PDB NEWSLETTER

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Weekly PDB news is available on the Web at **http://www.rcsb.org/pdb/latest_news.html**

Links to this and previous PDB newsletters are available at **http://www.rcsb.org/pdb/newsletter.html**

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Snapshot: April 2, 2002

17,737 released atomic coordinate entries

Molecule Type

- 15,908 proteins, peptides, and viruses
- 1,063 nucleic acids
- 748 protein/nucleic acid complexes
- 18 carbohydrates

Experimental Technique

- 14,645 diffraction and other
- 6,968 structure factor files
- 2,713 NMR
- 1,277 NMR restraint files

Participating RCSB Members

SDSC: www.rcsb.org

Rutgers: rutgers.rcsb.org

NIST: nist.rcsb.org

E-mail: info@rcsb.org

FTP: ftp.rcsb.org

Message from the PDB

This newsletter highlights the new features (and quite a few structures) that have been added to the PDB Web site during the first quarter of 2002. In addition to these developments, the PDB has also been involved in a variety of outreach activities.

The PDB had an exhibit booth at the 46th Annual Meeting of the Biophysical Society, February 23-27, 2002, at the Moscone Convention Center in San Francisco, CA.

PDB Director Helen M. Berman was profiled in the Jan/Feb issue of *Bioinformatics World*. The article looks at Dr. Berman's career and the history of the PDB resource.

In the next few months, we are looking forward to seeing everyone at the American Crystallographic Association's Annual Meeting in San Antonio, Texas (May 25-30). The PDB will be exhibiting at Booth #413. On Friday, May 24, a PDB talk will be given as part of the International School of Crystallography Meeting in Erice, Italy. We look forward to seeing you at one of these events!

The PDB ✦

PDB exhibit at the Biophysical Society Meeting.

The Protein Data Bank (PDB) is the single worldwide repository for the processing and distribution of 3-D biological macromolecular structure data. The PDB is operated by Rutgers, the State University of New Jersey; the San Diego Supercomputer Center (SDSC) at the University of California, San Diego; and the National Institute of Standards and Technology (NIST) — three members of the Research Collaboratory for Structural Bioinformatics, a non-profit consortium dedicated to improving our understanding of biological systems.

MIRROR SITES

Cambridge Crystallographic Data Centre (UK): **http://pdb.ccdc.cam.ac.uk/**

National University of Singapore: **http://pdb.bic.nus.edu.sg/**

Osaka University (Japan): **http://pdb.protein.osaka-u.ac.jp/**

Universidade Federal de Minas Gerais (Brazil): **http://www.pdb.ufmg.br/**

Data Deposition and Processing

PDB Deposition Statistics

More than 800 structures were deposited to the PDB in the first quarter of the year 2002. Approximately 73% of all of the structures received during this period were deposited with a "hold until publication" release status; 11% were deposited with a specific hold date; and 15% were deposited with a "release immediately" status. 81% were the result of X-ray crystallographic experiments; 15% from NMR.

PDB Focus: Annotating Data Around the World

PDB data is processed by an international effort. ADIT deposition sites are located at the RCSB-Rutgers site (US) and at the Institute for Protein Research, Osaka University (Japan).

Structures deposited using ADIT are processed immediately and returned to the author. The files are fully processed and are released according to the release status provided by the author. Data are processed by staff from the RCSB (at Rutgers University in New Jersey and remotely at the Center for Complex Molecular Systems and Biomolecules in the Czech Republic) and from the Institute for Protein Research at Osaka University. The procedures used for processing these data are described in the PDB Data Processing and Annotation Procedures at
http://www.rcsb.org/pdb/info.html#File_Formats_and_Standards.

PDB around the world. Annotator Kyle Burkhardt (Rutgers; second from left) meets with annotators from the Institute for Protein Research, Osaka University, Japan (Yumiko Kengaku, Reiko Igarashi, and Takashi Kosada).

