

# 2014

International Year of  
Crystallography

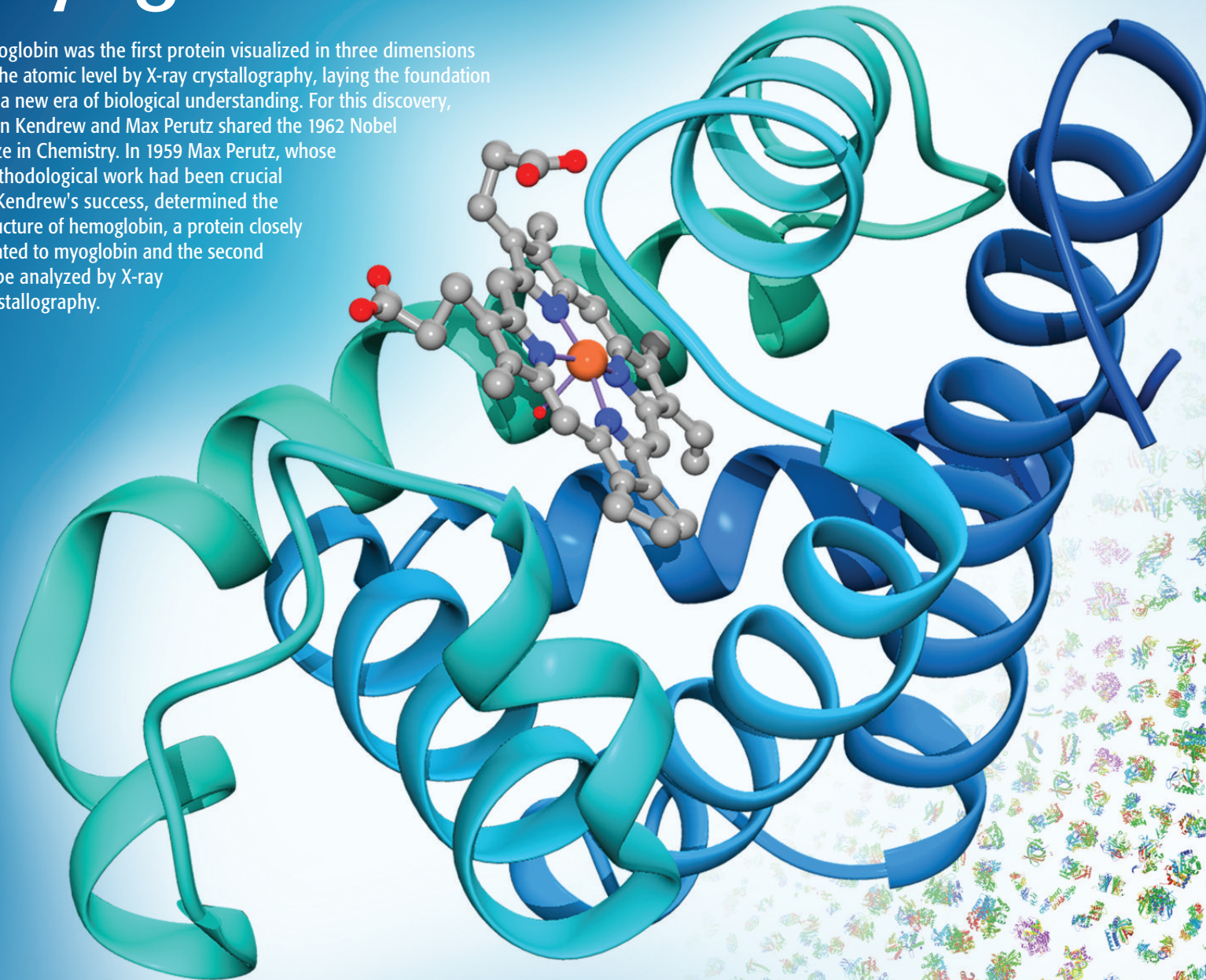


WORLDWIDE  
 **PDB**  
PROTEIN DATA BANK

Celebrating 

# Myoglobin

Myoglobin was the first protein visualized in three dimensions at the atomic level by X-ray crystallography, laying the foundation for a new era of biological understanding. For this discovery, John Kendrew and Max Perutz shared the 1962 Nobel Prize in Chemistry. In 1959 Max Perutz, whose methodological work had been crucial to Kendrew's success, determined the structure of hemoglobin, a protein closely related to myoglobin and the second to be analyzed by X-ray crystallography.

