

Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

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COVID-19 Genomics and Precision Public Health Weekly Update Content

- Pathogen and Human Genomics Studies
- Non-Genomics Precision Health Studies
- News, Reviews and Commentaries

Pathogen and Human Genomics Studies

- [Racial/Ethnic Variation in Nasal Gene Expression of Transmembrane Serine Protease 2 \(TMPRSS2\) \(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=164\)](#)
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- [Exploring the coronavirus pandemic with the WashU Virus Genome Browser \(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=170\)](#)
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Despite the novelty of the virus, global sequencing efforts have already identified genomic variation across isolates. To enable easy exploration and spatial visualization of the potential implications of SARS-CoV-2 mutations in infection, host immunity and drug development, we have developed COVID-3D.

- [Molecular architecture of the SARS-CoV-2 virus \(/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=179\)](#)
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Molecular architecture of the authentic SARS-CoV-2 virus is unveiled. Native structures of S in RBD down, one RBD up and postfusion conformations are solved. Compositions of the glycans from the native S are characterized. Structure and

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We show that SARS-CoV-2 spike protein interacts with both cellular heparan sulfate and angiotensin converting enzyme 2 (ACE2) through its Receptor Binding Domain (RBD). Docking studies suggest a heparin/heparan sulfate-binding site adjacent to the ACE2 binding site. Both ACE2 and heparin can bind independently to spike protein in vitro.

- Structural and Functional Analysis of the D614G SARS-CoV-2 Spike Protein Variant (/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=182)
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The SARS-CoV-2 D614G S protein variant supplanted the ancestral virus in people. D614G increases infectivity on human lung cells or cells with bat or pangolin ACE2. D614G is potently neutralized by antibodies targeting the receptor binding domain D614G shifts S protein conformation towards an ACE2-binding fusion-competent state.

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We describe a simple test for detection of SARS-CoV-2. The sensitivity of this test is similar to that of reverse-transcription-quantitative polymerase-chain-reaction (RT-qPCR) assays. STOP (SHERLOCK testing in one pot) is a streamlined assay that combines simplified extraction of viral RNA with isothermal amplification and CRISPR-mediated detection.

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