Supplementary Data (Supporting Online Materials) for:

Cataloguing the HIV-1 Human Protein Interaction Network

Roger G. Ptak, William Fu, Brigitte E. Sanders-Beer, Jonathan E. Dickerson, John W. Pinney, David L. Robertson, Mikhail N. Rozanov, Kenneth S. Katz, Donna R. Maglott, Kim D. Pruitt, and Carl W. Dieffenbach

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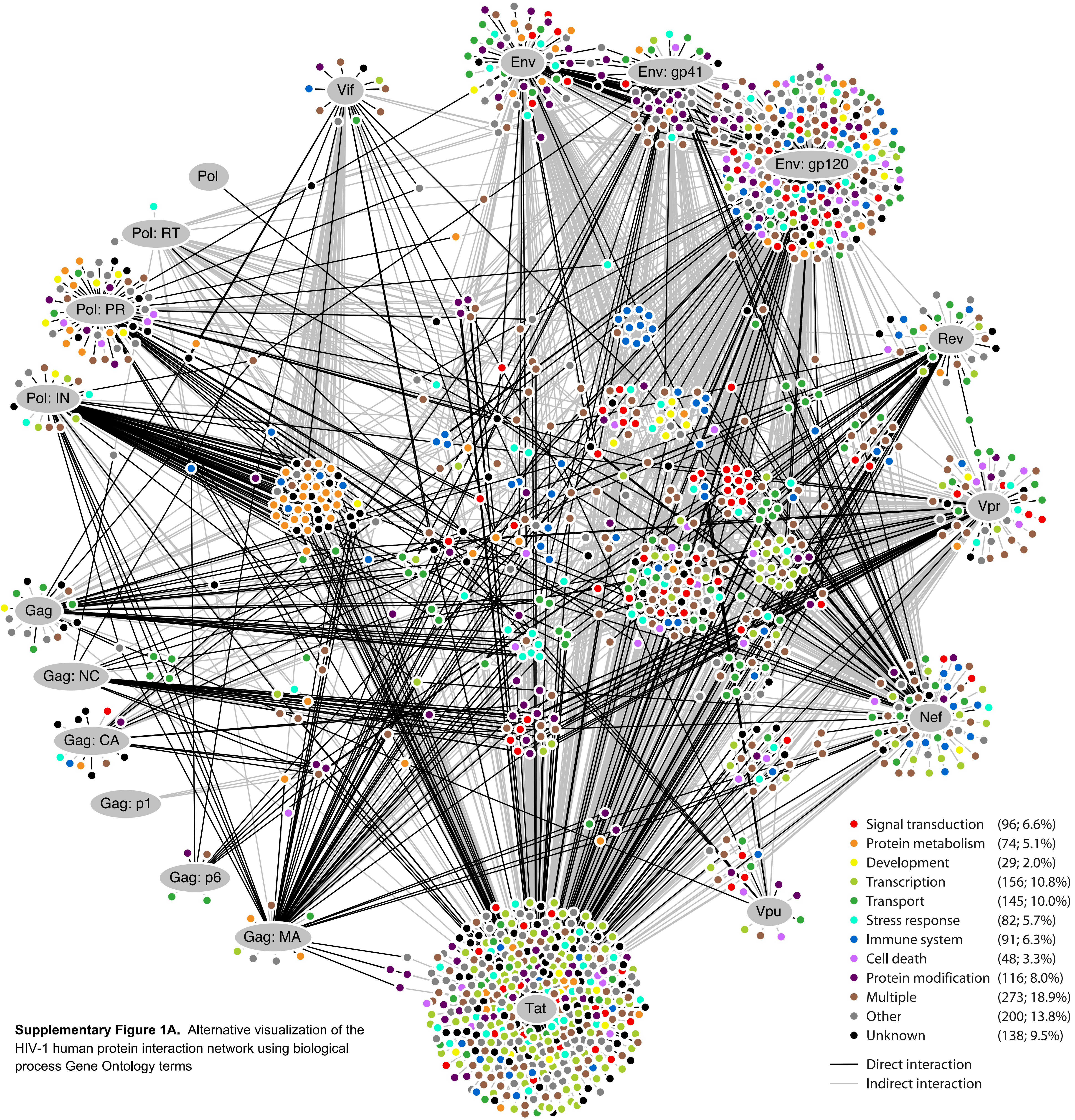
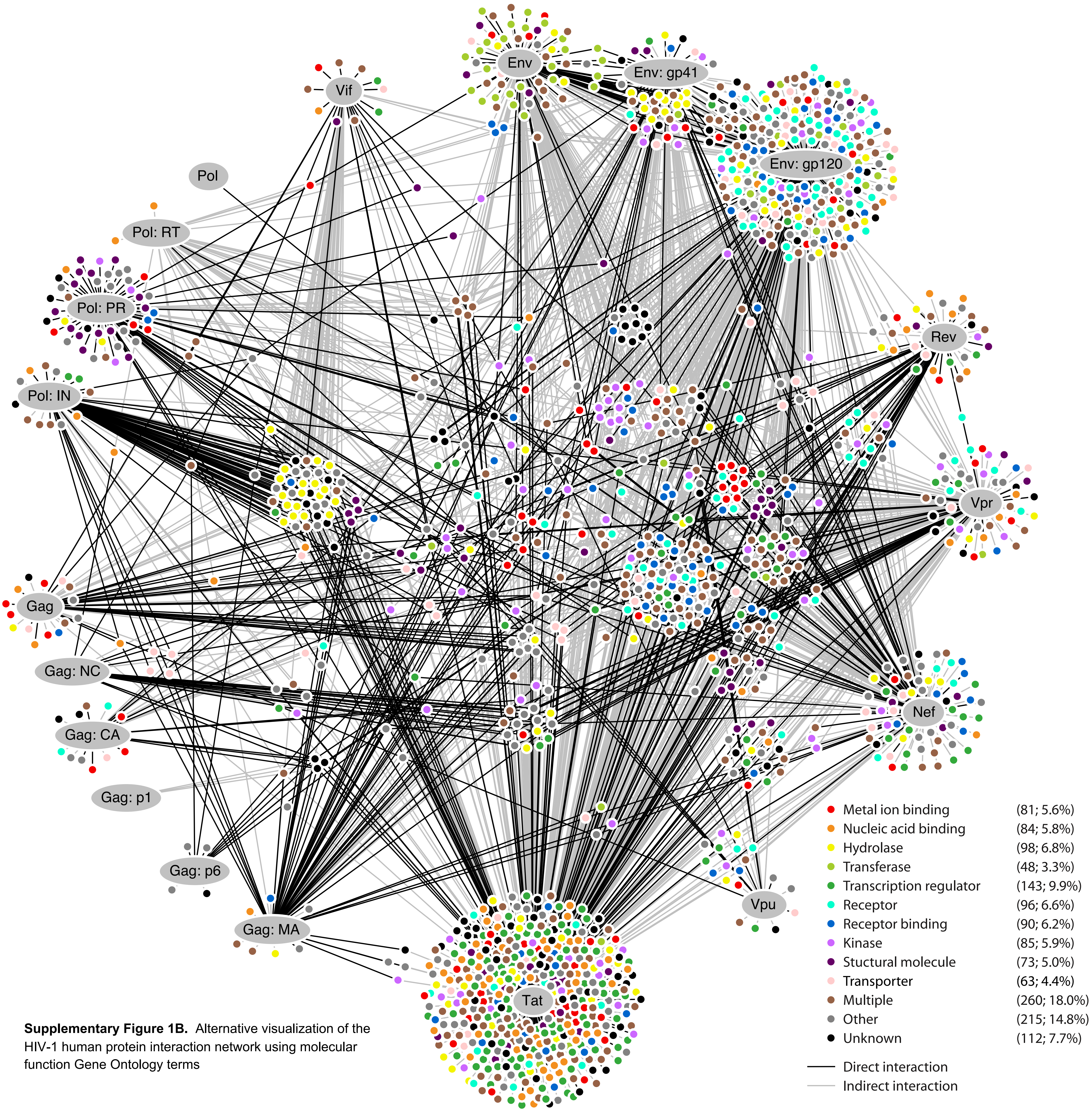


Supplementary Figure 1A. Alternative visualization of the HIV-1 human protein interaction network using biological process Gene Ontology terms



Supplementary Figure 1B. Alternative visualization of the HIV-1 human protein interaction network using molecular function Gene Ontology terms

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2	A2M	alpha-2-macroglobulin	2	Tat; retropepsin
19	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	1	Nef
58	ACTA1	actin, alpha 1, skeletal muscle	5	Envelope transmembrane glycoprotein gp41; Tat; matrix; retropepsin; reverse transcriptase
59	ACTA2	actin, alpha 2, smooth muscle, aorta	5	Envelope transmembrane glycoprotein gp41; Tat; matrix; retropepsin; reverse transcriptase
60	ACTB	actin, beta	8	Envelope transmembrane glycoprotein gp41; Nef; Rev; Tat; matrix; nucleocapsid; retropepsin; reverse transcriptase
70	ACTC1	actin, alpha, cardiac muscle 1	5	Envelope transmembrane glycoprotein gp41; Tat; matrix; retropepsin; reverse transcriptase
71	ACTG1	actin, gamma 1	8	Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; matrix; nucleocapsid; retropepsin; reverse transcriptase
72	ACTG2	actin, gamma 2, smooth muscle, enteric	5	Envelope transmembrane glycoprotein gp41; Tat; matrix; retropepsin; reverse transcriptase
81	ACTN4	actinin, alpha 4	1	Envelope transmembrane glycoprotein gp41
87	ACTN1	actinin, alpha 1	1	retropepsin
100	ADA	adenosine deaminase	1	Envelope surface glycoprotein gp120
103	ADAR	adenosine deaminase, RNA-specific	1	Envelope surface glycoprotein gp120
104	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	1	Envelope surface glycoprotein gp120
105	ADARB2	adenosine deaminase, RNA-specific, B2 (RED2 homolog rat)	1	Envelope surface glycoprotein gp120

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
107	ADCY1	adenylate cyclase 1 (brain)	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
108	ADCY2	adenylate cyclase 2 (brain)	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
109	ADCY3	adenylate cyclase 3	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
111	ADCY5	adenylate cyclase 5	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
112	ADCY6	adenylate cyclase 6	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
113	ADCY7	adenylate cyclase 7	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
114	ADCY8	adenylate cyclase 8 (brain)	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
115	ADCY9	adenylate cyclase 9	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
135	ADORA2A	adenosine A2a receptor	1	Tat
142	PARP1	poly (ADP-ribose) polymerase family, member 1	6	Envelope surface glycoprotein gp120; Nef; Tat; Vpr; integrase; retropepsin
143	PARP4	poly (ADP-ribose) polymerase family, member 4	1	retropepsin
160	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	3	Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
161	AP2A2	adaptor-related protein complex 2, alpha 2 subunit	3	Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat
162	AP1B1	adaptor-related protein complex 1, beta 1 subunit	1	Nef
163	AP2B1	adaptor-related protein complex 2, beta 1 subunit	4	Envelope transmembrane glycoprotein gp41; Nef; Pr55(Gag); Tat
164	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	2	Envelope transmembrane glycoprotein gp41; Nef
187	AGTRL1	angiotensin II receptor-like 1	1	Envelope surface glycoprotein gp120
207	AKT1	v-akt murine thymoma viral oncogene homolog 1	3	Envelope surface glycoprotein gp120; Tat; Vpr
208	AKT2	v-akt murine thymoma viral oncogene homolog 2	3	Envelope surface glycoprotein gp120; Tat; Vpr
213	ALB	albumin	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
240	ALOX5	arachidonate 5-lipoxygenase	1	Envelope surface glycoprotein gp120
248	ALPI	alkaline phosphatase, intestinal	1	Envelope surface glycoprotein gp120
249	ALPL	alkaline phosphatase, liver/bone/kidney	1	Envelope surface glycoprotein gp120
250	ALPP	alkaline phosphatase, placental (Regan isozyme)	1	Envelope surface glycoprotein gp120
262	AMD1	adenosylmethionine decarboxylase 1	1	Rev
291	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	1	Vpr
302	ANXA2	annexin A2	2	Pr55(Gag); Tat
317	APAF1	apoptotic peptidase activating factor 1	1	Envelope surface glycoprotein gp120

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
329	BIRC2	baculoviral IAP repeat-containing 2	1	Vpr
330	BIRC3	baculoviral IAP repeat-containing 3	1	Tat
332	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	1	Vpr
335	APOA1	apolipoprotein A-I	2	Envelope surface glycoprotein gp120; Nef
348	APOE	apolipoprotein E	2	Envelope surface glycoprotein gp120; Tat
350	APOH	apolipoprotein H (beta-2-glycoprotein I)	1	Pr55(Gag)
351	APP	amyloid beta (A4) precursor protein (peptidase nexin-II, Alzheimer disease)	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat; retropepsin
355	FAS	Fas (TNF receptor superfamily, member 6)	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpu
356	FASLG	Fas ligand (TNF superfamily, member 6)	3	Envelope surface glycoprotein gp120; Nef; Tat
375	ARF1	ADP-ribosylation factor 1	1	Nef
382	ARF6	ADP-ribosylation factor 6	2	Nef; Pr55(Gag)
387	RHOA	ras homolog gene family, member A	2	Tat; Vpr
388	RHOB	ras homolog gene family, member B	1	Vpr
391	RHOG	ras homolog gene family, member G (rho G)	1	Vpr
396	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	2	Tat; Vpr
466	ATF1	activating transcription factor 1	1	Vpr
467	ATF3	activating transcription factor 3	1	Nef
468	ATF4	activating transcription factor 4 (tax-responsive enhancer element B67)	1	Vpu

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
472	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	3	Rev; Vpr; integrase
545	ATR	ataxia telangiectasia and Rad3 related	2	Vpr; integrase
567	B2M	beta-2-microglobulin	1	Tat
572	BAD	BCL2-antagonist of cell death	3	Envelope surface glycoprotein gp160, precursor; Nef; Tat
573	BAG1	BCL2-associated athanogene	1	Tat
581	BAX	BCL2-associated X protein	3	Envelope surface glycoprotein gp120; Tat; Vpr
595	CCND1	cyclin D1	2	Nef; Tat
596	BCL2	B-cell CLL/lymphoma 2	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr; retropepsin
597	BCL2A1	BCL2-related protein A1	1	Vpu
598	BCL2L1	BCL2-like 1	5	Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr; Vpu
604	BCL6	B-cell CLL/lymphoma 6 (zinc finger protein 51)	1	Tat
627	BDNF	brain-derived neurotrophic factor	1	Envelope surface glycoprotein gp120
637	BID	BH3 interacting domain death agonist	1	retropepsin
649	BMP1	bone morphogenetic protein 1	1	Tat
650	BMP2	bone morphogenetic protein 2	1	Tat
659	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	1	Tat
661	POLR3D	polymerase (RNA) III (DNA directed) polypeptide D, 44kDa	1	Tat
672	BRCA1	breast cancer 1, early onset	1	Vpr

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
682	BSG	basigin (Ok blood group)	1	Envelope surface glycoprotein gp160, precursor
687	KLF9	Kruppel-like factor 9	1	Tat
708	C1QBP	complement component 1, q subcomponent binding protein	2	Rev; Tat
710	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)	2	Tat; retropepsin
712	C1QA	complement component 1, q subcomponent, A chain	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
713	C1QB	complement component 1, q subcomponent, B chain	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
714	C1QC	complement component 1, q subcomponent, C chain	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
718	C3	complement component 3	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef
721	C4B	complement component 4B (Childo blood group)	1	Envelope surface glycoprotein gp120
727	C5	complement component 5	1	Envelope surface glycoprotein gp120
728	C5AR1	complement component 5a receptor 1	2	Envelope surface glycoprotein gp120; Nef
735	C9	complement component 9	1	Envelope surface glycoprotein gp120
801	CALM1	calmodulin 1 (phosphorylase kinase, delta)	5	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; matrix; retropepsin

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
805	CALM2	calmodulin 2 (phosphorylase kinase, delta)	4	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; matrix
808	CALM3	calmodulin 3 (phosphorylase kinase, delta)	4	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; matrix
811	CALR	calreticulin	1	Envelope surface glycoprotein gp160, precursor
815	CAMK2A	calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha	1	Tat
816	CAMK2B	calcium/calmodulin-dependent protein kinase (CaM kinase) II beta	1	Tat
821	CANX	calnexin	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
823	CAPN1	calpain 1, (mu/I) large subunit	1	Envelope surface glycoprotein gp120
824	CAPN2	calpain 2, (m/II) large subunit	1	Envelope surface glycoprotein gp120
825	CAPN3	calpain 3, (p94)	1	Envelope surface glycoprotein gp120
834	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2	Envelope surface glycoprotein gp120; Vpr
836	CASP3	caspase 3, apoptosis-related cysteine peptidase	7	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; Vpu; retropepsin
839	CASP6	caspase 6, apoptosis-related cysteine peptidase	1	Envelope surface glycoprotein gp120
841	CASP8	caspase 8, apoptosis-related cysteine peptidase	4	Nef; Tat; Vpr; retropepsin

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
842	CASP9	caspase 9, apoptosis-related cysteine peptidase	4	Envelope surface glycoprotein gp120; Nef; Vpr; retropepsin
847	CAT	catalase	1	Envelope surface glycoprotein gp160, precursor
857	CAV1	caveolin 1, caveolae protein, 22kDa	1	Envelope transmembrane glycoprotein gp41
867	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	1	Nef
890	CCNA2	cyclin A2	1	Tat
891	CCNB1	cyclin B1	3	Envelope surface glycoprotein gp120; Tat; Vpr
892	CCNC	cyclin C	1	Tat
896	CCND3	cyclin D3	1	Tat
898	CCNE1	cyclin E1	3	Envelope surface glycoprotein gp120; Nef; Tat
902	CCNH	cyclin H	2	Tat; Vpr
904	CCNT1	cyclin T1	2	Tat; Vpr
905	CCNT2	cyclin T2	1	Tat
909	CD1A	CD1a molecule	1	Nef
912	CD1D	CD1d molecule	2	Envelope surface glycoprotein gp120; Nef
914	CD2	CD2 molecule	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; capsid
915	CD3D	CD3d molecule, delta (CD3-TCR complex)	5	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; capsid
916	CD3E	CD3e molecule, epsilon (CD3-TCR complex)	5	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; capsid
917	CD3G	CD3g molecule, gamma (CD3-TCR complex)	5	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; capsid
919	CD247	CD247 molecule	3	Nef; Tat; capsid

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
920	CD4	CD4 molecule	8	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vif; Vpr; Vpu
925	CD8A	CD8a molecule	1	Nef
926	CD8B	CD8b molecule	1	Nef
928	CD9	CD9 molecule	2	Envelope surface glycoprotein gp120; Pr55(Gag)
929	CD14	CD14 molecule	1	Nef
933	CD22	CD22 molecule	1	Nef
939	CD27	CD27 molecule	1	Envelope surface glycoprotein gp120
940	CD28	CD28 molecule	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr
941	CD80	CD80 molecule	4	Envelope surface glycoprotein gp120; Nef; Tat; Vpr
942	CD86	CD86 molecule	3	Nef; Tat; Vpr
945	CD33	CD33 molecule	1	Vpr
952	CD38	CD38 molecule	1	Envelope surface glycoprotein gp120
958	CD40	CD40 molecule, TNF receptor superfamily member 5	4	Envelope surface glycoprotein gp120; Tat; Vpr; Vpu
959	CD40LG	CD40 ligand (TNF superfamily, member 5, hyper-IgM syndrome)	2	Envelope surface glycoprotein gp120; Nef
960	CD44	CD44 molecule (Indian blood group)	1	Vpr
965	CD58	CD58 molecule	2	Envelope surface glycoprotein gp120; Nef
966	CD59	CD59 molecule, complement regulatory protein	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; matrix
967	CD63	CD63 molecule	1	capsid
969	CD69	CD69 molecule	4	Envelope surface glycoprotein gp120; Nef; Tat; Vpr

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
972	CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	1	Nef
974	CD79B	CD79b molecule, immunoglobulin-associated beta	1	Envelope surface glycoprotein gp120
975	CD81	CD81 molecule	2	Envelope surface glycoprotein gp120; Pr55(Gag)
977	CD151	CD151 molecule (Raph blood group)	1	Envelope surface glycoprotein gp120
983	CDC2	cell division cycle 2, G1 to S and G2 to M	4	Envelope surface glycoprotein gp120; Rev; Tat; Vpr
990	CDC6	cell division cycle 6 homolog (S. cerevisiae)	1	Tat
991	CDC20	cell division cycle 20 homolog (S. cerevisiae)	1	Tat
995	CDC25C	cell division cycle 25 homolog C (S. pombe)	2	Tat; Vpr
998	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	1	Nef
999	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	1	Vpr
1017	CDK2	cyclin-dependent kinase 2	1	Tat
1019	CDK4	cyclin-dependent kinase 4	1	Tat
1020	CDK5	cyclin-dependent kinase 5	1	Tat
1022	CDK7	cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase)	2	Tat; Vpr
1024	CDK8	cyclin-dependent kinase 8	1	Tat
1025	CDK9	cyclin-dependent kinase 9 (CDC2-related kinase)	3	Nef; Tat; Vpr

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	3	Envelope surface glycoprotein gp120; Tat; Vpr
1027	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	2	Envelope surface glycoprotein gp120; Tat
1051	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	2	Tat; Vpr
1056	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	1	Envelope surface glycoprotein gp120
1068	CETN1	centrin, EF-hand protein, 1	1	Pr55(Gag)
1069	CETN2	centrin, EF-hand protein, 2	2	Pr55(Gag); Vpr
1070	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	1	Pr55(Gag)
1072	CFL1	cofilin 1 (non-muscle)	2	Pr55(Gag); Tat
1073	CFL2	cofilin 2 (muscle)	1	Tat
1111	CHEK1	CHK1 checkpoint homolog (S. pombe)	1	Vpr
1134	CHRNA1	cholinergic receptor, nicotinic, alpha 1 (muscle)	1	Envelope surface glycoprotein gp120
1140	CHRNB1	cholinergic receptor, nicotinic, beta 1 (muscle)	1	Envelope surface glycoprotein gp120
1141	CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)	1	Envelope surface glycoprotein gp120
1147	CHUK	conserved helix-loop-helix ubiquitous kinase	2	Envelope surface glycoprotein gp120; Nef
1173	AP2M1	adaptor-related protein complex 2, mu 1 subunit	4	Envelope transmembrane glycoprotein gp41; Nef; Pr55(Gag); Tat
1174	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	2	Envelope transmembrane glycoprotein gp41; Nef
1175	AP2S1	adaptor-related protein complex 2, sigma 1 subunit	3	Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
1179	CLCA1	chloride channel, calcium activated, family member 1	1	Envelope surface glycoprotein gp120
1213	CLTC	clathrin, heavy chain (Hc)	1	Nef
1230	CCR1	chemokine (C-C motif) receptor 1	2	Envelope surface glycoprotein gp120; Tat
1231	CCR2	chemokine (C-C motif) receptor 2	2	Envelope surface glycoprotein gp120; Tat
1232	CCR3	chemokine (C-C motif) receptor 3	2	Envelope surface glycoprotein gp120; Tat
1233	CCR4	chemokine (C-C motif) receptor 4	2	Envelope surface glycoprotein gp120; Tat
1234	CCR5	chemokine (C-C motif) receptor 5	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
1235	CCR6	chemokine (C-C motif) receptor 6	1	Envelope surface glycoprotein gp120
1236	CCR7	chemokine (C-C motif) receptor 7	1	Envelope surface glycoprotein gp120
1237	CCR8	chemokine (C-C motif) receptor 8	1	Envelope surface glycoprotein gp120
1238	CCBP2	chemokine binding protein 2	1	Envelope surface glycoprotein gp120
1240	CMKLR1	chemokine-like receptor 1	1	Envelope surface glycoprotein gp120
1267	CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	1	Tat
1277	COL1A1	collagen, type I, alpha 1	1	Tat
1278	COL1A2	collagen, type I, alpha 2	1	Tat
1281	COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	1	Tat
1282	COL4A1	collagen, type IV, alpha 1	1	Envelope surface glycoprotein gp160, precursor
1284	COL4A2	collagen, type IV, alpha 2	1	Envelope surface glycoprotein gp160, precursor
1285	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	1	Envelope surface glycoprotein gp160, precursor

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
1286	COL4A4	collagen, type IV, alpha 4	1	Envelope surface glycoprotein gp160, precursor
1287	COL4A5	collagen, type IV, alpha 5 (Alport syndrome)	1	Envelope surface glycoprotein gp160, precursor
1315	COPB1	coatomer protein complex, subunit beta 1	1	Nef
1366	CLDN7	claudin 7	1	Envelope surface glycoprotein gp120
1374	CPT1A	carnitine palmitoyltransferase 1A (liver)	1	Envelope surface glycoprotein gp160, precursor
1375	CPT1B	carnitine palmitoyltransferase 1B (muscle)	1	Envelope surface glycoprotein gp160, precursor
1376	CPT2	carnitine palmitoyltransferase II	1	Envelope surface glycoprotein gp160, precursor
1380	CR2	complement component (3d/Epstein Barr virus) receptor 2	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
1385	CREB1	cAMP responsive element binding protein 1	1	Tat
1386	ATF2	activating transcription factor 2	1	Envelope surface glycoprotein gp120
1387	CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	2	Tat; Vpr
1390	CREM	cAMP responsive element modulator	1	Tat
1432	MAPK14	mitogen-activated protein kinase 14	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Vpr
1436	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog	1	Nef

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1437	CSF2	colony stimulating factor 2 (granulocyte-macrophage)	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
1445	CSK	c-src tyrosine kinase	1	Tat
1457	CSNK2A1	casein kinase 2, alpha 1 polypeptide	5	Rev; Vpu; matrix; retropepsin; reverse transcriptase
1459	CSNK2A2	casein kinase 2, alpha prime polypeptide	4	Rev; Vpu; matrix; retropepsin
1460	CSNK2B	casein kinase 2, beta polypeptide	5	Rev; Vpu; matrix; retropepsin; reverse transcriptase
1493	CTLA4	cytotoxic T-lymphocyte-associated protein 4	3	Envelope surface glycoprotein gp160, precursor; Nef; Vpr
1495	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	1	Envelope transmembrane glycoprotein gp41
1499	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	1	Vpu
1509	CTSD	cathepsin D	1	Envelope surface glycoprotein gp120
1510	CTSE	cathepsin E	1	Envelope surface glycoprotein gp120
1524	CX3CR1	chemokine (C-X3-C motif) receptor 1	1	Envelope surface glycoprotein gp120
1536	CYBB	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	1	capsid
1537	CYC1	cytochrome c-1	1	Vpr
1594	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	1	matrix
1595	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	1	Nef
1604	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	1	Envelope surface glycoprotein gp120

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GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
1636	ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	1	Envelope surface glycoprotein gp160, precursor
1647	GADD45A	growth arrest and DNA-damage-inducible, alpha	1	Vpr
1649	DDIT3	DNA-damage-inducible transcript 3	1	Tat
1653	DDX1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	1	Rev
1654	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	1	Rev
1660	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	2	Pr55(Gag); Rev
1667	DEFA1	defensin, alpha 1	1	Envelope surface glycoprotein gp120
1668	DEFA3	defensin, alpha 3, neutrophil-specific	1	Envelope surface glycoprotein gp120
1669	DEFA4	defensin, alpha 4, corticostatin	1	Envelope surface glycoprotein gp120
1674	DES	desmin	1	retropepsin
1676	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	1	retropepsin
1677	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	1	retropepsin
1755	DMBT1	deleted in malignant brain tumors 1	1	Envelope surface glycoprotein gp120
1794	DOCK2	dedicator of cytokinesis 2	1	Nef
1803	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
1805	DPT	dermatopontin	1	Nef
1810	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
1869	E2F1	E2F transcription factor 1	2	Envelope surface glycoprotein gp120; Tat
1874	E2F4	E2F transcription factor 4, p107/p130-binding	1	Tat
1906	EDN1	endothelin 1	3	Envelope surface glycoprotein gp120; Nef; Tat
1915	EEF1A1	eukaryotic translation elongation factor 1 alpha 1	3	Tat; integrase; matrix
1917	EEF1A2	eukaryotic translation elongation factor 1 alpha 2	1	Tat
1936	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	1	Tat
1938	EEF2	eukaryotic translation elongation factor 2	1	Vpr
1950	EGF	epidermal growth factor (beta-urogastrone)	1	Tat
1956	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	1	Pr55(Gag)
1958	EGR1	early growth response 1	1	Tat
1959	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	1	Tat
1960	EGR3	early growth response 3	1	Tat
1965	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	1	Tat
1968	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
1977	EIF4E	eukaryotic translation initiation factor 4E	1	Envelope surface glycoprotein gp120
1981	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	1	retropepsin
1984	EIF5A	eukaryotic translation initiation factor 5A	1	Rev
1991	ELA2	elastase 2, neutrophil	1	Envelope transmembrane glycoprotein gp41
2002	ELK1	ELK1, member of ETS oncogene family	1	Nef
2010	EMD	emerin (Emery-Dreifuss muscular dystrophy)	1	integrase
2021	ENDOG	endonuclease G	1	Tat
2023	ENO1	enolase 1, (alpha)	1	Tat
2033	EP300	E1A binding protein p300	3	Envelope surface glycoprotein gp120; Tat; Vpr
2056	EPO	erythropoietin	1	Envelope surface glycoprotein gp120
2068	ERCC2	excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D)	1	Tat
2071	ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	1	Tat
2099	ESR1	estrogen receptor 1	1	Envelope surface glycoprotein gp120
2100	ESR2	estrogen receptor 2 (ER beta)	1	Envelope surface glycoprotein gp120
2147	F2	coagulation factor II (thrombin)	1	Envelope surface glycoprotein gp120
2185	PTK2B	PTK2B protein tyrosine kinase 2 beta	3	Envelope surface glycoprotein gp120; Nef; Tat
2203	FBP1	fructose-1,6-bisphosphatase 1	1	matrix

