Proasis3

Rich Internet Application

Proasis3 is a new Rich Internet Application (RIA) built on top of DesertSci's Proasis2 database and visualization system and comes with many powerful new features

'Rich Internet applications (RIA) are Web applications that have the features and functionality of traditional desktop applications. RIAs typically transfer the processing necessary for the user interface to the Web client but keep the bulk of the data (i.e., maintaining the state of the program, the data etc) back on the application server.'

Wikipedia

Proasis3 is a browser application that works like a desktop application

Proasis3 Advantages

- Created with *'state of the art'* technology Proasis3 responds instantly for users and improves real time productivity.

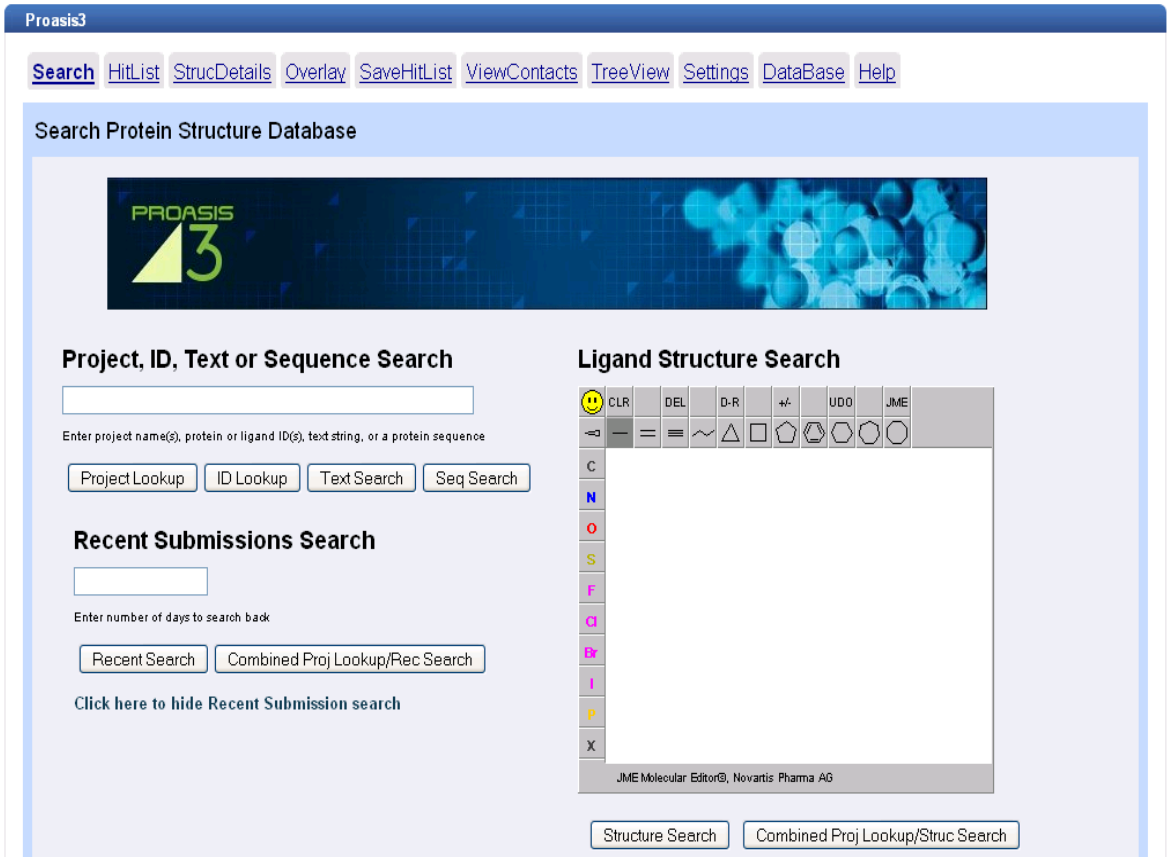
- Built to be 'future proof' for the next decade

- Improved user experiences. Behaves like a desktop application by minimizing client-server communications and providing richer functionality. For example, Proasis3 sorts 'on the client' making data manipulation easier. It provides text completion for easy project identification and structure retrieval

- Linkages to ViewContacts - the highest quality protein-ligand interaction software available

- Engineered using 'best in class' techniques so that the system is:
  - robust
  - easy to understand
  - scalable
  - fast to implement
  - easy to maintain

Introducing Proasis3



Cutting-Edge Technology:

- GWT (Google web toolkit)

