SERIAL CLONER 2.0
September 2009

Handling Features/Annotations

Serial Cloner 2.0 now handle annotations and features. Here are some description and hints about these new possibilities.

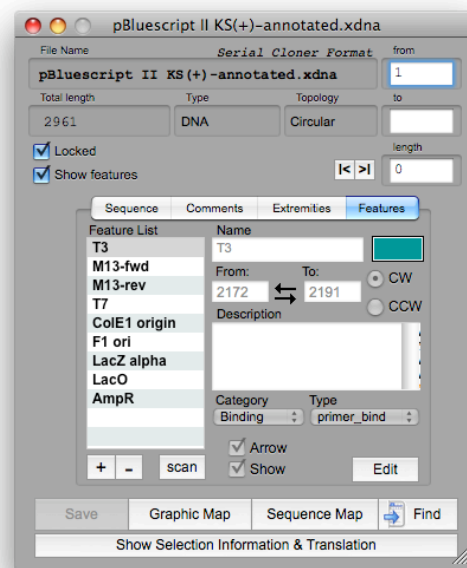## I. Accessing features in the Sequence window

A new tab has been added (*Features*) that gives access to features characteristics and management. A list of Features is shown on the left; double clicking on one will select the corresponding nucleotide sequence. To edit (*add/delete/modify*) Features, one has to be in the *'Edit'* mode. The Edit button is used to toggle between the *'protected'* mode where no unwanted modification can be done and the *'Edit'* mode.

One can select whether a feature will actually be displayed on the map (using the *'Show'* checkbox). Shown features are listed in Bold characters. To decide to Show or Hide all features at once, press the [ALT] key before clicking on the checkbox.

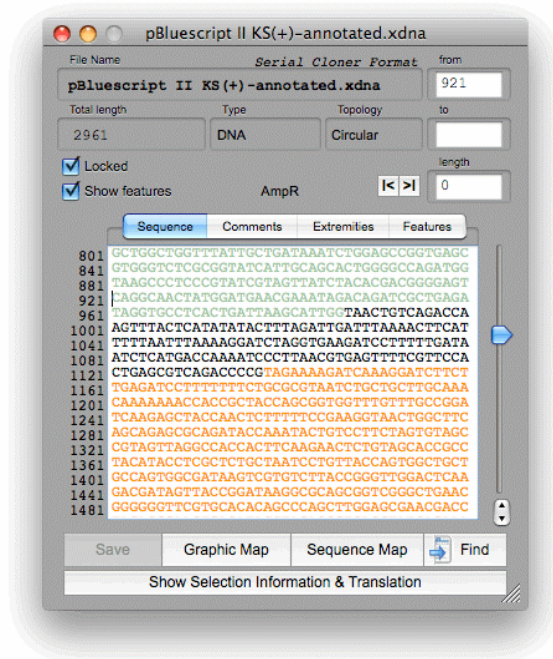A feature can have or not a pointing arrow (*'Arrow'* checkbox).

To change the Feature color, click on the *colored box* and select another color.

