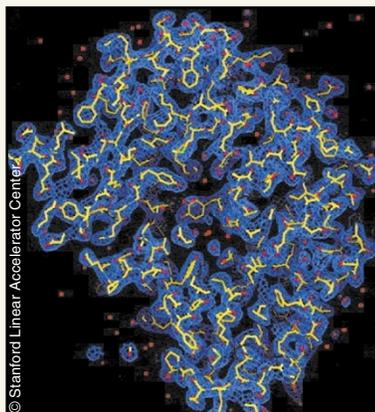


Structures without crystals



X-ray crystallography is a valuable tool with a serious handicap—the need to grow protein crystals to solve three-dimensional structure. Crystallization problems could be a thing of the past if a method described in the *Proc. Natl. Acad. Sci. USA* (98, 6641–6645, 2001) is realized one day. The method proposed in the paper requires a powerful X-ray free electron laser (X-FEL), a device that is currently under construction at the Stanford Linear Accelerator Center (Stanford, CA) and scheduled to begin operation in 2006. In the meantime, the Stanford researchers report that they have cleared a critical theoretical hurdle, developing an algorithm that can solve protein structures from the types of diffraction patterns that the X-FEL will produce. A computer simulation of the process, in which single molecules of an enzyme (ribulose-1,5-bisphosphate carboxylase/oxygenase) were analyzed 120 times a second, produced an accurate three-dimensional model of the protein at 2.5 Å resolution. “If you can make full use of the beam, then in principle you can solve a three-dimensional structure within a few hours,” says lead author John Miao. AD

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Off air benzene degradation

Benzene is a common environmental pollutant resulting from spillages of fuels, solvents, or chemicals. Because it is both highly toxic and soluble in water, it represents a significant environmental hazard for humans. To date, the aromatic hydrocarbon has confounded clean-up efforts because it seeps into air-free soils and sediments, which do not support the benzene-degrading *Pseudomonas putida* strains that require oxygen used in bioremediation. The alternative has been to apply a mixture of unidentified bacteria that degrade the hydrocarbon, but results tend to be rather unpredictable. Now, researchers at Southern Illinois University have successfully identified two *Dechloromonas* strains that can break down benzene into simpler hydrocarbons and carbon dioxide in an oxygen-free environment. Senior author John Coates and his colleagues have isolated two strains—RCB and JJ—that can decompose benzene under anaerobic conditions. RCB can use both chlorates and nitrates instead of oxygen as electron acceptors, whereas JJ can only use nitrates as an electron acceptor. As nitrates are much more common in airtight sediment and soil affected by benzene-contaminated groundwater, these strains should prove useful in bioremediation efforts. JB

Research News Briefs written by Jackie Barlow, Alan Dove, and Andrew Marshall.

ES cells leave their imprint

Animals produced by nuclear transfer cloning may be destined to inherit genetic abnormalities, even if they are cloned from embryonic stem (ES), rather than adult, cells. Previously, researchers had found a variety of defects in embryos cloned from somatic cell lines, but ES cell-derived clones were thought to be less prone to these abnormalities because undifferentiated ES cell nuclei are more likely to retain more of their original epigenetic imprinting than adult cells. Research in *Science* (293, 95–97, 2001) now shows that mice ES cell lines exhibit significant defects in imprinting, and although animals cloned from these cells appear normal, they actually harbor subtle genetic abnormalities. By tracking the expression levels of several genes that are imprinted—expressed differently depending on which parent contributed the gene—scientists found that separate subclones of a single mouse ES cell line showed variation in gene expression. Expression abnormalities due to loss of imprinting in ES cells were transmitted to the cells of mice cloned from them, even ones that survived to adulthood. “No one’s really figured out exactly what’s going on during the culturing process that causes this [imprinting] information to be lost,” says lead author David Humpherys, but “once that information is lost there’s really no way it can be regained.” AD

Protein ID resource

A freely accessible platform for rapidly analyzing protein mass spectrometry data has been made available over the web (<http://www.labonweb.com>). The platform, termed Protocall MS, allows researchers to use Compugen’s (Tel-Aviv, Israel) scoring and recalibration algorithms to query raw spectra (or a list of monoisotopic peaks) against a database that includes not only predicted human proteins from the company’s database, but also proteins deposited in the public NCBI_nr and SwissProt databases. At present, more than 70,000 human sequences and their derived proteins can be searched for matches. Results are displayed as a list of protein candidates best matching the measured peptide masses and include a information about each protein, a graphical summary of the matching peptides, and a link to more detailed information. Additional ProtoCall components and product line extensions are likely to be made available later this year, but according to Compugen, these will not be freely available. Users require an Internet Explorer version 5.5 browser. AM

Piezoelectric arrays

Because of relative insensitivity of the fluorescent detection systems used, DNA microarrays usually require PCR amplification of the sample before application to the array. Now, Israeli researchers have developed two detection formats that rely on a highly sensitive piezoelectric electrode, potentially dispensing with the need for an amplification step. In one format (*Angew. Chem. Int. Ed.* 40, 2261–2265, 2001), hybridization of target RNA to the array probe is detected by binding an additional oligonucleotide labeled with biotin, and then a streptavidin–alkaline phosphatase conjugate, which can catalyze the precipitation of a colorless substrate onto a piezoelectric electrode, producing a signal. In the second format (*J. Am. Chem. Soc.* 123, 5194–5205, 2001), attachment of the target to the array is again detected by binding a second biotinylated DNA probe, but this time signal is amplified by binding streptavidin/biotin-derivatized liposomes, which link together to form a branching network that also distorts the electrode. Although piezoelectric sensors are traditionally prone to false positives, senior author Itamar Willner says “we are orders of magnitude more sensitive than [other] available methods.” AD