



# **AZURESEQ RUO qPCR KIT SARS- CoV-2 FOR 200 REACTIONS**

## **INSTRUCTIONS FOR USE**

For Research Use Only

PROTOCOL VERSION V1.0

DOCUMENT VERSION 01

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### Document History – Important notes and updates

Protocol Version	Document Version	Date	Author	Summary of changes	Authorized by
1	v1	03/12/2020	Noémi Petrovicz	First version	Gergely Tölgyesi

## 1. Principle of the method

The test is a real-time reverse transcription polymerase chain reaction (rRT-PCR) test which is designed to detect RNA from two different regions of the SARS-CoV-2 nucleocapsid gene in nasopharyngeal (NP) and oropharyngeal (OP) swabs from patients with signs and symptoms of infection who are suspected of COVID-19. The kit primer and probe set also detects human RNase P (RP) in a clinical sample as internal control.

The target nucleic acid sequences from the genome of SARS-CoV-2 are the same sequences utilized by the CDC for their 2019 Novel Coronavirus (2019-nCoV) Real-Time RT-PCR Diagnostic Panel. These sequences are contained within 2 different regions (N1 and N2) of the virus nucleocapsid (N) gene.

Nucleic acids are isolated and purified from nasopharyngeal and oropharyngeal swabs using well established nucleic acid extraction systems. Sample input and elution volumes are system dependent. Samples collected in specific Viral Transport Medium which have undergone a heat incubation can be also used as inputs to the subsequent steps.

The purified nucleic acid, or the heat extracted sample is reverse transcribed into cDNA by combining nucleic acid with the AzureSeq RUO qPCR Kit SARS-CoV-2 for 200 Reactions (further referred as AzureSeq-200 RUO) master mix which is then subsequently amplified in the real time PCR instrument. In the process, the probe anneals to a specific target sequence located between the forward and reverse primers. During the extension phase of the PCR cycle, the 5' nuclease activity of Taq polymerase degrades the probe, causing the reporter dye to separate from the quencher dye, generating a fluorescent signal. With each cycle, additional reporter dye molecules are cleaved from their respective probes, increasing the fluorescence intensity. Fluorescence intensity is monitored at each PCR cycle by the real time PCR instrument.

## 2. Kit content

Product Code	Product Name	Number of tubes	Volume (μL)
OA-ITMP-MM-100	2X InhibiTaq Multiplex HotStart MasterMix	2	1000
OA-RT-200	RTScript Reverse Transcriptase, 200U/μL	1	100
OA-CPPM-100uL	CoVi Primer/Probe Mix 3	2	100
OA-NFW-350uL	Nuclease Free Water	2	350
OA-CVNC-150	CoVi Negative Control	1	150
OA-CVPC-150	CoVi Positive Control	1	150

## 3. Shipping and Storage

The AzureSeq–200 RUO kit is shipped on dry ice. The kit components should arrive frozen. Please contact [azureseq.support@omixon.com](mailto:azureseq.support@omixon.com) if any components are not frozen upon receipt or are compromised during shipment.

To prevent the reagents from degradation, all components should be stored immediately at -20°C.

It is recommended to have a back-up generator for your freezer as well as a temperature data log to ensure that the AzureSeq–200 RUO kit components remain frozen at -20°C if you work in an area prone to power outages.

Expires 12 months after date of manufacture. Do not use it after the expiration date.

Do not use the kit if it is defective.

Repeated freezing/thawing must be avoided because it can cause reagent degradation that leads to decrease in sensitivity.

Dispose of unused reagents and waste according to country regulations.

## 4. Specimen collection, transfer and storage

Inadequate or inappropriate specimen collection, transfer and storage can increase the probability of false negative results.

### 4.1 Collection

Refer to CDC's webpage for Interim Guidelines for Collecting, Handling and Testing Clinical Specimens from Patients Under Investigation (OUIs) for 2019 Novel Coronavirus (2019-nCoV).

<https://www.cdc.gov/coronavirus/2019-nCoV/guidelines-clinical-specimens.html>

Use only synthetic fiber swabs with plastic shafts. Do not use calcium alginate swabs or swabs with wooden shafts, as they may contain substances that inactivate some viruses and inhibit PCR testing.