The most powerful toolkit for creating Ajax applications

- Pyjamas

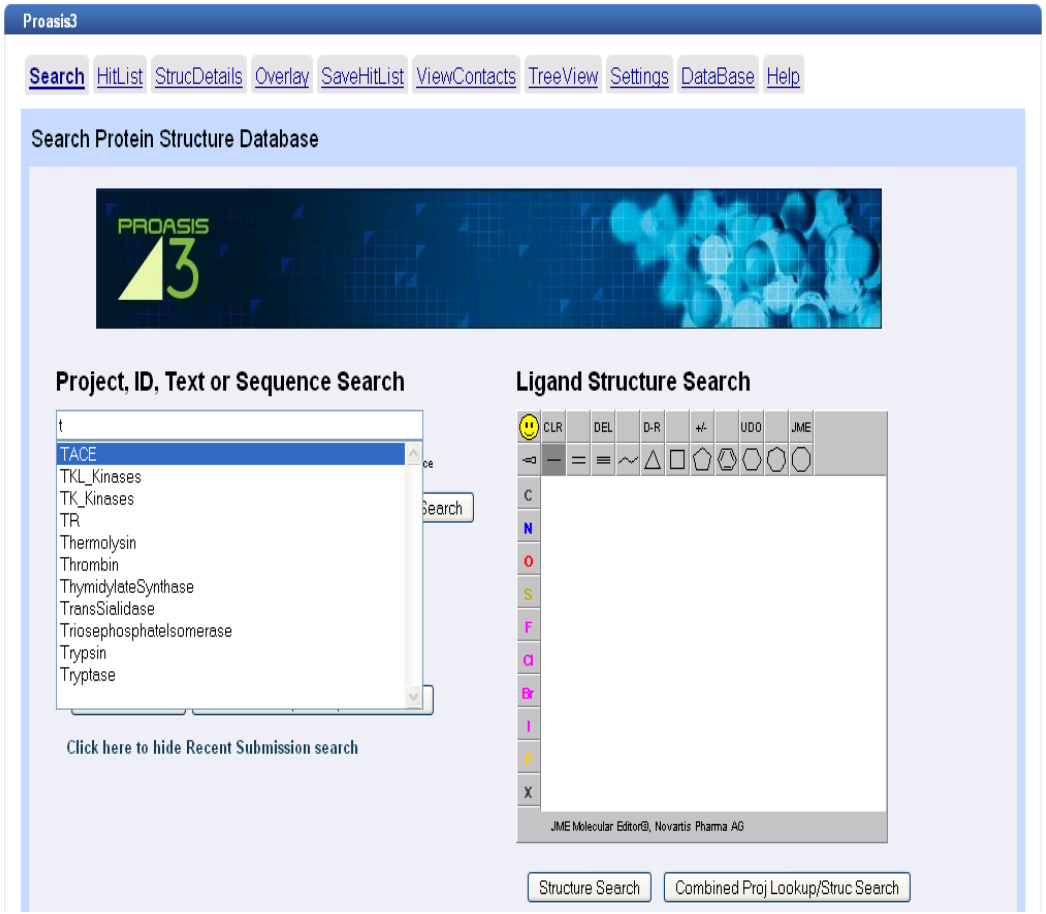
The python version of the GWT

- PureMVC python

A powerful framework based on MVC

Proasis3 runs highly optimized javascript (compiled from python code!) so in all popular browsers it is **fast to load and fast to execute**

