

RIDA®Plex Respiratory Pathogens 24 well

REF 80617



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1. INTENDED PURPOSE

This panel of assays is a qualitative, semi-automated in vitro diagnostic (IVD) multiplexed nucleic acid test. The test utilises multiplex-tandem polymerase chain reaction (MT-PCR) for the identification of pathogens in nucleic acid extracts from an appropriate respiratory specimen or cultured isolate (Stanley and Szewczuk, 2005). Respiratory specimens can be taken from the upper respiratory tract (e.g. nasal swabs, nasopharyngeal swabs, nasal aspirates and throat swabs) or lower respiratory tract (e.g. sputum, bronchial washings, bronchoalveolar lavage and endotracheal aspirates), or a saliva specimen for the detection of SARS-CoV-2, following the manufacturer's instructions for the associated specimen collection device. Use of the test is restricted to suitably trained personnel in qualified laboratories using the RIDA®Xplore (REF 96521), HighPlex (REF 91501), RIDA®Jump (REF 96221) or UltraPlex 3 (REF 94601).

The panel of assays is intended for the detection and identification of nucleic acid from the pathogens described in **SUMMARY AND EXPLANATION OF THE TEST**.

Nucleic acids from the pathogens identified by this test are typically detectable in respiratory specimens during the acute phase of infection. The detection of target nucleic acids in symptomatic individuals is indicative of the presence of the identified pathogen and supports the diagnosis of a respiratory infection when used in conjunction with other clinical evaluations, diagnostic procedures and epidemiological evidence.

The results of this test should not be used as the exclusive basis for patient management decisions. Positive results are indicative of the presence of the identified pathogen in the sample and cannot exclude the presence of other pathogens or confirm the definitive cause of the clinical presentation.

A negative result does not exclude the possibility of infection with pathogens not detected by this test or novel variants of included pathogens. A negative result cannot be relied upon for a definitive diagnosis. A lower respiratory tract infection may not be detected where an upper respiratory tract specimen is used. Negative results should be used in conjunction with information available from clinical evaluations and other diagnostic procedures. Failure or delay in treatment of an infected patient may lead to death, with immunocompromised patients being at highest risk.

2. FURTHER INSTRUCTIONS REQUIRED

The Instructions for Use (IFU) for this panel includes product-specific information not provided in other IFUs. The IFU for this product can be viewed by visiting the Knowledge Centre using the URL printed on the outer box label. Additionally, a copy is available upon request by contacting customer service via phone, email, or mail (see **TECHNICAL ENQUIRIES**).

These instructions for use must be read in conjunction with the IFU for:

- RIDA®Xplore (REF 96521) or HighPlex (REF 91501)
- RIDA®Jump (REF 96221) or UltraPlex 3 (REF 94601)
- RIDA®Plex L RNA Cassette (REF 40331)
- RIDA®Plex Medium RNA Reservoir (REF 40521)
- RIDA®Plex S RNA Reservoir (REF 40731)
- RIDA®Plex M RNA Reservoir (REF 40721)
- RIDA®Plex L RNA Reservoir (REF 40711)

and if applicable:

- RIDA®Plex Positive Control Respiratory Pathogens (REF 91011)
- RIDA®Plex Extraction Control (REF 91401)

3. SUMMARY AND EXPLANATION OF THE TEST

These tests utilise a multiplex-tandem polymerase chain reaction (MT-PCR) for the amplification of targeted DNA and/or RNA (Stanley and Szewczuk, 2005). For the full description of the principle of the method, refer to the relevant robotic system IFU (section “**PRINCIPLE OF THE METHOD**”).

The panel is intended to detect the following targets that have been associated with respiratory infections:

RIDA® PLEX RESPIRATORY PATHOGENS 24 WELL REF 80617 VER 10

Assay	Target
Viral targets	
EV	Enterovirus (types A, B, C and D)
HAdV	Human Adenovirus (includes groups B, C, E, excludes HAdV-21)
hMPV	Human Metapneumovirus (type A and B are differentiated)
hPIV1 and hPIV4	Human Parainfluenza viruses 1, 4A and 4B
hPIV2 and hPIV3	Human Parainfluenza viruses 2 and 3
Influenza A	Influenza virus A (includes H1, H3, H5 and H7)
Flu Typing	Influenza virus A serotypes pdH1N1 (H1(2009)) and HA-H3 (including H3N2)
Influenza B	Influenza virus B (Yamagata and Victoria lineages)
Parechovirus	Human Parechovirus (includes types 1-8)
RSV	Respiratory Syncytial Virus (includes and differentiates types A and B)
RV/EV	Rhinovirus (types A, B and C) and Enterovirus (types A, B, C and D)
SARS-CoV-2 ORF1	Severe Acute Respiratory Syndrome Coronavirus 2 (ORF1 gene)
SARS-CoV-2 ORF8	Severe Acute Respiratory Syndrome Coronavirus 2 (ORF8 gene)
Seasonal CoV	Human seasonal Coronaviruses OC43, 229E, HKU1 and NL63
Bacterial targets	
Bordetella	<i>Bordetella</i> IS481 (<i>Bordetella</i> spp., which includes <i>B. pertussis</i> and <i>B. holmesii</i>)
B. parapertussis	<i>Bordetella</i> IS1001 (includes all strains of <i>B. parapertussis</i> and some <i>B. bronchiseptica</i>)
B. pertussis	<i>Bordetella pertussis</i>
C. pneumoniae	<i>Chlamydomphila pneumoniae</i> (includes all strains)
C. psittaci	<i>Chlamydomphila psittaci</i> (includes all strains)
Legionella	<i>Legionella pneumophila</i> (all serotypes) and <i>Legionella longbeachae</i> (all strains)
M. pneumoniae	<i>Mycoplasma pneumoniae</i> (includes types 1 and 2, and their variants)

Fungal targets	
PCP	<i>Pneumocystis jirovecii</i> (includes all strains)
Control(s)	
Sample Adequacy	Human reference gene for sample adequacy control
SPIKE	Artificial sequence for assay control.

