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Research Collaboratory for Structural Bioinformatics Protein Data Bank

RCSB PDB PROTEIN DATA BANK NEWSLETTER

www.pdb.org • info@rcsb.org

Weekly RCSB PDB news is available online at www.pdb.org

Contents

SNAPSHOT: JULY 1, 2010

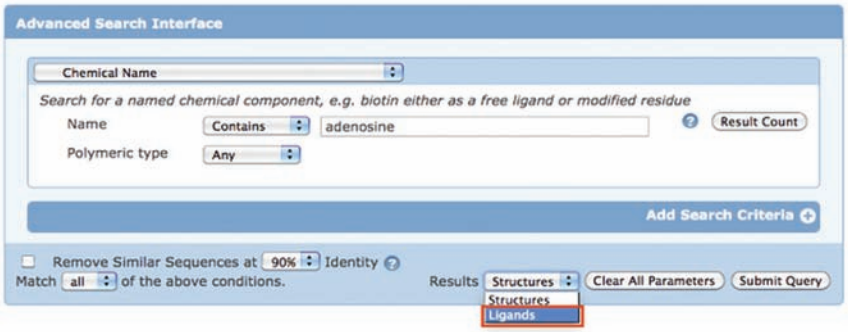
66212 released atomic coordinate entries

MOLECULE TYPE		EXPERIMENTAL TECHNIQUE	
61,280	proteins, peptides, and viruses	57,298	X-ray
2,148	nucleic acids	8,449	NMR
2,746	protein/nucleic acid complexes	295	electron microscopy
38	other	24	hybrid
		146	other
		46,690	structure factor files
		5,742	NMR restraint files

This Newsletter is printed on recycled paper

Message from the RCSB PDB

June Release of Website Features



Several options for searching and reporting chemical components have been added. For example, a search for "Chemical name contains adenosine" will return all PDB entries that match that search; many of these structures will also contain ligands that do not have "adenosine" in their chemical name. *Advanced Search* now provides the option to display either only the ligands that match the search criteria (those with "adenosine" in name) or all of the ligands associated with the PDB entries returned in the search (those with "adenosine" in the name and those without) in the Ligand Hits tab for query results.

The latest release of the website includes many other new features, such as enhancements to

- *Comparison Tool* for exploring sequence and structure alignments
- Chemical component searching
- Generation customized and interactive tabular reports
- *Molecule of the Month*

For an overview, see the **New Features** widget box on the home page.

PSI SBKB Reports on 10 Years of the Protein Structure Initiative (PSI)

Visit www.sbkb.org for a unique view of the current state of structural biology. From July - October 2010, the PSI Structural Biology Knowledgebase (PSI SBKB) is publishing a series of articles that highlight the progress made by the PSI over the past decade in the areas of

- METHODS (July)
  Cloning; expression and purification; crystallization; NMR; crystallography
- MODELS (August)
  Target selection; servers and databases; annotation; methods and workshops
- STRUCTURES (September)
  Metagenomics; membrane proteins; pathways; fold and sequence coverage; achievements and milestones
- OUTREACH (October)
  Working with industry and the biological community; functional annotations

Data Deposition and Annotation

ADIT 2.0 Offers Improved Deposition Process

A new and improved version of ADIT, a tool for validating and submitting structures to the PDB archive, has been released.

ADIT 2.0 indicates file format errors and provides suggestions for solutions; automatically runs validation checks; and reviews the consistency between sequence and coordinates. Improved help information and documentation are provided. The forms for entering sequence information, structure title, author names, and citation information have also been streamlined.

This version of ADIT was developed based on user feedback and suggestions, and implemented after a period of testing.

ADIT and its related tools are available from **deposit.rcsb.org**. Deposition sessions currently in process will not be disrupted; depositors will not have to update any bookmarks or session ID.

Use Ligand Expo When Depositing Structures with Ligands

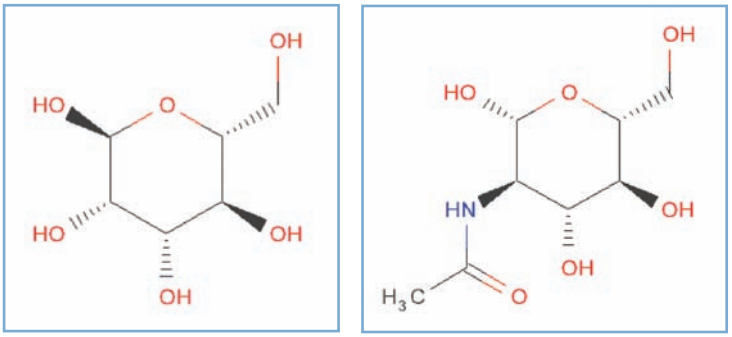
Ligand Expo (**ligand-expo.rcsb.org**) accesses chemical and structural information about all small molecule components found in PDB entries. It is based upon the Chemical Component Dictionary maintained by the wwPDB.

When depositing a structure with a ligand

- Search Ligand Expo for a chemical component that matches your ligand
- If a match is found, use the corresponding three-character code for the ligand in your coordinates
- If the ligand is not found, choose a new, unused three-character code. When depositing this new ligand during your ADIT deposition, upload the chemical name and formula and/or a file showing the chemical image for the new ligand into the Ligand Information section

Ligand Expo can search the Chemical Component Dictionary using uploaded data files (*e.g.*, PDB, MOL/SDF, Refmac/ Phenix monomer library (mmCIF)); chemical name; formula; SMILES string; and ID code.

