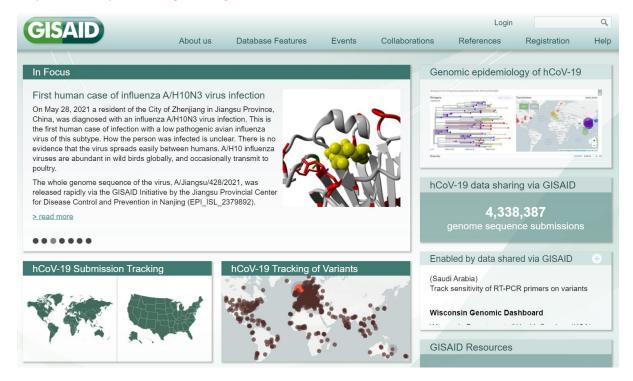
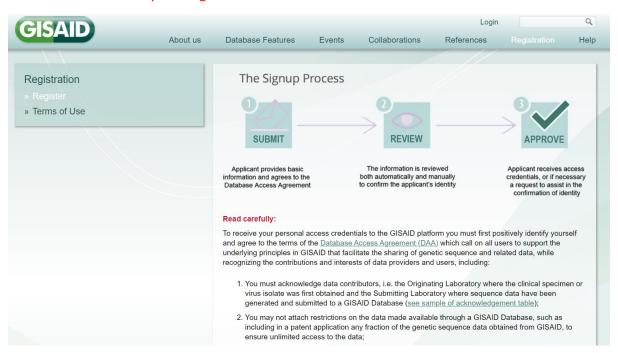
## **Instructions to Access to GISAID Database**

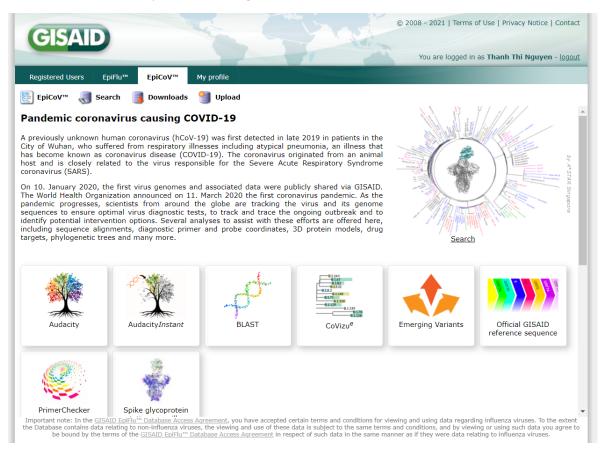
Step 1: Visit <a href="https://www.gisaid.org/">https://www.gisaid.org/</a>



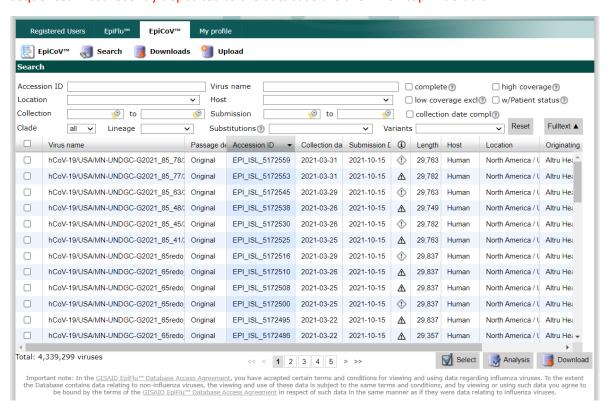
Step 2: You need to register before you can login. Your registration information will be reviewed, so it will take a while before you can get access credentials.



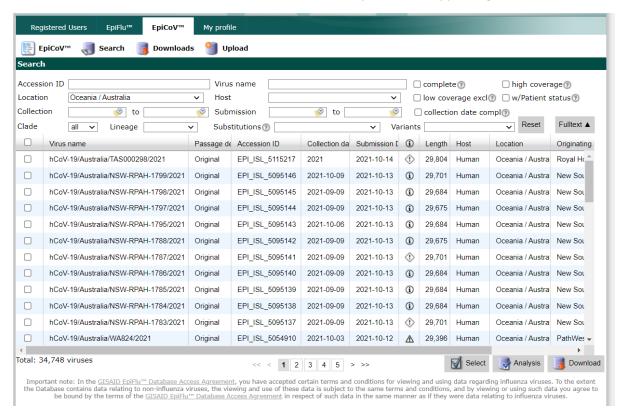
Step 3: After you login in, you can will have the options to explore genomic sequences of Flu or CoV. You can select the Tab EpiCoV to investigate SARS CoV.