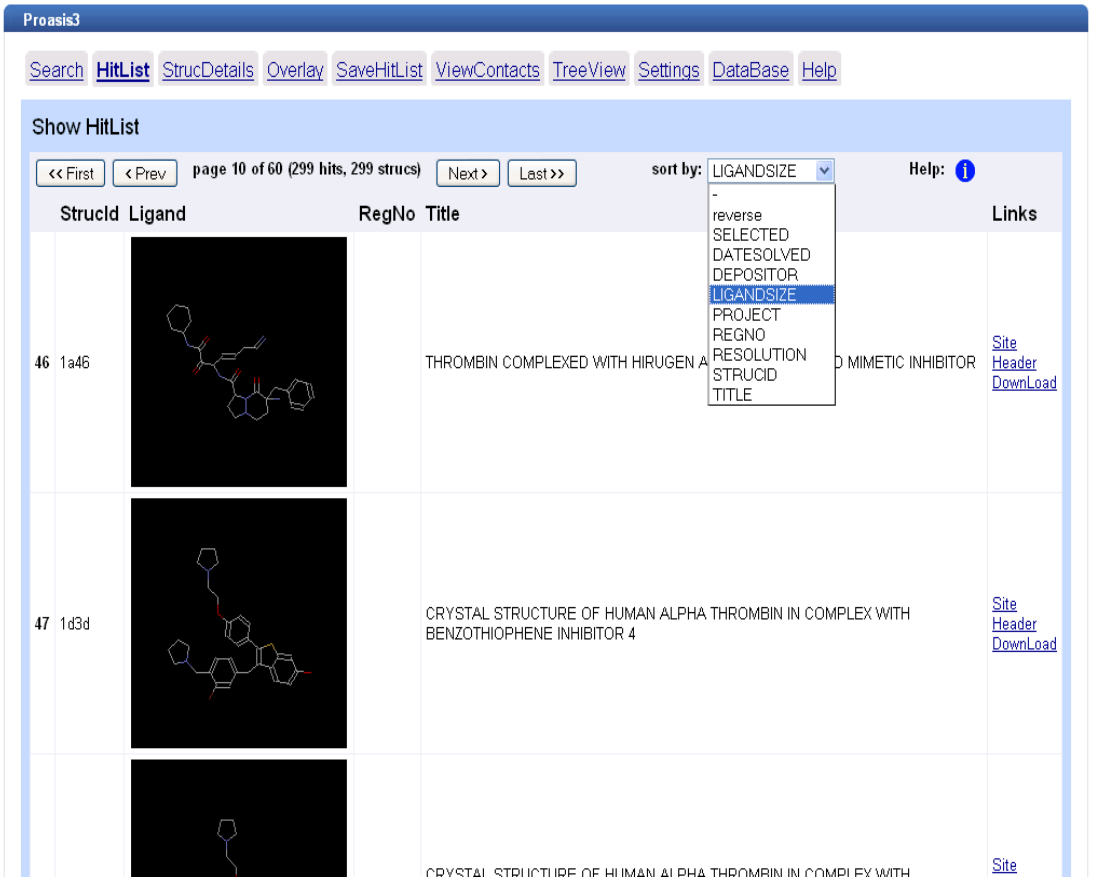
Easier Searching



- In-house project names are loaded automatically
- Simply typing a letter **lists all projects starting with that letter**.
- Select one and click ‘Project Lookup’ and all project structures are retrieved
- There is new, fast searching using ligand ID numbers or just the last few digits of a ligand ID
- A button for Combined Project/Structure searches makes these even easier

Many **different types of searches are easily available** from just one page of the interface, making Proasis3 even more user friendly

More like a Desktop Application



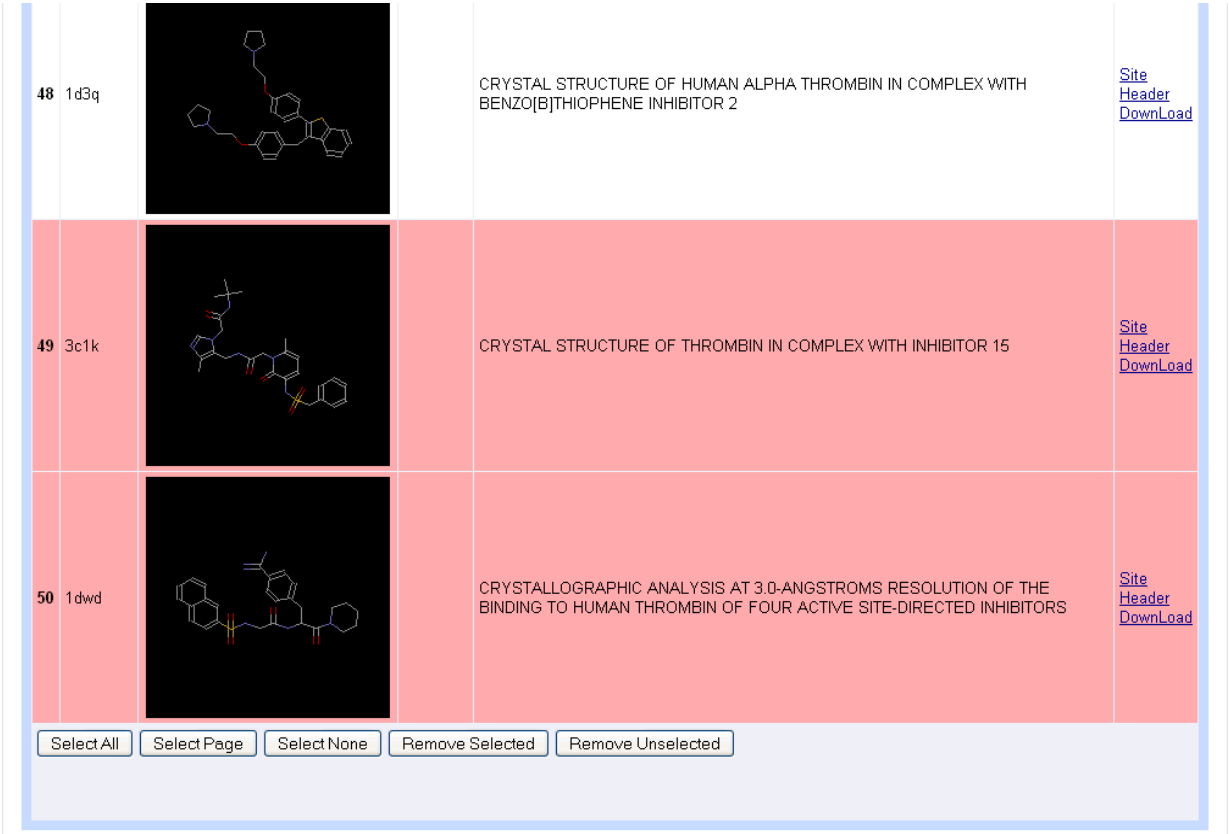
- Hitlists can be re-sorted according to different properties and dynamically re-sized entirely on the client

- The desktop application retrieves data from the database more efficiently (using asynchronous javascript technology)

