

# ZCURVE\_CoV database

an updated database of annotated protein-coding genes and proteinase cleavage sites in thousands of coronavirus genomes

ZCURVE\_CoV database is an updated database of annotated protein-coding genes in coronavirus genomes and proteinase cleavage sites in their polyproteins, based on the prediction of ZCURVE\_CoV software. The current release of database includes the prediction results for more than 2800 coronavirus genomes, which will be updated periodically to include more entries, and to integrate more information for each entry. The new coronavirus genomes which are not included temporarily can be predicted by the online service of ZCURVE\_CoV 2.0, which is available at <http://tubic.tju.edu.cn/sars>

If you have any problems, please send email to [Feng Gao](#).

## About

[People](#)

[Publication](#)

[History](#)

## Databases

[DEG](#)

[DoriC](#)

[DeOri](#)

[pDEG](#)

## Tools

[GC-Profile](#)

[Ori-Finder](#)

[Ori-Finder 2](#)

[Zcurve 3.0](#)

## TUBIC

School of

Science

Tianjin

University,

Greglist

300072  
No. 92 Weijin  
Road  
Nankai District,  
Tianjin  
China  
Tel: (Phone &  
Fax) +86-22-  
27402697

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