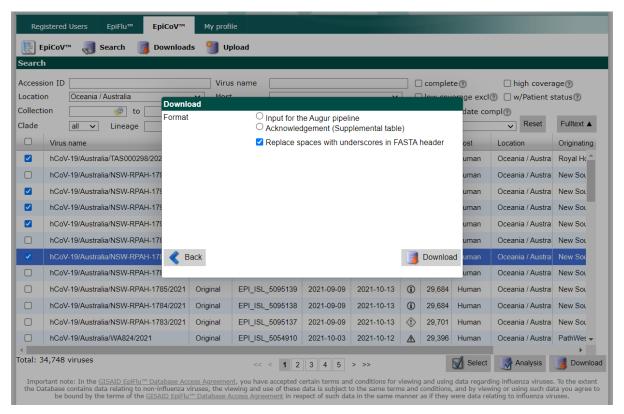
Step 4: You can select the Tab Search to search for genomic sequences based on different criteria. The sequences most recently deposited to the database are shown on top in default.



Step 5: For example, if I select the Location Oceania/Australia, I will see the total number of sequences available so far in this location is 34,748. And the latest sequences are appearing in the screen:



Step 6: You can select the checkboxes corresponding to the sequences you want to download. For example, I selected 5 sequences and hit the Download button:



Step 7: After downloading, you will obtain a FASTA file containing the genomic sequences of the 5 viruses you selected. Each sequence is separated with others by its header, starting with symbol ">":

gisaid\_hcov-19\_2021\_10\_15\_12 - Notepad

File Edit Format View Help

hCoV-19/Australia/NSW-RPAH-1787/2021 EPI ISL 5095141 2021-09-09 AGATCTGTTCTCTAAACGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACTCACGCAGTATAATT AATAACTAATTACTGTCGTTGACAGGACACGAGTAACTCGTCTATCTTCTGCAGGCTGCTTACGGTTTCGTCCGTTTTTGC AGCCGATCATCAGCACATCTAGGTTTTGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTCCCTGGTTTCAACGA GAAAACACGTCCAACTCAGTTTGCCTGTTTTACAGGTTCGCGACGTGCTCGTACGTGGCTTTGGAGACTCCGTGGAGG AGGTCTTATCAGAGGCACGTCAACATCTTAAAGATGGCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAA CTTGAACAGCCCTATGTGTTCATCAAACGTTCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGC AGAACTCGAAGGCATTCAGTACGGTCGTAGTGGTGAGACACTTGGTGTCCCTCATGTGGGCGAAATACCAGTGG CTTACCGCAAGGTTCTTCTTCGTAAGAACGGTAATAAAGGAGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTT GACTTAGGCGACGAGCTTGGCACTGATCCTTATGAAGATTTTCAAGAAAACTGGAACACTAAACATAGCAGTGGTGTTAC CCGTGAACTCATGCGTGAGCTTAACGGAGGGGCATACACTCGCTATGTCGATAACAACTTCTGTGGCCCTGATGGCTACC CTCTTGAGTGCATTAAAGACCTTCTAGCACGTGCTGGTAAAGCTTCATGCACTTTGTCCGAACAACTGGACTTTATTGAC ACTAAGAGGGGTGTATACTGCTGCCGTGAACATGAGCATGAAATTGCTTGGTACACGGAACGTTCTGAAAAAGAGCTATGA ATTGCAGACACCTTTTGAAATTAAATTGGCAAAGAAATTTGACACCTTCAATGGGGAATGTCCAAATTTTGTATTTCCCT TAAATTCCATAATCAAGACTATTCAACCAAGGGTTGAAAAGAAAAGCTTGATGGCTTTATGGGTAGAATTCGATCTGTC TATCCAGTTGCGTCACCAAATGAATGCAACCAAATGTGCCTTTCAACTCTCATGAAGTGTGATCATTGTGGTGAAACTTC ATGGCAGACGGCGATTTTGTTAAAGCCACTTGCGAATTTTGTGGCACTGAGAATTTTGACTAAAGAAGGTGCCACTACTT GTGGTTACTTACCCCAAAATGCTGTTGTTAAAATTTATTGTCCAGCATGTCACAATTCAGAAGTAGGACCTGAGCATAGT GTTCTCTTATGTTGGTTGCCATAACAAGTGTGCCTATTGGGTTCCACGTGCTAGCGCTAACATAGGTTGTAACCATACAG GTGTTGTTGGAGAAGGTTCCGAAGGTCTTAATGACAACCTTCTTGAAATACTCCAAAAAGGAAAGTCAACATCAATATT GTTGGTGACTTTAAACTTAATGAAGAGATCGCCATTATTTTGGCATCTTTTTCTGCTTCCACAAGTGCTTTTGTGGAAAC TGTGAAAGGTTTGGATTATAAAGCATTCAAACAAATTGTTGAATCCTGTGGTAATTTTAAAGTTACAAAAGGAAAAGCTA AAAAAGGTGCCTGGAATATTGGTGAACAGAAATCAATACTGAGTCCTCTTTATGCATTTGCATCAGAGGCTGCTCGTGTT GTACGATCAATTTTCTCCCGCACTCTTGAAACTGCTCAAAATTCTGTGCGTGTTTTTACAGAAGGCCGCTATAACAATACT AGATGGAATTTCACAGTATTCACTGAGACTCATTGATGCTATGATGTTCACATCTGATTTTGGCTACTAACAATCTAGTTG