

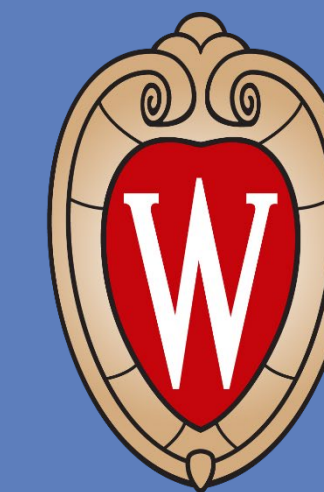


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# Identification of potential SARS-CoV-2 intermediate host species using SeqAPASS

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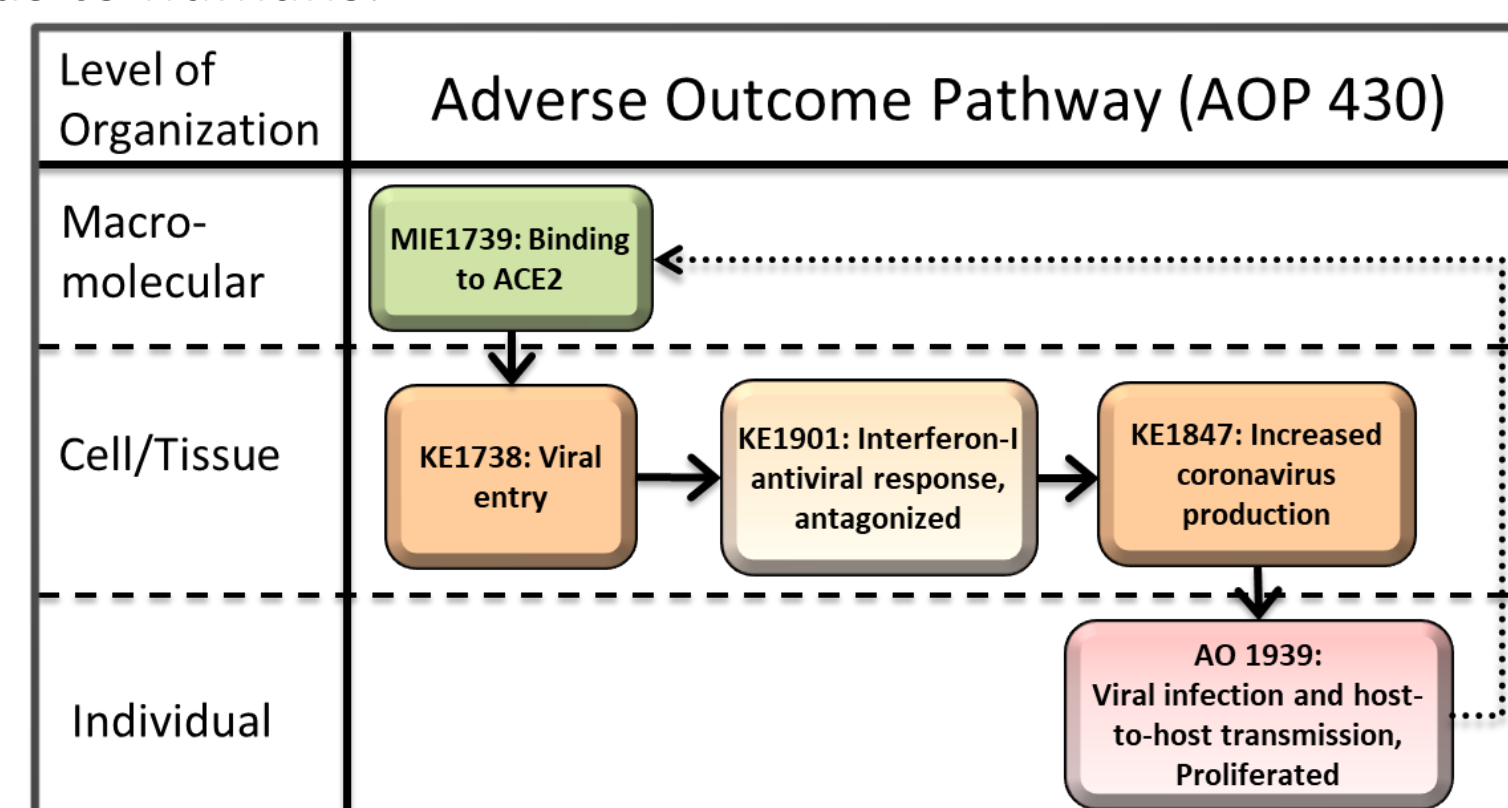
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## Introduction

SARS-CoV-2 is a zoonotic coronavirus responsible for the COVID-19 pandemic. Bats are known reservoirs for coronaviruses and may transmit them to other species. Recently-published evidence indicates the Huanan seafood market in Wuhan, China was the source of the pandemic. SARS-CoV-2 was detected in samples from market stalls that housed live animals including red foxes and racoon dogs, implicating these species as intermediate hosts that potentially carried the virus to humans.<sup>§</sup>

**The virus has been proven to be transmitted from humans to other mammals and back to humans, which could result in mutations that increase virulence or transmissibility.**



The SARS-CoV-2 spike protein utilizes the host angiotensin converting enzyme 2 (ACE2) as a receptor to enter the host cell. Thus far, only the ACE2 protein sequences have been compared across species to identify potential alternate hosts. However, viral proteins attack many proteins in the Interferon (IFN-I) antiviral pathway to block host immune response, allowing viral replication and transmission.