Follow specimen collection devices manufacturer instructions for proper collection methods.

#### **Oropharyngeal swab**

Use a sterile swab to wipe the posterior pharynx, avoiding the tongue. Place swabs immediately into labeled sterile tubes containing viral transport medium. Break each applicator sticks off at the score line (flocked swabs) or near the tip or cut with sterile scissors to permit tightening of the cap. Ship sample immediately on cold packs.

#### **Nasopharyngeal swab**

Insert a sterile swab into nostril parallel to the palate. Swab should reach depth equal to distance from nostrils to outer opening of the ear. Leave swab in place for several seconds to absorb secretions. Slowly remove swab while rotating it. Place swabs immediately into labeled sterile tubes containing viral transport medium. Break each applicator sticks off at the score line (flocked swabs) or near the tip or cut with sterile scissors to permit tightening of the cap. Ship sample immediately on cold packs.

### 4.2 Transport

All specimen must be transported with ice cool / ice-gel box / dry ice and securely sealed and handled.

Transport of clinical samples must obey local regulations. The biosafety local regulations for SARS-CoV-2 must be followed.

### 4.3 Handling

During handling potentially infectious specimens, laboratory workers should wear appropriate personal protective equipment (PPE), which includes disposable gloves, laboratory coat/gown, and eye protection.

For specific instructions on the handling of clinical specimens for coronavirus disease 2019, see also the CDC's webpage mentioned above.

### 4.4 Storing

Specimens can be stored at 2-8°C for up to 48 hours after collection. For storage longer than 2 days, specimens should be frozen at -70°C.

If the sample is stored for more than 48 hours, extraction of the RNA using validated RNA isolation system is required.

If the sample is not frozen and stored for less than 48 hours, direct approach of workflow can be used.

Repeated freezing and thawing of a specimen should be avoided. If a specimen is kept for retesting, it should be aliquoted in different tubes to avoid freezing and thawing cycles.

Depending on the type of sample and the transport medium used, specific storage and, for RNA isolation, pre-treatment of the sample may be required. Please observe the instructions provided by the manufacturer.

## 5. Materials and Equipment needed, but not provided

### 5.1. Equipment

- Real-time PCR thermal cycler able to detect FAM, HEX or ROX (or equivalent) channels
- Thermoblock (suitable for 1.5 mL microcentrifuge tubes, capable of heating up to 95°C)
- 100 µL and 1000 µL micropipettes
- 10 µL and 100 µL multichannel pipette
- Vortex mixer
- Centrifuge

### 5.2. Reagents

- Viral RNA/total RNA extraction kit
- Viral Transport Medium (Clinichem, Copan, Puritan, CDC VTM, mwe Medical Wire)

### 5.3. Materials

- Optical 96-well plates or 0.2 ml optical tubes
- Optical seal compatible with the qPCR instrument
- Disposable DNase/RNase free pipette tips with filters (10 µL, 20 µL, and 200 µL)
- DNase/RNase free 1.5 ml tubes
- Disposable powder-free gloves
- Surface decontaminant products such as "RNase away"
- Material necessary for nucleic acid extraction



## 6. Warning and Precaution

Good laboratory practices are essential to the proper performance of this assay. Due to the high sensitivity of the test, care should be taken while handling samples and materials while performing the assay to keep reagents and amplification mixtures free of contamination.

Users should pay attention to the following:

- Read the Instructions for Use carefully before processing samples. Any deviation from procedures written here may affect optimal performance.
- Use disinfectant to clean and disinfect the area around the sample
- Decontaminate and dispose of all specimens, reagents, and other potentially contaminated materials in accordance with local regulations
- Use universal precautions when performing the assay. Handle samples as if capable of transmitting infection.
- Wear personal protective equipment throughout the assay procedure.
- Thoroughly wash hands after removing gloves, and dispose of gloves as hazardous wastes
- Do not reconstitute or dilute the reagents in volumes other than described in this IFU. Do not use less volume of the reagents other than specified in this IFU. These activities can lead to performance errors.
- Omixon cannot provide support for any problems resulting from not following the protocol steps described in this IFU.
- Do not use the product in case of detectable damage to the components (broken vials, plate, loose caps etc.).
- Do not use reagents past their expiration date.
- Do not substitute or mix the AzureSeq–200 RUO kit reagents with reagents from other manufacturers.
- All instruments must be maintained and operated according to manufacturer’s instructions.
- Every workplace must be equipped with its own set of variable-volume pipettes, necessary auxiliary materials, and equipment.
- Do not pool reagents from different lots or from different vials of the same lot.
- Do not smoke, drink, eat or apply cosmetics in areas in which specimens or Kit components are handled.

