

# The PIMRider(R) platform V3.1

## Release notes

June 2004

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### 1) Summary

#### 11) Improvements V3.1

Application runs on MAC-OS X panther 10.3 / Safari.

Minor Improvements were done on the PIMViewer and the DomainViewer .

#### 12) Improvements V3.0

Major improvement of this version is the possibility to handle within the tool sheer integrated PIMs or 'multiple PIM'. A 'multiple PIM' can be defined as the result of complete integration of 2H screen results initially clustered with several 'unitary' PIMs or PIM program.

Last version tool (V2.4) could handle simultaneous exploration of multiple PIM, but data were not actually integrated and neither application ergonomomy nor functionalities were thought to studies of such PIMs.

Main principles:

- PIMRider can access one multiple PIM at the time,
- a multiple PIM can include up to 8 unitary PIMs,
- an unitary PIM contains one or two PROTEOMEs (if two: one is the bait proteome, other is the prey proteome),
- a CDS/ PROTEIN belongs at least to one or more than one PROTEOMEs,
- an 'atomic' INTERACTION belongs to one and only one PIM program. Nonetheless there can be several INTERACTIONs found between two PROTEINs.

## 2) New functionalities V3.1

### 2.1) PIMViewer

#### 211) « add protein» function

Usually a protein is displayed with its immediate neighborhood. Sometimes, it is more practical to load a serie of proteins of interest, arrange their positions on the graph, select them all and display their neighborhood once for all.

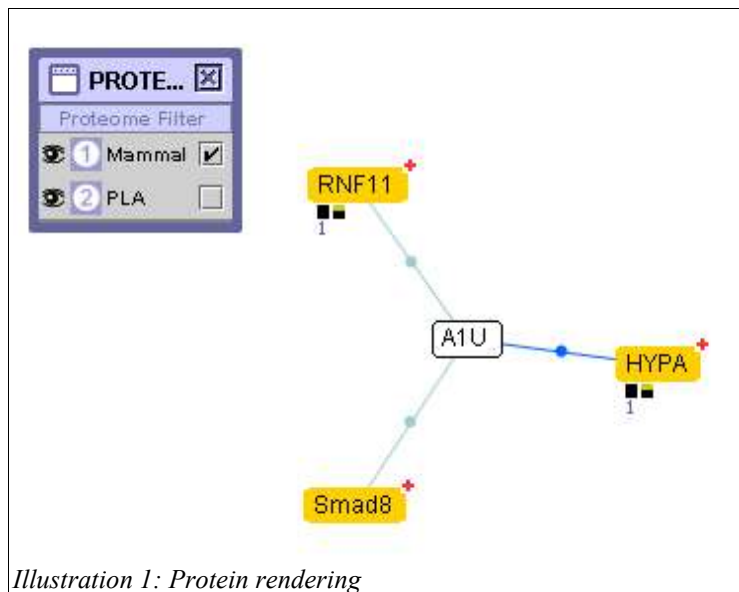
Select a protein of interest within the list then click on the «add» button next to the «neighborhood» button. Protein is displayed within the graph as is (with no neighbors displayed).

#### 212) display 2- and 3-component of a graph

Right-click on the graph and check pop-up menu items. This operation is not reversible.

#### 213) Protein rendering simplification

If a protein belongs to only one proteome, then no proteome symbol is displayed.



Example:

- RNF11, HYPA belong to proteomes Mammals and PLA,
- Smad 8 belongs to Mammals only,
- A1U belongs to PLA only.

## 214) Interaction rendering simplification

If an interaction was not found in a given program PIM then no empty circle is drawn anymore.

## 2.2) DomainViewer

221) Filter protein on domains and compare domains used a criteria with sid or bait.

Sid and bait domain cannot act as filter criteria anymore. The benefit is that you can now filter protein that contains a given domain (as usual) and then display sid or bait domains within the proteins filtered without affecting the current filter.

222) Display of Coiled-coil domain (obtained from Ncoil algorithm).

Coiled-coil domains were obtained from Ncoil algorithm. They can act as protein filters criteria.