- Tooltips and PopUps link directly to helpful hints

More data can be stored on the client, making for **faster navigation**

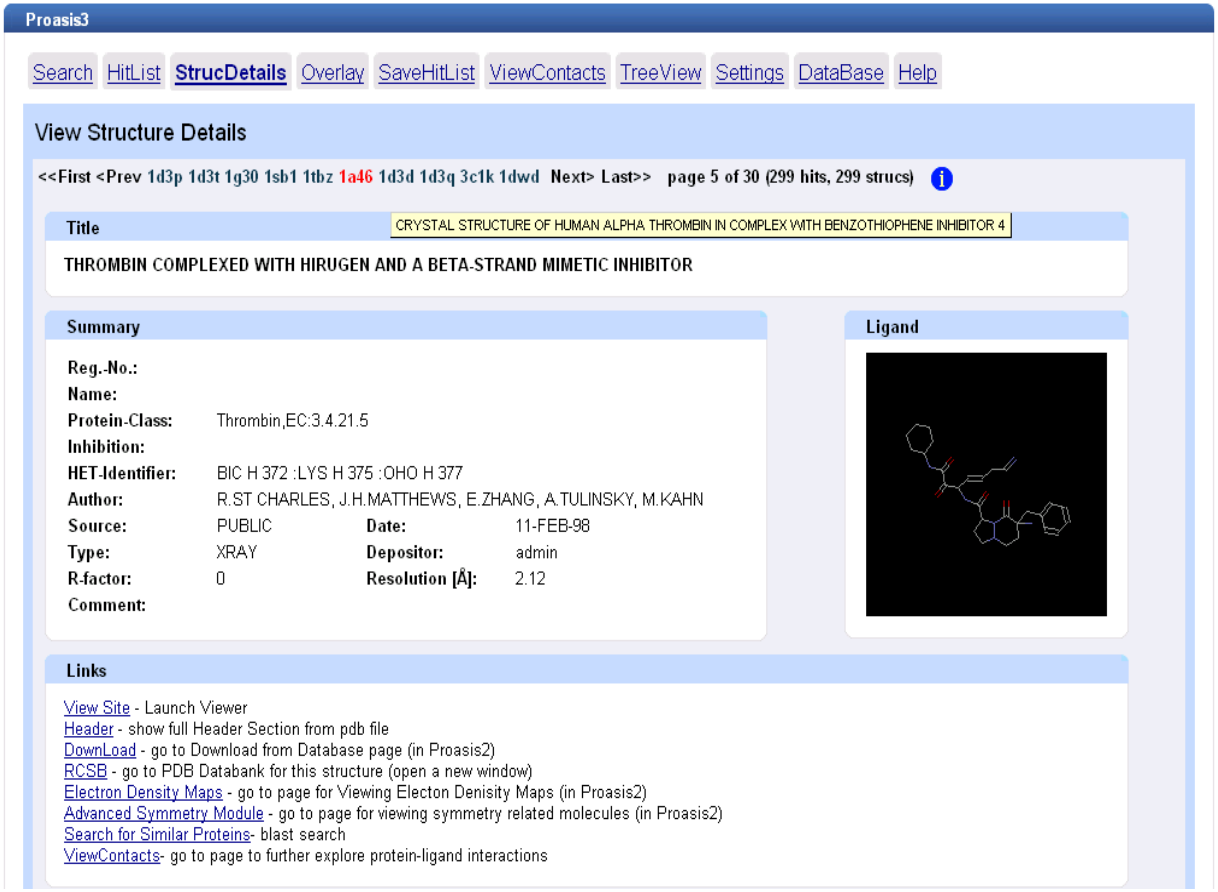
New Hitlist Tools



- Individual and multiple rows can be selected and manipulated
- Hitlists can be pruned and/or extended
- Hitlist rows easy to customize
- Hyperlinks easy to extend to connect to other inhouse and external resources

Hitlists can be exported in multiple formats – in report style or as a set of pdb files

