

**s8a.m9.o5** **Structural studies of influenza virus neutralization by antibodies.** M. Knossow<sup>1</sup>, C. Barbey-Martin<sup>1</sup>, B. Gigant<sup>1</sup>, T. Bizebard<sup>1</sup> & J.J. Skehel<sup>2</sup> (1) *L.E.B.S. C.N.R.S. 91198 Gif sur Yvette France* (2) *N.I.M.R. Mill Hill London NW7 1AA U.K.*

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*Notes*

The haemagglutinin (HA) is the influenza surface glycoprotein which interacts with infectivity neutralizing antibodies. As a consequence of this immune pressure, it is the variable virus component important in the antigenic drift which results in recurrent epidemics of influenza. The structures of the complexes of HA with neutralizing antibodies we have determined provide information on the mechanism of virus infectivity neutralization and on the mechanism of virus escape from neutralization<sup>1,2</sup>.

The range of antigenic mutations observed during successive epidemics indicates that antibodies with a wide variety of specificities are elicited by influenza viruses. Despite that and despite the existence of a few conserved amino acids on the surface of HA, antibodies that cross-react with more than two successive epidemic strains are extremely rare. The structure of the complex of one such antibody with HA accounts for the mutations that allow escape from neutralization by this antibody and provides a rationale for the recurrence of influenza epidemics in spite of the intense selective pressure exerted by the immune response.

[1] Fleury, D., Wharton, S., Skehel, J.J., Knossow, M., and Bizebard, T. 'Antigen Distortion Allows Influenza Virus To Escape Neutralization' (1998) *Nature Structural Biology*, 5, 119-123.

[2] Fleury, D., Barrère, B., Bizebard, T., Daniels, R.S., Skehel, J.J. and Knossow, M. 'A complex of influenza hemagglutinin with a neutralizing antibody that binds outside the virus receptor binding site' (1999) *Nature Structural Biology*, 6, 530-534.