Structures are also deposited using AutoDep at the European Bioinformatics Institute (EBI) in the United Kingdom. Data deposited using AutoDep are processed by the EBI.

ADIT:
RCSB **http://pdb.rutgers.edu/adit/**
Osaka University **http://pdbdep.protein.osaka-u.ac.jp/adit/**

AutoDep:
EBI **http://autodep.ebi.ac.uk/**

Data Query, Reporting, and Access

Experimental Data Availability Included in Status Search Results

A search of unreleased structures now indicates if the structure factor or constraint file has been deposited, and when this file will be released. This feature was added to the primary PDB Web site and its mirrors after a period of testing on the beta web site. Feedback on this new feature may be sent to **info@rcsb.org**.

STING Millennium Suite Released on PDB Web Site

After a period of testing at the PDB beta test site, select components of STING Millennium Suite (SMS) are now available from the Structure Explorer pages of the primary PDB Web site and its mirrors. SMS, a set of Java-based tools for the simultaneous display of information about macromolecular structure and sequence, was developed by Dr. Goran Neshich of Embrapa-CNPTIA (Campinas, Brazil) and colleagues, in collaboration with Dr. Barry Honig's laboratory at Columbia University in New York City, NY. The SMS links from the PDB site are served by an SMS mirror that is being maintained at the San Diego Supercomputer Center.

The "Sequence Details" and "View Structure" sections of the Structure Explorer now link to two interactive structure and sequence SMS views for any PDB structure, which include options to access features such as a graphical display of amino acid contacts; these views require Chime and a Java-enabled Web browser. A simpler "Protein Dossier" view is also available from the "Sequence Details" section, offering a static graphical summary of sequence-and structure-based properties, such as relative entropy and temperature factors.

The "Geometry" section of the Structure Explorer now links to a Ramachandran plot for each PDB entry, also served from SMS, with options including the inter-connection of data in a dihedral angle plot with the 3-D structure of the molecule. This view also requires Java and Chime. SMS is also accessible from the "Other Sources" section of the Structure Explorer for each PDB entry, under the category of Visualization resources.

Further information about this suite of tools is available from the SMS home page at **http://mirrors.rcsb.org/SMS/**, and at **http://www.rcsb.org/pdb/help-results.html**. Comments may be sent to **info@rcsb.org**.

Phase Out of BNL FTP Archive

Since 1999, the Research Collaboratory for Structural Bioinformatics (RCSB) has maintained two distinct FTP sites: the RCSB Protein Data Bank (PDB) site at **ftp://ftp.rcsb.org/** (and its mirrors; see **http://www.rcsb.org/pdb/mirrors.html**), and the Brookhaven National Laboratory (BNL) PDB site at **ftp://bnlarchive.rcsb.org/**.

In order to conserve resources and avoid confusion arising through the existence of two distinct PDB FTP sites, the RCSB has phased out the BNL PDB archive as of March 1, 2002, as announced on October 19, 2001

(**http://www.rcsb.org/pdb/lists/pdb-l/200110/msg00024.html**). This decision was made after consultation with the PDB Advisory Committee and review by members of the PDB user community.

The files previously available only at **ftp://bnlarchive.rcsb.org/pub/resources/index/** are now available at **ftp://ftp.rcsb.org/pub/pdb/derived_data/index/**.

Current users of the BNL PDB archive are encouraged to consider the option of mirroring the RCSB FTP archive. The RCSB FTP archive can be found at **ftp://ftp.rcsb.org** and instructions for mirroring it can be found at **http://www.rcsb.org/pdb/ftpproc.final.html**.

A Perl script is provided to assist with conversion of existing BNL FTP directory structure to the RCSB FTP directory structure. Further information about the script is available at **ftp://ftp.rcsb.org/pub/pdb/software/bnl2rcsb.pl**.

Please send your questions or concerns, or requests for assistance regarding this change, to **info@rcsb.org**.

