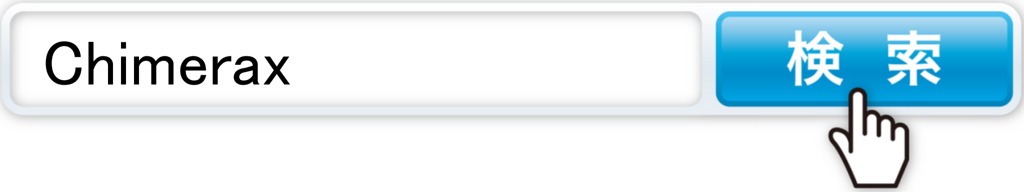
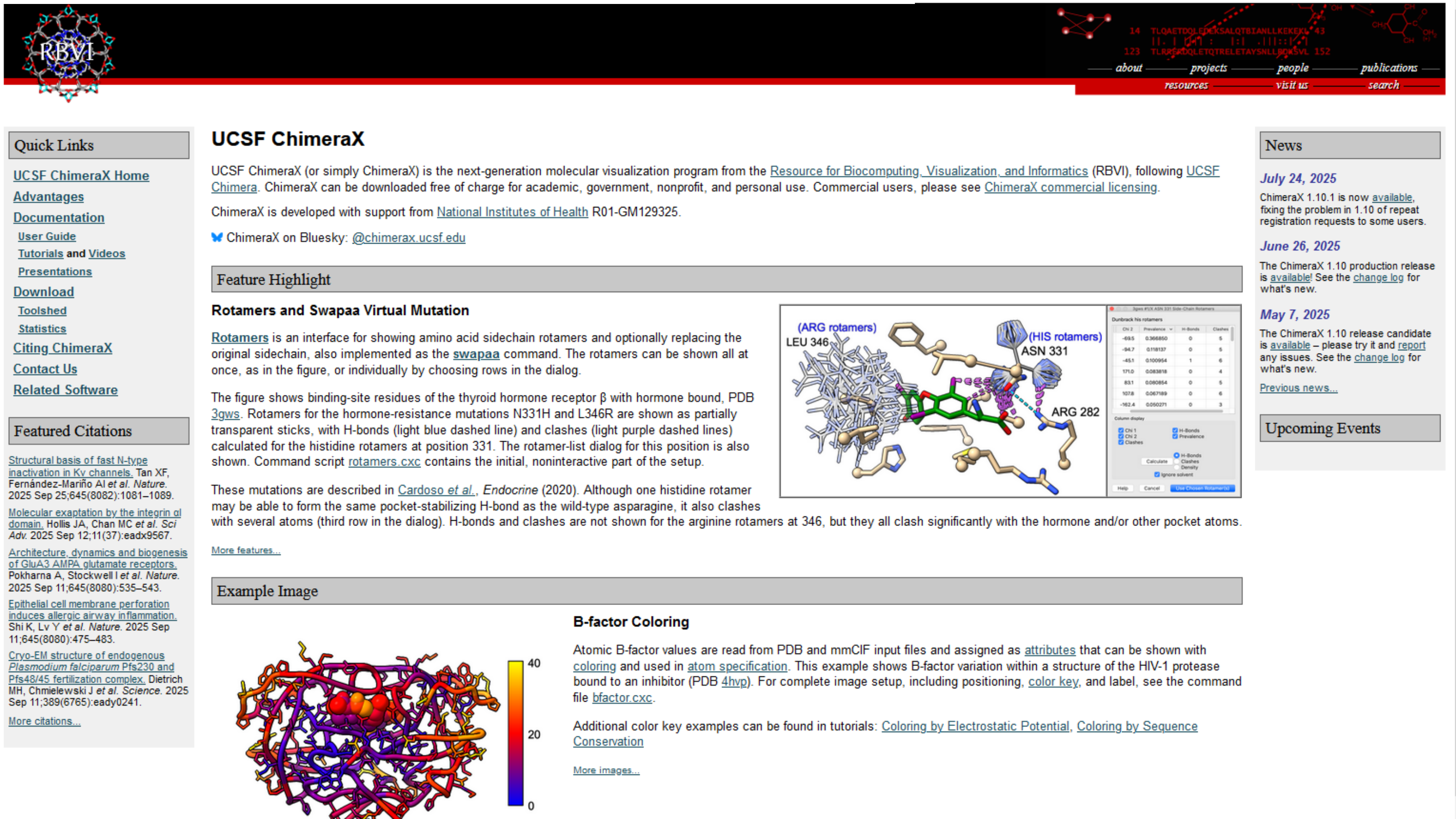
分子グラフィックスソフト Chimeraxのインストール

UCSF Chimeraの最新版Chimeraxをインストールします

以下のサイトにアクセスしてください

https://www.cgl.ucsf.edu/chimerax/





Quick Links

- UCSF ChimeraX Home
- Advantages
- Documentation
  - User Guide
  - Tutorials and Videos
  - Presentations
- Download
  - Toolshed
  - Statistics
- Citing ChimeraX
- Contact Us
- Related Software

Featured Citations

Structural basis of fast N-type inactivation in Kv channels. Tan XF, Fernández-Mariño AI *et al. Nature*. 2025 Sep 25;645(8082):1081–1089.

Molecular exaptation by the integrin αI domain. Hollis JA, Chan MC *et al. Sci Adv.* 2025 Sep 12;11(37):eadx9567.

Architecture, dynamics and biogenesis of GluA3 AMPA glutamate receptors. Pokharna A, Stockwell I *et al. Nature*. 2025 Sep 11;645(8080):535–543.

Epithelial cell membrane perforation induces allergic airway inflammation. Shi K, Lv Y *et al. Nature*. 2025 Sep 11;645(8080):475–483.

Cryo-EM structure of endogenous *Plasmodium falciparum* Pfs230 and Pfs48/45 fertilization complex. Dietrich MH, Chmielewski J *et al. Science*. 2025 Sep 11;389(6765):eady0241.

More citations...

UCSF ChimeraX

UCSF ChimeraX (or simply ChimeraX) is the next-generation molecular visualization program from the Resource for Biocomputing, Visualization, and Informatics (RBVI), following UCSF Chimera. ChimeraX can be downloaded free of charge for academic, government, nonprofit, and personal use. Commercial users, please see ChimeraX commercial licensing.

ChimeraX is developed with support from National Institutes of Health R01-GM129325.

ChimeraX on Bluesky: @chimerax.ucsf.edu

Feature Highlight

Rotamers and Swapaa Virtual Mutation

Rotamers is an interface for showing amino acid sidechain rotamers and optionally replacing the original sidechain, also implemented as the swapaa command. The rotamers can be shown all at once, as in the figure, or individually by choosing rows in the dialog.

The figure shows binding-site residues of the thyroid hormone receptor β with hormone bound, PDB 3gws. Rotamers for the hormone-resistance mutations N331H and L346R are shown as partially transparent sticks, with H-bonds (light blue dashed line) and clashes (light purple dashed lines) calculated for the histidine rotamers at position 331. The rotamer-list dialog for this position is also shown. Command script rotamers.cxc contains the initial, noninteractive part of the setup.

These mutations are described in Cardoso *et al.*, *Endocrine* (2020). Although one histidine rotamer may be able to form the same pocket-stabilizing H-bond as the wild-type asparagine, it also clashes with several atoms (third row in the dialog). H-bonds and clashes are not shown for the arginine rotamers at 346, but they all clash significantly with the hormone and/or other pocket atoms.

More features...

Example Image

B-factor Coloring

Atomic B-factor values are read from PDB and mmCIF input files and assigned as attributes that can be shown with coloring and used in atom specification. This example shows B-factor variation within a structure of the HIV-1 protease bound to an inhibitor (PDB 4hvp). For complete image setup, including positioning, color key, and label, see the command file bfactor.cxc.

Additional color key examples can be found in tutorials: Coloring by Electrostatic Potential, Coloring by Sequence Conservation

More images...

News

July 24, 2025

ChimeraX 1.10.1 is now available, fixing the problem in 1.10 of repeat registration requests to some users.

