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► **COVER:** 'Exit strategies' by Tom Wilson, inspired by the review on p811.



DAVID O'CONNELL



SUSAN JONES



SHEILAGH MOLLOY

August 2006 saw the final days of the sixteenth International AIDS conference in Toronto overshadowed by the protests of a large group of South African HIV-positive delegates who sought asylum in Canada, claiming they faced severe discrimination in their home country. It is now 25 years since the first AIDS cases were reported in the United States but, as these events testify, people living with HIV infection in the developing world still face unacceptable hardships.

Although HAART (highly active anti-retroviral therapy) has revolutionized the treatment of HIV infection, only one in five people in low and middle-income countries have access to these therapies, and so preventative treatments for HIV remain the ideal solution and an effective vaccine the ultimate goal. This month, Amalio Telenti and David Goldstein share their vision of how scientists can harness genomics techniques in the search for a vaccine against HIV (page 865). They focus not on the virus, but on the host genome, explaining how recent advances in our knowledge of human genetic variation — exemplified by data gleaned from the HapMap project — can be used to identify genes that influence the immune response to HIV.

In light of the global spread of the highly pathogenic H5N1 avian influenza virus, new technologies to survey the species specificity of such viruses are much needed. Influenza viruses bind to host-cell glycans that differ in structure among species, and the nature of the interaction between virus and host glycans is an important determinant of the species barrier. On page 857, James Stevens and colleagues describe how recently developed glycan microarrays can be used to rapidly assess and characterize influenza virus receptor specificity, providing valuable information about the potential emergence of pandemic influenza virus strains.

EDITORIAL OFFICES

LONDON NatureReviews@nature.com
The Macmillan Building, 4 Crinan Street,
London N1 9XW, UK

Tel: +44 (0)20 7843 3620;
Fax: +44 (0)20 7843 3629

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MANAGEMENT OFFICES

LONDON nature@nature.com
The Macmillan Building,
4 Crinan Street,
London N1 9XW, UK

Tel: +44 (0)20 7833 4000;
Fax: +44 (0)20 7843 4596/7

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NEW YORK nature@natureny.com

Nature Publishing Group, 75 Varick Street,
9th floor, New York, NY 10013-1917, USA

Tel: +1 212 726 9200;

Fax: +1 212 696 9006

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Chiyoda Building 5F, 2-37-1 Ichigayatamachi,
Shinjuku-ku, Tokyo 162-0843, Japan

Tel: +81 3 3267 8751;

Fax: +81 3 3267 8746

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