

**Digital Biology<sup>®</sup>**



Digital Biology

**geneious**

**Geneious Prime 2022**

**主な新機能と変更点**

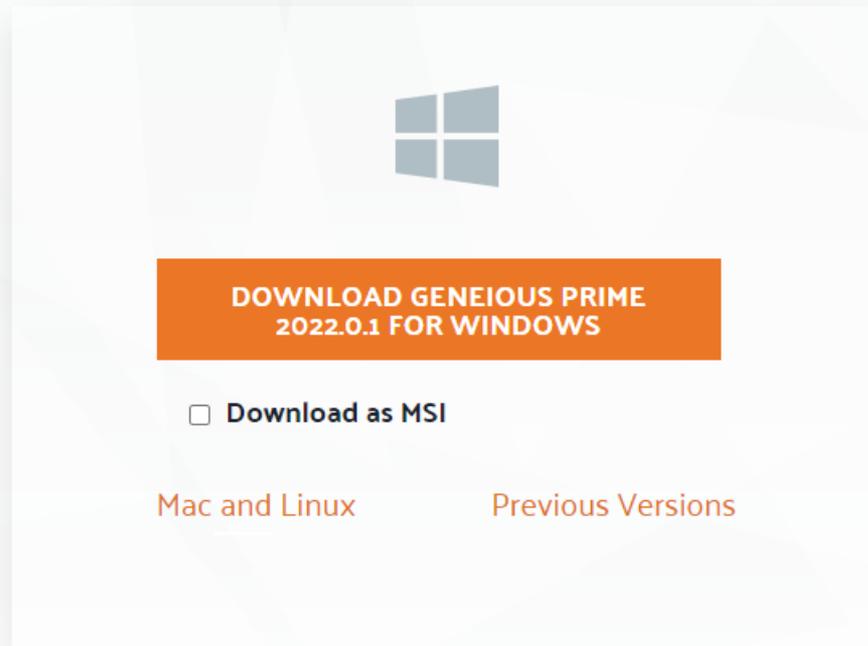
トミーデジタルバイオロジー株式会社

2021/11/16 リリース

# Geneious Prime 2022が公開されました

## Geneious Prime 2022 Download

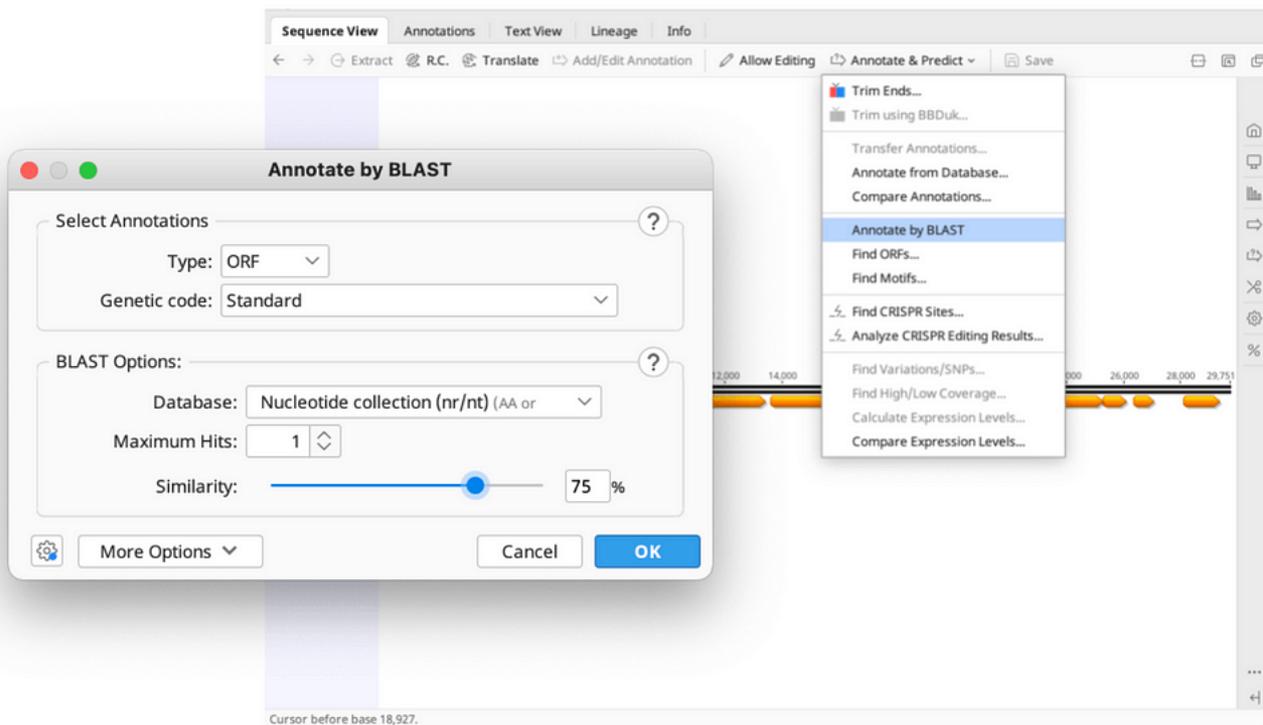
Download and install the the world's leading bioinformatics software platform used by over 4,000 institutes in more than 125 countries.