June 26, 2025

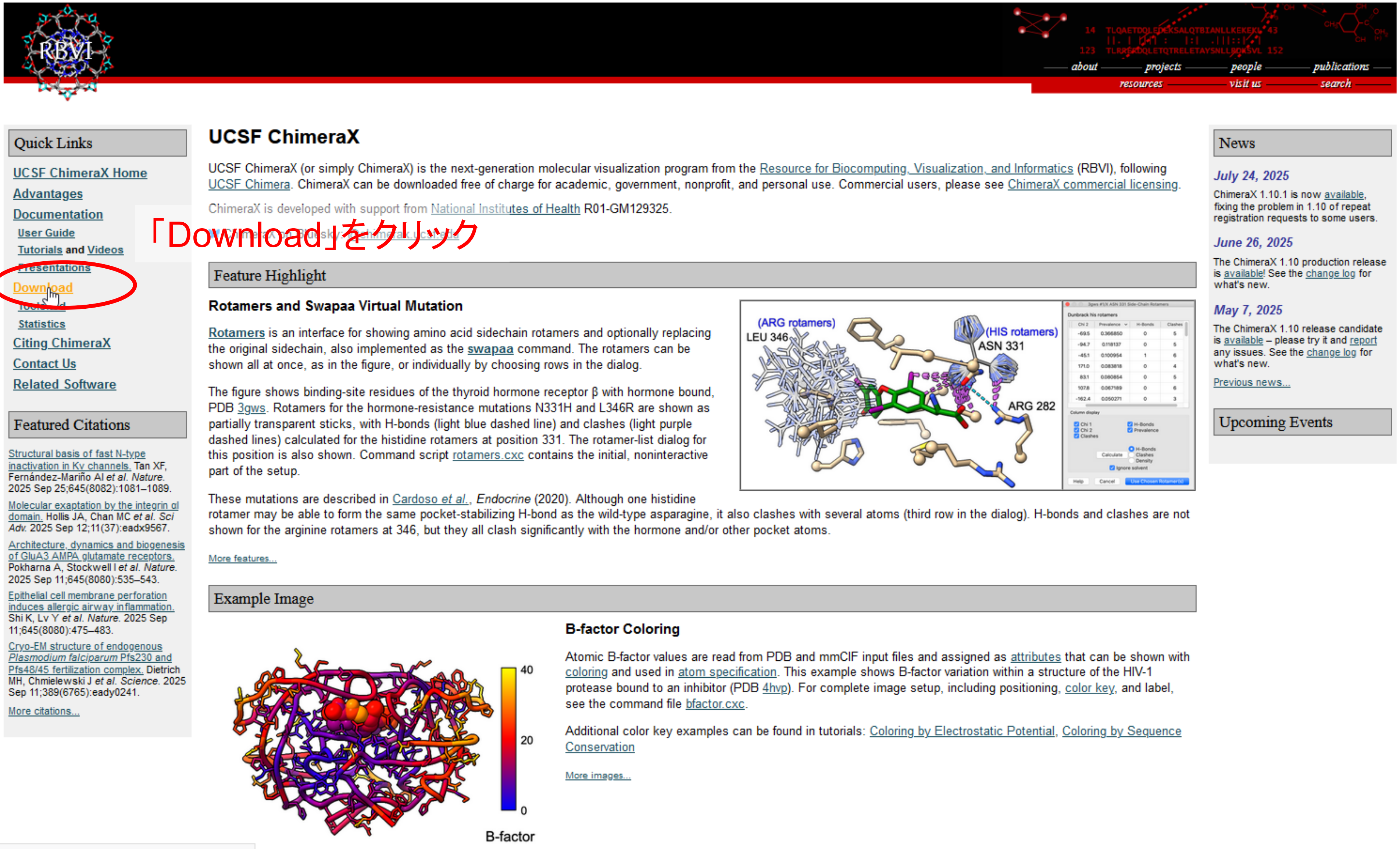
The ChimeraX 1.10 production release is available! See the change log for what's new.

May 7, 2025

The ChimeraX 1.10 release candidate is available – please try it and report any issues. See the change log for what's new.

Previous news...

Upcoming Events



「Download」をクリック

Quick Links

- UCSF ChimeraX Home
- Advantages
- Documentation
  - User Guide
  - Tutorials and Videos
  - Presentations
- Download
  - Toolshed
  - Statistics
- Citing ChimeraX
- Contact Us
- Related Software

Featured Citations

Structural basis of fast N-type inactivation in Kv channels. Tan XF, Fernández-Mariño AI *et al.* *Nature*. 2025 Sep 25;645(8082):1081–1089.

Molecular exaptation by the integrin αI domain. Hollis JA, Chan MC *et al.* *Sci Adv.* 2025 Sep 12;11(37):eadx9567.

Architecture, dynamics and biogenesis of GluA3 AMPA glutamate receptors. Pokharna A, Stockwell I *et al.* *Nature*. 2025 Sep 11;645(8080):535–543.

Epithelial cell membrane perforation induces allergic airway inflammation. Shi K, Lv Y *et al.* *Nature*. 2025 Sep 11;645(8080):475–483.

Cryo-EM structure of endogenous *Plasmodium falciparum* Pfs230 and Pfs48/45 fertilization complex. Dietrich MH, Chmielewski J *et al.* *Science*. 2025 Sep 11;389(6765):eady0241.

More citations...

UCSF ChimeraX

UCSF ChimeraX (or simply ChimeraX) is the next-generation molecular visualization program from the Resource for Biocomputing, Visualization, and Informatics (RBVI), following UCSF Chimera. ChimeraX can be downloaded free of charge for academic, government, nonprofit, and personal use. Commercial users, please see ChimeraX commercial licensing.

ChimeraX is developed with support from National Institutes of Health R01-GM129325.

ChimeraX on Bluesky: @chimerax.ucsf.edu

Feature Highlight

Rotamers and Swapaa Virtual Mutation

Rotamers is an interface for showing amino acid sidechain rotamers and optionally replacing the original sidechain, also implemented as the swapaa command. The rotamers can be shown all at once, as in the figure, or individually by choosing rows in the dialog.

The figure shows binding-site residues of the thyroid hormone receptor β with hormone bound, PDB 3gws. Rotamers for the hormone-resistance mutations N331H and L346R are shown as partially transparent sticks, with H-bonds (light blue dashed line) and clashes (light purple dashed lines) calculated for the histidine rotamers at position 331. The rotamer-list dialog for this position is also shown. Command script rotamers.cxc contains the initial, noninteractive part of the setup.

These mutations are described in Cardoso *et al.*, *Endocrine* (2020). Although one histidine rotamer may be able to form the same pocket-stabilizing H-bond as the wild-type asparagine, it also clashes with several atoms (third row in the dialog). H-bonds and clashes are not shown for the arginine rotamers at 346, but they all clash significantly with the hormone and/or other pocket atoms.

More features...

Example Image

B-factor Coloring

Atomic B-factor values are read from PDB and mmCIF input files and assigned as attributes that can be shown with coloring and used in atom specification. This example shows B-factor variation within a structure of the HIV-1 protease bound to an inhibitor (PDB 4hvp). For complete image setup, including positioning, color key, and label, see the command file bfactor.cxc.

Additional color key examples can be found in tutorials: Coloring by Electrostatic Potential, Coloring by Sequence Conservation

More images...

News

July 24, 2025

ChimeraX 1.10.1 is now available, fixing the problem in 1.10 of repeat registration requests to some users.

June 26, 2025

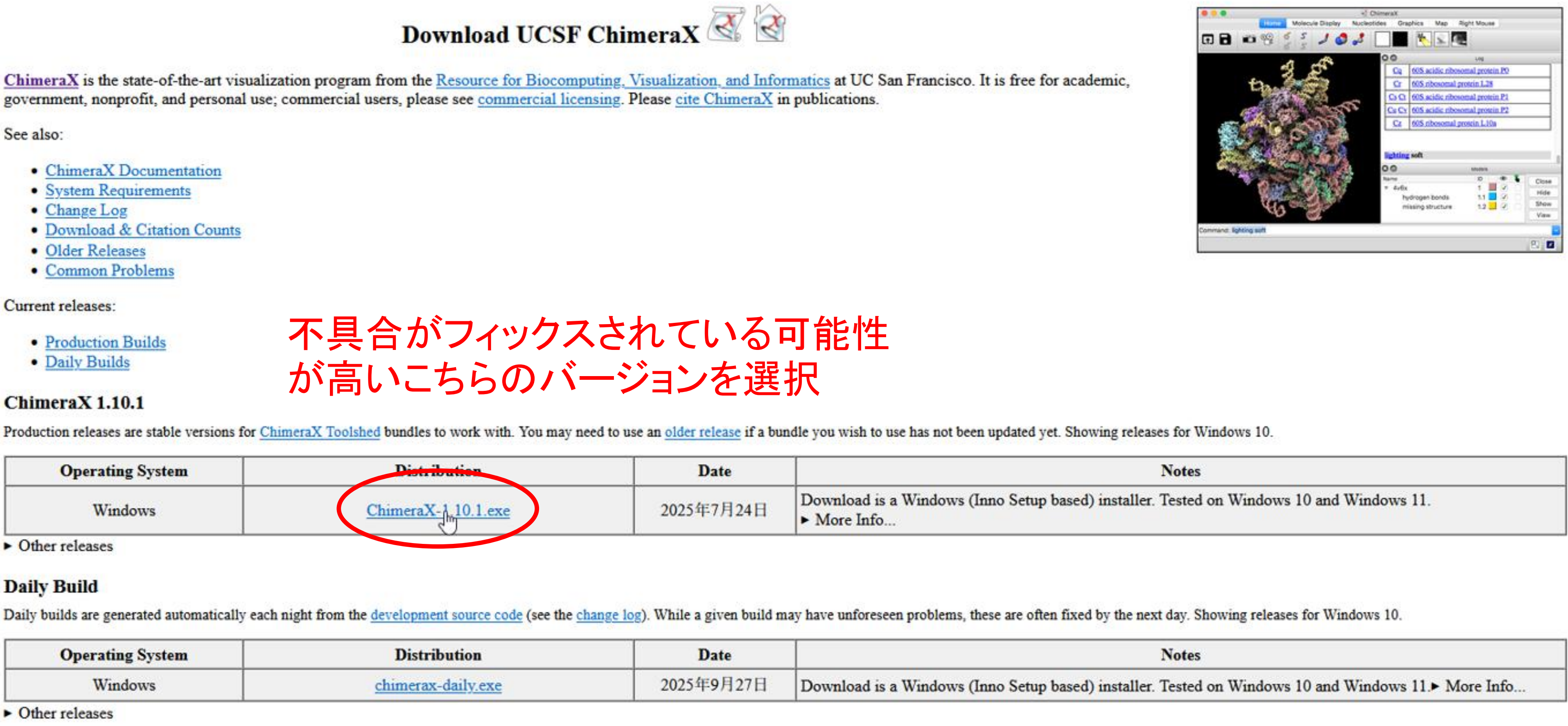
The ChimeraX 1.10 production release is available! See the change log for what's new.