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2204	FCAR	Fc fragment of IgA, receptor for	1	Envelope surface glycoprotein gp120
2208	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23)	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef
2209	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	1	Nef
2212	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	1	Nef
2213	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	1	Nef
2214	FCGR3A	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	1	Tat
2215	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	1	Tat
2217	FCGRT	Fc fragment of IgG, receptor, transporter, alpha	1	Envelope surface glycoprotein gp120
2237	FEN1	flap structure-specific endonuclease 1	1	integrase
2246	FGF1	fibroblast growth factor 1 (acidic)	2	Envelope surface glycoprotein gp120; Tat
2247	FGF2	fibroblast growth factor 2 (basic)	2	Envelope surface glycoprotein gp120; Tat
2280	FKBP1A	FK506 binding protein 1A, 12kDa	1	Envelope surface glycoprotein gp120
2309	FOXO3A	forkhead box O3A	1	Vpr
2316	FLNA	filamin A, alpha (actin binding protein 280)	1	retropepsin
2317	FLNB	filamin B, beta (actin binding protein 278)	1	retropepsin
2318	FLNC	filamin C, gamma (actin binding protein 280)	1	retropepsin

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2321	FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	1	Tat
2335	FN1	fibronectin 1	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; retropepsin
2353	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr
2357	FPR1	formyl peptide receptor 1	1	Envelope surface glycoprotein gp120
2358	FPRL1	formyl peptide receptor-like 1	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
2475	FRAP1	FK506 binding protein 12-rapamycin associated protein 1	1	Envelope surface glycoprotein gp120
2530	FUT8	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	1	Envelope surface glycoprotein gp160, precursor
2534	FYN	FYN oncogene related to SRC, FGR, YES	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef
2539	G6PD	glucose-6-phosphate dehydrogenase	1	Tat
2547	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)	3	Tat; Vif; integrase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2548	GAA	glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II)	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
2568	GABRP	gamma-aminobutyric acid (GABA) A receptor, pi	1	Envelope surface glycoprotein gp120
2595	GANC	glucosidase, alpha; neutral C	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
2619	GAS1	growth arrest-specific 1	1	Envelope surface glycoprotein gp120
2623	GATA1	GATA binding protein 1 (globin transcription factor 1)	1	Nef
2624	GATA2	GATA binding protein 2	1	Tat
2625	GATA3	GATA binding protein 3	1	Nef
2629	GBA	glucosidase, beta; acid (includes glucosylceramidase)	1	Tat
2648	GCN5L2	GCN5 general control of amino-acid synthesis 5-like 2 (yeast)	1	Tat
2670	GFAP	glial fibrillary acidic protein	4	Envelope surface glycoprotein gp120; Nef; Tat; retropepsin
2683	B4GALT1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	1	Envelope surface glycoprotein gp160, precursor
2688	GH1	growth hormone 1	1	Tat
2736	GLI2	GLI-Kruppel family member GLI2	1	Tat
2770	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2775	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	1	Nef
2821	GPI	glucose phosphate isomerase	1	Envelope surface glycoprotein gp120
2825	GPR1	G protein-coupled receptor 1	1	Envelope surface glycoprotein gp120
2833	CXCR3	chemokine (C-X-C motif) receptor 3	2	Nef; Tat
2838	GPR15	G protein-coupled receptor 15	1	Envelope surface glycoprotein gp120
2872	MKNK2	MAP kinase interacting serine/threonine kinase 2	1	Vpr
2876	GPX1	glutathione peroxidase 1	2	Envelope surface glycoprotein gp120; Tat
2877	GPX2	glutathione peroxidase 2 (gastrointestinal)	1	Tat
2878	GPX3	glutathione peroxidase 3 (plasma)	1	Tat
2879	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	1	Tat
2880	GPX5	glutathione peroxidase 5 (epididymal androgen-related protein)	1	Tat
2882	GPX7	glutathione peroxidase 7	1	Tat
2885	GRB2	growth factor receptor-bound protein 2	2	Nef; Tat
2896	GRN	granulin	1	Tat
2902	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	2	Envelope surface glycoprotein gp120; Tat
2903	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	2	Envelope surface glycoprotein gp120; Tat
2904	GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	2	Envelope surface glycoprotein gp120; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2905	GRIN2C	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	2	Envelope surface glycoprotein gp120; Tat
2906	GRIN2D	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	2	Envelope surface glycoprotein gp120; Tat
2907	GRINA	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	1	Envelope surface glycoprotein gp120
2908	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	1	Vpr
2911	GRM1	glutamate receptor, metabotropic 1	1	Tat
2919	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	1	Envelope surface glycoprotein gp120
2923	PDIA3	protein disulfide isomerase family A, member 3	1	Envelope surface glycoprotein gp120
2932	GSK3B	glycogen synthase kinase 3 beta	1	Tat
2934	GSN	gelsolin (amyloidosis, Finnish type)	1	Tat
2937	GSS	glutathione synthetase	1	Tat
2957	GTF2A1	general transcription factor IIA, 1, 19/37kDa	1	Tat
2958	GTF2A2	general transcription factor IIA, 2, 12kDa	1	Tat
2959	GTF2B	general transcription factor IIB	3	Tat; Vpr; nucleocapsid
2960	GTF2E1	general transcription factor IIE, polypeptide 1, alpha 56kDa	1	Tat
2961	GTF2E2	general transcription factor IIE, polypeptide 2, beta 34kDa	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
2962	GTF2F1	general transcription factor IIF, polypeptide 1, 74kDa	2	Envelope surface glycoprotein gp120; Tat
2963	GTF2F2	general transcription factor IIF, polypeptide 2, 30kDa	2	Envelope surface glycoprotein gp120; Tat
2965	GTF2H1	general transcription factor IIH, polypeptide 1, 62kDa	2	Tat; Vpr
2966	GTF2H2	general transcription factor IIH, polypeptide 2, 44kDa	1	Tat
2967	GTF2H3	general transcription factor IIH, polypeptide 3, 34kDa	1	Tat
2968	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	1	Tat
2975	GTF3C1	general transcription factor IIIC, polypeptide 1, alpha 220kDa	1	Tat
2976	GTF3C2	general transcription factor IIIC, polypeptide 2, beta 110kDa	1	Tat
2993	GYPA	glycophorin A (MNS blood group)	1	Tat
3001	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	1	Nef
3012	HIST1H2AE	histone cluster 1, H2ae	1	Tat
3013	HIST1H2AD	histone cluster 1, H2ad	1	Tat
3014	H2AFX	H2A histone family, member X	2	Tat; Vpr
3015	H2AFZ	H2A histone family, member Z	1	Tat
3017	HIST1H2BD	histone cluster 1, H2bd	1	Tat
3018	HIST1H2BB	histone cluster 1, H2bb	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3020	H3F3A	H3 histone, family 3A	1	Tat
3021	H3F3B	H3 histone, family 3B (H3.3B)	1	Tat
3055	HCK	hemopoietic cell kinase	2	Nef; Vif
3065	HDAC1	histone deacetylase 1	1	Tat
3075	CFH	complement factor H	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
3077	HFE	hemochromatosis	1	Nef
3082	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	1	Envelope surface glycoprotein gp120
3094	HINT1	histidine triad nucleotide binding protein 1	1	Envelope surface glycoprotein gp120
3096	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	1	Tat
3105	HLA-A	major histocompatibility complex, class I, A	8	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Pol; Pr55(Gag); Tat; Vpu
3106	HLA-B	major histocompatibility complex, class I, B	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpu
3107	HLA-C	major histocompatibility complex, class I, C	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpu
3108	HLA-DMA	major histocompatibility complex, class II, DM alpha	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3109	HLA-DMB	major histocompatibility complex, class II, DM beta	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3111	HLA-DOA	major histocompatibility complex, class II, DO alpha	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3112	HLA-DOB	major histocompatibility complex, class II, DO beta	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3113	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3115	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3117	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3118	HLA-DQA2	major histocompatibility complex, class II, DQ alpha 2	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3119	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3120	HLA-DQB2	major histocompatibility complex, class II, DQ beta 2	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3122	HLA-DRA	major histocompatibility complex, class II, DR alpha	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Pr55(Gag); Tat; capsid
3123	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Pr55(Gag); Tat; capsid
3125	HLA-DRB3	major histocompatibility complex, class II, DR beta 3	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat; capsid
3126	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat; capsid
3127	HLA-DRB5	major histocompatibility complex, class II, DR beta 5	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat; capsid
3133	HLA-E	major histocompatibility complex, class I, E	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3134	HLA-F	major histocompatibility complex, class I, F	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat
3135	HLA-G	HLA-G histocompatibility antigen, class I, G	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat
3156	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	1	Nef
3159	HMGA1	high mobility group AT-hook 1	2	integrase; matrix
3163	HMOX2	heme oxygenase (decycling) 2	1	Envelope surface glycoprotein gp120
3164	NR4A1	nuclear receptor subfamily 4, group A, member 1	1	Vpr
3178	HNRPA1	heterogeneous nuclear ribonucleoprotein A1	1	Rev
3190	HNRPK	heterogeneous nuclear ribonucleoprotein K	1	Rev
3265	HRAS	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	3	Envelope surface glycoprotein gp160, precursor; Nef; Tat
3266	ERAS	ES cell expressed Ras	2	Envelope surface glycoprotein gp160, precursor; Tat
3267	HRB	HIV-1 Rev binding protein	1	Rev
3268	HRBL	HIV-1 Rev binding protein-like	1	Rev
3297	HSF1	heat shock transcription factor 1	1	Vpr
3300	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	1	Vpr
3303	HSPA1A	heat shock 70kDa protein 1A	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3304	HSPA1B	heat shock 70kDa protein 1B	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix
3306	HSPA2	heat shock 70kDa protein 2	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix
3308	HSPA4	heat shock 70kDa protein 4	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix
3309	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Pr55(Gag); Tat; Vpr; matrix
3310	HSPA6	heat shock 70kDa protein 6 (HSP70B')	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix
3312	HSPA8	heat shock 70kDa protein 8	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix
3313	HSPA9	heat shock 70kDa protein 9 (mortalin)	5	Envelope surface glycoprotein gp120; Pr55(Gag); Tat; Vpr; matrix
3320	HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	1	Tat
3329	HSPD1	heat shock 60kDa protein 1 (chaperonin)	3	Envelope transmembrane glycoprotein gp41; Pr55(Gag); integrase
3336	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	1	integrase
3337	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	1	Nef
3339	HSPG2	heparan sulfate proteoglycan 2	1	Tat
3383	ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; matrix

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3397	ID1	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	1	Tat
3428	IFI16	interferon, gamma-inducible protein 16	1	Tat
3429	IFI27	interferon, alpha-inducible protein 27	1	Tat
3430	IFI35	interferon-induced protein 35	1	Tat
3431	SP110	SP110 nuclear body protein	1	Tat
3437	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	1	Tat
3439	IFNA1	interferon, alpha 1	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat; Vif; reverse transcriptase
3440	IFNA2	interferon, alpha 2	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Vif; reverse transcriptase
3444	IFNA7	interferon, alpha 7	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Vif; reverse transcriptase
3449	IFNA16	interferon, alpha 16	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Vif; reverse transcriptase
3454	IFNAR1	interferon (alpha, beta and omega) receptor 1	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3456	IFNB1	interferon, beta 1, fibroblast	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
3458	IFNG	interferon, gamma	9	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; capsid; matrix; reverse transcriptase
3460	IFNGR2	interferon gamma receptor 2 (interferon gamma transducer 1)	1	Envelope surface glycoprotein gp120
3467	IFNW1	interferon, omega 1	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
3479	IGF1	insulin-like growth factor 1 (somatomedin C)	2	Envelope surface glycoprotein gp120; Tat
3480	IGF1R	insulin-like growth factor 1 receptor	1	Envelope surface glycoprotein gp120
3487	IGFBP4	insulin-like growth factor binding protein 4	1	Tat
3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	2	Envelope surface glycoprotein gp120; Nef
3552	IL1A	interleukin 1, alpha	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat
3553	IL1B	interleukin 1, beta	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Pr55(Gag); Tat; retropepsin
3554	IL1R1	interleukin 1 receptor, type I	1	Tat
3557	IL1RN	interleukin 1 receptor antagonist	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3558	IL2	interleukin 2	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; matrix
3559	IL2RA	interleukin 2 receptor, alpha	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
3560	IL2RB	interleukin 2 receptor, beta	2	Envelope surface glycoprotein gp120; Tat
3561	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	1	Envelope surface glycoprotein gp120
3562	IL3	interleukin 3 (colony-stimulating factor, multiple)	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
3565	IL4	interleukin 4	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr; matrix
3566	IL4R	interleukin 4 receptor	1	Tat
3569	IL6	interleukin 6 (interferon, beta 2)	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; matrix
3570	IL6R	interleukin 6 receptor	2	Envelope surface glycoprotein gp160, precursor; Tat
3574	IL7	interleukin 7	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
3575	IL7R	interleukin 7 receptor	1	Tat
3576	IL8	interleukin 8	5	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3586	IL10	interleukin 10	7	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; capsid; reverse transcriptase
3592	IL12A	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr; matrix
3593	IL12B	interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40)	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat; matrix
3596	IL13	interleukin 13	3	Envelope surface glycoprotein gp120; Tat; reverse transcriptase
3600	IL15	interleukin 15	3	Envelope surface glycoprotein gp120; Nef; matrix
3603	IL16	interleukin 16 (lymphocyte chemoattractant factor)	2	Envelope surface glycoprotein gp120; Tat
3609	ILF3	interleukin enhancer binding factor 3, 90kDa	1	Rev
3620	INDO	indoleamine-pyrrole 2,3 dioxygenase	2	Envelope surface glycoprotein gp120; Vpr
3627	CXCL10	chemokine (C-X-C motif) ligand 10	3	Envelope surface glycoprotein gp120; Nef; Tat
3630	INS	insulin	1	Vpr
3655	ITGA6	integrin, alpha 6	1	Vpr
3659	IRF1	interferon regulatory factor 1	2	Nef; Tat
3660	IRF2	interferon regulatory factor 2	1	Nef
3661	IRF3	interferon regulatory factor 3	1	Nef
3665	IRF7	interferon regulatory factor 7	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3669	ISG20	interferon stimulated exonuclease gene 20kDa	1	Tat
3675	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	3	Envelope surface glycoprotein gp120; Tat; retropepsin
3676	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	1	Envelope surface glycoprotein gp120
3678	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	2	Tat; Vpr
3683	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat
3684	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	2	Envelope surface glycoprotein gp120; Nef
3685	ITGAV	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	2	Envelope surface glycoprotein gp120; Tat
3687	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	1	Envelope surface glycoprotein gp120
3688	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1	Tat
3689	ITGB2	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit)	2	Envelope surface glycoprotein gp120; Tat
3690	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3691	ITGB4	integrin, beta 4	2	Tat; retropepsin
3693	ITGB5	integrin, beta 5	1	Tat
3704	ITPA	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	1	Rev
3708	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	2	Nef; Tat
3709	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	1	Tat
3710	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	1	Tat
3716	JAK1	Janus kinase 1 (a protein tyrosine kinase)	1	Envelope surface glycoprotein gp120
3718	JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	1	Envelope surface glycoprotein gp120
3725	JUN	jun oncogene	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr
3732	CD82	CD82 molecule	1	Pr55(Gag)
3735	KARS	lysyl-tRNA synthetase	4	Pr55(Gag); Vpr; capsid; retropepsin
3777	KCNK3	potassium channel, subfamily K, member 3	1	Vpu
3778	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	1	Envelope surface glycoprotein gp120
3780	KCNN1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3781	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	1	Envelope surface glycoprotein gp120
3782	KCNN3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	1	Envelope surface glycoprotein gp120
3783	KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	1	Envelope surface glycoprotein gp120
3791	KDR	kinase insert domain receptor (a type III receptor tyrosine kinase)	1	Tat
3815	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	1	Nef
3835	KIF22	kinesin family member 22	1	Rev
3836	KPNA1	karyopherin alpha 1 (importin alpha 5)	3	Vpr; integrase; matrix
3837	KPNB1	karyopherin (importin) beta 1	5	Rev; Tat; Vpr; integrase; matrix
3838	KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	3	Vpr; integrase; matrix
3839	KPNA3	karyopherin alpha 3 (importin alpha 4)	2	integrase; matrix
3840	KPNA4	karyopherin alpha 4 (importin alpha 3)	2	integrase; matrix
3841	KPNA5	karyopherin alpha 5 (importin alpha 6)	2	integrase; matrix
3842	TNPO1	transportin 1	5	Rev; Tat; Vpr; integrase; matrix
3843	RANBP5	RAN binding protein 5	5	Rev; Tat; Vpr; integrase; matrix

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3845	KRAS	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1	Envelope surface glycoprotein gp160, precursor
3908	LAMA2	laminin, alpha 2 (merosin, congenital muscular dystrophy)	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
3909	LAMA3	laminin, alpha 3	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
3910	LAMA4	laminin, alpha 4	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
3911	LAMA5	laminin, alpha 5	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
3912	LAMB1	laminin, beta 1	1	Tat
3913	LAMB2	laminin, beta 2 (laminin S)	1	Tat
3914	LAMB3	laminin, beta 3	1	Tat
3915	LAMC1	laminin, gamma 1 (formerly LAMB2)	1	Tat
3916	LAMP1	lysosomal-associated membrane protein 1	1	capsid
3918	LAMC2	laminin, gamma 2	1	Tat
3932	LCK	lymphocyte-specific protein tyrosine kinase	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat
3936	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	2	Envelope surface glycoprotein gp160, precursor; retropepsin
3939	LDHA	lactate dehydrogenase A	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat
3945	LDHB	lactate dehydrogenase B	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
3948	LDHC	lactate dehydrogenase C	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
3949	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	1	Nef
3956	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	1	Envelope surface glycoprotein gp120
3958	LGALS3	lectin, galactoside-binding, soluble, 3	2	Rev; Tat
3976	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	1	Envelope surface glycoprotein gp120
3998	LMAN1	lectin, mannose-binding, 1	1	Envelope surface glycoprotein gp120
4000	LMNA	lamin A/C	3	Rev; Tat; Vpr
4001	LMNB1	lamin B1	2	Tat; Vpr
4035	LRP1	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1	Tat
4049	LTA	lymphotoxin alpha (TNF superfamily, member 1)	2	Envelope surface glycoprotein gp120; Tat
4057	LTF	lactotransferrin	1	Envelope surface glycoprotein gp120
4064	CD180	CD180 molecule	1	Tat
4067	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	2	Envelope surface glycoprotein gp120; Nef
4087	SMAD2	SMAD family member 2	1	Envelope surface glycoprotein gp120
4088	SMAD3	SMAD family member 3	1	Tat
4089	SMAD4	SMAD family member 4	1	Tat
4091	SMAD6	SMAD family member 6	1	Tat
4092	SMAD7	SMAD family member 7	1	Envelope surface glycoprotein gp120
4099	MAG	myelin associated glycoprotein	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
4121	MAN1A1	mannosidase, alpha, class 1A, member 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4122	MAN2A2	mannosidase, alpha, class 2A, member 2	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4123	MAN2C1	mannosidase, alpha, class 2C, member 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4124	MAN2A1	mannosidase, alpha, class 2A, member 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4125	MAN2B1	mannosidase, alpha, class 2B, member 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4126	MANBA	mannosidase, beta A, lysosomal	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4130	MAP1A	microtubule-associated protein 1A	1	retropepsin
4133	MAP2	microtubule-associated protein 2	2	Envelope surface glycoprotein gp120; retropepsin
4149	MAX	MYC associated factor X	1	Envelope surface glycoprotein gp120
4153	MBL2	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	1	Envelope surface glycoprotein gp120
4166	CHST6	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6	1	Envelope surface glycoprotein gp160, precursor

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
4193	MDM2	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)	1	Tat
4217	MAP3K5	mitogen-activated protein kinase kinase kinase 5	1	Nef
4234	METTL1	methyltransferase like 1	1	Tat
4246	SCGB2A1	secretoglobin, family 2A, member 1	1	Tat
4247	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
4250	SCGB2A2	secretoglobin, family 2A, member 2	1	Tat
4261	CIITA	class II, major histocompatibility complex, transactivator	1	Tat
4283	CXCL9	chemokine (C-X-C motif) ligand 9	1	Tat
4288	MKI67	antigen identified by monoclonal antibody Ki-67	1	Nef
4296	MAP3K11	mitogen-activated protein kinase kinase kinase 11	1	Envelope surface glycoprotein gp120
4311	MME	membrane metallo-endopeptidase	1	Tat
4312	MMP1	matrix metallopeptidase 1 (interstitial collagenase)	2	Envelope surface glycoprotein gp120; Tat
4313	MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
4314	MMP3	matrix metallopeptidase 3 (stromelysin 1, progelatinase)	1	Envelope surface glycoprotein gp120
4316	MMP7	matrix metallopeptidase 7 (matrilysin, uterine)	1	Tat
4318	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	3	Envelope surface glycoprotein gp120; Nef; Tat
4331	MNAT1	menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	2	Tat; Vpr
4360	MRC1	mannose receptor, C type 1	3	Envelope surface glycoprotein gp120; Nef; Tat
4363	ABCC1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	1	Tat
4478	MSN	moesin	2	Envelope surface glycoprotein gp120; Pr55(Gag)
4489	MT1A	metallothionein 1A (functional)	1	Tat
4490	MT1B	metallothionein 1B (functional)	1	Tat
4493	MT1E	metallothionein 1E (functional)	1	Tat
4494	MT1F	metallothionein 1F (functional)	1	Tat
4495	MT1G	metallothionein 1G	1	Tat
4496	MT1H	metallothionein 1H	1	Tat
4499	MT1M	metallothionein 1M	1	Tat
4501	MT1X	metallothionein 1X	1	Tat
4502	MT2A	metallothionein 2A	1	Tat
4504	MT3	metallothionein 3	1	Tat
4599	MX1	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
4609	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	2	Envelope surface glycoprotein gp120; Tat
4624	MYH6	myosin, heavy chain 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)	1	retropepsin
4625	MYH7	myosin, heavy chain 7, cardiac muscle, beta	1	retropepsin
4627	MYH9	myosin, heavy chain 9, non-muscle	1	retropepsin
4628	MYH10	myosin, heavy chain 10, non-muscle	1	retropepsin
4629	MYH11	myosin, heavy chain 11, smooth muscle	1	retropepsin
4676	NAP1L4	nucleosome assembly protein 1-like 4	1	Envelope surface glycoprotein gp120
4691	NCL	nucleolin	2	matrix; reverse transcriptase
4734	NEDD4	neural precursor cell expressed, developmentally down-regulated 4	2	Vif; p6
4758	NEU1	sialidase 1 (lysosomal sialidase)	1	Envelope surface glycoprotein gp120
4759	NEU2	sialidase 2 (cytosolic sialidase)	1	Envelope surface glycoprotein gp120
4771	NF2	neurofibromin 2 (bilateral acoustic neuroma)	1	Nef
4772	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	5	Envelope surface glycoprotein gp120; Nef; Tat; Vpr; reverse transcriptase
4773	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	4	Envelope surface glycoprotein gp120; Tat; Vpr; reverse transcriptase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
4775	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	3	Envelope surface glycoprotein gp120; Tat; Vpr
4776	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	3	Envelope surface glycoprotein gp120; Tat; Vpr
4782	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	1	Tat
4790	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	7	Envelope surface glycoprotein gp120; Nef; Tat; Vpr; Vpu; nucleocapsid; retropepsin
4791	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	2	Envelope surface glycoprotein gp120; Tat
4792	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Rev; Tat; Vpr; Vpu
4793	NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta	2	Envelope surface glycoprotein gp120; Tat
4803	NGFB	nerve growth factor, beta polypeptide	1	Tat
4826	NNAT	neuronatin	1	Envelope surface glycoprotein gp120
4836	NMT1	N-myristoyltransferase 1	2	Nef; matrix
4842	NOS1	nitric oxide synthase 1 (neuronal)	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
4843	NOS2A	nitric oxide synthase 2A (inducible, hepatocytes)	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
4846	NOS3	nitric oxide synthase 3 (endothelial cell)	2	Envelope transmembrane glycoprotein gp41; Tat
4853	NOTCH2	Notch homolog 2 (Drosophila)	1	Tat
4869	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	2	Rev; Tat
4893	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	1	Envelope surface glycoprotein gp160, precursor
4904	YBX1	Y box binding protein 1	1	Tat
4928	NUP98	nucleoporin 98kDa	1	Rev
4938	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	1	Tat
4939	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	1	Tat
4940	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	1	Tat
4950	OCLN	occludin	1	Envelope surface glycoprotein gp120
4968	OGG1	8-oxoguanine DNA glycosylase	1	Tat
4986	OPRK1	opioid receptor, kappa 1	1	Envelope surface glycoprotein gp120
4988	OPRM1	opioid receptor, mu 1	1	Envelope surface glycoprotein gp120
5004	ORM1	orosomucoid 1	1	Envelope surface glycoprotein gp120
5005	ORM2	orosomucoid 2	1	Envelope surface glycoprotein gp120
5034	P4HB	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	1	Envelope surface glycoprotein gp120
5045	FURIN	furin (paired basic amino acid cleaving enzyme)	2	Envelope surface glycoprotein gp160, precursor; Tat
5046	PCSK6	proprotein convertase subtilisin/kexin type 6	1	Envelope surface glycoprotein gp160, precursor

