

Supplementary materials

HIV genome-wide protein associations: A review of 30 years of research

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Supplementary tables

Table S 1: Summary of HIV-1 PDB codes used for our structural visualization

Gene	<i>gag</i>						<i>pol</i>			<i>vif</i>	<i>vpr</i>	<i>tat</i>	<i>rev</i>	<i>Vpu</i>	<i>env</i>		<i>nef</i>
Protein	Matrix	Capsid	SP1	Nucleocapsid	SP2	p6	Protease	RT	Integrase	Vif	Vpr	Tat	Rev	Vpu	GP120	GP41	Nef
Number of units	3	5,6	1	1	1	1	2	2	4	2,3,4	1	2	2,6	1	3	3	2
Multimeric protein	1HIW #	3H4E 4XFZ	-	-	-	-	1A30 4LL3	3V4I 3V81	1K6Y	-	-	-	3LPH		4NCO 4TVP	2XRA 4TVP	-
Monomeric protein	-	-	1U57	1A1T	-	2C55	-	-	-	4N9F	1M8L	1K5K	-	1VPU 1PJE	-	-	4EMZ 1AVV

#: HIV PDB codes were extracted from the RCSB Protein Data Bank (<http://www.rcsb.org/>) using the protein sequence search.

-: a PDB code does not exist or is not available.

For GP41, we used 4TVP to visualize the pre-fusion state, and 2XRA to visualize the post-fusion state. Most protein structures are crystalized from HIV-1 strains, except for SIV Vpx (PDB: 4CC9) and prototype foamy virus integrase (PDB: 3L2V).

In **Figure 5A**, the following HIV-1 PDB codes are used to show the structure of Env in complex with CD4 and CXCR4.

- (A) GP120 positions: 31–505 (PDB codes: 4JM2, 4TVP, 4NCO);
- (B) GP41 positions: 518–664 (PDB codes: 4JM2, 4TVP, 4NCO);
- (C) CXCR4 positions: 27–328 (PDB code: 3ODU);
- (D) CD4 positions: 26–388, 397–458 (PDB codes: 1WIO, 2KLU).

In **Figure 10B**, the following HIV-1 PDB codes are used to visualize protease structures crystalized with 6 substrate peptides derived from Gag and GagPol cleavage sites.

- (A) The MA–CA cleavage site (PDB: 1KJ4);
- (B) The SP1–NC cleavage site (PDB: 1KJ7);
- (C) The NC–SP2 cleavage site (PDB: 1TSQ);
- (D) The SP2–p6 cleavage site (PDB: 1KJF);
- (E) The p51–p15 cleavage site (PDB: 1KJG);
- (F) The p15–IN cleavage site (PDB: 1KJH).

Table S2: Summary of publication citations implying the citation level of HIV pairwise protein interactions.

Protein interaction	References	Citation numbers extracted from Google Scholar	Level
GP120 – GP41	(1-11)	228+130+19+3+71+93+24+274+235+6+63=1146	High
GP41 ^{Env} – Matrix	(12-19)	190+45+290+18+15+2+13+323=896	High
GP120 – Tat	(20-23)	41+4+28+4=77	Median
RT – Integrase	(24-31)	72+54+20+222+6+174+2+115=665	High
RT – Nucleocapsid	(32-35)	86+99+190+97=472	High
RT – Vif	(36)	20	Low
RT – Tat	(37)	28	Low
RT – Nef	(38, 39)	16+5=21	Median
Integrase – Rev	(40-42)	34+56+21=111	High
Integrase – Matrix	(43)	421	High
Matrix – Vpr	(44)	32	Low
Integrase – Nef	(39)	5	Low
Tat – Vpr	(45)	111	Median
Tat – Rev	(46)	1	Low
Tat – Nef	(47)	34	Low
Tat – Nucleocapsid	(48)	1	Low
Vif – Vpr	(49)	18	Low
NC ^{Gag} – Vif	(50-53)	155+68+6+109=338	High
NC ^{Gag} – Vpr	(54-56)	33+83+119=235	High
p6 ^{Gag} – Vpr	(56-67)	178+87+77+104+409+112+18+119+62+14+29+136=1345	High
p6 ^{Gag} – Vpx	(56, 57, 68, 69)	87+119+15+26=247	High
GP41 ^{Env} – Nef	(70)	53	Low
Gag – RT	(71, 72)	12+20=32	Median
Protease – Gag/GagPol	(73-75)	225+8+1=234	High
Protease – Vif	(76-78)	17+28+13=58	Median

Protease – RT	(79)	36	Low
Protease – Tat	(80)	42	Low
Protease – Nef	(81-85)	28+45+55+94+20=242	High
Protease – GP41CT	(86, 87)	33+14=47	Median

(i) Protein interaction, HIV pairwise protein interactions listed in our main text; (ii) References, publications that have characterized HIV protein interactions; (iii) Citation numbers extracted from Google Scholar, the total number of citations of references based on Google Scholar search on March 1, 2016. (iv) Level, the citation level measured by the number of publications and their citation numbers. (a) High: well-known interactions that have been cited more than 300 times, or have been recorded by at least 3 publications with more than 100 citations in total. (b) Low, little-known interactions that have been reported by a single paper with less than 100 citations. (c) Median, lesser-known interactions include the remaining interactions.