## 3) New functionalities V3.0

### 3.1) Protein Advanced Search Tool

'Advanced Search Tool' offers the possibility to build sophisticated queries on the 'multiple PIM'. Previous search tool (called now 'basic search tool') is still available.

During a session, requests built can be memorized. They can be restored in the same session, and serve as a start for new requests.

Protein can be initially searched at a proteome or a PIM program scope. Then additional clauses can be inserted line by line.

1. open tool from basic search tool.

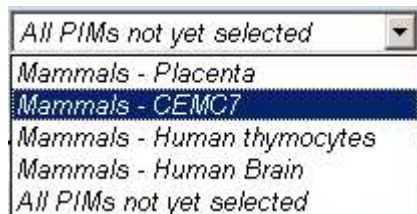


screenshot 1: basic search tool

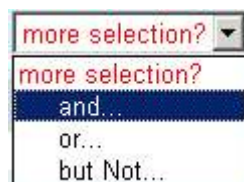
2. select search scope, here a PIM program.



3. precise search scope. Here 'mammal-Cemc7' PIM program.

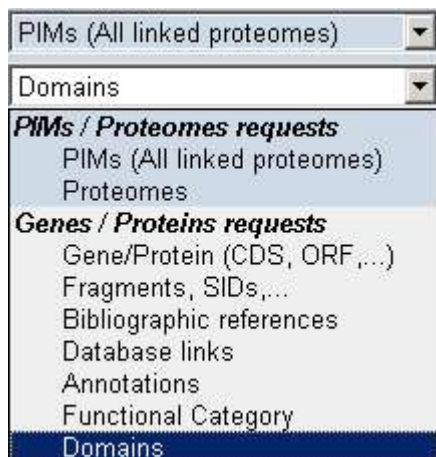


4. add new criteria. First select logical operator to combine new clause with previous ones.




Remark: 'OR' and 'BUT NOT' operators can only be applied to 'PIM / Proteom' requests and not to 'Gene / protein' requests.

'Genes / Protein' request can be applied to proteic functional domain for instance:



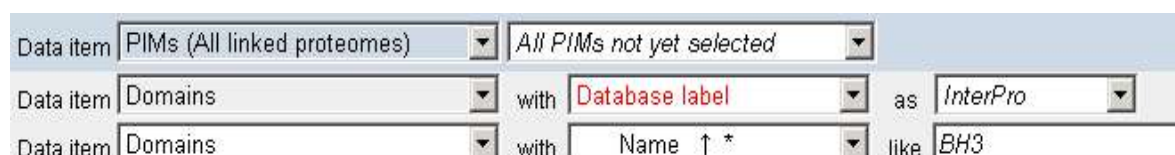
The criteria one selected must be precised:



Launch search using , icon **Searching** is then displayed.

Remark: once a search launched please do not click inside the window.

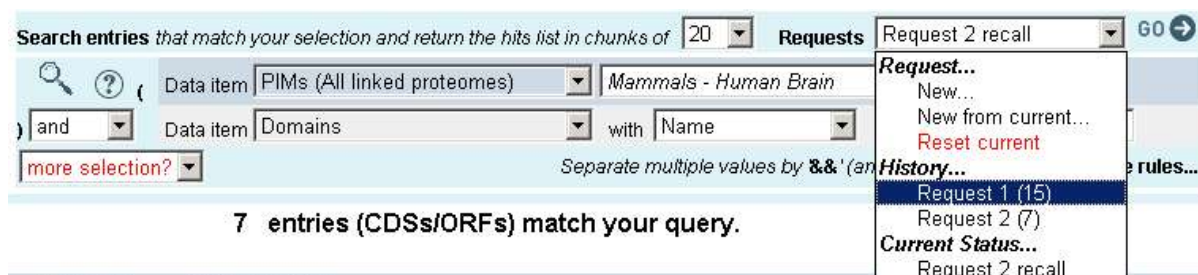
Example : query : "*seek all 'Mammals – CEMC7' proteins that contain at least one 'InterPro' BH3 domain*" is built as follows:



Screenshot 2: advanced search tool

For 'Genes / Protein request', you can use in-field boolean operator '&&', '||' et '&!' within the 'like' field (for example if you want to specify a list of possible value use '||').