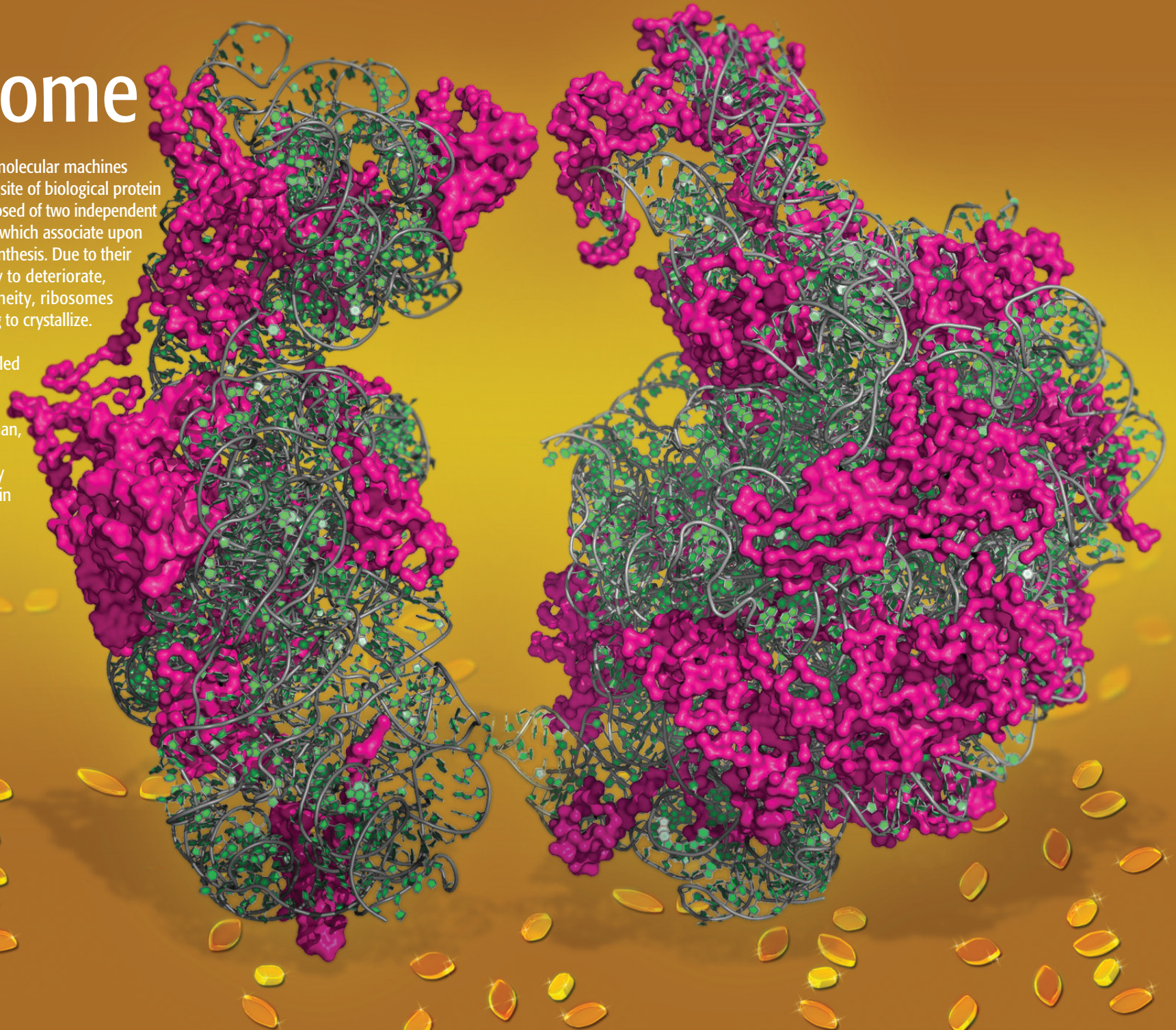




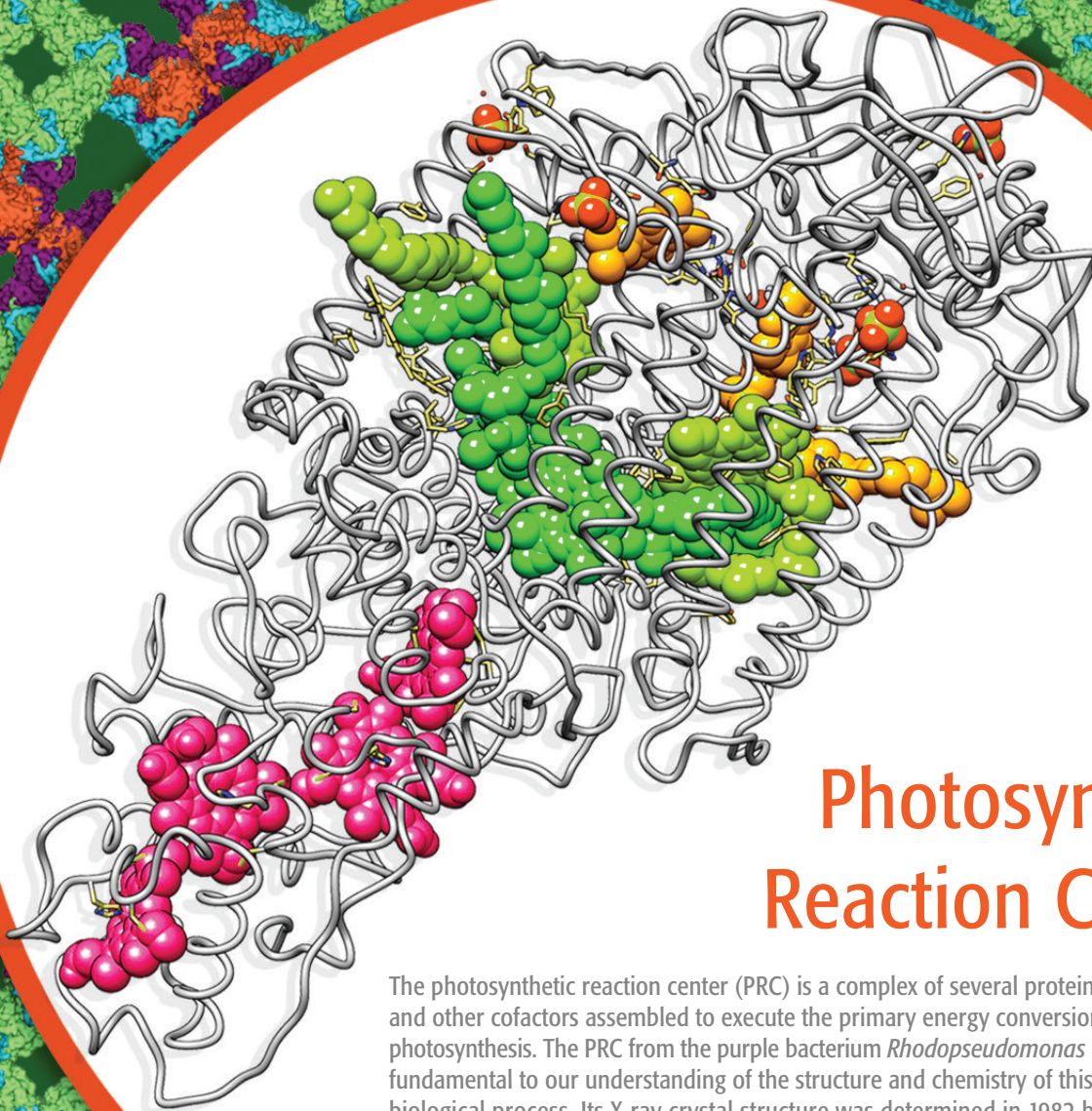
# Ribosome

Ribosomes are complex molecular machines that serve as the primary site of biological protein synthesis. They are composed of two independent subunits of unequal size, which associate upon initiation of protein biosynthesis. Due to their enormous size, tendency to deteriorate, and functional heterogeneity, ribosomes are extremely challenging to crystallize.

For determining the detailed structure and mechanism of the ribosome Venkatraman Ramakrishnan, Thomas A. Steitz and Ada E. Yonath were jointly awarded the Nobel Prize in Chemistry in 2009.





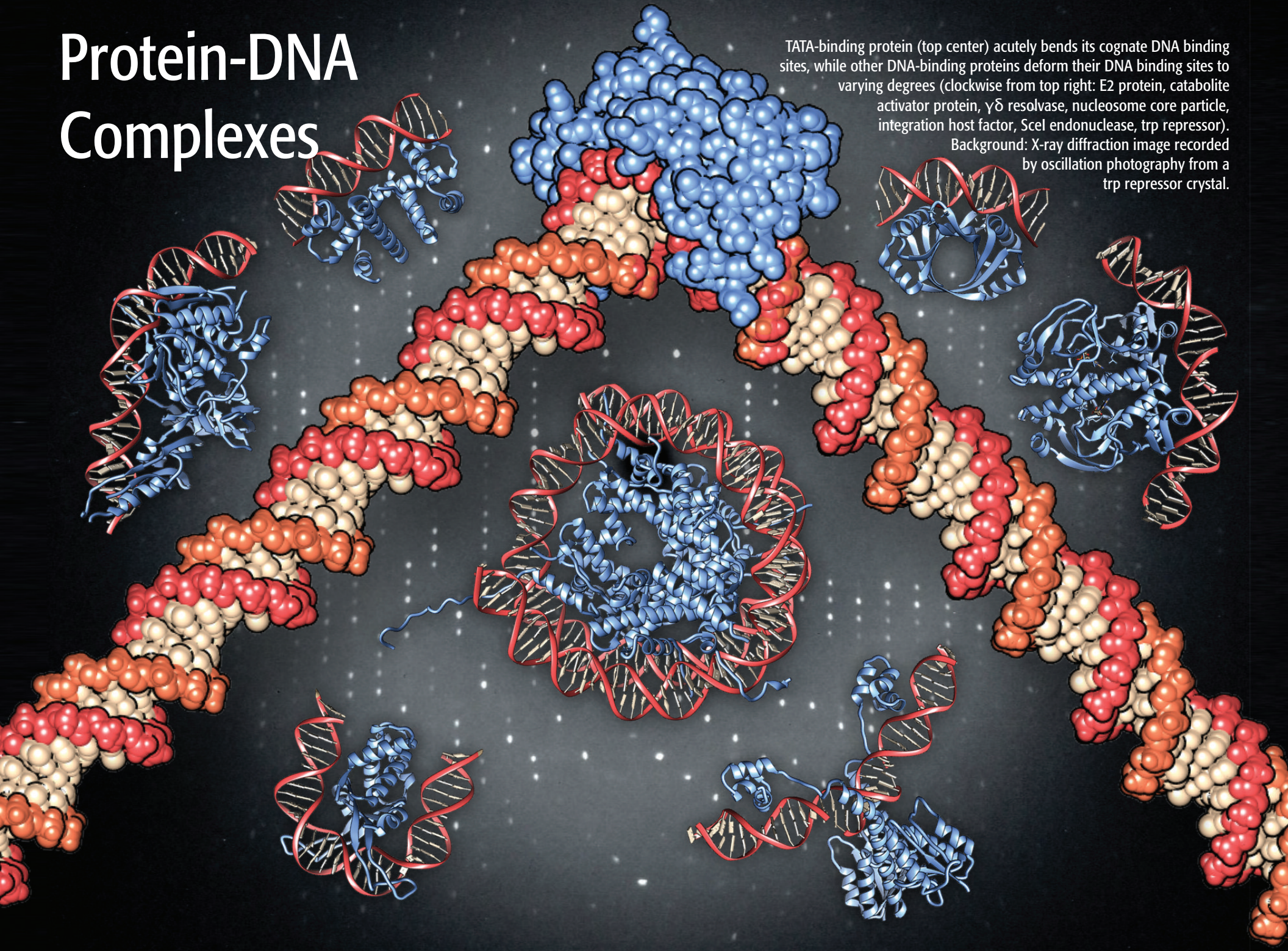


## Photosynthetic Reaction Center

The photosynthetic reaction center (PRC) is a complex of several proteins, chlorophyll, and other cofactors assembled to execute the primary energy conversion reactions of photosynthesis. The PRC from the purple bacterium *Rhodospseudomonas viridis* was fundamental to our understanding of the structure and chemistry of this critical biological process. Its X-ray crystal structure was determined in 1982 by Hartmut Michel, Johann Deisenhofer and Robert Huber, for which they shared the Nobel Prize in Chemistry in 1988. PRC represented the first structure of an integral membrane protein.



# Protein-DNA Complexes



TATA-binding protein (top center) acutely bends its cognate DNA binding sites, while other DNA-binding proteins deform their DNA binding sites to varying degrees (clockwise from top right: E2 protein, catabolite activator protein,  $\gamma\delta$  resolvase, nucleosome core particle, integration host factor, SclI endonuclease, trp repressor).

