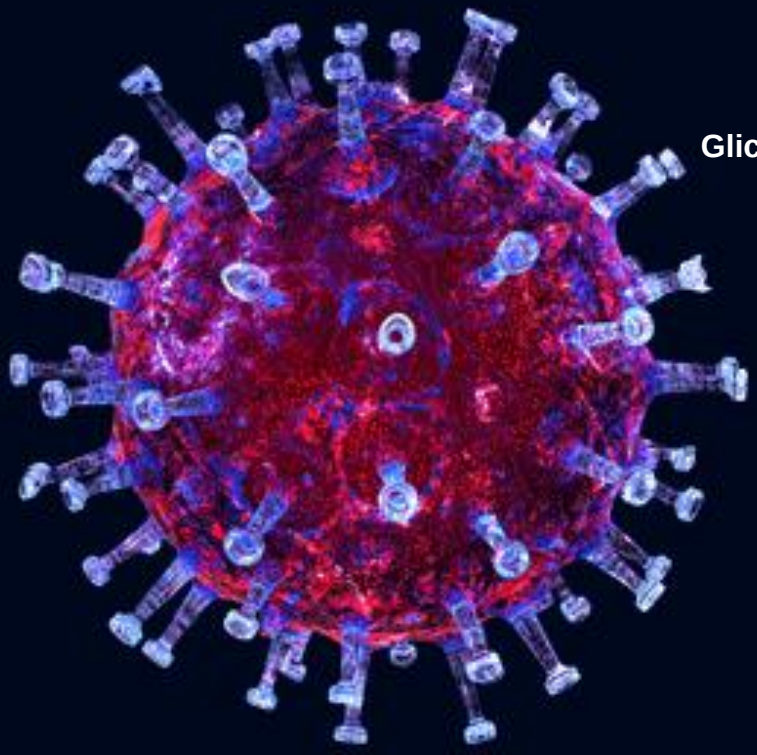
Infecção pelo SARS-CoV-2

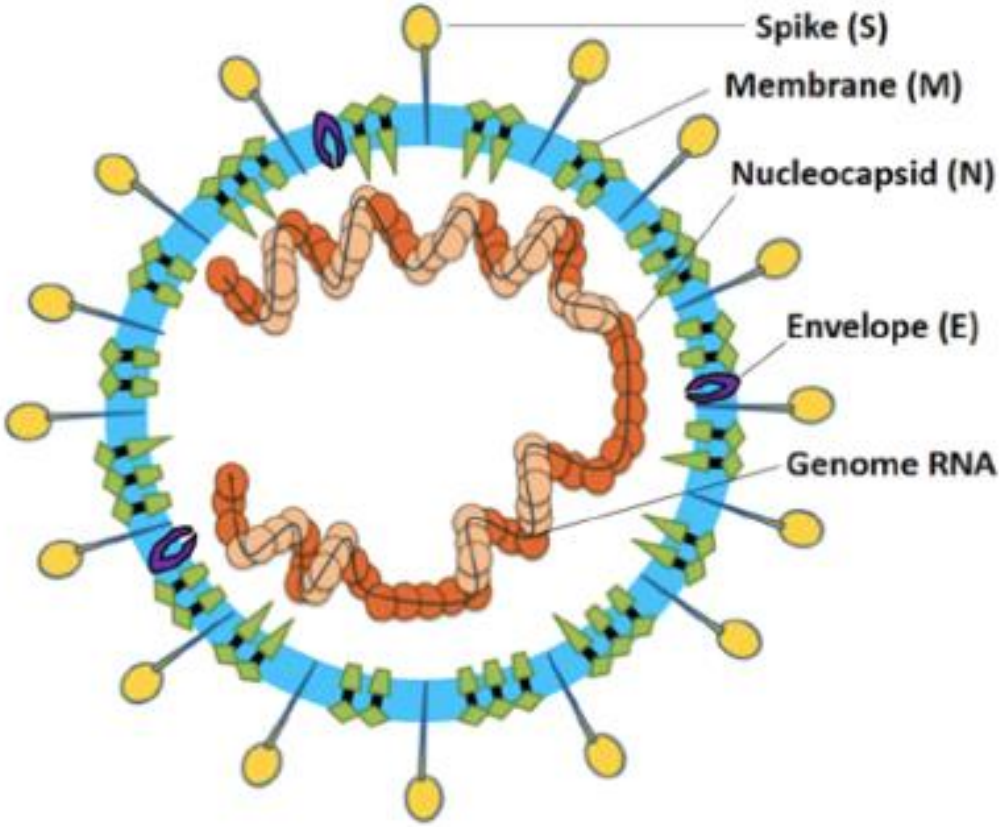
Prof. Dr. Walter F. de Azevedo Jr.