最新版はこちらのサイトよりダウンロードができます

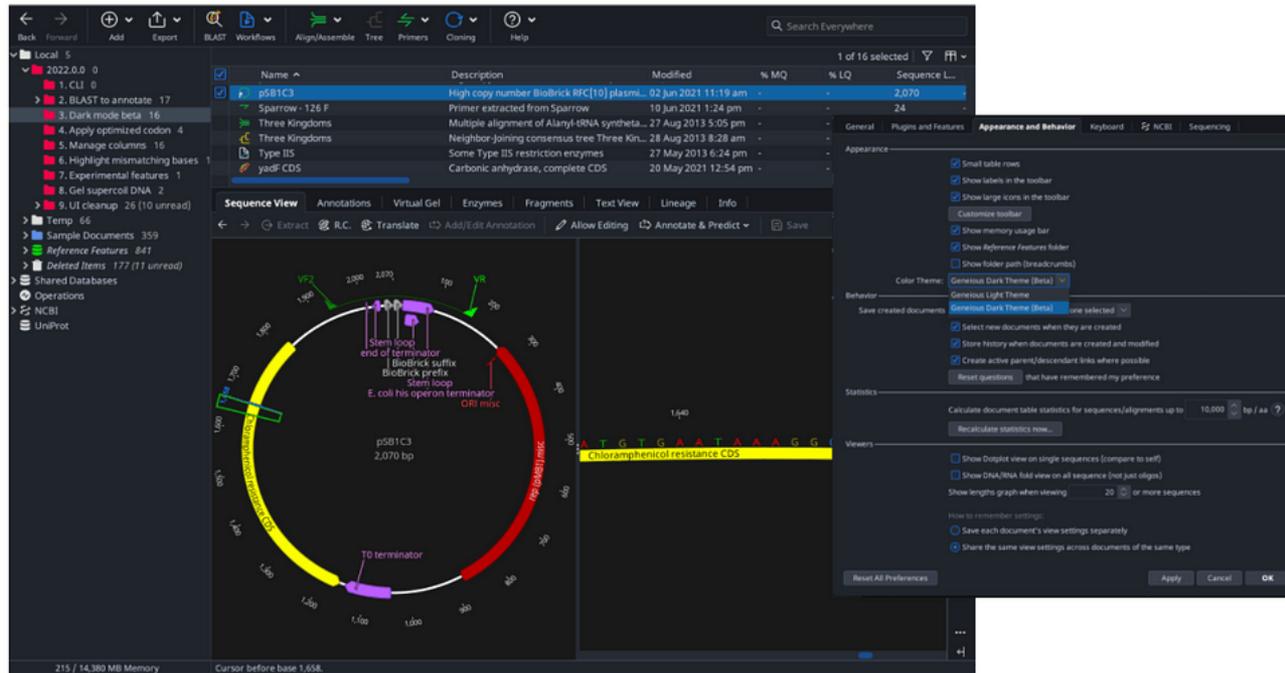
<https://www.geneious.com/download/>