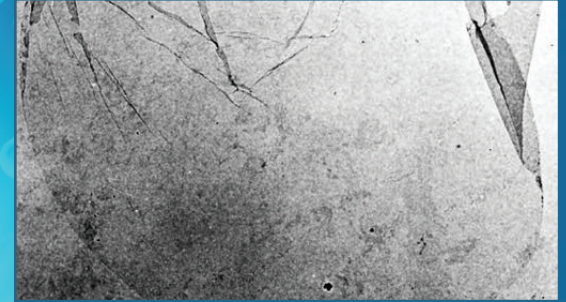
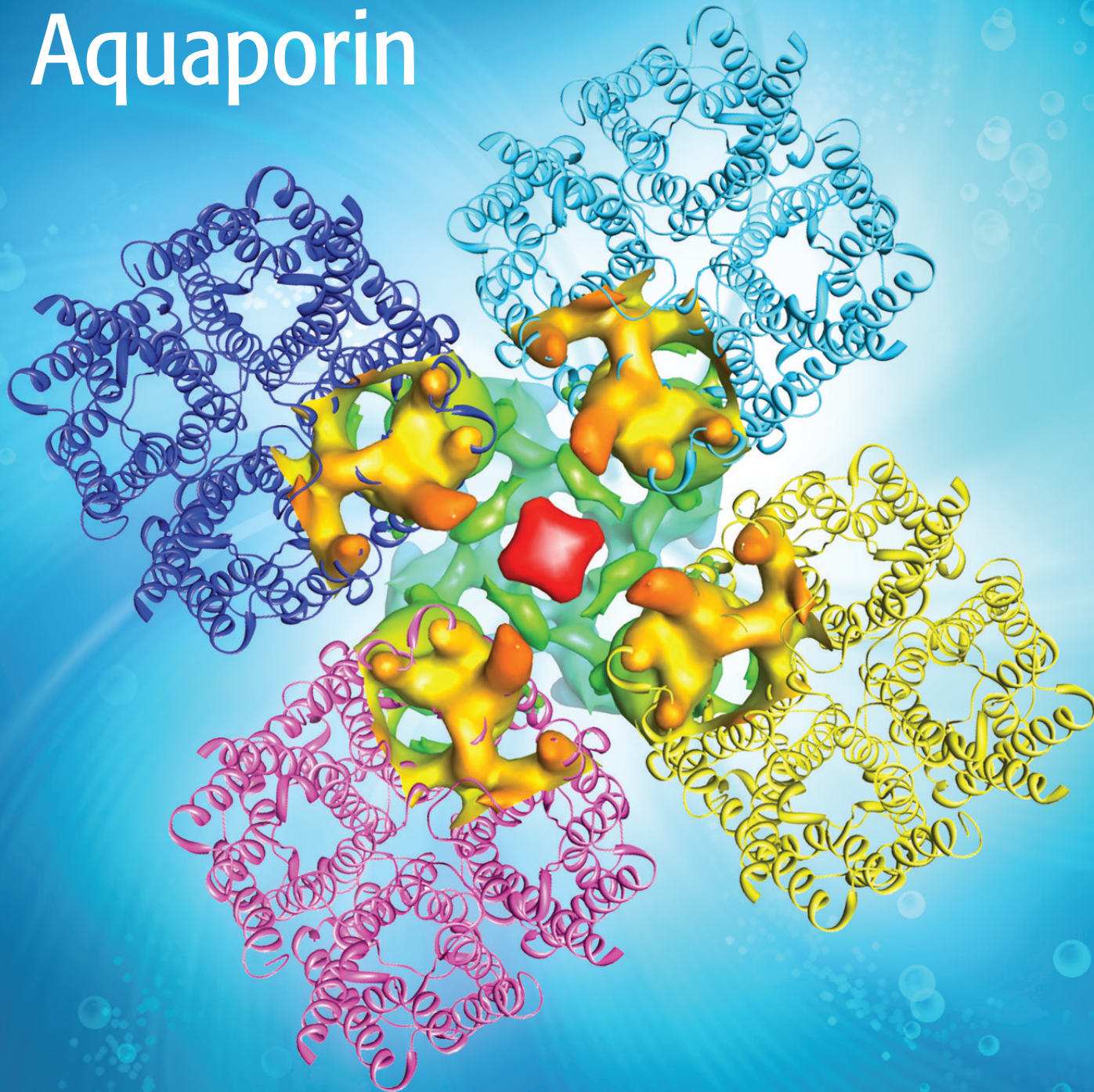
Background: X-ray diffraction image recorded by oscillation photography from a trp repressor crystal.



# April 2014

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# Aquaporin

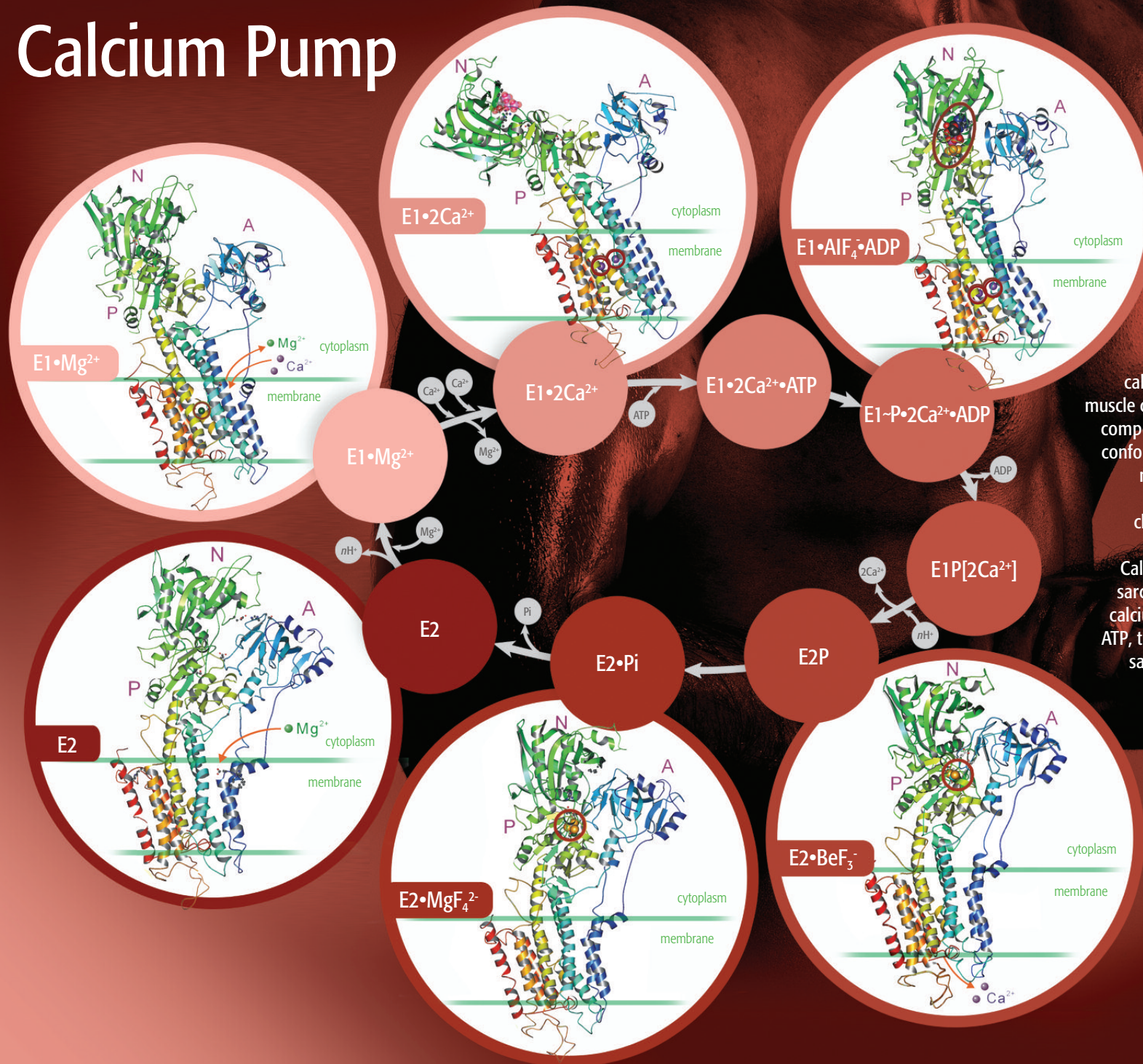


Two-dimensional crystals consist of a single layer of molecules arranged in an ordered array. They are particularly useful for studying proteins embedded in lipid bilayer membranes, like those found in eukaryotic and bacterial cell walls. Electron diffraction, rather than X-ray diffraction, is the most effective tool for studying such systems at the atomic level. Yoshinori Fujiyoshi has designed a series of cryo-electron microscopes for this purpose and determined several important structures, including aquaporin 4, a channel that selectively conducts water across the cell wall.

# May 2014

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# Calcium Pump



To activate muscle contraction, nerve excitation releases a flood of calcium ions from a special intracellular compartment, known as the sarcoplasmic reticulum. The calcium rapidly spreads throughout the muscle cell and binds to troponin, an integral component of thin filaments, producing a conformational change that allows myosin motors to climb up the thin filaments. Trillions of myosin motors continue climbing until the calcium is removed.

Calcium pumps in the membrane of the sarcoplasmic reticulum stop this frenetic calcium-induced contraction. Powered by ATP, they pump calcium ions back into the sarcoplasmic reticulum, which reduces the calcium level inside muscle cells leading to relaxation.

Crystallographic studies by Chikashi Toyoshima and colleagues inspired the structural model of the calcium ATPase pump cycle shown here.