## 7. Procedure

The AzureSeq–200 RUO kit contains a control assay targeting the RNaseP. This is an internal control needed to confirm the presence of nucleic acid in every sample run with the AzureSeq–200 RUO test kit and is used to generally confirm functionality of the test kit components.

Other than that, there are no external controls provided with the AzureSeq–200 RUO test kit. Users are expected to supply commercially available positive and negative controls from Omixon as a separate product (catalog numbers are listed in Section 5) or they can use their in-house ones.

### 7.1. Instructions for setting up the reactions

In case of direct approach without separate RNA extraction (heat treatment), please follow the instructions from step 1. In case of starting with RNA purified with regular, validated RNA extraction kits, skip steps 1-4 and start with step 5.

#### 7.1.1. Instructions

Recommended for use only with OP or NP swabs in Viral Transport Media (VTM) from the following manufacturers: Clinichem, Copan, Puritan, CDC VTM, mwe Medical Wire

Sample in VTM can be stored for up to 48 hours on 4°C.

1. Obtain swabbed OP/NP material in VTM.
2. Transfer 100-200µL of swabbed OP/NP VTM material into compatible DNase/RNase free tubes.
3. Heat sample for 5 minutes at 95°C.
4. Following incubation, spin the heated sample on ~1500 x rpm for 30 seconds to collect material at the bottom of the tube. Store on ice until needed. The sample is now ready to be added to the RT-qPCR reaction (see following steps).
5. Completely thaw the CoVi Primer/Probe mix 3 (brown tube/cap) by setting it on ice for ~30 minutes. Once thawed, briefly centrifuge to collect at the bottom of the tube, then add **384 µL** of nuclease free water to the tube. Mark the tube with water added.
6. Vortex the tube at max speed for 10 seconds to mix, then spin down briefly to collect at bottom of the tube.
7. Proceed to master mix setup as shown below in a clean room or designated setup area.

Reaction set-up for 20 $\mu$ L reaction volume:

Component	Volume/ reaction ( $\mu$ L)	Volume/100 reactions ( $\mu$ L)	Final concentration
2x InhibiTaq Multiplex qPCR MasterMix	10	1000	1x
RTScript Reverse Transcriptase, 200U/ $\mu$ L	0.5	50	5U/ $\mu$ L
Diluted Primer/Probe Mix (step #5)	4.5	450	1x

8. Mix the master mix by pipetting up and down repeatedly with pipette set to volume of 2X master mix added, or by capping the tube, vortexing briefly, and spinning down briefly to collect mix.
9. Distribute **15  $\mu$ l** of the master mix using an appropriate pipette to all wells of a plate that will be used.
10. Add **5  $\mu$ l** of the samples, positive control, or negative control to appropriate wells.
11. Seal the plate, vortex briefly or flick to mix; spin down in a centrifuge to collect the mixed samples.
12. Place the plate into the designated real-time machine and run the following program.

Recommended cycling conditions:

