GISAID
Data Science Initiative
Seamless integration of tools inside the GISAID platform (log-in once) provides you comprehensive views from multiple angles and all info in one place.

- **Full entry meta-data**
- **Subsampled summary tree**
- **Full list and summary of all related sequences in the database (not just subsample)**
- **Full mutation phenotype annotation**
Emerging Variants Tracker

Monitoring emerging Fast Spreading hCoV-19 variants

Monitor AA changes with potential effects on receptor or antibody binding as annotated in CoVsurver

2388 literature entries (antibody escape, ACE2 binding, Spike expression and stability)


Search GISAID EpiCoV database

View mutations in Spike 3D Structure

Constellation

Recent Spread

RANKED BY 2 METHODS

Acceleration

Filter by Country

Filter by Mutation

Tool to see new variants before they have a lineage name

356 antibody binding sites
CoVsurver real-time surveillance for mutations that can affect viral fitness

![Image](https://gisaid.org/covsurver)

**Spike S477N**

- **Protein:** Spike
- **Coronavirus type:** SARS-CoV-2 (2019)
- **Mutation (as in paper):** S477N

**Comment:**
In a deep mutational scanning experiment that expresses spike RD6 in a yeast-display platform, S477N mildly increases the binding to ACE2 (apparent dissociation constant (Kd) log10 value: 0.06)

**Receptor binding**
- **Mutated:** Spike
- **Wildtype:** Spike
- **Effect:** Host Change

**Antibody interface**
- **Spike glycoprotein mutation surveillance**

### Literature-curated mutation effect database
- **>2400 entries**
  - drug resistance: 7
  - virulence: 23
  - antigenic drift / escape mutant: 1336
  - host specificity change/shift: 369
  - Other (enzyme activity, affects protein accumulation/ stability/function): 496

### 3D structure interaction mutation position database
- **>3800 entries**
  - self/oligomerization: 2686
  - small ligand: 497
  - antibody: 356
  - host protein: 241
  - host cell receptor: 46

### Tool to judge relevance of new mutations in variants