3.1 TARGET DESCRIPTIONS: VIRUSES

Enteroviruses (EV)

EV is a picornavirus and the most common cause of viral meningitis. EV serotypes were initially defined by their pathogenicity as either polioviruses, coxsackieviruses, or echoviruses, however they have since been re-classified as species Enterovirus A to Enterovirus J to reflect their molecular distinctions (Bruu, 2002). This assay is designed to detect human infectious Enterovirus groups A to D, which includes a wide range of echoviruses, coxsackieviruses A and B, and enteroviruses 70 to 71.

Note: The RV/EV and EV assay outputs are used by the RIDA®Result or MT-PCR Results software to discriminate between Rhinovirus and Enterovirus. Refer to the Diagnostic window for result. More information can be found in **INTERPRETATION OF RHINOVIRUS AND ENTEROVIRUS**.

Human Adenoviruses (HAdV)

Human adenovirus can cause infections of the upper and lower respiratory tract throughout the year. Most people have had at least one adenovirus infection by the age of 10 years (Public Health England, 2014b). HAdV species B (types 3 and 7), C (types 1, 2 and 5) and E (type 4) are most frequently associated with respiratory disease (Centers for Disease Control and Prevention, 2015). The HAdV assay is designed to detect all three species except for type 21 of HAdV species B.

Warning: This assay could also detect some variants of HAdV species A or D.

Human Metapneumovirus (hMPV)

Human Metapneumovirus (hMPV) was first isolated in 2001, but has been in circulation prior to this (Public Health England, 2014b). hMPV is divided into two subgroups (A and B) and different lineages circulate from year to year (Sloots et al., 2006). hMPV shows similar symptoms to RSV, however unlike RSV no particular subgroup of hMPV has yet been shown to result in more severe disease than another (Sloots et al., 2006). The hMPV assay is designed to detect hMPV A and B, and the RIDA®Result or MT-PCR Results software will distinguish between the two subgroups.

Human Parainfluenza Viruses (hPIV1, hPIV2, hPIV3, and hPIV4)

Human Parainfluenza viruses cause significant respiratory infections in pre-school children and immunocompromised patients worldwide (Public Health England, 2014b). Of the four hPIV types, types 1 to 3 are more commonly isolated from respiratory infections (Liu et al., 2013). The hPIV assays are designed to detect hPIV1 to hPIV4.

Influenza A

Influenza virus A is the most virulent influenza virus in humans and is sub-typed depending on surface haemagglutinin (HA) and neuraminidase (NA). The most significant H1 subtype has been H1N1, causing the Spanish Flu in 1918 (Public Health England, 2014b). A novel H1N1 strain emerged in 2009 (pdH1N1 or “swine flu”) that contained viral segments from human, pig and avian influenza (Bishop, Murnane and Owen, 2009). The most common H3 variant is H3N2, which had its first known outbreak in 1968 in Hong Kong (Bean et al., 1992). H5 and H7 variants are hosted by birds with certain strains transmissible to humans (causing “avian influenza”) where sporadic infections are a public health concern. H5N1 has a mortality rate of about 60% of all known cases, where most sources of infection were from infected birds or contaminated environments (World Health Organization, 2015). Several H7 subtype infections with high pathogenicity have been reported in recent years, however there have been limited reports of human-to-human transmission (World Health Organization, 2015). The Influenza A assay is designed to detect Influenza A subtypes H1, H3, H5 and H7.

Flu Typing

The Flu Typing assay is designed to detect pdH1N1 (H1(2009)) and HA-H3 (including H3N2).

Note: If the Flu Typing assay calls positive and the Influenza A assay calls negative, then the test result for the sample is positive for Influenza A and the result for the Flu Typing assay is correct.

Influenza B

Influenza virus B is less common than Influenza virus A and causes influenza outbreaks when population immunity is overcome by viral mutations. The Influenza virus B assay is designed to detect both Influenza B variants, Victoria and Yamagata (Rota et al., 1990).

Human Parechovirus (hPeV)

Human Parechovirus (hPeV) is a picornavirus that is most associated with infection in neonates or children under 10 years of age. Like EV, it is difficult to culture, and makes up 2% of “EV” isolates in clinical laboratories using cell culture (Scheld, Whitley and Marra, 2014). hPeV1 and hPeV2 are the most common hPeV types to be isolated worldwide, and hPeV3 is the most common cause of hPeV meningitis (Scheld, Whitley and Marra, 2014). The Parechovirus assay is designed to detect hPeV types 1 to 8.

Respiratory Syncytial Virus (RSV)

Respiratory Syncytial Virus (RSV) is a leading cause of lower respiratory tract infections in young children and accounts for 50 – 90% of bronchiolitis hospital admissions (Public Health England, 2014b). Out of the two A and B strains in circulation, RSV A is the predominating strain. The RSV assay is designed to detect and distinguish both RSV A and B.

Warning: Discrimination between RSV A and B strains is for information purposes only.

Rhinovirus and Enterovirus (RV/EV)

Rhinovirus and Enterovirus are members of picornaviruses, which are regarded as the most common cause of viral infection worldwide notably the “common cold”. EV serotypes were initially defined by their pathogenicity as either polioviruses, coxsackieviruses or echoviruses, however they have since been re-classified as species Enterovirus A to Enterovirus J to reflect their molecular distinctions (Scheld et al., 2014). Rhinoviruses (RV) are associated with high rates of upper respiratory infections and colds in children and the elderly (Mackay, 2008). The RV/EV assay is designed to detect human Rhinovirus groups A to C and human Enterovirus groups A to D, which includes previous virus classification groups: echoviruses; coxsackieviruses A and B; and enteroviruses 68, 70 and 71.

Note: The RV/EV and EV assay outputs are used by the RIDA®Result or MT-PCR Results software to discriminate between Rhinovirus and Enterovirus. Refer to the Diagnostic window for result. More information in **INTERPRETATION OF RHINOVIRUS AND ENTEROVIRUS**.

SARS-CoV-2

Coronaviruses are a large family of RNA viruses which may cause illness in animals or humans. In humans, several coronaviruses are known to cause respiratory infections ranging from the common cold to more severe diseases such as Middle East Respiratory Syndrome (MERS) and severe acute respiratory syndrome (SARS). SARS-CoV-2 causes coronavirus disease COVID-19 and was first observed in Wuhan, China.

