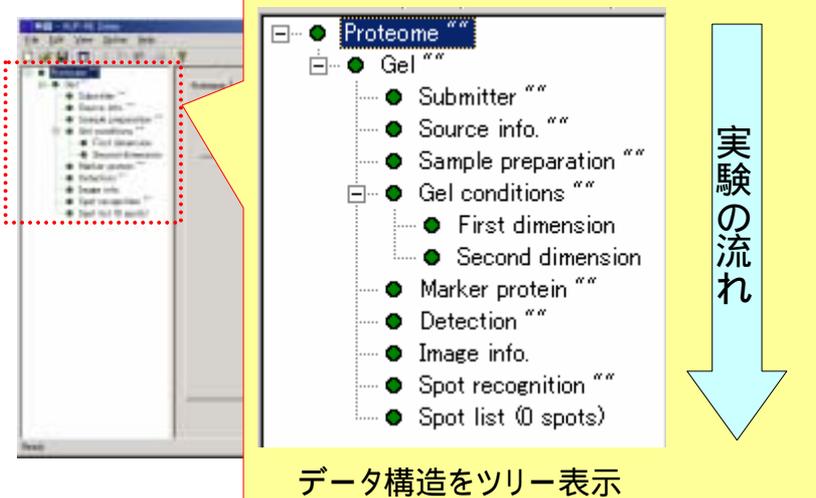


HUP-MLエディタ - データ入力の実際 -

データ入力の実際

(0) 起動画面



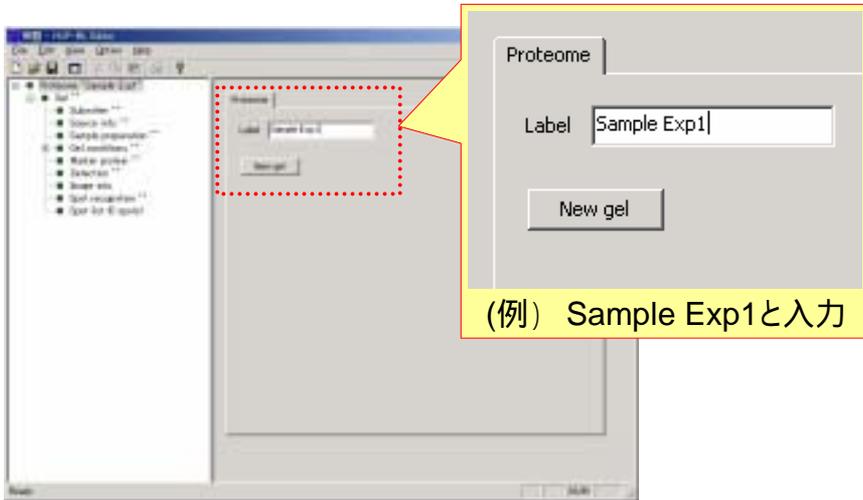
The screenshot shows the Proteome software interface. On the left, a sidebar contains a list of categories with a red dotted box highlighting the 'Gel' category. The main window displays a tree view of the data structure for a 'Gel' experiment. The tree is as follows:

- Proteome ""
 - Gel ""
 - Submitter ""
 - Source info. ""
 - Sample preparation ""
 - Gel conditions ""
 - First dimension
 - Second dimension
 - Marker protein ""
 - Detection ""
 - Image info.
 - Spot recognition ""
 - Spot list (0 spots)

On the right side of the screenshot, a large light blue arrow points downwards, labeled '実験の流れ' (Flow of experiment). Below the screenshot, the text 'データ構造をツリー表示' (Display data structure as a tree) is written.