# BLASTによるアノテーション



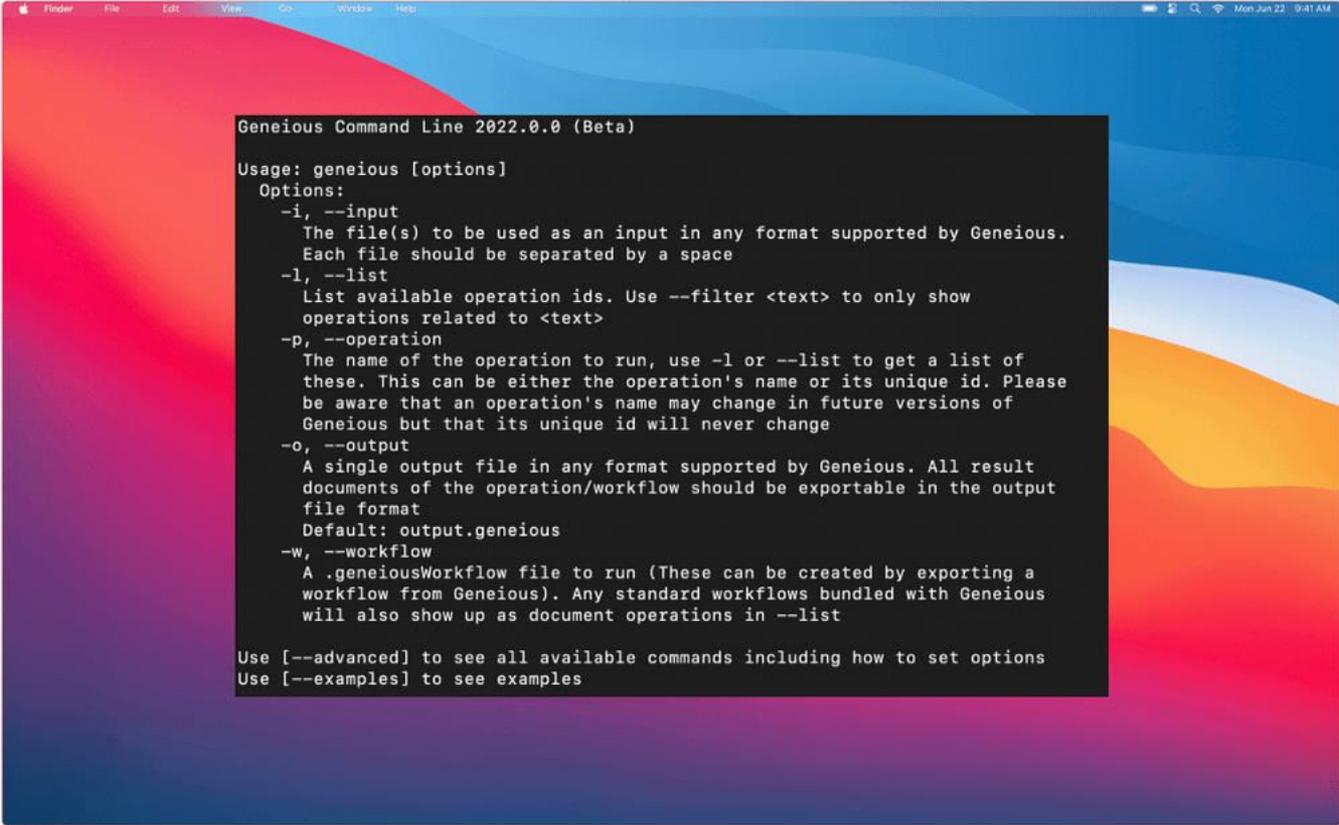
BLASTを利用してORF, CDS, mRNA領域を自動的にアノテーションできます

