount multiple filesystem types. We recommend storage presented as NFS or CIFS. The form (and volume) of data to be stored will depend on customer requirements:

- Storing POD5 files with raw read data in will permit re-basecalling of data when new algorithms are released by Oxford Nanopore. In such cases, new releases of basecallers have enabled significant improvements in basecalling accuracy of existing datasets through re-basecalling. Further, selected Oxford Nanopore and third-party tools use the raw signal information contained within the POD5 to extract additional information from the raw signal e.g. modified bases calling, reference-guided SNP calling or polishing of data.

- Retaining just FASTQ files will allow use of standard downstream analysis tools using the DNA/RNA sequence, but no further sequence data can be generated when improvements in basecalling become available.

Frequently asked questions

Can I use an uninterruptible power supply (UPS) with the GridION? Yes you can use a UPS, however we are unable to recommend a specific product.

Do you have any recommendations for how to move data off the GridION in real time during a sequencing run? Currently we recommend moving the data off the box using **rsync** run hourly through **crontab**. For further details, please email support@nanoporetech.com