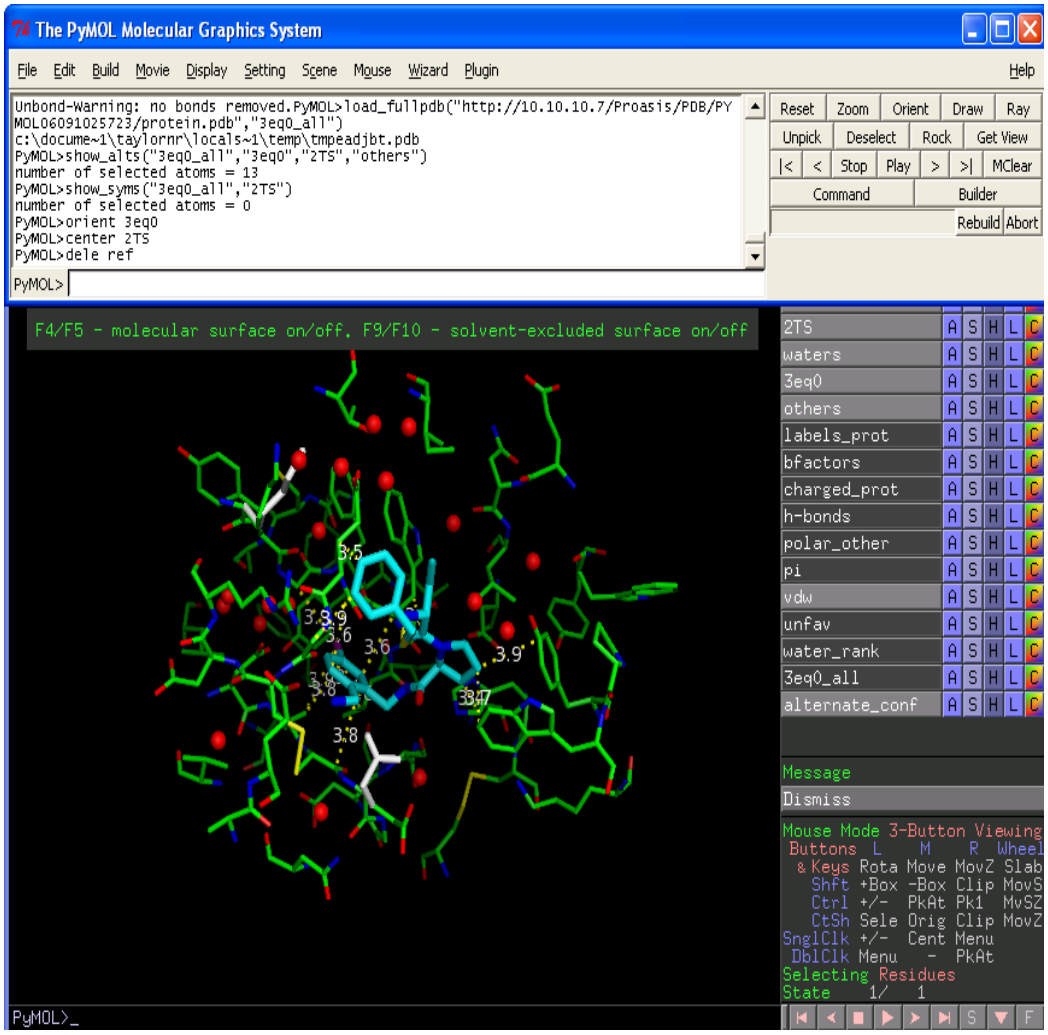
Updated Look and Feel



- Structure information has a new improved look and layout, with all the familiar details and functionality
- Includes easy access to the Advanced Symmetry Module

Ajax facilitates **faster browsing** from one structure to the next

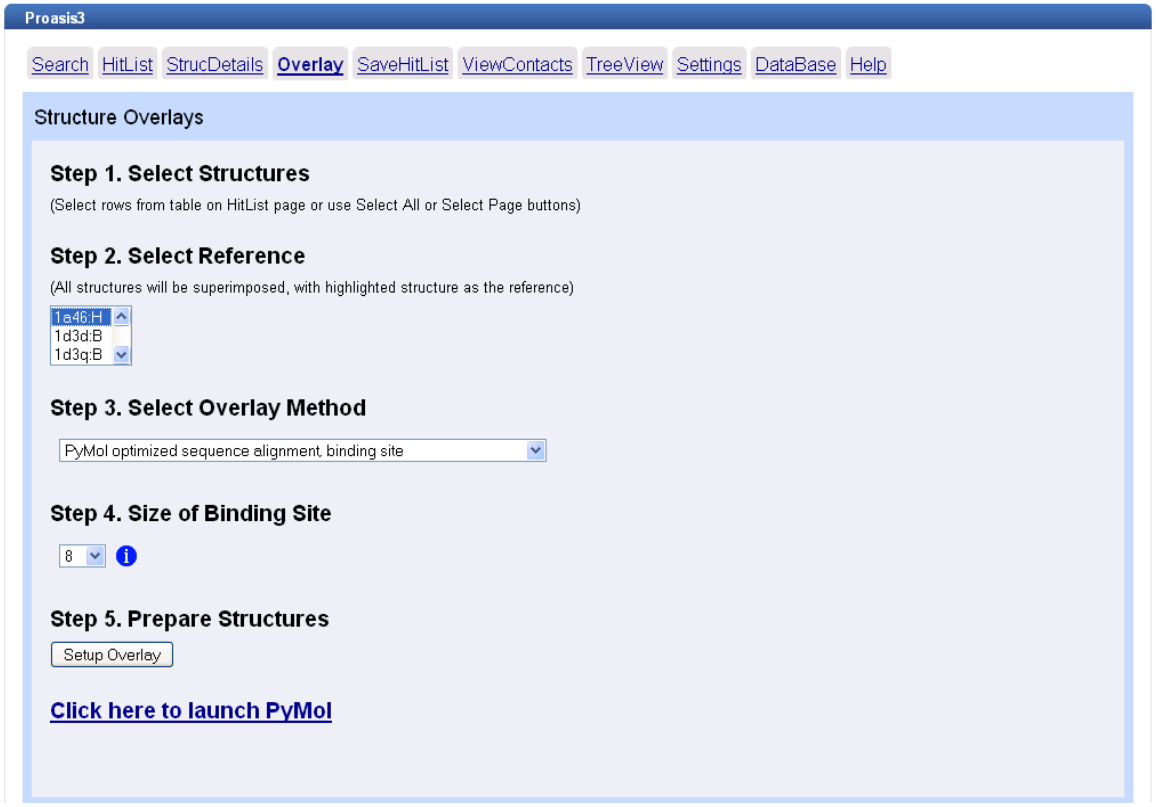
New PyMol Viewing Features



Enhanced PyMol viewing all in one session:

- binding site views include both the binding site and the entire protein
- alternative conformations in the binding site are highlighted
- all symmetry molecules making contact with the binding site are shown
- fine-tuned protein-ligand interactions are illustrated, including unfavorable contacts, and water-mediated interactions

Additional Overlay Functionality



- In addition to fast sequence and ligand based alignments, it is now possible to use PyMol's inbuilt optimized alignment algorithms
- Larger numbers of structures can be superimposed in one session
- Size of the binding site region can be fine-tuned
- Overlayed structures can be exported as pdb files

Protein-ligand interactions can now be viewed for overlayed structures …

Linkages to ViewContacts™
Identifcation of Interactions

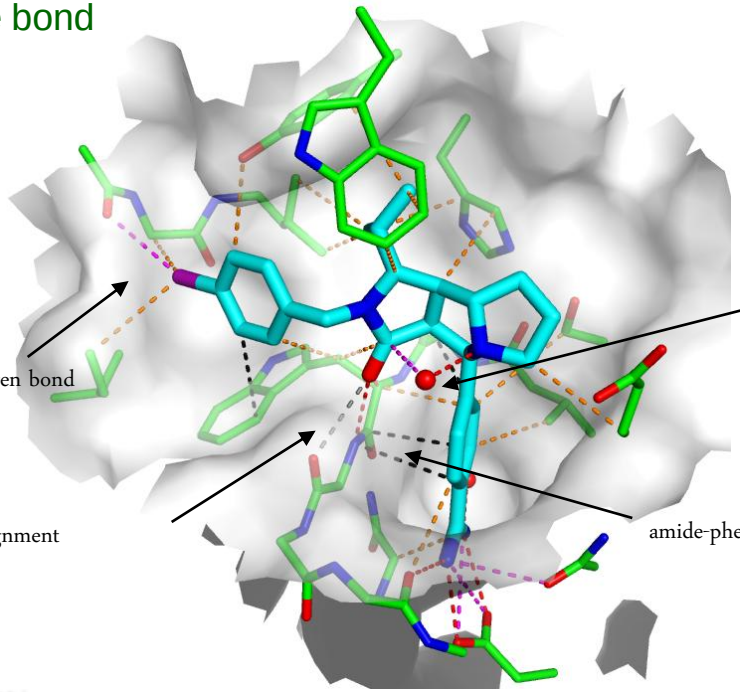
All of the important non-covalent interactions in a protein-ligand complex can be thoroughly explored using the link between Proasis3 and ViewContacts

1. hydrogen bond
2. metal
3. ionic
4. cation-dipole
5. cation-pi
6. dipolar
7. σ-hole bond
8. h_donor-pi
9. pi-pi
10. vdW
11. unfavorable of 1, 2, 3, 6
12. polar and non-polar clashes
13. polar-nonpolar contacts with likely desolvation penalties

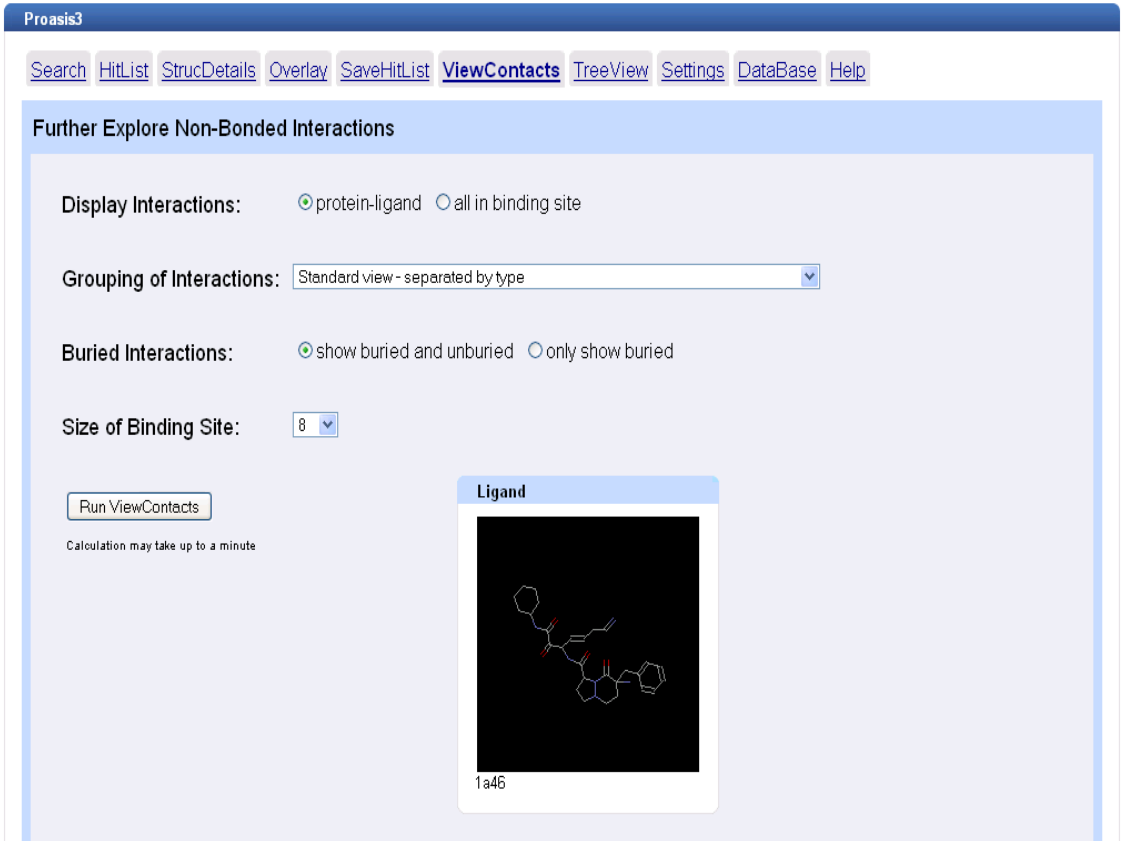
Water and rank score molecules:

$$Rank = \sum_{n}\left\{(2.80A/r_n)+\left[\sum_{m}\cos(\Theta_{Td}-\Theta_{nm})\right]/6\right\}$$

Ex. 2cf8 (thrombin)



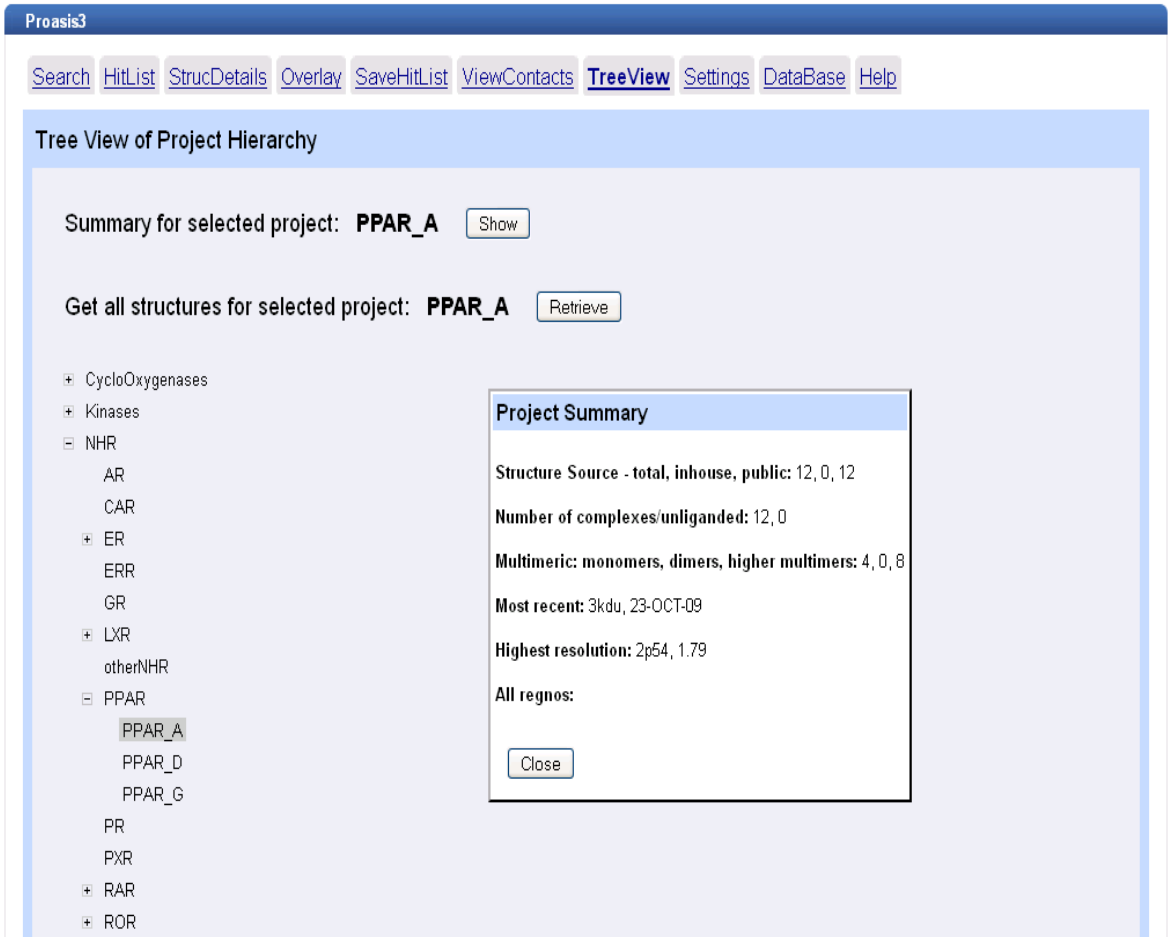
Additional Functionality for Interactions



