

Molecular basis for epitope recognition by non-neutralizing anti-gp41 antibody F240

Neelakshi Gohain^{1,2}, William D. Tolbert^{1,2}, Chiara Orlandi^{1,3}, Jonathan Richard^{4,5}, Shilei Ding^{4,5}, Xishan Chen^{1,2}, Daniel A. Bonsor^{1,6}, Eric J. Sundberg^{1,3,6}, Wuyuan Lu^{1,2}, Krishanu Ray², Andrés Finzi^{4,5,8}, George K. Lewis^{1,3}, Marzena Pazgier^{1,2#}

¹Division of Vaccine Research of Institute of Human Virology and ²Department of Biochemistry and Molecular Biology and ³Department of Microbiology and Immunology of University of Maryland School of Medicine, Baltimore, USA

⁴Centre de Recherche du CHUM and ⁵Department of Microbiology, Infectiology and Immunology, Université de Montréal, Montreal, Quebec, Canada,

⁶Division of Basic Science of Institute of Human Virology and Department of Medicine of University of Maryland School of Medicine, Baltimore, USA

⁸Department of Microbiology and Immunology, McGill University, Montreal, Quebec, Canada,

#To whom correspondence should be addressed:

Email: mpazgier@ihv.umaryland.edu

725 West Lombard Street, Baltimore, MD 21201, USA

Tel: (410)706-4780

Fax: (410)706-7583

Supplementary Figures and tables

Table S1. Buried surface area as calculated by the EBI PISA server (http://www.ebi.ac.uk/msd-srv/prot_int/cgi-bin/piserver).

		Fab F240-gp41			Fab 7B2-gp41		
		1 st copy	2 nd copy	Average	1 st copy	2 nd copy	Average
Buried Surface Area, Å²	gp41 total	808.7	876.3	842.5	735.3	727.1	731.2
	Heavy chain total	462.3	470.4	466.4	425	425.9	425.5
	FWR H	4.1`	7.9	6.0	0	0	0
	CDR H1	58	57.7	57.9	42.3	45.1	43.7
	CDR H2	18.8	18.9	18.85	20.5	19.6	20.1
	CDR H3	381.4	385.9	383.7	362.2	361.2	361.7
	Light chain total	255	294.6	274.8	182.8	177.7	180.3
	FWR L	52	51.5	51.7	56.8	56.1	56.5
	CDR L1	88.8	133.4	111.2	0	0	0
	CDR L2	101.3	96.6	99.0	112.8	109.5	111.2
	CDR L3	12.9	13.1	13.0	13.2	12.1	12.7
	Heavy and light chain total	717.3	765	741.2	607.8	603.6	605.7