# ダークモード(β版)



ダークモードにより昼夜を問わず快適にデータを解析することができます

# コマンドライン・インターフェース



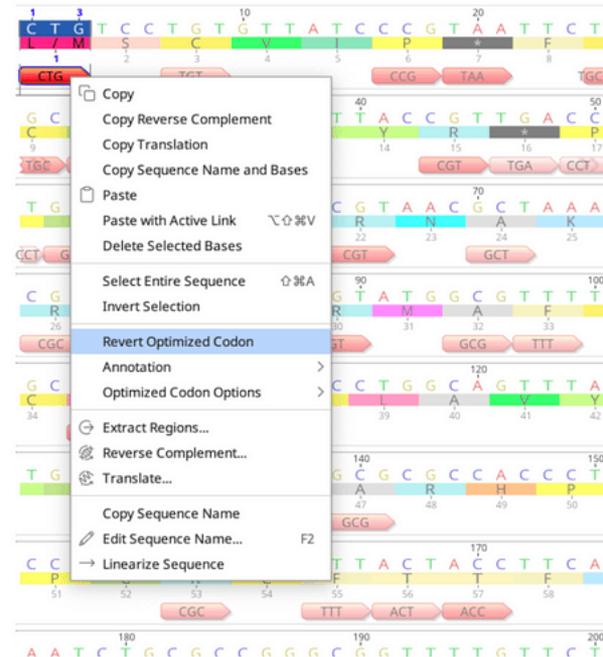
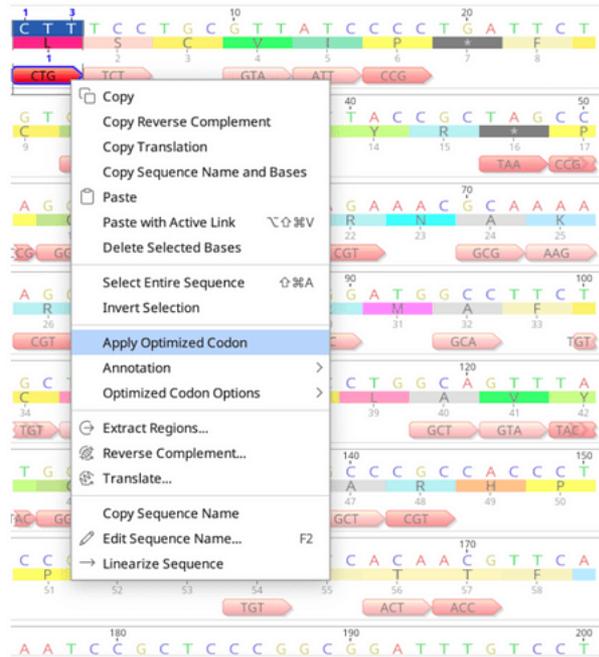
```
Geneious Command Line 2022.0.0 (Beta)

Usage: geneious [options]
Options:
  -i, --input
    The file(s) to be used as an input in any format supported by Geneious.
    Each file should be separated by a space
  -l, --list
    List available operation ids. Use --filter <text> to only show
    operations related to <text>
  -p, --operation
    The name of the operation to run, use -l or --list to get a list of
    these. This can be either the operation's name or its unique id. Please
    be aware that an operation's name may change in future versions of
    Geneious but that its unique id will never change
  -o, --output
    A single output file in any format supported by Geneious. All result
    documents of the operation/workflow should be exportable in the output
    file format
    Default: output.geneious
  -w, --workflow
    A .geneiousWorkflow file to run (These can be created by exporting a
    workflow from Geneious). Any standard workflows bundled with Geneious
    will also show up as document operations in --list

Use [--advanced] to see all available commands including how to set options
Use [--examples] to see examples
```

Geneious Primeの操作やワークフローをパイプラインの一部として  
ローカルに実行したり、より強力なサーバーで実行したりすることができます  
<https://www.geneious.com/api-developers/>