May 7, 2025

The ChimeraX 1.10 release candidate is available – please try it and report any issues. See the change log for what's new.

Previous news...

Upcoming Events



Download UCSF ChimeraX

ChimeraX is the state-of-the-art visualization program from the Resource for Biocomputing, Visualization, and Informatics at UC San Francisco. It is free for academic, government, nonprofit, and personal use; commercial users, please see commercial licensing. Please cite ChimeraX in publications.

See also:

- ChimeraX Documentation
- System Requirements
- Change Log
- Download & Citation Counts
- Older Releases
- Common Problems

Current releases:

- Production Builds
- Daily Builds

不具合がフィックスされている可能性
が高いこちらのバージョンを選択

ChimeraX 1.10.1

Production releases are stable versions for ChimeraX Toolshed bundles to work with. You may need to use an older release if a bundle you wish to use has not been updated yet. Showing releases for Windows 10.

Operating System	Distribution	Date	Notes
Windows	ChimeraX-1.10.1.exe	2025年7月24日	Download is a Windows (Inno Setup based) installer. Tested on Windows 10 and Windows 11. ▸ More Info...

▸ Other releases

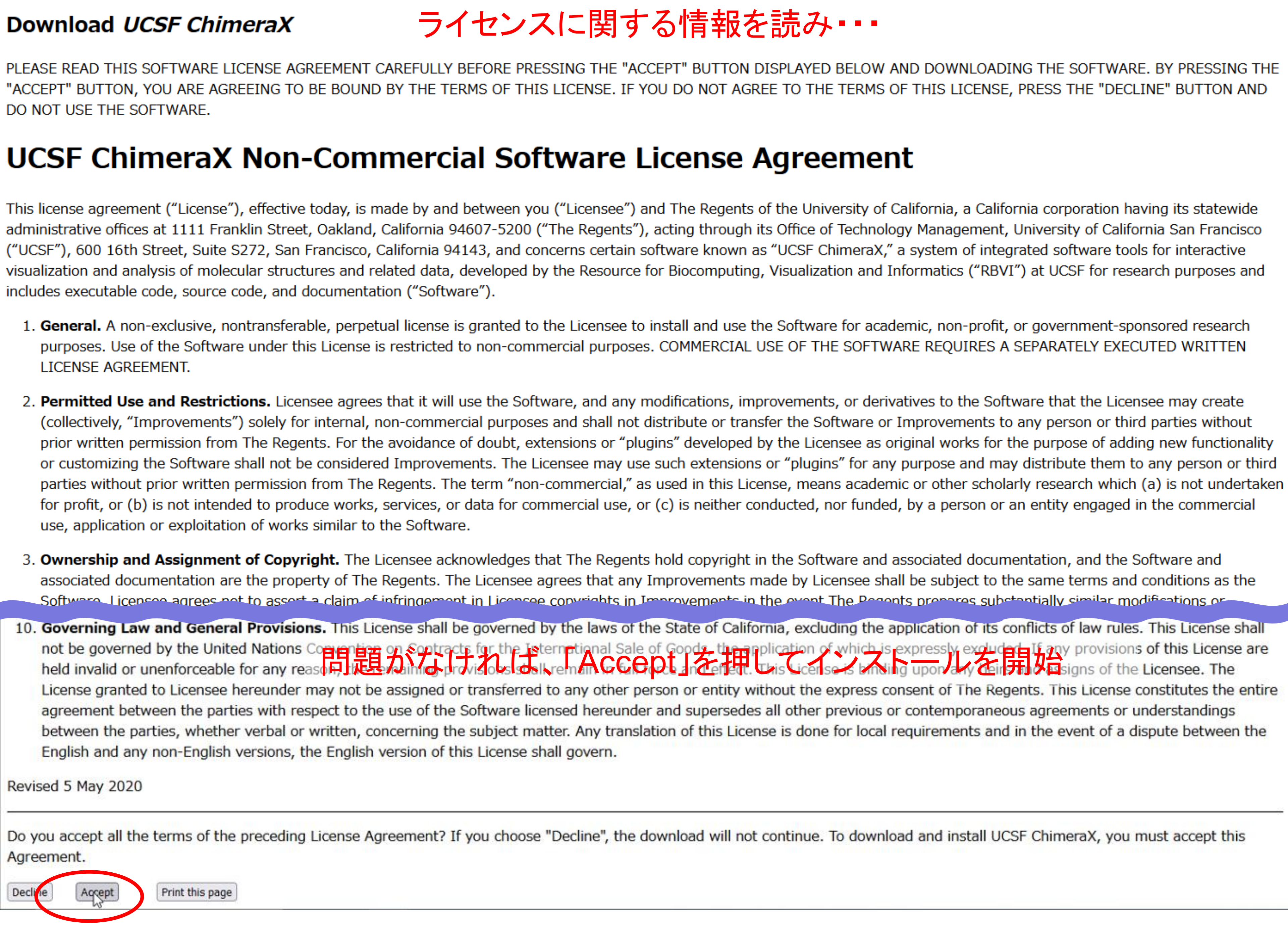
Daily Build

Daily builds are generated automatically each night from the development source code (see the change log). While a given build may have unforeseen problems, these are often fixed by the next day. Showing releases for Windows 10.

Operating System	Distribution	Date	Notes
Windows	chimerax-daily.exe	2025年9月27日	Download is a Windows (Inno Setup based) installer. Tested on Windows 10 and Windows 11.▸ More Info...

▸ Other releases

ライセンスに関する情報を読み・・・



Download *UCSF ChimeraX*

PLEASE READ THIS SOFTWARE LICENSE AGREEMENT CAREFULLY BEFORE PRESSING THE "ACCEPT" BUTTON DISPLAYED BELOW AND DOWNLOADING THE SOFTWARE. BY PRESSING THE "ACCEPT" BUTTON, YOU ARE AGREEING TO BE BOUND BY THE TERMS OF THIS LICENSE. IF YOU DO NOT AGREE TO THE TERMS OF THIS LICENSE, PRESS THE "DECLINE" BUTTON AND DO NOT USE THE SOFTWARE.

UCSF ChimeraX Non-Commercial Software License Agreement

This license agreement (“License”), effective today, is made by and between you (“Licensee”) and The Regents of the University of California, a California corporation having its statewide administrative offices at 1111 Franklin Street, Oakland, California 94607-5200 (“The Regents”), acting through its Office of Technology Management, University of California San Francisco (“UCSF”), 600 16th Street, Suite S272, San Francisco, California 94143, and concerns certain software known as “UCSF ChimeraX,” a system of integrated software tools for interactive visualization and analysis of molecular structures and related data, developed by the Resource for Biocomputing, Visualization and Informatics (“RBVI”) at UCSF for research purposes and includes executable code, source code, and documentation (“Software”).

1. **General.** A non-exclusive, nontransferable, perpetual license is granted to the Licensee to install and use the Software for academic, non-profit, or government-sponsored research purposes. Use of the Software under this License is restricted to non-commercial purposes. COMMERCIAL USE OF THE SOFTWARE REQUIRES A SEPARATELY EXECUTED WRITTEN LICENSE AGREEMENT.