Supplementary text S1

In this supplementary, we will summarize the basic functions of 16 HIV proteins. Additional information about their reference sequences, natural polymorphisms, protein structures and genomic localization is provided in our online platform (<http://www.virusface.com/>).

Matrix: HIV matrix, encoded by the *gag* gene, is a structural protein that builds the basic infrastructure of HIV particles. After the protease-mediated cleavage of Gag and Gagpol precursors, HIV matrix trimmers organize into ordered hexamers to create a structural layer beneath the viral membrane, which protects the integrity of HIV particles (88). The myristoylated N-terminal domain of HIV matrix is critical for targeting plasma membrane and for promoting viral assembly (89). To prevent nonspecific binding, matrix^{Gag} in the Gag polyprotein binds to nucleic acids in a PIP2-dependent manner (PIP2: phosphatidylinositol 4,5-bisphosphate) (88).

Capsid: HIV capsid, encoded by the *gag* gene, is a structural protein that builds the basic infrastructure of viral particles (88). The hexamer and pentamer forms of HIV capsid constitute the conical fullerene core of mature viral particles (90). The interactions between HIV capsid and host proteins allow for the packaging of host proteins (e.g. cyclophilin A) (91). HIV capsid also interacts with the host restriction factor TRIM5 α to prevent the viral uncoating at the early stage (92). Multifaceted functions of HIV capsid have been summarized in a recent review (93).

Nucleocapsid: Nucleocapsid is a structural protein encoded by the *gag* gene (88, 94-96). To prevent viral RNA from nucleases, HIV nucleocapsid coats the genomic RNA within the viral core (97). Nucleocapsid also interacts with many host proteins (e.g. the ESCRT-associated protein ALIX) to promote viral budding (98). As a RNA chaperone, nucleocapsid enhances nucleic acid-dependent steps in the HIV life cycle. For instance, it not only promotes the DNA strand-transfer reaction during reverse transcription, but also stimulates viral integration (99).

p6: p6 is a structural protein located at the C terminus of the *gag* gene (88). During viral budding, HIV p6^{Gag} recruits the host machinery to release the virus outwards from the cell surface (100). Moreover, HIV-1 p6^{Gag} binds to Vpr and host proteins (e.g. AIP1/ALIX) for their viral packaging (88).

Protease: HIV protease is the first viral enzyme encoded by the *pol* gene. During viral maturation, protease cleaves Gag polyproteins at the cleavage sites to produce structural proteins (matrix, capsid, nucleocapsid, p6). In a similar fashion, protease cleaves the GagPol precursors to produce viral enzymes (protease, reverse transcriptase, integrase). Moreover, the protease activity depends on the concentration of GagPol precursors, whilst the rate of protease-mediated autoprocessing is modulated by the adjacent p6* sequence (101).

Reverse transcriptase (RT): RT is the second enzyme encoded by the *pol* gene. To produce dsDNA from viral single-stranded RNA genome, RT in the reverse transcriptase complex (RTC) undertakes both the RNA-dependent and the DNA-dependent polymerization reactions. During reverse transcription, RT jumps from one template to another on two copies of single-stranded genomic RNAs. The frequent template switch promotes the generation of new recombinant genomes derived from two parental RNA sequences (99). Numerous mutations occur because of the error-prone reverse transcription.

Integrase: Integrase is the third enzyme encoded by the *pol* gene. After the nuclear import of the pre-integration complex (PIC), viral integrase performs two major reactions (3'-processing and strand-transfer reactions) to insert the double-stranded viral DNA into human chromosomes. Inside mature viral particles, HIV integrase is cleaved from GagPol polyproteins by viral protease. Moreover, reverse transcriptase interacts with integrase to prevent the catalytic activity of integrase before viral integration (29). As part of the reverse transcriptase complex (RTC), integrase also plays a crucial role during reverse transcription (99).

Vif: Viral infectivity factor is an accessory protein encoded by all lentiviruses except the equine infectious anemia virus (102). Vif is notorious for hijacking the human ubiquitin ligase complex CBF- β to counteract the antiviral activity of host proteins such as APOBEC-3G and APOBEC-3F (103, 104). APOBEC3 proteins from the human APOBEC3 family of DNA cytosine deaminases are known as anti-HIV proteins that potently inhibit HIV-1 by introducing G-to-A hypermutation of the viral genome to impair DNA synthesis and integration (102, 105-107). Vif also interacts with Gag polyproteins to modulate the protease-mediated proteolytic processing (102). Notably, Vif is incorporated into HIV particles during viral budding (102).