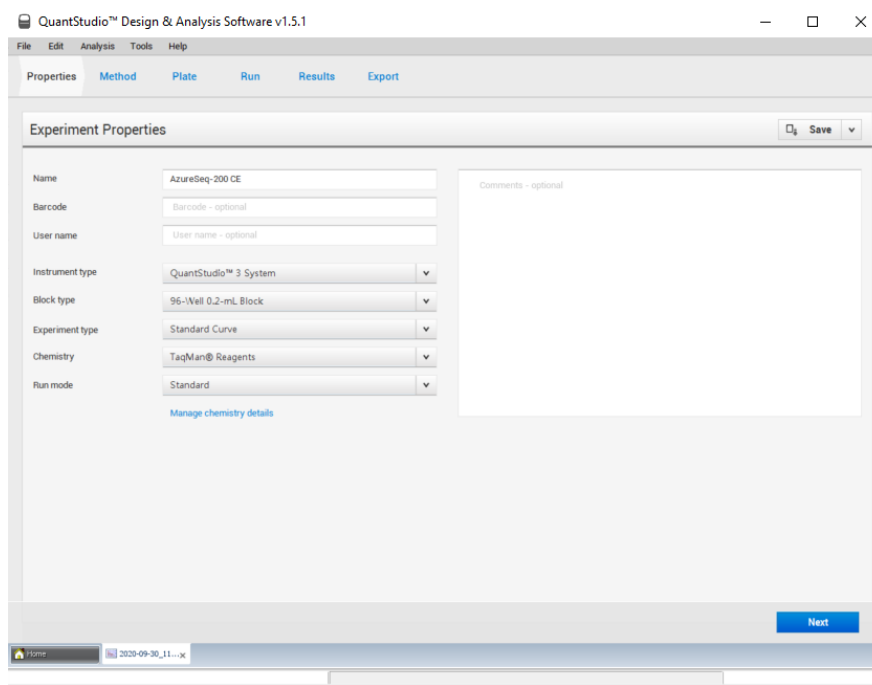
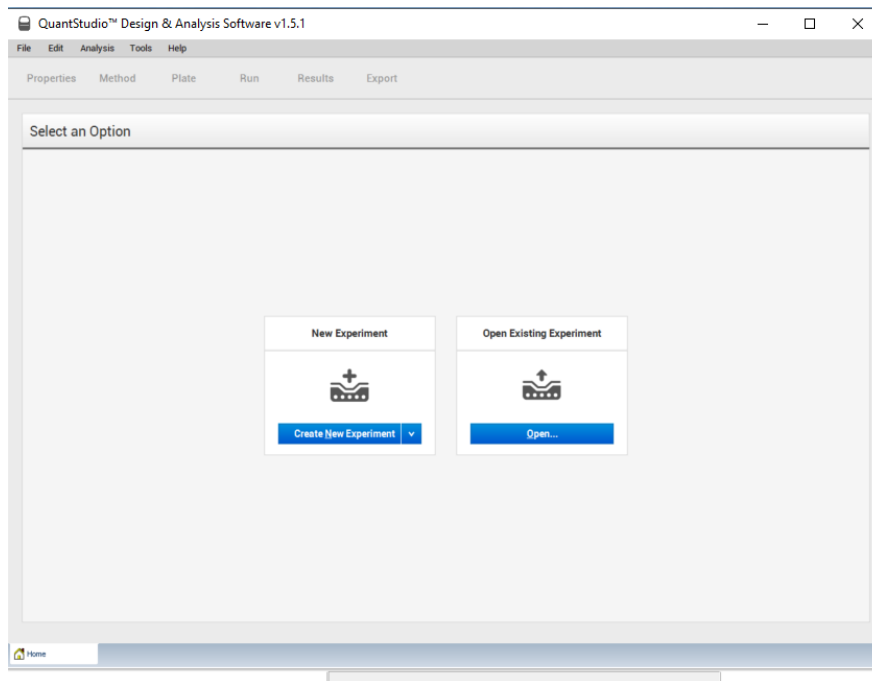
Cycling step	Stage	No. of cycles	Temperature ( $^{\circ}$ C)	Time
RT incubation	1	1	50	15 minutes
Enzyme activation	2	1	95	2 minutes
Amplification	3	45	95	3 seconds
			60**	30 seconds

\*\*Collect fluorescence during annealing/extension phase (60 $^{\circ}$ C) step on FAM, HEX, and ROX channels (or equivalent channels).