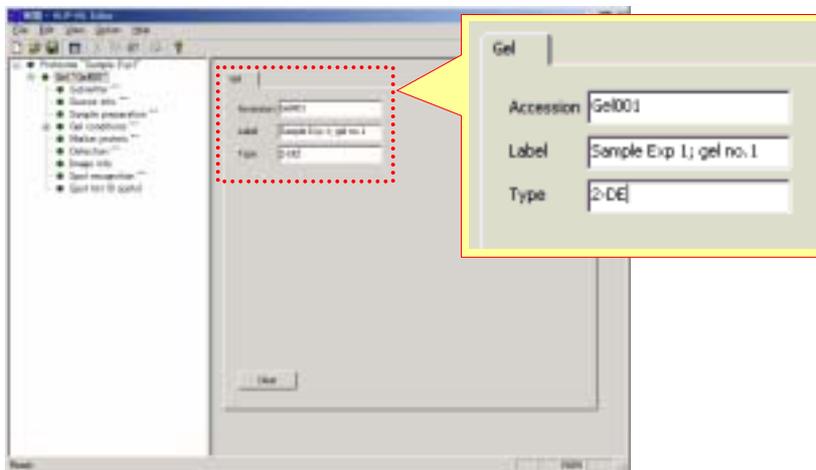
データ入力の実際

(1) 実験としてのラベル付け



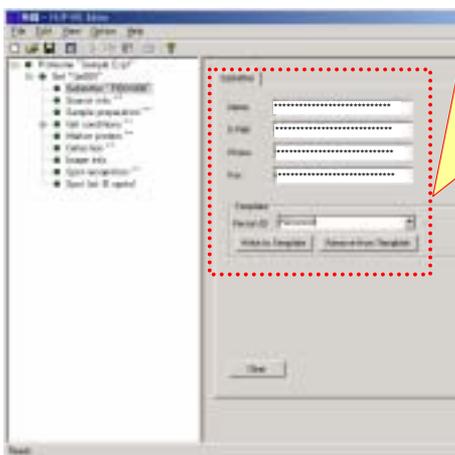
データ入力の実際

(2) ゲルへのラベル付け



データ入力の実際

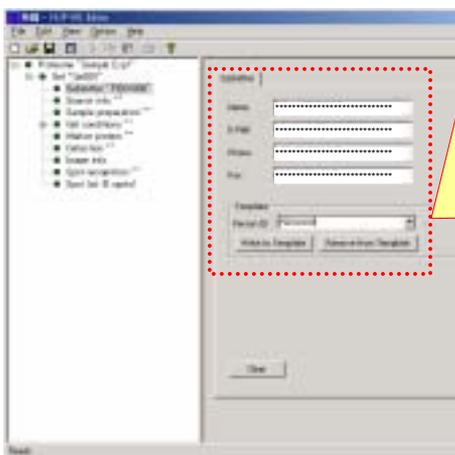
(3) 実験者情報を入力



名前、連絡先(メール、電話、FAX)をひとまとめにして保存可能

データ入力の実際

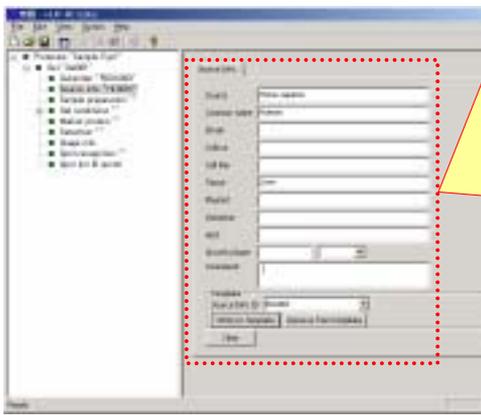
(3 - 2) 実験者情報の再利用



リストから選択して再利用

データ入力の実際

(4) サンプル情報を入力



Source Info

Source:

Common name:

Strain:

Cultiva:

Cell line:

Tissue:

Strain:

Induction:

Host:

Growth phase:

Comment:

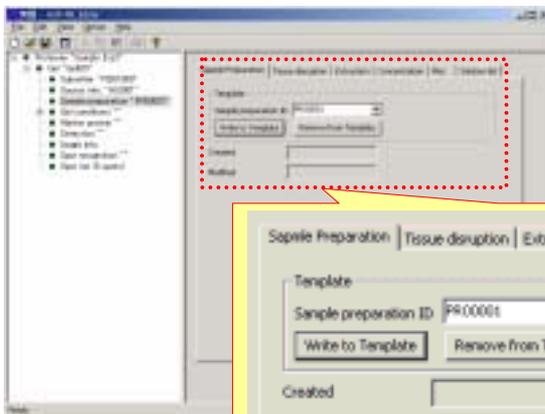
Template

Source Info ID:

サンプル情報をまとめて
保存・再利用可能

データ入力の実際

(5) サンプル調整方法・条件を入力



Sample Preparation | Tissue disruption | Extraction | Concentration | Misc | Solution list

Template

Sample preparation ID:

Created:

Modified:

サンプルの破碎、抽出、溶液成分などを
まとめて保存・再利用可能

データ入力の実際

(5 - 2) タンパク質抽出手順の入力例

The screenshot shows a software window with a tree view on the left and a main panel on the right. The main panel has tabs for 'Sample Preparation', 'Tissue disruption', 'Extraction', 'Concentration', 'Rec.', and 'Solution kit'. The 'Extraction' tab is active, showing an 'Extraction procedure' table with columns: No., Action, Sample, Time, Temp., and Granity. The table contains three rows: 1. 'homogenize precipitate' at 60.0min and 37 (degree in C); 2. 'centrifuge supernatant' at 20.0min and 1000; 3. 'store supernatant' at -80 (degree in C). Below the table are 'Up', 'Down', 'Insert', 'Edit', and 'Delete' buttons. A 'Comment' text box is below that. The 'Protease inhibitor' section has a table with columns 'Name' and 'Concentration', containing 'ADDFP' (1.04 μM D), 'Aprotinin' (0.6 μM D), and 'Leupeptin' (21 μM D). It also has 'Up', 'Down', 'New', 'Edit', 'Delete', and 'Clear' buttons. A red dashed box highlights the 'Extraction procedure' table area in the main window.

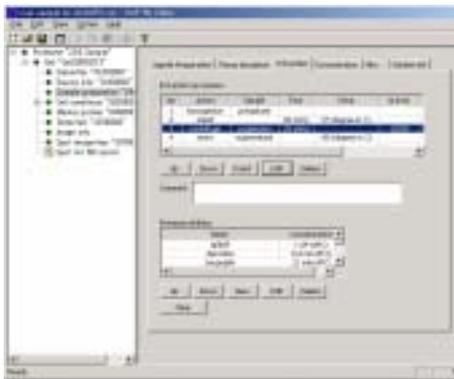
データ入力の実際

(5 - 2) 抽出手順の入力例

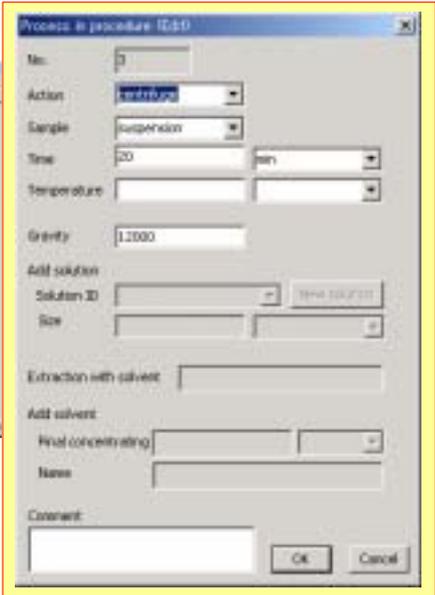
This screenshot is identical to the one above, showing the 'Extraction procedure' table and 'Protease inhibitor' section. A green speech bubble with the Japanese word 'クリック' (click) points to the 'Edit' button in the 'Extraction procedure' section.

