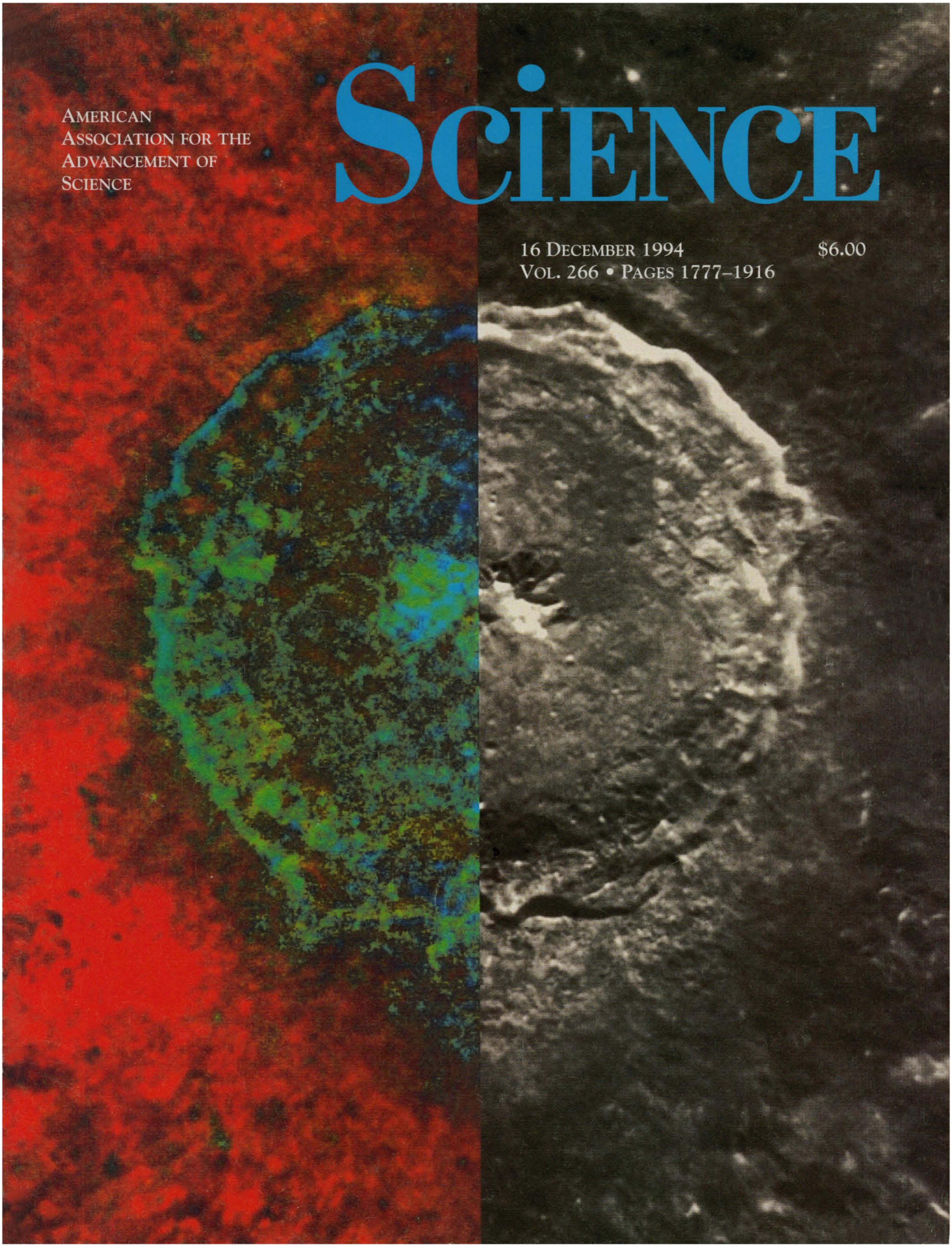
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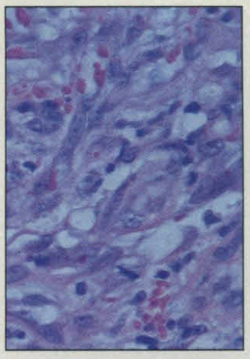
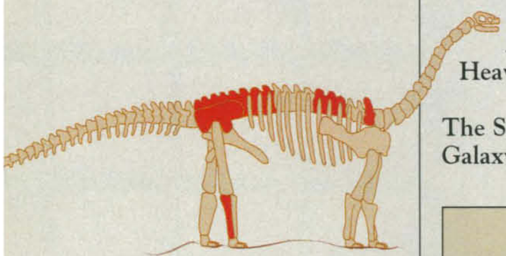


1803 & 1865
Herpes link to Kaposi's?