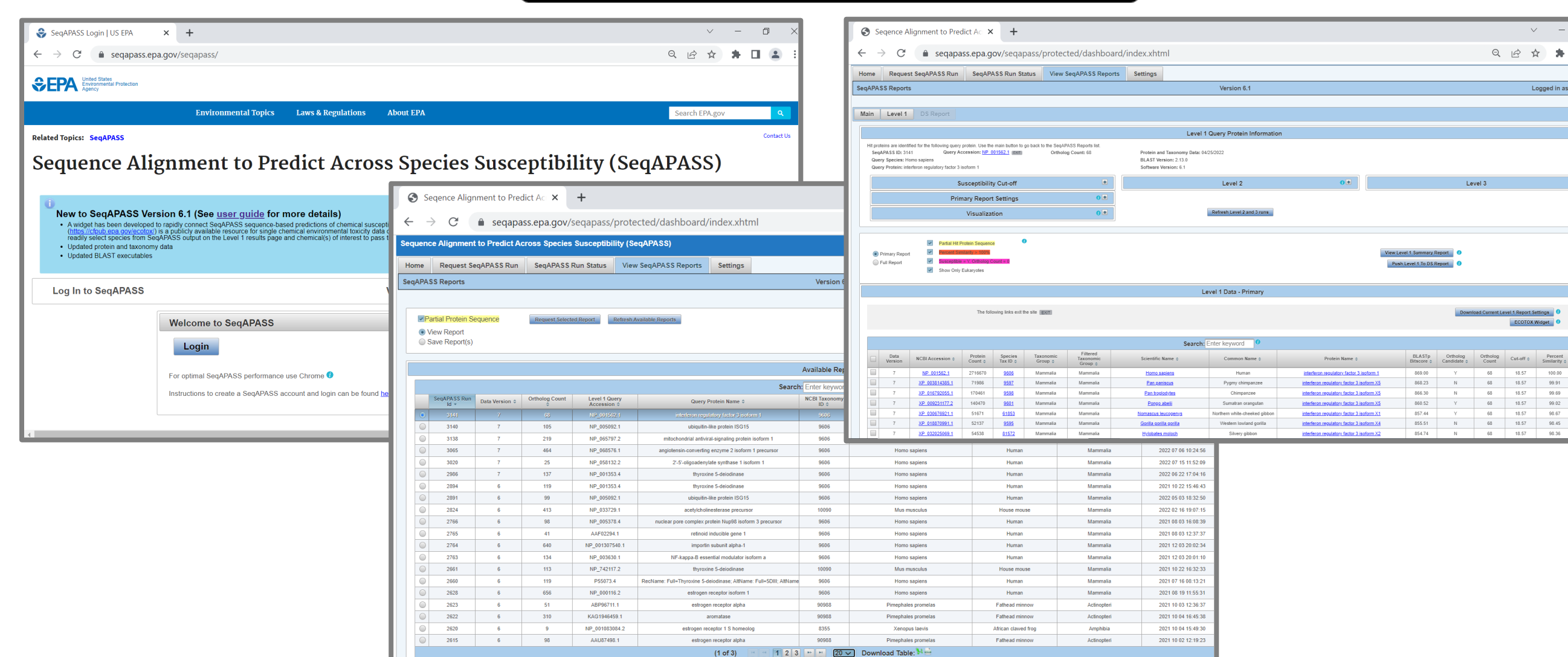
**Determining cross-species similarity of multiple host antiviral proteins could provide stronger evidence of species potential to transmit SARS-CoV-2.**

§ Worobey et al., Science 10.1126/science.abb8715 (2022).

## Methods: Literature review and SeqAPASS (Sequence Alignment to Predict Across Species Susceptibility)

- Literature was searched to identify IFN-I pathway target proteins and critical amino acids involved in the host protein-viral protein interactions (See References).
- The U.S. EPA's **SeqAPASS** bioinformatic tool was used in a systematic approach to evaluate IFN-I pathway protein sequence similarity and compare critical amino acids across literature-reported infected and non-infected species.

- Level 1 Primary Amino Acid Sequence Alignments
- Level 2 Conserved Functional Domain Alignments
- Level 3 Critical (Close Contact) Amino Acid Conservation



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## SeqAPASS provides a robust multi-protein analysis of species potential to transmit COVID-19

### Interferon (IFN-I) Antiviral Pathway proteins attacked by SARS-CoV-2 proteins