データ入力の実際

(5 - 2) 抽出手順の入力例

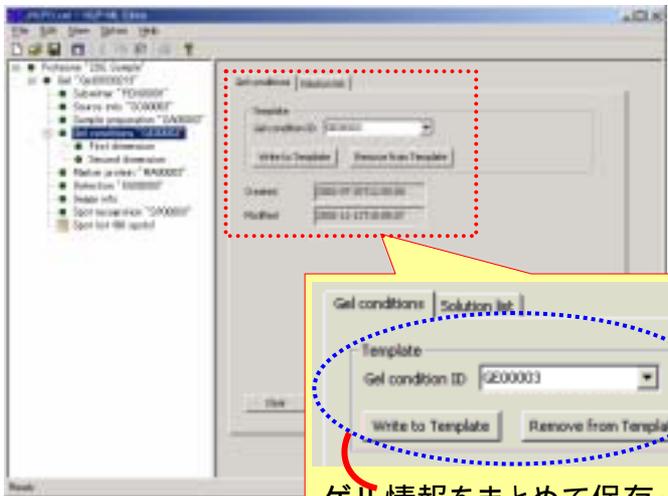


1手順ごとに
入力・編集



データ入力の実際

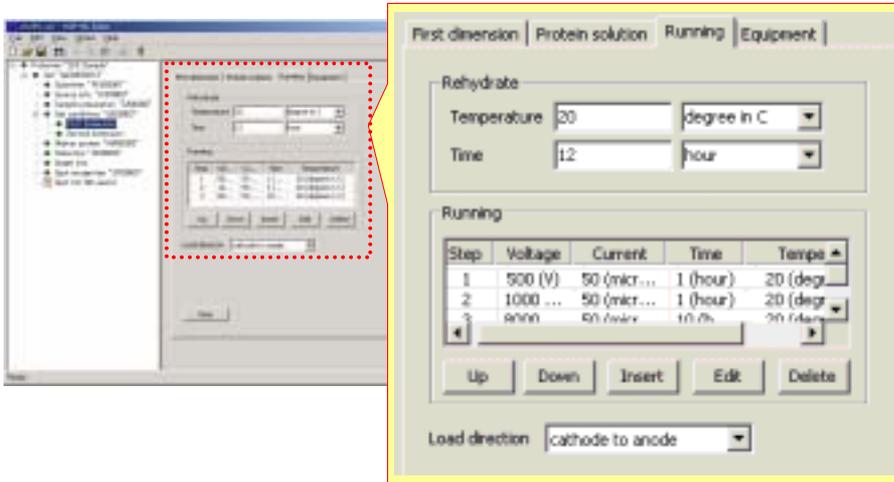
(6) ゲル情報(1次元目と2次元目に共通)を入力



ゲル情報をまとめて保存・再利用可能

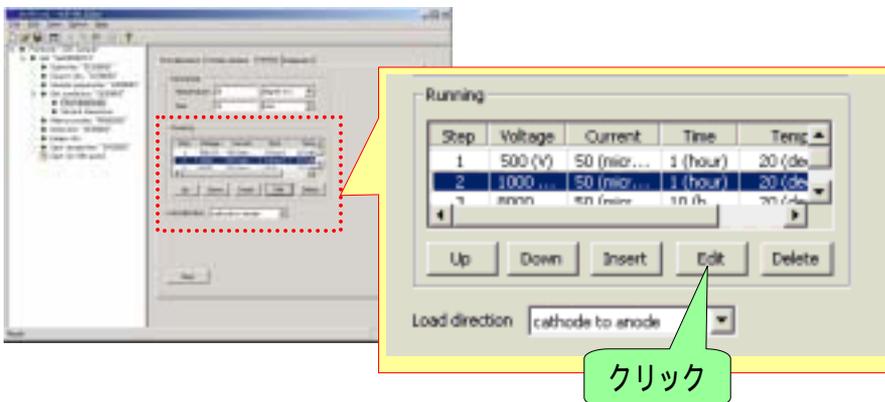
データ入力の実際

(7) 電気泳動1次元目の条件を入力



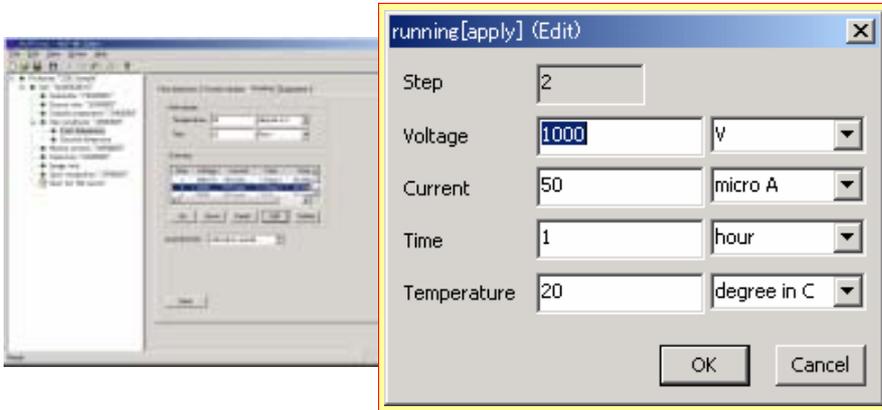
データ入力の実際

(7) 電気泳動1次元目の条件を入力



データ入力の実際