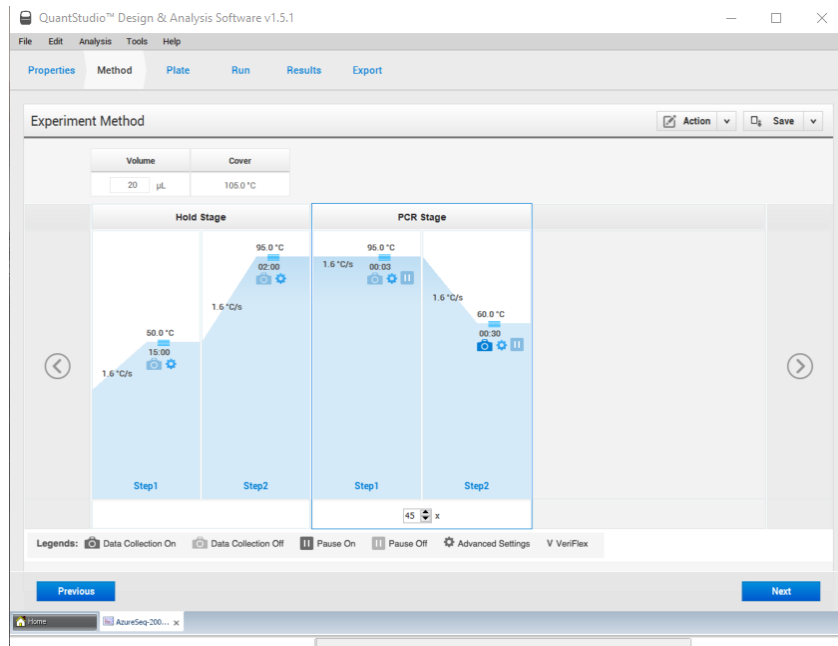
## 7.2 qPCR setup

### 7.2.1 QuantStudio 3, 5, 7 Pro

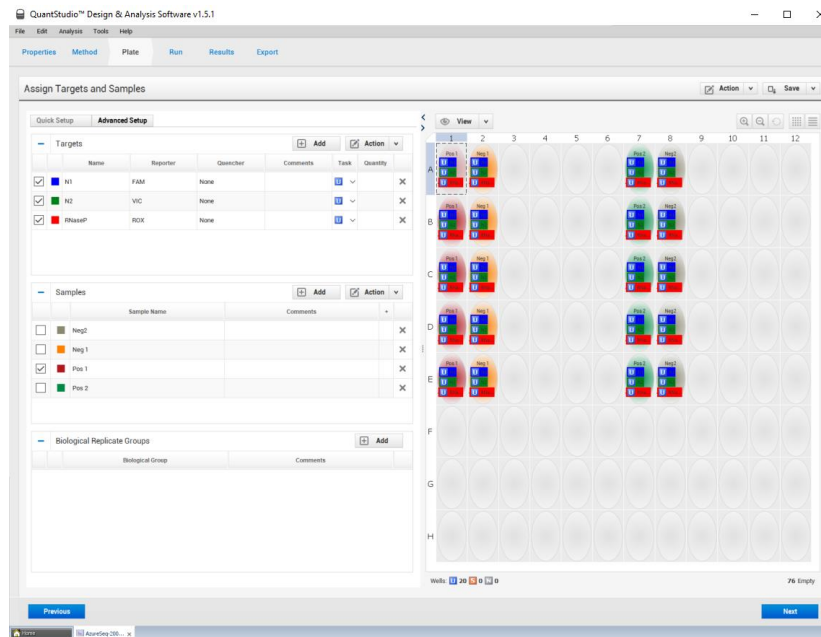
- Create a new experiment and then setup the Properties (Instrument Type, Block Type, Experiment Type, Chemistry, Run mode) according to the picture below.



- Set the method according to the PCR program detailed above.



- Set the targets and the samples on the Plate tab and assign the channels.



- Export the protocol to an USD drive.
- Load the Experiment from the USB drive on the qPCR instrument, insert the plate and start the Run.

## 7.2.2 Roche LightCycler 480 System

Please refer to the LightCycler 480 instrument Operator's manual for additional information on using the instrument.

- Create a 'Detection Format' to setup the targets (N1, N2, RNase P) and channels (FAM, HEX, ROX – or equivalent).
- Restart a software to access the newly created Detection Format.
- Select the color of the plate and create a New Experiment.
- Choose the new Detection Format from the drop-down list.
- Set the Block Size to 96 and the Reaction Volume to 20  $\mu$ L.
- Input the PCR program detailed in step 7.1.1.
- Set the Analysis Mode 'None' for RT incubation and Enzyme activation and 'Quantification' for the Amplification step.
- Set the Ramp to 4.4 for Stage 1, 2 and the first step of Stage 3 and to 2.2 for the second step of Stage 3.
- Load the plate and start the run.