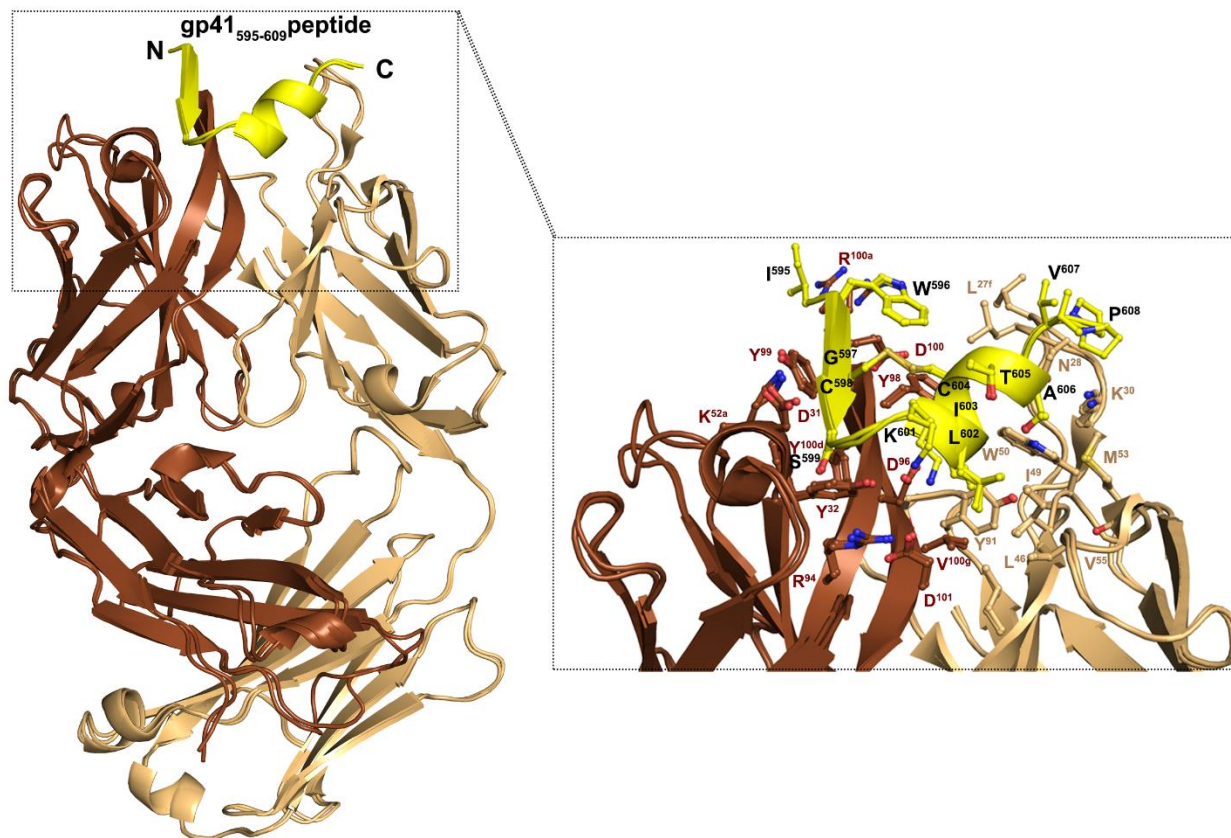


Figure S1: Ribbon diagram of superposition of the two copies of F240 Fab- gp41₅₈₃₋₆₁₈ complex from the asymmetric unit of the crystal. The blow up shows the F240 Fab-gp41₅₈₃₋₆₁₈ binding interface with residues contributing to the interface shown as sticks. Overall structures of these copies are very similar with the root mean square deviation (RMSD) of equivalent C α atoms of 0.61 Å for the complex, 0.62 Å for Fab molecules and 0.47 Å for gp41₅₈₃₋₆₁₈ peptide.

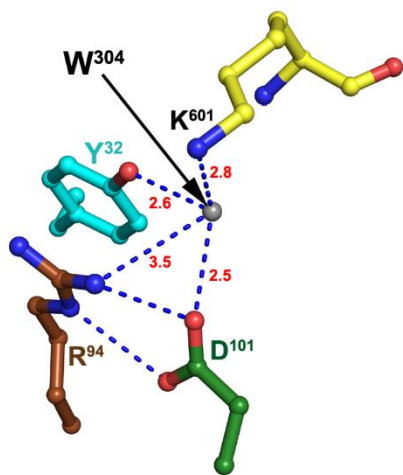


Figure S2: Network of water mediated H-bonds at the F240Fab- gp41₅₈₃₋₆₁₈ interface.

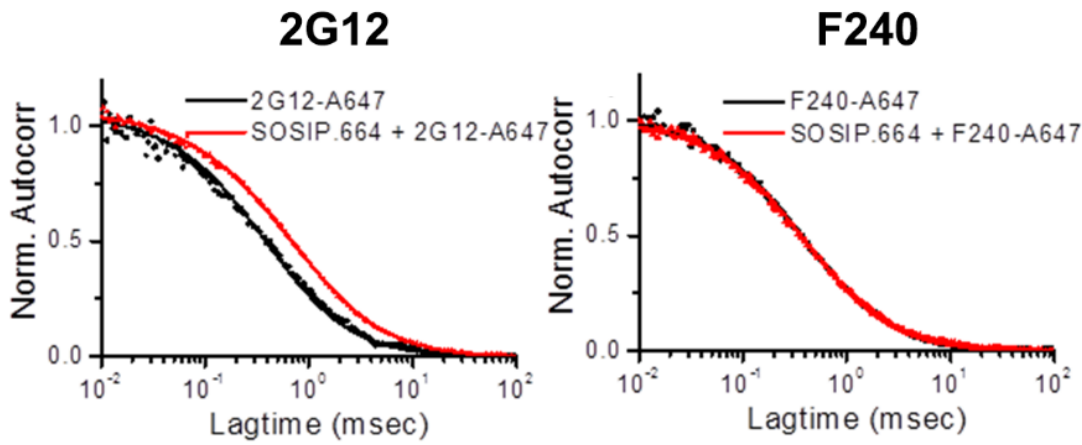


Figure S3: Autocorrelation curves of Alexa 647 labeled mAb 2G12 and F240 in the presence or absence of SOSIP. From the FCS measurements, the translational diffusion coefficient of Alexa 647 labeled 2G12 or F240 is determined to be $60 \pm 3 \mu\text{m}^2/\text{sec}$ after fitting the autocorrelation curves with a diffusion model. The diffusion coefficient of F240 remain unchanged even after incubating with BG505 SOSIP suggesting F240 does not bind to SOSIP which is in accordance with the binding profile of F240 to SOSIP as reported earlier. To confirm the binding profile of F240 to SOSIP in solution, we included Alexa 647 labeled 2G12 as a positive control. The diffusion coefficient of Alexa 647 labeled 2G12 has been significantly decreased upon binding to BG505 SOSIP. The diffusion coefficient for this 2G12-SOSIP complex is determined to be $20 \pm 2 \mu\text{m}^2/\text{sec}$. By fitting the autocorrelation curve of 2G12-SOSIP complex, the fraction of bound 2G12 is determined to be 50% as shown in Figure 4B.