The order in the list dictate the order by which Features will be drawn, and this can be important in case they overlap. To alter the order simply drag the Feature at another position in the list.
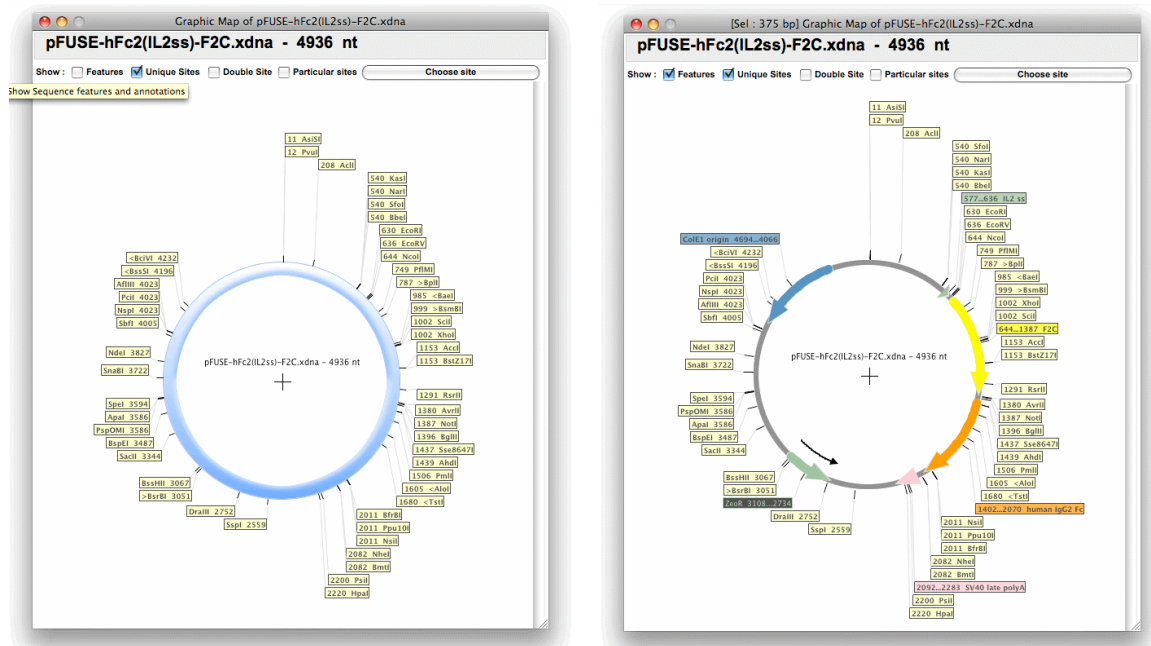
II. Display of Features in the Sequence Window

Features are visible in color in the sequence window. It is possible to show/hide them using the *'Show Features'* checkbox. When the insertion point is located within a Feature, the *corresponding Feature's name* is indicated above the Sequence Field.
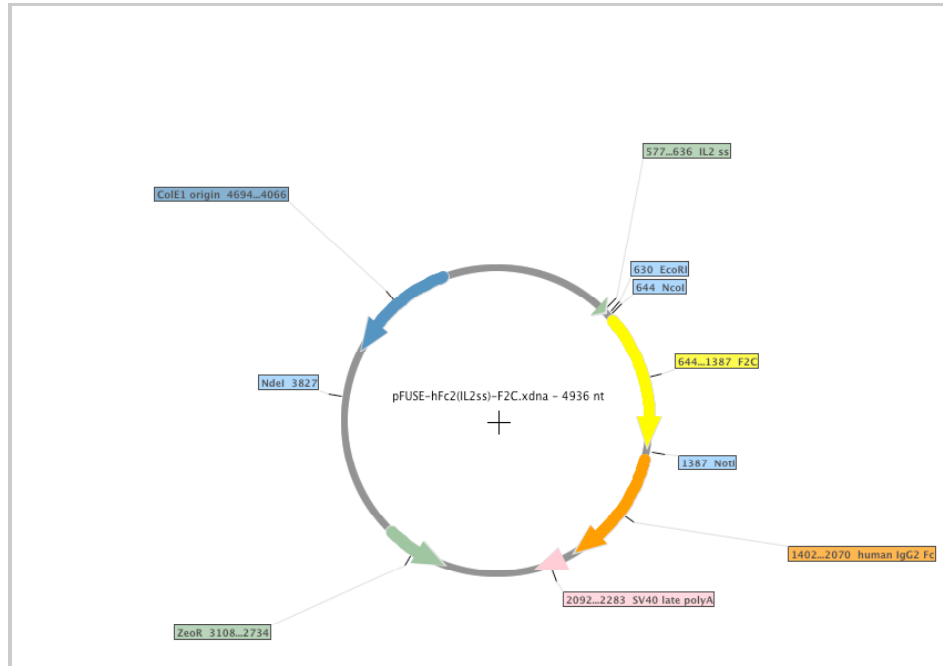
III. Graphical display of Feature.

Features can be displayed in the Graphic Map. They are represented by colored boxes with or without a pointing arrow. It is possible to switch between a Graphic Map with and without Feature using the checkbox present in the top left of the window (*'Features'*).

A *simple click* on a Feature name selects the corresponding portion in the map. A *double Click* selects the corresponding sequence in the parent Sequence Window.

