translation during and immediately after mitosis (Fig. 1b), indicating the protein's crucial role in regulating translation during mitosis. Instead, in cells lacking 14-3-3 $\sigma$ , cell division is impaired, with a loss of the Plk1 protein — a regulator of mitotic progression — at the mid-body region between dividing cells, and an accumulation of binucleated and fused cells.

Wilker and colleagues then searched for proteins that both were translated during mitosis in a cap-independent manner and had been implicated in mitotic events. They identified a proposed target of this defective switch in translation — the cell's own IRES-dependent form of a protein involved in cell-cycle progression (the cyclin-dependent kinase cdk11), called p58-PITSLRE. This is one of a large family of proteins involved in regulating cell-cycle progression. It contains an IRES element in its mRNA-coding region, and its activity is regulated by the cell cycle, thereby permitting translation of p58-PITSLRE immediately before and during mitosis9. The evidence for p58-PITSLRE as a target of  $14-3-3\sigma$  is compelling, but it is unlikely to be the only cap-independent mRNA affected by the defective switch in translation that is regulated by 14-3-30. It will be essential to identify other cap-independent mRNAs involved in this response.

Wilker *et al.*<sup>2</sup> also showed that some cellular defects observed after the 'knockdown' of 14-3-3 $\sigma$  can be reversed by using the drug rapamycin to suppress cap-dependent translation and increase cap-independent translation during mitosis. The authors therefore argue that, in the absence of 14-3-3 $\sigma$ , aberrant mitotic translation impairs termination of mitosis and produces binucleated cells; this implies that 14-3-3 $\sigma$  may be involved in tumorigenesis.

The identification of 14-3-3σ as a protein required for the mitotic switch from capdependent to cap-independent translation shines a brighter light on mRNA translation as an underappreciated factor in cell-cycle control. These findings also suggest that transition from cap-dependent to cap-independent translation is a potential chemotherapeutic target, as the effects of rapamycin may be partly explained by its ability to alter translation. Thus, there could be potential in exploiting the mitotic regulation of mRNA translation for therapeutic purposes. Anthony Wynshaw-Boris is in the Departments of Pediatrics and Medicine, Center for Human

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## Total surveillance

Ferdinand Schmidt-Kaler

Trapped by mirrors, a photon can be monitored from birth to death by a stream of passing atoms. The technique could also be used to entangle the quantum states of many atoms — a possible boon for quantum computing.

"You measured this only once?" Such enquiries from professor to student are often heard in the experimental laboratory. But although the necessity of repeat measurements might be self-evident in the classical world, things are not quite so straightforward for quantum measurements. This is because the tiny objects of quantum desire — single photons, for instance — are easily destroyed simply by measuring them. On page 297 of this issue, Serge Haroche and colleagues (Gleyzes *et al.*)<sup>1</sup> observe for the first time a single photon in a sequence of about 100 consecutive measurements, recording it from the instant of its birth to the moment of its death.

What are the necessary ingredients for this experimental masterwork? First, you must trap a photon for long enough to measure it over and over again. The longer the photon is trapped, the better. In Gleyzes and colleagues' experiment, a cavity in the form of a box 2.7 cm long, with walls made from ultra-reflective, superconducting mirrors (Fig. 1), serves to hold a photon for about 0.13 seconds. This is an impressive achievement: in that same time, a free photon would travel about a tenth of the distance to the Moon.

Second, a 'transparent' counter must be used instead of a normal photodetector. A conventional light detector works by absorbing the energy of an incident photon, and in so doing destroys it. But even if the photon is not destroyed during the measurement process, its properties will change dramatically. Gleyzes et al. use what is known as a quantum non-demolition technique. This involves a stream of atoms crossing the box in which the photon is trapped. Light is an electromagnetic wave, and the electric field of the photon shifts the energy levels of the atom, but without giving the atom a chance to absorb energy from the field. Once the atoms have emerged from the interaction region, they can be analysed precisely to ascertain whether a photon was in the box or not.

The principle of this measurement process is akin to each atom carrying its own clock, with orbiting electrons acting as the pendulum. The frequency of this pendulum is slowed down by the photon's electric field while the atom is in the box with a photon. This creates a delay in the atom's clock when compared with the clock of an atom that has not interacted with a photon. Measuring this minuscule difference requires the sensitive technique, devised by Norman Ramsey<sup>2</sup>, that is widely used for



**Figure 1** | **They do it with mirrors.** Gleyzes and colleagues' cavity for trapping photons<sup>1</sup>.

receiving the signal of modern atomic clocks.

We must still remember, however, that according to the strict laws of the quantum world, any measurement of a photon causes an unavoidable disturbance. For a classical electric field, both phase and amplitude may be determined independently with infinite precision. By contrast, the fluctuation in the phase and amplitude of a quantum field - such as that of the trapped photon — are interconnected. These two 'non-commuting' variables obey the Heisenberg uncertainty relation: that is, increased precision in measuring one of them will reduce the precision in measuring the other. In Gleyzes and colleagues' experiments<sup>1</sup>, the amplitude of the photon field is determined with certainty, meaning necessarily that the phase of the photon wave is fully mixed up.