# 最適化されたコドンの適用



最適化されたコドンシーケンスに簡単に追加・削除することができます

# ドキュメントテーブルのカラムの管理

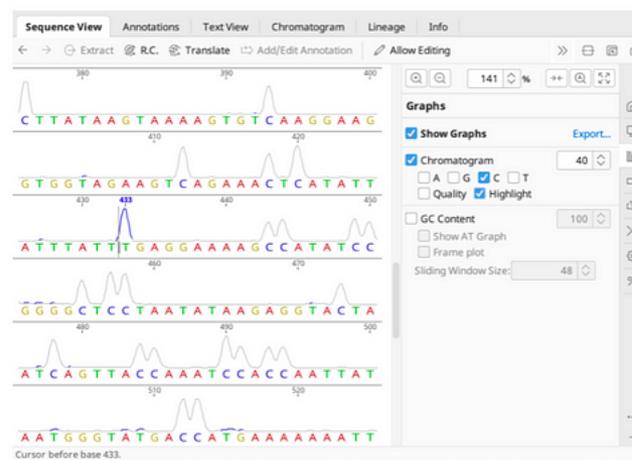
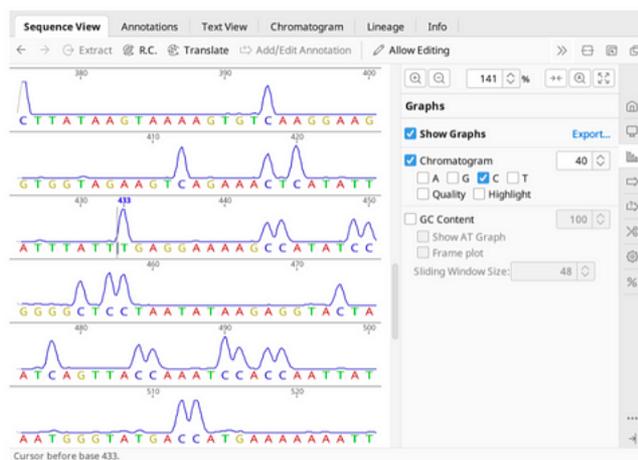
The screenshot displays a software interface for managing sequence data. At the top, a table lists various biological entries with columns for Name, Description, Organism, and Sequence length. Below the table, a 'Sequence View' tab is active, showing a detailed view of five selected sequences (JX560779 to JX560783). These sequences are represented as horizontal bars with a color-coded scale from 1 to 314. A settings panel on the right side of the interface allows for the selection and management of columns. The panel includes a list of columns with checkboxes, such as '# Disagreements', '# Indel Disagreements', '# Nucleotides', '# Nucleotide Sequences', '# Nucleotide Sequences With Mates', '# Nucleotide Sequences With Quality', '# Protein Sequences', '# Sequences', '% GC', '% GC Primer Bind', '% HQ', '% Identical Sites', '% LQ', '% MQ', '% Pairwise Identity', 'Accession', and 'Lock Column Order'. The '1 of 16 selected' indicator is visible at the top right of the settings panel.

Name	Description	Organism	Sequence
COI Assembly	Assembly of 2 reads: COI rev read (reversed), COI fwd read	-	758
COI rev read	Reverse Sanger read of COI gene	-	721
Ig variable region	5 immunoglobulin heavy chain variable regions	-	-
Image	An image	-	-
LysR family	7 LysR protein sequences	-	-
MK910749	Expression vector pDEST17-AceKMs, complete sequence	Expression vector pDEST17-AceK...	5,842
NARH	RecName: Full=Respiratory nitrate reductase 1 beta chain; EC=1.7.99.4; AltName: Full=Nit...	Escherichia coli	512
Notes	-	-	-
Protein complex (1A4Y)	Ribonuclease inhibitor-angiogenin complex	Homo sapiens	-
pSB1C3	High copy number BioBrick RFC[10] plasmid carrying chloramphenicol resistance.	pSB1C3 cloning vector	2,070
pSB1C3	High copy number BioBrick RFC[10] plasmid carrying chloramphenicol resistance.	pSB1C3 cloning vector	2,070
Sparrow - 126 F	Primer extracted from Sparrow	Aimophila botterii	24
Three Kingdoms	Multiple alignment of Alanyl-tRNA synthetase from organisms of three different kingdoms	-	1,156
Three Kingdoms	Neighbor-joining consensus tree Three Kingdoms	-	1,156
Type IIS	Some Type IIS restriction enzymes	-	-
yadF CDS	Carbonic anhydrase, complete CDS	Pseudomonas stutzeri ATCC 175...	645

複数のカラムを選択してデータを素早く整理することができます



# ミスマッチ塩基のハイライト



クロマトグラム中のミスマッチな塩基をハイライト表示することができます

# その他の試験的機能

The screenshot displays the Geneious Prime software interface. The main window shows a file browser on the left with a tree view containing folders like 'DemoData 47', 'DemoData1 52', 'test 26338 (11 unread)', 'Tutorials 758', 'Sample Documents 1272', 'Reference Features 842', 'Deleted Items 43', 'Shared Databases', 'Operations', 'NCBI', and 'UniProt'. The main workspace shows a sequence viewer with a sequence alignment. A 'Preferences' dialog box is open, with the 'Plugins and Features' tab selected. Within this dialog, the 'Customize Feature Set' sub-dialog is open, showing a list of plugins and features with checkboxes indicating their status. All features are currently checked and set to 'Enabled'. The 'Features' section at the bottom of the 'Customize Feature Set' dialog has two buttons: 'Customize Feature Set...' and 'Experimental Features...'. The 'Experimental Features...' button is highlighted, indicating it is the focus of the text below. The 'Preferences' dialog also has 'Reset All Preferences', 'OK', 'Cancel', and 'Apply' buttons at the bottom.