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5047	PAEP	progestagen-associated endometrial protein (placental protein 14, pregnancy-associated endometrial alpha-2-globulin, alpha uterine protein)	1	Envelope surface glycoprotein gp120
5048	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit 45kDa	1	Tat
5054	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	1	Tat
5055	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	1	Envelope surface glycoprotein gp120
5058	PAK1	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)	2	Nef; Tat
5062	PAK2	p21 (CDKN1A)-activated kinase 2	2	Nef; matrix
5074	PAWR	PRKC, apoptosis, WT1, regulator	1	Tat
5105	PCK1	phosphoenolpyruvate carboxykinase 1 (soluble)	1	integrase
5111	PCNA	proliferating cell nuclear antigen	1	Tat
5116	PCNT	pericentrin (kendrin)	1	Vpr
5122	PCSK1	proprotein convertase subtilisin/kexin type 1	1	Envelope surface glycoprotein gp160, precursor
5125	PCSK5	proprotein convertase subtilisin/kexin type 5	1	Envelope surface glycoprotein gp160, precursor
5136	PDE1A	phosphodiesterase 1A, calmodulin-dependent	1	Tat
5137	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5138	PDE2A	phosphodiesterase 2A, cGMP-stimulated	1	Tat
5139	PDE3A	phosphodiesterase 3A, cGMP-inhibited	1	Tat
5140	PDE3B	phosphodiesterase 3B, cGMP-inhibited	1	Tat
5141	PDE4A	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)	1	Tat
5142	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	1	Tat
5143	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	1	Tat
5144	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	1	Tat
5150	PDE7A	phosphodiesterase 7A	1	Tat
5151	PDE8A	phosphodiesterase 8A	1	Tat
5153	PDE1B	phosphodiesterase 1B, calmodulin-dependent	1	Tat
5199	CFP	complement factor properdin	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
5243	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	2	Envelope surface glycoprotein gp120; Tat
5244	ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5255	PHKA1	phosphorylase kinase, alpha 1 (muscle)	1	retropepsin
5256	PHKA2	phosphorylase kinase, alpha 2 (liver)	1	retropepsin
5257	PHKB	phosphorylase kinase, beta	1	retropepsin
5265	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	1	Envelope surface glycoprotein gp160, precursor
5286	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat; reverse transcriptase
5287	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5288	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5289	PIK3C3	phosphoinositide-3-kinase, class 3	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5290	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat
5291	PIK3CB	phosphoinositide-3-kinase, catalytic, beta polypeptide	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5293	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5294	PIK3CG	phosphoinositide-3-kinase, catalytic, gamma polypeptide	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5295	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	4	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat
5296	PIK3R2	phosphoinositide-3-kinase, regulatory subunit 2 (p85 beta)	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5304	PIP	prolactin-induced protein	1	Envelope surface glycoprotein gp120
5319	PLA2G1B	phospholipase A2, group IB (pancreas)	1	Envelope surface glycoprotein gp120
5320	PLA2G2A	phospholipase A2, group IIA (platelets, synovial fluid)	1	Envelope surface glycoprotein gp120
5321	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	1	Envelope surface glycoprotein gp120
5322	PLA2G5	phospholipase A2, group V	1	Envelope surface glycoprotein gp120
5328	PLAU	plasminogen activator, urokinase	3	Envelope surface glycoprotein gp120; Pr55(Gag); Tat
5329	PLAUR	plasminogen activator, urokinase receptor	1	capsid
5330	PLCB2	phospholipase C, beta 2	2	Envelope surface glycoprotein gp120; Tat
5331	PLCB3	phospholipase C, beta 3 (phosphatidylinositol-specific)	2	Envelope surface glycoprotein gp120; Tat
5332	PLCB4	phospholipase C, beta 4	2	Envelope surface glycoprotein gp120; Tat
5333	PLCD1	phospholipase C, delta 1	2	Envelope surface glycoprotein gp120; Tat
5335	PLCG1	phospholipase C, gamma 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
5336	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	2	Envelope surface glycoprotein gp120; Tat
5339	PLEC1	plectin 1, intermediate filament binding protein 500kDa	1	Vif

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5357	PLS1	plastin 1 (I isoform)	1	retropepsin
5358	PLS3	plastin 3 (T isoform)	1	retropepsin
5371	PML	promyelocytic leukemia	2	Tat; integrase
5396	PRRX1	paired related homeobox 1	1	Tat
5423	POLB	polymerase (DNA directed), beta	1	Tat
5426	POLE	polymerase (DNA directed), epsilon	1	Tat
5430	POLR2A	polymerase (RNA) II (DNA directed) polypeptide A, 220kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5431	POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5432	POLR2C	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5433	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	3	Envelope surface glycoprotein gp120; Tat; Vpr
5434	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5435	POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	3	Envelope surface glycoprotein gp120; Tat; Vpr
5436	POLR2G	polymerase (RNA) II (DNA directed) polypeptide G	3	Envelope surface glycoprotein gp120; Tat; Vpr
5437	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	3	Envelope surface glycoprotein gp120; Tat; Vpr
5438	POLR2I	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5439	POLR2J	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5440	POLR2K	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5441	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	3	Envelope surface glycoprotein gp120; Tat; Vpr
5443	POMC	proopiomelanocortin (adrenocorticotropin/ beta-lipotropin/ alpha-melanocyte stimulating hormone/ beta-melanocyte stimulating hormone/ beta-endorphin)	1	Envelope surface glycoprotein gp120
5451	POU2F1	POU domain, class 2, transcription factor 1	1	Tat
5468	PPARG	peroxisome proliferator-activated receptor gamma	1	Nef
5473	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	1	retropepsin
5478	PPIA	peptidylprolyl isomerase A (cyclophilin A)	7	Envelope surface glycoprotein gp120; Nef; Pr55(Gag); Vif; Vpr; capsid; matrix
5479	PPIB	peptidylprolyl isomerase B (cyclophilin B)	2	Envelope surface glycoprotein gp120; capsid
5499	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	1	Tat
5500	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	2	Envelope surface glycoprotein gp120; Tat
5501	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isoform	1	Tat
5511	PPP1R8	protein phosphatase 1, regulatory (inhibitor) subunit 8	1	Tat
5515	PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	3	Tat; Vpr; nucleocapsid
5516	PPP2CB	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	3	Tat; Vpr; nucleocapsid

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5518	PPP2R1A	protein phosphatase 2 (formerly 2A), regulatory subunit A , alpha isoform	3	Tat; Vpr; nucleocapsid
5519	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	3	Tat; Vpr; nucleocapsid
5520	PPP2R2A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform	3	Tat; Vpr; nucleocapsid
5521	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	3	Tat; Vpr; nucleocapsid
5522	PPP2R2C	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	3	Tat; Vpr; nucleocapsid
5523	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	3	Tat; Vpr; nucleocapsid
5524	PPP2R4	protein phosphatase 2A activator, regulatory subunit 4	3	Tat; Vpr; nucleocapsid
5525	PPP2R5A	protein phosphatase 2, regulatory subunit B', alpha isoform	3	Tat; Vpr; nucleocapsid
5526	PPP2R5B	protein phosphatase 2, regulatory subunit B', beta isoform	4	Envelope surface glycoprotein gp120; Tat; Vpr; nucleocapsid
5527	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	3	Tat; Vpr; nucleocapsid
5528	PPP2R5D	protein phosphatase 2, regulatory subunit B', delta isoform	3	Tat; Vpr; nucleocapsid
5529	PPP2R5E	protein phosphatase 2, regulatory subunit B', epsilon isoform	3	Tat; Vpr; nucleocapsid

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5530	PPP3CA	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	1	Tat
5532	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	1	Tat
5533	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	1	Tat
5534	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform	1	Tat
5535	PPP3R2	protein phosphatase 3 (formerly 2B), regulatory subunit B, beta isoform	1	Tat
5551	PRF1	perforin 1 (pore forming protein)	1	Tat
5566	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	5	Envelope surface glycoprotein gp120; Nef; Tat; capsid; matrix
5567	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	4	Envelope surface glycoprotein gp120; Tat; capsid; matrix
5568	PRKACG	protein kinase, cAMP-dependent, catalytic, gamma	4	Envelope surface glycoprotein gp120; Tat; capsid; matrix
5571	PRKAG1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	2	Tat; matrix
5573	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	3	Envelope surface glycoprotein gp120; Tat; matrix
5575	PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	2	Tat; matrix
5576	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	3	Envelope surface glycoprotein gp120; Tat; matrix

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5577	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	2	Tat; matrix
5578	PRKCA	protein kinase C, alpha	9	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Rev; Tat; matrix; retropepsin; reverse transcriptase
5579	PRKCB1	protein kinase C, beta 1	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; retropepsin; reverse transcriptase
5580	PRKCD	protein kinase C, delta	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat; retropepsin; reverse transcriptase
5581	PRKCE	protein kinase C, epsilon	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; retropepsin; reverse transcriptase
5582	PRKCG	protein kinase C, gamma	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat; retropepsin; reverse transcriptase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5583	PRKCH	protein kinase C, eta	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat; retropepsin; reverse transcriptase
5584	PRKCI	protein kinase C, iota	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat; retropepsin; reverse transcriptase
5587	PRKD1	protein kinase D1	1	Tat
5588	PRKCQ	protein kinase C, theta	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; retropepsin; reverse transcriptase
5590	PRKCZ	protein kinase C, zeta	6	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Tat; retropepsin; reverse transcriptase
5591	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	2	Tat; integrase
5594	MAPK1	mitogen-activated protein kinase 1	10	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Rev; Tat; Vif; Vpr; matrix; p6; reverse transcriptase
5595	MAPK3	mitogen-activated protein kinase 3	9	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Rev; Tat; Vif; matrix; p6; reverse transcriptase
5596	MAPK4	mitogen-activated protein kinase 4	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5597	MAPK6	mitogen-activated protein kinase 6	1	Envelope surface glycoprotein gp120
5598	MAPK7	mitogen-activated protein kinase 7	1	Envelope surface glycoprotein gp120
5599	MAPK8	mitogen-activated protein kinase 8	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef; Tat; Vpr
5600	MAPK11	mitogen-activated protein kinase 11	1	Envelope surface glycoprotein gp120
5601	MAPK9	mitogen-activated protein kinase 9	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
5602	MAPK10	mitogen-activated protein kinase 10	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
5603	MAPK13	mitogen-activated protein kinase 13	1	Envelope surface glycoprotein gp120
5604	MAP2K1	mitogen-activated protein kinase kinase 1	4	Envelope surface glycoprotein gp120; Nef; Tat; reverse transcriptase
5605	MAP2K2	mitogen-activated protein kinase kinase 2	4	Envelope surface glycoprotein gp120; Nef; Tat; Vpr
5609	MAP2K7	mitogen-activated protein kinase kinase 7	1	Vpr
5610	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	1	Tat
5621	PRNP	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia)	1	Tat
5644	PRSS1	protease, serine, 1 (trypsin 1)	1	Envelope surface glycoprotein gp120
5645	PRSS2	protease, serine, 2 (trypsin 2)	1	Envelope surface glycoprotein gp120
5682	PSMA1	proteasome (prosome, macropain) subunit, alpha type, 1	3	Tat; Vif; integrase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5683	PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	3	Tat; Vif; integrase
5684	PSMA3	proteasome (prosome, macropain) subunit, alpha type, 3	3	Tat; Vif; integrase
5685	PSMA4	proteasome (prosome, macropain) subunit, alpha type, 4	3	Tat; Vif; integrase
5686	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	3	Tat; Vif; integrase
5687	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	3	Tat; Vif; integrase
5688	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	3	Tat; Vif; integrase
5689	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	3	Tat; Vif; integrase
5690	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	3	Tat; Vif; integrase
5691	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	3	Tat; Vif; integrase
5692	PSMB4	proteasome (prosome, macropain) subunit, beta type, 4	4	Nef; Tat; Vif; integrase
5693	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5	3	Tat; Vif; integrase
5694	PSMB6	proteasome (prosome, macropain) subunit, beta type, 6	3	Tat; Vif; integrase
5695	PSMB7	proteasome (prosome, macropain) subunit, beta type, 7	3	Tat; Vif; integrase
5696	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	4	Tat; Vif; integrase; reverse transcriptase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5698	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	3	Tat; Vif; integrase
5699	PSMB10	proteasome (prosome, macropain) subunit, beta type, 10	3	Tat; Vif; integrase
5700	PSMC1	proteasome (prosome, macropain) 26S subunit, ATPase, 1	3	Tat; Vif; integrase
5701	PSMC2	proteasome (prosome, macropain) 26S subunit, ATPase, 2	3	Tat; Vif; integrase
5702	PSMC3	proteasome (prosome, macropain) 26S subunit, ATPase, 3	3	Tat; Vif; integrase
5704	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	3	Tat; Vif; integrase
5705	PSMC5	proteasome (prosome, macropain) 26S subunit, ATPase, 5	3	Tat; Vif; integrase
5706	PSMC6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	3	Tat; Vif; integrase
5707	PSMD1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	3	Tat; Vif; integrase
5708	PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	3	Tat; Vif; integrase
5709	PSMD3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	3	Tat; Vif; integrase
5710	PSMD4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	3	Tat; Vif; integrase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5711	PSMD5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	3	Tat; Vif; integrase
5713	PSMD7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog)	3	Tat; Vif; integrase
5714	PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	3	Tat; Vif; integrase
5715	PSMD9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	3	Tat; Vif; integrase
5716	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	3	Tat; Vif; integrase
5717	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	3	Tat; Vif; integrase
5718	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	3	Tat; Vif; integrase
5719	PSMD13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	3	Tat; Vif; integrase
5720	PSME1	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	3	Tat; Vif; integrase
5721	PSME2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	3	Tat; Vif; integrase
5725	PTBP1	polypyrimidine tract binding protein 1	2	Rev; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5728	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	1	Tat
5742	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	1	Envelope surface glycoprotein gp120
5743	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	2	Envelope surface glycoprotein gp120; Tat
5747	PTK2	PTK2 protein tyrosine kinase 2	1	Tat
5756	TWF1	twinfilin, actin-binding protein, homolog 1 (Drosophila)	1	Envelope surface glycoprotein gp120
5757	PTMA	prothymosin, alpha (gene sequence 28)	1	Rev
5781	PTPN11	protein tyrosine phosphatase, non-receptor type 11 (Noonan syndrome 1)	1	Envelope surface glycoprotein gp120
5786	PTPRA	protein tyrosine phosphatase, receptor type, A	1	Envelope surface glycoprotein gp120
5787	PTPRB	protein tyrosine phosphatase, receptor type, B	1	Envelope surface glycoprotein gp120
5788	PTPRC	protein tyrosine phosphatase, receptor type, C	1	Envelope surface glycoprotein gp120
5800	PTPRO	protein tyrosine phosphatase, receptor type, O	1	Envelope surface glycoprotein gp120
5813	PURA	purine-rich element binding protein A	1	Tat
5829	PXN	paxillin	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5879	RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	2	Nef; Tat
5880	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	2	Nef; Tat
5884	RAD17	RAD17 homolog (S. pombe)	1	Vpr
5886	RAD23A	RAD23 homolog A (S. cerevisiae)	1	Vpr
5888	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	3	Tat; Vpr; integrase
5894	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1	2	Envelope surface glycoprotein gp120; Nef
5901	RAN	RAN, member RAS oncogene family	2	Rev; matrix
5902	RANBP1	RAN binding protein 1	1	Rev
5923	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	1	Envelope surface glycoprotein gp120
5925	RB1	retinoblastoma 1 (including osteosarcoma)	3	Envelope surface glycoprotein gp120; Nef; Tat
5934	RBL2	retinoblastoma-like 2 (p130)	2	Envelope surface glycoprotein gp120; Tat
5962	RDX	radixin	1	Envelope surface glycoprotein gp120
5966	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
5970	RELA	v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian)	2	Tat; Vpr
5971	RELB	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian)	1	Tat
5981	RFC1	replication factor C (activator 1) 1, 145kDa	1	Tat
5982	RFC2	replication factor C (activator 1) 2, 40kDa	1	Tat
5983	RFC3	replication factor C (activator 1) 3, 38kDa	1	Tat
5984	RFC4	replication factor C (activator 1) 4, 37kDa	1	Tat
5985	RFC5	replication factor C (activator 1) 5, 36.5kDa	1	Tat
6059	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	2	Pr55(Gag); Vif
6117	RPA1	replication protein A1, 70kDa	3	Tat; Vpr; reverse transcriptase
6118	RPA2	replication protein A2, 32kDa	2	Vpr; reverse transcriptase
6119	RPA3	replication protein A3, 14kDa	1	reverse transcriptase
6122	RPL3	ribosomal protein L3	1	Tat
6125	RPL5	ribosomal protein L5	1	Rev
6198	RPS6KB1	ribosomal protein S6 kinase, 70kDa, polypeptide 1	1	Envelope transmembrane glycoprotein gp41
6300	MAPK12	mitogen-activated protein kinase 12	2	Envelope surface glycoprotein gp120; reverse transcriptase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6303	SAT1	spermidine/spermine N1-acetyltransferase 1	2	Tat; Vif
6346	CCL1	chemokine (C-C motif) ligand 1	2	Tat; Vpr
6347	CCL2	chemokine (C-C motif) ligand 2	3	Envelope surface glycoprotein gp120; Nef; Tat
6348	CCL3	chemokine (C-C motif) ligand 3	6	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; matrix
6351	CCL4	chemokine (C-C motif) ligand 4	5	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr
6352	CCL5	chemokine (C-C motif) ligand 5	5	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr
6354	CCL7	chemokine (C-C motif) ligand 7	2	Envelope surface glycoprotein gp120; Tat
6355	CCL8	chemokine (C-C motif) ligand 8	2	Envelope surface glycoprotein gp120; Tat
6356	CCL11	chemokine (C-C motif) ligand 11	1	Envelope surface glycoprotein gp120
6364	CCL20	chemokine (C-C motif) ligand 20	1	Envelope surface glycoprotein gp120
6366	CCL21	chemokine (C-C motif) ligand 21	1	Envelope surface glycoprotein gp120
6367	CCL22	chemokine (C-C motif) ligand 22	1	Envelope surface glycoprotein gp120
6375	XCL1	chemokine (C motif) ligand 1	2	Envelope surface glycoprotein gp120; Tat
6376	CX3CL1	chemokine (C-X3-C motif) ligand 1	2	Envelope surface glycoprotein gp120; Tat
6382	SDC1	syndecan 1	2	Envelope surface glycoprotein gp120; Tat
6383	SDC2	syndecan 2	2	Envelope surface glycoprotein gp120; Tat
6385	SDC4	syndecan 4	2	Envelope surface glycoprotein gp120; Tat
6386	SDCBP	syndecan binding protein (syntenin)	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6387	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	3	Envelope surface glycoprotein gp120; Nef; Tat
6390	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	1	Tat
6401	SELE	selectin E (endothelial adhesion molecule 1)	1	Tat
6402	SELL	selectin L (lymphocyte adhesion molecule 1)	1	Envelope surface glycoprotein gp120
6403	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	1	Envelope surface glycoprotein gp120
6422	SFRP1	secreted frizzled-related protein 1	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
6426	SFRS1	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	2	Rev; Tat
6427	SFRS2	splicing factor, arginine/serine-rich 2	1	Rev
6430	SFRS5	splicing factor, arginine/serine-rich 5	1	Rev
6432	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	1	Tat
6441	SFTPD	surfactant, pulmonary-associated protein D	1	Envelope surface glycoprotein gp120
6449	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	2	Pr55(Gag); Vpu
6464	SHC1	SHC (Src homology 2 domain containing) transforming protein 1	1	Tat
6482	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1	Envelope surface glycoprotein gp160, precursor

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6483	ST3GAL2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	1	Envelope surface glycoprotein gp160, precursor
6484	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	1	Envelope surface glycoprotein gp160, precursor
6487	ST3GAL3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	1	Envelope surface glycoprotein gp160, precursor
6502	SKP2	S-phase kinase-associated protein 2 (p45)	1	Tat
6506	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	1	Envelope surface glycoprotein gp120
6520	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	1	Envelope surface glycoprotein gp160, precursor
6523	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	1	Tat
6531	SLC6A3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	2	Envelope surface glycoprotein gp120; Tat
6545	SLC7A4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	1	Envelope surface glycoprotein gp120
6580	SLC22A1	solute carrier family 22 (organic cation transporter), member 1	1	Tat
6582	SLC22A2	solute carrier family 22 (organic cation transporter), member 2	1	Tat
6590	SLPI	secretory leukocyte peptidase inhibitor	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6595	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	1	Tat
6596	HLTF	helicase-like transcription factor	1	Nef
6597	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	1	Tat
6598	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	2	Tat; integrase
6609	SMPD1	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	2	Envelope surface glycoprotein gp120; Nef
6610	SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	1	Envelope surface glycoprotein gp120
6626	SNRPA	small nuclear ribonucleoprotein polypeptide A	1	Nef
6627	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	2	Rev; Tat
6628	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	1	Tat
6629	SNRPB2	small nuclear ribonucleoprotein polypeptide B''	1	Tat
6632	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6633	SNRPD2	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	1	Tat
6634	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	1	Tat
6647	SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
6648	SOD2	superoxide dismutase 2, mitochondrial	2	Envelope surface glycoprotein gp160, precursor; Tat
6649	SOD3	superoxide dismutase 3, extracellular	2	Envelope surface glycoprotein gp160, precursor; Tat
6667	SP1	Sp1 transcription factor	3	Tat; Vpr; nucleocapsid
6670	SP3	Sp3 transcription factor	1	Tat
6671	SP4	Sp4 transcription factor	1	Tat
6693	SPN	sialophorin (leukosialin, CD43)	1	Envelope surface glycoprotein gp120
6708	SPTA1	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	1	retropepsin
6709	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	1	retropepsin
6710	SPTB	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)	1	retropepsin
6711	SPTBN1	spectrin, beta, non-erythrocytic 1	1	retropepsin
6712	SPTBN2	spectrin, beta, non-erythrocytic 2	1	retropepsin
6714	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	2	Nef; Tat
6721	SREBF2	sterol regulatory element binding transcription factor 2	1	Nef

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6722	SRF	serum response factor (c-fos serum response element-binding transcription factor)	1	Envelope transmembrane glycoprotein gp41
6726	SRP9	signal recognition particle 9kDa	1	Envelope surface glycoprotein gp120
6737	TRIM21	tripartite motif-containing 21	1	capsid
6741	SSB	Sjogren syndrome antigen B (autoantigen La)	1	Tat
6742	SSBP1	single-stranded DNA binding protein 1	1	Tat
6750	SST	somatostatin	1	Envelope surface glycoprotein gp120
6772	STAT1	signal transducer and activator of transcription 1, 91kDa	3	Envelope surface glycoprotein gp120; Nef; Tat
6774	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	3	Envelope surface glycoprotein gp120; Nef; Tat
6776	STAT5A	signal transducer and activator of transcription 5A	2	Envelope surface glycoprotein gp120; capsid
6777	STAT5B	signal transducer and activator of transcription 5B	2	Envelope surface glycoprotein gp120; capsid
6778	STAT6	signal transducer and activator of transcription 6, interleukin-4 induced	1	Tat
6780	STAU1	staufen, RNA binding protein, homolog 1 (Drosophila)	1	Pr55(Gag)
6827	SUPT4H1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	1	Tat
6829	SUPT5H	suppressor of Ty 5 homolog (S. cerevisiae)	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6863	TAC1	tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide gamma)	1	Envelope surface glycoprotein gp120
6872	TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	1	Tat
6873	TAF2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	1	Tat
6874	TAF4	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	1	Tat
6877	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	1	Tat
6878	TAF6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	1	Tat
6879	TAF7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	1	Tat
6880	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6881	TAF10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa	1	Tat
6882	TAF11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 28kDa	1	Tat
6883	TAF12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20kDa	1	Tat
6884	TAF13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	1	Tat
6890	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1	Tat
6894	TARBP1	Tar (HIV-1) RNA binding protein 1	1	Tat
6895	TARBP2	Tar (HIV-1) RNA binding protein 2	1	Tat
6908	TBP	TATA box binding protein	3	Envelope surface glycoprotein gp120; Tat; Vpr
6917	TCEA1	transcription elongation factor A (SII), 1	1	Tat
6919	TCEA2	transcription elongation factor A (SII), 2	1	Tat
6920	TCEA3	transcription elongation factor A (SII), 3	1	Tat
6921	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	1	Vif

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
6923	TCEB2	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)	2	Tat; Vif
6924	TCEB3	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	1	Nef
6925	TCF4	transcription factor 4	1	Tat
6929	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	1	Tat
6934	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	1	Tat
6935	ZEB1	zinc finger E-box binding homeobox 1	1	Nef
7015	TERT	telomerase reverse transcriptase	2	Envelope surface glycoprotein gp120; Tat
7023	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)	1	Tat
7024	TFCP2	transcription factor CP2	1	Tat
7025	NR2F1	nuclear receptor subfamily 2, group F, member 1	1	Tat
7037	TFRC	transferrin receptor (p90, CD71)	2	Envelope surface glycoprotein gp120; Nef
7039	TGFA	transforming growth factor, alpha	1	Tat
7040	TGFB1	transforming growth factor, beta 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat
7042	TGFB2	transforming growth factor, beta 2	1	Tat
7047	TGM4	transglutaminase 4 (prostate)	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
7051	TGM1	transglutaminase 1 (K polypeptide epidermal type I, protein-glutamine-gamma-glutamyltransferase)	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
7052	TGM2	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Rev
7053	TGM3	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
7054	TH	tyrosine hydroxylase	1	Tat
7057	THBS1	thrombospondin 1	3	Envelope surface glycoprotein gp120; Tat; Vpr
7067	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	1	Tat
7070	THY1	Thy-1 cell surface antigen	1	matrix
7076	TIMP1	TIMP metallopeptidase inhibitor 1	1	Tat
7077	TIMP2	TIMP metallopeptidase inhibitor 2	1	Tat
7082	TJP1	tight junction protein 1 (zona occludens 1)	1	Envelope surface glycoprotein gp120
7094	TLN1	talin 1	1	retropepsin
7099	TLR4	toll-like receptor 4	1	Vpr
7122	CLDN5	claudin 5 (transmembrane protein deleted in velocardiofacial syndrome)	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
7124	TNF	tumor necrosis factor (TNF superfamily, member 2)	7	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41; Nef; Tat; Vpr; matrix
7125	TNNC2	troponin C type 2 (fast)	1	retropepsin
7132	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	1	Tat
7133	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	2	Envelope surface glycoprotein gp120; Tat
7134	TNNC1	troponin C type 1 (slow)	1	retropepsin
7150	TOP1	topoisomerase (DNA) I	2	nucleocapsid; reverse transcriptase
7157	TP53	tumor protein p53 (Li-Fraumeni syndrome)	5	Envelope surface glycoprotein gp120; Nef; Tat; Vpr; reverse transcriptase
7161	TP73	tumor protein p73	1	Tat
7168	TPM1	tropomyosin 1 (alpha)	1	retropepsin
7169	TPM2	tropomyosin 2 (beta)	1	retropepsin
7170	TPM3	tropomyosin 3	1	retropepsin
7185	TRAF1	TNF receptor-associated factor 1	1	Vpu
7188	TRAF5	TNF receptor-associated factor 5	1	Envelope surface glycoprotein gp120
7251	TSG101	tumor susceptibility gene 101	1	p6
7277	TUBA4A	tubulin, alpha 4a	3	Envelope surface glycoprotein gp120; Rev; Tat
7278	TUBA3C	tubulin, alpha 3c	3	Envelope surface glycoprotein gp120; Rev; Tat
7280	TUBB2A	tubulin, beta 2A	2	Rev; Tat
7283	TUBG1	tubulin, gamma 1	1	Vpr
7295	TXN	thioredoxin	2	Envelope surface glycoprotein gp120; Nef
7314	UBB	ubiquitin B	7	Rev; Tat; capsid; matrix; nucleocapsid; p1; p6
7316	UBC	ubiquitin C	7	Rev; Tat; capsid; matrix; nucleocapsid; p1; p6

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
7317	UBE1	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing)	1	Tat
7321	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	1	Tat
7329	UBE2I	ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast)	1	p6
7332	UBE2L3	ubiquitin-conjugating enzyme E2L 3	1	Nef
7341	SUMO1	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	1	p6
7342	UBP1	upstream binding protein 1 (LBP-1a)	1	Tat
7368	UGT8	UDP glycosyltransferase 8 (UDP-galactose ceramide galactosyltransferase)	1	Envelope surface glycoprotein gp120
7374	UNG	uracil-DNA glycosylase	2	Vpr; integrase
7409	VAV1	vav 1 oncogene	2	Envelope surface glycoprotein gp160, precursor; Nef
7410	VAV2	vav 2 oncogene	1	Envelope surface glycoprotein gp160, precursor
7412	VCAM1	vascular cell adhesion molecule 1	3	Envelope surface glycoprotein gp120; Tat; Vpu
7414	VCL	vinculin	1	Nef
7416	VDAC1	voltage-dependent anion channel 1	1	Vpr
7421	VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor	1	Envelope surface glycoprotein gp120
7422	VEGFA	vascular endothelial growth factor A	2	Envelope surface glycoprotein gp120; Tat
7430	VIL2	villin 2 (ezrin)	3	Envelope surface glycoprotein gp120; Pr55(Gag); Vpr
7431	VIM	vimentin	3	Envelope surface glycoprotein gp120; Vif; retropepsin

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
7432	VIP	vasoactive intestinal peptide	1	Envelope surface glycoprotein gp120
7433	VIPR1	vasoactive intestinal peptide receptor 1	1	Envelope surface glycoprotein gp120
7448	VTN	vitronectin	2	Envelope surface glycoprotein gp120; Tat
7453	WARS	tryptophanyl-tRNA synthetase	1	capsid
7465	WEE1	WEE1 homolog (S. pombe)	1	Vpr
7469	WHSC2	Wolf-Hirschhorn syndrome candidate 2	1	Tat
7490	WT1	Wilms tumor 1	1	Nef
7514	XPO1	exportin 1 (CRM1 homolog, yeast)	3	Rev; Vpr; matrix
7520	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa)	2	Tat; integrase
7528	YY1	YY1 transcription factor	1	Tat
7529	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	2	Envelope surface glycoprotein gp120; Vpr
7531	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2	Envelope surface glycoprotein gp120; Vpr
7532	YWHAG	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	1	Vpr