Warning: If either of the SARS-CoV-2 assays calls positive, the test result for the sample is positive for SARS-CoV-2.

Human Coronaviruses (hCoV)

Human Coronaviruses (hCoV) are a large family of RNA viruses that are the second most frequent cause of the common cold behind rhinoviruses and are responsible for more severe infections such as Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS) (Turner, 2012). Four types are continuously distributed worldwide: hCoV-HKU1, -229E, -OC43 and -NL63. Out of the coronaviruses, hCoV-229E and hCoV-OC43 are the most frequently isolated (Gaunt et al., 2010). The recently discovered coronavirus SARS-CoV-2 causes coronavirus disease COVID-19 and was first observed in Wuhan, China.

Warning: The 'Seasonal Coronavirus' assay is not intended to detect MERS-CoV, SARS-CoV or SARS-CoV-2.

Warning: Samples containing high concentrations of SARS-CoV-2 (Ct values of less than 10) may result in present calls for seasonal coronavirus.

3.2 TARGET DESCRIPTIONS: BACTERIA

***Bordetella* spp.**

Bordetella spp. are the cause of “whooping cough” and are highly prevalent amongst young, unvaccinated populations (Mattoo and Cherry, 2005). However, they are also re-emerging in highly vaccinated populations. The *Bordetella* spp. assay designed to detect *Bordetella* IS481 which is present within *B. pertussis* and *B. holmesii* species.

Note: Other *Bordetella* species possessing IS481 will also be detected. For example, some variants of *B. bronchiseptica* can possess IS481.

Bordetella parapertussis

Bordetella parapertussis is a human pathogen that causes a milder pertussis-like disease, but does not express the pertussis toxin (Kilgore et al., 2016). Unlike *B. pertussis*, *B. parapertussis* can infect other mammals and causes a mild cough in adults or more serious infections in immunocompromised patients (Mattoo and Cherry, 2005). The *B. parapertussis* assay is designed to detect IS1001 which is present in *B. parapertussis* but can also be found in some variants of *B. bronchiseptica*.

Warning: Other *Bordetella* species possessing IS1001 will be identified as *B. parapertussis*.

Bordetella pertussis

Bordetella pertussis is the primary pathogen that causes whooping cough. It is a strictly human pathogen, with no other known reservoir (Mattoo and Cherry, 2005). The *B. pertussis* assay is designed to detect *B. pertussis*.

Chlamydophila pneumoniae

Chlamydophila pneumoniae is a cause of milder community-acquired pneumonia. *C. pneumoniae* is often identified in the presence of other bacterial pathogens (e.g. *S. pneumoniae*) (Harris et al., 2011). The *C. pneumoniae* assay is designed to detect all strains of *C. pneumoniae*.

Chlamydophila psittaci

Chlamydophila psittaci causes respiratory disease in humans and birds, with poultry handlers at higher risk of transmission (Public Health England, 2014a). All serovars of *C. psittaci* are considered transmittable to humans and can result in mild flu-like symptoms through to fatal pneumonia (Rodolakis and Yousef Mohamad, 2010). The *C. psittaci* assay is designed to detect all strains of *C. psittaci*.

Warning: Samples containing high concentrations of closely related *Chlamydia* species such as *C. abortus* or *C. caviae* may yield a positive result for *C. psittaci* due to the high degree of sequence homology between these organisms.

Legionella longbeachae

Legionella longbeachae has been isolated from potting mixes/soils and it can infect humans after inhalation of dust (from dry potting mix), aerosols or poor gardening hygiene (lack of hand washing before eating or smoking after soil contact) (O'Connor et al., 2007). The *L. longbeachae* assay is designed to detect all known strains of *L. longbeachae*.

Legionella pneumophila

Legionella pneumophila causes up to 90% of cases of Legionellosis (Fields, Benson and Besser, 2002). *L. pneumophila* is a ubiquitous aquatic organism which grows best in warm water so is often found in large air conditioning systems, cooling towers, water tanks and can spread via the formation of aerosols. The *L. pneumophila* assay is designed to detect all known strains of *L. pneumophila*.

Mycoplasma pneumoniae

Mycoplasma pneumoniae is second to *Streptococcus pneumoniae* as the most common cause of community acquired pneumonia. Epidemics caused by *M. pneumoniae* can occur every 4-5 years (PHE, SMI B 57) (Public Health England, 2015). This assay is designed to detect both recognised types of *M. pneumoniae*: type 1 and type 2 and their variants.

3.3 TARGET DESCRIPTIONS: FUNGI

Pneumocystis jirovecii

Pneumocystis jirovecii causes pneumocystis pneumonia (PCP) and is a common opportunistic disease in the immunosuppressed, particularly in post-transplant and HIV-positive persons (Krajicek, Thomas and Limper, 2009). In people with a healthy immune system, *P. jirovecii* is suggested to be a common asymptomatic infection (Ponce et al., 2010). The PCP assay is designed to detect *P. jirovecii*.

4. PANEL COMPONENTS AND REAGENTS: MATERIALS AND STORAGE

Note: Step 1 and Step 2 products and associated reagents do not contain hazardous substances, as listed in CLP Regulation (EC) No 1272/2008 and according to the Globally Harmonised System (GHS) classification.

Panel Name	Panel components	REF
RIDA®Plex Respiratory Pathogens 24 well	RIDA®Plex Respiratory Pathogens 24 well Step 1	80617S
	RIDA®Plex Respiratory Pathogens 24 well Step 2	80617P
To be used with:	RIDA®Plex L RNA Cassette	40331
	RIDA®Plex Medium RNA Reservoir	40521
	RIDA®Plex S RNA Reservoir	40731
	RIDA®Plex M RNA Reservoir	40721
	RIDA®Plex L RNA Reservoir	40711

4.1 RIDA®PLEX STEP 1

Step 1 for this panel contains reagents for up to 96 samples.

