## Abstractions

**SECOND AUTHOR**

The damage caused by meteorites and asteroids when they strike planets or satellites is an area of research that can attract more than its fair share of hyperbole. And when Earth is brought into the equation, disaster movies are never far from the public's thoughts.

Clark Chapman of the Southwest Research Institute in Boulder, Colorado, is interested in the real effects of these objects. On page 1125 of this issue, Chapman and his colleagues assess what caused the craters on the surface of Jupiter's moon Europa. They calculate that most of Europa's smaller craters were not caused by the direct 'primary' impacts of asteroids and comets, as was previously believed. Instead they are the result of 'secondary' impacts, which occur when smaller pieces of debris are kicked up after the initial crash of the incoming body.

**As most craters on Europa now seem to have been caused by secondary impacts, does that mean that the chance of an asteroid hitting Earth is lower than previously calculated?**

For the small bodies — asteroids the size of a house — yes. But this does not really apply to kilometre-size asteroids hitting Earth and wiping out the planet.

**According to your work, too many craters have been counted as 'primary' impacts. What was responsible for the miscount?**

In the past, we assumed that apart from obvious secondary impacts, such as prominent clusters of craters, all other impacts were primary craters caused by asteroids.

**Are there any new techniques that bolster your theoretical predictions?**

There are independent estimates of the number of craters caused by secondary impacts from sources such as telescopic surveys. We believe that our results are consistent with these data.

**How dramatically do your results go against conventional wisdom?**

Our study of Europa, and some recent studies of Mars, are the first to raise the possibility that there are many more secondary craters than primary ones.

**Do you expect some controversy or resistance?**

A lot of people have spent a lot of time counting craters. There will be some inertia.

**Do films about asteroids hitting Earth bother you?**

Hollywood depictions of disasters are a little over-the-top. It's good that they increase the awareness that there are asteroids and comets out there, but the scientific details are way off. ■

## MAKING THE PAPER

### Robert Sauer

**Building an enzyme gives an insight into protein degradation.**

Robert Sauer (right) with Tania Baker (left) and Andreas Martin.

On page 1115 of this issue, Robert Sauer and his colleagues offer an insight into what makes molecular machines work. Their focus is an enzyme called ClpX, which unfolds proteins and prepares them for degradation in the cell.

The group's interest in protein degradation began with the question why do some proteins get degraded but not others? The key, it seems, is that for proteins to be unfolded by ClpX, they need to have recognition tags so that the enzyme can bind to them. ClpX also needs to hydrolyse ATP to drive the unfolding process. "ClpX is a molecular machine and ATP is the fuel that powers it," Sauer says.

The key to understanding this molecular machine for Sauer and his colleagues Tania Baker and Andreas Martin involved taking apart this machine and observing how its individual components drove protein degradation.

But ClpX is not a simple enzyme — it is made up of six identical building blocks or subunits. Earlier experiments had revealed that ClpX was inactive if none of its subunits could hydrolyse ATP, but there was no simple way to see whether ClpX could unfold proteins if one or more of its subunits was inactive.

Martin reasoned that, to understand the unfolding process, he would need to manipulate the enzyme's subunits one at a time. This proved easier said than done. He first tried to connect ClpX's subunits by making genes that expressed enzymes in which individual subunits were connected by different peptide linker sequences. But nothing worked. "It was very discouraging," Sauer says. "I was ready to quit, but Andreas persisted. He just refused to give up."

After six months of frustration, Martin found that deleting a non-essential segment of ClpX allowed him to stitch the subunits together and generate an active enzyme. But this, too, proved to be a lengthy business. Martin began by deleting the non-essential domain and then linked two separate subunits together. He then did some careful chemical engineering to link in the other four subunits to make a six-sided molecule.

To test how this re-engineered machine worked with ATP, Martin then made mutant enzymes in which only some subunits could use ATP as a power source. He found that only one active ClpX subunit was needed to allow protein degradation.

This contradicted the two prevailing models, one in which all six subunits had to bind and hydrolyse ATP simultaneously to trigger degradation, and another in which the six subunits had to hydrolyse ATP in a strict sequence, like the sequential firing of pistons in a car engine. This means that the six building blocks of ClpX provide some sort of redundancy to keep the process of protein degradation going even if one of the subunits becomes damaged. "We were very surprised," Sauer says. "But that's why we do experiments."

And more experiments lie ahead, Sauer says. "We want to understand how ATP binding and hydrolysis change the structure of ClpX and allow it to take other proteins apart," he says. This is unlikely to be a straightforward task, but persistence may, once again, pay off. ■

## QUANTIFIED **SOUTH KOREA**

**A numerical perspective on *Nature* authors.**

Kyeong Kyu Kim of the Sungkyunkwan University in Suwon, South Korea, describes himself as a "structural biologist trying to elucidate the fundamental biological phenomena at a molecular level, and developing new bionanomaterials and pharmaceuticals". Although his primary motivation for publishing his research is to share the results with other scientists, Kim admits that there is some pressure from his university, which has its own ambitions and emphasizes publications as a measure of scientific performance. This week, Kim and his colleagues describe the crystal structure of junctions between right-handed B-DNA and left-handed Z-DNA and demonstrate nature's simple solution for changing the form of DNA from one to the other by flipping two bases from the helix (see page 1183).

**112** original research submissions to *Nature* in 2005 came from South Korea (total number of submissions = 10,896)

**12** papers published in *Nature* this year had contributing authors working in South Korea (total number of papers published = 690)

**83%** of authors in South Korea who have contributed to *Nature* this year work in biological sciences.

**3** authors working in South Korea report original research in *Nature* this week.