PHYSICS UPDATE

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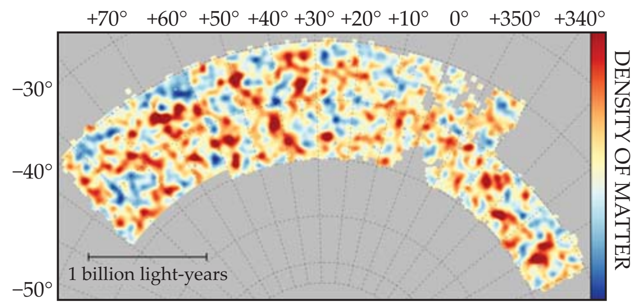
GALACTIC CENSUS REAFFIRMS STANDARD MODEL OF COSMOLOGY

The Rosetta Stone for cosmologists is the cosmic microwave background (CMB), remnant radiation from the surface of last scatter some 380 000 years after the Big Bang. Through increasingly precise microwave-band measurements, most recently by the *Planck* satellite, scientists have refined their basic model of the universe. Known as ΛCDM, the model posits the existence alongside normal matter of cold (that is, nonrelativistic) dark matter and dark energy in the form of the cosmological constant. Yet for all the useful clues embodied in the CMB, there is a complementary cosmological story to be told by analyzing more modern structures, particularly galaxy clusters.



CHIHWAY CHANG AND THE DES COLLABORATION

Enter the Dark Energy Survey, a galactic census of unprecedented detail conducted with a 570-megapixel camera mounted on a 4-meter optical telescope in Chile (see the article by Josh Frieman, PHYSICS TODAY, April 2014, page 28). In the first phase of the project, conducted over five-plus months in 2013–14, researchers charted 26 million galaxies in 1300 square degrees of sky (see the map). They focused on two features: the spatial distribution of the galaxies and the distortions in the galaxies' apparent shape as their light was weakly gravitationally lensed by 650 000 foreground galaxies.

The results rival the precision of *Planck*'s and are largely consistent with both the ΛCDM model itself and the model's parameters as derived mostly from the CMB. Determinations of the density of matter in the universe and the sum of the neutrino masses, for example, yielded values that deviated slightly but are compatible with those from *Planck*. The survey data are also consistent with an unvarying cosmological constant. When combined with *Planck* measurements, the survey brings the value of the Hubble constant closer to the value deduced by observations of supernovae and Cepheid variable stars (see the article by Mario Livio and Adam Riess, PHYSICS TODAY, October 2013, page 41).

The survey's error bars should shrink further once researchers crunch more data, first from three years of observing and then from five. Ultimately, the Large Synoptic Survey Telescope, currently under construction in Chile, will grab the baton when its camera captures 3.2-gigapixel images of more than 30 billion galaxies. (Dark Energy Survey collaboration, papers presented at the American Physical Society's division of particles and fields meeting, 3 August 2017.) —AG

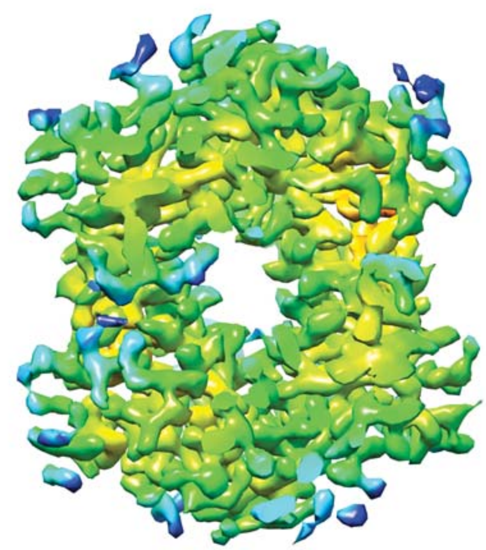
RESOLVING SMALLER MOLECULES WITH CRYO-EM

At this year's annual meeting of the American Crystallographic Association in New Orleans, Maryam Khoshouei of the Max Planck Institute of Biochemistry (MPIB) described how she and her collaborators used a novel technique to obtain a 3.2-Å-resolution structure of human hemoglobin (see accompanying figure). The feat is significant because, at 64 kDa, the protein complex is smaller than the 100 kDa lower limit that had previously prevailed when using cryo-electron microscopy (cryo-EM) to determine the structure of protein complexes.

In EM, contrast arises from differences in phase between scattered and unscattered electrons. (See the article by Bob Glaeser, PHYSICS TODAY, January 2008, page 48.) To create that difference, microscopists either defocus their beams or insert an ultrathin phase plate with a micron-sized hole at the focus; scattered electrons that pass through the plate acquire a phase shift of $\pi/2$ with respect to unscattered electrons that fly straight through the hole. Neither approach is ideal. Defocus leads to the diminution or even loss of low spatial frequencies, whereas holed phase plates are challenging to align and keep stable.

To mitigate either of those problems, the MPIB team developed a phase plate that lacks a central hole. Made from a 10-nm-thick sliver of amorphous carbon, the phase plate imposes a phase difference between the central, unscattered beam and its scattered periphery through the spontaneous interaction of the beam's electrons and the plate's atoms. At first, the MPIB researchers thought they needed to use their phase plate with a tightly focused—and therefore painstakingly aligned—beam. They later discovered that they could retain most of the setup's performance with a slightly defocused beam.

In single-particle cryo-EM, molecules in aqueous solution are abruptly frozen and imaged in whatever conformational state they happen to be. Not only does that step dispense with the need to make a crystal, it also makes it possible to analyze the range of states that enzymes and other proteins adopt *in vivo*. Recent advances in electron detectors have greatly reduced the time it



takes to determine structures with cryo-EM. (See PHYSICS TODAY, August 2016, page 13.) The new phase plate will likely help to bring cryo-EM even closer to joining x-ray crystallography as a routine method for high-resolution protein-structure determination. (M. Khoshouei et al., *Nat. Commun.* **8**, 16099, 2017.) —CD