2. **Permitted Use and Restrictions.** Licensee agrees that it will use the Software, and any modifications, improvements, or derivatives to the Software that the Licensee may create (collectively, “Improvements”) solely for internal, non-commercial purposes and shall not distribute or transfer the Software or Improvements to any person or third parties without prior written permission from The Regents. For the avoidance of doubt, extensions or “plugins” developed by the Licensee as original works for the purpose of adding new functionality or customizing the Software shall not be considered Improvements. The Licensee may use such extensions or “plugins” for any purpose and may distribute them to any person or third parties without prior written permission from The Regents. The term “non-commercial,” as used in this License, means academic or other scholarly research which (a) is not undertaken for profit, or (b) is not intended to produce works, services, or data for commercial use, or (c) is neither conducted, nor funded, by a person or an entity engaged in the commercial use, application or exploitation of works similar to the Software.

3. **Ownership and Assignment of Copyright.** The Licensee acknowledges that The Regents hold copyright in the Software and associated documentation, and the Software and associated documentation are the property of The Regents. The Licensee agrees that any Improvements made by Licensee shall be subject to the same terms and conditions as the Software. Licensee agrees not to assert a claim of infringement in Licensee copyrights in Improvements in the event The Regents prepares substantially similar modifications or

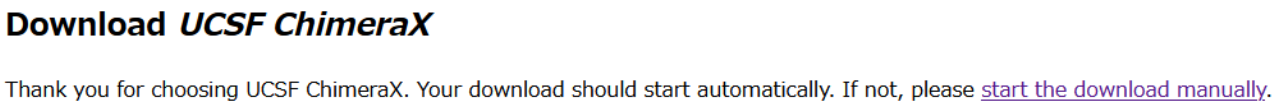
10. **Governing Law and General Provisions.** This License shall be governed by the laws of the State of California, excluding the application of its conflicts of law rules. This License shall not be governed by the United Nations Convention on Contracts for the International Sale of Goods, the application of which is expressly excluded. If any provisions of this License are held invalid or unenforceable for any reason, the remaining provisions shall remain in full force and effect. This License is binding upon any heirs and assigns of the Licensee. The License granted to Licensee hereunder may not be assigned or transferred to any other person or entity without the express consent of The Regents. This License constitutes the entire agreement between the parties with respect to the use of the Software licensed hereunder and supersedes all other previous or contemporaneous agreements or understandings between the parties, whether verbal or written, concerning the subject matter. Any translation of this License is done for local requirements and in the event of a dispute between the English and any non-English versions, the English version of this License shall govern.

問題がなければ、「Accept」を押してインストールを開始

Revised 5 May 2020

Do you accept all the terms of the preceding License Agreement? If you choose "Decline", the download will not continue. To download and install UCSF ChimeraX, you must accept this Agreement.

ダウンロードが行われる
開始しない場合は、「start the download manually」をクリック

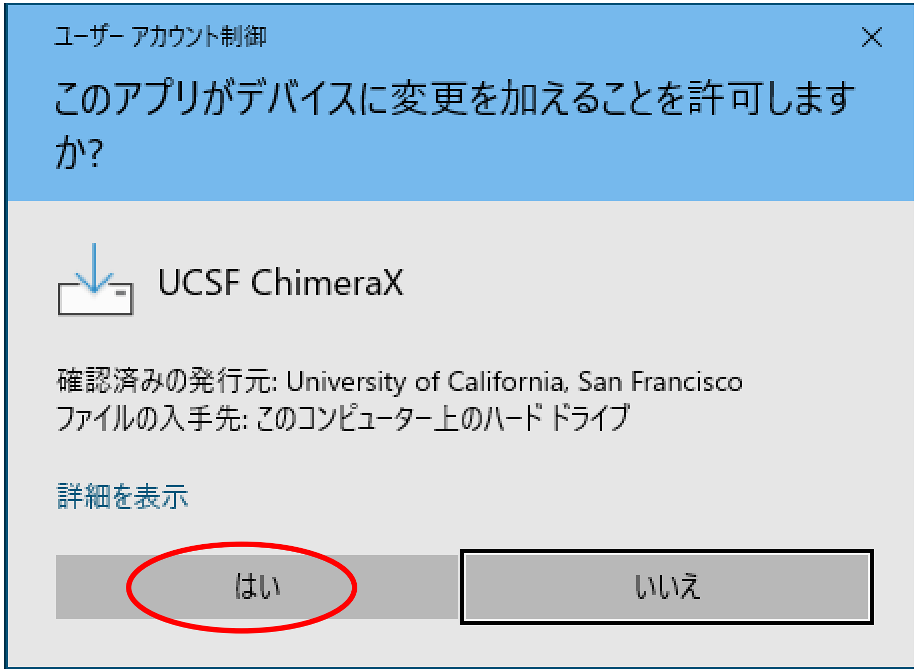


Download *UCSF ChimeraX*

Thank you for choosing UCSF ChimeraX. Your download should start automatically. If not, please start the download manually.

ダウンロードしたプログラムを実行すると、次の画面が現れる

Windows 10における表示の例）



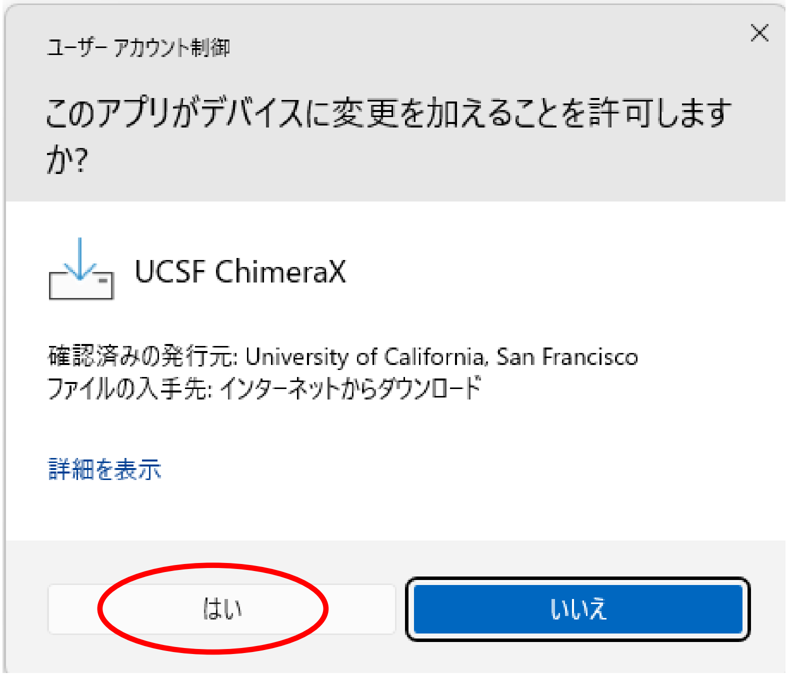
ユーザー アカウント制御

このアプリがデバイスに変更を加えることを許可しますか?