Searches for instances of ligands associated with macromolecular structures can also be performed at **www.pdb.org** using a variety of options, including the top bar Chemical Name/ID Search, *Advanced Search*, and the *Chemical Structure Search*. Users can then explore the ligand structures and the related PDB entries. Online screencasts are available at the RCSB PDB site to help users explore these features.



Ligand Expo can also be used to check and confirm the chemistry of a chemical component.Shown is the correct stereochemistry for alpha-D-mannose (ID: MAN) on the left, and for N-acetyl-D-glucosamine (ID: NAG) on the right.

wwPDB News from wwpdb.org

Validation Reports Available as PDFs

Review output from validation programs

Respond to any issues

Share with journals and coauthors

As part of the structure annotation process, wwPDB members provide depositors with detailed PDF reports that include the results of geometric and experimental data checking. These reports can be easily reviewed and shared by depositors.

As these validation reports provide an assessment of structure quality while keeping the coordinate data confidential, we encourage journal editors and referees to request them from depositors as part of the manuscript submission and review process. PDB validation reports are already required by the International Union of Crystallography (IUCr) journals[1] as part of their submission process.

The reports are date-stamped, and display the wwPDB processing site logo. They contain essentially the same information, regardless of PDB annotation site. The reports will continue to be developed and improved as we receive recommendations from our Validation Task Forces for X-ray, NMR, EM, and small angle scattering methods, and as we further develop our data deposition and processing procedures.

Questions about these reports and the annotation process may be sent to **info@wwpdb.org**.

Version 2 NMR Restraint Files Available from the wwPDB FTP

A new set of NMR restraint data files have been added to the wwPDB FTP with the June 30 update. These restraint files, identified as Version 2 files, are represented in NMR-STAR

Deposition Statistics

In the second quarter of 2010, 2312 experimentally-determined structures were deposited to the PDB archive. The entries were processed and annotated by wwPDB teams at the RCSB PDB, PDBe, and PDBj.

Of the structures deposited, 76.7% were deposited with a release status of "hold until publication"; 16.5% were released as soon as annotation of the entry was complete; and 6.8% were held until a particular date. 92.5% of these entries were determined by X-ray crystallographic methods; 6.8% were determined by NMR methods.

During the same time period, 1906 structures were released in the PDB, for a total of 4342 structures released in 2010.

Data Query, Reporting, and Access

Home Page Widgets

The entire RCSB PDB home page is comprised of customizable web widgets. Boxes with a dark blue bar on top are widgets that can be moved on the page by dragging the arrow buttons, hidden by selecting "Hide," or included in a customized view.

The Customize This Page button in the top right corner lets users select which widgets are displayed by default. To only see query-related options, add widgets to download files and search by sequence and remove the **Featured Molecules Widget** that displays the RCSB PDB's *Molecule of the Month* and the Protein Structure Initiative's *Featured Molecule*.

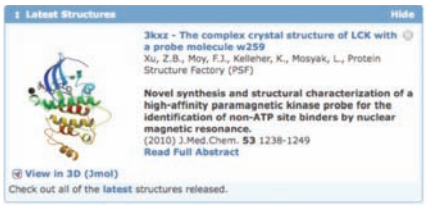
Other widgets that can be displayed on the home page include the *Comparison Tool* for running pairwise structural and sequence alignments, links to ADIT for new and existing depositions sessions, and the **New Features** and **Latest Structures** widgets described below.

New Website Features

Descriptions of features added in any release can be accessed with this widget.

Want to learn about the latest RCSB PDB tools and developments? The **New Features Widget** on the home page scrolls through the latest website applications and improvements. It also links to descriptions of all recent website releases.

Latest Structures



This widget rotates through all of the structures released in the most recent update.

A new widget on the home page displays a slideshow of the latest PDB entries.

The **Latest Structures Widget** randomly cycles through all the entries that have been released in the most recent update. It displays the entry title, image, citation and PubMed abstract, if available. Users can pause the slideshow at any point to read the entire abstract, or click on the entry title to view the entry's *Structure Summary* page.

3.1 format, contain current PDB atom nomenclature, and provide accurate atom-level correspondences to the NMR model coordinate files in the current archive. Restraint files containing restraint data as originally deposited (Version 1 files) will remain on the site and will continue to be updated regularly as new NMR entries are released.

The Version 2 NMR restraint files were generated for the wwPDB by the BMRB in collaboration with PDBe and the Centre for Molecular and Biomolecular Informatics/Institute for Molecules and Materials at the Radboud University Nijmegen. NMR restraints were parsed from their original format (Version 1), and harmonized with the coordinates using the software packages *Wattos* (BMRB; and CMBI/IMM), *FormatConverter* and *NMRStarExport* (PDBe), and the CCPN framework. The complexity of this process may have led to minor modifications or loss of data in the Version 2 restraint files due to parsing or conversion errors. The PDB coordinate file and the Version 1 restraint files remain the primary reference for these data. More information about the process used to generate these files is available.[2-4]

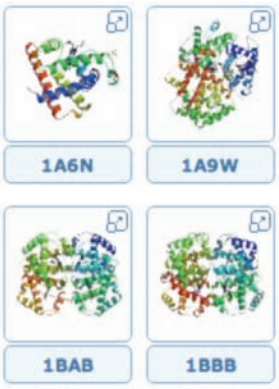
The initial release of the Version 2 NMR restraint files added more than 5700 new files (~310 Mbytes) to the FTP site. Version 2 restraint files for new PDB entries will be processed and made available after the PDB entry has been released. Version 1 restraint files for new PDB entries will continue to be released weekly.