PDB Focus: Pretest New Query Features at the PDB Beta Web Site

New query features, such as the recent additions of the STING Millennium Suite to Structure Explorer pages and the ability to search on a subset of non-homologous structures, are always made available for public testing at the PDB Beta Web Site at **http://beta.rcsb.org/pdb/**.

New developments ready for testing are announced on these pages. After the new features have been reviewed by the public, they are incorporated into all of the PDB sites. Comments about features being tested at the PDB Beta Test Site should be sent to **notify@rcsb.org**. We thank all of you who have used this site and have provided feedback!

PDB Web Site Statistics

The PDB is available from several Web and FTP sites located around the world. The access statistics are given below for the main PDB Web site at **http://www.pdb.org/**.

Access Statistics for **www.pdb.org**

	DAILY AVERAGE			MONTHLY TOTALS		
MONTH	HITS	FILES	SITES	KBYTES	FILES	HITS
Mar 01	154,276	119,291	79,787	198,774,855	3,698,029	4,782,566
Feb 01	151,127	120,164	80,852	147,930,455	3,244,452	4,231,581
Jan 01	134,639	103,042	71,236	124,463,080	3,194,326	4,173,829

PDB Mirrors

SDSC/UCSD (US) **http://www.pdb.org/**
Rutgers (US) **http://rutgers.rcsb.org/**
NIST (US) **http://nist.rcsb.org/**
CCDC (UK) **http://pdb.ccdc.cam.ac.uk/**
National University of Singapore **http://pdb.bic.nus.edu.sg/**
Osaka University (Japan) **http://pdb.protein.osaka-u.ac.jp/**
Universidade Federal de Minas Gerais (Brazil) **http://www.pdb.ufmg.br/**

PDB Outreach

Data Uniformity Paper Published

The latest Nucleic Acids Research issue features a paper from the PDB entitled "The Protein Data Bank: unifying the archive", that describes the ongoing efforts of the data uniformity project which addresses inconsistencies in the archive.

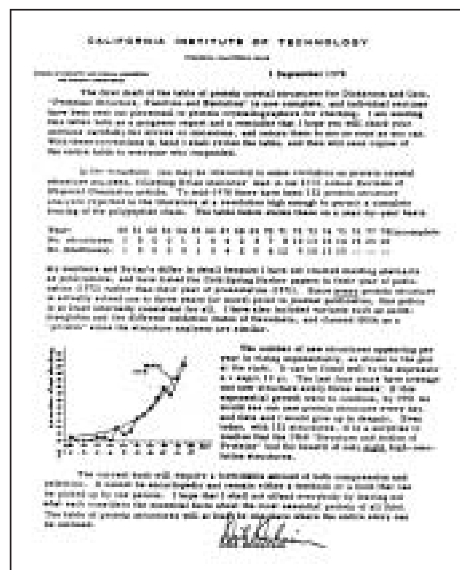
Updates on the Data Uniformity Project are posted at **http://www.rcsb.org/pdb/uniformity/index.html**.

Nucleic Acids Research, 2002, Vol. 30, No. 1 245-248 © 2002 Oxford University Press

"The Protein Data Bank: Unifying the Archive"
John Westbrook, Zukang Feng, Shri Jain, T. N. Bhat, Narmada Thanki, Veerasamy Ravichandran, Gary L. Gilliland, Wolfgang Bluhm, Helge Weissig, Douglas S. Greer, Philip E. Bourne and Helen M. Berman

Rate of PDB Holdings Growth Predicted in 1978?

In 1978, Richard E. Dickerson examined the number of available crystal structures. Based upon that number, he came upon an equation to describe the exponential growth for solved crystal structures.



The 1978 Dickerson letter.