Aqui está descrito o processo de infecção do SARS-CoV-2. O foco está na descrição das proteínas envolvidas no processo de infecção do SARS-CoV-2. O agente causador da COVID-19 é o vírus SARS-CoV-2. Este apresenta no seu capsídeo a glicoproteína *spike*. Esta proteína liga-se à enzima conversora de angiotensina 2 (ACE2) das células do hospedeiro e promove a infecção destas.



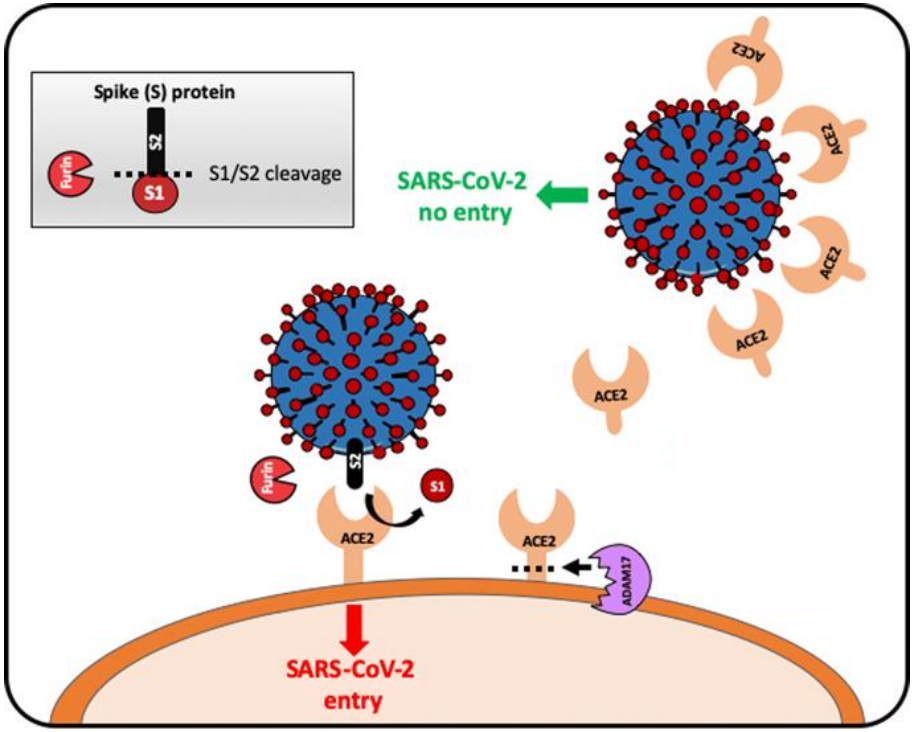
Glicoproteína Spike

SARS-CoV-2



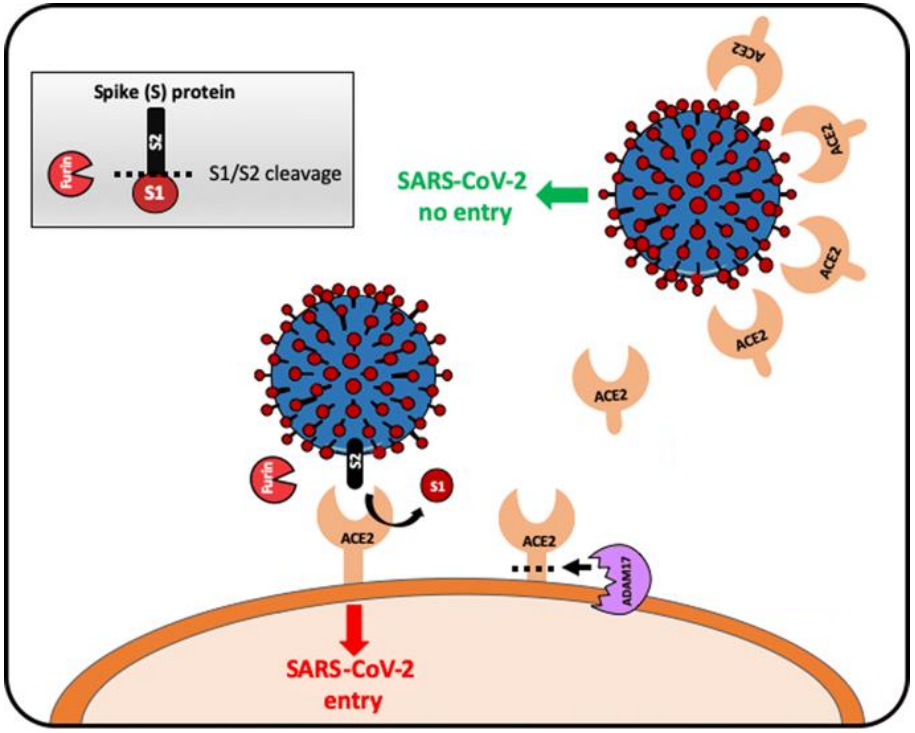
Fonte: Li G et al. Coronavirus infections and immune responses. J Med Virol. 2020, 92(4):424-432.

O agente causador da COVID-19 é o vírus SARS-CoV-2. Este apresenta no seu capsídeo a glicoproteína *spike*. Esta proteína liga-se à enzima conversora de angiotensina 2 (*ACE2*) das células do hospedeiro e promove a infecção destas. A figura abaixo ilustra o processo de encaixe da glicoproteína *spike* na enzima conversora de angiotensina 2 localizada na superfície da membrana plasmática da célula que será infectada.



Processo de infecção pelo SARS-CoV-2. Imagem disponível em: < https://link.springer.com/article/10.1007/s00395-020-0791-5>. Acesso em: 24 de maio de 2020.

Para a infecção da célula pelo SARS-CoV-2 ocorrer é necessária a clivagem proteolítica do sítio S_1/S_2 da glicoproteína *spike* pela protease furina. Os níveis de ACE2 na membrana plasmática são modulados pela proteína ADAM17, que cortam a ACE2.



