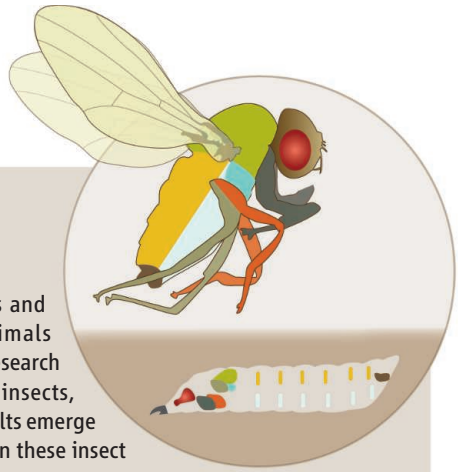
EDITED BY GILBERT CHIN AND JAKE YESTON



DEVELOPMENT

Coordinated Growth

Animal species display specific developmental stages and growth rates, with individual organs and whole animals attaining a characteristic shape and size. Considerable research on growth has been performed with holometabolous insects, such as the tobacco hornworm *Manduca sexta*, where adults emerge at a size determined by the end of the last larval stage. In these insect larvae, imaginal discs specify subsequent adult organs.

Using x-ray irradiation of *Drosophila* larvae, Stieper *et al.* examine size as it is regulated by imaginal disc growth. With a low dose of x-rays, the time to final pupariation increases but ultimate size is not affected; therefore, imaginal discs adjust metamorphosis time. In addition, critical size—the minimum size of larvae at which starvation does not delay metamorphosis—increases and pupariation is delayed when ribosomal protein S3 is disrupted by RNA interference methods. — BAP

Dev. Biol. 10.1016/j.ydbio.2008.05.556 (2008).

CELL BIOLOGY

Like Ps in a Pod

In the budding yeast, the 26*S* proteasome degrades many proteins involved in cell-cycle progression and thus is essential for cell proliferation. In actively growing yeast, 80% of the 26*S* proteasome, which comprises a *20S* core particle and a 19*S* regulatory particle, is localized inside the nucleus. In quiescent cells, proteasome proteolytic activity decreases and correlates with release of the regulatory particle, but the fate of the disassembled subcomplexes remains unclear.

Laporte *et al.* found that when cells exhausted their carbon source and entered quiescence, subunits from the 20*S* and 19*S* particles colocalized into cytoplasmic foci termed proteasome storage granules (PSGs). Consistent with the proposal that PSGs act as storage depots, refeeding the cells resulted in rapid relocalization of proteasomes into the nucleus and did not require de novo protein synthesis. Other macromolecular assemblies triggered by quiescence have been described, such as P-bodies, which contain RNA and RNA-modifying proteins, suggesting that there may be a major reorganization of cellular structures upon entry into quiescence. — VV

J. Cell Biol. **181**, 737 (2008).

MOLECULAR BIOLOGY

Reengineering Engrailed

The potential for engineering transcription factors so that they bind to specified DNA sequences and work as chemotherapeutic agents or sensors has generated a great deal of excitement. AT-rich sequences have been particularly challenging targets for zinc finger–domain approaches.

Noyes *et al.* have turned to the other large category of sequence-specific transcription factors, homeodomain proteins. They have carried out a comprehensive survey of the breadth of specificity of the 84 known *Drosophila* homeodomains that function independently of other DNA-binding domains. The relations between particular amino acid residues and preferred binding sequence were complex, but general determinants were assigned according to whether they cooperated or competed in binding character, leading to predictions for the binding specificity of roughly 75% of the homeodomains in the human genome and allowing them to modify Engrailed to exhibit a binding specificity resembling that of TGIF even though these proteins share only 25% amino acid identity. On the basis of their analysis, the authors have created a Web-based tool that supports the prediction of specificities for homeodomains from other organisms. — BJ

A close-up of homeodomain-DNA interaction.

Cell **133**, 1277 (2008).

