

PIMRider®

ULTimate Y2H™ interaction data visualization tool

PIMRider® is Hybrigenics' functional proteomics software platform, dedicated to the exploration of Protein Interaction Maps (PIM®).

Fed by our reliable interaction data, PIMRider allows the exploration of biological functions and the understanding of pathways.

PIMRider® integrates 4 viewers:

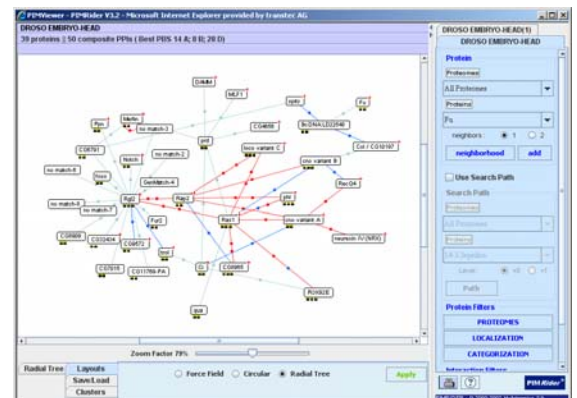
> **Protein Viewer® – Browse proteins and annotations**

- > Advanced search engine: selection of protein entry point using various filters and keywords
- > Functional and structural annotations: description, aliases, function, localization, links to bibliographic and external databases, protein sequence and genomic information
- > List of interacting proteins: interactions scored with PBS®, our proprietary confidence score.



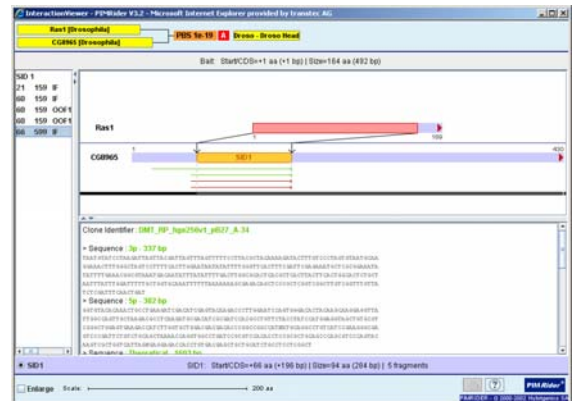
> **PIM Viewer® – Ride the interactions**

- > Graphical PIM display: different graph layouts, expand/hide and path search functions
- > Multiple-PIM display: for comparative proteomics
- > Filtering options: by PBS, proteome, library, subcellular localization, function
- > Import/export: save, load, and print graph options.



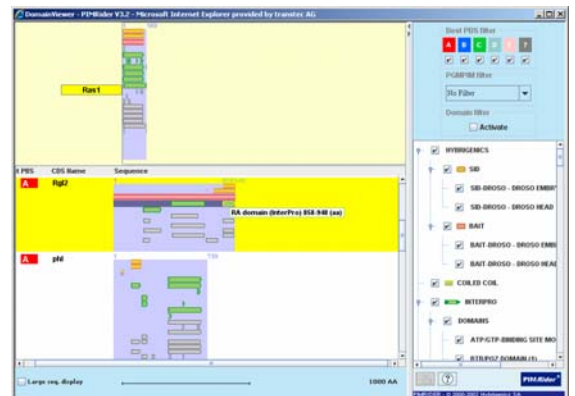
> Interaction Viewer® – Review details of experimental data

- > Bait domain definition: relative position in the bait protein
- > Detailed list of selected prey fragments: positions, clone identifiers, experimental and theoretical 5' and 3' sequences
- > Definition of SID®: interacting region common to all selected prey fragments.



> Domain Viewer® – Ride the interactions

- > Domain mapping: graphical view of experimental binding domains (bait and SID), structural domains (signal peptides, transmembrane segments, coiled-coil regions, secondary structures), and functional domains (InterPro)
- > Filtering options: by PBS, domain type or PIM
- > Sorting options: by PBS, protein name or protein size.



Access to Hybrigenics interaction data through the PIMRider software under special conditions. Please [contact us](#)