In a letter describing a book he was working on with Irving Geis, Dickerson noted (and illustrated with a hand-drawn graph) that the number of new structures appeared to be following the exponential law, n = exp(0.19 y), where n is the number of new structures per year and y is the year number since 1960. This equation predicted that at the end of 2001, there would be 13,941 crystal structure entries available in the PDB (approximately 14,000 crystal structures were available in Feb., 2002). Using this equation, there should be 24,667 crystal structures in 2004.

A copy of the letter is available at **http://www.rcsb.org/pdb/dickerson_letter.html**.

Thanks to Arthur Arnone, who noticed that there were 57 structures more than Dickerson's equation predicted in March 2001. Predictions for the rate of NMR structures may be sent to **info@rcsb.org**.

"The Art of Science"—a PDB Art Gallery Exhibit

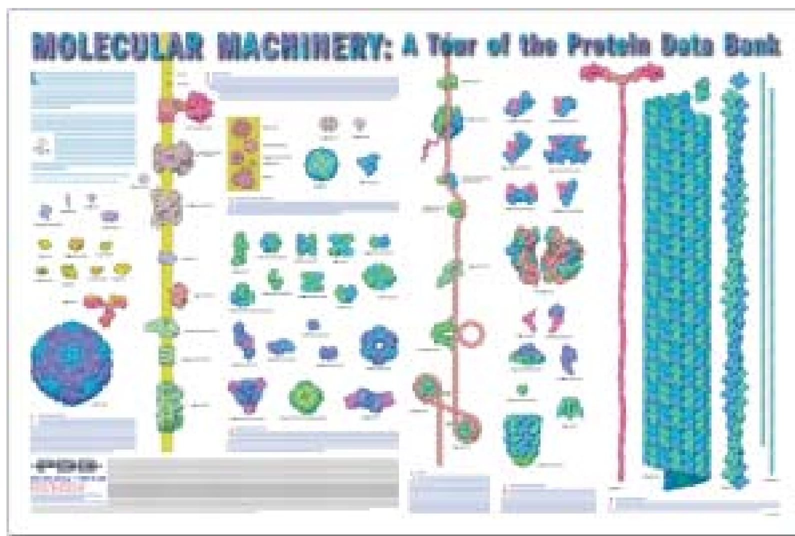
Images from the Protein Data Bank were presented as "The Art of Science", an art exhibit displayed at Rutgers University that focused on the beauty inherent in the three-dimensional structures of proteins. Various representations of proteins found in the PDB were highlighted, including large scale depictions of the images available from PDB Structure Explorer pages, images of collagen by Jordi Bella, and pictures from the PDB's Molecule of the Month series by David S. Goodsell. The exhibit, which was open from January 21 –February 9, was curated by Christine Zardecki.

Visitors admire images of proteins at "The Art of Science" exhibit.

"The Art of Science" exhibit turned out to be one of the more popular shows held at The Gallery, a space dedicated to art exhibits at Rutgers University. Many students, professors, and local educators viewed the exhibit during its run. Many commented on how they were surprised by how beautiful they found the images, and how interested they were in the scientific descriptions that accompanied the pictures. The exhibit was also the focus of several newspaper articles, including a story in The Star-Ledger and a front page article in The Bergen Record.

PDB Molecular Machinery Poster Released

The PDB is pleased to announce the release of a poster entitled, "Molecular Machinery: A Tour of the Protein Data Bank". This poster features illustrations of 75 select structures from the PDB, showing their relative sizes at a scale of three million to one, and generally describes their critical roles in the functions of living cells. Content for the poster was provided by David Goodsell of The Scripps Research Institute, with graphic design by Gail Bamber of the San Diego Supercomputer Center. Copies of this poster will be distributed at the ACA, ISMB, IUCr, and Protein Society conferences this summer.