Note that it is now possible to *move* the Restriction site and Features name boxes to highlight some of them before printing or copying the map. It is also possible to display only certain sites with the Features. Finally, it is now possible to resize the Graphic map in Height AND Width.
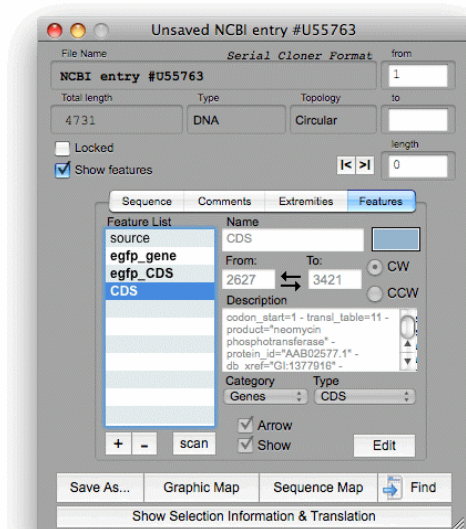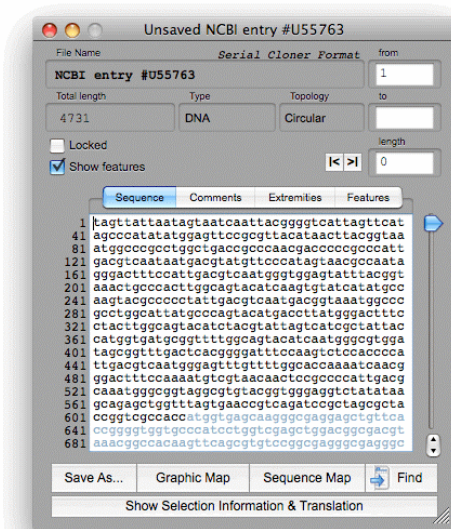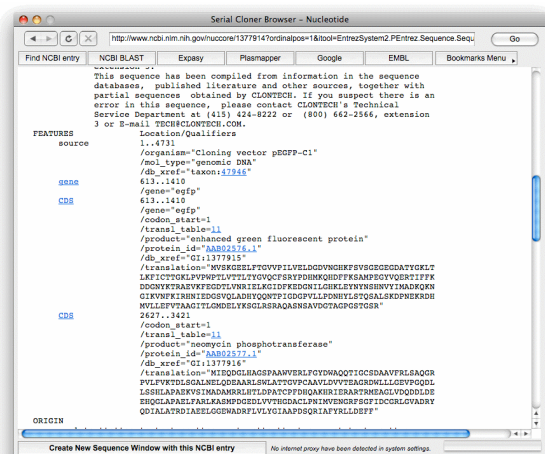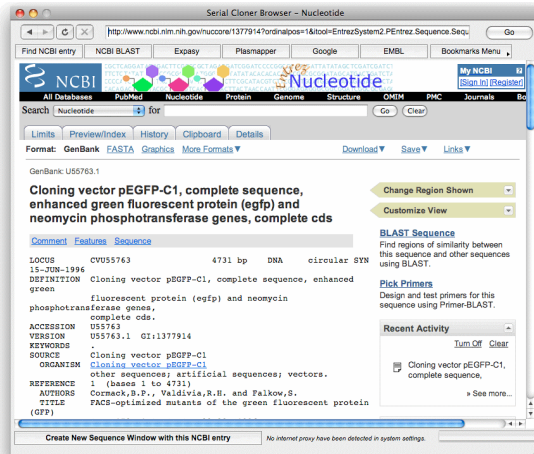

IV. File Format

Serial Cloner uses an extended DNA Strider file format. It is still readable by DNA Strider and by any software that respects the recommendations of the DNA Strider format. Strider will just ignore additional information, and in particular features and annotations. Of course, if one then saves the sequence using DNA Strider for example, Feature data will be lost.

V. Import of feature-enriched sequences

Serial Cloner 2.0 imports features-containing sequences saved by *ApE* or *Vector NTI*. Feature colors should be correctly imported.

Import of *Genbank* and *EMBL* have been improved and features should now be recognized and parsed. This is true for sequences saved in files or imported from the Genbank/EMBL web interface using Serial Cloner mini-Web Browser (using its bottom-left button). See the example bellow. [Note that other formats devoid of Features are still recognized by Serial Cloner : *Fasta*, *pDRAW32*, *raw text*].