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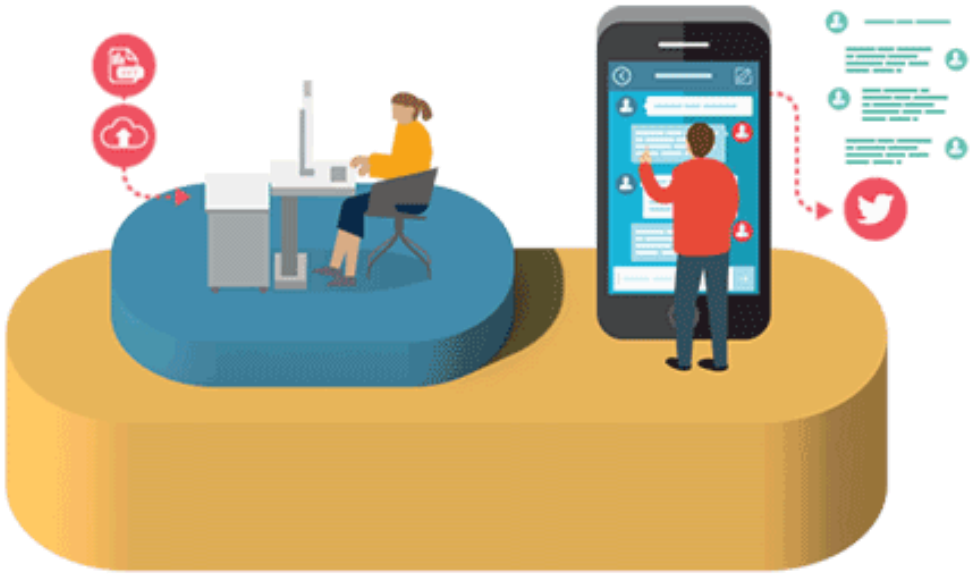
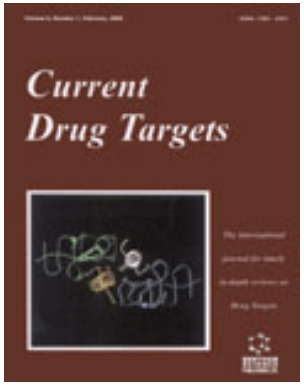
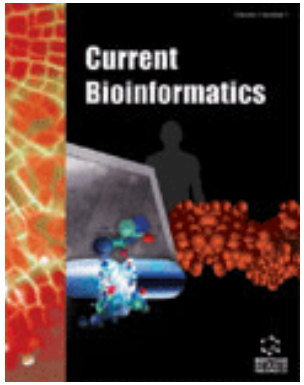


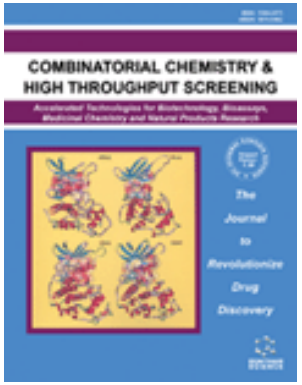
1) Qual a protease catalisa a clivagem do domínio S1/S2 da glicoproteína spike do SARS-CoV-2?

2) Como o conhecimento do processo de infecção pode ajudar no desenvolvimento de um fármaco para tratar a COVID-19?

Prof. Azevedo is Frontiers Section Editor (Bioinformatics and Biophysics) of the Current Drug Targets, section editor (Bioinformatics in Drug Design and Discovery) of the Current Medicinal Chemistry, section editor (Combinatorial/Medicinal Chemistry) for the Combinatorial Chemistry & High Throughput Screening, member of the editorial board of Current Bioinformatics, and editor of Docking Screens for Drug Discovery (Methods of Molecular Biology)(Springer Nature). He is also member of the editorial board of PeerJ, PeerJ Physical Chemistry, Organic & Medicinal Chemistry International Journal, and section editor in chief (Bioinformatics) of the Bioengineering International. He graduated in Physics (BSc in Physics) from the University of São Paulo (USP) in 1990. He completed a Master Degree in Applied Physics also from the USP (1992), working under the supervision of Prof. Yvonne P. Mascarenhas, the founder of crystallography in Brazil. His dissertation was about X-ray crystallography applied to organometallics compounds (De Azevedo Jr. et al., 1995). During his PhD, he worked under the supervision of Prof. Sung-Hou Kim (University of California, Berkeley), on a split Ph.D. program with a fellowship from Brazilian Research Council (CNPq)(1993-1996). His PhD was about the crystallographic structure of CDK2 (De Azevedo Jr. et al., 1996). His current position is coordinator of the Structural Biochemistry Laboratory at Pontifical Catholic University of Rio Grande do Sul (PUCRS). His research interests are interdisciplinary with two major emphases: molecular simulations and protein-ligand interactions. He published over 190 scientific papers about protein structures and computer models to assess intermolecular interactions involving biomolecules and potential ligands (H-index: 37, RG Index > 41.0). These publications have over 4900 citations in the Web of Science (Publons h-index: 37), more than 5600 citations in the Scopus (h-index: 41), and over 7100 citations in the Google Scholar (h-index: 44).