PDB Molecules of the Quarter

Thrombin, Nitrogenase, and Bacteriorhodopsin

The Molecule of the Month series explores the functions and significance of selected biological macromolecules for a general audience. These features, written and illustrated by Dr. David S. Goodsell of the Scripps Research Institute, are available at **http://www.rcsb.org/pdb/molecules/molecule_list.html**:

Thrombin: In the Right Place at the Right Time

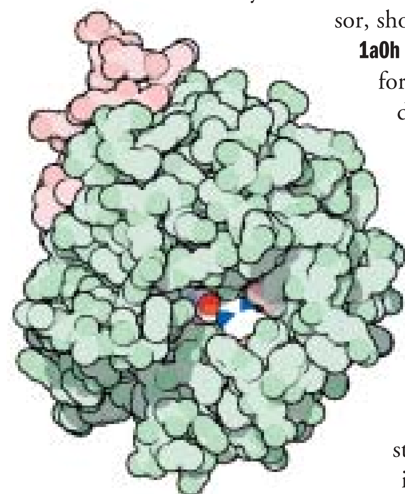
January, 2002—Oxygen and nutrients are delivered throughout our bodies through the watery transport system of the blood. Using a liquid delivery method poses two challenges. First, it leaves the entire body open to infection, since bacteria and viruses will be quickly distributed everywhere that the blood goes. The immune system, with antibodies as the first line of defense, fights this danger. Second, there is the constant danger of damage to the blood circulatory system. Blood is pumped throughout the body under pressure, and any small leak could lead to a rapid emptying of the entire system. Fortunately, the blood carries an emergency repair system: the blood clotting system. When we are cut or wounded, our blood builds a temporary dam to block the damage, giving the surrounding tissues time to build a more permanent repair.

Thrombin is at the center of this process of blood clotting. Blood clotting starts with molecules that sense that something is wrong. For instance, the protein tissue factor is found on the surfaces of cells that are not normally in contact with the blood. If tissue is cut, the blood flows out of the blood vessels and encounters tissue factor. Then, a cascade of signaling starts, beginning with a few tissue factor molecules and amplifying, like a pyramid scheme, into a response large enough to cure the entire problem. Tissue factor activates a few molecules of Factor VII. These then activate a lot of Factor X. And finally, these activate even more thrombin. Thrombin, when activated, then translates this signal into action. It clips a little piece off of the large protein fibrinogen, causing it to assemble into large stringy networks. These networks then trap lots of blood cells, forming the dark red scab that blocks the damage.

Thrombin is a serine protease: a protein-cutting enzyme that uses a serine amino acid to perform the cleavage. Other examples of serine proteases are trypsin and chymotrypsin, enzymes involved in digestion. Thrombin, however, is more specific than these gastrointestinal cleavage machines. It is designed to perform the specific cleavage needed to activate fibrinogen, without digesting all the other important proteins in the blood. The active site can

be seen in the structure of activated thrombin from PDB entry **1ppb**, at the base of a deep groove. A key serine amino acid is actived by a histidine here. An aspartate also helps in the activation.

Of course, blood clotting must be carefully regulated, otherwise the blood would be clotting in all of the wrong places. Errors in blood clotting have disastrous effects: improper blood clots in the heart can cause heart attacks and misplaced blood clots in the brain cause strokes. Thrombin is controlled in two ways. First, it is built as an inactive precursor, shown in part in PDB files **1a0h** and **2pf2**. The inactive form has several extra domains that are clipped off when the protein is activated. Calcium ions bind to specially modified glutamate amino acids. The strong positive charge on these ions tether the protein to the surfaces of blood vessels, so that thrombin stays put. Since thrombin is not free to spread, blood clots, once they start, will not spread everywhere. Only the thrombin right next to damage will be activated. Second, once thrombin is activated, as in PDB entry **1ppb**, it lasts only seconds, also limiting the clot to the area of damage.



