

Review

Herpes Virus Fusion and Entry: A Story with Many Characters

Roselyn J. Eisenberg ^{1,*}, Doina Atanasiu ², Tina M. Cairns ², John R. Gallagher ²,
Claude Krummenacher ² and Gary H. Cohen ²

¹ Department of Pathobiology, School of Veterinary Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA

² School of Dental Medicine, University of Pennsylvania, 240 South 40th Street, Philadelphia, PA 19104, USA; E-Mails: doinaa2@biochem.dental.upenn.edu (D.A.); tmcairns@biochem.dental.upenn.edu (T.M.C.); joga@dental.upenn.edu (J.R.G.); ckrummen@dental.upenn.edu (C.K.); ghc@dental.upenn.edu (G.H.C.)

* Author to whom correspondence should be addressed; E-Mail: roselyn@dental.upenn.edu; Tel.: +1-215-898-6552; Fax: +1-215-898-8385.

Received: 25 April 2012; in revised form: 4 May 2012 / Accepted: 9 May 2012 /

Published: 10 May 2012

Note: A recent paper by Connolly and Longnecker (J.Virol. epub ahead of print, April 4, 2012) has presented data to support a model for refolding of HSV gB. Using mutagenesis as their main tool, they show that residues within the C-terminal arm of the gB ectodomain contribute to its refolding during the fusion step of virus entry and provide a model for how gB refolds from a prefusion to postfusion structure. In their model, the refolding is reminiscent of the six-helix bundle that provides the energy for fusion in class I fusogens. It will be of interest to test the accuracy of this model in future studies.