- Fine-grained representations of non-covalent interactions can be viewed easily
- All contacts in a binding site can be shown
- Contacts involving only those residues in very close proximity to the ligand can be dsiplayed

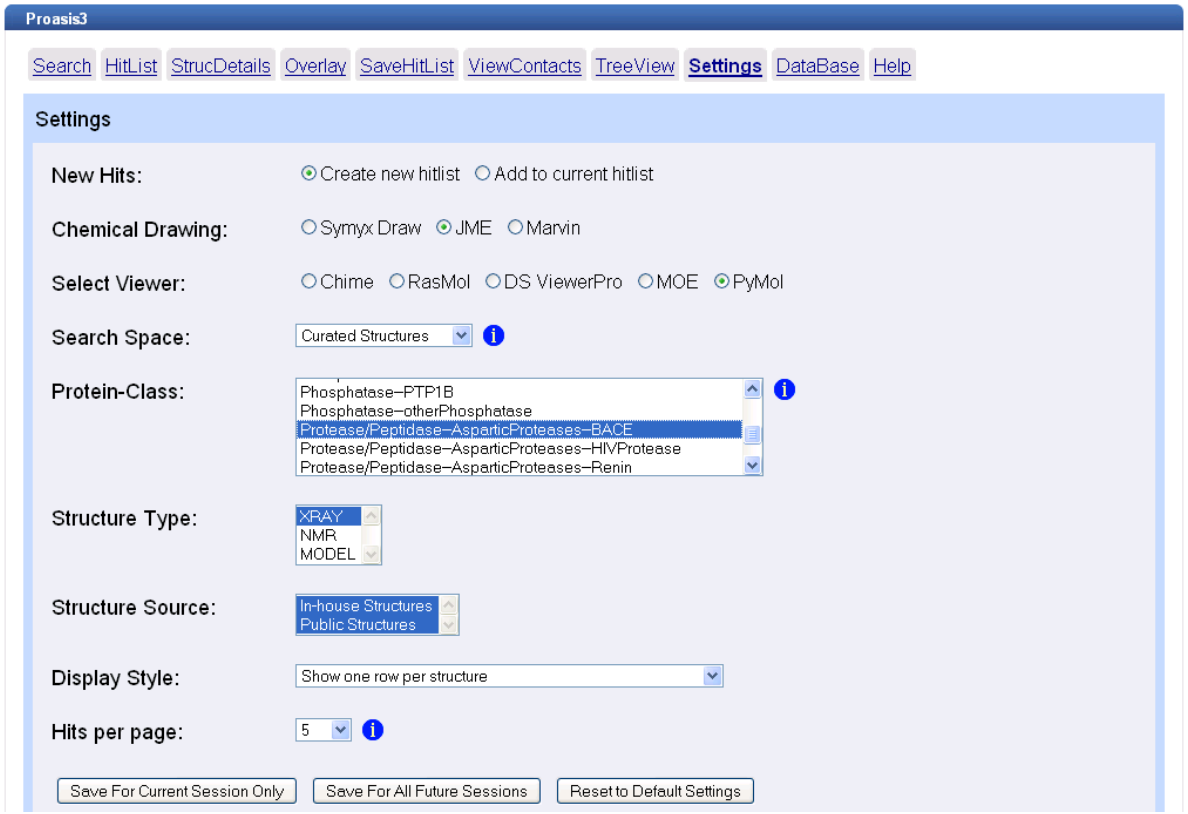
The desktop application, **VCWeb**, for non-database structures such as docking results and structures generated from interactive modeling sessions, is also available

Project Views



- The Project Tree is fast to load, fast to navigate, and its state is maintained when leaving the page
- Project summaries can now be quickly retrieved and inspected
- Structures from any project, or set of projects, are easy to retrieve

More Options and Settings Saved



- Powerful new options, including the ability to extend hitlists
- Users can choose their preferred molecular drawing package
- Users can choose their preferred molecular viewing package

End-user **settings can now be saved** from one session to the next

Other Features

- GWT/pyjamas means **just one version of code** is needed to support each of Internet Explorer, Firefox, Safari, Opera, Chrome, …
- Comprehensive test suite based on selenium
- Comprehensive on-line user manual
- Fine-tuned checking of input parameters
- Speed Tracer for Chrome (from Google) helps to achieve maximum performance

Future Enhancements

- Extend functionality for saving hitlists, eg:
  - Create reports with user defined columns
  - Export to Excel
- Session files maintained for each project
- Enable user structures not in the Proasis2 Database to be uploaded and compared and contrasted with experimental data
- Linking Proasis3 and PyMol on the desktop using PyMol's in-built web server functionality
- Providing hooks to DesertSci's *'Scorpion'* - **a new, innovative, state-of-the-art scoring function**
- Providing hooks to DesertSci's new **Ligand Design Tool** based on the '*Scorpion'* technology.