

Prediction Algorithm of Virus Mutation

Face the pathogens like SARS-Cov-2

Overview

To develop novel and effective diagnostic/therapeutic solutions against pathogenic viruses like SARS-Cov-2 in which the mutation frequencies are high, the technologies which enables to predict possible mutations before the spread of pathogenic variants with said mutations is required. In SARS-Cov-2, a trend in mutations was found by the analysis of various genomes from variants reported so far (reference 1), suggesting that this may be useful to identify possible mutation sites.

This invention disclose the methods and programs to predict the site and the mutations therein in virus genome in the future by AI-based model developed by using above trend for leaning.

Product Application

- ❑ Diagnostic kit for mutations/variants predicted.
- ❑ Therapeutic agent against variants with mutations predicted.
- ❑ Certification / rescission of immunity passport.

IP Data

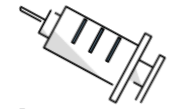
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Machine Learning

Mutation Prediction

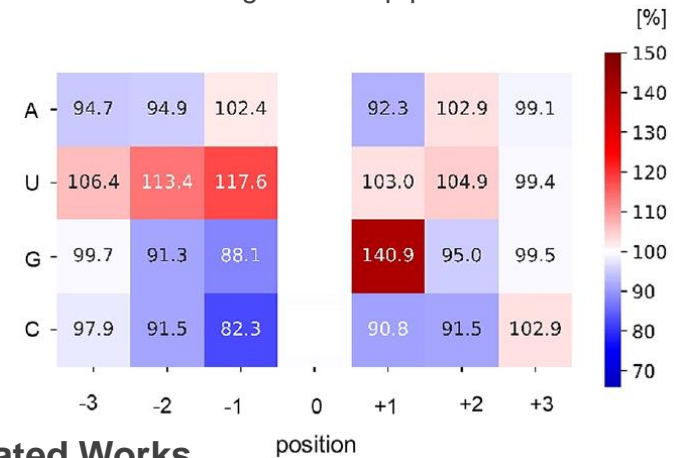


Prophylactic, Therapeutic and Diagnostic Agent



Context preferences at the mutation site

The mutations from cytosine (C) to uracil (U) was frequently found in SARS-CoV-2 variant genomes. Further analysis revealed a trend in sequences of C-to-U mutated site ± 3 base pairs. This trend is used for machine learning to develop prediction model.



Related Works

[1] Kosuge et. al., Scientific Reports (2020) 10:17766

Contact