Once request launched, to acces it again ('Request 1' here):



then click on :



Request is then restored.

### 3.2) Protein viewer

1. list of proteomes that contain the protein of interest.
2. interacting partner list with for each partner all interactions (with PBS category and value) found within all PIM programs.
3. interacting partner list sort functionalities:
  - 1. sort by best PBS,
  - 2. sort by protein name.

#### ProteinViewer

**PROTEIN A : Proteomes [ 3 ]**  
1. proteome1 2. proteome2 3. proteome3

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**PROTEIN A : Identification and Function**

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Original Name : PROTEIN A  
Biological Name : PROTEIN A  
Alias : alias for prot A  
Product : prot name  
Function : function

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**PROTEIN A : Functional Category [ 1 ]**

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Sub cellular localization : nucleus GO:0005634

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**PROTEIN A : Viewers [ 2 ]**

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[PIMViewer](#)  
[DomainViewer](#)

**PROTEIN A : Partners [ 1 ]**  
Sort table by:   

Protein Name	Best PBS	1 PROT. 1 - PROT. 2	2 PROT. 1 - PROT. 3
Total of partners	1	1	1
1 PROTEIN B	C	C (1e-4)	D (0.1)
Total of partners	1	1	1

screenshot 3: ProteinViewer

### 3.3) InteractionViewer

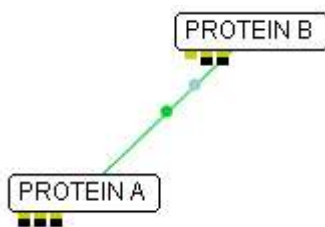
1. add proteome name for each interacting protein.

### 3.4) DomainViewer

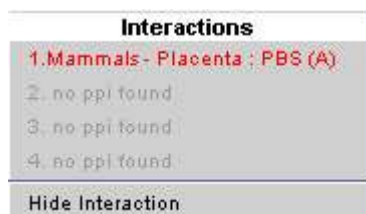
1. BAIT fragment tooltip: displays PIM programs list where fragment was used.
2. SID fragment tooltip: displays PIM program where fragment was defined.
3. highlight BAIT fragment SID partners: right-click on a bait fragmen will highlight all interacting SIDs within protein partner list.
4. show/hide BAIT and SID depending on PIM program they were used or found.
5. highlight BAIT and SID depending on PIM program they were used or found.
6. interacting partner PIM program filter. Restrict partner list to proteins involved in the PIM program specified.
7. interacting partner PIM domain filter. Possibility to filter protein.

### 3.5) PIMViewer

1. interactions: within the graph an edge represents all interactions found between two interacting proteins among different PIM programs. Here an interaction was found for each PIM program (2). (one is PBS C one is PBS D). Edge is colored according to the best PBS found: here B.



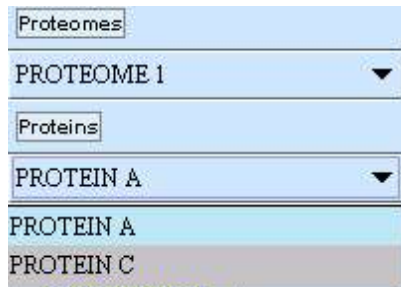
2. access to interactionViewer : get contextual menu (right-click on the edge). Here only one interaction was found, click on this item to get to InteractionViewer.