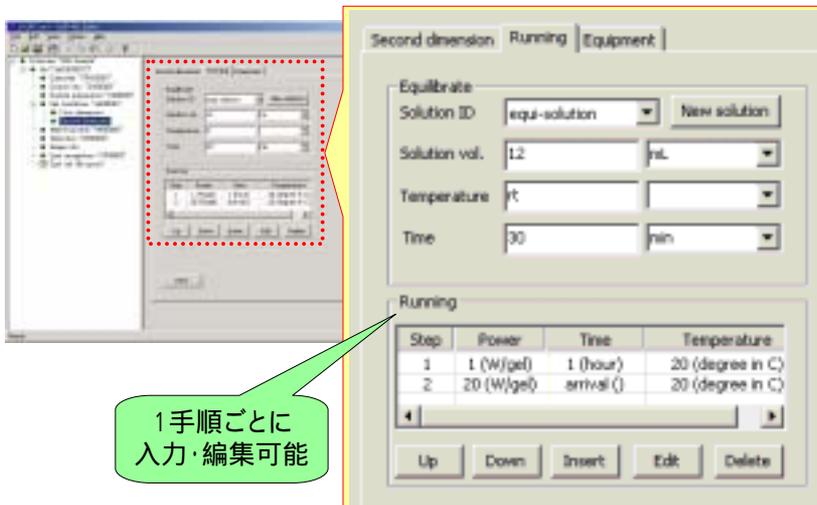
(7) 電気泳動1次元目の条件を入力



1手順ごとに入力・編集

データ入力の実際

(8) 電気泳動2次元目の条件を入力



1手順ごとに
入力・編集可能

データ入力の実際

(9) マーカープロテインの情報を入力

Marker protein

Name

Maker

Protein name	Amount	pI	MW

Up Down New Edit Delete

Template

Marker protein ID

Write to Template Remove from Template

セット名
メーカー

マーカープロテイン
各々の名前、量など

マーカーのセットとして保存・再利用可能

データ入力の実際