Roy Glauber<sup>3</sup> was the first to develop the quantum theory of photon detection in a destructive measurement process. Gleyzes *et al.* illustrate beautifully the detection of a single photon without its destruction. But their experimental scheme is not limited to simple cases such as that of a single photon, and further exciting experimental news is to be expected. With their current set-up, the authors are already in a position to detect quantum superpositions of two distinct, classical states of the photon's electric field. The photon statistics of such notorious 'Schrödinger's cat' states have escaped observation until now.

The successful demonstration<sup>1</sup> of a quantum non-demolition measurement of a single photon has significant implications for the rapidly evolving field of quantum computing<sup>4</sup>. Photons<sup>5</sup>, atoms<sup>6</sup>, ions<sup>7-9</sup> and also a menagerie of solid-state two-level systems<sup>10-12</sup> have been used to carry elementary units of quantum information ('qubits'), which live in superpositions of two quantum states, 0 and 1. To translate Gleyzes and colleagues' experiment into the language of information processing, they have demonstrated that a stream of atomic qubits can be fully controlled by the qubit state of a trapped photon. In the next experimental steps, we can hope to see the electromagnetic field being prepared in a quantum superposition of one photon and no photon. In this case, the atoms in the stream leaving the box will all be in that same superposition state. Moreover, the properties of all the atoms will be 'entangled' such that it no longer makes any sense to consider them individually, even if they are spatially well separated.

As Nobel-prizewinning physicist Richard Feynman said, "We do not understand quantum

The six-bond bound

Gernot Frenking and Ralf Tonner

What is the maximum number of covalent chemical bonds that two atoms can share? Six, according to the latest theoretical study — at least where just two atoms of the same element are concerned.

Every atom can make a small, integer number of covalent chemical bonds with neighbouring atoms. This number is usually not more than eight, although a precise statement is dangerous — in rare cases, atoms can have more than eight neighbours, but whether they are covalently bound is open to debate. By the nineteenth century, chemists had realized<sup>1</sup> that more than one bond may connect the same two atoms: most famously, adjacent carbon atoms can be bound twice or even three times. For many years, three seemed to be the limit. Then, in 1965, a salt compound was isolated with a fourfold rhenium-rhenium bond in its anion<sup>2</sup>. Five bonds followed in 2005, when the synthesis<sup>3</sup> of a complex organometallic compound was interpreted in terms of a quintuple bond between two chromium atoms<sup>4,5</sup>. In a thorough theoretical study in Angewandte Chemie International Edition, Roos, Borin and Gagliardi<sup>6</sup> use quantum chemistry to tackle the obvious question that arises — what is the maximum number of bonds that can bind two atoms?

Theoretical models of covalent bonding go back to 1916, when Gilbert Lewis<sup>7</sup> introduced the idea of electron pairing between neighbouring atoms. Remarkably, this simple model is still the most widespread conceptual description of the covalent bond<sup>8</sup>. The first quantum-chemical study<sup>9,10</sup>, however, struggled to reconcile the paired-electron idea with the delocalized nature of electron wavefunctions, which are smeared over large areas of an atom in 'orbitals' (Box 1). Since then, the paired-electron bond has become chemistry's unicorn — although everyone seems to know what one looks like, no one has actually ever seen one<sup>11</sup>.

mechanics" - but, as Gleyzes and colleagues'

achievement<sup>1</sup> shows, we do know increasingly

well how to handle it in our experiments.

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Roos et al.<sup>6</sup> simplify things by focusing

mainly on molecules made up of two atoms of the same elements, in which there are no further bonds to complicate the analysis. They considered all possible bonding and antibonding combinations of the two atoms' electron orbitals using 'multi-reference' wavefunctions. Here, the simple picture of molecular orbitals that are either empty or occupied by two electrons, one from each atom, does not apply. Instead, the authors calculated 'natural' molecular orbitals that retain the simple model, but have non-integer occupation numbers. By summing up the occupation numbers of all these orbitals (antibonding orbitals being negative in the sum), they could arrive at an overall, non-integer 'effective bond order' (EBO). To tie this in with the qualitative paired-electron bonding picture, the authors suggest that the true 'number' of bonds is the next integer larger than the molecules' EBO.

To find the molecules with the highest EBO, Roos *et al.* investigated the transition-metal dimers of chromium, molybdenum and tungsten, respectively Cr<sub>2</sub>, Mo<sub>2</sub> and W<sub>2</sub>. The atoms of these transition metals have six outer, or 'valence' orbitals, all of which are available for bonding (Fig. 1). (The availability of an orbital for bonding cannot be assumed: in dimers of atoms such as carbon, for instance, the antibonding combination of one pair of orbitals may be lower in energy than the bonding combination of another, effectively allowing a maximum of just three bonds to form.)

For  $Cr_2$ , however, the authors came up with an EBO of 3.5, which equates, following their method, to four paired-electron bonds, rather than the expected six for simple dimers. They explain this discrepancy with an imbalance between the optimal bond length for the outermost 4*s* and 3*d* orbital contributions to the Cr–Cr bond (Box 1). At the equilibrium bonding distance, 1.66 Å, the 4*s* component is already

> Figure 1 | Six bonds that bind. A depiction of the molecular orbitals of each bond in the sextuple bond between two transition-metal atoms, as investigated by Roos and colleagues6. Two bonds ( $\sigma$  bonds; top) each have a single component oriented along the bonding axis between the two atoms. which is horizontal here; two bonds (middle) have double components above and below, or to the sides of, the bonding axis ( $\pi$  bonds); two bonds (bottom) have four components around the axis  $\delta$  bonds).