3. proteins: within the graph: vertex indicates list of proteome it belong to. In the previous example protein B belongs to proteome 2 and 3 not 1, protein A belongs to all proteomes.
4. 'Multiple PIM' proteome list. Select one proteome refreshes proteins list below:



'PROTEOME' 1 protein list:



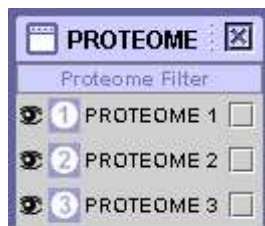
5. best PBS filter/highlight panel: click on the eye to filter interaction, check the box to highlight interactions:



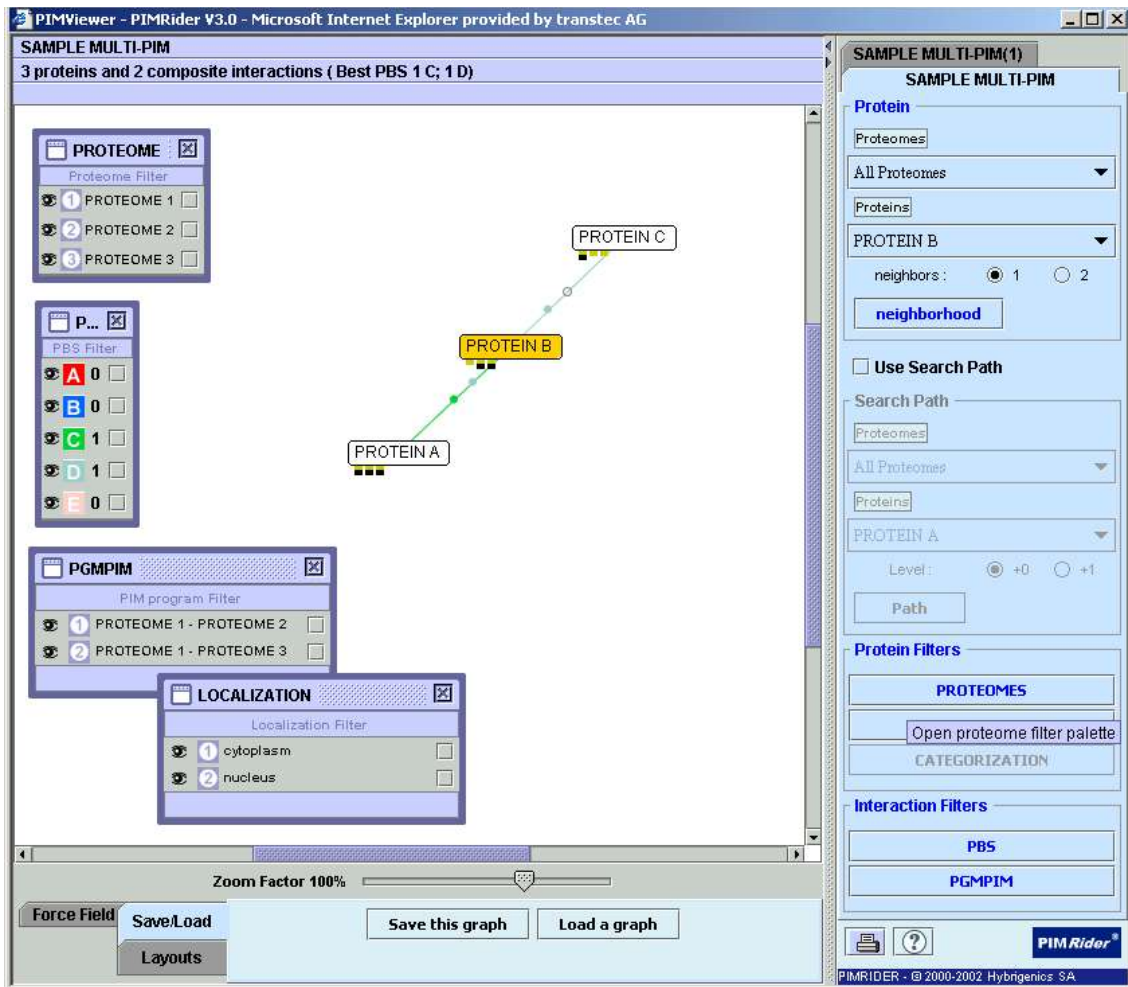
6. PIM program interaction filter/highlight panel:



7. proteome filter/highlight panel:



8. overview with filter tools open:



screenshot 4: PIMViewer