Bode, W., Mayr, I., Baumann, U., Huber, R., Stone, S. R., Hofsteenge, J. (1989): The refined 1.9 A crystal structure of human alpha-thrombin: interaction with D-Phe-Pro-Arg chloromethylketone and significance of the Tyr-Pro-Pro-Trp insertion segment. EMBO J ***8**, p. 3467.*

Blood clots are not always wanted. For instance, many people take small doses of aspirin, under the direction of their doctors, to reduce the chance of the blood clots that cause heart attacks. Aspirin acts on the protein cyclooxygenase, which is important in another aspect of clot formation that uses small cell fragments called platelets. The rat poison warfarin, not commonly used these days, blocks the formation of the modified glutamate amino acids that hold calcium ions. The unfortunate rats then die because of uncontrolled blood clotting. Leeches, as you might expect, also detest blood clots, because it means the end to their meal. They make special proteins that block thrombin (or other enzymes), stopping the formation of the clot. One example, a protein called hirudin, is shown in PDB entry **2hgt**. This leech protein blocks the active site of thrombin perfectly.

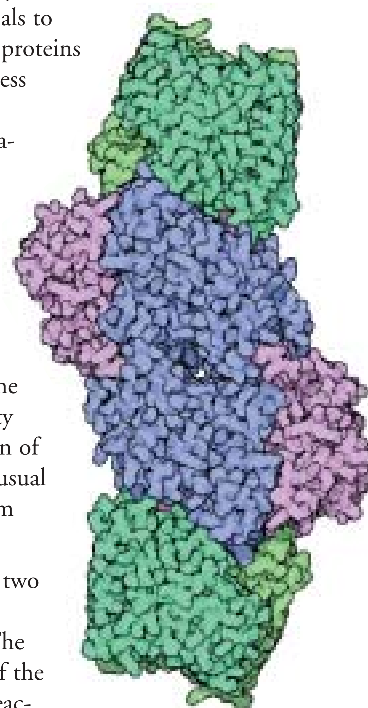
PDB entry **1mkx** is a perfect structure for exploring thrombin. It contains two molecules of the protein, one in inactive form (chain K) and one activated (chain H and L). In order to activate the protein, the protein strand must be cleaved between two segments on one side. Then, the two new ends separate and the whole protein relaxes into the active form. In the active form, the key catalytic serine amino acid changes position and points straight out into the active site, ready to perform the cleavage.

A list of all thrombin structures in the PDB as of January, 2002, is available at **http://www.rcsb.org/pdb/molecules/pdb25_report.html**. For additional information on thrombin, see **http://www.rcsb.org/pdb/molecules/pdb25_1.html**.

Nitrogenase: The Nitrogen-splitting Anvil

February, 2002—Nitrogen is needed by all living things to build proteins and nucleic acids. Nitrogen gas is very common on the earth, as it comprises just over 75% of the molecules in air. Nitrogen gas, however, is very stable and difficult to break apart into individual nitrogen atoms. Usable nitrogen, in the form of ammonia or nitrate salts, is scarce. Often, the growth of plants is limited by the amount of nitrogen available in the soil. Small amounts of usable forms of nitrogen are formed by lightning and the ultraviolet light from the sun. Significant amounts of nitrogen are fed to plants in the form of industrial fertilizers. But the lion's share of usable nitrogen is created by bacteria, using the enzyme nitrogenase.

Nitrogen-fixing bacteria have the ability to convert nitrogen gas into ammonia, which is easily combined with other raw materials to form the building blocks of proteins and nucleic acids. This process requires extreme measures, because nitrogen gas is so stable. The industrial process used to create ammonia requires high temperatures and pressures of 300 atmospheres, along with catalysts. In nitrogen-fixing bacteria, the enzyme nitrogenase drives the reaction with a large quantity of ATP, and uses a collection of metal ions, including an unusual molybdenum ion, to perform the reaction.