Materials	Description	Qty.
RIDA®Plex Step 1	1 x 96-slots plastic frame containing 12 x foil-sealed 8-well strips of plastic tubes with dried oligonucleotides.	96

STORAGE AND HANDLING CONDITIONS

The Step 1 are delivered with a 12-month shelf life providing the product is refrigerated at 2 - 8°C on arrival as per label instructions. Products are delivered at room temperature.

If the product is being partially used, the product may be removed from the refrigerator to remove the required Step 1, but remaining product must be returned to the refrigerator within 30 minutes.

The RIDA®Plex Step 1 may also be stored on arrival at 8 - 25° C but the shelf life is reduced to 6 months from the date of manufacture. In the case of ambient temperature storage, the provided labels must be applied to the product to indicate the ambient storage temperature and reduced shelf life.

Product is transported at ambient temperature and can withstand a total of 28 days (four weeks) in transit across all stages of the distribution channel, from the manufacturing facility through intermediate storage and handling by distributors to final delivery to the end user.

Warning: Once the product is stored at room temperature for beyond 30 minutes, it cannot be stored back at 2 - 8°C. Instead, the expiry date for storage at room temperature will apply, which is six months from the date of manufacture. Deviations from the stipulated storage of the product may lead to false or inconclusive results.

4.2 RIDA®PLEX STEP 2

The Step 2 box for this panel contains reagents for up to 192 samples.

Materials	Description	Qty.
RIDA®Plex Step 2	Sealed bag containing 1 X 384-well plate with dried oligonucleotides and two desiccant pouches.	12
Dilution plate	1 X Foil-sealed 96-well plate to prepare the Step 2 dilutions.	6

STORAGE AND HANDLING CONDITIONS

The Step 2 box must be stored between 15 - 25° C.

Warning: Ensure desiccant pouches are intact before removing product from sealed bag; do not use product if desiccant is compromised or missing.

The expiration of the product is provided on the label.

4.3 ADDITIONAL CONSUMABLES REQUIRED BUT NOT PROVIDED

Contact AusDiagnostics to purchase the following consumables (see **TECHNICAL ENQUIRIES**).

- Dilution Plates (REF 90020)
- Sealing Films for Step 2 (REF 90201)
- 100 µL A-line Non-conductive Tips, 4800 tips (REF 93250) (for RIDA®Xplore and HighPlex)
- HP-line Tip Disposal Bags (REF 91502) (for RIDA®Xplore and HighPlex)
- Bleach Tubes (REF 91503) (for RIDA®Xplore and HighPlex)
- 50 µL T-line Conductive Tips, 2304 tips (REF 93061) (for RIDA®Jump and UltraPlex 3)
- 200 µL T-line Conductive Tips, 2304 tips (REF 93062) (for RIDA®Jump and UltraPlex 3)
- 1000 µL T-line Conductive Tips, 2304 tips (REF 94741) (for RIDA®Jump)
- T-line Tip Disposal Bags (REF 94503) (for RIDA®Jump and UltraPlex 3)
- Reagent Reservoir Thawing Block (REF 94606) (for UltraPlex 3)
- Reagent Reservoir Thawing Block V2 (REF 94745) (for RIDA®Jump)
- RIDA®Plex Positive Control Respiratory Pathogens (REF 91011)
- RIDA®Plex Extraction Control (REF 91401)
- Reagents as per **PANEL COMPONENTS AND REAGENTS: MATERIALS AND STORAGE**

Required reagents and equipment that are not provided by AusDiagnostics are:

- Personal protective equipment (PPE)
- Bleach with 0.4% available chlorine (4 mL required per run)
- Nuclease-free and adjustable pipettes
- Nuclease-free and sterile filtered tips

5. SPECIMEN REQUIREMENTS

5.1 SPECIMEN TYPES AND VOLUME

A nucleic acid extract from an appropriate respiratory secretion, suitable for PCR testing, should be used with this product. Respiratory specimens may be taken from the upper respiratory tract (e.g. nasal swabs, nasopharyngeal swabs, nasal aspirates, and throat swabs) or the lower respiratory tract (e.g. sputum, bronchial washings, bronchoalveolar lavage, and endotracheal aspirates), as well as from cultured isolates, following the manufacturer's instructions for specimen collection devices. Important to note, that saliva specimen is only suitable for the detection of SARS-CoV-2.

Note: Store nucleic acid extract in tubes free from PCR inhibitors and nucleases.

When working with RNA samples, standard precautions to minimise RNA degradation should be used.

Warning: Always handle and dispose of specimens potentially containing human pathogens according to relevant safety procedures; refer to SDS where required.

Sample volume to be added to Step 1 tube must be 10 µL.

5.2 SUITABLE NUCLEIC ACID EXTRACTION METHODS

Warning: Manual extraction and pipetting of nucleic acid extracts into Step 1 tubes is best performed in a biological safety cabinet or PCR setup area.

If a specimen needs to be extracted for utilisation of this panel, refer to the Instructions for Use (IFU) provided with your extraction kit for details of the workflow and validated specimen types.

The following manual and automated nucleic acid extraction methods have been validated by AusDiagnostics customers and have been deemed suitable to produce nucleic acid extracts compatible with this panel of assays. For further details on the extraction protocols used, contact AusDiagnostics (see **TECHNICAL ENQUIRIES**).

Extraction System	Protocol Name	Type
RIDA®Xtract 24 or MT-Prep™ 24	RIDA®Xtract 24 Pathogen Kit or MT-Prep™ Viral/Pathogen Nucleic Acids Extraction Kit B (48 samples)	Automated
RIDA®Xtract 96 or MT-Prep™ XL	RIDA®Xtract 96 DNA/RNA Kit or Puryx Comprehensive DNA / RNA Extraction Kit	Automated
Abbott 2000	mSample Preparation System DNA	Automated
bioMerieux, NucliSENS easyMAG	NUCLISENS magnetic silica particles	Automated
bioMerieux EMAG	EMAG magnetic silica particles	Automated
PerkinElmer Chemagic Prepito-D	Chemagic Prepito-D	Automated
PerkinElmer JANUS	Chemagic DNA Kit	Automated
Qiagen QIAcube	QIAcube	Automated
Qiagen QIAasympy	DSP/Virus/Pathogen Mini Kit	Automated
Qiagen EZ1 Advanced	EZ1 DSP Virus Kit	Automated
Qiagen QIAamp	DNA mini kit	Manual
Roche High Pure series	High Pure Viral Nucleic Acid Kit	Manual

Roche MagNA Pure 96	Pathogen Universal 200	Automated
Roche MagNA Pure series	High Pure Viral Nucleic Acid Kit	Automated
Roche MagNA Pure LC 2.0	LC Total NA panel LV Kit	Automated

6. INTERPRETATION OF RESULTS

Warning: IVD performance claims do not extend to any changes made by the user to a result (i.e., “Reject” or “Confirm” a result). These user changes will be clearly indicated in the Analysis Report.

