

DATE OF BIRTH: **Not Provided**

SEX: **Not Provided**

SESSION ID: **f1d1cdaf07c14269b87ecbeb2d7a1f55**

ANALYSIS ID: **274555397**

SUBMITTER:

ANALYSIS VERSION: **1.0.0**

SPECIMEN RECEIVED: **01 September 2020**

DATE OF COLLECTION: **Not Provided**

SPECIMEN TYPE: **Not Provided**

Analysis Performed: Explify Respiratory ID/AMR Panel - Data Analysis Solution

For Research Use Only. Not for use in diagnostic procedures.

## RESULTS: ONE OR MORE POTENTIAL PATHOGENS DETECTED

READ CLASSIFICATION: **83.2% TARGETED**    9.6% Untargeted    4.0% Ambiguous    2.2% Unclassified

	CONFIDENCE SCORE	PROPORTION OF DETECTED	
<b>VIRUSES</b>			
SARS-CoV-2	3.00 (High)	93.3%	
Influenza A virus (H1N1)	2.12 (High)	6.7%	
<b>BACTERIA</b>			
<i>Staphylococcus aureus</i>	2.75 (High)	73.4%	
<i>Escherichia coli</i>	0.83 (Low)	26.6%	
<b>FUNGI</b>			
<i>Pneumocystis jirovecii</i>	2.90 (High)	100%	
<b>AMR</b>			
mecA	3.00 (High)	<u><i>Staphylococcus aureus</i></u>	Amoxicillin, Amoxicillin-Clavulanate, Cefazolin, Cefepime, Cefotaxime, Meropenem, Oxacillin
CTX-M	2.11 (Mid)	<i>Acinetobacter baumannii</i> <i>Enterobacter cloacae</i> complex <u><i>Escherichia coli</i></u> <i>Klebsiella pneumoniae</i> <i>Pseudomonas aeruginosa</i>	Amoxicillin, Cefazolin, Cefepime, Cefotaxime

## INTERPRETIVE DATA

### **For Research Use Only. Not for use in diagnostic procedures.**

The Respiratory Pathogen ID and AMR panel with Explify<sup>®</sup> analysis identifies 42 viruses, 187 bacteria, 53 fungi, and 1,218 antimicrobial resistance (AMR) markers based on target enriched next-generation sequencing (NGS) of pathogen transcriptome and genome sequences. Sequencing data are interpreted by the Explify software and potential pathogens that pass minimum Confidence Score thresholds are listed. Passing Confidence Scores range from 0 to 3 with higher values indicating greater confidence. Confidence Scores are categorized as High, Medium, and Low. If two or more microorganisms from a given class (e.g., bacteria) are identified, their relative abundance is calculated based on normalized sequencing read counts and listed as proportion (e.g., "Proportion of Detected Bacteria"). Associated Pathogen and Associated Resistance are listed for AMR Markers that pass a minimum Confidence Score threshold and are based on existing scientific knowledge. Associated Pathogen have been linked to resistance based on the identified AMR Marker. They may or may not have been identified in this specimen. See [www.idbydna.com/respiratoryidamrpanel](http://www.idbydna.com/respiratoryidamrpanel) for additional information.

## LIMITATIONS

Negative results do not rule out the presence of viruses, bacteria, fungi, and AMR markers. Due to complexities of next generation sequencing methodologies and sequence-based microbial identification, there may be a risk of false-positive and/or false-negative results. Contamination with microorganisms is possible during specimen collection, transport, and processing. The identification of cDNA or DNA sequences from a microorganism do not confirm that the identified microorganism is causing symptoms, is viable, or is infectious. Detection of genetic markers for antibiotic resistance does not always predict phenotypic resistance; lack of detection does not indicate susceptibility. Information provided by the Respiratory Pathogen ID and AMR panel with Explify<sup>®</sup> analysis is based on existing scientific knowledge and has been curated. However, scientific knowledge evolves and information about associated pathogen and associated resistance may not always be complete and/or correct. Results should be interpreted with caution. Other sources of data may be required for confirmation.