Description	Enabled	Info
Minimap2: A versatile mapper / pairwise aligner for genomic and	<input checked="" type="checkbox"/>	Info
Muscle alignment: MUSCLE: Multiple sequence comparison by	<input checked="" type="checkbox"/>	Info
Mutation/SNP Finder: Finds mutations such as SNPs in a contig	<input checked="" type="checkbox"/>	Info
My god, it's full of stars: My god, it's full of stars	<input checked="" type="checkbox"/>	Info
NCBI: Provides access to GenBank, BLAST, Custom BLAST, PubMed	<input checked="" type="checkbox"/>	Info
New Sequence: New sequence documents can be made by pasting or	<input checked="" type="checkbox"/>	Info
Newick importer/exporter: Provides Newick importing and exporting	<input checked="" type="checkbox"/>	Info
NextgenBiologics: Experimental operations for biologics on nextgen	<input checked="" type="checkbox"/>	Info
Nexus importer/exporter: Provides Nexus importing/exporting	<input checked="" type="checkbox"/>	Info
Nucleotide Sequence Quality Statistics: Provides statistics in the	<input checked="" type="checkbox"/>	Info
Open reading frame plugin: ORF analysis tools	<input checked="" type="checkbox"/>	Info
Operations Table: Displays local and remote jobs and allows	<input checked="" type="checkbox"/>	Info
PDF importer/exporter: Imports PDF documents	<input checked="" type="checkbox"/>	Info
PHYLIP importer/exporter: Provides Phylip import/export	<input checked="" type="checkbox"/>	Info
PIR/NBRF importer: Provides PIR/NBRF import	<input checked="" type="checkbox"/>	Info
Parent Descendant Viewer: Allows viewing of and managing the	<input checked="" type="checkbox"/>	Info
Pfam: Provides access to the Pfam databases. Provided for backward.	<input checked="" type="checkbox"/>	Info

Tools → Preferences → Experimental Featuresボタンより、いくつかの試験的機能をお試しいただくことができます

# Want more details?

これまでのバージョンと, Prime 2022で追加された機能に関しては  
下記のページでご確認いただけます(英語)

<https://www.geneious.com/whats-new/>

その他のマイナーチェンジや, バグの修正を含むすべてのアップデート情報は,  
下記のGeneious Primeリリースノートでご確認いただけます(英語)

<https://assets.geneious.com/documentation/geneious/release-notes.html>

# Geneious Prime 2022のシステム要件

OS: Windows 7/8/8.1/10/11 (64-bit)  
Mac OS 10.11 El Capitan以降  
Linux Ubuntu Desktop LTS (18.04 and 20.04)

CPU : x86 64-bit

メモリ : 2 GB以上のRAM

ハードディスク : 2 GB以上の空き容量

モニタ : 1024x768以上の解像度

※上記はアプリケーションが動作する最小の構成です  
NGS関連の解析機能などを使用される場合はデータ量に依存します

# Mac (Apple M1) ユーザーの方へのご注意

Prime 2019(=R12)以前のバージョンのGeneiousは、macOS Big Sur 11以降の環境で動作することができません

macOS Big Sur 11またはmacOS Monterey 12でGeneiousを使用されたい方は、Prime 2020以降のバージョンにアップグレードしていただく必要があります

GeneiousがサポートしているOSの詳細な情報につきましては以下をご参照ください

<https://help.geneious.com/hc/en-us/articles/360045071451-Supported-Operating-Systems>

# マニュアルのダウンロード

日本語版(Prime 2021.0) (2022版は準備中です)

<https://www.digital-biology.co.jp/datadownload/Geneious>

ユーザー名: geneious@biomatters

パスワード: orange

英語版(Prime 2022.0)

<https://assets.geneious.com/documentation/geneious/GeneiousPrimeManual2022.0.pdf>

Geneious内にあらかじめ入っているデモデータをクリックすると横に表示されるHelpパネル(英語)もご参照ください

# カスタマーサポート

トミーデジタルバイオロジー株式会社

TEL: 03-6240-0451

E-mail: support@digital-biology.co.jp

担当: 田中・越後

対応時間: 平日9:00～17:30



※メーカーの公式なサポートは最新バージョンと一つ前のバージョンまでが対象となっております(2021年12月現在、Prime 2021まで)

それ以前のバージョンはサポートできかねることがございますので何卒ご了承ください

旧バージョンをご利用の方でアップグレードをご希望の方は弊社までお問い合わせください