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
7533	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	1	Vpr
7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	1	Vpr
7535	ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
7841	GCS1	glucosidase I	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
7846	TUBA1A	tubulin, alpha 1a	3	Envelope surface glycoprotein gp120; Rev; Tat
7852	CXCR4	chemokine (C-X-C motif) receptor 4	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
7936	RDBP	RD RNA binding protein	1	Tat
7941	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	1	Envelope surface glycoprotein gp120
7994	MYST3	MYST histone acetyltransferase (monocytic leukemia) 3	1	integrase
8021	NUP214	nucleoporin 214kDa	1	Rev
8065	CUL5	cullin 5	1	Vif
8140	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	1	Envelope surface glycoprotein gp160, precursor

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID				
GeneID	**Symbol**	**Name**	**Number of HIV-1 Protein Interactions**	**Interacts with HIV-1 Proteins**
8148	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	1	Tat
8178	ELL	elongation factor RNA polymerase II	1	Tat
8202	NCOA3	nuclear receptor coactivator 3	1	Tat
8290	HIST3H3	histone cluster 3, H3	1	Tat
8294	HIST1H4I	histone cluster 1, H4i	1	Tat
8329	HIST1H2AI	histone cluster 1, H2ai	1	Tat
8330	HIST1H2AK	histone cluster 1, H2ak	1	Tat
8331	HIST1H2AJ	histone cluster 1, H2aj	1	Tat
8332	HIST1H2AL	histone cluster 1, H2al	1	Tat
8334	HIST1H2AC	histone cluster 1, H2ac	1	Tat
8335	HIST1H2AB	histone cluster 1, H2ab	1	Tat
8336	HIST1H2AM	histone cluster 1, H2am	1	Tat
8337	HIST2H2AA3	histone cluster 2, H2aa3	1	Tat
8338	HIST2H2AC	histone cluster 2, H2ac	1	Tat
8339	HIST1H2BG	histone cluster 1, H2bg	1	Tat
8340	HIST1H2BL	histone cluster 1, H2bl	1	Tat
8341	HIST1H2BN	histone cluster 1, H2bn	1	Tat
8342	HIST1H2BM	histone cluster 1, H2bm	1	Tat
8343	HIST1H2BF	histone cluster 1, H2bf	1	Tat
8344	HIST1H2BE	histone cluster 1, H2be	1	Tat
8345	HIST1H2BH	histone cluster 1, H2bh	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
8346	HIST1H2BI	histone cluster 1, H2bi	1	Tat
8347	HIST1H2BC	histone cluster 1, H2bc	1	Tat
8348	HIST1H2BO	histone cluster 1, H2bo	1	Tat
8349	HIST2H2BE	histone cluster 2, H2be	1	Tat
8350	HIST1H3A	histone cluster 1, H3a	1	Tat
8351	HIST1H3D	histone cluster 1, H3d	1	Tat
8352	HIST1H3C	histone cluster 1, H3c	1	Tat
8353	HIST1H3E	histone cluster 1, H3e	1	Tat
8354	HIST1H3I	histone cluster 1, H3i	1	Tat
8355	HIST1H3G	histone cluster 1, H3g	1	Tat
8356	HIST1H3J	histone cluster 1, H3j	1	Tat
8357	HIST1H3H	histone cluster 1, H3h	1	Tat
8358	HIST1H3B	histone cluster 1, H3b	1	Tat
8359	HIST1H4A	histone cluster 1, H4a	1	Tat
8360	HIST1H4D	histone cluster 1, H4d	1	Tat
8361	HIST1H4F	histone cluster 1, H4f	1	Tat
8362	HIST1H4K	histone cluster 1, H4k	1	Tat
8363	HIST1H4J	histone cluster 1, H4j	1	Tat
8364	HIST1H4C	histone cluster 1, H4c	1	Tat
8365	HIST1H4H	histone cluster 1, H4h	1	Tat
8366	HIST1H4B	histone cluster 1, H4b	1	Tat
8367	HIST1H4E	histone cluster 1, H4e	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
8368	HIST1H4L	histone cluster 1, H4l	1	Tat
8369	HIST1H4G	histone cluster 1, H4g	1	Tat
8370	HIST2H4A	histone cluster 2, H4a	1	Tat
8398	PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	1	Envelope surface glycoprotein gp120
8399	PLA2G10	phospholipase A2, group X	1	Envelope surface glycoprotein gp120
8459	TPST2	tyrosylprotein sulfotransferase 2	1	Envelope surface glycoprotein gp120
8460	TPST1	tyrosylprotein sulfotransferase 1	1	Envelope surface glycoprotein gp120
8487	SIP1	survival of motor neuron protein interacting protein 1	1	integrase
8519	IFITM1	interferon induced transmembrane protein 1 (9-27)	1	Rev
8520	HAT1	histone acetyltransferase 1	1	Envelope surface glycoprotein gp120
8534	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	1	Envelope surface glycoprotein gp160, precursor
8536	CAMK1	calcium/calmodulin-dependent protein kinase I	1	Tat
8567	MADD	MAP-kinase activating death domain	1	Envelope surface glycoprotein gp120
8600	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	2	Envelope surface glycoprotein gp120; Vpr
8605	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	1	Envelope surface glycoprotein gp120
8648	NCOA1	nuclear receptor coactivator 1	2	Tat; Vpr
8651	SOCS1	suppressor of cytokine signaling 1	1	Nef
8681	PLA2G4B	phospholipase A2, group IVB (cytosolic)	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
8685	MARCO	macrophage receptor with collagenous structure	1	Vpr
8702	B4GALT4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	1	Envelope surface glycoprotein gp160, precursor
8703	B4GALT3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	1	Envelope surface glycoprotein gp160, precursor
8704	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	1	Envelope surface glycoprotein gp160, precursor
8705	B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	1	Envelope surface glycoprotein gp160, precursor
8706	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	1	Envelope surface glycoprotein gp160, precursor
8707	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	1	Envelope surface glycoprotein gp160, precursor
8708	B3GALT1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	1	Envelope surface glycoprotein gp160, precursor
8717	TRADD	TNFRSF1A-associated via death domain	1	Envelope surface glycoprotein gp120
8721	EDF1	endothelial differentiation-related factor 1	1	Tat
8726	EED	embryonic ectoderm development	3	Nef; integrase; matrix
8732	RNGTT	RNA guanylyltransferase and 5'-phosphatase	1	Tat
8735	MYH13	myosin, heavy chain 13, skeletal muscle	1	retropepsin

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
8740	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	1	Nef
8743	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10	2	Envelope surface glycoprotein gp120; Tat
8766	RAB11A	RAB11A, member RAS oncogene family	1	Nef
8789	FBP2	fructose-1,6-bisphosphatase 2	1	matrix
8793	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	1	Envelope surface glycoprotein gp120
8794	TNFRSF10C	tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain	1	Envelope surface glycoprotein gp120
8795	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	1	Envelope surface glycoprotein gp120
8797	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	1	Envelope surface glycoprotein gp120
8815	BANF1	barrier to autointegration factor 1	3	Pr55(Gag); integrase; matrix
8850	PCAF	p300/CBP-associated factor	1	Tat
8851	CDK5R1	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	1	Tat
8862	APLN	apelin, AGTRL1 ligand	1	Envelope surface glycoprotein gp120
8874	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	1	Nef
8894	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	1	Tat
8900	CCNA1	cyclin A1	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
8905	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	2	Envelope transmembrane glycoprotein gp41; Nef
8906	AP1G2	adaptor-related protein complex 1, gamma 2 subunit	2	Envelope transmembrane glycoprotein gp41; Nef
8907	AP1M1	adaptor-related protein complex 1, mu 1 subunit	2	Envelope transmembrane glycoprotein gp41; Nef
8943	AP3D1	adaptor-related protein complex 3, delta 1 subunit	2	Nef; matrix
8945	BTRC	beta-transducin repeat containing	1	Vpu
8968	HIST1H3F	histone cluster 1, H3f	1	Tat
8969	HIST1H2AG	histone cluster 1, H2ag	1	Tat
8970	HIST1H2BJ	histone cluster 1, H2bj	1	Tat
8976	WASL	Wiskott-Aldrich syndrome-like	1	Nef
9020	MAP3K14	mitogen-activated protein kinase kinase kinase 14	1	Tat
9044	BTAF1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	1	Tat
9076	CLDN1	claudin 1	1	Tat
9131	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1	2	Envelope surface glycoprotein gp120; Vpr
9133	CCNB2	cyclin B2	1	Vpr
9138	ARHGEF1	Rho guanine nucleotide exchange factor (GEF) 1	1	Envelope transmembrane glycoprotein gp41
9146	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	1	Pr55(Gag)

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
9150	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	1	Tat
9159	PCSK7	proprotein convertase subtilisin/kexin type 7	1	Envelope surface glycoprotein gp160, precursor
9255	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	1	Tat
9308	CD83	CD83 molecule	2	Tat; Vpr
9328	GTF3C5	general transcription factor IIIC, polypeptide 5, 63kDa	1	Tat
9329	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	1	Tat
9330	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	1	Tat
9331	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	1	Envelope surface glycoprotein gp160, precursor
9333	TGM5	transglutaminase 5	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
9397	NMT2	N-myristoyltransferase 2	1	matrix
9412	SURB7	SRB7 suppressor of RNA polymerase B homolog (yeast)	1	Tat
9414	TJP2	tight junction protein 2 (zona occludens 2)	2	Envelope surface glycoprotein gp120; Tat
9435	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	1	Envelope surface glycoprotein gp160, precursor
9459	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	1	Nef

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
9469	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	1	Envelope surface glycoprotein gp160, precursor
9486	CHST10	carbohydrate sulfotransferase 10	1	Envelope surface glycoprotein gp160, precursor
9491	PSMF1	proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	3	Tat; Vif; integrase
9536	PTGES	prostaglandin E synthase	1	capsid
9555	H2AFY	H2A histone family, member Y	1	Tat
9564	BCAR1	breast cancer anti-estrogen resistance 1	1	Tat
9582	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	1	Pr55(Gag)
9601	PDIA4	protein disulfide isomerase family A, member 4	1	Envelope surface glycoprotein gp120
9618	TRAF4	TNF receptor-associated factor 4	1	Tat
9629	CLCA3	chloride channel, calcium activated, family member 3	1	Envelope surface glycoprotein gp120
9635	CLCA2	chloride channel, calcium activated, family member 2	1	Envelope surface glycoprotein gp120
9636	ISG15	ISG15 ubiquitin-like modifier	1	Tat
9641	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	1	Envelope surface glycoprotein gp120
9647	PPM1F	protein phosphatase 1F (PP2C domain containing)	1	Tat
9651	PLCH2	phospholipase C, eta 2	1	Envelope surface glycoprotein gp120
9669	EIF5B	eukaryotic translation initiation factor 5B	1	matrix
9672	SDC3	syndecan 3	2	Envelope surface glycoprotein gp120; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
9730	VPRBP	Vpr (HIV-1) binding protein	1	Vpr
9733	SART3	squamous cell carcinoma antigen recognized by T cells 3	1	Tat
9844	ELMO1	engulfment and cell motility 1	1	Nef
9861	PSMD6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	3	Tat; Vif; integrase
9902	MRC2	mannose receptor, C type 2	2	Envelope surface glycoprotein gp120; Tat
9972	NUP153	nucleoporin 153kDa	1	Rev
9978	RBX1	ring-box 1	1	Vif
10000	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	3	Envelope surface glycoprotein gp120; Tat; Vpr
10005	ACOT8	acyl-CoA thioesterase 8	1	Nef
10013	HDAC6	histone deacetylase 6	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
10015	PDCD6IP	programmed cell death 6 interacting protein	3	Nef; Pr55(Gag); p6
10018	BCL2L11	BCL2-like 11 (apoptosis facilitator)	1	Tat
10053	AP1M2	adaptor-related protein complex 1, mu 2 subunit	1	Envelope transmembrane glycoprotein gp41
10130	PDIA6	protein disulfide isomerase family A, member 6	1	Envelope surface glycoprotein gp120
10164	CHST4	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	1	Envelope surface glycoprotein gp160, precursor
10197	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	3	Tat; Vif; integrase

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
10204	NUTF2	nuclear transport factor 2	1	matrix
10226	M6PRBP1	mannose-6-phosphate receptor binding protein 1	3	Envelope transmembrane glycoprotein gp41; Pr55(Gag); matrix
10242	KCNMB2	potassium large conductance calcium-activated channel, subfamily M, beta member 2	1	Envelope surface glycoprotein gp120
10262	SF3B4	splicing factor 3b, subunit 4, 49kDa	1	Vpr
10317	B3GALT5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	1	Envelope surface glycoprotein gp160, precursor
10318	TNIP1	TNFAIP3 interacting protein 1	2	Nef; matrix
10319	LAMC3	laminin, gamma 3	1	Tat
10332	CLEC4M	C-type lectin domain family 4, member M	1	Envelope surface glycoprotein gp120
10346	TRIM22	tripartite motif-containing 22	1	Tat
10376	TUBA1B	tubulin, alpha 1b	3	Envelope surface glycoprotein gp120; Rev; Tat
10381	TUBB3	tubulin, beta 3	2	Rev; Tat
10382	TUBB4	tubulin, beta 4	2	Rev; Tat
10383	TUBB2C	tubulin, beta 2C	2	Rev; Tat
10397	NDRG1	N-myc downstream regulated gene 1	1	retropepsin
10399	GNB2L1	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	1	Nef
10451	VAV3	vav 3 oncogene	1	Envelope surface glycoprotein gp160, precursor
10488	CREB3	cAMP responsive element binding protein 3	3	Envelope transmembrane glycoprotein gp41; Pr55(Gag); Tat
10499	NCOA2	nuclear receptor coactivator 2	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
10507	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	1	Tat
10524	HTATIP	HIV-1 Tat interacting protein, 60kDa	1	Tat
10527	IPO7	importin 7	5	Vpr; integrase; matrix; nucleocapsid; reverse transcriptase
10537	UBD	ubiquitin D	7	Rev; Tat; capsid; matrix; nucleocapsid; p1; p6
10553	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	1	Tat
10561	IFI44	interferon-induced protein 44	1	Tat
10567	RABAC1	Rab acceptor 1 (prenylated)	1	Envelope transmembrane glycoprotein gp41
10575	CCT4	chaperonin containing TCP1, subunit 4 (delta)	2	Tat; integrase
10614	HEXIM1	hexamethylene bis-acetamide inducible 1	1	Tat
10621	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	1	Tat
10622	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	1	Tat
10623	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	1	Tat
10657	KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	1	Rev
10663	CXCR6	chemokine (C-X-C motif) receptor 6	1	Envelope surface glycoprotein gp120
10673	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
10728	PTGES3	prostaglandin E synthase 3 (cytosolic)	1	Vpr
10787	NCKAP1	NCK-associated protein 1	1	Envelope surface glycoprotein gp120
10825	NEU3	sialidase 3 (membrane sialidase)	1	Envelope surface glycoprotein gp120
10846	PDE10A	phosphodiesterase 10A	1	Tat
10855	HPSE	heparanase	1	Tat
10905	MAN1A2	mannosidase, alpha, class 1A, member 2	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
10914	PAPOLA	poly(A) polymerase alpha	2	Tat; Vpr
10915	TCERG1	transcription elongation regulator 1	1	Tat
10923	SUB1	SUB1 homolog (S. cerevisiae)	1	Tat
10947	AP3M2	adaptor-related protein complex 3, mu 2 subunit	1	Envelope transmembrane glycoprotein gp41
10954	PDIA5	protein disulfide isomerase family A, member 5	1	Envelope surface glycoprotein gp120
10971	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	1	Vpr
10980	COPS6	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	1	Vpr
10992	SF3B2	splicing factor 3b, subunit 2, 145kDa	1	Vpr
11004	KIF2C	kinesin family member 2C	1	Tat
11034	DSTN	destrin (actin depolymerizing factor)	1	Envelope surface glycoprotein gp120
11097	NUPL2	nucleoporin like 2	2	Rev; Vpr

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
11103	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	1	Rev
11128	POLR3A	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	1	Tat
11140	CDC37	cell division cycle 37 homolog (S. cerevisiae)	1	Tat
11143	MYST2	MYST histone acetyltransferase 2	1	integrase
11168	PSIP1	PC4 and SFRS1 interacting protein 1	1	integrase
11200	CHEK2	CHK2 checkpoint homolog (S. pombe)	1	Vpr
11253	MAN1B1	mannosidase, alpha, class 1B, member 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
11262	SP140	SP140 nuclear body protein	1	Vif
11282	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	2	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
11320	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	2	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
11346	SYNPO	synaptopodin	1	Nef
22798	LAMB4	laminin, beta 4	1	Tat
22802	CLCA4	chloride channel, calcium activated, family member 4	1	Envelope surface glycoprotein gp120
22861	NLRP1	NLR family, pyrin domain containing 1	1	Envelope surface glycoprotein gp120
22938	SNW1	SNW domain containing 1	1	Tat
22954	TRIM32	tripartite motif-containing 32	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
22984	PDCD11	programmed cell death 11	1	Tat
23007	PLCH1	phospholipase C, eta 1	1	Envelope surface glycoprotein gp120
23127	GLT25D2	glycosyltransferase 25 domain containing 2	1	Envelope surface glycoprotein gp120
23193	GANAB	glucosidase, alpha; neutral AB	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
23198	PSME4	proteasome (prosome, macropain) activator subunit 4	3	Tat; Vif; integrase
23236	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	2	Envelope surface glycoprotein gp120; Tat
23237	ARC	activity-regulated cytoskeleton-associated protein	1	Envelope surface glycoprotein gp120
23291	FBXW11	F-box and WD repeat domain containing 11	1	Vpu
23324	MAN2B2	mannosidase, alpha, class 2B, member 2	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
23405	DICER1	Dicer1, Dcr-1 homolog (Drosophila)	1	Tat
23411	SIRT1	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	1	Tat
23435	TARDBP	TAR DNA binding protein	1	Tat
23438	HARSL	histidyl-tRNA synthetase like	1	matrix
23443	SLC35A3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3	1	Envelope transmembrane glycoprotein gp41

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
23468	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	1	Tat
23522	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	1	integrase
23563	CHST5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	1	Envelope surface glycoprotein gp160, precursor
23583	SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1	1	Vpr
23613	ZMYND8	zinc finger, MYND-type containing 8	1	Envelope surface glycoprotein gp120
23633	KPNA6	karyopherin alpha 6 (importin alpha 7)	2	integrase; matrix
23636	NUP62	nucleoporin 62kDa	1	Rev
23683	PRKD3	protein kinase D3	1	Tat
24137	KIF4A	kinesin family member 4A	1	Pr55(Gag)
25834	MGAT4C	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)	2	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
25920	COBRA1	cofactor of BRCA1	1	Tat
25930	PTPN23	protein tyrosine phosphatase, non-receptor type 23	1	Tat
26279	PLA2G2D	phospholipase A2, group IID	1	Envelope surface glycoprotein gp120
26985	AP3M1	adaptor-related protein complex 3, mu 1 subunit	1	Nef
26986	PABPC1	poly(A) binding protein, cytoplasmic 1	2	Rev; retropepsin
26998	FETUB	fetuin B	1	Envelope surface glycoprotein gp160, precursor
27035	NOX1	NADPH oxidase 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Nef

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
27067	STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	1	Pr55(Gag)
27094	KCNMB3	potassium large conductance calcium-activated channel, subfamily M beta member 3	1	Envelope surface glycoprotein gp120
27113	BBC3	BCL2 binding component 3	1	Envelope surface glycoprotein gp120
27175	TUBG2	tubulin, gamma 2	1	Vpr
27336	HTATSF1	HIV-1 Tat specific factor 1	2	Nef; Tat
27345	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	1	Envelope surface glycoprotein gp120
27350	APOBEC3C	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C	1	Vif
29082	CHMP4A	chromatin modifying protein 4A	1	p6
29893	PSMC3IP	PSMC3 interacting protein	1	Tat
29935	RPA4	replication protein A4, 34kDa	1	reverse transcriptase
29949	IL19	interleukin 19	1	Tat
29969	MDFIC	MyoD family inhibitor domain containing	1	Tat
30009	TBX21	T-box 21	1	Tat
30814	PLA2G2E	phospholipase A2, group IIE	1	Envelope surface glycoprotein gp120
30835	CD209	CD209 molecule	2	Envelope surface glycoprotein gp120; Nef
50487	PLA2G3	phospholipase A2, group III	1	Envelope surface glycoprotein gp120
50489	CD207	CD207 molecule, langerin	1	Envelope surface glycoprotein gp120
50507	NOX4	NADPH oxidase 4	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
50508	NOX3	NADPH oxidase 3	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
50604	IL20	interleukin 20	1	Tat
50810	HDGFRP3	hepatoma-derived growth factor, related protein 3	4	Vpr; integrase; matrix; reverse transcriptase
50940	PDE11A	phosphodiesterase 11A	1	Tat
51022	GLRX2	glutaredoxin 2	1	retropepsin
51160	VPS28	vacuolar protein sorting 28 homolog (S. cerevisiae)	1	Pr55(Gag)
51182	HSPA14	heat shock 70kDa protein 14	1	Envelope surface glycoprotein gp120
51196	PLCE1	phospholipase C, epsilon 1	2	Envelope surface glycoprotein gp120; Tat
51218	GLRX5	glutaredoxin 5 homolog (S. cerevisiae)	1	retropepsin
51332	SPTBN5	spectrin, beta, non-erythrocytic 5	1	retropepsin
51341	ZBTB7A	zinc finger and BTB domain containing 7A	1	Tat
51422	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	2	Tat; matrix
51454	GULP1	GULP, engulfment adaptor PTB domain containing 1	1	Envelope surface glycoprotein gp120
51497	TH1L	TH1-like (Drosophila)	1	Tat
51606	ATP6V1H	ATPase, H+ transporting, lysosomal 50/57kDa, V1 subunit H	1	Nef
51652	VPS24	vacuolar protein sorting 24 homolog (S. cerevisiae)	1	Envelope surface glycoprotein gp120
51692	CPSF3	cleavage and polyadenylation specific factor 3, 73kDa	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
51728	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	1	Tat
51807	TUBA8	tubulin, alpha 8	3	Envelope surface glycoprotein gp120; Rev; Tat
53358	SHC3	SHC (Src homology 2 domain containing) transforming protein 3	1	Tat
53371	NUP54	nucleoporin 54kDa	1	Vpr
53840	TRIM34	tripartite motif-containing 34	1	capsid
54145	H2BFS	H2B histone family, member S	1	Tat
54205	CYCS	cytochrome c, somatic	5	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Tat; Vpr; retropepsin
54476	TRIAD3	TRIAD3 protein	1	Vif
55170	PRMT6	protein arginine methyltransferase 6	3	Envelope surface glycoprotein gp160, precursor; Rev; Tat
55506	H2AFY2	H2A histone family, member Y2	1	Tat
55512	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	1	Envelope surface glycoprotein gp120
55627	SMPD4	sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3)	1	Envelope surface glycoprotein gp120
55690	PACS1	phosphofurin acidic cluster sorting protein 1	1	Nef
55703	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	1	Tat
55718	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	1	Tat
55766	H2AFJ	H2A histone family, member J	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
55830	GLT8D1	glycosyltransferase 8 domain containing 1	1	Envelope surface glycoprotein gp120
55849	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	1	Envelope surface glycoprotein gp120
56548	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	1	Envelope surface glycoprotein gp160, precursor
56604	TUBB4Q	tubulin, beta polypeptide 4, member Q	1	Tat
56616	DIABLO	diablo homolog (Drosophila)	1	Vpr
56623	INPP5E	inositol polyphosphate-5-phosphatase, 72 kDa	1	Pr55(Gag)
56852	RAD18	RAD18 homolog (S. cerevisiae)	1	integrase
56903	PAPOLB	poly(A) polymerase beta (testis specific)	1	Tat
57134	MAN1C1	mannosidase, alpha, class 1C, member 1	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
57379	AICDA	activation-induced cytidine deaminase	1	Vif
57447	NDRG2	NDRG family member 2	1	retropepsin
57704	GBA2	glucosidase, beta (bile acid) 2	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
57731	SPTBN4	spectrin, beta, non-erythrocytic 4	1	retropepsin
57733	GBA3	glucosidase, beta, acid 3 (cytosolic)	3	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
58155	PTBP2	polypyrimidine tract binding protein 2	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
60489	APOBEC3G	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3G	4	Vif; nucleocapsid; p6; reverse transcriptase
64377	CHST8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	1	Envelope surface glycoprotein gp160, precursor
64600	PLA2G2F	phospholipase A2, group IIF	1	Envelope surface glycoprotein gp120
64714	PDIA2	protein disulfide isomerase family A, member 2	1	Envelope surface glycoprotein gp120
64895	PAPOLG	poly(A) polymerase gamma	1	Tat
64919	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	1	Tat
79400	NOX5	NADPH oxidase, EF-hand calcium binding domain 5	2	Envelope surface glycoprotein gp120; Envelope surface glycoprotein gp160, precursor
79694	MANEA	mannosidase, endo-alpha	2	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
79709	GLT25D1	glycosyltransferase 25 domain containing 1	1	Envelope surface glycoprotein gp120
79720	VPS37B	vacuolar protein sorting 37 homolog B (S. cerevisiae)	1	Pr55(Gag)
79784	MYH14	myosin, heavy chain 14	1	retropepsin
79902	NUP85	nucleoporin 85kDa	1	Vpr
81027	TUBB1	tubulin, beta 1	2	Rev; Tat
81579	PLA2G12A	phospholipase A2, group XIIA	1	Envelope surface glycoprotein gp120
81631	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	1	retropepsin
83468	GLT8D2	glycosyltransferase 8 domain containing 2	1	Envelope surface glycoprotein gp120
83539	CHST9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	1	Envelope surface glycoprotein gp160, precursor
83660	TLN2	talin 2	1	retropepsin

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
83737	ITCH	itchy homolog E3 ubiquitin protein ligase (mouse)	1	Vif
83740	H2AFB3	H2A histone family, member B3	1	Tat
83953	FCAMR	Fc receptor, IgA, IgM, high affinity	1	Envelope surface glycoprotein gp120
84148	MYST1	MYST histone acetyltransferase 1	1	integrase
84557	MAP1LC3A	microtubule-associated protein 1 light chain 3 alpha	1	retropepsin
84560	MT4	metallothionein 4	1	Tat
84617	TUBB6	tubulin, beta 6	2	Rev; Tat
84647	PLA2G12B	phospholipase A2, group XIIB	1	Envelope surface glycoprotein gp120
84717	HDGF2	hepatoma-derived growth factor-related protein 2	1	integrase
84790	TUBA1C	tubulin, alpha 1c	3	Envelope surface glycoprotein gp120; Rev; Tat
84812	PLCD4	phospholipase C, delta 4	2	Envelope surface glycoprotein gp120; Tat
84823	LMNB2	lamin B2	2	Tat; Vpr
85235	HIST1H2AH	histone cluster 1, H2ah	1	Tat
85236	HIST1H2BK	histone cluster 1, H2bk	1	Tat
85363	TRIM5	tripartite motif-containing 5	1	capsid
85417	CCNB3	cyclin B3	1	Vpr
89869	PLCZ1	phospholipase C, zeta 1	1	Envelope surface glycoprotein gp120
90678	LRSAM1	leucine rich repeat and sterile alpha motif containing 1	1	Pr55(Gag)
92140	MTDH	metadherin	1	Envelope surface glycoprotein gp120
92421	CHMP4C	chromatin modifying protein 4C	1	p6
92815	HIST3H2A	histone cluster 3, H2a	1	Tat
94239	H2AFV	H2A histone family, member V	1	Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
113026	PLCD3	phospholipase C, delta 3	2	Envelope surface glycoprotein gp120; Tat
116179	TGM7	transglutaminase 7	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
116443	GRIN3A	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	2	Envelope surface glycoprotein gp120; Tat
116444	GRIN3B	glutamate receptor, ionotropic, N-methyl-D-aspartate 3B	2	Envelope surface glycoprotein gp120; Tat
116835	HSPA12B	heat shock 70kD protein 12B	1	Envelope surface glycoprotein gp120
117854	TRIM6	tripartite motif-containing 6	1	capsid
121504	HIST4H4	histone cluster 4, H4	1	Tat
124790	HEXIM2	hexamthylene bis-acetamide inducible 2	1	Tat
126129	CPT1C	carnitine palmitoyltransferase 1C	1	Envelope surface glycoprotein gp160, precursor
126961	HIST2H3C	histone cluster 2, H3c	1	Tat
128312	HIST3H2BB	histone cluster 3, H2bb	1	Tat
128866	CHMP4B	chromatin modifying protein 4B	1	p6
129685	TBN	taube nuss homolog (mouse)	1	Tat
130340	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	1	Nef
140564	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D (putative)	1	Vif
144423	GLT1D1	glycosyltransferase 1 domain containing 1	1	Envelope surface glycoprotein gp120