Schindelin, H., Kisker, C., Schlessman, J. L., Howard, J. B., Rees, D. C. (1997): Structure of ADP x AIF4(-)-stabilized nitrogenase complex and its implications for signal transduction. Nature ***387**, p. 370.*

Nitrogenase is composed of two components, such as those found in PDB entry **1n2c**. The MoFe protein contains all of the machinery to perform the reaction, but requires a steady source of electrons. The reaction requires the addition of six electrons for each nitrogen molecule that is split into two ammonia molecules. The Fe protein uses the breakage of ATP to pump these electrons into the MoFe protein. In the typical reaction, two molecules of ATP are consumed for each electron transferred. Nitrogenase also converts hydrogen ions to hydrogen gas at the same time (this might be an obligatory part of the nitrogen splitting

reaction, or it might be a simple side effect), thus consuming even more ATP in the process.

This is a large investment in energy, but well worth the effort if nitrogen is not available in the environment. Fortunately, nitrogen fixing bacteria are found throughout the world, and are often found in partnerships with plants. For instance, legumes build special nodules in their roots that provide a perfect home for the bacteria. The plants provide shelter and even a few essential nutrients, jealously guarding their guests, and the bacteria provide a steady supply of nitrogen.

At the heart of nitrogenase is an unusual complex of iron, sulfur and a molybdenum ion, which is thought to perform the nitrogen-fixing reaction. A string of cofactors feed electrons to this MoFe-cluster. Electrons start at a pair of ATP molecules (two at each end of the dimeric complex), flow inwards into the iron-sulfur cluster, then to the P-cluster, and finally to the MoFe-cluster. A homocitrate molecule helps to stabilize this unusual metal ion. The P-cluster is in the middle and the iron-sulfur cluster of the Fe protein is at the top. In spite of the detailed knowledge provided by the beautiful structures of nitrogenase, such as that found in PDB entry **1n2c**, the actual binding site for nitrogen gas is still a subject of controversy and intense study.

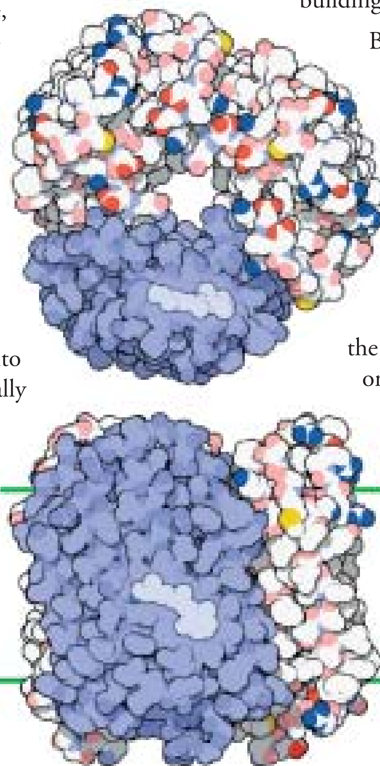
The metal clusters are the centerpiece of nitrogenase, and are the major attraction on any tour of the structures. PDB entry **1n2c** is a good place to start—it contains both the MoFe protein and two copies of the Fe protein dimer bound on either end. The metal ions can be easily displayed using a spacefilling representation, which reveals the iron-sulfur cluster, the P-cluster, and the FeMo-cluster arranged in a row. The ATP binding site is revealed in this structure by using an unusual analogue of ATP: an ADP molecule with an aluminum fluoride ion. Two of these molecules bind at each end, forming a stable but inactive complex with the Fe protein, essentially gluing the Fe protein to the FeMo protein so its structure can be solved.

A list of all nitrogenase structures in the PDB as of February, 2002, is available at **http://www.rcsb.org/pdb/molecules/pdb26_report.html**. For more information on nitrogenase, see **http://www.rcsb.org/pdb/molecules/pdb26_1.html**.

Bacteriorhodopsin: A Light-driven Pump

March, 2002—Sunlight powers the biological world. Through photosynthesis, plants capture sunlight and build sugars. These sugars then provide all of the starting materials for our growth and energy needs. As seen in the Molecule of Month last October, photosynthesis requires a complex collection of molecular antennas and photosystems. However, some bacteria have found a simpler solution to capturing sunlight.