The cycling curves and the melt curves of a run are displayed in the Result software (RIDA®Result or MT-PCR Results). Based on predefined parameters, the software will call the target as “Present”, “Check” or blank (not detected). Note that multiple infections are possible. Molecular target concentrations, expressed as arbitrary units, are calculated relative to the internal control SPIKE, which amplifies a known amount of target molecules. As the concentration of SPIKE is not measured, these values are in arbitrary units. Furthermore, in some panels of assays the relative concentration of each target may be inferred from the normalised percent (displayed in parentheses after the “Present” call).

For further details on analysis of results, refer to the following IFUs:

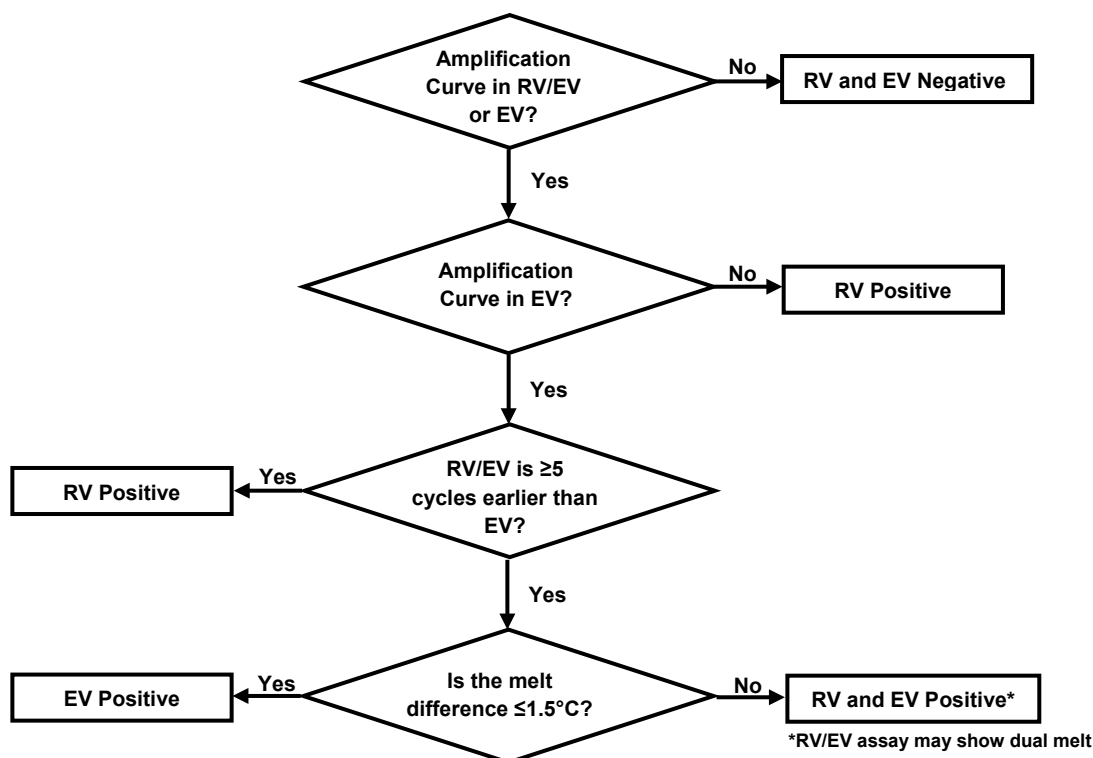
- RIDA®Xplore or RIDA®Jump (“**INTERPRETATION OF RESULTS**”),
- HighPlex IFU (“**INTERPRETING SOFTWARE RESULTS**”) or
- UltraPlex 3 IFU (“**MT-PCR RESULTS SOFTWARE**”).

Warning: For notifiable diseases, report results to applicable state or local public health departments.

6.1 INTERPRETATION OF RHINOVIRUS AND ENTEROVIRUS

Discrimination of Rhinovirus (RV/EV) and Enterovirus (EV) positive results is displayed in the “Diagnosis” or “Interpretation of Results” under the Results table and relevant output report files.

Warning: Automated calling for Rhinovirus and Enterovirus is unable to discriminate between the two pathogens when the Ct difference is ≤ 5 cycles or when there is a dual infection. The flowchart and description below can be applied to allow user interpretation of Rhinovirus (RV/EV) and Enterovirus (EV) positive results.



RV can be considered present if:

- The RV/EV assay is Present and the EV assay absent.
- The RV/EV and EV assays are Present, and the Ct of the RV/EV assay is earlier (>5 cycles) than the EV assay.

EV can be considered present if:

- The RV/EV and EV assays are Present and both assays have similar Ct's, and melts.

Both RV and EV can be considered present if:

- The RV/EV and EV assays are Present, and the melt difference is $>1.5^{\circ}\text{C}$, or dual melt peaks are present in the RV/EV assay.

The diagnosis window will display 'Low Concentration' if:

- RV/EV or EV Concentration is <100 .

For further details on analysis of results, refer to the System IFU.

Warning: Report results to state or local public health departments, if applicable.

7. CONTROLS

7.1 POSITIVE CONTROL

A positive control should be included in every run. Refer to individual laboratory procedures. The failure of a positive control should lead to the reassessment of any negative result obtained since the last control was run.

The RIDA®Plex Positive Control Respiratory Pathogens (REF 91011) contains all targets for this panel.

The RIDA®Plex Positive Control IFU must be read before using this product.