MATERIALS SCIENCE

Slippery When Wet

Diamond has low friction and wear, particularly in humid environments, but the cause of this behavior is an issue of debate. One idea is that the bonds rehybridize to an ordered sp^2 form, which is consistent with graphite being the thermodynamically stable allotrope at room temperature and pressure; graphite is also an excellent lubricant because of its layered structure. An alternative idea is that the surface becomes passivated, which is consistent with data that show lower wear and friction for diamond in hydrous or H_2 atmospheres compared to experiments in vacuum. To explore this question, Konicek *et al.* created films of ultrananocrystalline diamond (UNCD), which has an extremely smooth surface and shares many of the properties of large-grained or single-crystal diamond films. Spheres coated with UNCD were rubbed against the films, either at high or low loading and high or low humidity, and the wear tracks were measured and compared with the unworn areas. The most significant wear damage occurred under high loading/low humidity conditions, which also exhibited an initially higher friction coefficient (though all four systems showed similar steady-state values). A number of techniques failed to reveal the pres-

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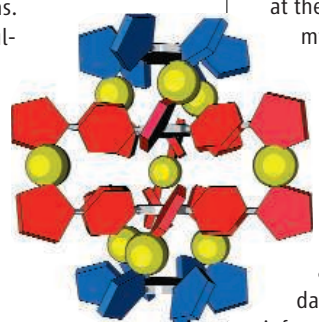
ence of graphitic bonding, indicating that rehybridization effects were negligible and that it is rapid passivation of dangling bonds that is responsible for the low friction and wear of diamond. — MSL

Phys. Rev. Lett. **100**, 235502 (2008).

CHEMISTRY

Spinning in Concert

In macroscopic machines, gears are commonly used to induce the synchronous motion of well-separated components. Hiraoka *et al.* observe a similar effect at the nanoscale in a stack of four ligands held together by mutual coordination to metal ions. The ligands consist of multiple oxazoline or thiazole rings appended to a central phenyl core. Upon binding silver or mercuric ions, these pendant rings adopt a common cant (shown at right) that creates an overall helicity, with the central ligands transmitting an orientational bias from one capping ligand to the other. Using solution-phase nuclear magnetic resonance spectroscopy, the authors demonstrate that a helix inversion in one component of the stack induces a cascade of inversions throughout, thereby correlating the motion of molecules spaced more than a nanometer apart. — JSY



J. Am. Chem. Soc. **130**, 10.1021/ja8014583 (2008).

PHYSICS

Quantum Privacy

For those that have it and for those that seek it, the saying that information is power is as true today as it ever was. Closely coupled to that, however, is the question of privacy—how to ensure that the information stored in a database is secure (data privacy), and that the information retrieved by users, as in a Web search, is not used against them (user privacy). For good reason, holders of information do not wish to compromise their advantage and so make it difficult to access the information (storing log files). That, however, tends to put users at the disadvantage of having to compromise their privacy or trust the database provider not to use the information in any dishonest way.

Giovannetti *et al.* show theoretically how quantum mechanics may be able to help ensure privacy for both parties. They have produced a quantum protocol that allows users to access information from a classical database without revealing which item of information it was they retrieved, and also allows perfect data privacy of the database. By quantum mechanically entangling the questions (queries would be addressed as a pulse of entangled photons, for example), any attempt by the database handler to identify which piece of information was retrieved would be scuppered as the user would be alerted. With such a quantum protocol, all parties retain their privacy. — ISO

Phys. Rev. Lett. **100**, 230502 (2008).

Science Signaling AAAS

<< Counting Phosphates

The kinases Rad53 and Dun1 are important components of a checkpoint kinase cascade activated in response to DNA damage in yeast. Both enzymes contain forkhead-associated (FHA) domains, which bind to phosphothreonine (pThr) residues. Rad53 has four Thr residues clustered in its N-terminal SCD1 domain. Upon phosphorylation by upstream kinases, Rad53 interacts with Dun1 through the Dun1-FHA domain to activate Dun1. Although mutant Rad53 proteins that contain only one of the four SCD1 Thr residues are readily activated by upstream kinases, they cannot activate Dun1. Lee *et al*. found that a recombinant Dun1-FHA domain bound with greater affinity to Rad53-SCD1–derived phosphopeptides containing both $pThr^5$ and $pThr^8$ than to phosphopeptides that had only one of these residues, consistent with the Dun1-FHA domain, unlike that of Rad53, having not one, but two high-affinity pThr-binding sites. Treatment of yeast strains expressing a mutant *rad53* allele with a DNA-damage–inducing agent showed that the presence of both Thr^5 and Thr^8 in the Rad53-SCD1 was required for optimal Dun1 activity. Mass spectrometry studies showed the presence of monophosphorylated and diphosphorylated Rad53 proteins in response to DNA damage in vivo. Together these data suggest that whereas monophosphorylation activates Rad53, diphosphorylation of Rad53 is required to activate the Dun1-dependent arm of the DNA-damage response. — JFF

Mol. Cell **30**, 767 (2008).

CREDIT: HIRAOKA *ET AL.*, *J. AM. CHEM. SOC.* 130, 10.1021/JA8014583 (2008)

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