NMR restraint files are named using extension .mr, as in "1abc.mr.gz" for PDB ID 1abc. Version 2 restraint files will be named "1abc_mr.str.gz", where "str" identifies the NMR-STAR (V3.1) data format. All restraint files are compressed (.gz) using the GNU gzip program.

Version 1 restraint files will remain in their current directory structure. Version 2 restraint files are stored in directories named by the middle two characters of their PDB ID in: **ftp.wwpdb.org/pub/pdb/data/structures/divided/nmr_restraints_v2/**

These data files are linked symbolically to the directory: **ftp.wwpdb.org/pub/pdb/data/structures/all/nmr_restraints_v2/**

Create a Collage of Structures

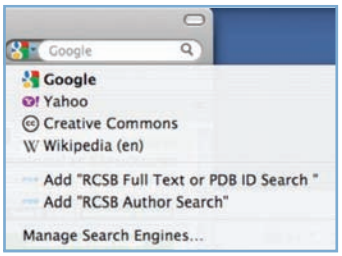


After searching for structures, select *Custom Report>Image Collage* to display the set of returned structures as a series of tiled molecular pictures. Moving your mouse over each image in the collage displays the structure title; clicking on the small image shows a larger version. The PDB ID listed links to the corresponding *Structure Summary* page.

Image collages can be customized by the size of the images displayed and how many images are shown per page.

This image collage shows some of the structures that were returned for a search of structures that contained the same sequence as chain A of hemoglobin structure 4hhb.

Search the RCSB PDB in Your Web Browser



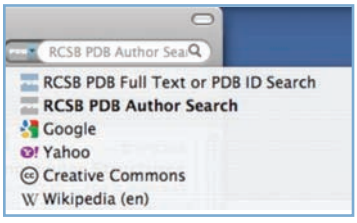
From Firefox, add RCSB PDB Search options by clicking on the arrow to the left of the search box.

In a hurry to search for a PDB entry? Add the RCSB PDB search engine to your web browser to perform queries directly through the browser's search box. RCSB Full Text or PDB ID Search and RCSB Author Search queries can be performed (alongside similar searches to Google and Yahoo) in the search box of modern browsers such as Firefox (versions 3+) and Internet Explorer (7+).

To add this OpenSearch functionality to your web browser:

- Visit **www.pdb.org**
- Click on the arrow near the search box
- For Firefox, select "Add RCSB Full Text or PDB ID Search/ Add RCSB Author Search"
- For IE, select the RCSB PDB search options from the "Add Search Providers" menu

Then select one of the RCSB PDB search engines from the query pulldown menu and search the RCSB PDB directly from your browser.

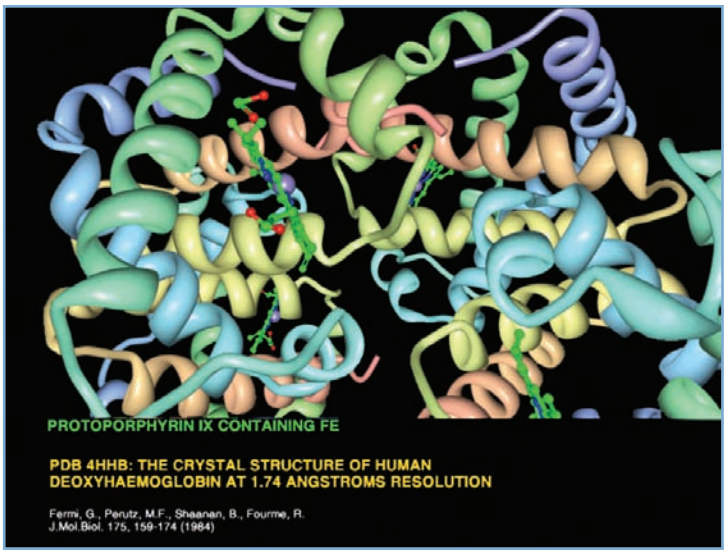


Queries can be performed using this search box while browsing any website.

Reading about a PDB entry in a paper? Use the "RCSB Full Text or PDB ID Search" to search by the PDB ID. Use the "RCSB Author Search" to search for structures by the same author. As you type the author name in the browser search box, the "autocomplete" functionality will suggest possible name matches.

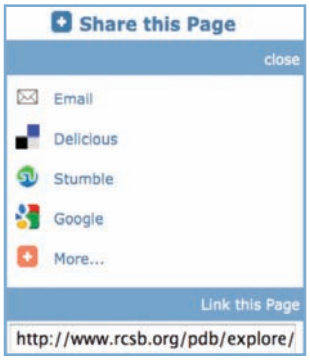
Turn Your Computer into a PDB Kiosk

Highlight structures from your lab, institution, or class with the *Molecules in Motion Kiosk Viewer*. Using a list of PDB IDs, this full-screen animation program will display any PDB structure from different angles and perspectives. This Java viewer can be downloaded or launched from the RCSB PDB's **Educational Resources** page.