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID				
GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
146664	MGAT5B	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	2	Envelope surface glycoprotein gp160, precursor; Envelope transmembrane glycoprotein gp41
171558	PTCRA	pre T-cell antigen receptor alpha	1	Envelope surface glycoprotein gp120
171568	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	1	Tat
196883	ADCY4	adenylate cyclase 4	4	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Nef; Tat
197257	LDHD	lactate dehydrogenase D	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
200315	APOBEC3A	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	1	Tat
200316	APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	2	Pr55(Gag); Vif
203068	TUBB	tubulin, beta	1	Tat
221613	HIST1H2AA	histone cluster 1, H2aa	1	Tat
225689	MAPK15	mitogen-activated protein kinase 15	1	Envelope surface glycoprotein gp120
255189	PLA2G4F	phospholipase A2, group IVF	1	Envelope surface glycoprotein gp120
255626	HIST1H2BA	histone cluster 1, H2ba	1	Tat
257202	GPX6	glutathione peroxidase 6 (olfactory)	1	Tat
283748	PLA2G4D	phospholipase A2, group IVD (cytosolic)	1	Envelope surface glycoprotein gp120
284217	LAMA1	laminin, alpha 1	3	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41; Tat

Supplementary Table 1. HIV-1 Human Protein Interaction Database: Listing of interactions by Entrez GeneID

GeneID	Symbol	Name	Number of HIV-1 Protein Interactions	Interacts with HIV-1 Proteins
317772	HIST2H2AB	histone cluster 2, H2ab	1	Tat
326343	MT1DP	metallothionein 1D (pseudogene)	1	Tat
340273	ABCB5	ATP-binding cassette, sub-family B (MDR/TAP), member 5	1	Envelope surface glycoprotein gp120
343641	TGM6	transglutaminase 6	2	Envelope surface glycoprotein gp120; Envelope transmembrane glycoprotein gp41
347688	TUBB8	tubulin, beta 8	2	Rev; Tat
347733	TUBB2B	tubulin, beta 2B	1	Tat
360203	GLT6D1	glycosyltransferase 6 domain containing 1	1	Envelope surface glycoprotein gp120
440738	MAP1LC3C	microtubule-associated protein 1 light chain 3 gamma	1	retropepsin
644314	MTE	metallothionein E	1	Tat
653361	NCF1	neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1)	1	Tat

Supplementary Table 2. Listing and Distribution of Keywords Associated with the HIV-1 Human Protein Interaction Database

Keyword	Number of Times Used	% of Total
interacts with	875	17.04
upregulates	609	11.86
binds	602	11.72
activates	499	9.72
downregulates	401	7.81
inhibits	352	6.85
inhibited by	213	4.15
processed by	132	2.57
regulated by	106	2.06
phosphorylated by	77	1.5
cleaves	71	1.38
imported by	66	1.29
enhances	65	1.27
complexes with	61	1.19
stimulates	59	1.15
induces phosphorylation of	58	1.13
inactivates	55	1.07
induces release of	47	0.92
degraded by	45	0.88
incorporates	45	0.88
co-localizes with	44	0.86
associates with	40	0.78
enhanced by	40	0.78
modulated by	40	0.78
requires	38	0.74
synergizes with	36	0.7
recruits	34	0.66
stimulated by	34	0.66
modulates	32	0.62
ubiquitinated by	30	0.58
stabilizes	29	0.56
relocalizes	23	0.45
mediated by	21	0.41
competes with	20	0.39
decreases phosphorylation of	20	0.39
cleaved by	18	0.35
regulates	16	0.31

Supplementary Table 2. Listing and Distribution of Keywords Associated with the HIV-1 Human Protein Interaction Database

Keyword	Number of Times Used	% of Total
degrades	15	0.29
depolymerizes	13	0.25
cooperates with	12	0.23
enhances polymerization of	12	0.23
induces cleavage of	12	0.23
activated by	10	0.19
modified by	10	0.19
acetylated by	9	0.18
induces rearrangement of	8	0.16
relocalized by	8	0.16
induces accumulation of	7	0.14
upregulated by	7	0.14
glycosylated by	6	0.12
induces acetylation of	6	0.12
sensitizes	6	0.12
disrupts	5	0.1
downregulated by	5	0.1
exported by	5	0.1
palmitoylated by	4	0.08
induces complex with	3	0.06
methylated by	3	0.06
myristoylated by	3	0.06
acetylates	2	0.04
fractionates with	2	0.04
isomerized by	2	0.04
recruited by	2	0.04
cleavage induced by	1	0.02
deglycosylates	1	0.02
inhibits acetylation of	1	0.02
phosphorylates	1	0.02
polarizes	1	0.02

Supplementary Table 3A. HIV-1 Human Protein Interaction Database: Distribution of cellular component Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0005575	cellular_component	1448	100.00%
0005623	cell	1140	78.73%
0044464	cell part	1140	78.73%
0005622	intracellular	860	59.39%
0044424	intracellular part	823	56.84%
0043226	organelle	669	46.20%
0043229	intracellular organelle	669	46.20%
0043231	intracellular membrane-bound organelle	589	40.68%
0043227	membrane-bound organelle	589	40.68%
0016020	membrane	476	32.87%
0005634	nucleus	447	30.87%
0005737	cytoplasm	428	29.56%
0044425	membrane part	370	25.55%
0043234	protein complex	361	24.93%
0031224	intrinsic to membrane	333	23.00%
0016021	integral to membrane	331	22.86%
0044422	organelle part	312	21.55%
0044446	intracellular organelle part	312	21.55%
0044444	cytoplasmic part	279	19.27%
0005886	plasma membrane	252	17.40%
0044459	plasma membrane part	198	13.67%
0043232	intracellular non-membrane-bound organelle	196	13.54%
0043228	non-membrane-bound organelle	196	13.54%
0005576	extracellular region	172	11.88%
0031226	intrinsic to plasma membrane	159	10.98%
0005887	integral to plasma membrane	158	10.91%
0044428	nuclear part	133	9.19%
0044421	extracellular region part	124	8.56%
0005856	cytoskeleton	113	7.80%
0031974	membrane-enclosed lumen	99	6.84%
0043233	organelle lumen	99	6.84%
0005615	extracellular space	96	6.63%
0000267	cell fraction	93	6.42%
0031981	nuclear lumen	91	6.28%
0005829	cytosol	90	6.22%
0005654	nucleoplasm	83	5.73%
0044430	cytoskeletal part	75	5.18%
0005694	chromosome	73	5.04%
0031090	organelle membrane	73	5.04%
0044451	nucleoplasm part	68	4.70%
0044427	chromosomal part	66	4.56%
0012505	endomembrane system	65	4.49%
0005624	membrane fraction	61	4.21%
0000785	chromatin	48	3.31%
0015630	microtubule cytoskeleton	47	3.25%
0005794	Golgi apparatus	45	3.11%
0005783	endoplasmic reticulum	44	3.04%
0005739	mitochondrion	42	2.90%
0000786	nucleosome	41	2.83%
0005667	transcription factor complex	40	2.76%
0031012	extracellular matrix	38	2.62%
0000502	proteasome complex (sensu the Eukaryota research community)	38	2.62%
0005578	extracellular matrix (sensu the Metazoa research community)	37	2.56%
0015629	actin cytoskeleton	37	2.56%
0016591	DNA-directed RNA polymerase II, holoenzyme	33	2.28%
0005874	microtubule	32	2.21%
0031975	envelope	32	2.21%
0031967	organelle envelope	32	2.21%
0005625	soluble fraction	31	2.14%
0044431	Golgi apparatus part	31	2.14%
0043235	receptor complex	29	2.00%
0000139	Golgi membrane	28	1.93%
0030529	ribonucleoprotein complex	28	1.93%
0016023	cytoplasmic membrane-bound vesicle	25	1.73%
0031410	cytoplasmic vesicle	25	1.73%
0031988	membrane-bound vesicle	25	1.73%
0031982	vesicle	25	1.73%
0044420	extracellular matrix part	23	1.59%
0005635	nuclear envelope	23	1.59%

Supplementary Table 3A. HIV-1 Human Protein Interaction Database: Distribution of cellular component Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0044433	cytoplasmic vesicle part	20	1.38%
0030659	cytoplasmic vesicle membrane	20	1.38%
0030135	coated vesicle	20	1.38%
0012506	vesicle membrane	20	1.38%
0005773	vacuole	19	1.31%
0044445	cytosolic part	19	1.31%
0030136	clathrin-coated vesicle	19	1.31%
0008287	protein serine/threonine phosphatase complex	19	1.31%
0048475	coated membrane	18	1.24%
0030662	coated vesicle membrane	18	1.24%
0009986	cell surface	18	1.24%
0030117	membrane coat	18	1.24%
0005604	basement membrane	18	1.24%
0005839	proteasome core complex (sensu the Eukaryota research community)	18	1.24%
0005905	coated pit	18	1.24%
0030120	vesicle coat	18	1.24%
0030125	clathrin vesicle coat	17	1.17%
0030880	RNA polymerase complex	17	1.17%
0030665	clathrin coated vesicle membrane	17	1.17%
0042995	cell projection	17	1.17%
0030118	clathrin coat	17	1.17%
0031965	nuclear membrane	16	1.10%
0044453	nuclear membrane part	16	1.10%
0005643	nuclear pore	15	1.04%
0046930	pore complex	15	1.04%
0005764	lysosome	15	1.04%
0031300	intrinsic to organelle membrane	15	1.04%
0000323	lytic vacuole	15	1.04%
0030054	cell junction	14	0.97%
0000159	protein phosphatase type 2A complex	14	0.97%
0031228	intrinsic to Golgi membrane	14	0.97%
0005768	endosome	14	0.97%
0005669	transcription factor TFIID complex	14	0.97%
0045202	synapse	14	0.97%
0000228	nuclear chromosome	13	0.90%
0005730	nucleolus	13	0.90%
0008305	integrin complex	13	0.90%
0005938	cell cortex	11	0.76%
0005942	phosphoinositide 3-kinase complex	11	0.76%
0044429	mitochondrial part	11	0.76%
0045211	postsynaptic membrane	11	0.76%
0043292	contractile fiber	11	0.76%
0005798	Golgi-associated vesicle	11	0.76%
0005657	replication fork	11	0.76%
0044456	synapse part	11	0.76%
0005681	spliceosome	10	0.69%
0005605	basal lamina	10	0.69%
0005911	intercellular junction	10	0.69%
0044449	contractile fiber part	10	0.69%
0019867	outer membrane	10	0.69%
0030133	transport vesicle	10	0.69%
0030119	membrane coat adaptor complex	10	0.69%
0030140	trans-Golgi network transport vesicle	10	0.69%
0001772	immunological synapse	10	0.69%
0030016	myofibril	10	0.69%
0005740	mitochondrial envelope	9	0.62%
0031966	mitochondrial membrane	9	0.62%
0005665	DNA-directed RNA polymerase II, core complex	9	0.62%
0030658	transport vesicle membrane	9	0.62%
0012510	trans-Golgi network transport vesicle membrane	9	0.62%
0042101	T cell receptor complex	9	0.62%
0044432	endoplasmic reticulum part	9	0.62%
0044448	cell cortex part	9	0.62%
0042612	MHC class I protein complex	9	0.62%
0044454	nuclear chromosome part	9	0.62%
0005875	microtubule associated complex	9	0.62%
0030660	Golgi-associated vesicle membrane	9	0.62%
0043256	laminin complex	9	0.62%
0030017	sarcomere	9	0.62%

Supplementary Table 3A. HIV-1 Human Protein Interaction Database: Distribution of cellular component Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0030130	clathrin coat of trans-Golgi network vesicle	9	0.62%
0042611	MHC protein complex	9	0.62%
0005838	proteasome regulatory particle (sensu the Eukaryota research community)	8	0.55%
0005815	microtubule organizing center	8	0.55%
0005882	intermediate filament	8	0.55%
0005581	collagen	8	0.55%
0030863	cortical cytoskeleton	8	0.55%
0030131	clathrin adaptor complex	8	0.55%
0045111	intermediate filament cytoskeleton	8	0.55%
0005813	centrosome	8	0.55%
0005666	DNA-directed RNA polymerase III complex	8	0.55%
0005792	microsome	7	0.48%
0008076	voltage-gated potassium channel complex	7	0.48%
0005606	laminin-1 complex	7	0.48%
0005819	spindle	7	0.48%
0031301	integral to organelle membrane	7	0.48%
0005952	cAMP-dependent protein kinase complex	7	0.48%
0042598	vesicular fraction	7	0.48%
0005884	actin filament	7	0.48%
0005793	ER-Golgi intermediate compartment	7	0.48%
0008091	spectrin	7	0.48%
0016459	myosin complex	7	0.48%
0005912	adherens junction	7	0.48%
0030139	endocytic vesicle	7	0.48%
0030864	cortical actin cytoskeleton	7	0.48%
0016327	apicolateral plasma membrane	6	0.41%
0030173	integral to Golgi membrane	6	0.41%
0005923	tight junction	6	0.41%
0043296	apical junction complex	6	0.41%
0005626	insoluble fraction	6	0.41%
0005663	DNA replication factor C complex	6	0.41%
0005802	Golgi trans face	6	0.41%
0030666	endocytic vesicle membrane	5	0.35%
0005662	DNA replication factor A complex	5	0.35%
0031968	organelle outer membrane	5	0.35%
0016323	basolateral plasma membrane	5	0.35%
0005876	spindle microtubule	5	0.35%
0005587	collagen type IV	5	0.35%
0005789	endoplasmic reticulum membrane	5	0.35%
0030055	cell-matrix junction	5	0.35%
0043005	neuron projection	5	0.35%
0005788	endoplasmic reticulum lumen	5	0.35%
0043596	replication fork (sensu the Eukaryota research community)	5	0.35%
0000127	transcription factor TFIIIC complex	5	0.35%
0005925	focal adhesion	5	0.35%
0031252	leading edge	5	0.35%
0019866	organelle inner membrane	5	0.35%
0030427	site of polarized growth	5	0.35%
0030935	sheet-forming collagen	5	0.35%
0005741	mitochondrial outer membrane	5	0.35%
0030894	replisome	5	0.35%
0005924	cell-substrate adherens junction	5	0.35%
0001726	ruffle	5	0.35%
0043601	replisome (sensu the Eukaryota research community)	5	0.35%
0009897	external side of plasma membrane	5	0.35%
0042175	nuclear envelope-endoplasmic reticulum network	5	0.35%
0030132	clathrin coat of coated pit	5	0.35%
0005865	striated muscle thin filament	5	0.35%
0005675	transcription factor TFIIH complex	5	0.35%
0030426	growth cone	4	0.28%
0045121	lipid raft	4	0.28%
0030121	AP-1 adaptor complex	4	0.28%
0016585	chromatin remodeling complex	4	0.28%
0044450	microtubule organizing center part	4	0.28%
0005743	mitochondrial inner membrane	4	0.28%
0045334	clathrin-coated endocytic vesicle	4	0.28%
0030532	small nuclear ribonucleoprotein complex	4	0.28%
0016604	nuclear body	4	0.28%
0005955	calcineurin complex	4	0.28%

Supplementary Table 3A. HIV-1 Human Protein Interaction Database: Distribution of cellular component Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0005840	ribosome	4	0.28%
0005859	muscle myosin complex	4	0.28%
0048471	perinuclear region	4	0.28%
0030425	dendrite	4	0.28%
0016460	myosin II complex	4	0.28%
0031672	A band	4	0.28%
0030128	clathrin coat of endocytic vesicle	4	0.28%
0019898	extrinsic to membrane	4	0.28%
0016605	PML body	4	0.28%
0030669	clathrin-coated endocytic vesicle membrane	4	0.28%
0030122	AP-2 adaptor complex	4	0.28%
0005863	striated muscle thick filament	4	0.28%
0000775	chromosome, pericentric region	4	0.28%
0000792	heterochromatin	3	0.21%
0016282	eukaryotic 43S preinitiation complex	3	0.21%
0005862	muscle thin filament tropomyosin	3	0.21%
0005583	fibrillar collagen	3	0.21%
0005684	U2-dependent spliceosome	3	0.21%
0016363	nuclear matrix	3	0.21%
0000793	condensed chromosome	3	0.21%
0000790	nuclear chromatin	3	0.21%
0030424	axon	3	0.21%
0000151	ubiquitin ligase complex	3	0.21%
0000794	condensed nuclear chromosome	3	0.21%
0005776	autophagic vacuole	3	0.21%
0000781	chromosome, telomeric region	3	0.21%
0042579	microbody	3	0.21%
0005941	unlocalized protein complex	3	0.21%
0043025	cell soma	3	0.21%
0005777	peroxisome	3	0.21%
0000119	mediator complex	3	0.21%
0005850	eukaryotic translation initiation factor 2 complex	3	0.21%
0005720	nuclear heterochromatin	3	0.21%
0044463	cell projection part	3	0.21%
0008537	proteasome activator complex	3	0.21%
0005830	cytosolic ribosome (sensu the Eukaryota research community)	3	0.21%
0000930	gamma-tubulin complex	2	0.14%
0031143	pseudopodium	2	0.14%
0000922	spindle pole	2	0.14%
0005602	complement component C1q complex	2	0.14%
0001739	sex chromatin	2	0.14%
0008023	transcription elongation factor complex	2	0.14%
0016281	eukaryotic translation initiation factor 4F complex	2	0.14%
0005732	small nucleolar ribonucleoprotein complex	2	0.14%
0005652	nuclear lamina	2	0.14%
0005892	nicotinic acetylcholine-gated receptor-channel complex	2	0.14%
0005697	telomerase holoenzyme complex	2	0.14%
0005759	mitochondrial matrix	2	0.14%
0044437	vacuolar part	2	0.14%
0044440	endosomal part	2	0.14%
0043189	H4/H2A histone acetyltransferase complex	2	0.14%
0031594	neuromuscular junction	2	0.14%
0035267	NuA4 histone acetyltransferase complex	2	0.14%
0005816	spindle pole body	2	0.14%
0005842	cytosolic large ribosomal subunit (sensu the Eukaryota research community)	2	0.14%
0000123	histone acetyltransferase complex	2	0.14%
0030496	midbody	2	0.14%
0000118	histone deacetylase complex	2	0.14%
0005903	brush border	2	0.14%
0015934	large ribosomal subunit	2	0.14%
0000776	kinetochore	2	0.14%
0044455	mitochondrial membrane part	2	0.14%
0005673	transcription factor TFIIE complex	2	0.14%
0005844	polysome	2	0.14%
0010008	endosome membrane	2	0.14%
0005610	laminin-5 complex	2	0.14%
0001740	Barr body	2	0.14%
0030530	heterogeneous nuclear ribonucleoprotein complex	2	0.14%
0000805	X chromosome	2	0.14%

Supplementary Table 3A. HIV-1 Human Protein Interaction Database: Distribution of cellular component Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0001533	cornified envelope	2	0.14%
0000803	sex chromosome	2	0.14%
0005774	vacuolar membrane	2	0.14%
0005791	rough endoplasmic reticulum	2	0.14%
0044452	nucleolar part	2	0.14%
0005584	collagen type I	2	0.14%
0043197	dendritic spine	2	0.14%
0005958	DNA-dependent protein kinase complex	2	0.14%
0005746	mitochondrial electron transport chain	2	0.14%
0000242	pericentriolar material	2	0.14%
0005686	snRNP U2	2	0.14%
0005579	membrane attack complex	2	0.14%
0031980	mitochondrial lumen	2	0.14%
0005765	lysosomal membrane	1	0.07%
0044447	axoneme part	1	0.07%
0005685	snRNP U1	1	0.07%
0005956	protein kinase CK2 complex	1	0.07%
0005795	Golgi stack	1	0.07%
0005954	calcium- and calmodulin-dependent protein kinase complex	1	0.07%
0043259	laminin-10 complex	1	0.07%
0045335	phagocytic vesicle	1	0.07%
0005586	collagen type III	1	0.07%
0005853	eukaryotic translation elongation factor 1 complex	1	0.07%
0046658	anchored to plasma membrane	1	0.07%
0005827	polar microtubule	1	0.07%
0000235	astral microtubule	1	0.07%
0030126	COPI vesicle coat	1	0.07%
0030667	secretory granule membrane	1	0.07%
0005638	lamin filament	1	0.07%
0000152	nuclear ubiquitin ligase complex	1	0.07%
0000133	polarisome	1	0.07%
0005871	kinesin complex	1	0.07%
0019717	synaptosome	1	0.07%
0043257	laminin-8 complex	1	0.07%
0016011	dystroglycan complex	1	0.07%
0005637	nuclear inner membrane	1	0.07%
0005790	smooth endoplasmic reticulum	1	0.07%
0008303	caspase complex	1	0.07%
0005851	eukaryotic translation initiation factor 2B complex	1	0.07%
0001725	stress fiber	1	0.07%
0005770	late endosome	1	0.07%
0031234	extrinsic to internal side of plasma membrane	1	0.07%
0016533	cyclin-dependent protein kinase 5 activator complex	1	0.07%
0031074	nucleocytoplasmic shuttling complex	1	0.07%
0030670	phagocytic vesicle membrane	1	0.07%
0043626	PCNA complex	1	0.07%
0000784	nuclear chromosome, telomeric region	1	0.07%
0000300	peripheral to membrane of membrane fraction	1	0.07%
0044423	virion part	1	0.07%
0005913	cell-cell adherens junction	1	0.07%
0000221	hydrogen-transporting ATPase V1 domain	1	0.07%
0019028	viral capsid	1	0.07%
0005672	transcription factor TFIIA complex	1	0.07%
0015935	small ribosomal subunit	1	0.07%
0005930	axoneme	1	0.07%
0048500	signal recognition particle	1	0.07%
0016010	dystrophin-associated glycoprotein complex	1	0.07%
0005861	troponin complex	1	0.07%
0005608	laminin-3 complex	1	0.07%
0005818	aster	1	0.07%
0005964	phosphorylase kinase complex	1	0.07%
0008274	gamma-tubulin ring complex	1	0.07%
0016469	proton-transporting two-sector ATPase complex	1	0.07%
0005674	transcription factor TFIIF complex	1	0.07%
0030663	COPI coated vesicle membrane	1	0.07%
0005918	septate junction	1	0.07%
0005843	cytosolic small ribosomal subunit (sensu the Eukaryota research community)	1	0.07%
0019897	extrinsic to plasma membrane	1	0.07%
0005607	laminin-2 complex	1	0.07%