(10) 染色方法を入力

Detection | Equipment

Detection Method

Comment

Template

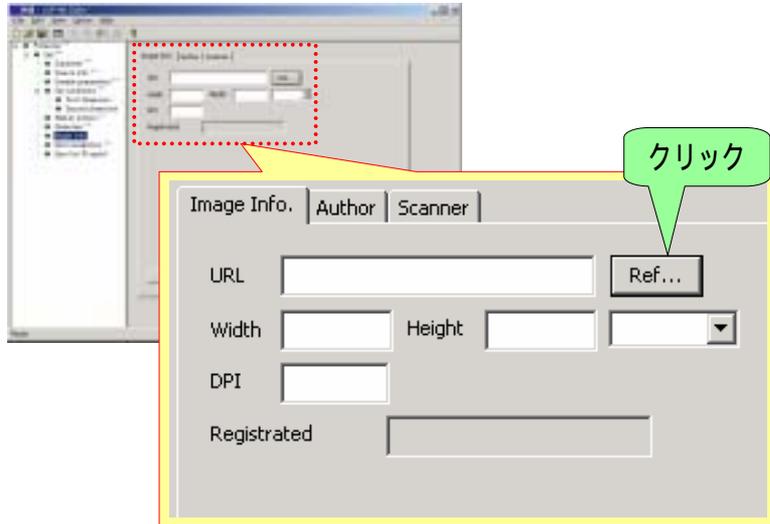
Detection ID

Write to Template Remove from Template

染色方法・装置をまとめて
保存・再利用可能

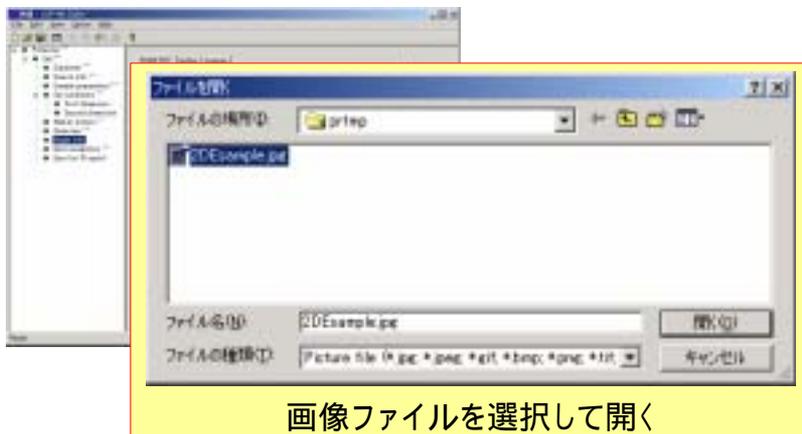
データ入力の実際

(11) ゲル画像の情報を入力



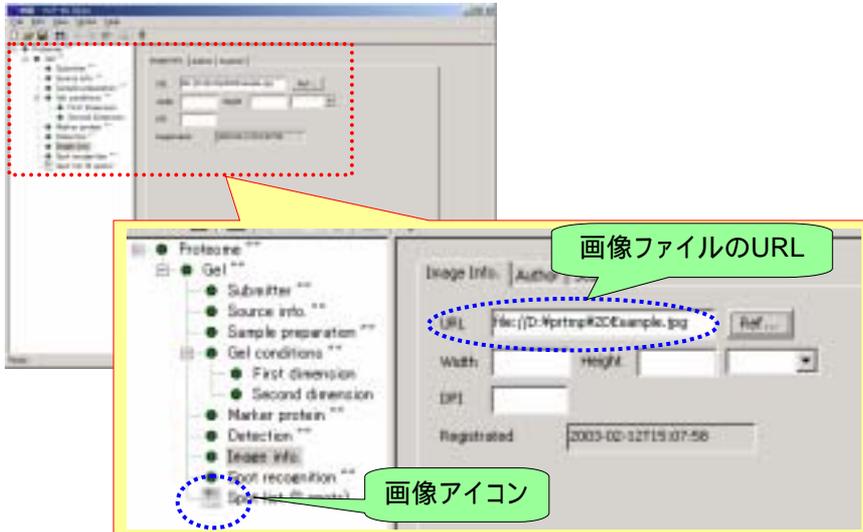
データ入力の実際

(11) ゲル画像の情報を入力