Vpr: Viral protein R is an accessory protein which enhances HIV-1 replications in the non-dividing cells (e.g. macrophages). During the HIV-1 life cycle, Vpr plays multiple functions such as the modulation of viral reverse transcription, the nuclear import of the HIV-1 pre-integration complex, the transactivation of HIV-1 long terminal repeat (LTR) promoter, and the induction of apoptosis and G2/M cell cycle arrest (see review (108)). Notably, Vpr is incorporated into HIV-1 particles during viral budding (109).

Vpu: HIV-1 viral protein U (Vpu) is a membrane-associated accessory protein with two major functions: CD4 downregulation and tetherin antagonism (110). First, Vpu hijacks the human ubiquitin machinery to target CD4, and induces the downregulation of CD4 receptors in the endoplasmic reticulum (ER). Second, Vpu antagonizes tetherin, an interferon-regulated human restriction factor, to enhance the release of viral particles. Notably, Vpu is not incorporated into HIV particles during viral budding (111).

Vpx: Vpx is an accessory protein in HIV-2 and SIV, which marks a distinct difference compared to HIV-1. Major functions of Vpx include: (i) Vpx induces the ubiquitin-proteasome-dependent degradation of SAMHD1, which is a host protein that restricts HIV-2 replication in myeloid cells (112-114). (ii) Vpx is required for HIV-2 reverse transcription (115). (iii) Vpx assists nuclear import of the viral pre-integration complex (PIC) (112-114). Notably, Vpx is incorporated into viral particles during viral budding.

Rev: Rev is an accessory protein that controls the nuclear export of unspliced and partially spliced viral RNAs from the nucleus to the cytoplasm (116). Rev multimers bind to the stem-loop structure of Rev response element (RRE) in the *env* coding region of viral RNA, forming a large oligomeric ribonucleoprotein (RNP) (99). The RNP complex interacts with human export factor CRM1 (exportin 1 or Xpo1) to shuttle from the nucleus to the cytoplasm through the nuclear pore complex (NPC). Overall, Rev activity exerts a strong influence on viral RNA transport, translation and packaging (117). Notably, Rev is not incorporated into viral particles (111).

Tat: HIV trans-activator of transcription (Tat) is a regulatory protein that plays essential roles in viral replication. Tat exists in all lentiviruses and is the first eukaryotic transcription factor known to interact with TAR (transactivating response element) in RNA instead of DNA (99). Tat interacts with various human proteins to execute multiple functions (99, 118, 119). (i) Tat activates the transcription initiation and elongation of HIV-1 LTR promoter, preventing the premature termination of transcription and polyadenylation. (ii) Tat acts as a nucleic acid chaperone to regulate the capping of HIV-1 mRNA. (iii) Tat induces the T cell apoptosis, neurodegeneration and oxidative stress. (iv) Tat regulates the expression of major histocompatibility complex (MHC) and downregulates many cell surface receptors. (v) Tat suppresses the activity of reverse transcriptase to prevent the premature synthesis of viral DNA. (vi) Extracellular Tat upregulates the CXCR4 expression on CD4⁺ T cells, stimulates the expression of cytokines and interacts with cell-surface receptors to activate cellular signal transduction pathways. Notably, Tat is not incorporated into viral particles.

GP120: Encoded by the *env* gene, the surface glycoprotein GP120 is exposed on the surface of HIV particles (120). On the virion surface, there are approximately 14 envelope spikes consisting of three molecules of GP120 and GP41 each, connected by non-covalent interactions (121). During viral entry, GP120 interacts with specific receptors (e.g. CD4) on the cell surface (122). Specifically, the binding of CD4 to GP120 induces the conformational changes of GP120, therefore exposing the V3 loop

of GP120 to interact with cellular coreceptors (e.g. CCR5). Many human neutralizing antibodies have been found to target GP120, whereas a few antibodies (e.g. PG9, PG16) have a broad neutralization activity against different HIV-1 strains (123-125).

GP41: The transmembrane glycoprotein GP41 is the second envelope protein encoded by the *env* gene. GP41 contains a glycine-rich region that is essential for membrane fusion activity (126). HIV GP41 plays multiple activities during the viral life cycle (126). (i) Env intracellular trafficking is regulated by the cytoplasmic tail of GP41 (GP41CT) which interacts with various cellular proteins. (ii) GP41CT interacts with viral Matrix to regulate Env incorporation. (iii) GP41CT regulates internalization exerted by the clathrin-mediated endocytosis. (iv) GP41CT regulates the cellular activation of host transcription factors (e.g. NF- κ B). (v) GP41 interacts with host proteins to regulate the activity of the actin cytoskeleton. (vi) HIV-1 GP41 membrane-proximal external region is targeted by human antibodies (e.g. 10E8) (127).

Nef: HIV negative regulatory factor (Nef) is an accessory protein which enhances viral pathogenesis (128). During the viral life cycle, Nef can play multiple roles (128). (i) Nef downregulates CD4 receptors and MHC molecules. (ii) Nef promotes the viral release and the cell-to-cell transmission. (iii) Nef activates the apoptosis and takes part in the clathrin-dependent endocytic pathways. Notably, Nef is incorporated into HIV particles (128).

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