## 7.2.3 BioRAD CFX96 Touch

Please refer to the CFX96™ Touch Instruction Manual for additional information on using the instrument.

- Run the CFX Manager software on the computer connected to the CFX96.
- Create a New Protocol by selecting the 'User-defined' run type.
- Click 'Edit Selected' on 'Protocol' tab to make changes to the protocol. Set the parameters of the PCR program detailed in Section 7.1.1.
- Click 'Edit Selected' on 'Plate' tab to setup the Plate.
- Click on 'Select Fluorophores', check the checkbox of the fluorophores (FAM, HEX, ROX – or equivalent).
- Specify the positive control well, set the sample type to "Positive Control", and set the detection fluorescences (N1 target - FAM, N2 target - HEX, Rnase P - ROX).
- Specify the negative control well, set the sample type to "Negative Control", and set the detection fluorescences (N1 target - FAM, N2 target - HEX, Rnase P - ROX).
- Wells with clinical specimens should be specified as Unknown, set the detection fluorescences (N1 target - FAM, N2 target - HEX, Rnase P - ROX).
- In the Setting menu set the plate type to BR white.
- Go to Start Run, select Block Name (PCR instrument) to use, close Lid and start the run.

## 8. Result interpretation

All test controls should be examined prior to interpretation of patient results. If the controls are not valid, the patient results cannot be interpreted. Collect fluorescence during annealing/extension phase (60°C) step on FAM (N1 marker), HEX (N2 marker), and ROX (RNaseP marker) channels (or equivalent channels). Ct values <40 are interpreted as positive by the user for the BioRad CFX96, Roche Lightcycler 480 System and QuantStudio 3, 5, and 7 Pro.

SARS-CoV-2 N1 (FAM)	SARS-CoV-2 N2 (HEX)	RNase P (Texas Red)	Result Interpretation	Action
+	+	+/-	Positive SARS-CoV-2	Report results to the healthcare provider and appropriate public health agencies.
If only one of the two targets is positive		+/-	Inconclusive	Repeat test.
-	-	+	SARS-CoV-2 Not Detected	Report results to the healthcare provider.
-	-	-	Invalid	Repeat test. If still invalid, collect another specimen. If another specimen is unavailable, report to the healthcare provider.

Use the table above as a general guide for result interpretation.

To report a patient test result, all controls within the same run must be valid and produce the expected results. If either or both of the controls is deemed invalid or produces unexpected results, no patient results from that run should be reported.

### RNase P (Extraction Control)

All clinical samples should exhibit fluorescence growth curves in the RNase P reaction that cross the threshold line within 40.00 cycles (< 40.00 Ct), thus indicating the presence of the human RNase P gene. Failure to detect RNase P in any clinical specimens may indicate:

- Improper extraction of nucleic acid/improper heat extraction from clinical materials resulting in loss of RNA and/or RNA degradation.
- Absence of sufficient human cellular material due to poor collection or loss of specimen integrity.
- Improper assay set up and execution.
- Reagent or equipment malfunction.

If the RP assay does not produce a positive result for human clinical specimens, interpret as follows:

- If the 2019-nCoV N1 and N2 are positive even in the absence of a positive RP, the result should be considered valid. It is possible that some samples may fail to exhibit RNase P growth curves due to low cell numbers in the original clinical sample. A negative RP signal does not preclude the presence of 2019-nCoV virus RNA in a clinical specimen.
- If all 2019-nCoV markers AND RNase P are negative for the specimen, the result should be considered invalid for the specimen. If residual specimen is available, repeat the extraction procedure and repeat the test. If all markers remain negative after re-test, report the results as invalid and a new specimen should be collected if possible.