The kiosk program will also focus on and label any chemical components in an entry, like the heme group shown here in hemoglobin entry 4hhb.

Bookmark and Share RCSB PDB Web pages



Easily send and store URLs by using the *Share this Page* button on the upper right side of all RCSB PDB web pages.

With this service, favorite PDB entries, *Molecule of the Month* features, and *Looking at Structures* pages can be emailed to colleagues or added to link sharing, bookmarking, and social networking sites such as Delicious, Facebook, and Twitter.

Want to send an interesting PDB entry to a colleague? Use the Share this Page *feature at the RCSB PDB site.*

Website Statistics

Website access statistics for second quarter of 2010 are given below.

Month	Unique Visitors	Number of Visits	Bandwidth
APRIL 2010	203139	486879	978.97 GB
MAY 2010	199620	473973	1058.45 GB
JUNE 2010	174582	429274	869.39 GB

Outreach and Education

Recent and Upcoming Meetings and Presentations

More than 75,000 people came to the Rutgers Day showcase of the varied resources, departments, and people at the university. Visitors to the RCSB PDB's table with the Department of Chemistry and Chemical Biology were able to learn about protein structure next to experiments and demonstrations of how chemistry impacts the food we eat, the air we breathe, the cars we drive, and the medicines we take.

RUTGERS DAY

Virus models were built using either marshmallows and toothpicks or the foldable template available for download from the Molecule of the Month *feature on the dengue virus.*

The RCSB PDB exhibited along with the PSI Structural Genomics Knowledgebase at the **American Society for Biochemistry and Molecular Biology's Annual Meeting** (April 24-28, Anaheim, CA), which was held in conjunction with the Experimental Biology conference.

Booth visitors at the Experimental Biology meeting were able to meet with RCSB PDB staff, explore new website features, and pick up the How Do Drugs Work? *poster.*

A pop-up edition of the *Art of Science* exhibit was staged as part of **Rutgers' Alumni Weekend** (May 14). The RCSB PDB's traveling exhibit includes large-scale depictions of proteins, including images and text from the *Molecule of the Month* series. To learn more about this program, please contact **info@rcsb.org.**

Photos: Jon Horowitz

As part of Alumni weekend, the Art of Science *exhibit was installed at Rutgers and included a lecture about protein structure and scientific art.*

The RCSB PDB will participate at the **24th Annual Symposium of The Protein Society** (August 1-5; Boston, MA) and in the *PDB and Chemistry Symposium* at the **240th National Meeting of the American Chemical Society** (August 22 - 26; Boston, MA).

Papers Published

Articles describing how the RCSB PDB incorporates open access literature and how scientific illustrators can utilize the PDB data and the RCSB PDB have been published:

- Integration of open access literature into the RCSB Protein Data Bank Using BioLit. Andreas Prlić, Marco A Martinez, Dimitris Dimitropoulos, Bojan Beran, Benjamin T Yukich, Peter W Rose, Philip E Bourne, J Lynn Fink (2010) *BMC Bioinformatics* **11**:220. doi:10.1186/1471-2105-11-220
- Getting the Most Out of the Protein Data Bank. David S Goodsell (2009) *The Journal of Biocommunication* **35**: E52-E57.

Congratulations to the National Protein Modeling Champions

In the 2010 Science Olympiad protein modeling trial event, high school teams were asked to demonstrate their understanding of hemagglutinin, neuraminidase, and how protein structure related to the H1N1 influenza virus.At these competitions held at regional and state levels, teams brought a model of hemagglutinin to the event to be judged, built a portion of a protein at the onsite competition, and answered questions on a written exam about H1N1.

The National Science Olympiad championships were held May 20-22 at the University of Illinois at Urbana-Champaign. Out of 44 participating teams, Troy High School from California won the protein modeling event in a tie break.

The protein modeling event focuses on structures highlighted by the *Molecule of the Month* series. The RCSB PDB also sponsors the events held in New Jersey. Information and resources can be found at **education.pdb.org** and **twitter.com/buildmodels**.

The event is organized nationally by the MSOE Center for BioMolecular Modeling. Full results, rubrics, and photos have been posted at **cbm.msoe.edu/stupro/so/NationalTournamentResults.html**. For the past few years, protein modeling has been a trial event offered in a few states. In 2011, protein modeling will be available as a full event offered to all states.

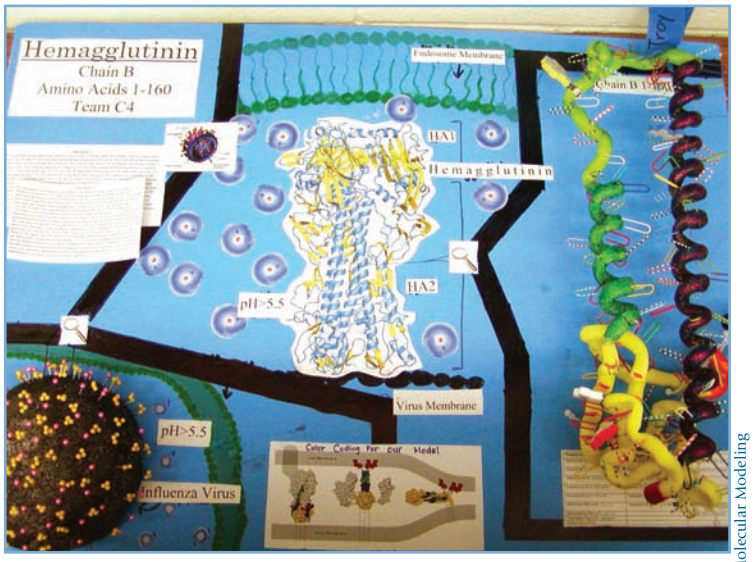
Protein Modeing Event at the National Science Olympiad
May 20-22, 2010
University of Illinois at Urbana-Champaign

