Quick-Start Protocol December 2017

QIAamp® 96 DNA QIAcube® HT Kit

This protocol is for use with QIAcube HT Prep Manager Software. If you are using QIAcube HT 4.17 Software, download the corresponding protocol at **www.qiagen.com/HB-1569**.

Further information

- *QIAamp 96 DNA QIAcube HT Handbook:* **www.qiagen.com/HB-2158**
- Safety Data Sheets: **www.qiagen.com/safety**
- Technical assistance: **support.qiagen.com**

Notes before starting

- This protocol is for the purification of gDNA from blood, cells and soft tissues, such as biopsies, mouse tails, brain, liver and muscle using the QIAamp 96 DNA QIAcube HT Kit with the QIAcube HT Prep Manager Software.
- For processing tissue samples, you will also need Collection Microtube Racks (cat. no. 19560) and Collection Microtube Caps (cat. no. 19566).
- Prepare Buffers ACB, AW1 and AW2 according to the instructions in the *QIAamp 96 DNA QIAcube HT Handbook*.
- For processing blood and cell samples, prepare a mixture of Buffer VXL and proteinase K immediately before starting the run according to Table 1. **Note**: If you use tissues, proteinase K is already used during sample disruption. In this case, load only an appropriate amount of Buffer VXL as shown on the virtual worktable.

1. Start the QIAcube HT Prep Manager Software. Click on the **Home** icon in the main toolbar to access the Home screen.
2. Select QIAamp 96 DNA from the **Create Experiment** list. Follow the instructions in the wizard and fill in all required fields.

3. In the **Setup** step, select **Sample type** and **Pre-treatment** for documentation.
4. Select the protocol: QIAamp DNA protocol. For information about optional steps and advanced options see the kit handbook.
5. Define samples in the **Labware selection** step.
6. Arrange samples to the output plate in the **Assignment** step. **Note**: The instrument must be switched on and connected to the software before entering the **Worktable** step.
7. Follow the instructions on the virtual worktable to prepare the instrument worktable.
8. Add the volume of sample as indicated on the virtual worktable to the selected S-Block wells.
9. Save the experiment by clicking the **Save** button in the button bar.
10. Click the **Start** run button to start the run. **Important**: If the optional Vacuum performance check has been selected, the software will show a dialog that needs to be confirmed after defined vacuum steps.
11. When the protocol is complete, cover the elution plate (EMTR) with the lid and remove it from the elution chamber. **Note**: If using Top Elute fluid, there may be 2 liquid phases in the elution microtubes. Top Elute fluid will be the top layer over the elution buffer.
12. Create a report (if required).
13. Follow the cleaning procedure.

Table 1. Buffer VXL mixture preparation.

Samples	24	32	40	48	56	64	72	80	88	96
Buffer VXL (ml)	2.48	3.2	4.0	4.72	5.44	6.16	6.88	7.68	8.4	9.12
Proteinase K (µl)	620	800	1000	1180	1360	1540	1720	1920	2100	2280

Scan QR code for handbook.

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Document revision history	
R2/2017	Notation paragraph for Proteinase K was added, step 4: part of sentence dealing with off-board lysis was erased