Structural basis of antagonism of human APOBEC3F by HIV-1 Vif

Yingxia Hu[1], Belete A. Desimmie[2], Henry C. Nguyen[1, 3], Samantha J. Ziegler[1], Tat Cheung Cheng[1, 4], John Chen[2], Jia Wang[5], Hongwei Wang[5], Kai Zhang[1], Vinay K. Pathak[2,*], and Yong Xiong[1,*]

[1]Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, Connecticut 06511, USA;

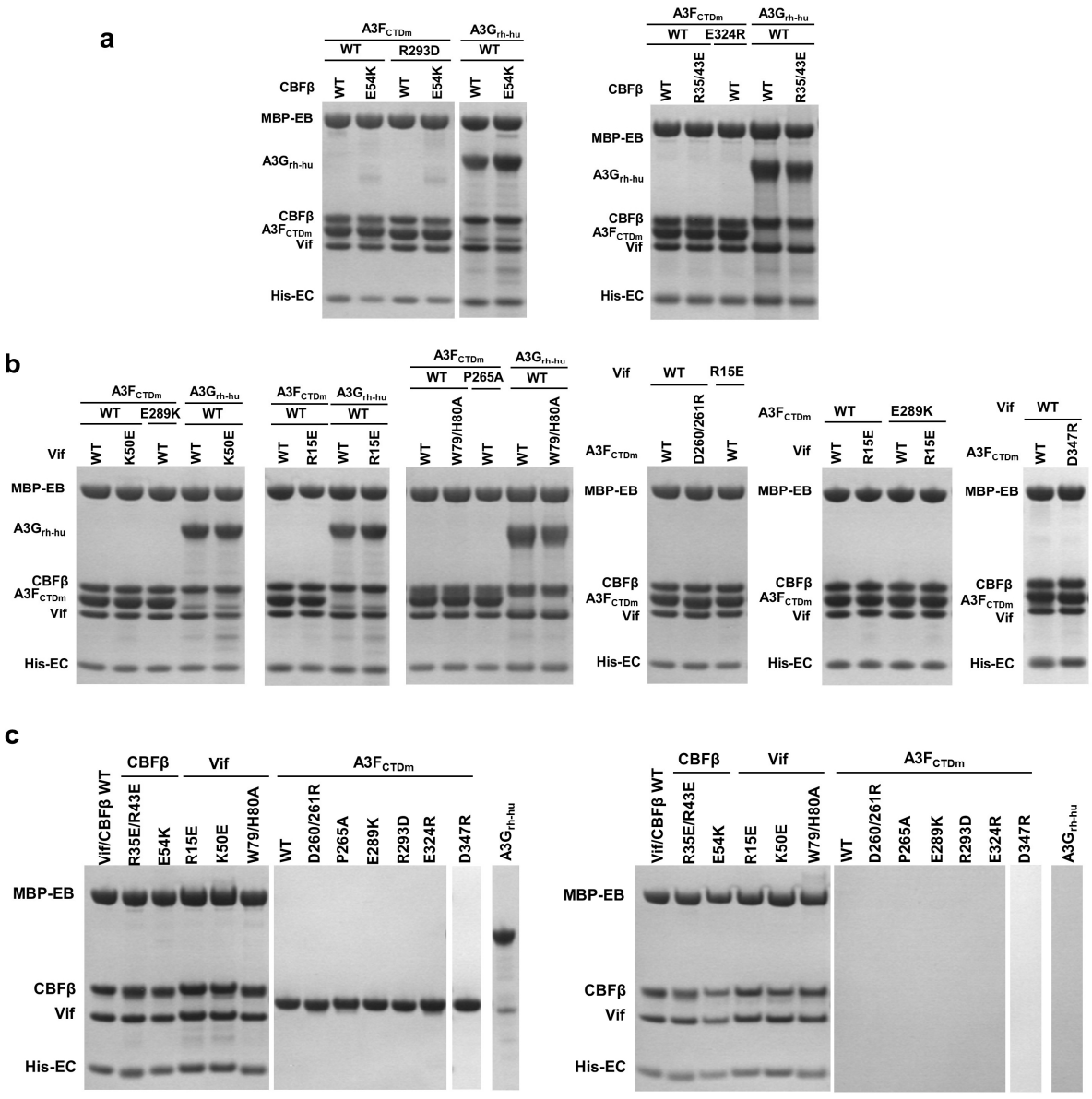
[2]Viral Mutation Section, HIV Dynamics and Replication Program, Center for Cancer Research, National Cancer Institute at Frederick, Frederick, Maryland 21702, USA;

[3]Present address: Department of Biochemistry and Biophysics, University of California, San Francisco, San Francisco, California 94158, USA;

[4]Present address: IGBMC, CNRS, Illkirch 67404, France;

[5]School of Life Sciences, Tsinghua University, Haidian District, Beijing 100084, China

*Corresponding authors. All correspondence should be addressed to: yong.xiong@yale.edu or pathakv@mail.nih.gov



Supplementary Fig. 1: The MBP column loading controls for the *in vitro* pull-down assay of the CBFβ-A3F interface (a) and the Vif-A3F interface (b), along with the loading (left) and elution (right) fractions of all Vif/CBFβ/EloB/EloC or A3F$_{CTDm}$ variants and A3G$_{rh-hu}$ alone (c).