1st Place:
Troy High School, CA

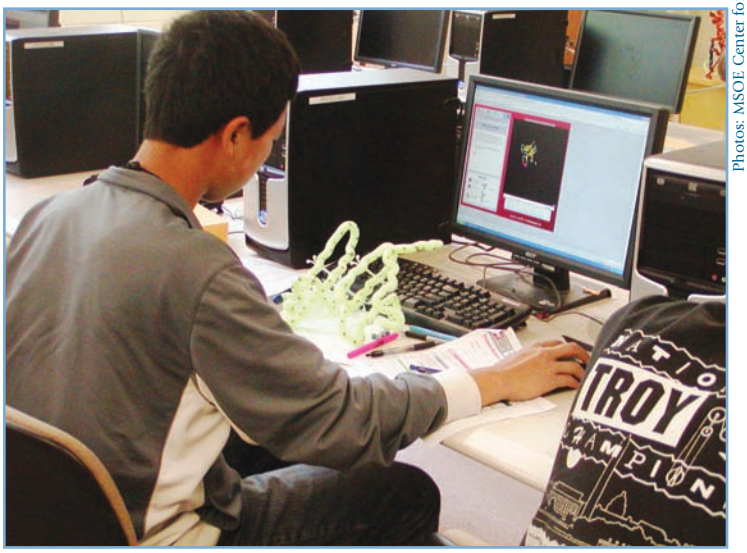
2nd Place:
West Windsor-Plainsboro South High School, NJ

3rd Place:
New Trier High School, IL

Congratulations to all of teams who participated!



Troy High School's model of hemagglutinin.



Teams built 3D models onsite using Jmol as a guide.

Photos: MSOE Center for BioMolecular Modeling

Questions from the Protein Modeling Event

- *Since our body develops immunity to the bacteria and viruses we are exposed to, whether through illness or vaccine, why do we need to get a flu shot every year?*
- *Influenza strains that are resistant to the antiviral Tamiflu have been emerging, which means that treating patients with Tamiflu is becoming less effective against the viral infection. What is the key mutation in neuraminidase that leads to resistance to the antiviral? What is significant about this mutation that prevents Tamiflu from working effectively?*
- *Hemagglutinin undergoes a major conformational change after the virus has been taken into the host cell through endocytosis. What triggers this conformational change and why is this change so essential to the function of hemagglutinin?*
- *Explain how antigenic shift and antigenic drift contribute to the appearance of novel strains of influenza viruses.*

Screencasts and Tutorials Demonstrate RCSB PDB Features

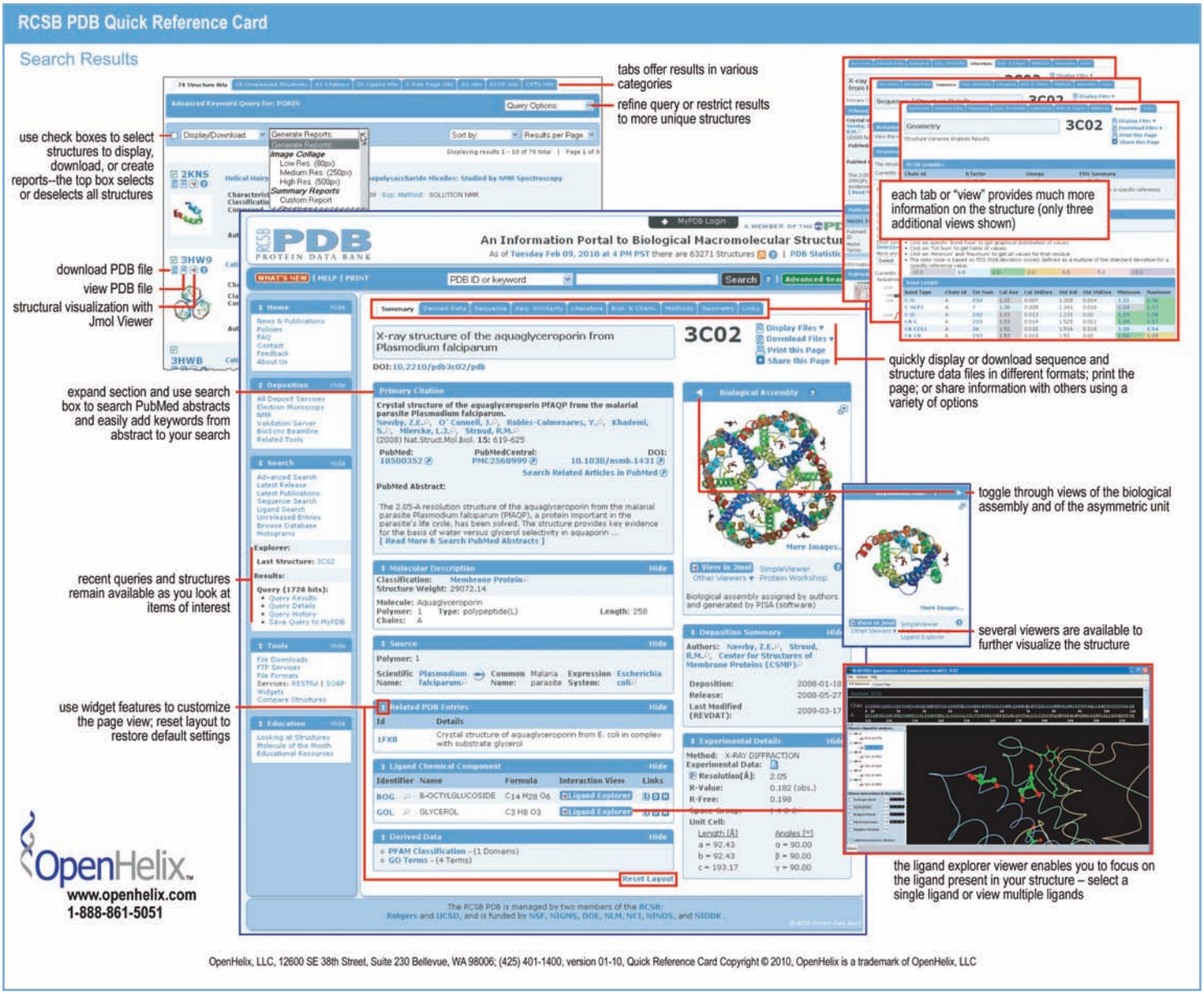
Short, online narrated videos describe how to use ligand searching and website customization tools.