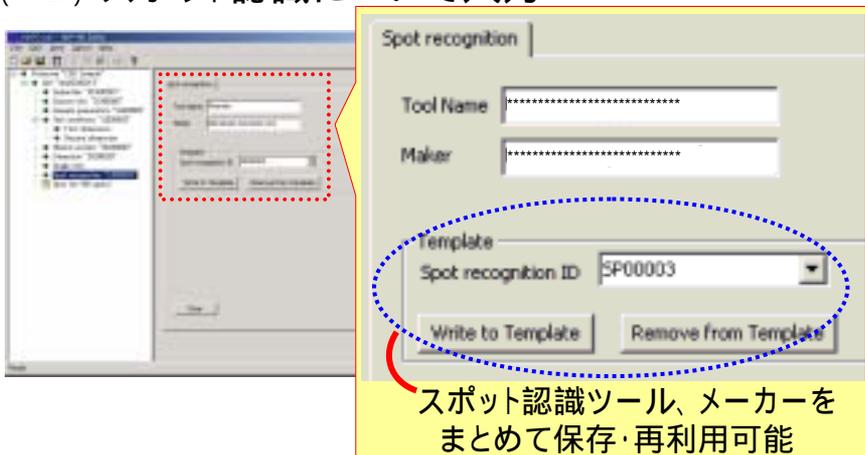
データ入力の実際

(11) ゲル画像の情報を入力



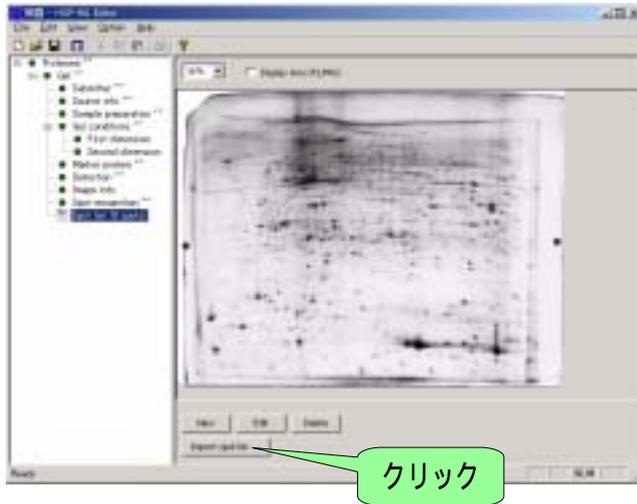
データ入力の実際

(12) スポット認識について入力



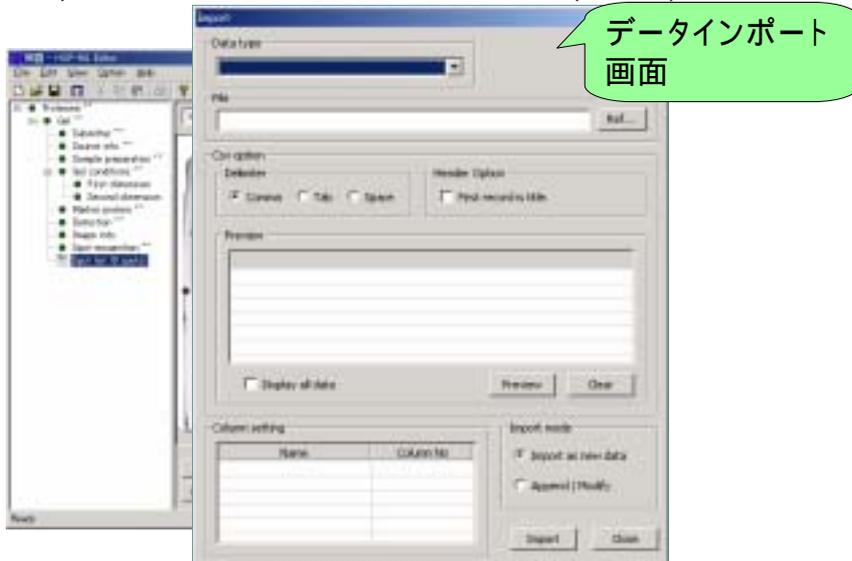
データ入力の実際

(13) スポット解析結果を取り込み(座標)



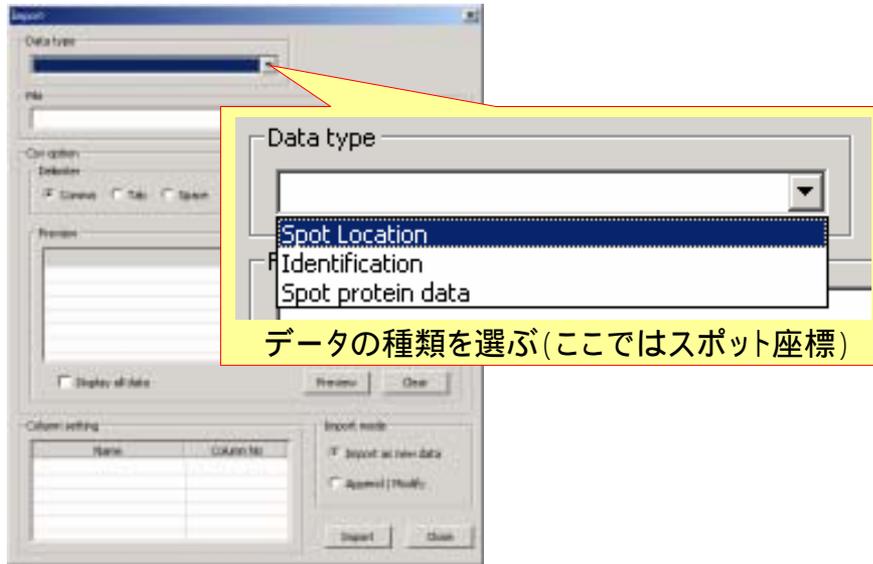
データ入力の実際

(13) スポット解析結果を取り込み(座標)



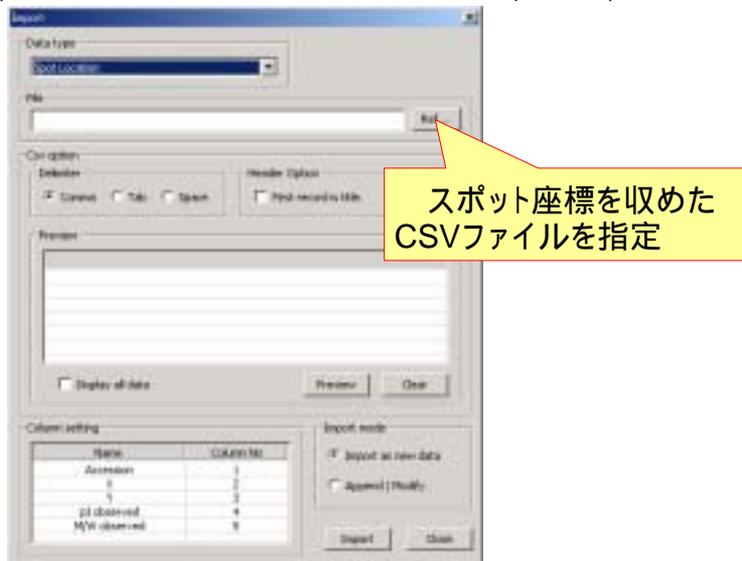
データ入力の実際

(13) スポット解析結果を取り込み(座標)