Bacteriorhodopsin is a compact molecular machine that pumps protons across a membrane powered by green sunlight. It is built by halophilic (salt loving) bacteria, found in high-temperature brine pools. They use sunlight to pump protons outwards across their cell membranes, making the inside 10,000-fold more alkaline than the outside. These protons are then allowed to flow back inwards through another protein, ATP synthase, building much of the ATP that powers the cell.



Subramaniam, S., Henderson, R. (2000): Molecular Mechanism of Vectorial Proton Translocation by Bacteriorhodopsin. Nature ***406**, p. 653.*

Bacteriorhodopsin, as shown in PDB entry **1fbb**, is composed of three protein chains. It is found embedded in dense arrays in the membranes of the bacteria. At the heart of each protein chain is a molecule of retinal, which is bound deep inside the protein and connected through a lysine amino acid. Retinal contains a string of carbons that strongly absorb light. When a photon is absorbed, it causes a change in the conformation of the molecule. In bacteriorhodopsin, this is a change from a straight form to a bent form. This change in shape powers the pumping of protons.

The capturing of light is so useful that these salt-loving bacteria actually build four different types of rhodopsins. Bacteriorhodopsin is used to generate energy. Halorhodopsin, which may be seen in PDB entry **1e12**, is also a pump that funnels chloride ions instead of protons. It is in charge of keeping the internal concentration of chloride at high levels that match the salty conditions outside the cell. The other two rhodopsins are sensory rhodopsins, such as the ones in PDB entries **1h68** or **1jgj**. These rhodopsins sense bluish light and send signals to the cell to move, finding an area with more useful, greenish light. All four of these rhodopsins are built along similar lines, with a retinal molecule securely held inside a compact container of protein.

We also build several forms of rhodopsin and use them in our eyes for seeing light. As in bacteriorhodopsin, our rhodopsin also contains a molecule of retinal. Bacteriorhodopsin, as seen in PDB entry **1fbb**, can be compared with rhodopsin from cows, as seen in PDB entry **1f88**. Retinal is made in our bodies from retinol, or vitamin A, which is essential in the diet, since we cannot synthesize vitamin A on our own. When it absorbs a photon, the retinal in rhodopsin changes shape from bent to straight--just the opposite of retinal in bacteriorhodopsin! This change of shape then pushes the surrounding protein into a slightly different shape, which is sensed by proteins inside the cell. Then, the message is passed through a cascade of proteins, each sending the message to the next, finally launching a nerve signal to the brain. The process is so sensitive that the eye can sense as few as 5 photons.

Many structures of bacteriorhodopsin are available in the PDB, showing many of the steps in the process of absorbing light and pumping protons. Two snapshots can be found in PDB entries

1c3w and **1dze**. The structure found in PDB entry **1c3w** is in the ground state, before it has absorbed light. The retinal is in the straight trans form. The structure from PDB entry **1dze** shows the molecule after absorbing light. Notice that the retinal now has a bent cis shape. This new shape has changed the orientation of the nitrogen at the end of the retinal. It has also shifted the position of several protein amino acids that are along the pathway of proton transfer. In particular, notice the large shift of arginine 82 at the bottom. Researchers are working to discover how these changes in shape power the transfer of a proton from the top to the bottom, through the middle of bacteriorhodopsin and across the bacterial membrane.

A list of all bacteriorhodopsin structures in the PDB as of March, 2002 is available at **http://www.rcsb.org/pdb/molecules/pdb27_report.html**. For suggestions for additional reading about bacteriorhodopsin, see **http://www.rcsb.org/pdb/molecules/pdb27_1.html**.

PDB Job Listings

PDB career opportunities are posted at **http://www.rcsb.org/pdb/jobs.html**.

PDB Project Team Leaders

The overall operation of the PDB is managed by the PDB Project Team Leaders. Technical and scientific support are provided by the PDB Members.

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