Supplementary Table 3A. HIV-1 Human Protein Interaction Database: Distribution of cellular component Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0030137	COPI-coated vesicle	1	0.07%
0031970	organelle envelope lumen	1	0.07%
0008328	ionotropic glutamate receptor complex	1	0.07%
0042627	chylomicron	1	0.07%
0008247	2-acetyl-1-alkylglycerophosphocholine esterase complex	1	0.07%
0030286	dynein complex	1	0.07%
0005902	microvillus	1	0.07%
0000015	phosphopyruvate hydratase complex	1	0.07%
0005858	axonemal dynein complex	1	0.07%
0030867	rough endoplasmic reticulum membrane	1	0.07%
0005758	mitochondrial intermembrane space	1	0.07%
0005677	chromatin silencing complex	1	0.07%
0000795	synaptonemal complex	1	0.07%
0016283	eukaryotic 48S initiation complex	1	0.07%
0009898	internal side of plasma membrane	1	0.07%
0017146	N-methyl-D-aspartate selective glutamate receptor complex	1	0.07%
0005901	caveola	1	0.07%
0016471	hydrogen-translocating V-type ATPase complex	1	0.07%
0046728	viral capsid (sensu the Retroviridae research community)	1	0.07%
0005814	centriole	1	0.07%
0005785	signal recognition particle receptor complex	1	0.07%
0008021	synaptic vesicle	1	0.07%
0005678	chromatin assembly complex	1	0.07%
0030141	secretory granule	1	0.07%
0019013	viral nucleocapsid	1	0.07%
0031092	platelet alpha granule membrane	1	0.07%
0005786	signal recognition particle (sensu the Eukaryota research community)	1	0.07%
0016599	caveolar membrane	1	0.07%
0031436	BRCA1-BARD1 complex	1	0.07%
0031227	intrinsic to endoplasmic reticulum membrane	1	0.07%
0016328	lateral plasma membrane	1	0.07%
0030176	integral to endoplasmic reticulum membrane	1	0.07%
0019012	virion	1	0.07%
0031091	platelet alpha granule	1	0.07%
0032432	actin filament bundle	1	0.07%
0005895	interleukin-5 receptor complex	1	0.07%
0008180	signalosome complex	1	0.07%
0030175	filopodium	1	0.07%
0005896	interleukin-6 receptor complex	1	0.07%
0016514	SWI/SNF complex	1	0.07%
0043034	costamere	1	0.07%
0031225	anchored to membrane	1	0.07%
0000178	exosome (RNase complex)	1	0.07%
0035030	phosphoinositide 3-kinase complex, class IA	1	0.07%
0046696	lipopolysaccharide receptor complex	1	0.07%
	unknown	203	14.02%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0008150	biological_process	1448	100.00%
0009987	cellular process	1232	85.08%
0008152	metabolic process	899	62.09%
0044238	primary metabolic process	862	59.53%
0044237	cellular metabolic process	836	57.73%
0043170	macromolecule metabolic process	766	52.90%
0043283	biopolymer metabolic process	574	39.64%
0065007	biological regulation	517	35.70%
0050789	regulation of biological process	512	35.36%
0007154	cell communication	475	32.80%
0050794	regulation of cellular process	460	31.77%
0007165	signal transduction	442	30.52%
0019538	protein metabolic process	424	29.28%
0044260	cellular macromolecule metabolic process	400	27.62%
0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	396	27.35%
0044267	cellular protein metabolic process	389	26.86%
0050896	response to stimulus	387	26.73%
0032502	developmental process	323	22.31%
0032501	multicellular organismal process	282	19.48%
0051179	localization	276	19.06%
0019222	regulation of metabolic process	269	18.58%
0016070	RNA metabolic process	267	18.44%
0016043	cell organization and biogenesis	264	18.23%
0031323	regulation of cellular metabolic process	252	17.40%
0006350	transcription	245	16.92%
0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	227	15.68%
0032774	RNA biosynthetic process	220	15.19%
0006351	transcription, DNA-dependent	220	15.19%
0045449	regulation of transcription	218	15.06%
0051234	establishment of localization	214	14.78%
0043412	biopolymer modification	213	14.71%
0030154	cell differentiation	210	14.50%
0048869	cellular developmental process	210	14.50%
0006810	transport	209	14.43%
0006464	protein modification	206	14.23%
0006355	regulation of transcription, DNA-dependent	201	13.88%
0007242	intracellular signaling cascade	200	13.81%
0006950	response to stress	198	13.67%
0002376	immune system process	194	13.40%
0048518	positive regulation of biological process	191	13.19%
0048468	cell development	174	12.02%
0007166	cell surface receptor linked signal transduction	172	11.88%
0048856	anatomical structure development	163	11.26%
0008219	cell death	163	11.26%
0006955	immune response	163	11.26%
0016265	death	163	11.26%
0048519	negative regulation of biological process	159	10.98%
0012501	programmed cell death	158	10.91%
0006915	apoptosis	157	10.84%
0007275	multicellular organismal development	156	10.77%
0006996	organelle organization and biogenesis	154	10.64%
0048522	positive regulation of cellular process	154	10.64%
0048523	negative regulation of cellular process	149	10.29%
0007049	cell cycle	149	10.29%
0022402	cell cycle process	135	9.32%
0006952	defense response	135	9.32%
0009605	response to external stimulus	135	9.32%
0006796	phosphate metabolic process	129	8.91%
0006793	phosphorus metabolic process	129	8.91%
0006259	DNA metabolic process	129	8.91%
0048731	system development	124	8.56%
0065003	macromolecule complex assembly	124	8.56%
0002217	physiological defense response	121	8.36%
0043067	regulation of programmed cell death	118	8.15%
0042981	regulation of apoptosis	117	8.08%
0008283	cell proliferation	116	8.01%
0051726	regulation of cell cycle	116	8.01%
0000074	regulation of progression through cell cycle	115	7.94%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0009058	biosynthetic process	115	7.94%
0016310	phosphorylation	112	7.73%
0042221	response to chemical stimulus	107	7.39%
0006468	protein amino acid phosphorylation	105	7.25%
0009611	response to wounding	104	7.18%
0006366	transcription from RNA polymerase II promoter	102	7.04%
0044249	cellular biosynthetic process	102	7.04%
0009056	catabolic process	98	6.77%
0051641	cellular localization	97	6.70%
0022610	biological adhesion	94	6.49%
0007155	cell adhesion	94	6.49%
0051649	establishment of cellular localization	93	6.42%
0006954	inflammatory response	93	6.42%
0007267	cell-cell signaling	92	6.35%
0046907	intracellular transport	92	6.35%
0009607	response to biotic stimulus	92	6.35%
0048513	organ development	92	6.35%
0006629	lipid metabolic process	83	5.73%
0006508	proteolysis	80	5.52%
0051707	response to other organism	77	5.32%
0008104	protein localization	77	5.32%
0009653	anatomical structure morphogenesis	75	5.18%
0042127	regulation of cell proliferation	74	5.11%
0045184	establishment of protein localization	74	5.11%
0065009	regulation of a molecular function	73	5.04%
0005975	carbohydrate metabolic process	72	4.97%
0009059	macromolecule biosynthetic process	72	4.97%
0050790	regulation of catalytic activity	69	4.77%
0015031	protein transport	69	4.77%
0007010	cytoskeleton organization and biogenesis	68	4.70%
0044248	cellular catabolic process	68	4.70%
0007610	behavior	68	4.70%
0007243	protein kinase cascade	67	4.63%
0051674	localization of cell	66	4.56%
0006928	cell motility	66	4.56%
0051276	chromosome organization and biogenesis	63	4.35%
0007001	chromosome organization and biogenesis (sensu the Eukaryota research community)	62	4.28%
0009057	macromolecule catabolic process	60	4.14%
0044255	cellular lipid metabolic process	60	4.14%
0065004	protein-DNA complex assembly	59	4.07%
0006323	DNA packaging	58	4.01%
0006357	regulation of transcription from RNA polymerase II promoter	57	3.94%
0006935	chemotaxis	57	3.94%
0006325	establishment and/or maintenance of chromatin architecture	57	3.94%
0007626	locomotory behavior	57	3.94%
0042330	taxis	57	3.94%
0007186	G-protein coupled receptor protein signaling pathway	56	3.87%
0006811	ion transport	56	3.87%
0043068	positive regulation of programmed cell death	54	3.73%
0044262	cellular carbohydrate metabolic process	54	3.73%
0006886	intracellular protein transport	54	3.73%
0006461	protein complex assembly	54	3.73%
0043065	positive regulation of apoptosis	54	3.73%
0009893	positive regulation of metabolic process	54	3.73%
0042592	homeostatic process	53	3.66%
0006959	humoral immune response	53	3.66%
0009892	negative regulation of metabolic process	53	3.66%
0006091	generation of precursor metabolites and energy	51	3.52%
0000902	cell morphogenesis	50	3.45%
0012502	induction of programmed cell death	50	3.45%
0006917	induction of apoptosis	50	3.45%
0043285	biopolymer catabolic process	50	3.45%
0031325	positive regulation of cellular metabolic process	50	3.45%
0006396	RNA processing	49	3.38%
0019752	carboxylic acid metabolic process	48	3.31%
0044265	cellular macromolecule catabolic process	48	3.31%
0051338	regulation of transferase activity	48	3.31%
0051246	regulation of protein metabolic process	48	3.31%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0043549	regulation of kinase activity	48	3.31%
0006082	organic acid metabolic process	48	3.31%
0043069	negative regulation of programmed cell death	48	3.31%
0009719	response to endogenous stimulus	47	3.25%
0009966	regulation of signal transduction	47	3.25%
0006333	chromatin assembly or disassembly	47	3.25%
0043066	negative regulation of apoptosis	47	3.25%
0045859	regulation of protein kinase activity	47	3.25%
0022403	cell cycle phase	46	3.18%
0050877	neurological process	46	3.18%
0006974	response to DNA damage stimulus	45	3.11%
0007399	nervous system development	43	2.97%
0006807	nitrogen compound metabolic process	43	2.97%
0008284	positive regulation of cell proliferation	43	2.97%
0000003	reproduction	43	2.97%
0016192	vesicle-mediated transport	42	2.90%
0031324	negative regulation of cellular metabolic process	42	2.90%
0031497	chromatin assembly	42	2.90%
0019725	cell homeostasis	42	2.90%
0006334	nucleosome assembly	41	2.83%
0030163	protein catabolic process	40	2.76%
0048878	chemical homeostasis	39	2.69%
0000278	mitotic cell cycle	39	2.69%
0016071	mRNA metabolic process	38	2.62%
0006916	anti-apoptosis	38	2.62%
0007167	enzyme linked receptor protein signaling pathway	38	2.62%
0065008	regulation of biological quality	38	2.62%
0043085	positive regulation of enzyme activity	38	2.62%
0006281	DNA repair	38	2.62%
0009308	amine metabolic process	37	2.56%
0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	37	2.56%
0030003	cation homeostasis	36	2.49%
0006873	cell ion homeostasis	36	2.49%
0051239	regulation of multicellular organismal process	36	2.49%
0001775	cell activation	36	2.49%
0050801	ion homeostasis	36	2.49%
0006397	mRNA processing	36	2.49%
0045941	positive regulation of transcription	36	2.49%
0009615	response to virus	35	2.42%
0051301	cell division	35	2.42%
0006875	metal ion homeostasis	35	2.42%
0030005	di-, tri-valent inorganic cation homeostasis	34	2.35%
0045786	negative regulation of progression through cell cycle	34	2.35%
0000279	M phase	34	2.35%
0045321	leukocyte activation	34	2.35%
0006605	protein targeting	33	2.28%
0002520	immune system development	33	2.28%
0008285	negative regulation of cell proliferation	33	2.28%
0006412	translation	33	2.28%
0006457	protein folding	32	2.21%
0006643	membrane lipid metabolic process	32	2.21%
0006260	DNA replication	32	2.21%
0006066	alcohol metabolic process	32	2.21%
0007169	transmembrane receptor protein tyrosine kinase signaling pathway	32	2.21%
0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	32	2.21%
0048534	hemopoietic or lymphoid organ development	32	2.21%
0044257	cellular protein catabolic process	32	2.21%
0016042	lipid catabolic process	32	2.21%
0022414	reproductive process	32	2.21%
0051603	proteolysis involved in cellular protein catabolic process	32	2.21%
0016481	negative regulation of transcription	31	2.14%
0046649	lymphocyte activation	31	2.14%
0019730	antimicrobial humoral response	31	2.14%
0019882	antigen processing and presentation	31	2.14%
0030097	hemopoiesis	31	2.14%
0007264	small GTPase mediated signal transduction	31	2.14%
0006913	nucleocytoplasmic transport	31	2.14%
0040007	growth	30	2.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0019735	antimicrobial humoral response (sensu the Vertebrata research community)	30	2.07%
0051169	nuclear transport	30	2.07%
0006897	endocytosis	29	2.00%
0019226	transmission of nerve impulse	28	1.93%
0008632	apoptotic program	28	1.93%
0050793	regulation of developmental process	28	1.93%
0006812	cation transport	28	1.93%
0007017	microtubule-based process	28	1.93%
0007249	I-kappaB kinase/NF-kappaB cascade	28	1.93%
0006519	amino acid and derivative metabolic process	27	1.86%
0030036	actin cytoskeleton organization and biogenesis	27	1.86%
0008361	regulation of cell size	27	1.86%
0016049	cell growth	27	1.86%
0030029	actin filament-based process	27	1.86%
0019932	second-messenger-mediated signaling	27	1.86%
0006874	calcium ion homeostasis	27	1.86%
0006512	ubiquitin cycle	27	1.86%
0006511	ubiquitin-dependent protein catabolic process	26	1.80%
0048002	antigen processing and presentation of peptide antigen	26	1.80%
0043632	modification-dependent macromolecule catabolic process	26	1.80%
0000087	M phase of mitotic cell cycle	26	1.80%
0002526	acute inflammatory response	26	1.80%
0019941	modification-dependent protein catabolic process	26	1.80%
0007067	mitosis	26	1.80%
0016477	cell migration	26	1.80%
0042110	T cell activation	25	1.73%
0009967	positive regulation of signal transduction	25	1.73%
0007268	synaptic transmission	25	1.73%
0045893	positive regulation of transcription, DNA-dependent	25	1.73%
0006644	phospholipid metabolic process	25	1.73%
0008380	RNA splicing	25	1.73%
0040008	regulation of growth	24	1.66%
0006520	amino acid metabolic process	24	1.66%
0006118	electron transport	24	1.66%
0006800	oxygen and reactive oxygen species metabolic process	23	1.59%
0016032	viral reproduction	22	1.52%
0009100	glycoprotein metabolic process	22	1.52%
0002682	regulation of immune system process	22	1.52%
0051240	positive regulation of multicellular organismal process	22	1.52%
0002521	leukocyte differentiation	22	1.52%
0017038	protein import	22	1.52%
0050776	regulation of immune response	22	1.52%
0015980	energy derivation by oxidation of organic compounds	22	1.52%
0001558	regulation of cell growth	22	1.52%
0030001	metal ion transport	22	1.52%
0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	22	1.52%
0000375	RNA splicing, via transesterification reactions	22	1.52%
0051336	regulation of hydrolase activity	22	1.52%
0045087	innate immune response	22	1.52%
0051170	nuclear import	22	1.52%
0000398	nuclear mRNA splicing, via spliceosome	22	1.52%
0002252	immune effector process	22	1.52%
0050778	positive regulation of immune response	21	1.45%
0005996	monosaccharide metabolic process	21	1.45%
0007265	Ras protein signal transduction	21	1.45%
0006470	protein amino acid dephosphorylation	21	1.45%
0022415	viral reproductive process	21	1.45%
0030705	cytoskeleton-dependent intracellular transport	21	1.45%
0009889	regulation of biosynthetic process	21	1.45%
0002684	positive regulation of immune system process	21	1.45%
0002460	adaptive immune response (sensu the Gnathostomata research community)	21	1.45%
0006606	protein import into nucleus	21	1.45%
0016337	cell-cell adhesion	21	1.45%
0019318	hexose metabolic process	21	1.45%
0016311	dephosphorylation	21	1.45%
0009101	glycoprotein biosynthetic process	21	1.45%
0002250	adaptive immune response	21	1.45%
0000165	MAPKKK cascade	21	1.45%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0051258	protein polymerization	21	1.45%
0009887	organ morphogenesis	21	1.45%
0051248	negative regulation of protein metabolic process	21	1.45%
0007018	microtubule-based movement	21	1.45%
0008015	circulation	20	1.38%
0002449	lymphocyte mediated immunity	20	1.38%
0046903	secretion	20	1.38%
0043413	biopolymer glycosylation	20	1.38%
0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	20	1.38%
0051347	positive regulation of transferase activity	20	1.38%
0051704	multi-organism process	20	1.38%
0002443	leukocyte mediated immunity	20	1.38%
0009117	nucleotide metabolic process	20	1.38%
0043122	regulation of I-kappaB kinase/NF-kappaB cascade	20	1.38%
0045860	positive regulation of protein kinase activity	20	1.38%
0050878	regulation of body fluids	19	1.31%
0019058	viral infectious cycle	19	1.31%
0051345	positive regulation of hydrolase activity	19	1.31%
0051325	interphase	19	1.31%
0006486	protein amino acid glycosylation	19	1.31%
0006261	DNA-dependent DNA replication	19	1.31%
0007600	sensory perception	18	1.24%
0006968	cellular defense response	18	1.24%
0006820	anion transport	18	1.24%
0006631	fatty acid metabolic process	18	1.24%
0000079	regulation of cyclin-dependent protein kinase activity	18	1.24%
0006417	regulation of translation	18	1.24%
0009888	tissue development	18	1.24%
0002253	activation of immune response	18	1.24%
0006352	transcription initiation	18	1.24%
0006936	muscle contraction	18	1.24%
0016568	chromatin modification	18	1.24%
0018193	peptidyl-amino acid modification	18	1.24%
0031326	regulation of cellular biosynthetic process	18	1.24%
0016051	carbohydrate biosynthetic process	17	1.17%
0019724	B cell mediated immunity	17	1.17%
0015698	inorganic anion transport	17	1.17%
0051329	interphase of mitotic cell cycle	17	1.17%
0016064	immunoglobulin mediated immune response	17	1.17%
0051247	positive regulation of protein metabolic process	17	1.17%
0045892	negative regulation of transcription, DNA-dependent	17	1.17%
0030098	lymphocyte differentiation	17	1.17%
0043281	regulation of caspase activity	16	1.10%
0019079	viral genome replication	16	1.10%
0009617	response to bacterium	16	1.10%
0015672	monovalent inorganic cation transport	16	1.10%
0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	16	1.10%
0008610	lipid biosynthetic process	16	1.10%
0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	16	1.10%
0019884	antigen processing and presentation of exogenous antigen	16	1.10%
0002495	antigen processing and presentation of peptide antigen via MHC class II	16	1.10%
0006979	response to oxidative stress	16	1.10%
0002478	antigen processing and presentation of exogenous peptide antigen	16	1.10%
0051249	regulation of lymphocyte activation	16	1.10%
0018212	peptidyl-tyrosine modification	16	1.10%
0043405	regulation of MAPK activity	16	1.10%
0043280	positive regulation of caspase activity	15	1.04%
0042742	defense response to bacterium	15	1.04%
0022613	ribonucleoprotein complex biogenesis and assembly	15	1.04%
0042060	wound healing	15	1.04%
0030155	regulation of cell adhesion	15	1.04%
0001816	cytokine production	15	1.04%
0006310	DNA recombination	15	1.04%
0007259	JAK-STAT cascade	15	1.04%
0007229	integrin-mediated signaling pathway	15	1.04%
0051128	regulation of cell organization and biogenesis	15	1.04%
0007050	cell cycle arrest	15	1.04%
0006919	caspase activation	15	1.04%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0007599	hemostasis	15	1.04%
0006817	phosphate transport	14	0.97%
0006383	transcription from RNA polymerase III promoter	14	0.97%
0050817	coagulation	14	0.97%
0048646	anatomical structure formation	14	0.97%
0045595	regulation of cell differentiation	14	0.97%
0019953	sexual reproduction	14	0.97%
0046651	lymphocyte proliferation	14	0.97%
0048858	cell projection morphogenesis	14	0.97%
0051049	regulation of transport	14	0.97%
0001501	skeletal development	14	0.97%
0009165	nucleotide biosynthetic process	14	0.97%
0050863	regulation of T cell activation	14	0.97%
0030030	cell projection organization and biogenesis	14	0.97%
0008154	actin polymerization and/or depolymerization	14	0.97%
0007596	blood coagulation	14	0.97%
0007517	muscle development	14	0.97%
0007204	elevation of cytosolic calcium ion concentration	14	0.97%
0018108	peptidyl-tyrosine phosphorylation	14	0.97%
0051480	cytosolic calcium ion homeostasis	14	0.97%
0030217	T cell differentiation	14	0.97%
0043086	negative regulation of enzyme activity	14	0.97%
0042325	regulation of phosphorylation	14	0.97%
0051174	regulation of phosphorus metabolic process	14	0.97%
0000122	negative regulation of transcription from RNA polymerase II promoter	14	0.97%
0019220	regulation of phosphate metabolic process	14	0.97%
0040011	locomotion	13	0.90%
0031589	cell-substrate adhesion	13	0.90%
0042107	cytokine metabolic process	13	0.90%
0009891	positive regulation of biosynthetic process	13	0.90%
0051789	response to protein stimulus	13	0.90%
0044403	symbiosis, encompassing mutualism through parasitism	13	0.90%
0044275	cellular carbohydrate catabolic process	13	0.90%
0042089	cytokine biosynthetic process	13	0.90%
0050954	sensory perception of mechanical stimulus	13	0.90%
0006006	glucose metabolic process	13	0.90%
0043406	positive regulation of MAPK activity	13	0.90%
0006986	response to unfolded protein	13	0.90%
0005976	polysaccharide metabolic process	13	0.90%
0007605	sensory perception of sound	13	0.90%
0007266	Rho protein signal transduction	13	0.90%
0051270	regulation of cell motility	13	0.90%
0016052	carbohydrate catabolic process	13	0.90%
0007160	cell-matrix adhesion	13	0.90%
0002541	activation of plasma proteins during acute inflammatory response	13	0.90%
0006956	complement activation	13	0.90%
0040012	regulation of locomotion	13	0.90%
0044419	interspecies interaction between organisms	13	0.90%
0009187	cyclic nucleotide metabolic process	13	0.90%
0006790	sulfur metabolic process	13	0.90%
0006953	acute-phase response	13	0.90%
0051052	regulation of DNA metabolic process	13	0.90%
0006469	negative regulation of protein kinase activity	12	0.83%
0006521	regulation of amino acid metabolic process	12	0.83%
0048514	blood vessel morphogenesis	12	0.83%
0051348	negative regulation of transferase activity	12	0.83%
0008064	regulation of actin polymerization and/or depolymerization	12	0.83%
0001932	regulation of protein amino acid phosphorylation	12	0.83%
0030099	myeloid cell differentiation	12	0.83%
0050730	regulation of peptidyl-tyrosine phosphorylation	12	0.83%
0030832	regulation of actin filament length	12	0.83%
0030522	intracellular receptor-mediated signaling pathway	12	0.83%
0019221	cytokine and chemokine mediated signaling pathway	12	0.83%
0043623	cellular protein complex assembly	12	0.83%
0019935	cyclic-nucleotide-mediated signaling	12	0.83%
0051251	positive regulation of lymphocyte activation	12	0.83%
0001568	blood vessel development	12	0.83%
0016055	Wnt receptor signaling pathway	12	0.83%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0030518	steroid hormone receptor signaling pathway	12	0.83%
0042035	regulation of cytokine biosynthetic process	12	0.83%
0006092	main pathways of carbohydrate metabolic process	12	0.83%
0001525	angiogenesis	12	0.83%
0001944	vasculature development	12	0.83%
0007187	G-protein signaling, coupled to cyclic nucleotide second messenger	12	0.83%
0006958	complement activation, classical pathway	11	0.76%
0030334	regulation of cell migration	11	0.76%
0051056	regulation of small GTPase mediated signal transduction	11	0.76%
0002455	humoral immune response mediated by circulating immunoglobulin	11	0.76%
0046578	regulation of Ras protein signal transduction	11	0.76%
0044264	cellular polysaccharide metabolic process	11	0.76%
0022618	protein-RNA complex assembly	11	0.76%
0008202	steroid metabolic process	11	0.76%
0007276	gametogenesis	11	0.76%
0042113	B cell activation	11	0.76%
0045045	secretory pathway	11	0.76%
0000187	activation of MAPK activity	11	0.76%
0006171	cAMP biosynthetic process	10	0.69%
0048015	phosphoinositide-mediated signaling	10	0.69%
0050870	positive regulation of T cell activation	10	0.69%
0016044	membrane organization and biogenesis	10	0.69%
0046058	cAMP metabolic process	10	0.69%
0044242	cellular lipid catabolic process	10	0.69%
0000075	cell cycle checkpoint	10	0.69%
0048699	generation of neurons	10	0.69%
0030182	neuron differentiation	10	0.69%
0009190	cyclic nucleotide biosynthetic process	10	0.69%
0009628	response to abiotic stimulus	10	0.69%
0043543	protein amino acid acylation	10	0.69%
0045727	positive regulation of protein biosynthetic process	10	0.69%
0022008	neurogenesis	10	0.69%
0031328	positive regulation of cellular biosynthetic process	10	0.69%
0051129	negative regulation of cell organization and biogenesis	10	0.69%
0019883	antigen processing and presentation of endogenous antigen	10	0.69%
0051186	cofactor metabolic process	10	0.69%
0051261	protein depolymerization	10	0.69%
0006354	RNA elongation	10	0.69%
0009790	embryonic development	10	0.69%
0007417	central nervous system development	10	0.69%
0008544	epidermis development	9	0.62%
0045944	positive regulation of transcription from RNA polymerase II promoter	9	0.62%
0030834	regulation of actin filament depolymerization	9	0.62%
0051168	nuclear export	9	0.62%
0051318	G1 phase	9	0.62%
0016125	sterol metabolic process	9	0.62%
0030835	negative regulation of actin filament depolymerization	9	0.62%
0030521	androgen receptor signaling pathway	9	0.62%
0015674	di-, tri-valent inorganic cation transport	9	0.62%
0006073	glucan metabolic process	9	0.62%
0035023	regulation of Rho protein signal transduction	9	0.62%
0006813	potassium ion transport	9	0.62%
0006112	energy reserve metabolic process	9	0.62%
0051701	interaction with host	9	0.62%
0006732	coenzyme metabolic process	9	0.62%
0042108	positive regulation of cytokine biosynthetic process	9	0.62%
0051090	regulation of transcription factor activity	9	0.62%
0006665	sphingolipid metabolic process	9	0.62%
0050670	regulation of lymphocyte proliferation	9	0.62%
0042100	B cell proliferation	9	0.62%
0007173	epidermal growth factor receptor signaling pathway	9	0.62%
0008203	cholesterol metabolic process	9	0.62%
0030042	actin filament depolymerization	9	0.62%
0031098	stress-activated protein kinase signaling pathway	9	0.62%
0005977	glycogen metabolic process	9	0.62%
0008624	induction of apoptosis by extracellular signals	9	0.62%
0007398	ectoderm development	9	0.62%
0051016	barbed-end actin filament capping	9	0.62%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0007254	JNK cascade	9	0.62%
0051693	actin filament capping	9	0.62%
0048666	neuron development	9	0.62%
0042770	DNA damage response, signal transduction	9	0.62%
0045926	negative regulation of growth	9	0.62%
0006487	protein amino acid N-linked glycosylation	8	0.55%
0002483	antigen processing and presentation of endogenous peptide antigen	8	0.55%
0030308	negative regulation of cell growth	8	0.55%
0016569	covalent chromatin modification	8	0.55%
0045792	negative regulation of cell size	8	0.55%
0051259	protein oligomerization	8	0.55%
0046365	monosaccharide catabolic process	8	0.55%
0006801	superoxide metabolic process	8	0.55%
0051321	meiotic cell cycle	8	0.55%
0046164	alcohol catabolic process	8	0.55%
0002474	antigen processing and presentation of peptide antigen via MHC class I	8	0.55%
0007188	G-protein signaling, coupled to cAMP nucleotide second messenger	8	0.55%
0050792	regulation of viral life cycle	8	0.55%
0046209	nitric oxide metabolic process	8	0.55%
0006690	icosanoid metabolic process	8	0.55%
0007260	tyrosine phosphorylation of STAT protein	8	0.55%
0019933	cAMP-mediated signaling	8	0.55%
0007088	regulation of mitosis	8	0.55%
0006898	receptor-mediated endocytosis	8	0.55%
0006473	protein amino acid acetylation	8	0.55%
0019320	hexose catabolic process	8	0.55%
0006809	nitric oxide biosynthetic process	8	0.55%
0019885	antigen processing and presentation of endogenous peptide antigen via MHC class I	8	0.55%
0006607	NLS-bearing substrate import into nucleus	8	0.55%
0051235	maintenance of localization	8	0.55%
0016570	histone modification	8	0.55%
0007005	mitochondrion organization and biogenesis	8	0.55%
0008629	induction of apoptosis by intracellular signals	8	0.55%
0046916	transition metal ion homeostasis	8	0.55%
0031175	neurite development	8	0.55%
0006367	transcription initiation from RNA polymerase II promoter	8	0.55%
0007028	cytoplasm organization and biogenesis	8	0.55%
0046466	membrane lipid catabolic process	8	0.55%
0042098	T cell proliferation	8	0.55%
0051093	negative regulation of developmental process	7	0.48%
0045069	regulation of viral genome replication	7	0.48%
0050657	nucleic acid transport	7	0.48%
0006633	fatty acid biosynthetic process	7	0.48%
0042129	regulation of T cell proliferation	7	0.48%
0048667	neuron morphogenesis during differentiation	7	0.48%
0000904	cellular morphogenesis during differentiation	7	0.48%
0009395	phospholipid catabolic process	7	0.48%