UCSF ChimeraX

確認済みの発行元: University of California, San Francisco
ファイルの入手先: このコンピューター上のハード ドライブ

Windows 11における表示の例）



ユーザー アカウント制御

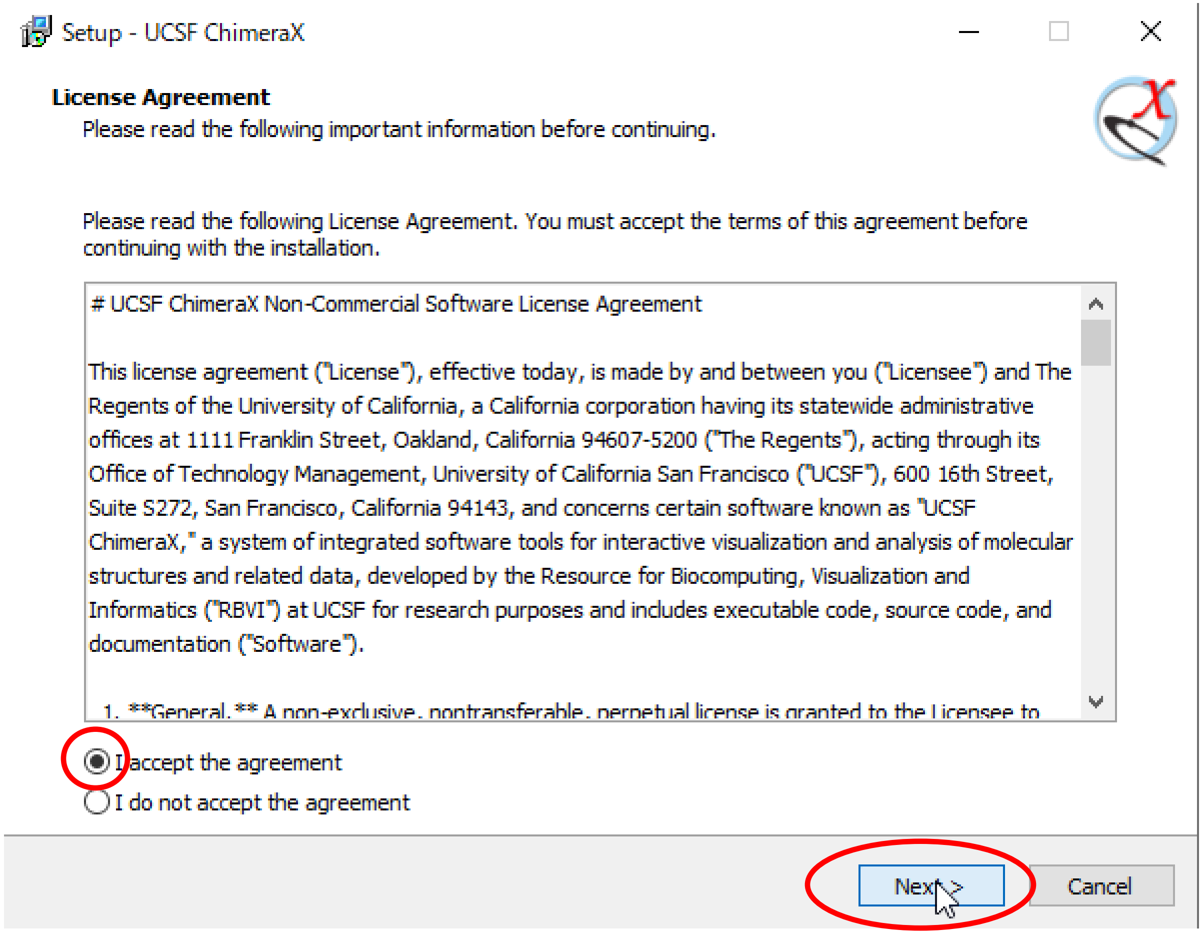
このアプリがデバイスに変更を加えることを許可しますか?

UCSF ChimeraX

確認済みの発行元: University of California, San Francisco
ファイルの入手先: インターネットからダウンロード

「はい」を選択

ダウンロードしたプログラム「ChimeraX-1.6.1.exe」を実行



License Agreement

Please read the following important information before continuing.

Please read the following License Agreement. You must accept the terms of this agreement before continuing with the installation.

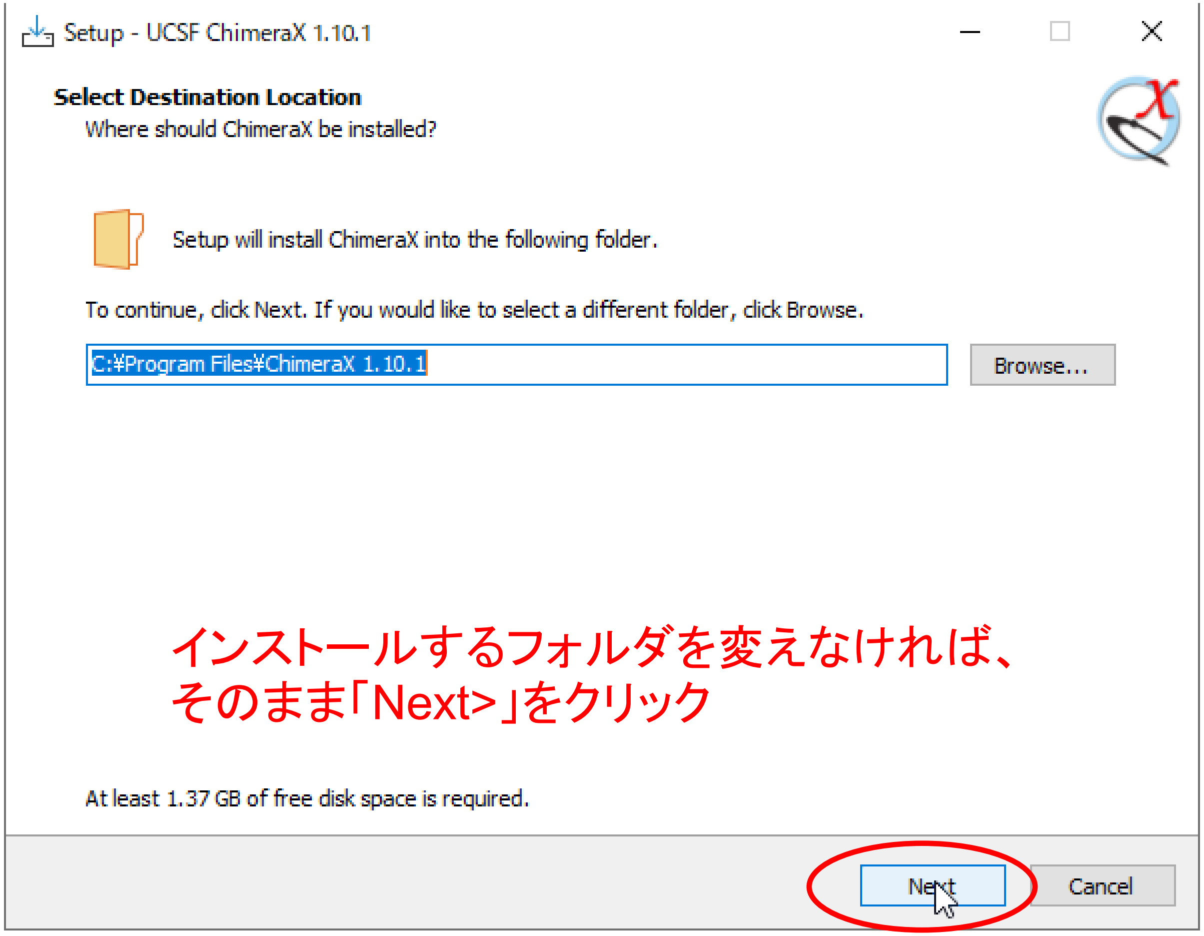
UCSF ChimeraX Non-Commercial Software License Agreement

This license agreement ("License"), effective today, is made by and between you ("Licensee") and The Regents of the University of California, a California corporation having its statewide administrative offices at 1111 Franklin Street, Oakland, California 94607-5200 ("The Regents"), acting through its Office of Technology Management, University of California San Francisco ("UCSF"), 600 16th Street, Suite S272, San Francisco, California 94143, and concerns certain software known as "UCSF ChimeraX," a system of integrated software tools for interactive visualization and analysis of molecular structures and related data, developed by the Resource for Biocomputing, Visualization and Informatics ("RBVI") at UCSF for research purposes and includes executable code, source code, and documentation ("Software").

1. **General.** A non-exclusive, nontransferable, perpetual license is granted to the Licensee to

● I accept the agreement

○ I do not accept the agreement



Setup - UCSF ChimeraX 1.10.1

Select Destination Location

Where should ChimeraX be installed?

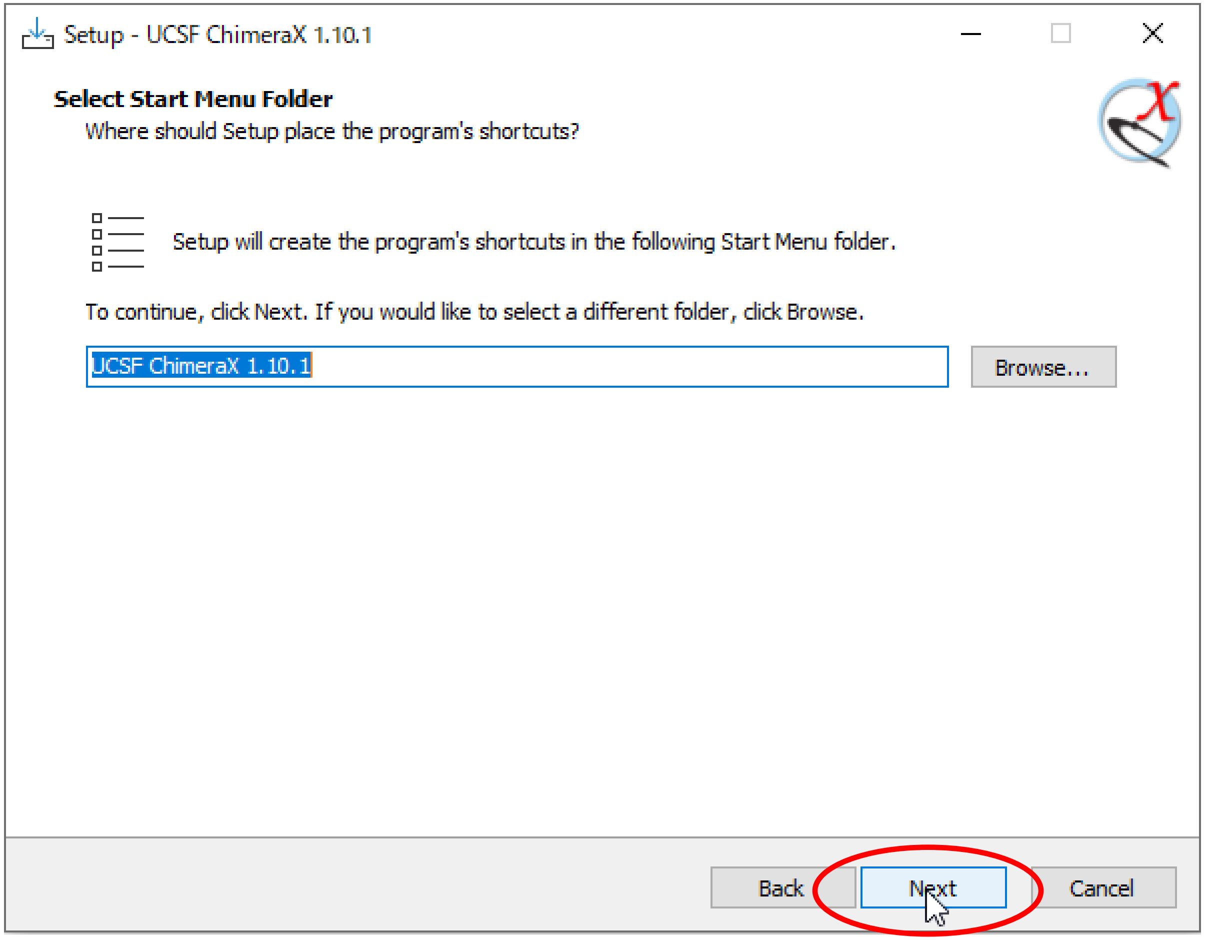
Setup will install ChimeraX into the following folder.