7.2 NEGATIVE CONTROL

A negative control should be used according to the individual laboratory procedures. Amplification of the negative control indicates contamination from the environment (e.g., from handling during set-up or spillages of sample material on the robot deck). In this case, the surface of the robot deck (including the thermal cycler cover) should be wiped with a non-corrosive nucleic acid denaturing reagent (e.g., DNA-OFF™) and then UV treated. The relevant samples should be retested.

Warning: Do not use bleach to clean the instrument.

7.3 SAMPLE ADEQUACY CONTROL

The Sample Adequacy Control assay targets a human DNA reference gene, to indicate the presence of human DNA in the nucleic acid extract or direct sampling specimen.

Note: If both the assay and Sample Adequacy Control call negative, a new sample should be collected. If the assay calls positive and the human DNA control calls negative, the sample is positive.

7.4 RIDA®PLEX EXTRACTION CONTROL

An extraction control should be used during the extraction process. Refer to the IFU for RIDA®Plex Extraction Control (REF 91401) “**PROCEDURE FOR USE**” to determine the concentration of extraction control required.

Warning: if the extraction control is not detected during analysis with RIDA®Plex panels, negative results cannot be relied upon. It is recommended that any sample with a negative extraction control should be re-extracted if appropriate and analysis repeated.

7.5 SAMPLE INHIBITION AND INSTRUMENT FUNCTION CONTROL

SPIKE is an artificial sequence that is present in Step 1 to monitor sample inhibition and instrument performance. SPIKE has been designed to have no cross-reactivity with diagnostic targets or assays. If SPIKE is shown to be inhibited, then this suggests that the sample contained inhibitory substances, or that the reaction conditions are suboptimal. In this case a negative result cannot be relied upon, and it is recommended that the sample should be re-extracted if appropriate, and analysis repeated. For further details on analysis of SPIKE, refer to “**INHIBITED**” in the IFU of the relevant robotic system.

8. PERFORMANCE CHARACTERISTICS

8.1 REPRODUCIBILITY AND REPEATABILITY

The reproducibility of assays on the RIDA®Xplore, HighPlex and UltraPlex 3 systems was assessed by testing five samples on three batches across three days (with each batch tested once per day) and three systems with three operators. The coefficient of variation (CV) for the resulting mean cycle take-off values (Ct values) for each of the samples were calculated. It was found that the Ct values for all samples at all concentrations were highly reproducible with CV values ranging from 2.08% to 4.86%, averaging 3.40%.

The reproducibility of assays on the RIDA®Jump system was assessed by testing five samples on three batches across three days (with each batch tested once per day) and three systems with three operators. The CV for the resulting mean cycle take-off values (Ct values) for each of the samples were calculated. It was found that the Ct values for all samples at all concentrations were highly reproducible with CV values ranging from 1.85% to 5.81%, averaging 3.13%.

The repeatability of assays on the RIDA®Xplore, HighPlex and UltraPlex 3 systems was assessed by testing five samples on three batches with one batch tested three times each day on one system. It was found that the Ct values for all samples at all concentrations were highly repeatable with CV values ranging from 2.26% to 5.11%, averaging 3.84%.

The repeatability of the assays on the RIDA®Jump system was assessed by testing sixty-three samples, three times, using the same system and product batch on the same day. It was found that the Ct values for all samples at all concentrations were highly repeatable with CV values ranging from 0.54% to 5.60%, averaging 2.58%.

The low CV from these studies provides evidence that the RIDA®Xplore, HighPlex, RIDA®Jump and UltraPlex 3 systems are suitably precise for IVD use.

8.2 INTERFERING SUBSTANCES

A range of exogenous and endogenous substances including those expected to be found in the sample types for this panel were tested for potential PCR interference. Minimal or no interference was seen due to the presence of any one of the substances tested

The presence of the internal control SPIKE in all AusDiagnostics panels controls for possible PCR interference in each sample.

For further details on interfering substances, refer to “**INTERFERING SUBSTANCES**” in the IFU of the relevant robotic system.

8.3 ANALYTICAL SPECIFICITY

Pathogens that are likely to be present in the specimen types used during the clinical validation were tested for cross-reactivity with the assays in this product. No cross-reactivity was seen. Pathogens tested include: *Staphylococcus aureus*, *Staphylococcus epidermidis*, coagulase negative *Staphylococcus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter cloacae*, *Streptococcus pneumoniae*, *Proteus mirabilis*, *Salmonella typhi*, *Bacteroides fragilis*, *Klebsiella oxytoca*, *Enterococcus faecalis*, *Pseudomonas aeruginosa*, *Streptococcus gordonii*, *Streptococcus pyogenes*, *Streptococcus constellatus*, *Streptococcus salivarius*, *Sphingobacterium spiritivorum*, *Corynebacterium jeikeium* and *Propionibacterium acnes*.

8.4 ANALYTICAL SENSITIVITY

For assays marked with an *, the limit of detection (LoD) was determined using a serial dilution of plasmids quantified by dPCR. For assays marked with an **, the LoD was determined using a serial dilution of clinical isolates quantified by dPCR. Both * and ** marked assays were assessed with a multiplexed Step 1 amplification and 24 replicates per dilution tested. The LoD was determined by Probit analysis as detection with a 95% CI. The LoD calculation is given as copies per 10µL which equates to copies per reaction.

For all other assays, the limit of detection (LoD) was determined using serial dilutions of plasmids, with a multiplexed Step 1 amplification and 16 replicates per dilution tested. The LoD was determined to be the lowest concentration that showed 100% target amplification. Ranges are used when samples with higher concentrations were not detected, contrary to 100% amplification of samples with lower concentrations. The LoDs calculation is given as copies per 10 µL which equates to copies per reaction.