The pEGFP-C1 has been obtained from the NCBI web interface using Serial Cloner mini-Web Browser. Because a GenBank formatted sequence has been detected by Serial Cloner, the button "Create a New Sequence Window…" at the bottom left was enabled. Clicking on it imported the Genbank entry in a new Sequence Window, correctly parsing the Features.

VI. Adding Features

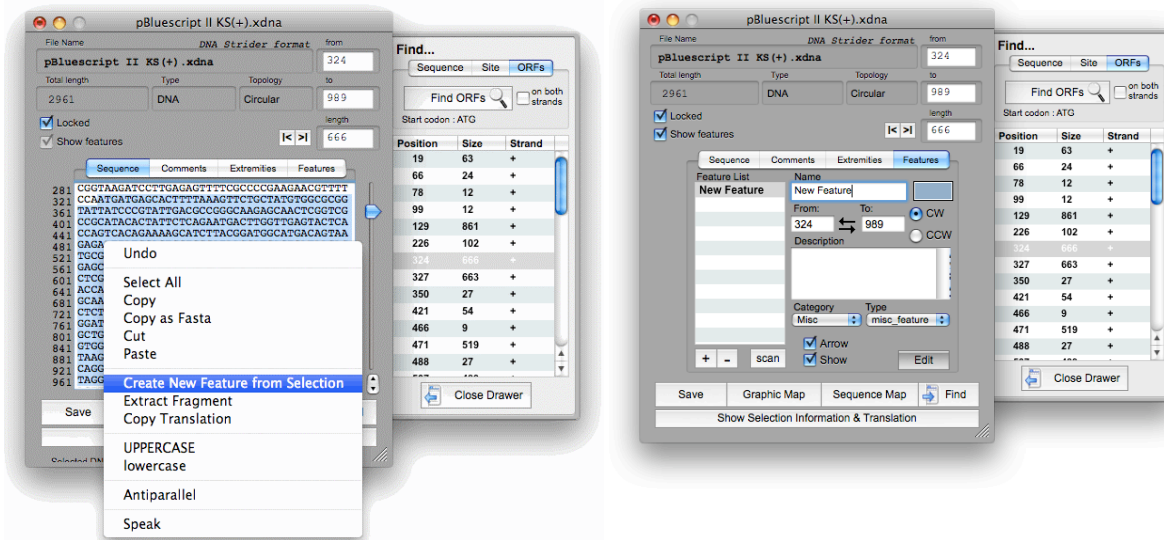Several ways exist to add new Features to a sequence.

A. Manual entry

Simply go in the Feature section (*Features* Tab) and press the '+' button. Then, enter numerically the coordinates of the feature and set the different values. If a portion of sequence has been selected before pressing the '+' button, then the coordinates of the current selection will be automatically proposed as default values for the features (and in some cases the translation pasted as indicated bellow).
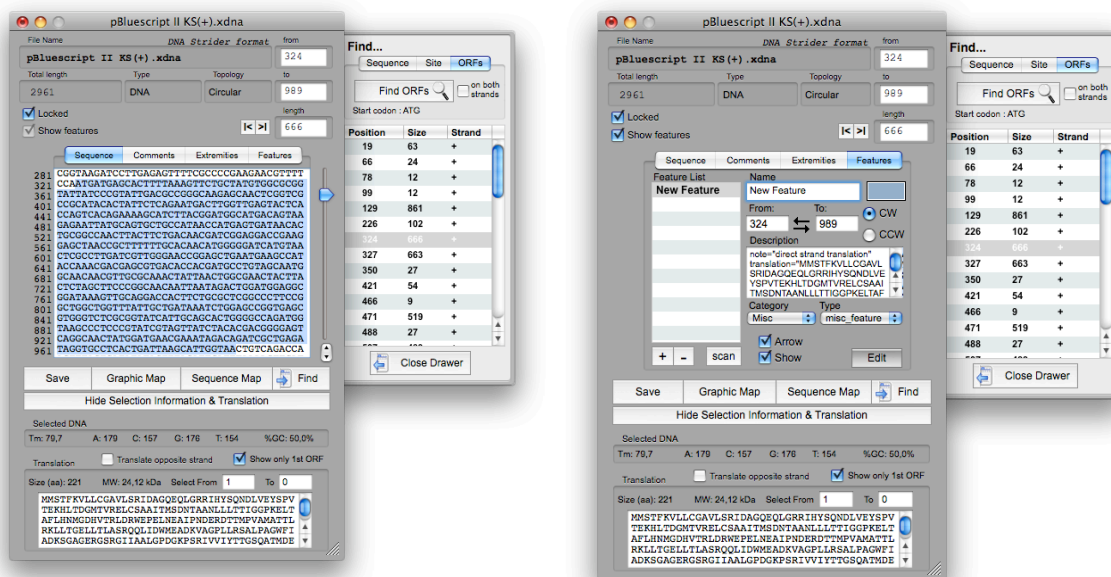
B. After selecting a nucleotide fragment in the sequence window.