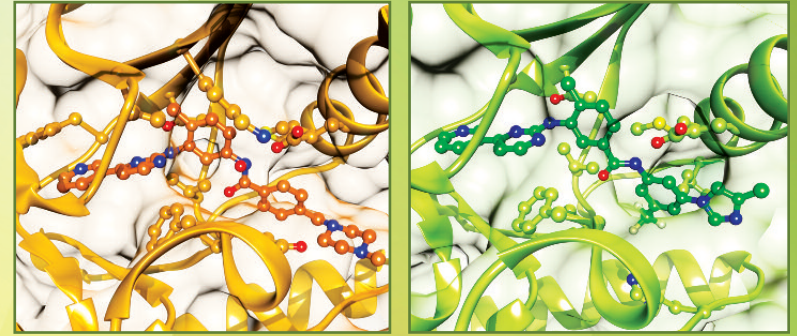
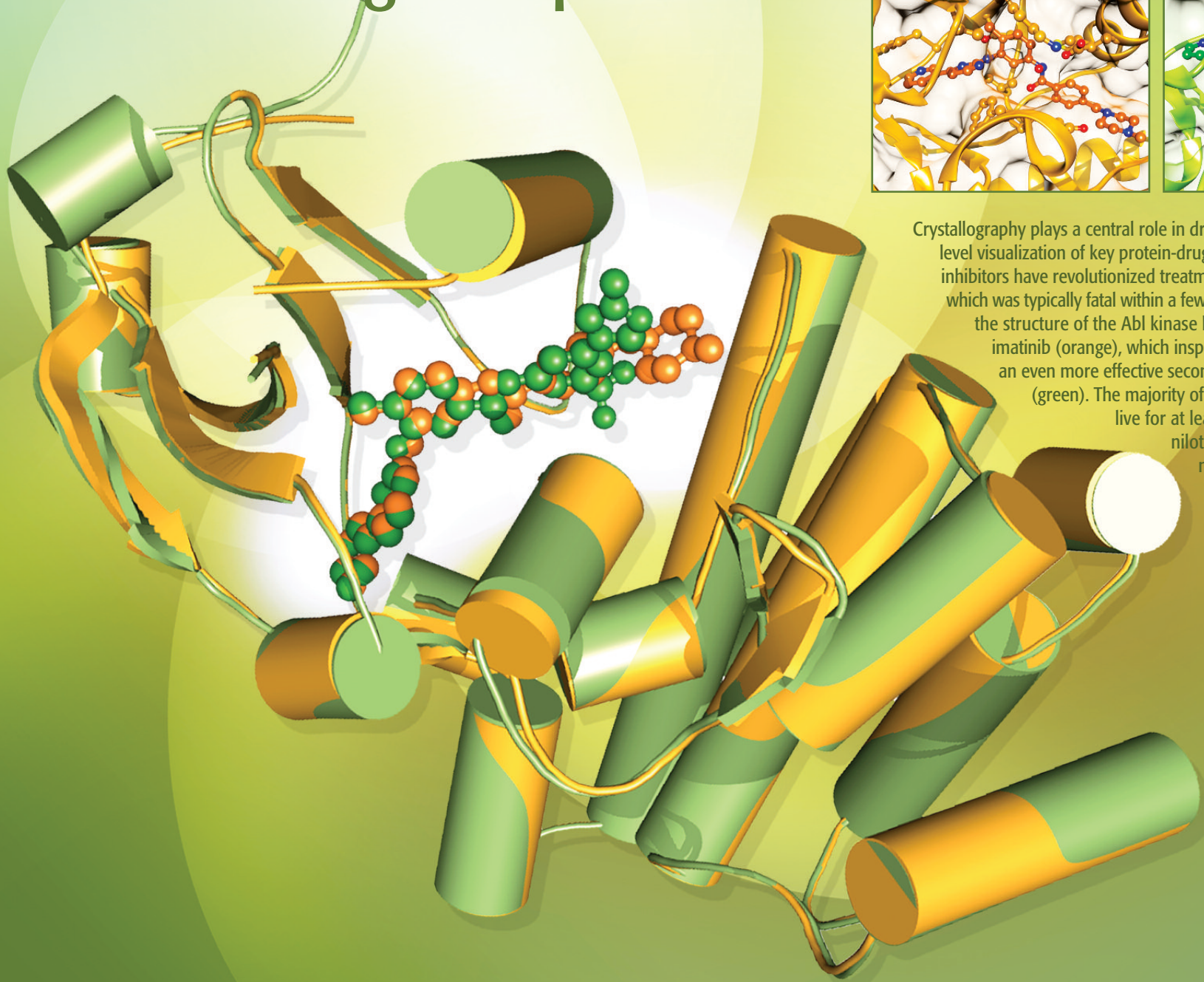
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# Protein-Drug Complexes



Crystallography plays a central role in drug discovery by providing atomic level visualization of key protein-drug interactions. Abl tyrosine-kinase inhibitors have revolutionized treatment of chronic myeloid leukemia, which was typically fatal within a few years of diagnosis. Shown here is the structure of the Abl kinase bound to a first-generation drug, imatinib (orange), which inspired medicinal chemists to design an even more effective second-generation treatment, nilotinib (green). The majority of patients treated with these drugs live for at least a decade. While imatinib and nilotinib are very similar in structure, nilotinib is less vulnerable to the emergence of drug resistance, as it makes a better fit to the enzyme active site.

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# Tobacco Mosaic Virus

Tobacco mosaic virus (TMV), the first virus to be discovered, was purified by Wendell Stanley via crystallization. He demonstrated that the virus is primarily composed of protein. Others showed that TMV contains a single-stranded RNA genome. Prominent structural biologists (including J. D. Bernal, Rosalind Franklin, Ken Holmes, Aaron Klug, Don Caspar, and Gerald Stubbs) used X-ray diffraction and electron microscopy to study TMV's 3D structure. The RNA strand (purple) is enveloped by a protective coat of capsid proteins (pink) arranged in a cylinder. Stanley and John Northrop shared the 1946 Nobel Prize in Chemistry "for their preparation of enzymes and virus proteins in a pure form."

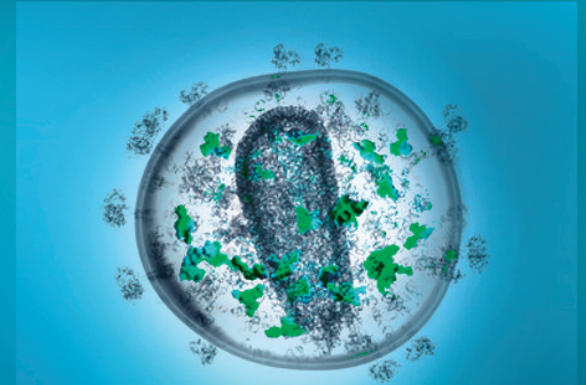
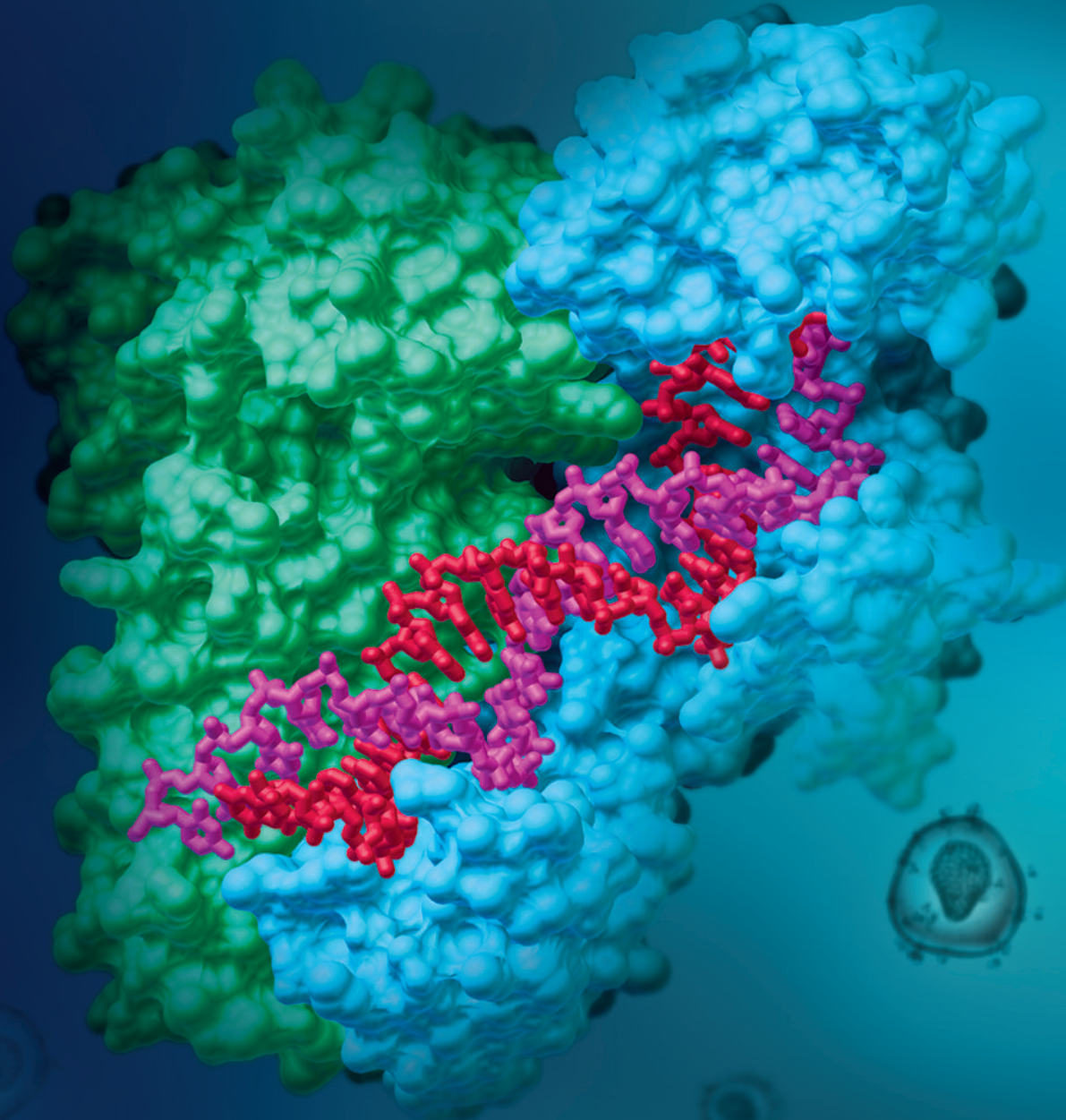
Detail shows Rosalind Franklin and Aaron Klug's TMV model, sculpted by John Ernest for the 1958 Brussels World Exhibition International Science Pavilion.