1805
It could be a contender

NEWS & COMMENT

RESEARCH NEWS

POLICY FORUM

PERSPECTIVE

ARTICLE

RESEARCH ARTICLE

DEPARTMENTS

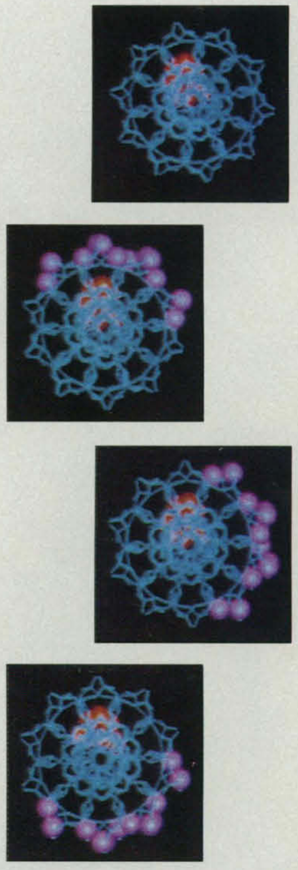
COVER

Mosaic of three image sets from the Clementine spacecraft ultraviolet-visible camera of the lunar impact crater Tycho (85-kilometer diameter). A color composite is shown in mirror format on the left. The colors emphasize variations in surface units, where blues and greens indicate relatively recently exposed material, and green indicates a higher abundance of iron-bearing minerals. The red area surrounding Tycho is a ring of lower albedo impact melt. See page 1844 and related Reports on Clementine data beginning on page 1835. [Color composite image: produced at Brown University]

REPORTS

CLEMENTINE

TECHNICAL COMMENTS



◩ Indicates accompanying feature

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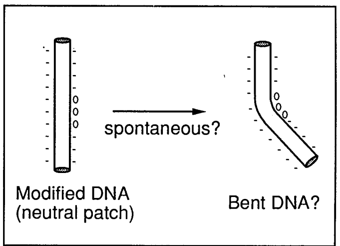
edited by PHIL SZUROMI

Bending DNA

Protein binding can bend a DNA double helix. In some cases, it is thought that cationic peptide side chains on the protein neutralize the negative charge on phosphate groups on one backbone; this charge im-



balance leads to a force that bends the helix. Strauss and Maher (p. 1829; see the Perspective by Crothers, p. 1819) tested this idea by synthesizing DNA double helixes that contained short segments of neutral methylphosphonates instead of phosphates in one of the backbone strands. They show that such DNA strands are bent in toward the charge-neutralized surface.

■

Clementine's view of the moon

Earlier this year Clementine, a lightweight spacecraft developed by NASA and the Defense Department, orbited the moon for more than 2 months, mapping and surveying the entire surface. Seven Reports in this issue recount the mission and the unprecedented detail of results that it achieved. Nozette *et al.* (p. 1835) describe the instrumentation Clementine carried, which included multiwavelength imaging capacity from the infrared to the ultraviolet, as well as a laser-ranging system. The latter yielded a topographic survey of the lunar surface, which in conjunction with gravity data derived from the spacecraft's trajectory produced the high-resolution map of the moon's shape and crustal structure discussed by Zuber *et al.* (p. 1839). Pieters *et al.* (p. 1844) used ultraviolet and visible light images to investigate the lithography of the impact craters Copernicus, Tycho, and Giordano Bruno. Impact melts and different components of excavated minerals are readily identified. By means of laser altimetry, Spudis *et al.* (p. 1848) identified several partly obliterated multiring basins due to impacts early in lunar history; some previously tentative identifications are now confirmed, and a number of newly identified basins are described. Shoemaker *et al.* (p. 1851) offer a wholly new view of the moon's south polar region, much of which is permanently in shadow because of encircling mountains and crater rims. Topographic and geological differences between the near and far sides of the moon are discussed by Lucey *et al.* (p. 1855). The heavily cratered far side, which does not have the large basaltic plains so prominent on the near side, has significantly different surface mineralogy and a different distribution of elevations. Finally, McEwen *et al.* (p. 1858) use Clementine's capabilities to study the already-much-studied Aristarchus region, showing how detailed mineralogical and stratigraphic information can be used to reconstruct the history of a portion of the moon's surface.

Put differently

Activation of growth factor receptors or other tyrosine kinases leads to formation of complexes of signaling proteins. The tyrosine phosphorylated substrates, which include the receptors themselves, can be bound by other proteins that contain SH2 domains–100-residue regions that recognize phosphotyrosine in the context of specific adjacent residues. Kavanaugh and Williams (p. 1862) show that SHC—a protein that has an SH2 domain and appears to participate in activation of Ras—has another domain that recognizes phosphotyrosine. This phosphotyrosine-binding (PTB) domain allows SHC to interact with a 145-kilodalton protein of unknown function in cells stimulated with growth factors. The PTB domain may provide another mechanism by which growth factors and oncogenes lead to interaction of specific proteins and thus to alterations in cellular function.