0007283	spermatogenesis	7	0.48%
0050658	RNA transport	7	0.48%
0000080	G1 phase of mitotic cell cycle	7	0.48%
0006007	glucose catabolic process	7	0.48%
0018149	peptide cross-linking	7	0.48%
0006040	amino sugar metabolic process	7	0.48%
0006405	RNA export from nucleus	7	0.48%
0009405	pathogenesis	7	0.48%
0043284	biopolymer biosynthetic process	7	0.48%
0048812	neurite morphogenesis	7	0.48%
0046822	regulation of nucleocytoplasmic transport	7	0.48%
0022411	cellular structure disassembly	7	0.48%
0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	7	0.48%
0006909	phagocytosis	7	0.48%
0006403	RNA localization	7	0.48%
0030595	leukocyte chemotaxis	7	0.48%
0016053	organic acid biosynthetic process	7	0.48%
0046394	carboxylic acid biosynthetic process	7	0.48%
0050900	leukocyte migration	7	0.48%
0040029	regulation of gene expression, epigenetic	7	0.48%
0045937	positive regulation of phosphate metabolic process	7	0.48%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0007519	striated muscle development	7	0.48%
0051327	M phase of meiotic cell cycle	7	0.48%
0048232	male gamete generation	7	0.48%
0007126	meiosis	7	0.48%
0048609	reproductive process in a multicellular organism	7	0.48%
0050671	positive regulation of lymphocyte proliferation	7	0.48%
0045216	intercellular junction assembly and maintenance	7	0.48%
0007611	learning and/or memory	7	0.48%
0008286	insulin receptor signaling pathway	7	0.48%
0042327	positive regulation of phosphorylation	7	0.48%
0051236	establishment of RNA localization	7	0.48%
0007200	G-protein signaling, coupled to IP3 second messenger (phospholipase C activating)	6	0.41%
0009968	negative regulation of signal transduction	6	0.41%
0006413	translational initiation	6	0.41%
0051223	regulation of protein transport	6	0.41%
0006044	N-acetylglucosamine metabolic process	6	0.41%
0000059	protein import into nucleus, docking	6	0.41%
0030216	keratinocyte differentiation	6	0.41%
0051091	positive regulation of transcription factor activity	6	0.41%
0051050	positive regulation of transport	6	0.41%
0002573	myeloid leukocyte differentiation	6	0.41%
0000082	G1/S transition of mitotic cell cycle	6	0.41%
0030574	collagen catabolic process	6	0.41%
0006338	chromatin remodeling	6	0.41%
0050731	positive regulation of peptidyl-tyrosine phosphorylation	6	0.41%
0051606	detection of stimulus	6	0.41%
0008630	DNA damage response, signal transduction resulting in induction of apoptosis	6	0.41%
0016485	protein processing	6	0.41%
0006650	glycerophospholipid metabolic process	6	0.41%
0007043	intercellular junction assembly	6	0.41%
0022604	regulation of cell morphogenesis	6	0.41%
0006399	tRNA metabolic process	6	0.41%
0006096	glycolysis	6	0.41%
0042509	regulation of tyrosine phosphorylation of STAT protein	6	0.41%
0006041	glucosamine metabolic process	6	0.41%
0010033	response to organic substance	6	0.41%
0045764	positive regulation of amino acid metabolic process	6	0.41%
0009314	response to radiation	6	0.41%
0042306	regulation of protein import into nucleus	6	0.41%
0001906	cell killing	6	0.41%
0008637	apoptotic mitochondrial changes	6	0.41%
0006692	prostanoid metabolic process	6	0.41%
0050864	regulation of B cell activation	6	0.41%
0006302	double-strand break repair	6	0.41%
0006693	prostaglandin metabolic process	6	0.41%
0006275	regulation of DNA replication	6	0.41%
0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	6	0.41%
0007157	heterophilic cell adhesion	6	0.41%
0007016	cytoskeletal anchoring	6	0.41%
0008360	regulation of cell shape	6	0.41%
0032446	protein modification by small protein conjugation	6	0.41%
0046425	regulation of JAK-STAT cascade	6	0.41%
0030100	regulation of endocytosis	6	0.41%
0001934	positive regulation of protein amino acid phosphorylation	6	0.41%
0022603	regulation of anatomical structure morphogenesis	6	0.41%
0006816	calcium ion transport	6	0.41%
0032147	activation of protein kinase activity	6	0.41%
0048771	tissue remodeling	5	0.35%
0016567	protein ubiquitination	5	0.35%
0046364	monosaccharide biosynthetic process	5	0.35%
0031644	regulation of neurological process	5	0.35%
0042102	positive regulation of T cell proliferation	5	0.35%
0006575	amino acid derivative metabolic process	5	0.35%
0032508	DNA duplex unwinding	5	0.35%
0051828	entry into other organism during symbiotic interaction	5	0.35%
0006268	DNA unwinding during replication	5	0.35%
0030031	cell projection biogenesis	5	0.35%
0007163	establishment and/or maintenance of cell polarity	5	0.35%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0019319	hexose biosynthetic process	5	0.35%
0006289	nucleotide-excision repair	5	0.35%
0006308	DNA catabolic process	5	0.35%
0042493	response to drug	5	0.35%
0000302	response to reactive oxygen species	5	0.35%
0046718	entry of virus into host cell	5	0.35%
0031327	negative regulation of cellular biosynthetic process	5	0.35%
0006921	cell structure disassembly during apoptosis	5	0.35%
0050727	regulation of inflammatory response	5	0.35%
0042348	NF-kappaB import into nucleus	5	0.35%
0051262	protein tetramerization	5	0.35%
0006094	gluconeogenesis	5	0.35%
0030260	entry into host cell	5	0.35%
0007015	actin filament organization	5	0.35%
0019059	initiation of viral infection	5	0.35%
0042345	regulation of NF-kappaB import into nucleus	5	0.35%
0048583	regulation of response to stimulus	5	0.35%
0019835	cytolysis	5	0.35%
0044409	entry into host	5	0.35%
0002274	myeloid leukocyte activation	5	0.35%
0006090	pyruvate metabolic process	5	0.35%
0042516	regulation of tyrosine phosphorylation of Stat3 protein	5	0.35%
0031570	DNA integrity checkpoint	5	0.35%
0009311	oligosaccharide metabolic process	5	0.35%
0051651	maintenance of cellular localization	5	0.35%
0006022	aminoglycan metabolic process	5	0.35%
0002768	immune response-regulating cell surface receptor signaling pathway	5	0.35%
0006013	mannose metabolic process	5	0.35%
0030203	glycosaminoglycan metabolic process	5	0.35%
0009890	negative regulation of biosynthetic process	5	0.35%
0032392	DNA geometric change	5	0.35%
0051092	activation of NF-kappaB transcription factor	5	0.35%
0002764	immune response-regulating signal transduction	5	0.35%
0050804	regulation of synaptic transmission	5	0.35%
0050803	regulation of synapse structure and function	5	0.35%
0031347	regulation of defense response	5	0.35%
0008635	caspase activation via cytochrome c	5	0.35%
0015837	amine transport	5	0.35%
0042503	tyrosine phosphorylation of Stat3 protein	5	0.35%
0045076	regulation of interleukin-2 biosynthetic process	5	0.35%
0002429	immune response-activating cell surface receptor signaling pathway	5	0.35%
0046849	bone remodeling	5	0.35%
0046165	alcohol biosynthetic process	5	0.35%
0045884	regulation of survival gene product activity	5	0.35%
0002440	production of molecular mediator of immune response	5	0.35%
0002377	immunoglobulin production	5	0.35%
0032623	interleukin-2 production	5	0.35%
0048193	Golgi vesicle transport	5	0.35%
0006997	nuclear organization and biogenesis	5	0.35%
0007215	glutamate signaling pathway	5	0.35%
0006368	RNA elongation from RNA polymerase II promoter	5	0.35%
0000226	microtubule cytoskeleton organization and biogenesis	5	0.35%
0045058	T cell selection	5	0.35%
0050871	positive regulation of B cell activation	5	0.35%
0042991	transcription factor import into nucleus	5	0.35%
0009306	protein secretion	5	0.35%
0042094	interleukin-2 biosynthetic process	5	0.35%
0002757	immune response-activating signal transduction	5	0.35%
0006957	complement activation, alternative pathway	5	0.35%
0000270	peptidoglycan metabolic process	5	0.35%
0046456	icosanoid biosynthetic process	5	0.35%
0007586	digestion	5	0.35%
0051969	regulation of transmission of nerve impulse	5	0.35%
0007409	axonogenesis	5	0.35%
0048729	tissue morphogenesis	5	0.35%
0042254	ribosome biogenesis and assembly	5	0.35%
0042990	regulation of transcription factor import into nucleus	5	0.35%
0007179	transforming growth factor beta receptor signaling pathway	5	0.35%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0017148	negative regulation of protein biosynthetic process	5	0.35%
0051806	entry into cell of other organism during symbiotic interaction	5	0.35%
0007346	regulation of progression through mitotic cell cycle	5	0.35%
0016573	histone acetylation	5	0.35%
0007159	leukocyte adhesion	5	0.35%
0007172	signal complex formation	5	0.35%
0001666	response to hypoxia	5	0.35%
0045995	regulation of embryonic development	5	0.35%
0050851	antigen receptor-mediated signaling pathway	5	0.35%
0050852	T cell receptor signaling pathway	5	0.35%
0006418	tRNA aminoacylation for protein translation	4	0.28%
0016338	calcium-independent cell-cell adhesion	4	0.28%
0015849	organic acid transport	4	0.28%
0007498	mesoderm development	4	0.28%
0051297	centrosome organization and biogenesis	4	0.28%
0030218	erythrocyte differentiation	4	0.28%
0051028	mRNA transport	4	0.28%
0006937	regulation of muscle contraction	4	0.28%
0006865	amino acid transport	4	0.28%
0046467	membrane lipid biosynthetic process	4	0.28%
0009416	response to light stimulus	4	0.28%
0006491	N-glycan processing	4	0.28%
0002562	somatic diversification of immune receptors via germline recombination within a single locus	4	0.28%
0006414	translational elongation	4	0.28%
0040017	positive regulation of locomotion	4	0.28%
0006869	lipid transport	4	0.28%
0009259	ribonucleotide metabolic process	4	0.28%
0007089	traversing start control point of mitotic cell cycle	4	0.28%
0045428	regulation of nitric oxide biosynthetic process	4	0.28%
0030111	regulation of Wnt receptor signaling pathway	4	0.28%
0006839	mitochondrial transport	4	0.28%
0002208	somatic diversification of immunoglobulins during immune response	4	0.28%
0006406	mRNA export from nucleus	4	0.28%
0051272	positive regulation of cell motility	4	0.28%
0009260	ribonucleotide biosynthetic process	4	0.28%
0030384	phosphoinositide metabolic process	4	0.28%
0001516	prostaglandin biosynthetic process	4	0.28%
0002204	somatic recombination of immunoglobulin genes during immune response	4	0.28%
0050767	regulation of neurogenesis	4	0.28%
0000060	protein import into nucleus, translocation	4	0.28%
0002200	somatic diversification of immune receptors	4	0.28%
0019048	virus-host interaction	4	0.28%
0046426	negative regulation of JAK-STAT cascade	4	0.28%
0000245	spliceosome assembly	4	0.28%
0048730	epidermis morphogenesis	4	0.28%
0007507	heart development	4	0.28%
0046631	alpha-beta T cell activation	4	0.28%
0007009	plasma membrane organization and biogenesis	4	0.28%
0051051	negative regulation of transport	4	0.28%
0008625	induction of apoptosis via death domain receptors	4	0.28%
0050732	negative regulation of peptidyl-tyrosine phosphorylation	4	0.28%
0048167	regulation of synaptic plasticity	4	0.28%
0040013	negative regulation of locomotion	4	0.28%
0045763	negative regulation of amino acid metabolic process	4	0.28%
0042532	negative regulation of tyrosine phosphorylation of STAT protein	4	0.28%
0007568	aging	4	0.28%
0046519	sphingoid metabolic process	4	0.28%
0006672	ceramide metabolic process	4	0.28%
0009309	amine biosynthetic process	4	0.28%
0030168	platelet activation	4	0.28%
0006364	rRNA processing	4	0.28%
0050673	epithelial cell proliferation	4	0.28%
0009411	response to UV	4	0.28%
0046942	carboxylic acid transport	4	0.28%
0045185	maintenance of protein localization	4	0.28%
0006818	hydrogen transport	4	0.28%
0051271	negative regulation of cell motility	4	0.28%
0031023	microtubule organizing center organization and biogenesis	4	0.28%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0009108	coenzyme biosynthetic process	4	0.28%
0008643	carbohydrate transport	4	0.28%
0046457	prostanoid biosynthetic process	4	0.28%
0006029	proteoglycan metabolic process	4	0.28%
0009620	response to fungus	4	0.28%
0051098	regulation of binding	4	0.28%
0015992	proton transport	4	0.28%
0009410	response to xenobiotic stimulus	4	0.28%
0044272	sulfur compound biosynthetic process	4	0.28%
0016444	somatic cell DNA recombination	4	0.28%
0006879	iron ion homeostasis	4	0.28%
0044271	nitrogen compound biosynthetic process	4	0.28%
0016445	somatic diversification of immunoglobulins	4	0.28%
0030258	lipid modification	4	0.28%
0000077	DNA damage checkpoint	4	0.28%
0045619	regulation of lymphocyte differentiation	4	0.28%
0001933	negative regulation of protein amino acid phosphorylation	4	0.28%
0042518	negative regulation of tyrosine phosphorylation of Stat3 protein	4	0.28%
0050678	regulation of epithelial cell proliferation	4	0.28%
0065002	intracellular protein transport across a membrane	4	0.28%
0006941	striated muscle contraction	4	0.28%
0050679	positive regulation of epithelial cell proliferation	4	0.28%
0016447	somatic recombination of immunoglobulin gene segments	4	0.28%
0008217	blood pressure regulation	4	0.28%
0045190	isotype switching	4	0.28%
0045580	regulation of T cell differentiation	4	0.28%
0045086	positive regulation of interleukin-2 biosynthetic process	4	0.28%
0001508	regulation of action potential	4	0.28%
0046777	protein amino acid autophosphorylation	4	0.28%
0002381	immunoglobulin production during immune response	4	0.28%
0051188	cofactor biosynthetic process	4	0.28%
0043038	amino acid activation	4	0.28%
0042445	hormone metabolic process	4	0.28%
0030183	B cell differentiation	4	0.28%
0043039	tRNA aminoacylation	4	0.28%
0042157	lipoprotein metabolic process	4	0.28%
0009991	response to extracellular stimulus	4	0.28%
0009451	RNA modification	4	0.28%
0051402	neuron apoptosis	4	0.28%
0019722	calcium-mediated signaling	4	0.28%
0006887	exocytosis	4	0.28%
0045936	negative regulation of phosphate metabolic process	4	0.28%
0030262	apoptotic nuclear changes	4	0.28%
0006163	purine nucleotide metabolic process	4	0.28%
0006611	protein export from nucleus	4	0.28%
0006309	DNA fragmentation during apoptosis	4	0.28%
0016072	rRNA metabolic process	4	0.28%
0006576	biogenic amine metabolic process	4	0.28%
0006164	purine nucleotide biosynthetic process	4	0.28%
0001505	regulation of neurotransmitter levels	4	0.28%
0021700	developmental maturation	4	0.28%
0007098	centrosome cycle	4	0.28%
0001503	ossification	4	0.28%
0016540	protein autoprocessing	4	0.28%
0032507	maintenance of cellular protein localization	4	0.28%
0042036	negative regulation of cytokine biosynthetic process	4	0.28%
0006359	regulation of transcription from RNA polymerase III promoter	4	0.28%
0042326	negative regulation of phosphorylation	4	0.28%
0031214	biomineral formation	4	0.28%
0045596	negative regulation of cell differentiation	4	0.28%
0030330	DNA damage response, signal transduction by p53 class mediator	4	0.28%
0009152	purine ribonucleotide biosynthetic process	4	0.28%
0009150	purine ribonucleotide metabolic process	4	0.28%
0050880	regulation of blood vessel size	4	0.28%
0007569	cell aging	4	0.28%
0030101	natural killer cell activation	4	0.28%
0001907	killing of host cells	3	0.21%
0009913	epidermal cell differentiation	3	0.21%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0032609	interferon-gamma production	3	0.21%
0006303	double-strand break repair via nonhomologous end joining	3	0.21%
0015749	monosaccharide transport	3	0.21%
0031640	killing of cells of another organism	3	0.21%
0045597	positive regulation of cell differentiation	3	0.21%
0007162	negative regulation of cell adhesion	3	0.21%
0030335	positive regulation of cell migration	3	0.21%
0030336	negative regulation of cell migration	3	0.21%
0045664	regulation of neuron differentiation	3	0.21%
0043407	negative regulation of MAPK activity	3	0.21%
0007127	meiosis I	3	0.21%
0019395	fatty acid oxidation	3	0.21%
0051339	regulation of lyase activity	3	0.21%
0048747	muscle fiber development	3	0.21%
0048469	cell maturation	3	0.21%
0009206	purine ribonucleoside triphosphate biosynthetic process	3	0.21%
0046824	positive regulation of nucleocytoplasmic transport	3	0.21%
0006270	DNA replication initiation	3	0.21%
0019836	hemolysis of host red blood cells	3	0.21%
0009205	purine ribonucleoside triphosphate metabolic process	3	0.21%
0048741	skeletal muscle fiber development	3	0.21%
0031667	response to nutrient levels	3	0.21%
0051260	protein homooligomerization	3	0.21%
0000018	regulation of DNA recombination	3	0.21%
0030195	negative regulation of blood coagulation	3	0.21%
0048675	axon extension	3	0.21%
0030193	regulation of blood coagulation	3	0.21%
0030316	osteoclast differentiation	3	0.21%
0006446	regulation of translational initiation	3	0.21%
0009201	ribonucleoside triphosphate biosynthetic process	3	0.21%
0006878	copper ion homeostasis	3	0.21%
0006023	aminoglycan biosynthetic process	3	0.21%
0009792	embryonic development (sensu the Metazoa research community)	3	0.21%
0006024	glycosaminoglycan biosynthetic process	3	0.21%
0044003	modification of host morphology or physiology	3	0.21%
0042771	DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis	3	0.21%
0006378	mRNA polyadenylation	3	0.21%
0000726	non-recombinational repair	3	0.21%
0051094	positive regulation of developmental process	3	0.21%
0031124	mRNA 3'-end processing	3	0.21%
0044004	disruption of host cells	3	0.21%
0042401	biogenic amine biosynthetic process	3	0.21%
0030888	regulation of B cell proliferation	3	0.21%
0006476	protein amino acid deacetylation	3	0.21%
0031123	RNA 3'-end processing	3	0.21%
0045927	positive regulation of growth	3	0.21%
0007205	protein kinase C activation	3	0.21%
0043550	regulation of lipid kinase activity	3	0.21%
0007034	vacuolar transport	3	0.21%
0006100	tricarboxylic acid cycle intermediate metabolic process	3	0.21%
0007033	vacuole organization and biogenesis	3	0.21%
0042310	vasoconstriction	3	0.21%
0000723	telomere maintenance	3	0.21%
0002286	T cell activation during immune response	3	0.21%
0030166	proteoglycan biosynthetic process	3	0.21%
0015833	peptide transport	3	0.21%
0002285	lymphocyte activation during immune response	3	0.21%
0045807	positive regulation of endocytosis	3	0.21%
0006888	ER to Golgi vesicle-mediated transport	3	0.21%
0006814	sodium ion transport	3	0.21%
0051883	killing of cells of other organism during symbiotic interaction	3	0.21%
0048259	regulation of receptor mediated endocytosis	3	0.21%
0006725	aromatic compound metabolic process	3	0.21%
0007202	phospholipase C activation	3	0.21%
0051238	sequestering of metal ion	3	0.21%
0045090	retroviral genome replication	3	0.21%
0051283	negative regulation of sequestering of calcium ion	3	0.21%
0045787	positive regulation of progression through cell cycle	3	0.21%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0048637	skeletal muscle development	3	0.21%
0051282	regulation of sequestering of calcium ion	3	0.21%
0030307	positive regulation of cell growth	3	0.21%
0042542	response to hydrogen peroxide	3	0.21%
0016126	sterol biosynthetic process	3	0.21%
0045785	positive regulation of cell adhesion	3	0.21%
0051640	organelle localization	3	0.21%
0000188	inactivation of MAPK activity	3	0.21%
0046632	alpha-beta T cell differentiation	3	0.21%
0045637	regulation of myeloid cell differentiation	3	0.21%
0008654	phospholipid biosynthetic process	3	0.21%
0007589	fluid secretion	3	0.21%
0007588	excretion	3	0.21%
0015758	glucose transport	3	0.21%
0009593	detection of chemical stimulus	3	0.21%
0007250	activation of NF-kappaB-inducing kinase	3	0.21%
0051817	modification of morphology or physiology of other organism during symbiotic interaction	3	0.21%
0051818	disruption of cells of other organism during symbiotic interaction	3	0.21%
0050768	negative regulation of neurogenesis	3	0.21%
0006911	phagocytosis, engulfment	3	0.21%
0050832	defense response to fungus	3	0.21%
0019642	anaerobic glycolysis	3	0.21%
0051715	cytolysis of cells of another organism	3	0.21%
0048041	focal adhesion formation	3	0.21%
0006914	autophagy	3	0.21%
0018065	protein-cofactor linkage	3	0.21%
0030149	sphingolipid catabolic process	3	0.21%
0043525	positive regulation of neuron apoptosis	3	0.21%
0043523	regulation of neuron apoptosis	3	0.21%
0016575	histone deacetylation	3	0.21%
0009199	ribonucleoside triphosphate metabolic process	3	0.21%
0043367	CD4-positive, alpha beta T cell differentiation	3	0.21%
0006471	protein amino acid ADP-ribosylation	3	0.21%
0042307	positive regulation of protein import into nucleus	3	0.21%
0051209	release of sequestered calcium ion into cytosol	3	0.21%
0051208	sequestering of calcium ion	3	0.21%
0008037	cell recognition	3	0.21%
0046034	ATP metabolic process	3	0.21%
0030041	actin filament polymerization	3	0.21%
0051216	cartilage development	3	0.21%
0050920	regulation of chemotaxis	3	0.21%
0045454	cell redox homeostasis	3	0.21%
0009141	nucleoside triphosphate metabolic process	3	0.21%
0051801	cytolysis of cells of other organism during symbiotic interaction	3	0.21%
0009142	nucleoside triphosphate biosynthetic process	3	0.21%
0050854	regulation of antigen receptor-mediated signaling pathway	3	0.21%
0009144	purine nucleoside triphosphate metabolic process	3	0.21%
0009145	purine nucleoside triphosphate biosynthetic process	3	0.21%
0000086	G2/M transition of mitotic cell cycle	3	0.21%
0006684	sphingomyelin metabolic process	3	0.21%
0000041	transition metal ion transport	3	0.21%
0031279	regulation of cyclase activity	3	0.21%
0005980	glycogen catabolic process	3	0.21%
0000272	polysaccharide catabolic process	3	0.21%
0003006	reproductive developmental process	3	0.21%
0000271	polysaccharide biosynthetic process	3	0.21%
0045429	positive regulation of nitric oxide biosynthetic process	3	0.21%
0019062	virion attachment to host cell surface receptor	3	0.21%
0005513	detection of calcium ion	3	0.21%
0007565	pregnancy	3	0.21%
0045761	regulation of adenylate cyclase activity	3	0.21%
0042095	interferon-gamma biosynthetic process	3	0.21%
0008645	hexose transport	3	0.21%
0006752	group transfer coenzyme metabolic process	3	0.21%
0006635	fatty acid beta-oxidation	3	0.21%
0030593	neutrophil chemotaxis	3	0.21%
0050819	negative regulation of coagulation	3	0.21%
0006753	nucleoside phosphate metabolic process	3	0.21%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0051101	regulation of DNA binding	3	0.21%
0045765	regulation of angiogenesis	3	0.21%
0048525	negative regulation of viral life cycle	3	0.21%
0006766	vitamin metabolic process	3	0.21%
0043087	regulation of GTPase activity	3	0.21%
0006754	ATP biosynthetic process	3	0.21%
0045072	regulation of interferon-gamma biosynthetic process	3	0.21%
0042093	T-helper cell differentiation	3	0.21%
0002263	cell activation during immune response	3	0.21%
0042092	T-helper 2 type immune response	3	0.21%
0008634	negative regulation of survival gene product activity	3	0.21%
0001897	cytolysis of host cells	3	0.21%
0032200	telomere organization and biogenesis	3	0.21%
0042993	positive regulation of transcription factor import into nucleus	3	0.21%
0008016	regulation of heart contraction	3	0.21%
0006821	chloride transport	3	0.21%
0030890	positive regulation of B cell proliferation	3	0.21%
0045793	positive regulation of cell size	3	0.21%
0050818	regulation of coagulation	3	0.21%
0045582	positive regulation of T cell differentiation	3	0.21%
0048009	insulin-like growth factor receptor signaling pathway	3	0.21%
0042391	regulation of membrane potential	3	0.21%
0045621	positive regulation of lymphocyte differentiation	3	0.21%
0009251	glucan catabolic process	3	0.21%
0019228	generation of action potential	3	0.21%
0006695	cholesterol biosynthetic process	3	0.21%
0042730	fibrinolysis	3	0.21%
0045191	regulation of isotype switching	3	0.21%
0006401	RNA catabolic process	3	0.21%
0009312	oligosaccharide biosynthetic process	3	0.21%
0006694	steroid biosynthetic process	3	0.21%
0006284	base-excision repair	3	0.21%
0042346	positive regulation of NF-kappaB import into nucleus	3	0.21%
0009249	protein-lipoylation	3	0.21%
0019369	arachidonic acid metabolic process	3	0.21%
0006826	iron ion transport	3	0.21%
0002366	leukocyte activation during immune response	3	0.21%
0006805	xenobiotic metabolic process	3	0.21%
0002292	T cell differentiation during immune response	3	0.21%
0007131	meiotic recombination	3	0.21%
0044247	cellular polysaccharide catabolic process	3	0.21%
0007420	brain development	3	0.21%
0007040	lysosome organization and biogenesis	3	0.21%
0002293	alpha-beta T cell differentiation during immune response	3	0.21%
0019229	regulation of vasoconstriction	3	0.21%
0001909	leukocyte mediated cytotoxicity	3	0.21%
0051222	positive regulation of protein transport	3	0.21%
0042398	amino acid derivative biosynthetic process	3	0.21%
0043631	RNA polyadenylation	3	0.21%
0002294	CD4-positive, alpha-beta T cell differentiation during immune response	3	0.21%
0046483	heterocycle metabolic process	3	0.21%
0042133	neurotransmitter metabolic process	2	0.14%
0006739	NADP metabolic process	2	0.14%
0050654	chondroitin sulfate proteoglycan metabolic process	2	0.14%
0051224	negative regulation of protein transport	2	0.14%
0046795	intracellular virion transport	2	0.14%
0006265	DNA topological change	2	0.14%
0019362	pyridine nucleotide metabolic process	2	0.14%
0007041	lysosomal transport	2	0.14%
0007262	STAT protein nuclear translocation	2	0.14%
0051607	defense response to virus	2	0.14%
0051220	cytoplasmic sequestering of protein	2	0.14%
0016139	glycoside catabolic process	2	0.14%
0006266	DNA ligation	2	0.14%
0006733	oxidoreduction coenzyme metabolic process	2	0.14%
0046794	virion transport	2	0.14%
0042033	chemokine biosynthetic process	2	0.14%
0031281	positive regulation of cyclase activity	2	0.14%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0016137	glycoside metabolic process	2	0.14%
0042440	pigment metabolic process	2	0.14%
0050729	positive regulation of inflammatory response	2	0.14%
0009581	detection of external stimulus	2	0.14%
0030225	macrophage differentiation	2	0.14%
0016547	RNA editing	2	0.14%
0009725	response to hormone stimulus	2	0.14%
0007286	spermatid development	2	0.14%
0050999	regulation of nitric-oxide synthase activity	2	0.14%
0046486	glycerolipid metabolic process	2	0.14%
0050650	chondroitin sulfate proteoglycan biosynthetic process	2	0.14%
0001836	release of cytochrome c from mitochondria	2	0.14%
0031349	positive regulation of defense response	2	0.14%
0042446	hormone biosynthetic process	2	0.14%
0007269	neurotransmitter secretion	2	0.14%
0051187	cofactor catabolic process	2	0.14%
0051250	negative regulation of lymphocyte activation	2	0.14%
0006119	oxidative phosphorylation	2	0.14%
0031069	hair follicle morphogenesis	2	0.14%
0042994	cytoplasmic sequestering of transcription factor	2	0.14%
0006664	glycolipid metabolic process	2	0.14%
0042531	positive regulation of tyrosine phosphorylation of STAT protein	2	0.14%
0007422	peripheral nervous system development	2	0.14%
0009103	lipopolysaccharide biosynthetic process	2	0.14%
0001894	tissue homeostasis	2	0.14%
0006400	tRNA modification	2	0.14%
0030259	lipid glycosylation	2	0.14%
0045885	positive regulation of survival gene product activity	2	0.14%
0042347	negative regulation of NF-kappaB import into nucleus	2	0.14%
0042992	negative regulation of transcription factor import into nucleus	2	0.14%
0016197	endosome transport	2	0.14%
0007281	germ cell development	2	0.14%
0045616	regulation of keratinocyte differentiation	2	0.14%
0046488	phosphatidylinositol metabolic process	2	0.14%
0007423	sensory organ development	2	0.14%
0006662	glycerol ether metabolic process	2	0.14%
0006337	nucleosome disassembly	2	0.14%
0050672	negative regulation of lymphocyte proliferation	2	0.14%
0006661	phosphatidylinositol biosynthetic process	2	0.14%
0046489	phosphoinositide biosynthetic process	2	0.14%
0008406	gonad development	2	0.14%
0006283	transcription-coupled nucleotide-excision repair	2	0.14%
0006687	glycosphingolipid metabolic process	2	0.14%
0009894	regulation of catabolic process	2	0.14%
0006282	regulation of DNA repair	2	0.14%
0006685	sphingomyelin catabolic process	2	0.14%
0051668	localization within membrane	2	0.14%
0009266	response to temperature stimulus	2	0.14%
0048821	erythrocyte development	2	0.14%
0045622	regulation of T-helper cell differentiation	2	0.14%
0045079	negative regulation of chemokine biosynthetic process	2	0.14%
0050853	B cell receptor signaling pathway	2	0.14%
0007411	axon guidance	2	0.14%
0050856	regulation of T cell receptor signaling pathway	2	0.14%
