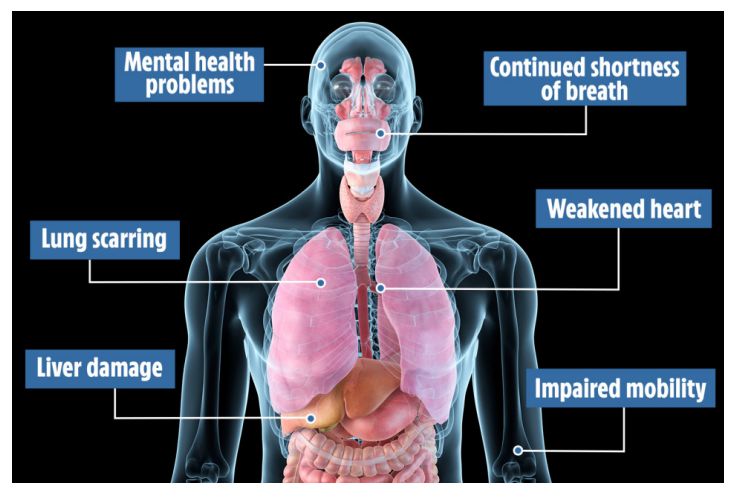
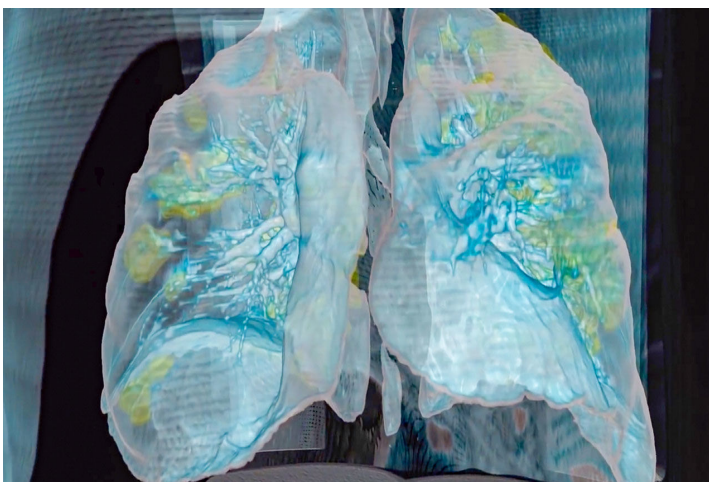
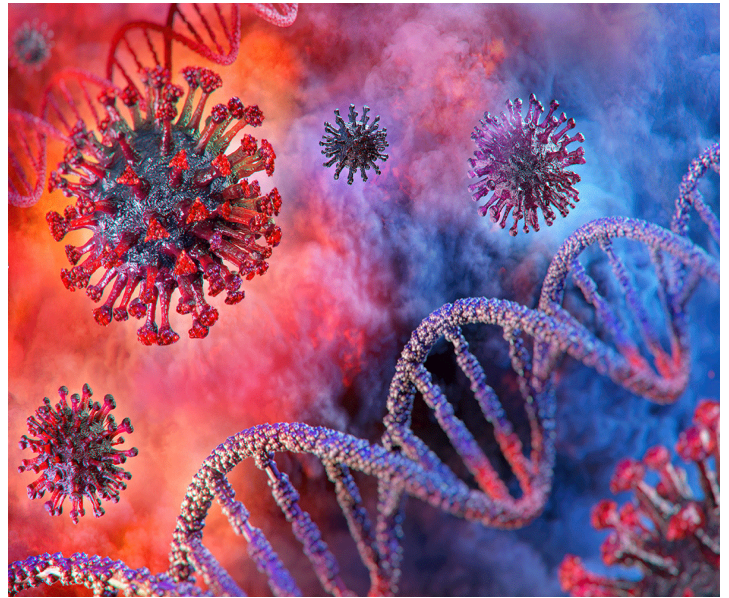


# Covid-19 Genomics



## Genomic Testing for Covid-19 Prognosis & Diagnosis

Covid-19 global pandemic caused by SARS-CoV-2 is sweeping through 212 countries affecting 3,566,542 (as of 04/05/2020) individuals and killing more than 250,000 in a matter of months. Covid-19 forced more than half of the global population locked in doors thereby devastating global economy. It is apparent now that each individual responds differently to this debilitating disease. This lethal pathogen is accumulating mutations in its genome and already has differentiated into more than ten strains with ever increasing pathogenicity and lethality. The Spike protein of this pathogen has to bind to ACE2 receptor in humans to initiate the infection cycle. Binding affinity between the S protein of the virus and ACE2 receptor of the human host is major determinant of Covid-19 disease severity. Thus Gene expression and variant analysis of ACE2 in the epithelial cells of nasal and bronchial cells would be critical for both prognosis and diagnosis of Covid-19

# Clinical Genomics

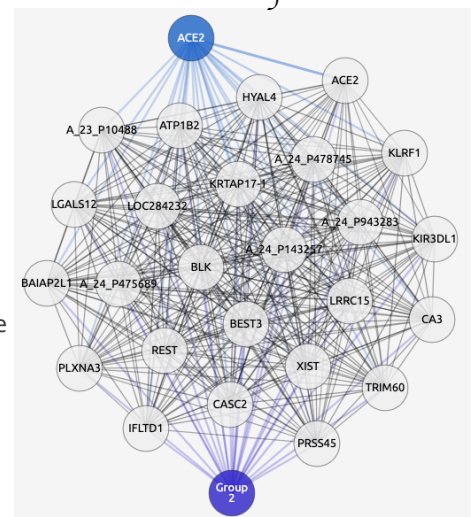


## Molecular Genetics

*Covid-19 disease caused by SARS-CoV-2 is an RNA virus that hijacks the functionality of nearly 338 host (human) proteins to enter, multiply and exit. ACE2 gene of humans is critical in determining the entry of the virus pathogen through nasal and bronchial epithelial cells. Besides ACE2, TMPRSS2, CTSB and CTSB genes may also play a key role in this entry process. More than 50 genes have been identified that are associated with the elevated expression of ACE2 during Covid-19 disease onset. Some of the notable genes are IDO1, TRAK3, NOS2, TNFSF10, OAS1 and MX1. Nearly 75 genes have been mapped to the brain functionality subsequent to SARS-CoV-2 infection.*

## Pharmacogenomics

- Presence of variant rs1805087 in gene **MTR** is associated with increased response to Hydroxychloroquine
- Presence of variant rs1045642 in gene **ABCB1** is associated with decreased concentration of Azithromycin
- Presence of variant rs6051702 in gene **ITPA** with genotype AA may increase the risk of anemia when treated with Ribavirin



## Why myClinGen?

*myClinGen is a complete and comprehensive solution from sample collection to NGS Sequencing to BIG data analytics on Supercomputer to Customized reports to Cloud based Knowledgebase hosting to Genetic Counselling at affordable rates and a faster Turn Around Time (TAT).*

*Please see: [www.myclinngen.com](http://www.myclinngen.com) for more information.*