■

Superantigen binding

Peptide antigens bind to specific types of molecules of the major histocompatibility complex (MHC) in a surface groove, but superantigens, which are proteins produced by many bacteria and viruses, bind less specifically to many types of MHC molecules outside of this groove. Thibodeau *et al.* (p. 1874) use mutant MHC class II molecules to show that although two superantigens, enterotoxin B from *Staphylococcus aureus* (SEB) and toxic shock syndrome toxin–1 (TSST-1), bind to the same region of different subsets of the human class II MHC molecule HLA-DR1, peptide binding into the groove of the MHC molecule affects superantigen binding. Kim *et al.* (p. 1870) determined the x-ray crystal structure of TSST-1 bound to HLA-DR1 and found that, unlike a previously determined structure for SEB bound to HLA-DR1, the TSST-1 binding site extends over half of the peptide binding site. These results suggest that peptide antigens can play a role in the activation of T cells by superantigens.

■

Kaposi's sarcoma and herpesvirus

Because gay and bisexual men are much more likely to develop Kaposi's sarcoma (KS) tumors than other people with acquired immunodeficiency syndrome, it has been thought that a sexually transmitted infection agent may underlie its cause. Chang *et al.* (p. 1865) identified DNA sequences in KS tissues that are rare or absent in healthy tissue. These sequences are homologous to but distinct from other herpesviruses and may represent a new human herpesvirus. In a news story, Cohen (p. 1803) discusses whether such a virus could be an infectious agent that causes KS or is a virus that colonizes KS lesions.

■

Back to basics

In order to understand how a transcription factor functions in a specific context in vivo, it is necessary to define the domains of the protein that are required. Rørth (p. 1878) has substituted various domains in CCAAT/enhancer binding protein (C/EBP) of *Drosophila* with heterologous domains and tested if the chimeric proteins could substitute for wild-type C/EBP during development. The chimeras could rescue a C/EBP mutant if they contained the C/EBP-specific basic region, but could contain heterologous activation and leucine zipper dimerization domains. These experiments support the model that the basic region dictates C/EBP-specific activity in vivo.

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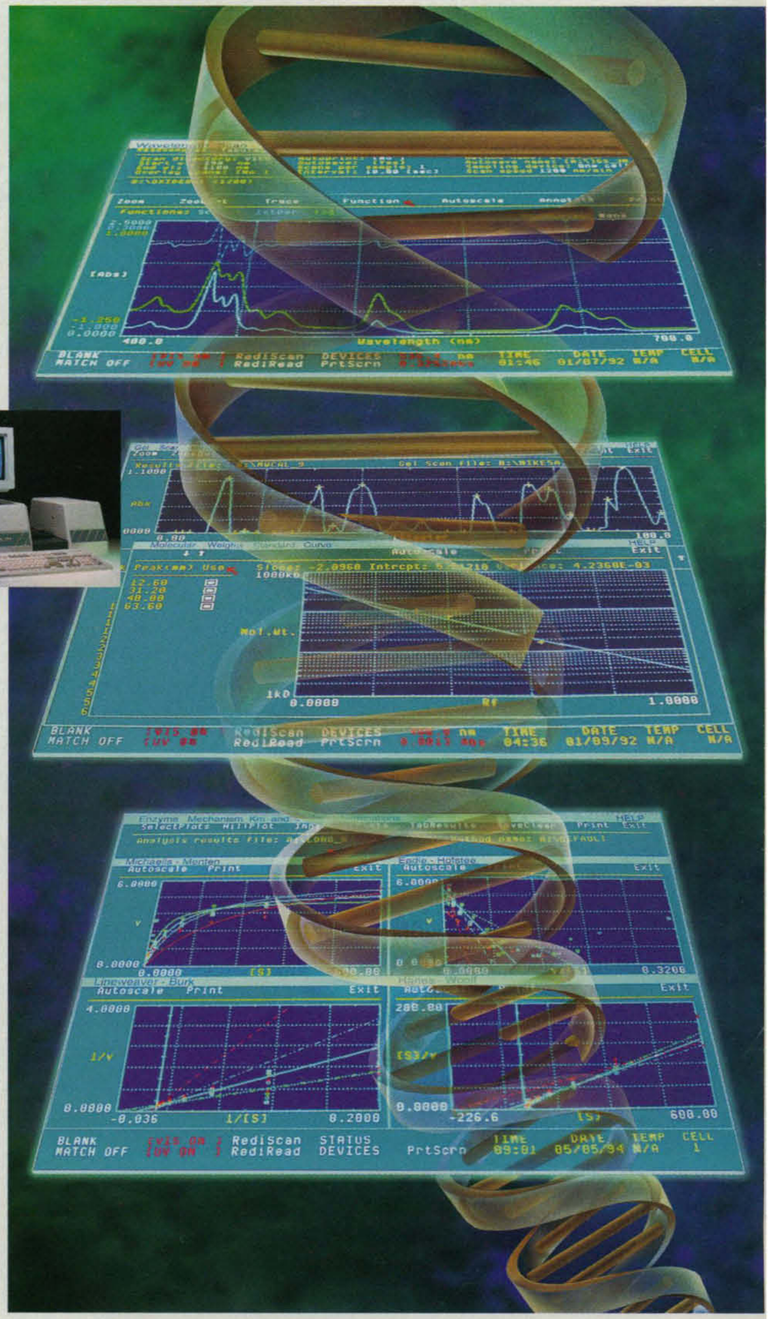

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