# Reverse Transcriptase



HIV (human immunodeficiency virus), the cause of Acquired Immune Deficiency Syndrome or AIDS, is composed of two RNA strands, 15 distinct viral proteins, and a few proteins derived from the last host cell it infected, all surrounded by a lipid bilayer membrane. Together, these molecules allow the virus to infect cells of the immune system, thereby disabling the cells and forcing them to build new copies of the virus.

Reverse transcriptase, highlighted in the image above and to the left, makes a DNA copy of the HIV RNA genome. The large image shows the enzyme assembling a DNA strand (magenta) from the viral RNA (red). Thereafter, the same enzyme destroys the original viral RNA as it builds a matching second DNA strand. The new double-stranded DNA can then be used to make both viral proteins and viral RNAs, which assemble to form new viruses.

One component of the multidrug regimen currently used to fight HIV infection blocks the action of reverse transcriptase.

# September 2014

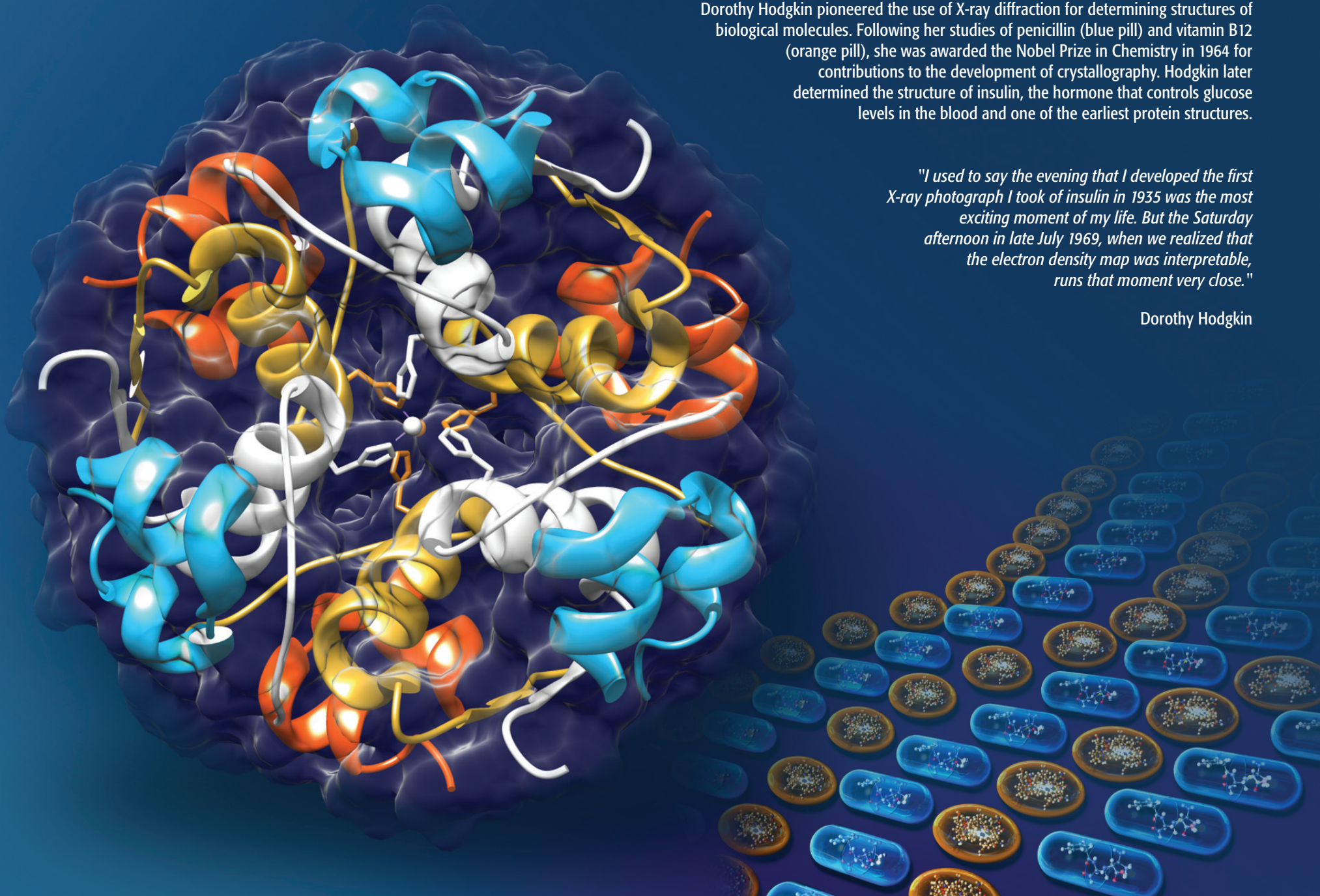
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# Insulin

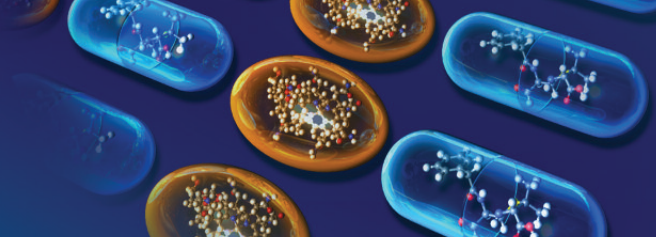
Dorothy Hodgkin pioneered the use of X-ray diffraction for determining structures of biological molecules. Following her studies of penicillin (blue pill) and vitamin B12 (orange pill), she was awarded the Nobel Prize in Chemistry in 1964 for contributions to the development of crystallography. Hodgkin later determined the structure of insulin, the hormone that controls glucose levels in the blood and one of the earliest protein structures.

*"I used to say the evening that I developed the first X-ray photograph I took of insulin in 1935 was the most exciting moment of my life. But the Saturday afternoon in late July 1969, when we realized that the electron density map was interpretable, runs that moment very close."*

Dorothy Hodgkin

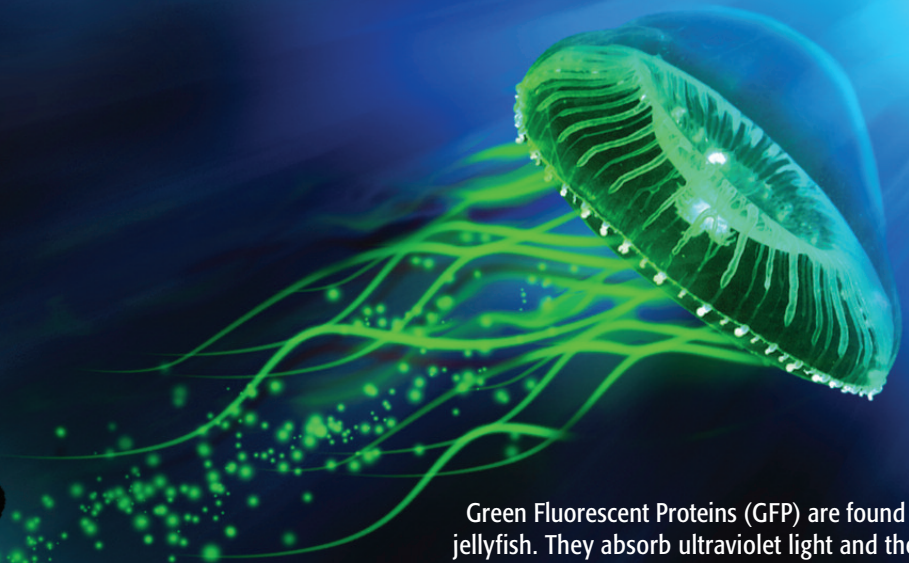
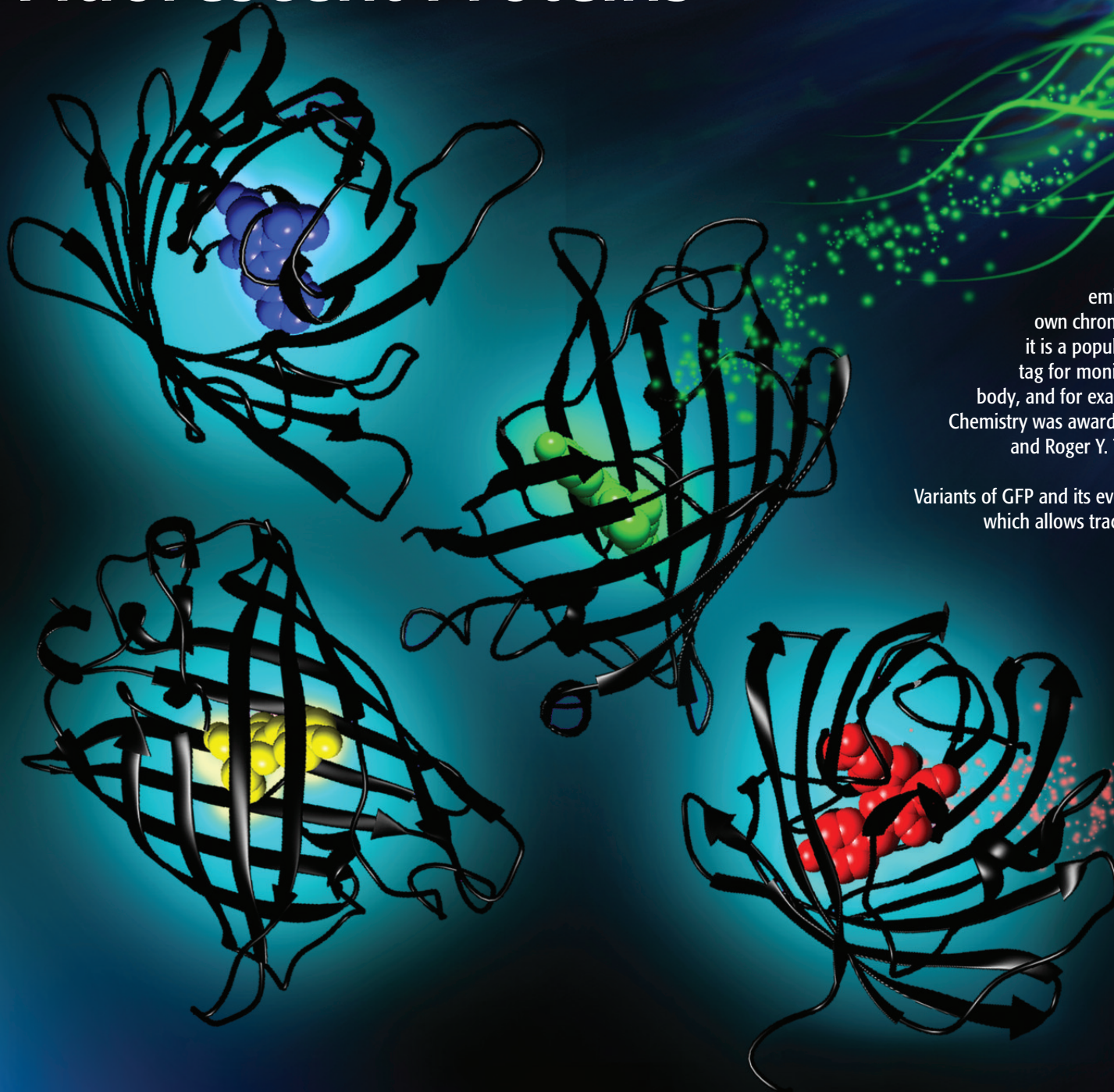