Assay	LoD (copies/10 µL)
Viral targets	
EV	3
HAdV	43
hMPV A	4
hMPV B	13 - 25
hPIV1*	11
hPIV2*	4
hPIV3*	13
hPIV4*	9
Influenza A*	10
H1(2009)*	48
HA-H3*	10
Influenza B	21
Parechovirus	4 - 40
RSV A*	11
RSV B	85
RV/EV	41
SARS-CoV-2 ORF1**	18
SARS-CoV-2 ORF8	7
PanCorona	84 - 167
Bacterial targets	
Bordetella*	4
B. pertussis*	7
B. parapertussis*	4
C. pneumoniae*	2

C. psittaci*	2
L. longbeachae*	100
L. pneumophila*	49
M. pneumoniae*	4
Fungal targets	
PCP*	2

8.5 CLINICAL PERFORMANCE USING NUCLEIC ACID EXTRACTS

Clinical performance is provided on samples extracted via the methods outlined in **SUITABLE NUCLEIC ACID EXTRACTION METHODS**. The clinical performance for the targets used in this product were assessed by multiple clinical laboratories in Australia, New Zealand and the United Kingdom. Each institution's alternative method was considered the reference method for this assessment.

Assay	PPA % (95% CI)	NPA % (95% CI)
Viral targets		
EV	92.1 (83.9 – 96.5)	>99.0 (98.1 – 100.0)
HAdV	>99.0 (92.6 – 100.0)	>99.0 (98.8 – 100.0)
hMPV (hMPV A and B)	>99.0 (87.0 – 100.0)	>99.0 (99.1 – 100.0)
hPIV1	>99.0 (82.4 – 100.0)	>99.0 (98.3 – 100.0)
hPIV2	>99.0 (82.4 – 100.0)	>99.0 (98.3 – 100.0)
hPIV3	>99.0 (84.6 – 100.0)	>99.0 (98.3 – 100.0)
hPIV4	>99.0 (82.4 – 100.0)	>99.0 (98.3 – 100.0)
Influenza A	96.8 (83.3 – 99.9)	>99.0 (98.3 – 100.0)
H1(2009)	>99.0 (95.2 – 100.0)	>99.0 (94.9 – 100.0)
HA-H3	>99.0 (85.8 – 100.0)	>99.0 (98.3 – 100.0)
Influenza B	>99.0 (88.6 – 100.0)	>99.0 (99.2 – 100.0)
Parechovirus	88.2 (71.6 – 96.1)	>99.0 (97.4 – 99.8)
RSV A	>99.0 (83.9 – 100.0)	>99.0 (98.3 – 100.0)
RSV B	>99.0 (94.1 – 100.0)	>99.0 (99.1 – 100.0)
RV/EV	>99.0 (90.4 – 100.0)	>99.0 (96.4 – 100.0)

SARS-CoV-2**	99.0 (96.4 – 99.7)	>99.0 (97.6 – 99.6)
PanCorona	76.0 (54.5 – 89.8)	>99.0 (96.6 – 100.0)
Bacterial targets		
Bordetella	>99.0 (93.0 – 100.0)	>99.0 (96.4 – 100.0)
B. parapertussis*	>99.0 (From 3 positive samples)	>99.0 (94.7 – 100.0)
B. pertussis	>99.0 (81.5 – 100.0)	>99.0 (71.7 – 100.0)
C. pneumoniae	>99.0 (83.4 – 100.0)	>99.0 (98.7 – 100.0)
C. psittaci	>99.0 (92.5 – 100.0)	>99.0 (97.9 – 100.0)
L. longbeachae	>99.0 (81.5 – 100.0)	>99.0 (86.7 – 100.0)
L. pneumophila	>99.0 (90.8 – 100.0)	>99.0 (87.4 – 100.0)
M. pneumoniae	94.2 (85.1 – 98.1)	>99.0 (98.5 – 100.0)
Fungal targets		
PCP	>99.0 (91.4 – 100.0)	>99.0 (97.2 – 100.0)

*This assay has been validated with <20 confirmed positive samples. During primer design for each assay, bioinformatics analysis is conducted whereby the target sequence of the primer is analysed in all publicly available sequences. This analysis is based on published research and in-house studies on the importance of any mismatches in primer sequence on the efficiency of qPCR. This provides evidence that AusDiagnostics assays should detect all specified targets, and therefore assays validated with a low number of confirmed samples can be relied upon.

** If either of the SARS-CoV-2 assays calls positive, the test result for the sample is positive for SARS-CoV-2.

9. WARNINGS AND LIMITATIONS

- IVD performance claims are only applicable when the instructions provided are followed.
- Do not use if the product or packaging is compromised in any way.
- Do not use Step 1 or Step 2 panel components with different catalogue and/or version numbers.
- Do not use expired products.
- Always handle and dispose of specimens potentially containing human pathogens according to relevant safety procedures.
- This panel of assays must only be used with the robotic system(s) as provided in **INTENDED PURPOSE**.
- Good laboratory practice is essential for the intended performance of this panel of assays. For further safety information, consult the relevant Safety Data Sheets (SDS). **Note:** Step 1 and Step 2 products and associated reagents do not contain hazardous substances, as listed in CLP Regulation (EC) No 1272/2008 and according to the Globally Harmonised System (GHS) classification. AusDiagnostics SDS's can be accessed online at www.r-biopharm.com.au/login.
- Manual extraction and pipetting of nucleic acid extracts into Step 1 tubes is best performed in a biological safety cabinet or PCR setup area.

9.1 LIMITATIONS OF THE PROCEDURE

- The detection of nucleic acid is dependent upon proper specimen collection, handling, transportation, storage, and preparation (using the manufacturer's specimen collection device instructions). Failure to follow proper procedures can lead to incorrect results.
- This product is only for use by suitably trained personnel in qualified laboratories.
- The performance of this panel has only been established on the RIDA®Xplore, HighPlex, RIDA®Jump and UltraPlex 3 systems.
- The assays in this product do not provide a quantitative value for the pathogen(s) in the sample.
- The performance of the test has been evaluated for use with human specimen material only.
- The performance of this test has been demonstrated using nucleic acid extracts from upper and lower respiratory excretion samples from the following specimen types: nasal swab, throat swab, nasopharyngeal swab, sputum, and cultured isolates.
- Saliva specimen is only suitable for the detection of SARS-CoV-2.
- Upper and lower tract excretions are defined in accordance with the Clinical and Laboratory Standards Institute (CLSI) guideline MM17.
- Numerous published studies have demonstrated saliva to be a valid specimen type for the detection of SARS-CoV-2 with a percentage positive agreement in the range of 82 to 100% when compared to a throat/nasal swab collection method for PCR. Saliva is less sensitive at the early and late stages of disease and in asymptomatic cases compared with using throat/nasal swabs.
- The performance of this test has not been established for specimens collected from individuals without signs or symptoms of respiratory infection.
- The performance of this test has not been established for immunocompromised individuals.
- This panel is designed to measure specific nucleic acid sequences. Therefore, a negative result does not exclude the possibility that an unusual sequence variant is present. A negative result cannot be relied upon for a definitive diagnosis. The results obtained with this product should be used in conjunction with information available from clinical evaluations and other diagnostic procedures. Failure or delay in treatment of an infected patient may lead to death, with immunocompromised patients being at highest risk.
- Discrimination between RSV A and RSV B strains is for information purposes only.
- Discrimination of RV and EV provided by the Diagnosis Window is indicative only.