The screencasts currently offered at **www.pdb.org** demonstrate:

- Ligand searching: Using the MarvinSketch applet
- Ligand searching: Advanced MarvinSketch features
- Ligand searching: Using SMARTS features
- Ligand searching: Loading a PDB chemical component
- Customizing *Structure Summary* pages using Widgets
- Tour of the left hand menu

For a more detailed introduction to the features and functionality of the RCSB PDB, comprehensive training materials are available at **openhelix.com**. The training tools include an online narrated tutorial that demonstrates basic and advanced searching, report generation, exploring individual structures, and many other research and education tools. The full tutorial runs for about an hour, and can be navigated by specific chapters.

The animated PowerPoint slides used as a basis for the tutorial can be downloaded, along with slide handouts and exercises. These materials are freely available for teachers and professors to create classroom content.



To accompany the online tutorial, OpenHelix offers free Quick Reference Cards for the RCSB PDB that highlight search strategies, features and functionality. The cards can be ordered at **openhelix.com** *at no cost; shipping is free within the United States.*

Education Corner by Phil McFadden, Ph.D.

Undergraduate Course: Protein Portraits

Protein Portraits is a nontraditional college course developed around the question of what it might be like to shrink to the nanometer realm for a direct encounter with a protein molecule. Since this question invites artistic interpretation, the course is recommended to students whose tastes include both art and science.

The course has been offered in various versions around the Oregon State University (OSU) campus. In recent years it has found a home in our Honors College where the atmosphere is enriched by high-performing students from all academic majors. This spring, with nothing to lose and two credit-hours to gain, eleven Honors College students enrolled in *Protein Portraits* to boldly go where only their imagination could take them. These are the portraits of their ten-week voyage.

The instructor of the course, Phil McFadden, is a professor in the Department of Biochemistry and Biophysics. He teaches the course out of the belief that chemical modeling sets are one of the best toys for kids of all ages. The following interview is distilled from the *Protein Portraits* course blog at **blogs.oregonstate.edu/psquared.**

Q: *Dr. McFadden, how does a student taking your course decide which protein to portray?*

A: Easy. I show the students how to use the RCSB Protein Data Bank. David Goodsell's *Molecule of the Month* is an inspiring starting point. From there, the students are soon able to go off on their own, using the RCSB PDB's search and 3D visualization tools to find a protein structure that fits their personal interests. By the third or fourth week of the class, most students have made a firm choice of a protein. They know its name, its domain structure, what it does for the organism.

Q: *What kind of scientific guidance do you give your students for portraying a protein molecule?*

A: It is true that to understand the structures in the PDB archive, students need at least a basic understanding of how amino acids are connected into chains and how those chains fold according to the hierarchy of secondary, tertiary and quaternary structure. Many students have learned these essentials by high school, so all I generally need to do is throw more light on the subject by spinning PDB structures before their eyes. For this course I also feel fortunate that protein scientists have used a good deal of whimsy in the naming systems for various protein structures -what could be more visually affirming than zinc fingers, leucine zippers, and jelly roll domains as proof positive of the utility of depicting proteins as everyday forms?

PHIL MCFADDEN *is an Associate Professor of Biochemistry and Biophysics at Oregon State University. His ten-week lecture course in biochemistry opens the year-long sequence offered to undergraduate and graduate students seeking degrees in biochemistry and biophysics, American Chemical Society-certified chemistry degrees, and professional pharmacy degrees. He has conducted research in protein chemistry and biological sensory systems, and is currently working on the biology and phenomenology of shells with equal footing in Darwin, Schrodinger and Heidegger. Among his most prized possessions is his autographed copy of Albert Lehninger's 1975 edition of* Biochemistry.