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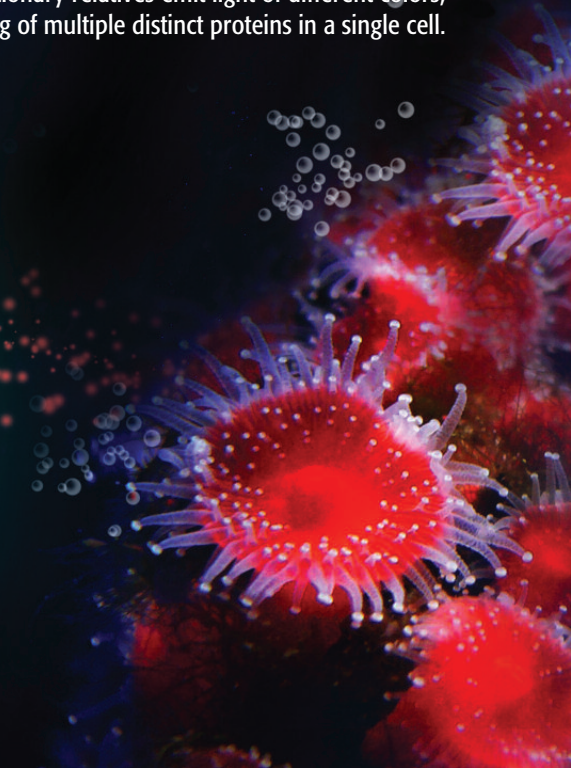
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# Fluorescent Proteins



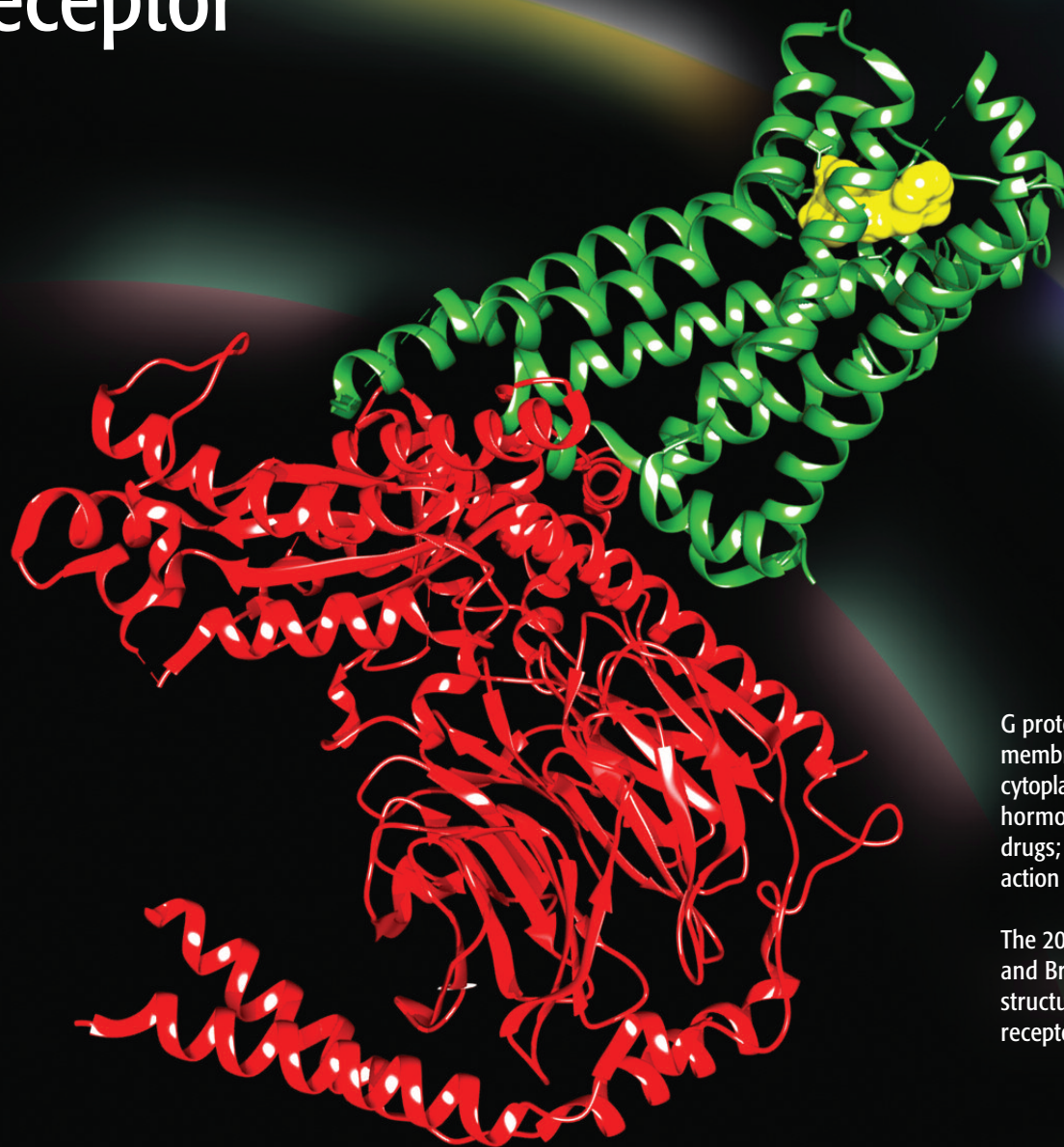
Green Fluorescent Proteins (GFP) are found in jellyfish. They absorb ultraviolet light and then emit lower-energy green light. Since GFP creates its own chromophore, the chemical group that produces color, it is a popular tool for genetic engineering. GFP is used as a tag for monitoring individual proteins in cells or even in the body, and for examining protein stability. The 2008 Nobel Prize in Chemistry was awarded jointly to Osamu Shimomura, Martin Chalfie, and Roger Y. Tsien for the discovery and development of GFP.

Variants of GFP and its evolutionary relatives emit light of different colors, which allows tracking of multiple distinct proteins in a single cell.





# G Protein-Coupled Receptor



G protein-coupled receptors (GPCRs) form the largest family of human integral membrane proteins. They transmit cellular signals from outside the cell to the cytoplasm and eventually the nucleus. They respond variously to neurotransmitters, hormones, and light as shown here. GPCRs represent important targets for drugs; more than 50% of approved drugs work by modulating the action of one or more GPCRs.

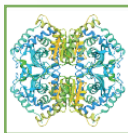
The 2012 Nobel Prize in Chemistry was awarded jointly to Robert J. Lefkowitz and Brian K. Kobilka for studies of GPCRs. The PDB holds many GPCR structures, including Kobilka's groundbreaking structure of the  $\beta_2$  adrenergic receptor bound to a G protein heterotrimer shown to the left.