First select a portion of sequence in the sequence window either directly or using the ORF search for example. Then either display a contextual menu (Right-Click or [CTRL]-Click) and select '*Create New Feature From Selection*'. Alternatively, use the '*New Feature From Selection*' (shortcut : [*C*]-@) from the *'Sequence'* menu.
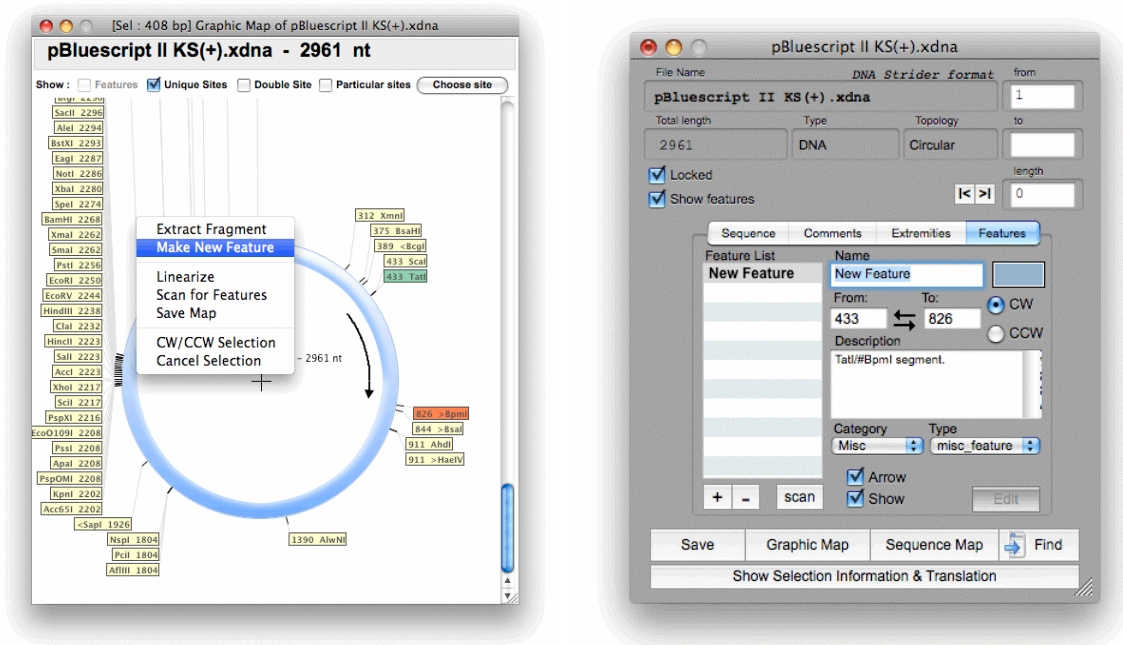

Note that if the '*Selection information and Translation*' was shown before creating the Feature, then the current translation will be added in the features comments (see bellow).

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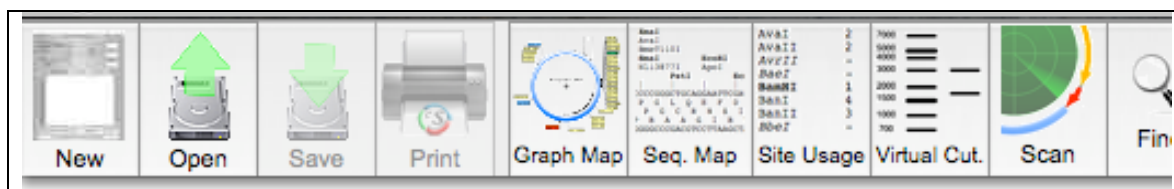## C. After selecting a nucleotide fragment in the Graphic Window.