Q: *What artistic advice do you offer?*

A: I advise them to make an allusion to the biological function of the protein in their artwork. Then I show them inspiring examples of the world's heritage of protein art: Irving Geiss's portrayal of sperm whale myoglobin, Roger Hayward's pastel illustrations of proteins for *Scientific American*, Jane Richardson's revolutionary depictions of the structural elements of proteins, and various other masterful illustrations from books and journals published since the 1960s. I also point to the works of contemporary artistic-scientists and scientific-artists such as David Goodsell's exciting graphics and Julian Voss-Andreae's wonderful sculptures. Finally, we are lucky on this campus to be able to stroll across the campus quad to visit the OSU library where Linus Pauling's many chemical models built out of many sorts of materials (including his earliest models of the alpha helix built from folded paper) are held as historical treasures along with the rest of his archived effects.

Q: *How did the students' public art show turn out at the end of the term?*

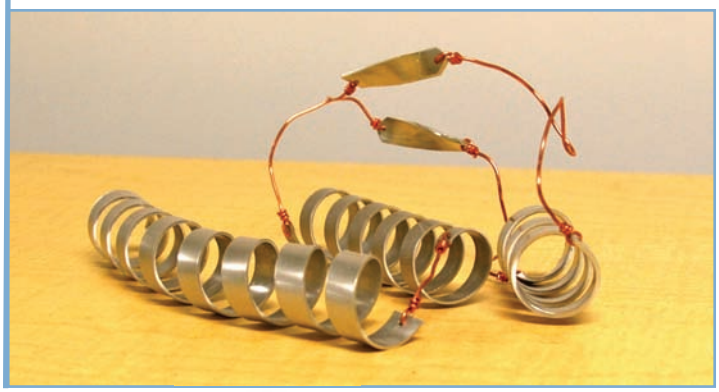
A: It was a lot of fun. Included here are photos of each student's work along with their authored caption. I should mention that the cost of artistic materials was capped at around $10 per portrait, so you did not see bronze castings or cut crystal at the show. Aside from cost, any artistic medium was permitted.

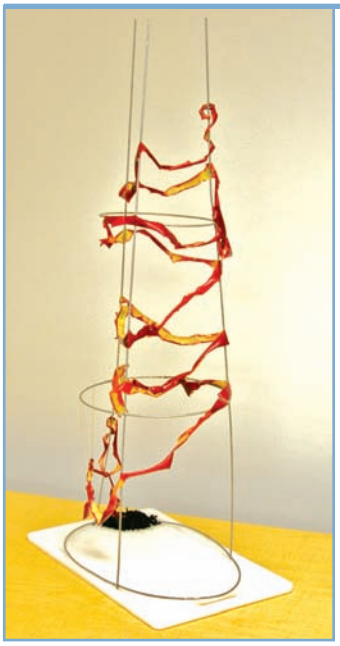
Now, if you have strong scientific credentials, it may be obvious that most of the portraits deviate from the precise 3D coordinates deposited in the PDB. Indeed, I gave the students artistic license to adjust the pose of a protein chain if it helped their art come together. As I explained to them, all of the structures deposited in the PDB have been determined as instrumental averages measured over large populations of protein molecules, so why not give a little extra flexibility to a particular molecule coming to life in the art studio?

Our end-of-term show attracted around a hundred visitors. Ballots were provided to collect votes for the **Most Artistic, Most Scientific, and Overall Awesome**, as noted.

Prion
based on PDB ID: 1qlx[5]
Artist: Dan Cheung

The human prion protein is found throughout the body, but its function is a mystery. The biggest mystery is how in the misfolded state, a prion can act like a cult figure–it converts normal prions into pathogenic forms, causing deadly neural diseases, such as Creutzfeldt-Jakob disease and the notorious mad cow disease.





Pectin Lyase
based on PDB ID: 1idk[7]
Artist: Karen Hoagland

You reach into the fruit bowl and pick up a juicy, bright red apple. You take a huge bite. . . yuck! A big rotten chunk of fruity flesh just spoiled your treat. Blame no other than pectin lyase, the protein that breaks down pectin in the middle lamella of that now-spoiled apple. But don't get too down on pectin lyase. . . if it wasn't busy breaking bonds, that apple would still be unripe and bitter!

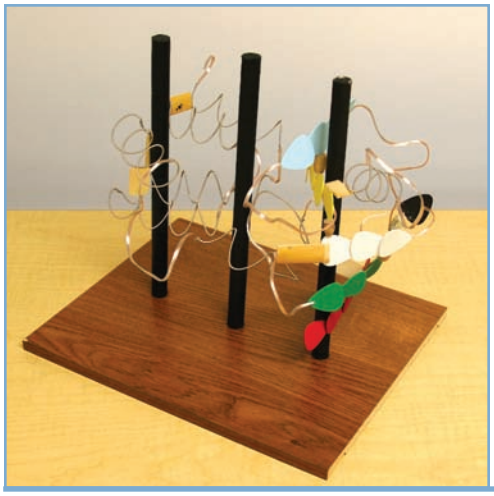
Ovalbumin
based on PDB ID: 1ova[8]
Artist: Danika Kusuma

The fluff of a marshmallow, the taste of a pretzel, the white of an egg omelet. . . To say that this egg protein is not all it's cracked up to be would be something of an outrageous fib! This storage protein has multifarious uses, one of which creates that slight crispy texture to the surface of your humble pretzel. Isn't it eggcellent?