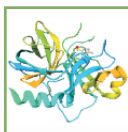


# References and Acknowledgements

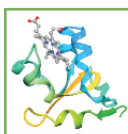
## Front Cover:



**PDB ID: 6ldh** C. Abad-Zapatero, J. P. Griffith, J. L. Sussman, M. G. Rossmann. (1987) Refined crystal structure of dogfish M4 apo-lactate dehydrogenase. *J.Mol.Biol.* **198**: 445-467.



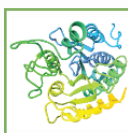
**PDB ID: 2cha** J. J. Birkoft, D. M. Blow. (1972). Structure of crystalline alpha-chymotrypsin. V. The atomic structure of tosyl-alpha-chymotrypsin at 2 Å resolution. *J.Mol.Biol.* **68**: 187-240.



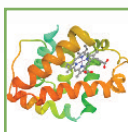
**PDB ID: 1cyo** R. C. Durley, F. S. Mathews. (1996) Refinement and structural analysis of bovine cytochrome b5 at 1.5 Å resolution. *Acta Crystallogr., Sect.D* **52**: 65-76.



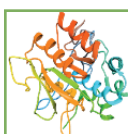
**PDB ID: 4pti** M. Marquart, J. Walter, J. Deisenhofer, W. Bode, R. Huber. (1983) The geometry of the reactive site and of the peptide groups in trypsin, trypsinogen and its complexes with inhibitors *Acta Crystallogr., Sect.B* **39**: 480-490.



**PDB ID: 3cpa** D. W. Christianson, W. N. Lipscomb. (1986) X-ray crystallographic investigation of substrate binding to carboxypeptidase A at subzero temperature. *Proc.Natl.Acad.Sci.USA* **83**: 7568-7572

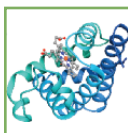


**PDB ID: 2lhb** R. B. Honzatko, W. A. Hendrickson, W. E. Love. (1985) Refinement of a molecular model for lamprey hemoglobin from *Petromyzon marinus*. *J.Mol.Biol.* **184**: 147-164.



**PDB ID: 1sbt** R. A. Alden, J. J. Birkoft, J. Kraut, J. D. Robertus, C.S. Wright. (1971). Atomic coordinates for subtilisin BPN' (or Novo). *Biochem.Biophys.Res. Commun.* **45**: 337-344.

## January: Myoglobin



**PDB ID: 1mbn** J. C. Kendrew, G. Bodo, H. M. Dintzis, R. G. Parrish, H. Wyckoff, D. C. Phillips. (1958) A three-dimensional model of the myoglobin molecule obtained by X-ray analysis. *Nature* **181**: 662-666.

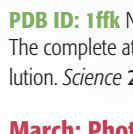
## February: Ribosome



**PDB ID: 1fjg** A. P. Carter, W. M. Clemons, D. E. Brodersen, R. J. Morgan-Warren, B. T. Wimberly, V. Ramakrishnan. (2000) Functional insights from the structure of the 30S ribosomal subunit and its interactions with antibiotics. *Nature* **407**: 340-348.

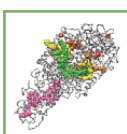


**PDB ID: 1fka** F. Schluenzen, A. Tocilj, R. Zarivach, J. Harms, M. Gluehmann, D. Janell, A. Bashan, H. Bartels, I. Agmon, F. Franceschi, A. Yonath. (2000) Structure of functionally activated small ribosomal subunit at 3.3 Å resolution. *Cell* **102**: 615-623.



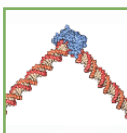
**PDB ID: 1ffk** N. Ban, P. Nissen, J. Hansen, P. B. Moore, T. A. Steitz. (2000) The complete atomic structure of the large ribosomal subunit at a 2.4 Å resolution. *Science* **289**: 905-920.

## March: Photosynthetic Reaction Center



**PDB ID: 1prc** J. Deisenhofer, O. Epp, I. Sinning, H. Michel. (1995) Crystallographic refinement at 2.3 Å resolution and refined model of the photosynthetic reaction centre from *Rhodospseudomonas viridis*. *J.Mol.Biol.* **246**: 429-457.

## April: Protein-DNA Complexes



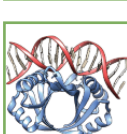
**PDB ID: 1vtl** J. L. Kim, D. B. Nikolov, S. K. Burley. (1993) Co-crystal structure of TBP recognizing the minor groove of a TATA element. *Nature* **365**: 520-527.



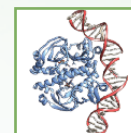
**PDB ID: 1lws** C. M. Moure, F. S. Gimble, F. A. Quijcho. (2002) Crystal structure of the intein homing endonuclease PI-SceI bound to its recognition sequence *Nat.Struct.Biol.* **9**: 764-770.



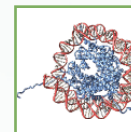
**PDB ID: 1tro** Z. Otwinowski, R. W. Schevitz, R.-G. Zhang, C. L. Lawson, A. Joachimiak, R. Q. Marmorstein, B. F. Luisi, P. B. Sigler. (1988) Crystal structure of trp repressor/operator complex at atomic resolution *Nature* **335**: 321-329.



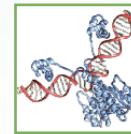
**PDB ID: 2bop** R. S. Hegde, S. R. Grossman, L. A. Laimins, P. B. Sigler. (1992) Crystal structure at 1.7 Å of the bovine papillomavirus-1 E2 DNA-binding domain bound to its DNA target *Nature* **359**: 505-512.



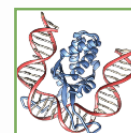
**PDB ID: 1j59** G. Parkinson, C. Wilson, A. Gunasekera, Y. W. Ebricht, R. E. Ebricht, H.M. Berman. (1996) Structure of the CAP-DNA complex at 2.5 Å resolution: a complete picture of the protein-DNA interface *J.Mol.Biol.* **260**: 395-408.



**PDB ID: 1aoi** K. Luger, A. W. Mader, R. K. Richmond, D. F. Sargent, T. J. Richmond. (1997) Crystal structure of the nucleosome core particle at 2.8 Å resolution *Nature* **389**: 251-260.

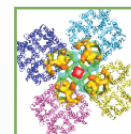


**PDB ID: 1gdt** W. Yang, T. A. Steitz. (1995) Crystal structure of the site-specific recombinase gamma delta resolvase complexed with a 34 bp cleavage site *Cell* **82**: 193-207.



**PDB ID: 2np2** K. W. Mouw, P. A. Rice. (2007) Shaping the *Borrelia burgdorferi* genome: crystal structure and binding properties of the DNA-bending protein Hbb *Mol.Microbiol.* **63**: 1319-1330.

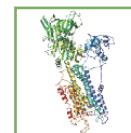
## May: Aquaporin



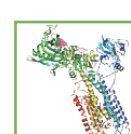
**PDB ID: 3iyz** T. Mitsuma, K. Tani, Y. Hiroaki, A. Kamegawa, H. Suzuki, H. Hibino, Y. Kurachi, Y. Fujiyoshi. (2010) Influence of the cytoplasmic domains of aquaporin-4 on water conduction and array formation *J.Mol.Biol.* **402**: 669-681

Photos courtesy of Professor Yoshinori Fujiyoshi (Nagoya University)  
Molecular image courtesy of Dr. Hirofumi Suzuki (Osaka University)

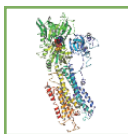
## June: Calcium Pump



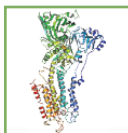
**PDB ID: 3w5a** C. Toyoshima, S. Iwasawa, H. Ogawa, A. Hirata, J. Tsueda, G. Inesi. (2013) Crystal structures of the calcium pump and sarcolipin in the Mg<sup>2+</sup>-bound E1 state. *Nature* **495**: 260-264.



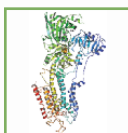
**PDB ID: 1su4** C. Toyoshima, M. Nakasako, H. Nomura, H. Ogawa. (2000) Crystal structure of the calcium pump of sarcoplasmic reticulum at 2.6 Å resolution. *Nature* **405**: 647-655.



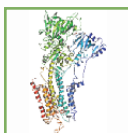
**PDB ID: 2zbd** C. Toyoshima, H. Nomura, T. Tsuda. (2004) Luminal gating mechanism revealed in calcium pump crystal structures with phosphate analogues. *Nature* **432**: 361-368.



**PDB ID: 2zbe** C. Toyoshima, Y. Norimatsu, S. Iwasawa, T. Tsuda, H. Ogawa. (2007) How processing of aspartylphosphate is coupled to luminal gating of the ion pathway in the calcium pump. *Proc.Natl.Acad.Sci.USA* **104**: 19831-19836.



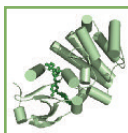
**PDB ID: 1wpg** C. Toyoshima, H. Nomura, T. Tsuda. (2004) Luminal gating mechanism revealed in calcium pump crystal structures with phosphate analogues. *Nature* **432**: 361-368.



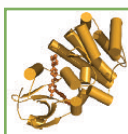
**PDB ID: 3w5c** C. Toyoshima, S. Iwasawa, H. Ogawa, A. Hirata, J. Tsueda, G. Inesi. (2013) Crystal structures of the calcium pump and sarcolipin in the Mg<sup>2+</sup>-bound E1 state. *Nature* **495**: 260-264.

