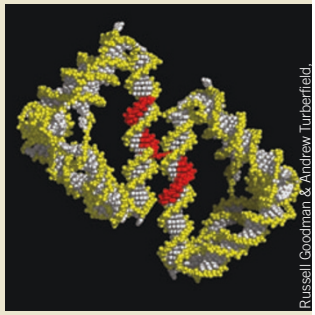
## Snap 'n go DNA nanostructures




Physicists have succeeded in designing a self-assembling DNA nanostructure that efficiently forms the shape of a tetrahedron, a simple and strong geometrical shape used extensively in architecture and engineering. Such tetrahedra could be exploited to construct more complex three-dimensional structures at the nano- and microscales. The authors obtained high yields of tetrahedra by subjecting four different DNA strands, each containing three sequences that specifically anneal with a sequence in one of the other three strands, to a simple process of heating and rapid cooling. Individual tetrahedra could also be connected using 'linker' DNA strands in geometrically prespecified ways (see picture). The ability to efficiently form complex architectures from DNA sequences opens up the possibility of creating templates for nanoscale electrical circuit manufacture, nanomaterials assembly and even novel drug delivery systems. (***Science* 310**, 1661–1665, 2005) ***GTO***

## Rice that's not to be sneezed at?

The escalating incidence of allergies across the globe is driving the search for new approaches to combat immunoglobulin E (IgE)-mediated allergic responses. Although several T-cell epitope peptide immunotherapies delivered by injection have been tested in the clinic, results thus far have proven disappointing. As an alternative delivery approach, Takagi *et al.* have created an edible peptide vaccine using rice. The vaccine consists of two epitope peptides, Cry j I and Cry j II, from a common allergen, Japanese cedar pollen, fused to a soybean seed storage protein under the control of a seed-specific promoter. When systemically challenged with Japanese cedar pollen, mice previously fed transgenic rice exhibited lower levels of allergen-specific serum IgE and IgG, reduced $CD4^+$ T cell responses and less allergic sneezing compared with controls. Although edible vaccines against allergens may simplify storage and administration, remaining issues include recombinant product consistency, efficacy and the potential to induce allergenic reactions. (*Proc. Natl. Acad. Sci. USA* **102**, 17525–17530, 2005) *PH*

## Setting the bar code

We know little about the diversity of life on this planet; of the estimated 10-million species on Earth, only 1.7 million have been properly identified. In addition, species are threatened with extinction and invasion by other species, events that could go by unnoticed without technologies for identifying them. Bar codes—short gene sequences (markers) uniquely identifying an organism—have been touted as a simple way to classify unknown species and identify new ones. However, a new study suggests some caveats in applying this technology. Using a short mitochondrial gene sequence, Meyer and Paulay created a comprehensive database of 2,000 individuals from 263 taxa of cowrie, a marine mollusk. They then asked how accurately new species could be identified using this data set in two taxonomic settings, one strictly morphological and one integrating morphological and genetic classification. Although the bar code performed well (98% accurate) in the latter case, it was less accurate (80%) when only morphological data were available. As cowries exhibit extensive intraspecies variation, they may be a particular challenge for this kind of analysis, but the study does reveal limitations in the use of bar coding to delineate closely related species in taxonomically understudied groups. (*PLoS Biol.*, published online 29 November 2005; 10.1371/journal.pbio.0030422) *LD*

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## Ratio predicts mAb activity

Different subclasses of mammalian immunoglobulin G (IgG) have long been known to elicit specific types of immune response. This variability, once thought to arise solely from differences in the ability of each IgG subclass to fix complement, has now been found to depend on the affinity of their Fc regions for different Fc receptors. Nimmerjahn and Ravetch propose that the type of immune response elicited by an IgG subclass can be predicted by each subclass's differential affinities for specific activating IgG Fc receptors and their specific inhibitory Fc receptor, expressed as a ratio of activating-to-inhibitory receptors (A/I). To test this hypothesis, the authors produced monoclonal IgGs that recognized either the melanosome gp75 antigen or a platelet integrin antigen, each containing Fc regions from one of the IgG1, IgG2a, IgG2b or IgG3 subclasses. The range of anti-gp75 IgG subclasses and anti-platelet integrin IgG subclasses were then tested in mouse models of metastatic melanoma or platelet clearance. The authors found that IgG subclasses IgG2a and IgG2b, which have the highest A/I ratios, lead to the most effective tumor and platelet clearance. This ability to predict and improve IgG efficacy may be useful in the early stages of monoclonal antibody design and also signals new opportunities to optimize subclass in second-generation molecules. (*Science* **310**, 1510–1512, 2005) *TM*

## Kinase substrate hunts

Most cancer drugs that inhibit protein kinases have been targeted directly at the kinase of interest; however, another option is to target key kinase substrates associated with malignancy. As only half of all protein kinases in budding yeast have known *in vivo* substrates, Ptacek *et al.* have developed a global unbiased approach for rapid identification of these substrates. Using protein microarrays containing ~4,400 yeast proteins, the authors identify over 4,000 phosphorylation events on 1,325 different proteins catalyzed by 87 protein kinases. By combining the protein phosphorylation data with transcription factor binding and protein interaction data, the authors were able to identify novel regulatory pathways that were not apparent from the individual data sets. As kinase signaling pathways are highly conserved from fungi to humans, these results may be of interest in cancer drug discovery. An alternative high-throughput strategy for identifying protein kinase substrates developed by Dephoure *et al.* relies on a combination of chemical genetics and proteomics. (*Nature* **438**, 679–684, 2005; *Proc. Natl. Acad. Sci. USA* **102**, 17940–17945, 2005) *JWT*

## Boxer sequence joins Shadow


The 2.4-billion-bp (7.5× coverage) sequence of a female boxer dog named Tasha (pictured), now published, surpasses the fidelity (1×) of the only other dog sequence (the poodle Shadow), released in 2003. The sequence should facilitate research using inbred dogs as models of human genetic diseases. (*Nature* **438**, 803–819, 2005) *GTO*