To continue, click Next. If you would like to select a different folder, click Browse.

C:¥Program Files¥ChimeraX 1.10.1

At least 1.37 GB of free disk space is required.

インストールするフォルダを変えなければ、
そのまま「Next>」をクリック



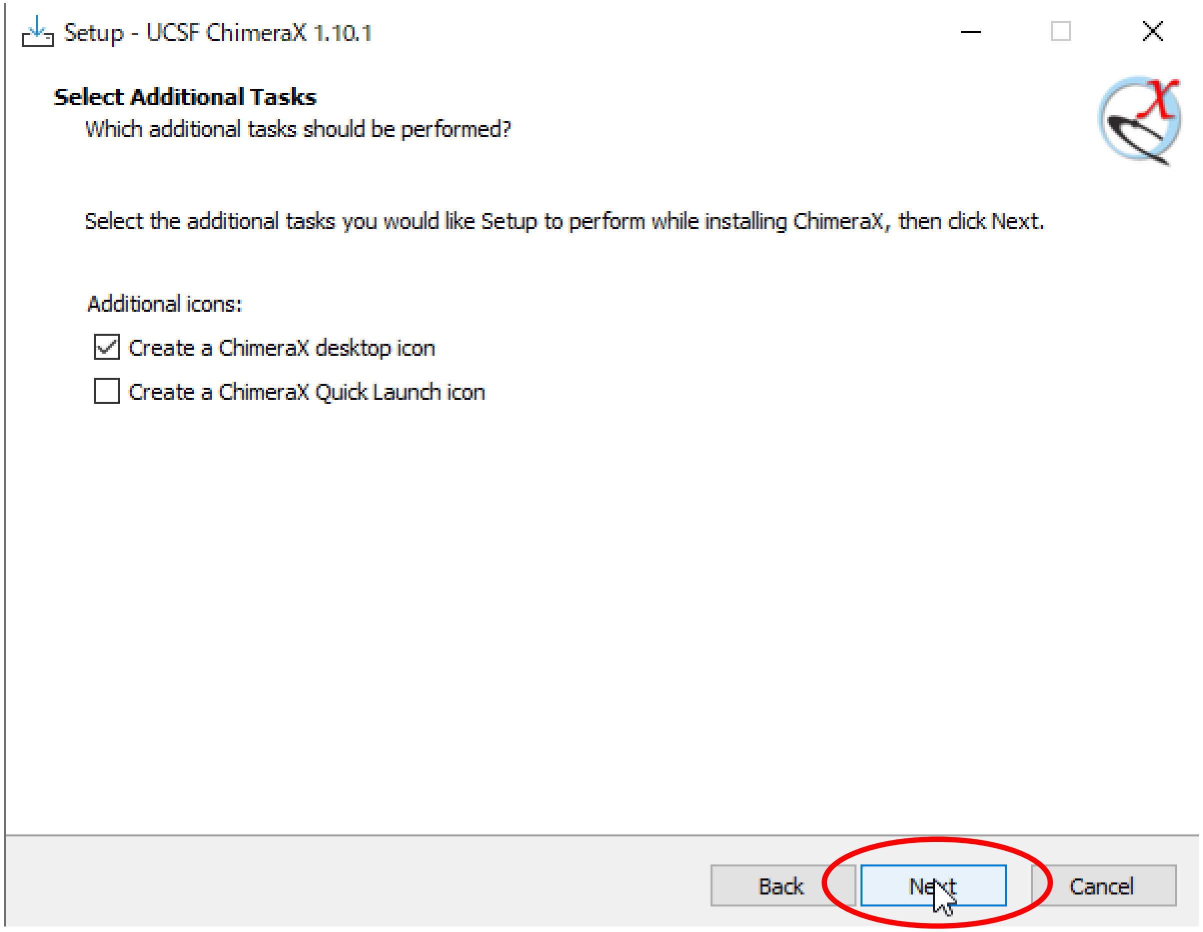
Select Start Menu Folder

Where should Setup place the program's shortcuts?

Setup will create the program's shortcuts in the following Start Menu folder.

To continue, click Next. If you would like to select a different folder, click Browse.

UCSF ChimeraX 1.10.1



Setup - UCSF ChimeraX 1.10.1

Select Additional Tasks

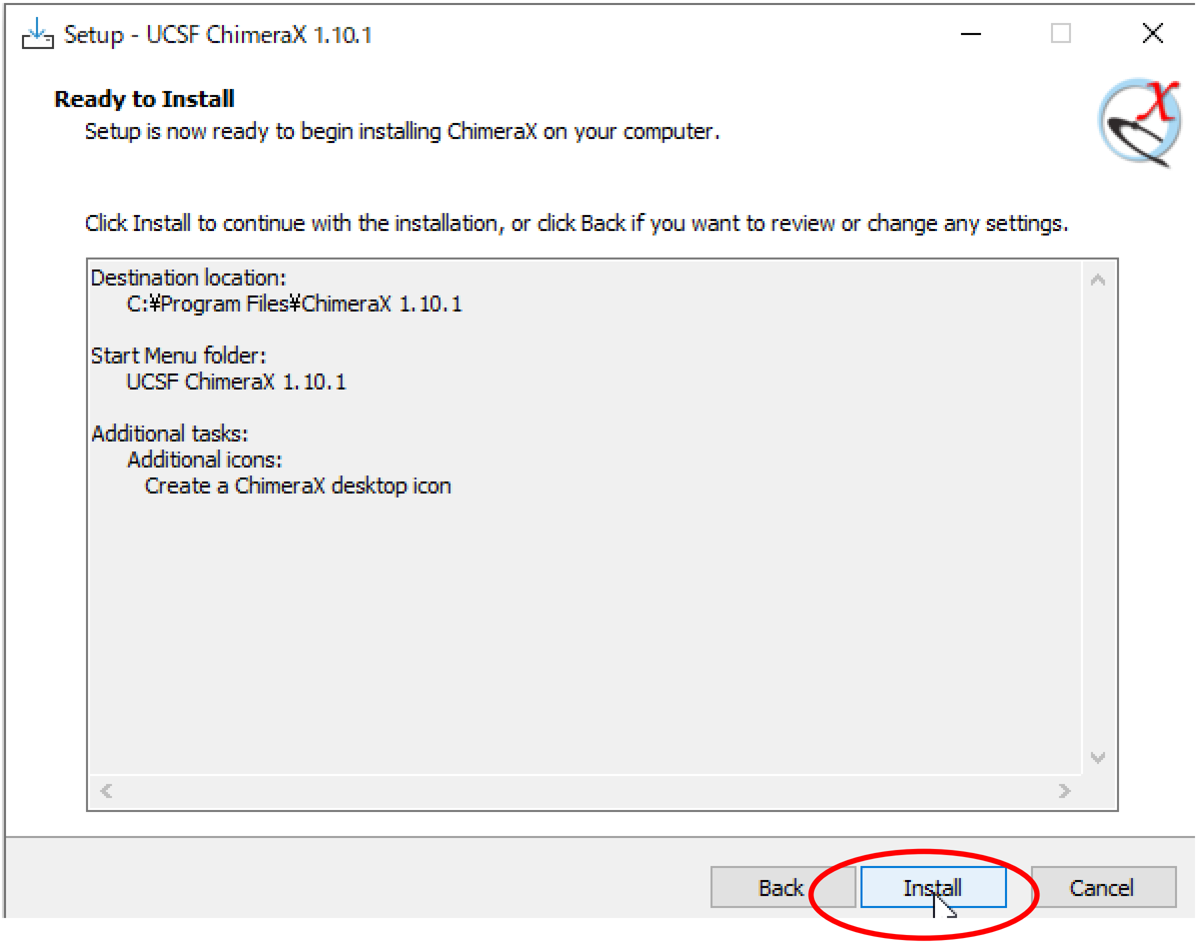
Which additional tasks should be performed?