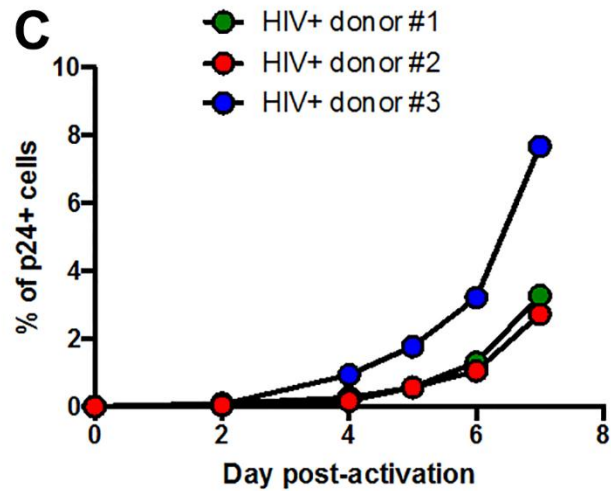
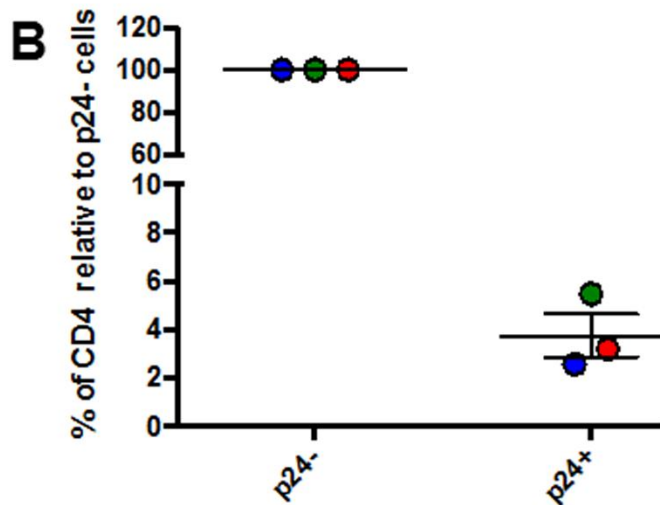
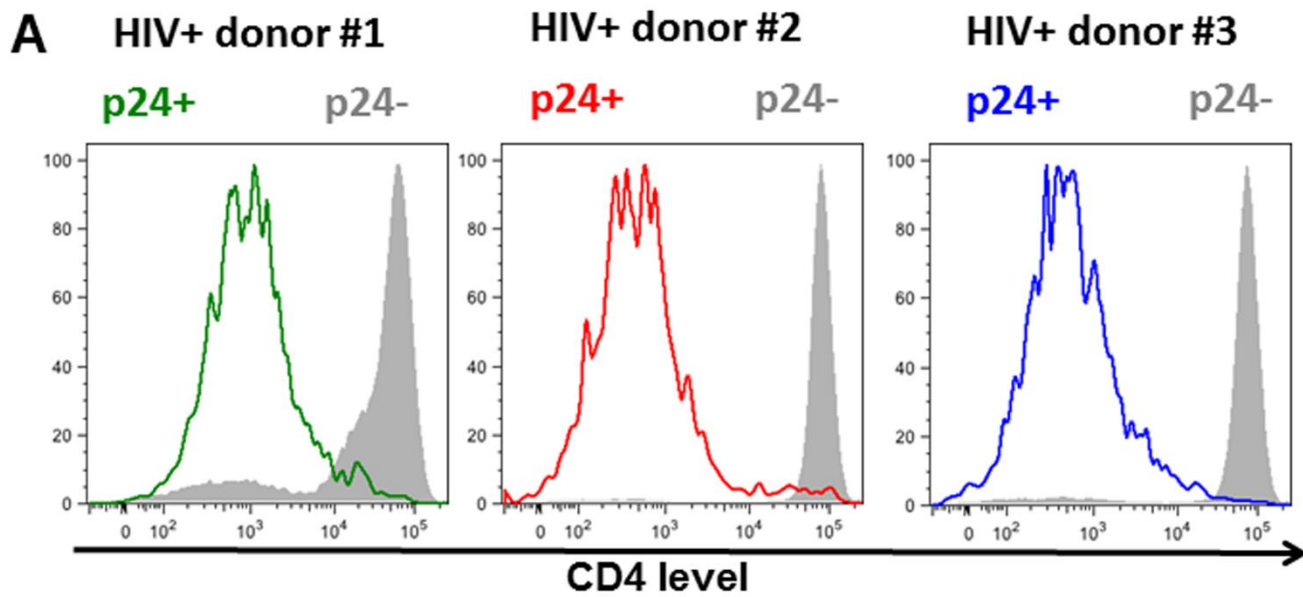


Figure S4: Level of cell-surface CD4 on endogenously-infected primary CD4+ T cells. Cell-surface staining of primary CD4+ T cells isolated from 3 HIV-1-infected individuals after activation, with an anti-CD4 mAbs. (A) Histograms depicting representative staining, (B) percentage of CD4 at the surface of HIV-1-infected (p24+) relative to uninfected (p24-) cells and (C) the kinetic of p24+ cells upon reactivation for the three HIV+ donors