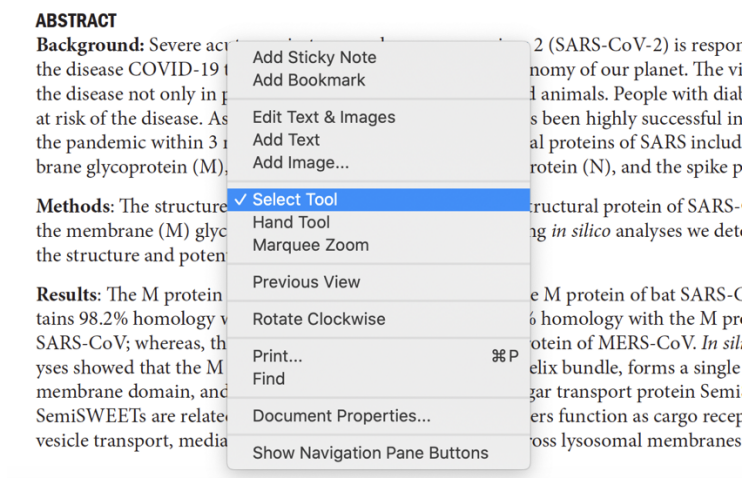
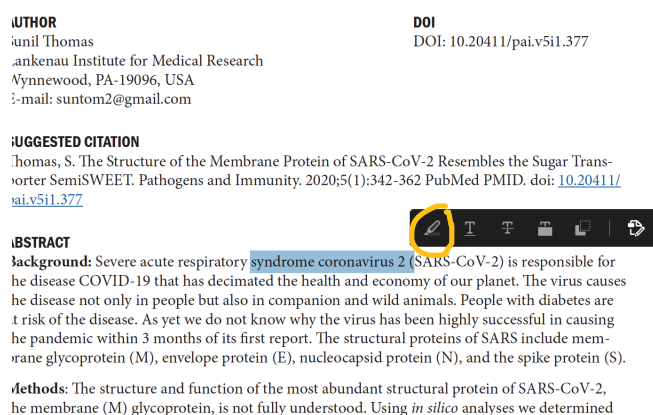


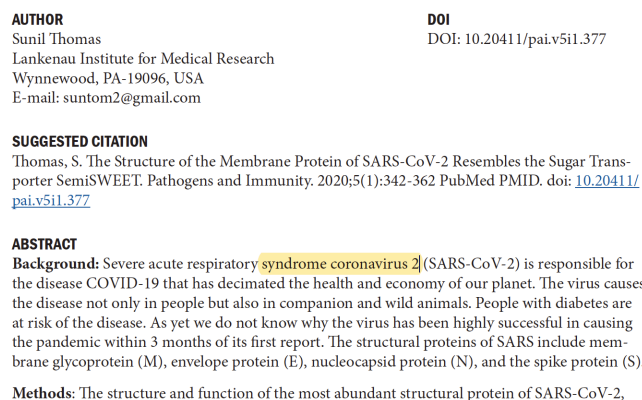
1. Right click on your document near the text you want to change. Click “Select Tool”



2. Then, highlight the copy you want to change and a little menu bar will pop up. Select the “highlighter tool” which is the first tool on this menu bar.



3. Drag your cursor over the copy you want to correct again so that it highlights:



4. Double click on the highlighted text and you will get a comment box. Type your correction into this comment box.

Sunil Thomas
Lankenau Institute for Medical Research
Wynnewood, PA-19096, USA
E-mail: suntom2@gmail.com

DOI: 10.20411/pai.v5i1.377

SUGGESTED CITATION

Thomas, S. The Structure of the Membrane Protein of SARS-CoV-2 Resembles the Sugar Transporter SemiSWEET. Pathogens and Immunity. 2020;5(1):342-362 PubMed PMID. doi: [10.20411/pai.v5i1.377](https://doi.org/10.20411/pai.v5i1.377)

ABSTRACT

Background: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the disease COVID-19 that has decimated the health and economy of the world. The disease not only in people but also in companion and wild animals is at risk of the disease. As yet we do not know why the virus has been the pandemic within 3 months of its first report. The structural proteins are membrane glycoprotein (M), envelope protein (E), nucleocapsid protein (N), and spike protein (S).

Methods: The structure and function of the most abundant structural protein, the membrane (M) glycoprotein, is not fully understood. Using *in silico* methods, the structure and potential function of the M protein.

Results: The M protein of SARS-CoV-2 is 98.6% similar to the M protein of bat SARS-CoV, maintains 98.2% homology with pangolin SARS-CoV, and has 90% homology with the M protein of SARS-CoV; whereas, the similarity is only 38% with the M protein of MERS-CoV. *In silico* analyses showed that the M protein of SARS-CoV-2 has a triple helix bundle, forms a single 3-transmembrane domain, and is homologous to the prokaryotic sugar transport protein SemiSWEET. SemiSWEETs are related to the PQ-loop family whose members function as cargo receptors in vesicle transport, mediate movement of basic amino acids across lysosomal membranes, and are

heatheronorati 12:45 PM Reply X

Add a comment...

@

Post

SAVE