figure). The thickness of the sheet can be varied from a one-octahedra-thick layer (n = 1) up to five-octahedra-thick layers (n = 5) by controlling the ratio of small MA to large BA cations. While studying single crystals ($n \leq 2$) of these materials with time-resolved photoluminescence, the authors noted that excitons generated in the bulk of the crystals recombined quickly (see the figure). Yet, surprisingly, for crystals with $n > 2$, excitons that reached the edge of the crystal within a picosecond time scale encountered new electronic states, called layer-edge states (LESs). In these states, the separated charge carriers survive for a long time before recombining to reemit a photon. Consequently, for $n > 2$ 2D perovskites, fabricating solar cells from polycrystalline films of crystal grain sizes smaller than the diffusion length of the excitons (10 to 100 nm) guarantees that a maximal number of excitons will reach LESs, and thus can be separated and collected efficiently. Indeed, the study observed very low PCEs for cells based on n = 1 and 2 (no LESs), and impressively high efficiencies as soon as n exceeded 2 (LESs present).

The discovery of LESs that protect charges from fast recombination in 2D perovskites is in stark contrast to 3D perovskite surfaces, which tend to be defective and riddled with undesirable trap states that prevent charge carriers from being collected. Additionally, from a fundamental physics and materials property standpoint, the precisely controlled quantum confinement of these 2D perovskites with LESs makes them ideal systems for studying the physics of highly confined free-carrier states—a situation that is difficult to replicate in other materials systems. The finding of Blancon *et al.* opens the possibility for engineering similar LESs in other members of the low-dimensional perovskite family; as such, a large group of materials that photovoltaic researchers mostly overlooked in the past now become prime competitors in optoelectronics, offering an expanded toolbox to remediate many of the impediments plaguing 3D perovskites. ■

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10.1126/science.aam7154

SELF-ASSEMBLY

Bringing proteins into the fold

A molecular origami method uses double-stranded DNA scaffolds and protein staples to create hybrid nanostructures

By **Shawn M. Douglas**

Molecular engineers have become increasingly adept at repurposing life's building blocks to make custom self-assembled shapes. Because a single drop of solution contains billions of such shapes, DNA origami smiley faces (*1*), RNA stars (*2*), and designer protein polyhedra (*3*) may vastly outnumber most other human-made objects on Earth. These shapes lack immediate practical utility, but they transmit a powerful message: Researchers are beginning to understand how molecules self-assemble. On page 1283 of this issue, Praetorius and Dietz make another leap forward by demonstrating a novel class of nanostructures, namely DNA-protein hybrid shapes (*4*). This is an important advance because it provides a method to create human-designed shapes out of ingredients that are generally compatible with living systems.

"Their proof of concept offers a tantalizing path toward a new generation of tools that could address important hypotheses about the role of DNA bending and compaction in biology."

In the DNA origami method, a kilobase-long single-stranded DNA (ssDNA) "scaffold" hybridizes with ssDNA oligonucleotide "staples" to form custom assemblies (see the figure). DNA origami provides a user-friendly approach for coaxing biomolecules into specific arrangements with nanoscale precision. It has been used to build imaging probes and prototype drug carriers (*5*), but early efforts have been limited to in vitro applications. This new work offers a promising route to building custom shapes for in vivo applications.

Praetorius and Dietz have reimagined DNA origami to create a hybrid approach, in which a double-stranded DNA plasmid serves as the scaffold, while engineered transcription activator–like (TAL) effectors act as staples. TAL effectors are proteins that are composed of compact modular DNA nucleotide–binding domains that can be concatenated to bind to arbitrary DNA sequences (*6*). The authors leveraged TAL effectors to design several custom DNA-binding modules, each with a distinct 20–base-pair DNA substrate. Pairs of TAL effector modules were spliced together to form double-TAL (dT) staple proteins that guided the assembly of the plasmid scaffolds into a variety of custom shapes (see the figure).

TAL effectors are perhaps most notable for their initial promise to supersede zinc-finger nucleases for genome editing (*7*). However, generating new TAL effectors that bind to a specific DNA sequence is a laborious process, so they were phased into early retirement in favor of clustered regularly interspaced short palindromic repeat (CRISPR)–based proteins that are less cumbersome to work with.

Fortunately, Praetorius and Dietz may not have received that memo. In a tour de force, they generated 12 dT staples and used them to fold 16 DNA plasmid scaffolds into different shapes. In doing so, they convincingly show that TAL effectors still hold tremendous potential for biotechnology. Their proof of concept offers a tantalizing path toward a new generation of tools that could address important hypotheses about the role of DNA bending and compaction in biology. Indeed, many natural protein complexes that perform gene regulation can be thought of as protein staples that create DNA loops or bends. The authors' approach could be extended to create synthetic enhancers or silencers and eventually a full suite of programmable nanoscale tools for validating models of three-dimensional genome architecture (*8*).

The hybrid DNA–protein origami method is particularly exciting because it demonstrates that DNA origami is not a one-off method. Instead, Rothemund happened to use DNA to invent a particularly successful instance of a general approach: staple-directed assembly of scaffold templates. It would not be surprising if other

Department of Cellular and Molecular Pharmacology, University of California, San Francisco, San Francisco, CA 94143, USA. Email: shawn.douglas@ucsf.edu

permutations of source materials could also be programmed to self-assemble.

Several challenges lie ahead. The method requires a lot of effort to generate new dT staples, which may limit adoption. The DNA-protein hybrid shapes are genetically encoded but have not yet been shown to work in living organisms, unlike alternative RNA-based methods (*9*) and protein scaffolds (*10*) that have been used to control metabolic flux in vivo. It may be difficult in general to translate complex self-assembly methods to work in vivo, even though simple DNA nanostructures have been expressed and folded in bacteria (*11*).