Select the additional tasks you would like Setup to perform while installing ChimeraX, then click Next.

Additional icons:

☑ Create a ChimeraX desktop icon

☐ Create a ChimeraX Quick Launch icon



Ready to Install

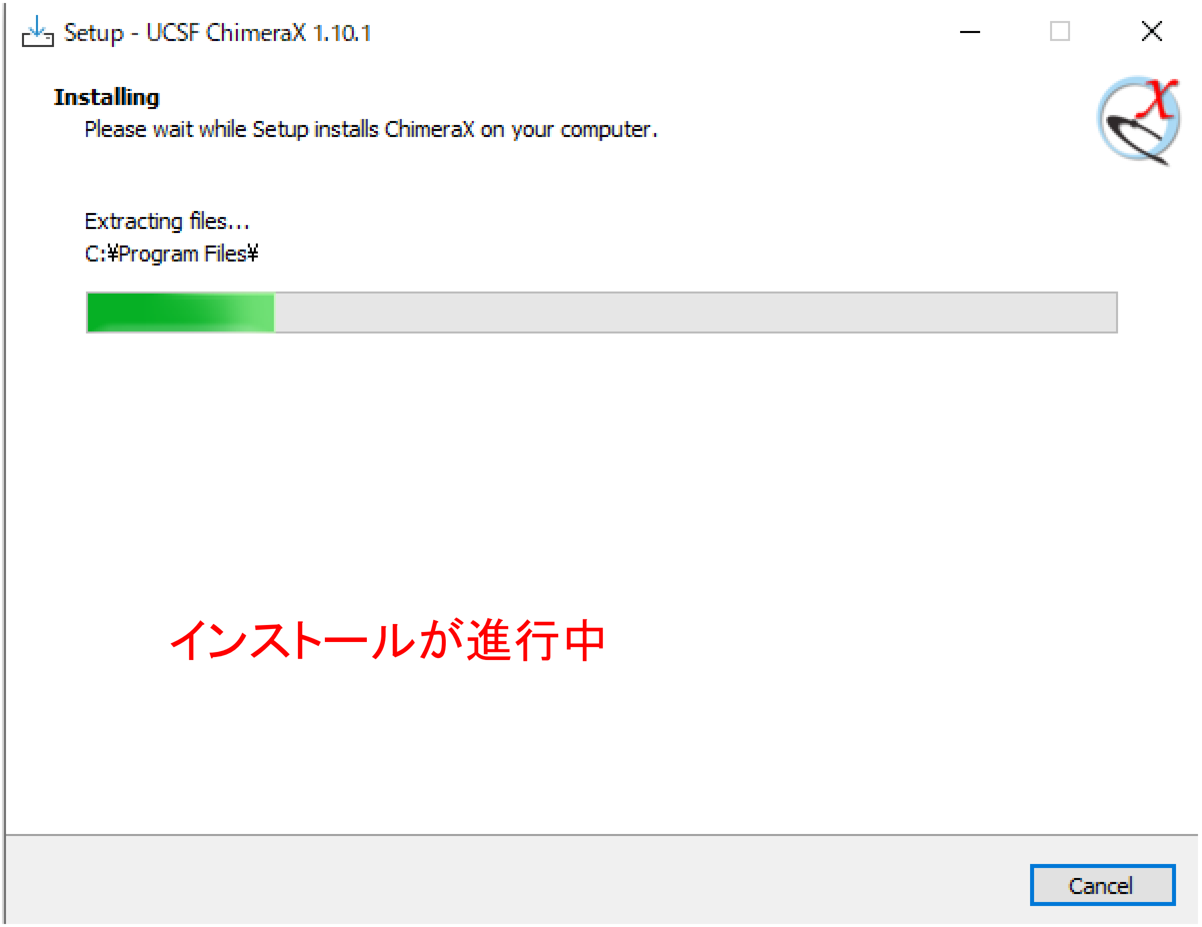
Setup is now ready to begin installing ChimeraX on your computer.

Click Install to continue with the installation, or click Back if you want to review or change any settings.

Destination location:
C:¥Program Files¥ChimeraX 1.10.1

Start Menu folder:
UCSF ChimeraX 1.10.1

Additional tasks:
Additional icons:
Create a ChimeraX desktop icon



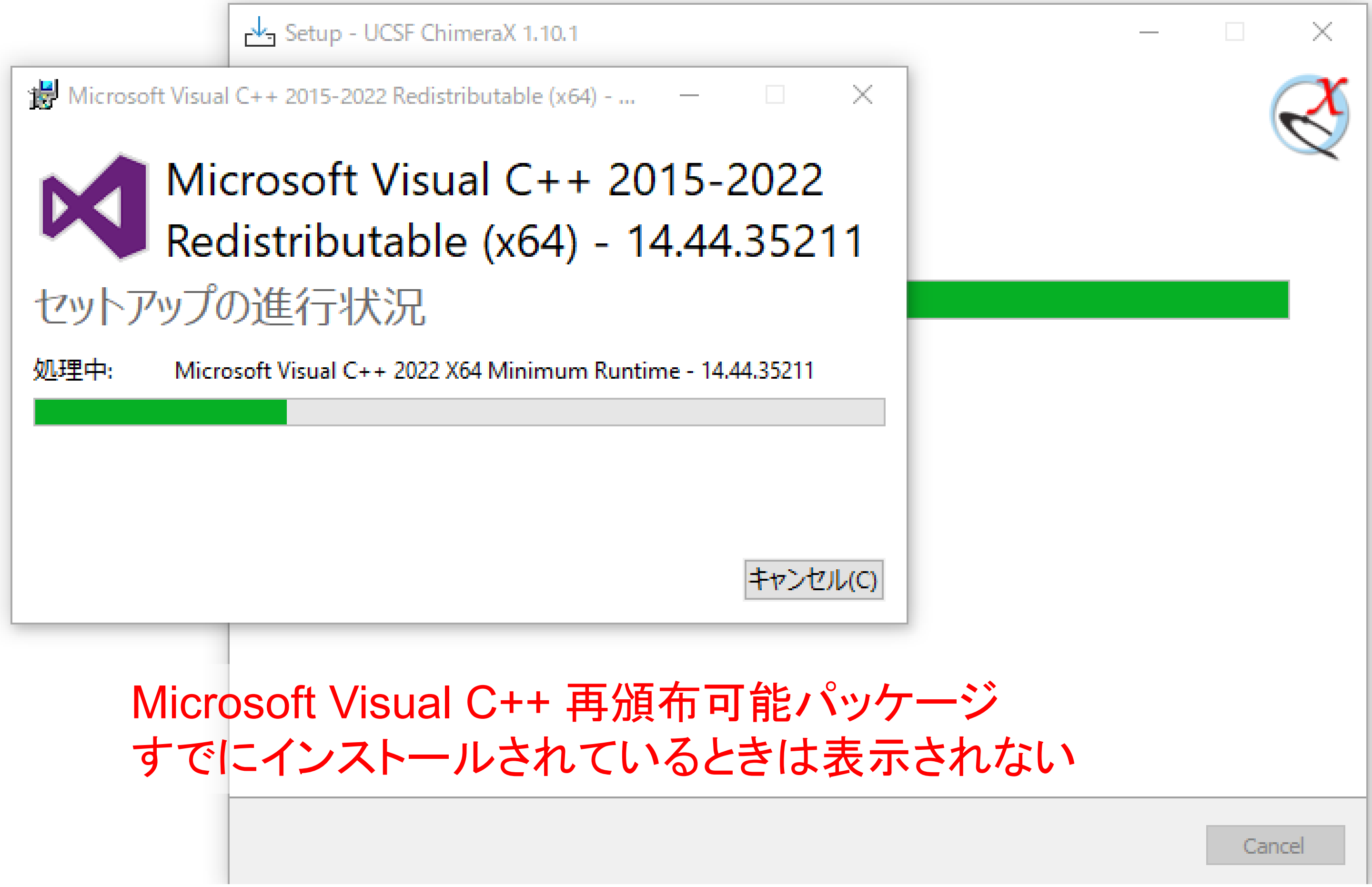
Installing

Please wait while Setup installs ChimeraX on your computer.