#### 2019-nCoV Markers (N1 and N2)

- When all controls exhibit the expected performance, a specimen is considered negative if all 2019-nCoV marker (N1, N2) cycle threshold growth curves DO NOT cross the threshold line within 40.00 cycles (< 40.00 Ct) AND the RNase P growth curve DOES cross the threshold line within 40.00 cycles (< 40.00 Ct).
- When all controls exhibit the expected performance, a specimen is considered positive for 2019-nCoV if all 2019-nCoV marker (N1, N2) cycle threshold growth curves cross the threshold line within 40.00 cycles (< 40.00 Ct). The RNase P may or may not be positive as described above, but the 2019-nCoV result is still valid.
- When all controls exhibit the expected performance and the growth curves for the 2019-nCoV markers (N1, N2) AND the RNase P marker DO NOT cross the cycle threshold growth curve within 40.00 cycles (< 40.00 Ct), the result is invalid. The extracted RNA (obtained by direct method or with regular isolation) from the specimen should be re-tested. If residual RNA is not available, re-extract RNA from residual specimen and re-test. If the re-tested sample is negative for all markers and RNase P, the result is invalid and collection of a new specimen from the patient should be considered.
- When all controls exhibit the expected performance and the cycle threshold growth curve for any one marker (N1 or N2, but not both markers) crosses the threshold line within 40.00 cycles (< 40.00 Ct) the result is inconclusive. The extracted RNA should be retested. If residual RNA is not available, re-extract RNA from residual specimen and re-test.



## 9. Procedure Limitation

- The intended users must be trained with this technology prior to the use of this device.
- It is the intended user's responsibility to validate system performance for any procedures used in their laboratory which are not covered by Omixon Biocomputing Ltd.'s performance studies.
- Use this product only with following human biological samples: nasopharyngeal (NP) and oropharyngeal (OP) swabs
- The efficiency of the direct approach (without RNA extraction; heat treatment) is highly dependent on the VTM media used during the sample collection process. Using VTM from the following manufacturers: Clinichem, Copan, Puritan, CDC VTM is highly recommended. Other manufacturers' VTM, mwe Medical Wire must be validated by the end user laboratory.
- Results are dependent on appropriate specimen collection and absence of inhibitors. The presence of PCR inhibitors may cause invalid or inconclusive results which requires repetition.
- False Positive results may occur due to the several reasons, most of which relate to RNA contamination during specimen handling and preparation.

## 10. Troubleshooting

Problems	Possible root cause	Recommendation
Fluorescent intensity is weak or does not appear in the positive control	Probe degradation	Use a new probe aliquot or repeat test with a new kit LOT
High inconsistency in the fluorescence signals in samples	Inaccurate pipetting	Use calibrated pipettes, make sure that an equal volume of reagents is added to each wells/tube
Fluorescent signal is detected in the negative control reaction	Carry over contamination	Always change tips between samples. Take care when dispensing samples, negative controls, and positive controls
	Contamination of the amplification master mix	Use a new aliquot of amplification mix
	Contamination of the extraction/preparation area	Use disinfectant to clean and disinfect the areas
No fluorescent signal is detected in all samples, including positive control	Probe degradation	Use new probe aliquot
	Thermal cycler setting error	Verify the correct program setting of the real time PCR instrument
	Wrongly prepared master mix, possible omitted component	Verify each component and repeat the PCR master mix preparation
False negative results	Presence of RT-PCR inhibitors	Validate the RNA extraction kit prior to use. Use VTM from the recommended manufacturers listed in this IFU
	Improper sample collection	Follow validated sample collection method
	Failure to follow instruction for use	Read the Instructions for Use carefully before processing samples. Any deviation from procedures written here may affect optimal performance.
	Using unauthorized reagents	Do not substitute or mix the AzureSeq-200 RUO kit reagents with reagents from other manufacturers.
False positive reaction	Cross contamination between samples	Take extra care when handle patient specimens, use straightforward and validated traceability processes in the laboratory
	Sample mix-up	

## 11. Quality Control

Validating the whole assay procedure (direct or including a separate RNA extraction) and amplification session by processing a negative tested sample and a positive tested sample or a calibrated reference material) is recommended.

## 12. Contact information

For general assistance with this protocol contact:

**Email Support:**

[azureseq.support@omixon.com](mailto:azureseq.support@omixon.com)

**Telephone Support:**

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