First, select a fragment by choosing an upstream (simple click) and downstream (double-click or [SHIFT]-Click) restriction site. Clockwise and Counter-Clockwise can be toggled using the spacebar. Then display a contextual menu by right-clicking (or [CTRL]-Clicking) on the map and select '*Make New Feature*'. Alternatively, use the '*New Feature From Selection*' (shortcut : [*C*]-@) from the *'Sequence'* menu. The feature will created between these two sites and the names on the enzymes added in the comment field.

D. By automatic scanning

Serial Cloner now includes an internal database that allows to automatically detect the presence of tens of frequent sequences like the β-lactamase, the ColE1 or the f1 sequence for example (see the list bellow). At the moment, there are no way to add user-defined sequences. This will be for the next release of Serial Cloner.

To use the database and detects the presence of these domains in your sequences, simply use the *Scan* button present in the *Toolbar* or the use the '*Scan Sequence*' command ([ALT]-[*C*]-S, in the *'Sequence'* menu). This can be done either while displaying the *Sequence Window* or the *Graphic Map*. In the latter case, the associated *Sequence Window* must not have been closed.

It is also possible to scan using the *'Scan'* button present it the *'Features'* tab of the Sequence Window. By default, all are *'Shown'* but the *'Show'* checkbox can be use to alter this state.

Note that if you scan more than once the same sequence, the same Features will of course be found and the new Features will replace the identical new ones. BUT if you change something on an automatically found annotation (like its name, color, etc.), it will not anymore be automatically erased upon a new scan (to protect your modifications). A new scan will thus result in a duplication of this Feature and the unwanted one will have to be deleted manually.

Serial Cloner 2.0 : Internal database of Features

The following features will be looked for upon scanning. Note that proper detection depends on correct matching to the consensus sequence stored in Serial Cloner. Please, do not hesitate to signal any lack of detection so that I can update the consensus sequence for this Feature. You can also propose to add your preferred Feature in the database (submitting by email a consensus sequence) but again, an interface allowing custom consensus sequence scanning should be present in the next version of Serial Cloner.

- T3
- M13-fwd
- M13-rev
- T7
- SP6
- ColE1 origin
- F1 ori
- 2u ori
- M13 origin
- LacZ alpha
- LacO
- AmpR
- LacI
- Kan/neoR
- KanR
- CmR
- TetR
- TetR
- ZeoR
- BlastiR
- PuroR
- TetA
- GentaR
- HygroR
- SV40 late polyA
- CMV promoter

- SV40 early promoter
- hGH polyA signal
- FRT
- LoxP
- IL2 ss
- human IgG1 Fc
- human IgG2 Fc
- human IgG3 Fc
- human IgG4 Fc
- mouse IgG2A Fc
- mouse IgG2B Fc
- mouse IgG3 Fc
- rabbit IgG Fc
- rat IgG2B Fc
- TRE
- U6 promoter
- EM7 promoter
- mPGK Prom
- bar
- Spec
- dhfr
- APH(3')-IIA
- aadA
- tsr
- pat
- aph
- oriVR6Kgamma
- oriS
- oriRg
- R6K ori
- 35S CMV
- PBAD
- AML-P
- NOS-P
- TrpC
- CaMV 35S
- mPGK Prom
- EGFP
- GST
- mRFP1
- mCherry
- EYFP
- ECFP
- hRluc1
- Rluc
- AcGFP

- 6His
- Cys
- IRES [1]
- IRES [2]
- attB4
- attB3
- AttB2
- AttB1
- attP4
- attP3
- AttP2
- AttP1
- attL4
- attL3
- AttL2
- AttL1
- attR4
- attR3
- AttR2
- AttR1
- ccdB
- KanMX
- URA3
- TRP1
- MET15
- LYS2
- LEU2
- HIS3
- ADE2
- 2 micron origin
- CEN-ARS pRS
- CEN-ARS YCp-lac
- CEN-ARS YCp50
- GAL4 terminator
- CYC1 terminator
- ADH1 terminator
- MET15 promoter
- GAL1-10 promoter
- GAL1 promoter
- ADH1 promoter
- Gal4 activation domain
- LexA DNA-binding domain
- Gal4 DNA-binding domain
- HIS1
- PDR5