データ入力の実際

(13) スポット解析結果を取り込み(座標)



データ入力の実際

(13) スポット解析結果を取り込み(座標)

データのプレビュー

データの列を指定して
インポート

インポート

Column No. 1	Column No. 2	Column No. 3	Column No. 4	Column No. 5
5		Observed yf	Observed yf	Protein
294	2941	3.28	14.11	Unkown
293	293	3.38	65.65	Unkown
424	1852	3.38	16.76	Unkown
492	886	3.75	43.71	Unkown

Name	Column No.
Accession	1
5	1
2	1
3	1
4	1
5	1
6	1
7	1
8	1
9	1
10	1

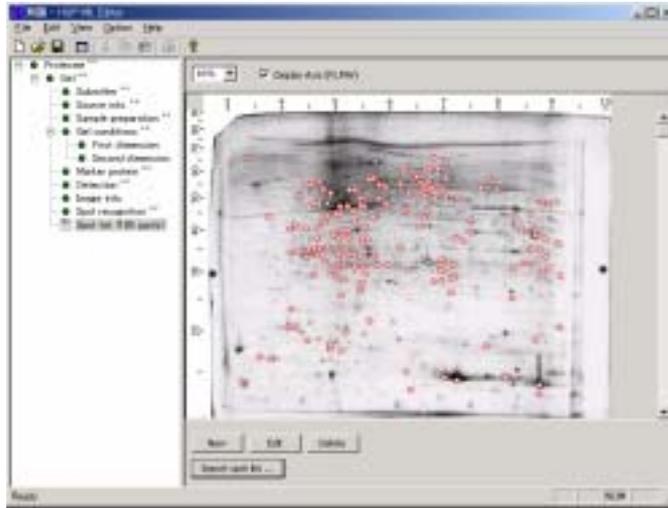
データ入力の実際

(13) スポット座標取り込み後

Spot list (200 spots)

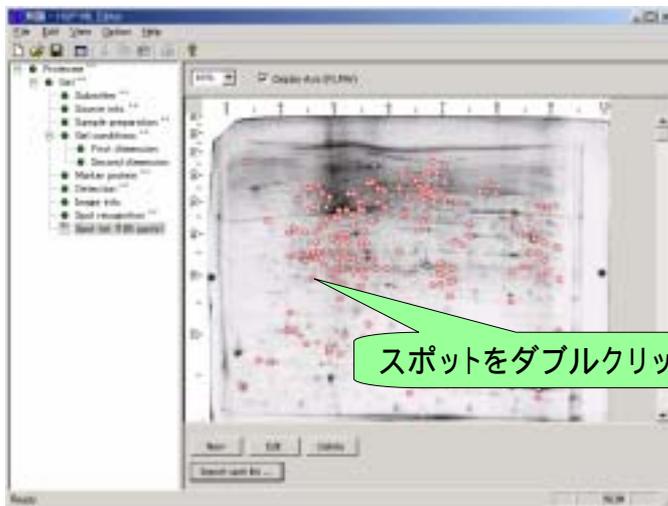
データ入力の実際

(13) タンパク質名などの取り込み後



ポスト・アナリシス支援

タンパク質同定結果から公共データベースを検索



ポスト・アナリシス支援

タンパク質同定結果から公共データベースを検索

The screenshot shows a software window titled "Spot '04K01280'". The left sidebar contains a tree view with categories: Spot location, Identifiers, Spot data, Protein data (selected), and Gene data. The main area has tabs for Protein data, Sequence, Function, Modification, Splicing, and Feature. The Protein data tab is active, showing fields for GI name (P00670), Accession(s), Submitted date, Protein name, and pI/theoretical. A "View" button is next to the Accession(s) field. A red arrow points from a green callout bubble "クリックすると" (Clicking here) to the "View" button. A second green callout bubble "公共DBを検索して表示" (Search and display in public DB) points to a smaller window that has opened, displaying a search result for "P00670" from the "Swiss-Prot" database. The search result window shows a table with columns for Accession, Name, and other details.

クリックすると

公共DBを検索して表示