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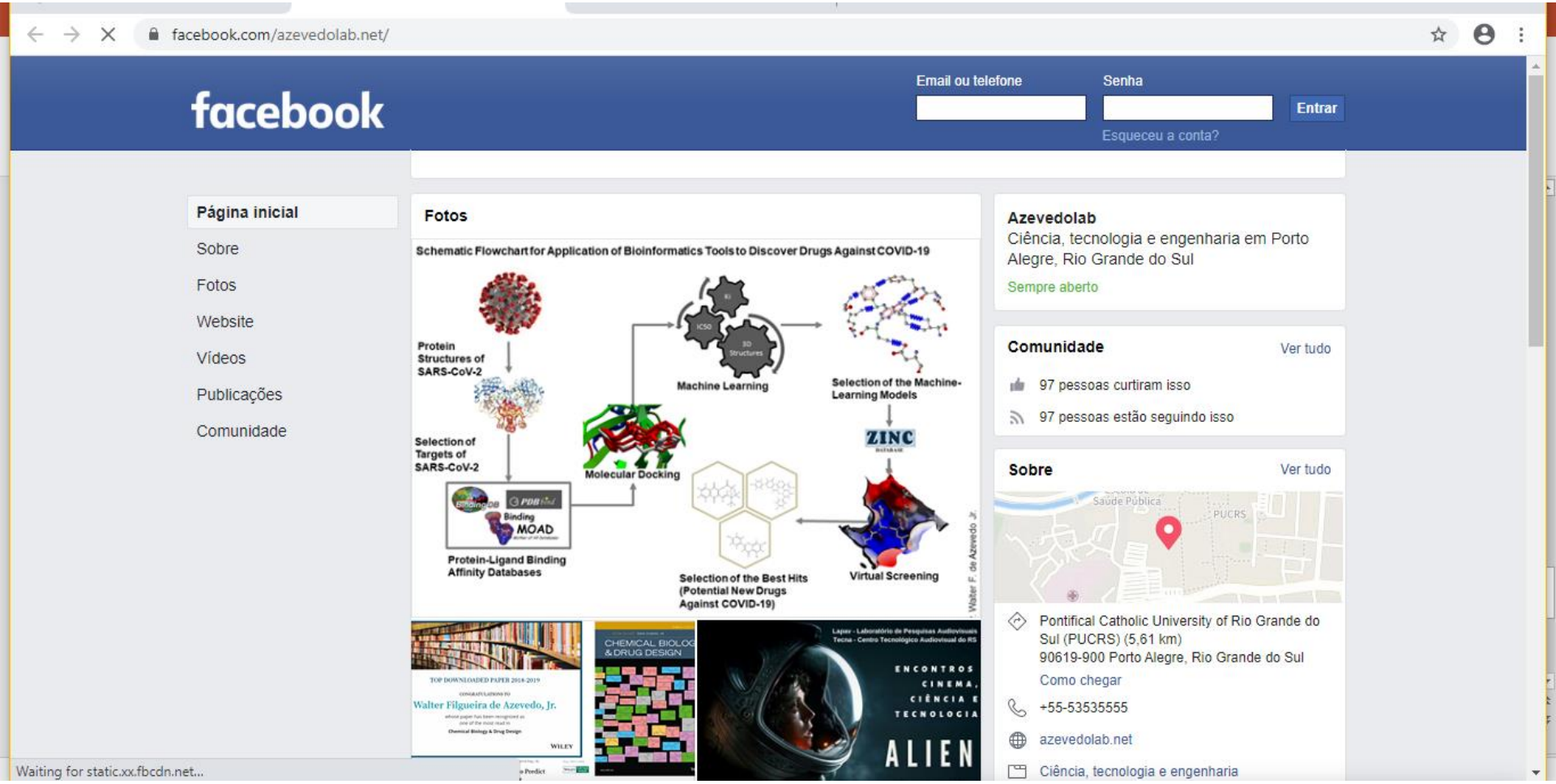

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