Most Scientific

Calcitonin
based on PDB ID: 2glh[6]
Artist: Nathan Forster

Bones are a surprisingly dynamic part of an organism's body in that they are constantly being torn down and built back up by the combined efforts of osteoclasts and osteoblasts. Calcitonin, a molecule produced by the thyroid gland, is the protein responsible for both calcium uptake and telling the osteoblasts to build up new bone. Salmon calcitonin, depicted here with salmon vertebrae as the amino acids, is a prescribed medication for the debilitating bone loss of osteoporosis. [Thanks go to Dr. Eric Forsman for providing dermestid beetles to clean the vertebrae, and to the Umatilla and Warm Springs Indian Tribes for providing the salmon material.]



Harmonin
based on PDB ID: 2kbs[9]
Artist: Jason S. Lusk

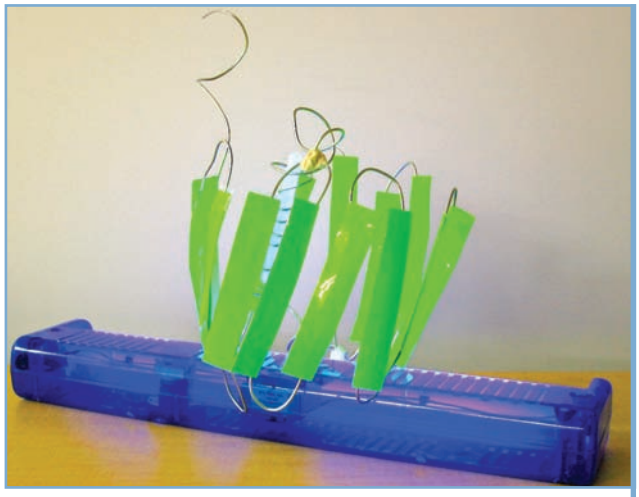
Of the myriad functions of proteins, among the most crucial are those that work in the ensembles that enable us to perceive our world. Harmonin is one such player in a chain of structures that give us our sense of hearing, from a beautiful chord played on a guitar to the powerful roar of thunder. This portrait of harmonin is built of materials (guitar picks, guitar strings, speaker wire and woodwind reeds) that would never have been invented were harmonin not working to help transmit sound vibrations through the inner ear.

ATP Synthase

based on PDB ID: 1e79[10] and 1c17[11]

Artist: Valerie Mullen

Imagine those lazy summer days–nothing to do but sip lemonade and sit in the garden reading. It seems as if you are expending a minimum amount of energy, but in truth your body is still producing massive quantities of ATP. The powerhouse protein that makes everything possible is ATP synthase: one of the most highly conserved and ubiquitous proteins you'll find in nature. Yet we still don't know its exact workings. Interested? Come take a closer look…



Dronpa

based on PDB ID: 2ie2[12]

Artist: Thi Nguyen

A careful balance between dark and light is achieved by dronpa, an engineered protein whose fluorescent glow is switched on and off by changing the wavelength of light that is shone upon it. This lovely behavior explains the name–a fusion of the ninja term for vanishing, dron, and the abbreviation for photoactivation, pa.

Dead Box Protein 5

based on PDB ID: 2kbf[13]

Artist: Callia Palioca

Like a hand carefully untangling precious jewelry, the Dead Box Protein 5 unravels RNA strands. Found in many organisms and performing many functions, it primarily serves as an RNA helicase that enables the RNA strand formed after transcription to be functional. Here, the protein moves the RNA as it opens and closes. Though ancient and perhaps weary from its continual labor, this protein is certainly not just a "dead" box.

Clathrin

based on PDB ID: 1xi4[14]

Artist: Audrey Riesen

You wouldn't want to brave the elements without the proper outerwear–and neither do the vesicles that carry cargo such as enzymes throughout the interior of the cell. These vesicles wear a coat of their own–a delicate and beautiful polyhedral lattice formed when numerous three-armed clathrin triskelions join forces. So, my dears, grab your hats! We're going out!

Green Fluorescent Protein (GFP)
PDB ID: 1ema[15]
Artist: Elizabeth Runde

GFP is composed of a barrel of beta sheets and a light-emitting chromophore within. By teaming up with aequorin (which glows blue), GFP produces the eerie green light that jellyfish are known for. GFP has spurred many new technologies, from tracer studies with fluorescent microscopes to those creepy glow-in-the-dark cats produced by genetic engineering.

Ubiquitin
based on PDB ID: 1ubq[16]
Artist: Minhazur Sarker

Garbage: it's all around us, even in our body! Ubiquitin is a special protein that functions to eliminate the proteins we do not need anymore. A link, via a covalent attachment, joins ubiquitin proteins together, and when 4 are strung together, they move the garbage protein to a proteasome, which runs the process of destruction.

[Note: One evening, the ubiquitin portrait was thrown out as trash by the custodial service. Evidently the protein was fully active, marking its own disposal.]

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