Variant Proportions, Region 6

HHS Region 6: 1/16/2022 – 4/23/2022


Region 6 - Arkansas, Louisiana, New Mexico, Oklahoma, and Texas

<table>
<thead>
<tr>
<th>WHO label</th>
<th>Lineage #</th>
<th>US Class</th>
<th>%Total</th>
<th>95%PI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Omicron</td>
<td>BA.2</td>
<td>VOC</td>
<td>87.0%</td>
<td>82.2-90.7%</td>
</tr>
<tr>
<td></td>
<td>BA.2.12.1</td>
<td>VOC</td>
<td>8.7%</td>
<td>5.2-13.9%</td>
</tr>
<tr>
<td></td>
<td>B.1.1.529</td>
<td>VOC</td>
<td>4.0%</td>
<td>2.9-5.5%</td>
</tr>
<tr>
<td>Delta</td>
<td>B.1.617.2</td>
<td>VBM</td>
<td>0.0%</td>
<td>0.0-0.0%</td>
</tr>
<tr>
<td>Other</td>
<td>Other*</td>
<td></td>
<td>0.3%</td>
<td>0.1-0.6%</td>
</tr>
</tbody>
</table>

- Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all weeks displayed.
- These data include Nowcast estimates, which are modeled projections that may differ from weighted estimates generated at later dates.
- AY.1-AY.133 and their sublineages are aggregated with B.1.1.617.2, BA.1, BA.3, BA.4, BA.5 and their sublineages (except BA.1.1 and its sublineages) are aggregated with B.1.1.529. For regional data, BA.1.1 and its sublineages are also aggregated with B.1.1.529, as they currently cannot be reliably called in each region. Except BA.2.12.1, BA.2 sublineages are aggregated with BA.2.

Source: https://covid.cdc.gov/covid-data-tracker/#variant-proportions

Regional proportions from specimens collected the week ending 4/23/2022.

Lineages called using pangolin v4.0.5 and pangolin-data v1.3.
Lineage BA.1.1 and its sublineages are aggregated with B.1.1.529 at the regional level as they currently cannot be reliably called in each region.

Updated April 26, 2022
Data From the Last 60 Days

B.1.617.2, Delta (India)

BA.1.1 Omicron

BA.2 Omicron

BA.2.12.1 Omicron

SARS-CoV-2 (hCoV-19) sequencing is not a random sample of mutations. As a result, this report does not indicate the true prevalence of the mutations but rather our best estimate now.