10. TECHNICAL ENQUIRIES

Further instructions and troubleshooting can be found in the relevant robotic system IFU.

For assistance or if any issues recur, contact AusDiagnostics at: support@r-biopharm.com.au.

In the event of a serious incident, immediately contact your local representative and notify the appropriate health authorities in accordance with regulatory requirements.

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11. GLOSSARY

11.1 SYMBOLS

The following symbols can be found on product labels. Use the definitions below as a guideline to interpret the symbols.

	IVD device code and name
	Name and address of the manufacturer
	For in vitro diagnostic use
	For research use in the laboratory research phase of development; not for therapeutic or in vitro diagnostic use
	Date of manufacture (YYYY-MM-DD)
	Use-by/expiration date (YYYY-MM-DD)
	Batch code (/ Serial number where applicable)
	Unique Device Identifier (UDI)
	Name and address of the Authorised Representative for EU
UKRP	Name and address of the Authorised Representative for UK
	CE marking Conformité Européene
	CE marking Conformité Européene Notified Body Reference no. 0123
	Indicates the use for medical devices placed on the Great Britain (England, Wales, Scotland) market.
	Consult e-labelling instructions for use
	Indicates the temperature limits to which the medical device can be safely exposed

	Indicates the upper limit of temperature to which the medical device can be safely exposed
	Indicates a medical device that is intended for one use, or for use on a single patient during a single procedure
	Indicates a control material that is intended to verify the performance characteristics of another medical device
	Indicates a control material that is intended to verify the results in the expected positive range
	Indicates a control material that is intended to verify the results in the expected negative range
	Importer - name and address of the importing entity adjacent to the symbol indicates the entity importing the medical device into the locale
	Distributor - name and address of the importing entity adjacent to the symbol indicates the entity distributing the device into the locale
	Indicates that there are potential biological risks associated with the medical device
	Do not use if package is damaged and consult instructions for use
	Indicates that caution is necessary when operating the device or control close to where the symbol is placed, or that the current situation needs operator awareness or operator action in order to avoid undesirable consequences.
	Indicates the version number of the product.
	Indicates the supplied quantity of the product.
	Indicates correct upright position of the transport package.

11.2 DEFINITIONS

AusDx: AusDiagnostics Pty Ltd.

Negative Percent Agreement (NPA): The proportion of comparative method positive results in which the test method result is negative when the comparative method is not a widely accepted best method of assessing a target condition.

Operator: The trained individual interacting with the system.

Panel of assays: Components comprising Step 1 and Step 2; to be used together for detecting a specific group (“panel”) of targets.

Panel-specific IFU: Instructions for Use (IFU) which contain information specific to a panel.

Primers: Short synthetic oligonucleotides specifically designed to bind to and amplify specific gene sequences under conditions provided during PCR.

Positive Percent Agreement (PPA): The proportion of comparative method positive results in which the test method result is positive when the comparative method is not a widely accepted best method of assessing a target condition.

Run: All steps from starting the Setup software (RIDA®Setup or MT-PCR Assay Setup) (see relevant section in robotic system IFU) to generation of the Result file is considered a “run”.

RUO: For research use only. No clinical performance claims are made.

Serious incident: A serious incident is defined as any incident that directly or indirectly leads to the death of a patient, user or other person; serious deterioration in health (temporary or permanent); or a serious public health threat.

Target: A gene or sequence that primers are designed to bind to.

Warning: A statement alerting the operator to precautionary measures necessary for safe and effective use of the device.

12. DISCLAIMER

Warranty expressly does not cover (a) consumable parts, damage caused by normal wear, (b) any good(s) that has been reconstructed, repaired by person(s) other than the AusDx and its authorised representatives or a third -party approved and certified to make such repair, (c) any good(s) that have been subject to abuse, misuse, neglect, negligence, accident, improper testing, improper installation, improper storage, improper handling, abnormal physical stress, abnormal environmental conditions or use contrary to any instructions issued by the AusDx.

AusDx may in its own discretion, change or replace goods, material, or services to cure a legal defect or to provide lacking use rights to Customer. AusDx has a termination right, if this is not possible.

AusDx does not assume liability for (a) user changes or modifications; (b) use or processing inconsistent with contractually agreed purpose or general product safety, (c) due to incorrect or unsuitable use or storage, or through chemical, electromagnetic, mechanical or electrolytic influences, (d) or which cannot be sufficiently traced to faulty material or workmanship, design, manufacturer materials or instructions for use is especially excluded.

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14. DOCUMENT HISTORY

Document ID	Date of Change	Changes
80617-r02	17 Jun 2026	Added information for RIDA®Jump. Corrected HPIV inclusivity in Section 3. Added CE0123 symbol on the cover page. Added EU REP, UK RP, importer and distributor to Technical Enquiries section. Added UKCA symbol to Glossary. Updated ORF1 Analytical Sensitivity, including description of methods.
80617-r01	15 Dec 2025	Ref 80617 is being distributed as Respiratory Pathogens 24-well since 2020 and now it is rebranded to RIDA®Plex Respiratory Pathogens 24 well. No changes are made to the device's intended purpose, performance or safety. Minor editorial changes for clarity and alignment with RIDA branding.