On a positive note, the hybrid DNA–protein structures reported by Praetorius and Dietz do not rely on any ssDNA components, which might be a major advantage because custom ssDNA is typically difficult to produce in cells. It will be interesting to see what kinds of functionalization can be added to dT staples, especially because applications in cells may require careful regulation of expression and folding conditions. Fortunately, there will be no shortage of options to explore as molecular engineers get ever closer to biological-level sophistication and complexity. ■

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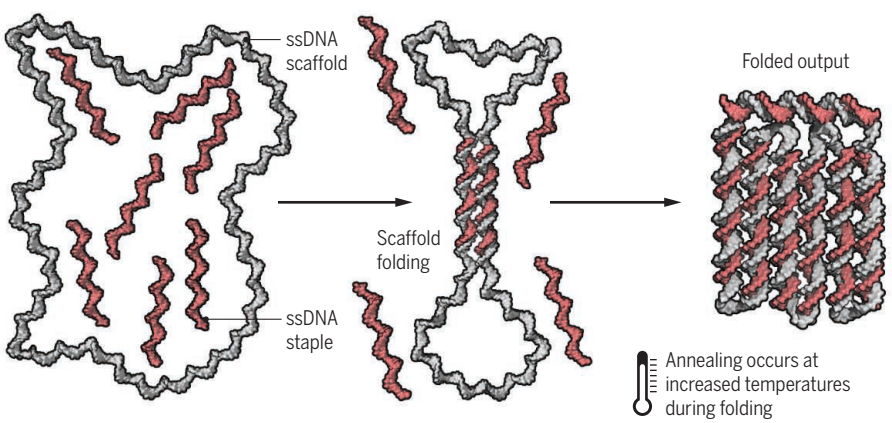
10.1126/science.aam9541

Bringing proteins into the fold

Biomolecular nanostructures can be built using a powerful approach—staple-directed folding of scaffold templates. This strategy has been extended to work with genetically encoded building blocks.

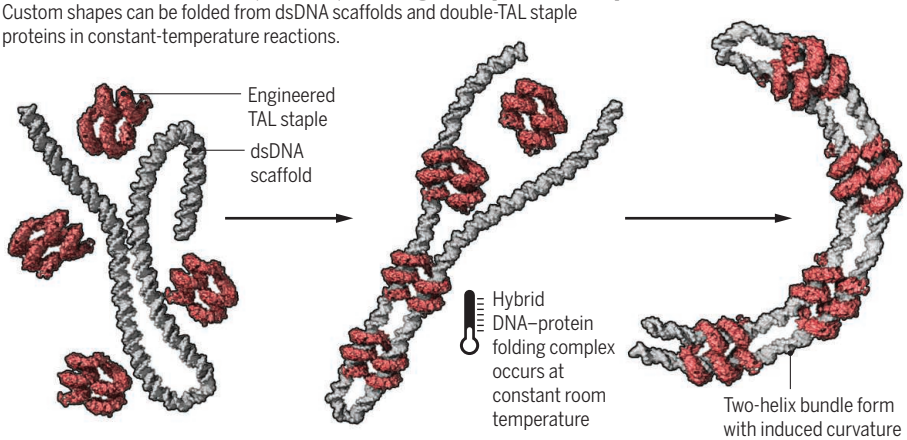
Traditional single-stranded DNA (ssDNA) origami folding

Long strands of ssDNA are folded together with ssDNA staples using thermal annealing ramps.



Double-stranded DNA (dsDNA) folding with protein staples

Custom shapes can be folded from dsDNA scaffolds and double-TAL staple proteins in constant-temperature reactions.



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ACTIVE MATTER

From chaos to order in active fluids

Random flows in an active fluid become directional under confinement

By **Alexander Morozov**

There are few sights more spectacular than the swarming of a school of fish or a flock of birds that suddenly gives way to a directional motion. Arguably, our admiration is rooted in the surprise that individual organisms, capable of self-propulsion on their own, organize to move en masse in a coherent fashion. Coherent motion is common in a large class of biological and synthetic materials that are often referred to as active matter. Such materials consist of particles immersed in a fluid that can extract energy from their surroundings (or internal fuel) and convert it into directed motion. Living organisms, biological tissues, rods on a vibrated plate, and self-phoretic colloids are just a few examples (*1*). Similar to schools of fish and flocks of birds, active matter often exhibits random swarming motion (*2*–*5*) that until now was impossible to control or use. On page 1284 of this issue, Wu *et al.* (*6*) demonstrate that an active fluid can be manipulated to flow in a particular direction without any external stimuli by confining it in microchannels.

Active systems can display unusual properties that develop from the motion of their individual components. Enhanced diffusion of passive tracers added to active fluids (*7*), superfluid-like behavior of bacterial suspensions (*8*), and an ongoing debate about how to define the pressure inside an active fluid (*9*, *10*) add to recent fascination with active matter across many disciplines. In physics, active systems act as a playground for developing new nonequilibrium methods applicable in situations in which usual statistical mechanics breaks down. In biology, it poses a fundamental question of what traits can be considered truly biological and what is emergent and caused by the activity of its constituents. In materials science, these fluids might be manipulated to per-

School of Physics and Astronomy, University of Edinburgh, Edinburgh EH9 3FD, UK. Email: alexander.morozov@ph.ed.ac.uk

Bringing proteins into the fold
Shawn M. Douglas (March 23, 2017)
Science **355** (6331), 1261-1262. [doi: 10.1126/science.aam9541]

Editor's Summary

Science (print ISSN 0036-8075; online ISSN 1095-9203) is published weekly, except the last week in December, by the American Association for the Advancement of Science, 1200 New York Avenue NW, Washington, DC 20005.