Molecular images courtesy of Dr. Ryuta Kanai (University of Tokyo)  
Background photo courtesy of zcool.com.cn

## July: Protein-Drug Complexes



**PDB ID: 3cs9** E. Weisberg, P. W. Manley, W. Breitenstein, J. Bruggen, S. W. Cowan-Jacob, A. Ray, B. Huntly, D. Fabbro, G. Fendrich, E. Hall-Meyers, A. L. Kung, J. Mestan, G. Q. Daley, L. Callahan, L. Catley, C. Cavazza, M. Azam, D. Neuberg, R. D. Wright, D. G. Gilliland, J. D. Griffin. (2005) Characterization of AMN107, a selective inhibitor of native and mutant Bcr-Abl. *Cancer Cell* **7**: 129-141.



**PDB ID: 2hyy** S. W. Cowan-Jacob, G. Fendrich, A. Floer-sheimer, P. Furet, J. Liebetanz, G. Rummel, P. Rheinberger, M. Centeleghe, D. Fabbro, P. W. Manley. (2007) Structural biology contributions to the discovery of drugs to treat chronic myelogenous leukaemia. *Acta Crystallog., Sect. D* **63**: 80-93.

**PDB ID 1iep** B. Nagar, W. Bornmann, P. Pellicena, T. Schindler, D. R. Veach, W. T. Miller, B. Clarkson, J. Kuriyan. (2002) Crystal structures of the kinase domain of c-Abl in complex with the small molecule inhibitors PD173955 and imatinib (STI-571). *Cancer Res.* **62**: 4236-4243.

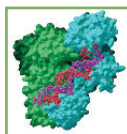
## August: Tobacco Mosaic Virus



**PDB ID: 2tmv** K. Namba, R. Pattanayek, G. Stubbs. (1989) Visualization of protein-nucleic acid interactions in a virus. Refined structure of intact tobacco mosaic virus at 2.9 Å resolution by X-ray fiber diffraction. *J.Mol.Biol.* **208**: 307-325.

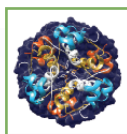
Inset image courtesy of MRC Laboratory of Molecular Biology  
Background photo courtesy of Darren Lewis (publicdomainpictures.net)

## September: Reverse Transcriptase



**PDB ID: 1hys** S. G. Sarafianos, K. Das, C. Tantillo, A. D. Clark, Jr., J. Ding, J. M. Whitcomb, P. L. Boyer, S. H. Hughes, E. Arnold. (2001) Crystal structure of HIV-1 reverse transcriptase in complex with a polypurine tract RNA:DNA. *EMBO J.* **20**: 1449-1461.

## October: Insulin



**PDB ID: 4ins** E. N. Baker, T. L. Blundell, J. F. Cutfield, S. M. Cutfield, E. J. Dodson, G. G. Dodson, D. M. Hodgkin, R. E. Hubbard, N. W. Isaacs, C. D. Reynolds, K. Sakabe, N. Sakabe, N. M. Vijayan. (1988) The structure of 2Zn pig insulin crystals at 1.5 Å resolution. *Philos.Trans.R.Soc.Lond.B.Biol.Sci.* **319**: 369-456.

## November: Fluorescent Proteins



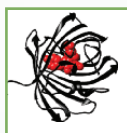
**PDB ID: 1ema** M. Ormo, A. B. Cubitt, K. Kallio, L. A. Gross, R. Y. Tsien, S. J. Remington. (1996) Crystal structure of the *Aequorea victoria* green fluorescent protein. *Science* **273**: 1392-1395.



**PDB ID: 1bfp** R. M. Wachter, B. A. King, R. Heim, K. Kallio, R. Y. Tsien, S. G. Boxer, S. J. Remington. (1997) Crystal structure and photodynamic behavior of the blue emission variant Y66H/Y145F of green fluorescent protein. *Biochemistry* **36**: 9759-9765.



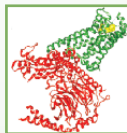
**PDB ID: 1yfp** R. M. Wachter, M. A. Elsliger, K. Kallio, G. T. Hanson, S. J. Remington. (1998) Structural basis of spectral shifts in the yellow-emission variants of green fluorescent protein. *Structure* **6**: 1267-1277.



**PDB ID: 1g7k** D. Yarbrough, R. M. Wachter, K. Kallio, M. V. Matz, S. J. Remington. (2001) Refined crystal structure of DsRed, a red fluorescent protein from coral, at 2.0-Å resolution. *Proc.Nat.Acad.Sci.USA* **98**: 462-467.

Molecular images courtesy of Dr. Hirofumi Suzuki (Osaka University)  
Image of *Aequorea victoria* based on photo by Sierra Blakely / CC-BY-SA-3.0  
Photo of *Corynactis californica* © Stan Shebs / Wikimedia Commons / CC-BY-SA-3.0 / GFDL

## December: G Protein-Coupled Receptor



**PDB ID: 3sn6** S. G. Rasmussen, B. T. DeVree, Y. Zou, A. C. Kruse, K. Y. Chung, T. S. Kobilka, F. S. Thian, P. S. Chae, E. Par-don, D. Calinski, J. M. Mathiesen, S. T. Shah, J. A. Lyons, M. Caffrey, S. H. Gellman, J. Steyaert, G. Skiniotis, W. I. Weis, R. K. Sunahara, B. K. Kobilka. (2011) Crystal structure of the beta2 adrenergic receptor-Gs protein complex. *Nature* **477**: 549-555.

Images courtesy of Dr. Hirofumi Suzuki (Osaka University)

## Back Cover References

1. J. C. Kendrew, G. Bodo, H. M. Dintzis, *et al.* (1958) A three-dimensional model of the myoglobin molecule obtained by X-ray analysis. *Nature* **181**: 662-666.
2. J. C. Kendrew, R. E. Dickerson, B. E. Strandberg, *et al.* (1960) Structure of myoglobin: A three-dimensional Fourier synthesis at 2 Å. resolution. *Nature* **185**: 422-427.
3. M. F. Perutz, M. G. Rossmann, A. F. Cullis, *et al.* (1960) Structure of haemoglobin: a three-dimensional Fourier synthesis at 5.5 Å resolution, obtained by X-ray analysis. *Nature* **185**: 416-422.
4. W. Bolton, M. F. Perutz. (1970) Three dimensional fourier synthesis of horse deoxyhaemoglobin at 2.8 Ångstrom units resolution. *Nature* **228**: 551-552.
6. C. C. F. Blake, D.F. Koenig, G.A. Mair, *et al.* (1965) Structure of hen egg-white lysozyme. A three dimensional Fourier synthesis at 2 Å resolution. *Nature* **206**: 757-761.
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Molecular images were created using **Chimera** (E.F. Pettersen, T.D. Goddard, C.C. Huang, *et al.* (2004) UCSF Chimera—a visualization system for exploratory research and analysis. *J Comput Chem* **25**: 1605-1612.), **PyMOL** (The PyMOL Molecular Graphics System, Version 1.5.0.4 Schrödinger, LLC.) and **autoPACK** (Graham Johnson, Ludovic Autin, Mostafa Al-Alusi, David Goodsell, Michel Sanner and Art Olson; open-source at [autopack.org](http://autopack.org)).

This calendar was developed by the wwPDB team, with special thanks to Gary Battle (PDBe) and to Luigi Di Costanzo, David S. Goodsell, Brian Hudson, Catherine Lawson, Maria Voigt and Christine Zardecki (RCSB PDB).

# Crystallography and the PDB: A Community Resource for Science

In the late 1950s, scientists began to decipher the 3D shapes of proteins at the level of individual atoms. As structures were determined using X-ray crystallography, early computer graphics programs provided interactive views of these macromolecules. The possibilities for science and knowledge seen in these glimpses of myoglobin,<sup>1,2</sup> hemoglobin,<sup>3,4</sup> lysozyme,<sup>5,6</sup> and ribonuclease<sup>7,8</sup> inspired a new field of structural biology. The potential research that could be enabled by archiving and sharing data from these experiments moved the scientific community to action.

Beginning with the seven structures pictured on the cover—carboxypeptidase, chymotrypsin, cytochrome, hemoglobin (lamprey), lactate dehydrogenase, subtilisin, and trypsin inhibitor—the PDB archive was established in 1971 to provide both a home and an access point for the data produced from these experiments.

Today, the PDB contains and supports online access to tens of thousands of biomacromolecular structures determined *via* X-ray crystallography and other methods. These structures help researchers understand innumerable aspects of biology ranging from biomedicine, agriculture, protein synthesis, health and disease, to biological energy. In 2014, the International Year of Crystallography, the holdings of the PDB archive will reach the 100,000 structure mark.

The PDB archive is managed by the Worldwide Protein Data Bank (wwPDB), a consortium of organizations that host deposition, annotation, and distribution centers for PDB data and collaborate on a variety of projects and outreach efforts.

The wwPDB partners include: the Research Collaboratory for Structural Bioinformatics Protein Data Bank (RCSB PDB) and BioMagResBank (BMRB) in the USA, the Protein Data Bank in Europe (PDBe) and the Protein Data Bank Japan (PDBj).

The PDB structures highlighted in this calendar illustrate how X-ray crystallography enables our understanding of biology at the atomic level.



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