Extracting files...

C:¥Program Files¥

インストールが進行中

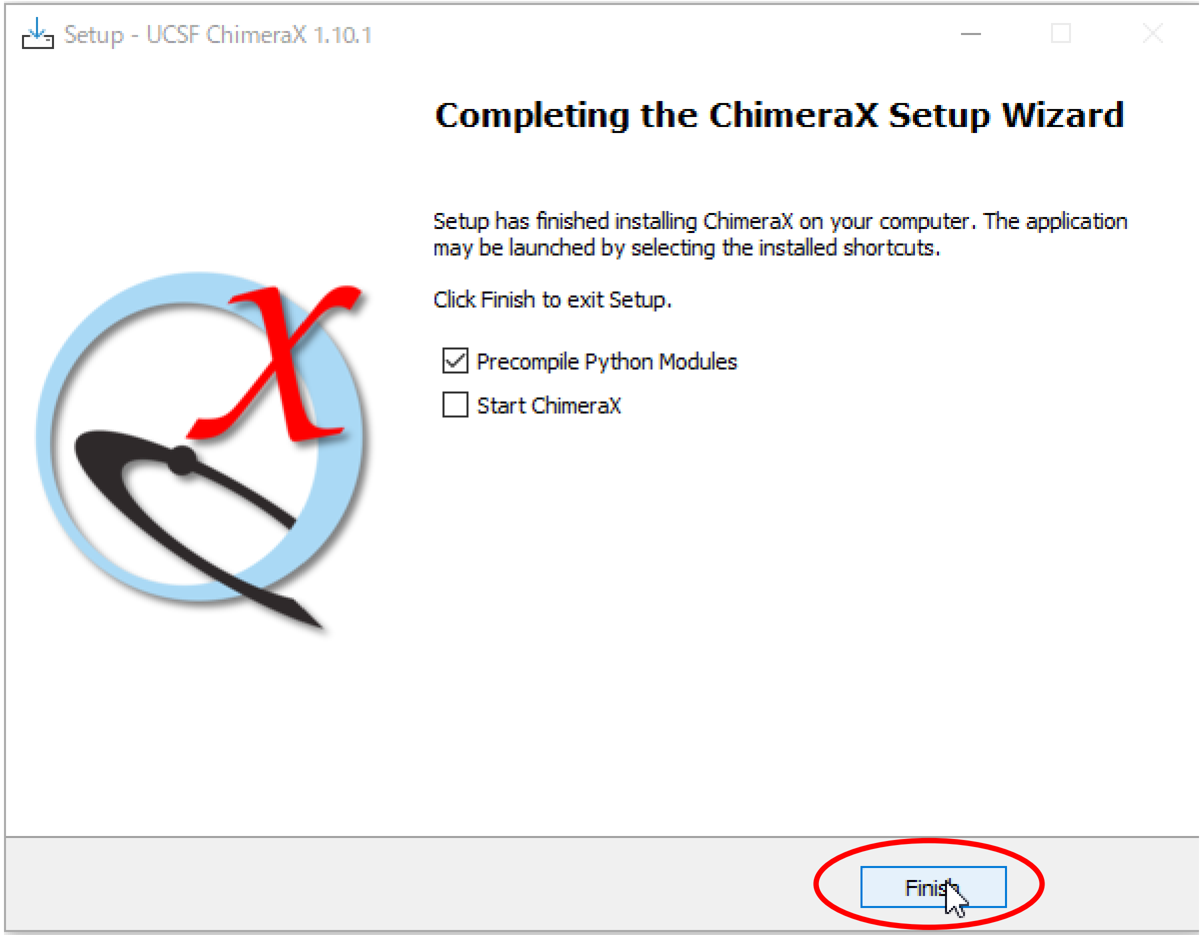


Microsoft Visual C++ 2015-2022 Redistributable (x64) - 14.44.35211

セットアップの進行状況

処理中: Microsoft Visual C++ 2022 X64 Minimum Runtime - 14.44.35211

Microsoft Visual C++ 再頒布可能パッケージ
すでにインストールされているときは表示されない



Setup - UCSF ChimeraX 1.10.1

Completing the ChimeraX Setup Wizard

Setup has finished installing ChimeraX on your computer. The application may be launched by selecting the installed shortcuts.

Click Finish to exit Setup.

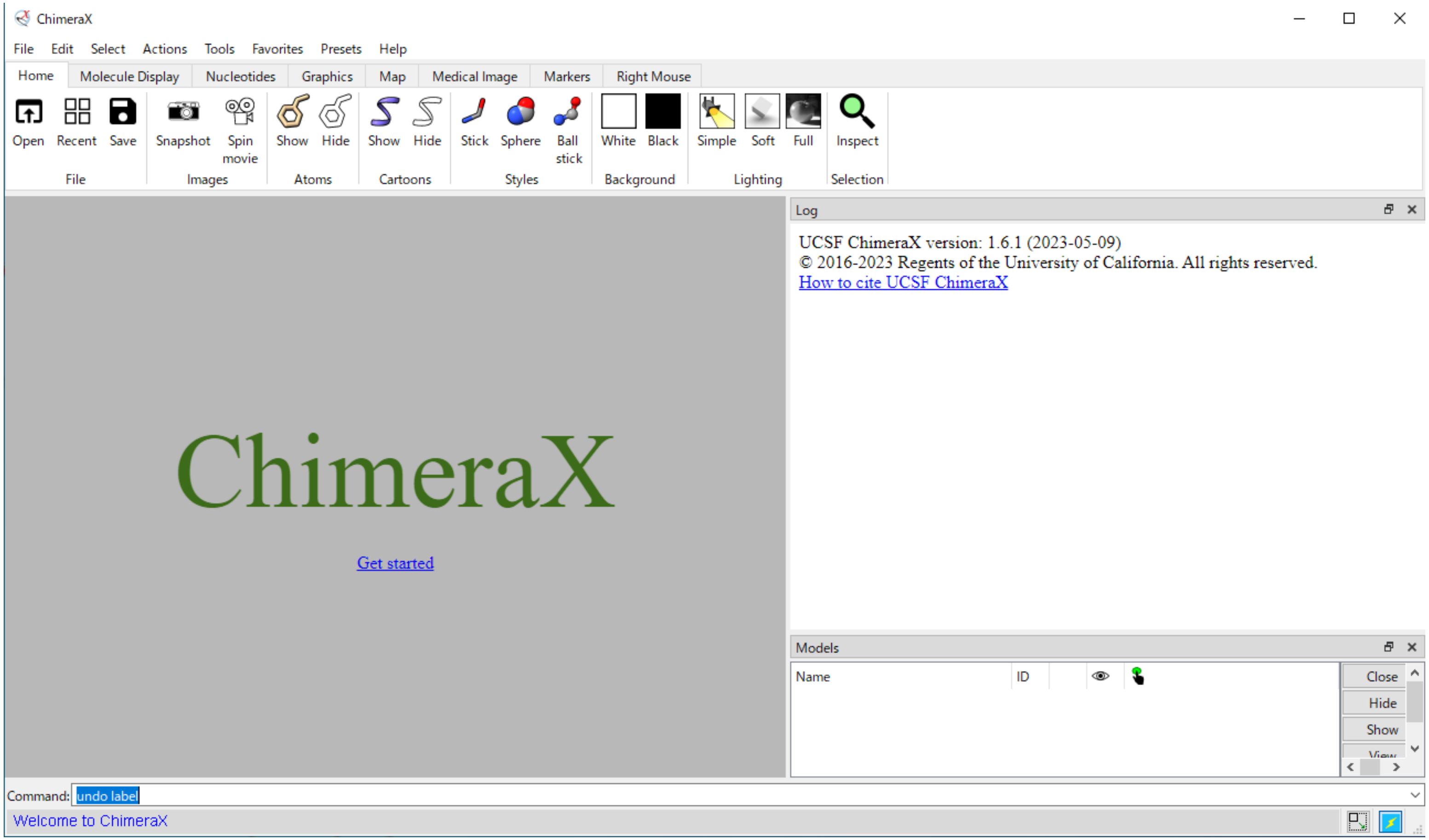
☑ Precompile Python Modules

☐ Start ChimeraX

デスクトップに以下のようなアイコンが表示される

これをクリックすると･･･

起動時の画面（初めて使うとき）



UCSF ChimeraX version: 1.6.1 (2023-05-09)
© 2016-2023 Regents of the University of California. All rights reserved.
How to cite UCSF ChimeraX

Command: undo label

Welcome to ChimeraX