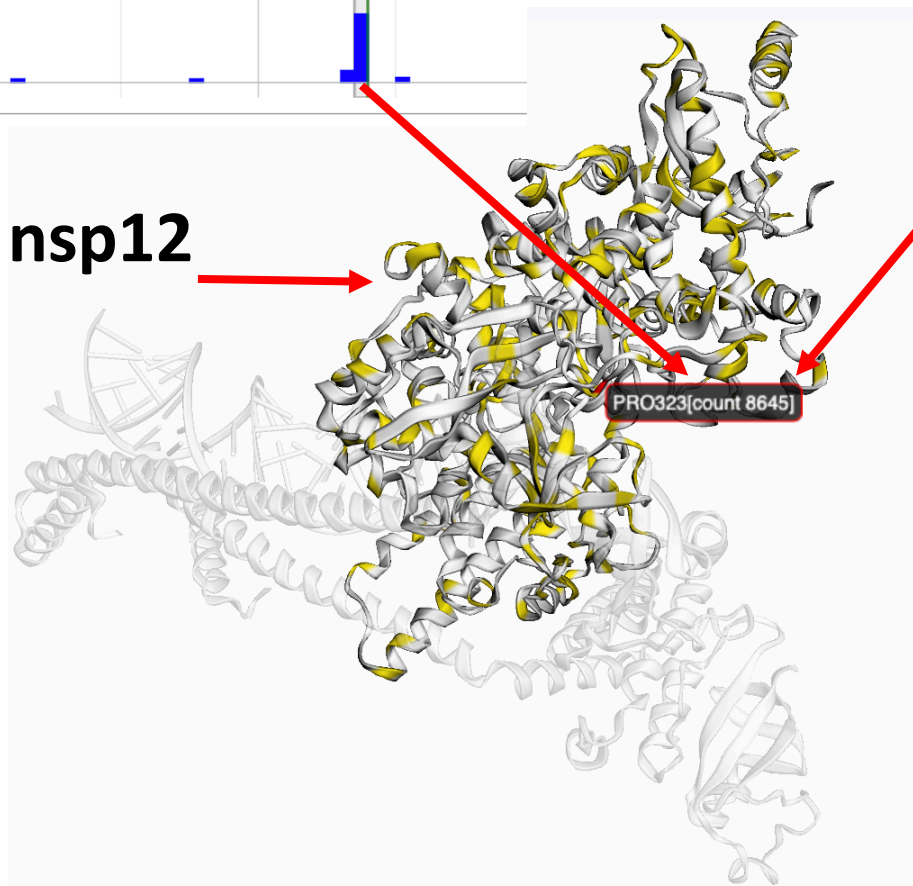




# The most common mutation in nsp12. nsp12 P323L (14408) is at the interface between nsp12 and nsp8.

nsp12



Click on any structure above to display 3d view or **display random structure**

Selected structure: 6yyt

Download ▾

PDB Chain 6yytA

Title Structure of replicating SARS-CoV-2 polymerase

Position 13531:16227

Method ELECTRON MICROSCOPY

Display as:

Ribbon

Stick

CA trace

Color by AA mutation frequency

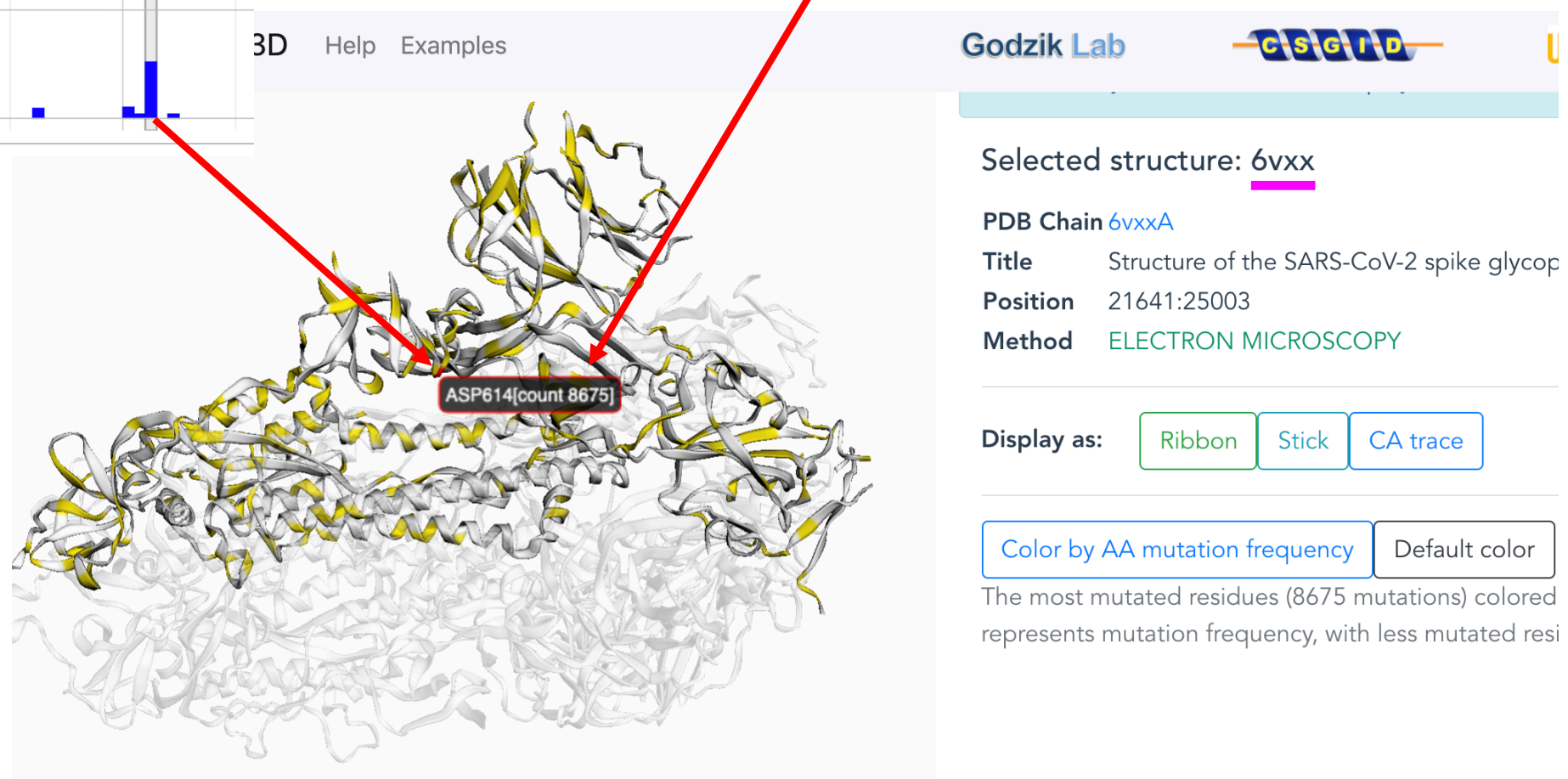
Default color

The most mutated residues (8645 mutations) colored red. Intensity of the color represents mutation frequency, with less mutated residues having lighter color.

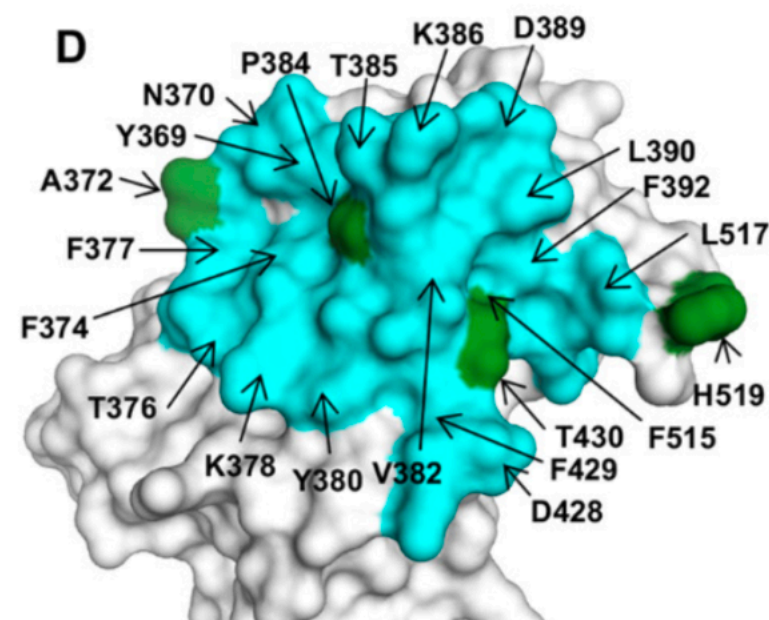
Last update **May-15-2020**: 6955 positions with mutations (based on 12775 genomes), 19 structures, and



# The most common mutation in surface glycoprotein D614G (23403)



Mutations of the epitope residues



		nearby
Y369		
N370		
A372		
F374		
T376		
F377		
K378	R	
Y380		
V382		
L390		P491->R
F392		P491->R
D428		
F429		
T430		
F515		
L517		
H519	P,Q	