0042744	hydrogen peroxide catabolic process	2	0.14%
0002228	natural killer cell mediated immunity	2	0.14%
0050857	positive regulation of antigen receptor-mediated signaling pathway	2	0.14%
0045078	positive regulation of interferon-gamma biosynthetic process	2	0.14%
0050921	positive regulation of chemotaxis	2	0.14%
0042743	hydrogen peroxide metabolic process	2	0.14%
0006939	smooth muscle contraction	2	0.14%
0042303	molting cycle	2	0.14%
0045624	positive regulation of T-helper cell differentiation	2	0.14%
0046475	glycerophospholipid catabolic process	2	0.14%
0051046	regulation of secretion	2	0.14%
0007257	activation of JNK activity	2	0.14%
0046474	glycerophospholipid biosynthetic process	2	0.14%
0043624	cellular protein complex disassembly	2	0.14%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0050926	regulation of positive chemotaxis	2	0.14%
0045059	positive thymic T cell selection	2	0.14%
0042308	negative regulation of protein import into nucleus	2	0.14%
0050927	positive regulation of positive chemotaxis	2	0.14%
0045333	cellular respiration	2	0.14%
0007253	cytoplasmic sequestering of NF-kappaB	2	0.14%
0007342	fusion of sperm to egg plasma membrane	2	0.14%
0001776	leukocyte homeostasis	2	0.14%
0045445	myoblast differentiation	2	0.14%
0006584	catecholamine metabolic process	2	0.14%
0006706	steroid catabolic process	2	0.14%
0007189	G-protein signaling, adenylate cyclase activating pathway	2	0.14%
0045073	regulation of chemokine biosynthetic process	2	0.14%
0051057	positive regulation of small GTPase mediated signal transduction	2	0.14%
0006345	loss of chromatin silencing	2	0.14%
0007584	response to nutrient	2	0.14%
0051054	positive regulation of DNA metabolic process	2	0.14%
0003001	generation of a signal involved in cell-cell signaling	2	0.14%
0031401	positive regulation of protein modification	2	0.14%
0050868	negative regulation of T cell activation	2	0.14%
0030520	estrogen receptor signaling pathway	2	0.14%
0045071	negative regulation of viral genome replication	2	0.14%
0045070	positive regulation of viral genome replication	2	0.14%
0050930	induction of positive chemotaxis	2	0.14%
0045091	regulation of retroviral genome replication	2	0.14%
0030204	chondroitin sulfate metabolic process	2	0.14%
0045830	positive regulation of isotype switching	2	0.14%
0006639	acylglycerol metabolic process	2	0.14%
0043241	protein complex disassembly	2	0.14%
0042339	keratan sulfate metabolic process	2	0.14%
0045767	regulation of anti-apoptosis	2	0.14%
0030503	regulation of cell redox homeostasis	2	0.14%
0006638	neutral lipid metabolic process	2	0.14%
0045806	negative regulation of endocytosis	2	0.14%
0030865	cortical cytoskeleton organization and biogenesis	2	0.14%
0045165	cell fate commitment	2	0.14%
0043249	erythrocyte maturation	2	0.14%
0006944	membrane fusion	2	0.14%
0042130	negative regulation of T cell proliferation	2	0.14%
0016601	Rac protein signal transduction	2	0.14%
0045137	development of primary sexual characteristics	2	0.14%
0046800	enhancement of virulence	2	0.14%
0048261	negative regulation of receptor mediated endocytosis	2	0.14%
0048524	positive regulation of viral life cycle	2	0.14%
0006376	mRNA splice site selection	2	0.14%
0051241	negative regulation of multicellular organismal process	2	0.14%
0051341	regulation of oxidoreductase activity	2	0.14%
0009988	cell-cell recognition	2	0.14%
0006767	water-soluble vitamin metabolic process	2	0.14%
0007271	synaptic transmission, cholinergic	2	0.14%
0006477	protein amino acid sulfation	2	0.14%
0007567	parturition	2	0.14%
0007338	fertilization (sensu the Metazoa research community)	2	0.14%
0045762	positive regulation of adenylate cyclase activity	2	0.14%
0015918	sterol transport	2	0.14%
0046427	positive regulation of JAK-STAT cascade	2	0.14%
0030206	chondroitin sulfate biosynthetic process	2	0.14%
0006769	nicotinamide metabolic process	2	0.14%
0002761	regulation of myeloid leukocyte differentiation	2	0.14%
0002762	negative regulation of myeloid leukocyte differentiation	2	0.14%
0048332	mesoderm morphogenesis	2	0.14%
0007270	nerve-nerve synaptic transmission	2	0.14%
0006478	peptidyl-tyrosine sulfation	2	0.14%
0051821	dissemination or transmission of organism from other organism during symbiotic interaction	2	0.14%
0031396	regulation of protein ubiquitination	2	0.14%
0031398	positive regulation of protein ubiquitination	2	0.14%
0007606	sensory perception of chemical stimulus	2	0.14%
0045576	mast cell activation	2	0.14%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0031399	regulation of protein modification	2	0.14%
0009299	mRNA transcription	2	0.14%
0045670	regulation of osteoclast differentiation	2	0.14%
0019748	secondary metabolic process	2	0.14%
0045736	negative regulation of cyclin-dependent protein kinase activity	2	0.14%
0042176	regulation of protein catabolic process	2	0.14%
0043507	positive regulation of JNK activity	2	0.14%
0042088	T-helper 1 type immune response	2	0.14%
0050770	regulation of axonogenesis	2	0.14%
0043506	regulation of JNK activity	2	0.14%
0018958	phenol metabolic process	2	0.14%
0006499	N-terminal protein myristoylation	2	0.14%
0007190	adenylate cyclase activation	2	0.14%
0045671	negative regulation of osteoclast differentiation	2	0.14%
0050773	regulation of dendrite development	2	0.14%
0045055	regulated secretory pathway	2	0.14%
0006271	DNA strand elongation during DNA replication	2	0.14%
0006497	protein amino acid lipidation	2	0.14%
0051656	establishment of organelle localization	2	0.14%
0050774	negative regulation of dendrite morphogenesis	2	0.14%
0051349	positive regulation of lyase activity	2	0.14%
0042158	lipoprotein biosynthetic process	2	0.14%
0001707	mesoderm formation	2	0.14%
0031649	heat generation	2	0.14%
0050755	chemokine metabolic process	2	0.14%
0042136	neurotransmitter biosynthetic process	2	0.14%
0042267	natural killer cell mediated cytotoxicity	2	0.14%
0007093	mitotic checkpoint	2	0.14%
0046823	negative regulation of nucleocytoplasmic transport	2	0.14%
0006000	fructose metabolic process	2	0.14%
0032602	chemokine production	2	0.14%
0031498	chromatin disassembly	2	0.14%
0006836	neurotransmitter transport	2	0.14%
0031647	regulation of protein stability	2	0.14%
0048813	dendrite morphogenesis	2	0.14%
0042554	superoxide release	2	0.14%
0045026	plasma membrane fusion	2	0.14%
0048814	regulation of dendrite morphogenesis	2	0.14%
0043062	extracellular structure organization and biogenesis	2	0.14%
0006612	protein targeting to membrane	2	0.14%
0001704	formation of primary germ layer	2	0.14%
0000910	cytokinesis	2	0.14%
0006927	transformed cell apoptosis	2	0.14%
0030032	lamellipodium biogenesis	2	0.14%
0018319	protein amino acid myristoylation	2	0.14%
0001660	fever	2	0.14%
0045061	thymic T cell selection	2	0.14%
0007156	homophilic cell adhesion	2	0.14%
0007548	sex differentiation	2	0.14%
0007549	dosage compensation	2	0.14%
0043433	negative regulation of transcription factor activity	2	0.14%
0050918	positive chemotaxis	2	0.14%
0022616	DNA strand elongation	2	0.14%
0019089	transmission of virus	2	0.14%
0009072	aromatic amino acid family metabolic process	2	0.14%
0042632	cholesterol homeostasis	2	0.14%
0042633	hair cycle	2	0.14%
0045815	positive regulation of gene expression, epigenetic	2	0.14%
0035051	cardiac cell differentiation	2	0.14%
0043368	positive T cell selection	2	0.14%
0022407	regulation of cell-cell adhesion	2	0.14%
0048515	spermatid differentiation	2	0.14%
0022405	hair cycle process	2	0.14%
0022404	molting cycle process	2	0.14%
0010038	response to metal ion	2	0.14%
0045840	positive regulation of mitosis	2	0.14%
0043163	cell envelope organization and biogenesis	2	0.14%
0048871	multicellular organismal homeostasis	2	0.14%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0008033	tRNA processing	2	0.14%
0031424	keratinization	2	0.14%
0009566	fertilization	2	0.14%
0048872	homeostasis of number of cells	2	0.14%
0043072	negative regulation of non-apoptotic programmed cell death	2	0.14%
0015695	organic cation transport	2	0.14%
0006621	protein retention in ER	2	0.14%
0010035	response to inorganic substance	2	0.14%
0007140	male meiosis	2	0.14%
0043070	regulation of non-apoptotic programmed cell death	2	0.14%
0048608	reproductive structure development	2	0.14%
0045088	regulation of innate immune response	2	0.14%
0045089	positive regulation of innate immune response	2	0.14%
0007219	Notch signaling pathway	2	0.14%
0016458	gene silencing	2	0.14%
0043297	apical junction assembly	2	0.14%
0031529	ruffle organization and biogenesis	2	0.14%
0050766	positive regulation of phagocytosis	2	0.14%
0001659	thermoregulation	2	0.14%
0007218	neuropeptide signaling pathway	2	0.14%
0018377	protein myristoylation	2	0.14%
0044007	dissemination or transmission of organism from host	2	0.14%
0050764	regulation of phagocytosis	2	0.14%
0051923	sulfation	2	0.14%
0030162	regulation of proteolysis	2	0.14%
0050663	cytokine secretion	2	0.14%
0046968	peptide antigen transport	2	0.14%
0042423	catecholamine biosynthetic process	2	0.14%
0042692	muscle cell differentiation	2	0.14%
0045346	regulation of MHC class II biosynthetic process	2	0.14%
0007052	mitotic spindle organization and biogenesis	2	0.14%
0001654	eye development	2	0.14%
0007051	spindle organization and biogenesis	2	0.14%
0042116	macrophage activation	2	0.14%
0045229	external encapsulating structure organization and biogenesis	2	0.14%
0015985	energy coupled proton transport, down electrochemical gradient	2	0.14%
0015986	ATP synthesis coupled proton transport	2	0.14%
0045638	negative regulation of myeloid cell differentiation	2	0.14%
0016358	dendrite development	2	0.14%
0030236	anti-inflammatory response	2	0.14%
0019731	antibacterial humoral response	2	0.14%
0007369	gastrulation	2	0.14%
0045342	MHC class II biosynthetic process	2	0.14%
0008653	lipopolysaccharide metabolic process	2	0.14%
0016244	non-apoptotic programmed cell death	2	0.14%
0030301	cholesterol transport	2	0.14%
0009595	detection of biotic stimulus	2	0.14%
0006749	glutathione metabolic process	2	0.14%
0001942	hair follicle development	2	0.14%
0008588	release of cytoplasmic sequestered NF-kappaB	2	0.14%
0032431	activation of phospholipase A2	1	0.07%
0051014	actin filament severing	1	0.07%
0046605	regulation of centrosome cycle	1	0.07%
0009063	amino acid catabolic process	1	0.07%
0045341	MHC class I biosynthetic process	1	0.07%
0006746	FADH2 metabolic process	1	0.07%
0048661	positive regulation of smooth muscle cell proliferation	1	0.07%
0051281	positive regulation of release of sequestered calcium ion into cytosol	1	0.07%
0048660	regulation of smooth muscle cell proliferation	1	0.07%
0009062	fatty acid catabolic process	1	0.07%
0008295	spermidine biosynthetic process	1	0.07%
0008584	male gonad development	1	0.07%
0045630	positive regulation of T-helper 2 cell differentiation	1	0.07%
0007617	mating behavior	1	0.07%
0030239	myofibril assembly	1	0.07%
0019733	antibacterial humoral response (sensu the Vertebrata research community)	1	0.07%
0048592	eye morphogenesis	1	0.07%
0046006	regulation of activated T cell proliferation	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0046606	negative regulation of centrosome cycle	1	0.07%
0008582	regulation of synaptic growth at neuromuscular junction	1	0.07%
0044416	induction of host defense response	1	0.07%
0032429	regulation of phospholipase A2 activity	1	0.07%
0006436	tryptophanyl-tRNA aminoacylation	1	0.07%
0042541	hemoglobin biosynthetic process	1	0.07%
0050828	regulation of liquid surface tension	1	0.07%
0015988	energy coupled proton transport, against electrochemical gradient	1	0.07%
0001915	negative regulation of T cell mediated cytotoxicity	1	0.07%
0006509	membrane protein ectodomain proteolysis	1	0.07%
0016486	peptide hormone processing	1	0.07%
0051017	actin filament bundle formation	1	0.07%
0045343	regulation of MHC class I biosynthetic process	1	0.07%
0016246	RNA interference	1	0.07%
0048103	somatic stem cell division	1	0.07%
0030641	hydrogen ion homeostasis	1	0.07%
0019511	peptidyl-proline hydroxylation	1	0.07%
0001539	ciliary or flagellar motility	1	0.07%
0007213	acetylcholine receptor signaling, muscarinic pathway	1	0.07%
0045639	positive regulation of myeloid cell differentiation	1	0.07%
0031114	regulation of microtubule depolymerization	1	0.07%
0006430	lysyl-tRNA aminoacylation	1	0.07%
0045606	positive regulation of epidermal cell differentiation	1	0.07%
0048255	mRNA stabilization	1	0.07%
0006778	porphyrin metabolic process	1	0.07%
0001914	regulation of T cell mediated cytotoxicity	1	0.07%
0042384	cilium biogenesis	1	0.07%
0050872	white fat cell differentiation	1	0.07%
0030885	regulation of myeloid dendritic cell activation	1	0.07%
0016553	base conversion or substitution editing	1	0.07%
0046600	negative regulation of centriole replication	1	0.07%
0031111	negative regulation of microtubule polymerization or depolymerization	1	0.07%
0031047	RNA-mediated gene silencing	1	0.07%
0051350	negative regulation of lyase activity	1	0.07%
0002683	negative regulation of immune system process	1	0.07%
0031110	regulation of microtubule polymerization or depolymerization	1	0.07%
0042476	odontogenesis	1	0.07%
0045347	negative regulation of MHC class II biosynthetic process	1	0.07%
0045749	negative regulation of S phase of mitotic cell cycle	1	0.07%
0045410	positive regulation of interleukin-6 biosynthetic process	1	0.07%
0009060	aerobic respiration	1	0.07%
0042119	neutrophil activation	1	0.07%
0006298	mismatch repair	1	0.07%
0042253	granulocyte macrophage colony-stimulating factor biosynthetic process	1	0.07%
0015074	DNA integration	1	0.07%
0030887	positive regulation of myeloid dendritic cell activation	1	0.07%
0006360	transcription from RNA polymerase I promoter	1	0.07%
0051646	mitochondrion localization	1	0.07%
0051099	positive regulation of binding	1	0.07%
0007026	negative regulation of microtubule depolymerization	1	0.07%
0043269	regulation of ion transport	1	0.07%
0000724	double-strand break repair via homologous recombination	1	0.07%
0016556	mRNA modification	1	0.07%
0051289	protein homotetramerization	1	0.07%
0010002	cardioblast differentiation	1	0.07%
0045348	positive regulation of MHC class II biosynthetic process	1	0.07%
0048010	vascular endothelial growth factor receptor signaling pathway	1	0.07%
0016525	negative regulation of angiogenesis	1	0.07%
0050708	regulation of protein secretion	1	0.07%
0006084	acetyl-CoA metabolic process	1	0.07%
0051097	negative regulation of helicase activity	1	0.07%
0007616	long-term memory	1	0.07%
0008366	axon ensheathment	1	0.07%
0050707	regulation of cytokine secretion	1	0.07%
0042355	L-fucose catabolic process	1	0.07%
0000725	recombinational repair	1	0.07%
0051648	vesicle localization	1	0.07%
0030855	epithelial cell differentiation	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0051095	regulation of helicase activity	1	0.07%
0042354	L-fucose metabolic process	1	0.07%
0007217	tachykinin signaling pathway	1	0.07%
0045349	interferon-alpha biosynthetic process	1	0.07%
0030951	establishment and/or maintenance of microtubule cytoskeleton polarity	1	0.07%
0051353	positive regulation of oxidoreductase activity	1	0.07%
0043029	T cell homeostasis	1	0.07%
0006907	pinocytosis	1	0.07%
0044270	nitrogen compound catabolic process	1	0.07%
0001913	T cell mediated cytotoxicity	1	0.07%
0001315	age-dependent response to reactive oxygen species	1	0.07%
0030952	establishment and/or maintenance of cytoskeleton polarity	1	0.07%
0048011	nerve growth factor receptor signaling pathway	1	0.07%
0045414	regulation of interleukin-8 biosynthetic process	1	0.07%
0007020	microtubule nucleation	1	0.07%
0045814	negative regulation of gene expression, epigenetic	1	0.07%
0045189	connective tissue growth factor biosynthetic process	1	0.07%
0045682	regulation of epidermis development	1	0.07%
0018208	peptidyl-proline modification	1	0.07%
0045415	negative regulation of interleukin-8 biosynthetic process	1	0.07%
0007141	male meiosis I	1	0.07%
0045416	positive regulation of interleukin-8 biosynthetic process	1	0.07%
0045684	positive regulation of epidermis development	1	0.07%
0045005	maintenance of fidelity during DNA-dependent DNA replication	1	0.07%
0048875	chemical homeostasis within a tissue	1	0.07%
0019377	glycolipid catabolic process	1	0.07%
0045604	regulation of epidermal cell differentiation	1	0.07%
0007059	chromosome segregation	1	0.07%
0031669	cellular response to nutrient levels	1	0.07%
0050806	positive regulation of synaptic transmission	1	0.07%
0009755	hormone-mediated signaling	1	0.07%
0031571	G1 DNA damage checkpoint	1	0.07%
0002009	morphogenesis of an epithelium	1	0.07%
0031668	cellular response to extracellular stimulus	1	0.07%
0050808	synapse organization and biogenesis	1	0.07%
0006020	myo-inositol metabolic process	1	0.07%
0045085	negative regulation of interleukin-2 biosynthetic process	1	0.07%
0051716	cellular response to stimulus	1	0.07%
0006622	protein targeting to lysosome	1	0.07%
0043193	positive regulation of gene-specific transcription	1	0.07%
0045084	positive regulation of interleukin-12 biosynthetic process	1	0.07%
0031572	G2/M transition DNA damage checkpoint	1	0.07%
0051705	behavioral interaction between organisms	1	0.07%
0030423	RNA interference, targeting of mRNA for destruction	1	0.07%
0001911	negative regulation of leukocyte mediated cytotoxicity	1	0.07%
0030516	regulation of axon extension	1	0.07%
0006982	response to lipid hydroperoxide	1	0.07%
0006713	glucocorticoid catabolic process	1	0.07%
0006980	redox signal response	1	0.07%
0006740	NADPH regeneration	1	0.07%
0002475	antigen processing and presentation via MHC class Ib	1	0.07%
0043161	proteasomal ubiquitin-dependent protein catabolic process	1	0.07%
0046504	glycerol ether biosynthetic process	1	0.07%
0001817	regulation of cytokine production	1	0.07%
0048535	lymph node development	1	0.07%
0006903	vesicle targeting	1	0.07%
0048016	inositol phosphate-mediated signaling	1	0.07%
0048511	rhythmic process	1	0.07%
0006890	retrograde vesicle-mediated transport, Golgi to ER	1	0.07%
0030261	chromosome condensation	1	0.07%
0030198	extracellular matrix organization and biogenesis	1	0.07%
0006891	intra-Golgi vesicle-mediated transport	1	0.07%
0006885	regulation of pH	1	0.07%
0045017	glycerolipid biosynthetic process	1	0.07%
0048286	alveolus development	1	0.07%
0032259	methylation	1	0.07%
0006892	post-Golgi vesicle-mediated transport	1	0.07%
0031575	G1/S transition checkpoint	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0032633	interleukin-4 production	1	0.07%
0009225	nucleotide-sugar metabolic process	1	0.07%
0030263	apoptotic chromosome condensation	1	0.07%
0008277	regulation of G-protein coupled receptor protein signaling pathway	1	0.07%
0006641	triacylglycerol metabolic process	1	0.07%
0007613	memory	1	0.07%
0016046	detection of fungus	1	0.07%
0006626	protein targeting to mitochondrion	1	0.07%
0031576	G2/M transition checkpoint	1	0.07%
0019098	reproductive behavior	1	0.07%
0016045	detection of bacterium	1	0.07%
0001910	regulation of leukocyte mediated cytotoxicity	1	0.07%
0031577	spindle checkpoint	1	0.07%
0042637	catagen	1	0.07%
0051971	positive regulation of transmission of nerve impulse	1	0.07%
0048289	isotype switching to IgE isotypes	1	0.07%
0006306	DNA methylation	1	0.07%
0042219	amino acid derivative catabolic process	1	0.07%
0000747	conjugation with cellular fusion	1	0.07%
0009156	ribonucleoside monophosphate biosynthetic process	1	0.07%
0009110	vitamin biosynthetic process	1	0.07%
0006305	DNA alkylation	1	0.07%
0007623	circadian rhythm	1	0.07%
0000746	conjugation	1	0.07%
0006304	DNA modification	1	0.07%
0051106	positive regulation of DNA ligation	1	0.07%
0045019	negative regulation of nitric oxide biosynthetic process	1	0.07%
0022408	negative regulation of cell-cell adhesion	1	0.07%
0006895	Golgi to endosome transport	1	0.07%
0051105	regulation of DNA ligation	1	0.07%
0045368	positive regulation of interleukin-13 biosynthetic process	1	0.07%
0030104	water homeostasis	1	0.07%
0046469	platelet activating factor metabolic process	1	0.07%
0050821	protein stabilization	1	0.07%
0015813	glutamate transport	1	0.07%
0031579	lipid raft organization and biogenesis	1	0.07%
0010212	response to ionizing radiation	1	0.07%
0007612	learning	1	0.07%
0006901	vesicle coating	1	0.07%
0043449	alkene metabolic process	1	0.07%
0045366	regulation of interleukin-13 biosynthetic process	1	0.07%
0035315	hair cell differentiation	1	0.07%
0050902	leukocyte adhesive activation	1	0.07%
0045351	interferon type I biosynthetic process	1	0.07%
0006882	zinc ion homeostasis	1	0.07%
0006467	protein thiol-disulfide exchange	1	0.07%
0015788	UDP-N-acetylglucosamine transport	1	0.07%
0051100	negative regulation of binding	1	0.07%
0008038	neuron recognition	1	0.07%
0045742	positive regulation of epidermal growth factor receptor signaling pathway	1	0.07%
0032640	tumor necrosis factor-alpha production	1	0.07%
0045362	positive regulation of interleukin-1 biosynthetic process	1	0.07%
0001701	embryonic development (sensu the Mammalia research community)	1	0.07%
0048819	regulation of hair follicle maturation	1	0.07%
0042262	DNA protection	1	0.07%
0035295	tube development	1	0.07%
0048818	positive regulation of hair follicle maturation	1	0.07%
0045360	regulation of interleukin-1 biosynthetic process	1	0.07%
0007530	sex determination	1	0.07%
0006929	substrate-bound cell migration	1	0.07%
0042552	myelination	1	0.07%
0046328	regulation of JNK cascade	1	0.07%
0032607	interferon-alpha production	1	0.07%
0032641	tumor necrosis factor-beta production	1	0.07%
0045823	positive regulation of heart contraction	1	0.07%
0007099	centriole replication	1	0.07%
0042228	interleukin-8 biosynthetic process	1	0.07%
0009074	aromatic amino acid family catabolic process	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0032606	interferon type I production	1	0.07%
0051293	establishment of spindle localization	1	0.07%
0006900	vesicle budding	1	0.07%
0015781	pyrimidine nucleotide-sugar transport	1	0.07%
0007158	neuron adhesion	1	0.07%
0006926	virus-infected cell apoptosis	1	0.07%
0051294	establishment of spindle orientation	1	0.07%
0046530	photoreceptor cell differentiation	1	0.07%
0045063	T-helper 1 cell differentiation	1	0.07%
0015780	nucleotide-sugar transport	1	0.07%
0042226	interleukin-6 biosynthetic process	1	0.07%
0031646	positive regulation of neurological process	1	0.07%
0050905	neuromuscular process	1	0.07%
0032604	granulocyte macrophage colony-stimulating factor production	1	0.07%
0045064	T-helper 2 cell differentiation	1	0.07%
0018350	protein amino acid esterification	1	0.07%
0046596	regulation of virion penetration into host	1	0.07%
0019083	viral transcription	1	0.07%
0042255	ribosome assembly	1	0.07%
0019371	cyclooxygenase pathway	1	0.07%
0046597	negative regulation of virion penetration into host	1	0.07%
0007095	mitotic G2 checkpoint	1	0.07%
0005978	glycogen biosynthetic process	1	0.07%
0006923	cleavage of cytoskeletal proteins during apoptosis	1	0.07%
0045354	regulation of interferon-alpha biosynthetic process	1	0.07%
0006099	tricarboxylic acid cycle	1	0.07%
0006493	protein amino acid O-linked glycosylation	1	0.07%
0007094	mitotic spindle checkpoint	1	0.07%
0000731	DNA synthesis during DNA repair	1	0.07%
0006922	cleavage of lamin	1	0.07%
0032601	connective tissue growth factor production	1	0.07%
0009612	response to mechanical stimulus	1	0.07%
0006098	pentose-phosphate shunt	1	0.07%
0045355	negative regulation of interferon-alpha biosynthetic process	1	0.07%
0042222	interleukin-1 biosynthetic process	1	0.07%
0046661	male sex differentiation	1	0.07%
0035088	establishment and/or maintenance of apical/basal cell polarity	1	0.07%
0006835	dicarboxylic acid transport	1	0.07%
0015844	monoamine transport	1	0.07%
0045408	regulation of interleukin-6 biosynthetic process	1	0.07%
0007492	endoderm development	1	0.07%
0050777	negative regulation of immune response	1	0.07%
0006857	oligopeptide transport	1	0.07%
0046599	regulation of centriole replication	1	0.07%
0051659	maintenance of mitochondrion localization	1	0.07%
0051298	centrosome duplication	1	0.07%
0009452	RNA capping	1	0.07%
0035025	positive regulation of Rho protein signal transduction	1	0.07%
0007090	regulation of S phase of mitotic cell cycle	1	0.07%
0001709	cell fate determination	1	0.07%
0019080	viral genome expression	1	0.07%
0046339	diacylglycerol metabolic process	1	0.07%
0051657	maintenance of organelle localization	1	0.07%
0009127	purine nucleoside monophosphate biosynthetic process	1	0.07%
0019370	leukotriene biosynthetic process	1	0.07%
0051299	centrosome separation	1	0.07%
0030833	regulation of actin filament polymerization	1	0.07%
0030299	cholesterol absorption	1	0.07%
0006498	N-terminal protein lipidation	1	0.07%
0006004	fucose metabolic process	1	0.07%
0045404	positive regulation of interleukin-4 biosynthetic process	1	0.07%
0007601	visual perception	1	0.07%
0001959	regulation of cytokine and chemokine mediated signaling pathway	1	0.07%
0046730	induction of host immune response by virus	1	0.07%
0046731	passive induction of host immune response by virus	1	0.07%
0050771	negative regulation of axonogenesis	1	0.07%
0046356	acetyl-CoA catabolic process	1	0.07%
0045423	regulation of granulocyte macrophage colony-stimulating factor biosynthetic process	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0051653	spindle localization	1	0.07%
0006788	heme oxidation	1	0.07%
0048762	mesenchymal cell differentiation	1	0.07%
0016142	O-glycoside catabolic process	1	0.07%
0046813	virion attachment, binding of host cell surface receptor	1	0.07%
0006787	porphyrin catabolic process	1	0.07%
0009126	purine nucleoside monophosphate metabolic process	1	0.07%
0045648	positive regulation of erythrocyte differentiation	1	0.07%
0000738	DNA catabolic process, exonucleolytic	1	0.07%
0050953	sensory perception of light stimulus	1	0.07%
0046579	positive regulation of Ras protein signal transduction	1	0.07%
0051650	establishment of vesicle localization	1	0.07%
0045646	regulation of erythrocyte differentiation	1	0.07%
0051319	G2 phase	1	0.07%
0043017	positive regulation of tumor necrosis factor-beta biosynthetic process	1	0.07%
0006517	protein deglycosylation	1	0.07%
0043030	regulation of macrophage activation	1	0.07%
0042177	negative regulation of protein catabolic process	1	0.07%
0006516	glycoprotein catabolic process	1	0.07%
0001953	negative regulation of cell-matrix adhesion	1	0.07%
0045425	positive regulation of granulocyte macrophage colony-stimulating factor biosynthetic process	1	0.07%
0032635	interleukin-6 production	1	0.07%
0001952	regulation of cell-matrix adhesion	1	0.07%
0040001	establishment of mitotic spindle localization	1	0.07%
0048339	paraxial mesoderm development	1	0.07%
0045579	positive regulation of B cell differentiation	1	0.07%
0045577	regulation of B cell differentiation	1	0.07%
0035020	regulation of Rac protein signal transduction	1	0.07%
0035194	RNA-mediated posttranscriptional gene silencing	1	0.07%
0050860	negative regulation of T cell receptor signaling pathway	1	0.07%
0048659	smooth muscle cell proliferation	1	0.07%
0031580	lipid raft distribution	1	0.07%
0006448	regulation of translational elongation	1	0.07%
0046627	negative regulation of insulin receptor signaling pathway	1	0.07%
0006940	regulation of smooth muscle contraction	1	0.07%
0043016	regulation of tumor necrosis factor-beta biosynthetic process	1	0.07%
0032288	myelin formation	1	0.07%
0015827	tryptophan transport	1	0.07%
0006510	ATP-dependent proteolysis	1	0.07%
0045402	regulation of interleukin-4 biosynthetic process	1	0.07%
0008088	axon cargo transport	1	0.07%
0050798	activated T cell proliferation	1	0.07%
0009214	cyclic nucleotide catabolic process	1	0.07%
0006568	tryptophan metabolic process	1	0.07%
0000045	autophagic vacuole formation	1	0.07%
0046626	regulation of insulin receptor signaling pathway	1	0.07%
0045739	positive regulation of DNA repair	1	0.07%
0009124	nucleoside monophosphate biosynthetic process	1	0.07%
0048247	lymphocyte chemotaxis	1	0.07%
0048268	clathrin cage assembly	1	0.07%
0042772	DNA damage response, signal transduction resulting in transcription	1	0.07%
0006379	mRNA cleavage	1	0.07%
0006569	tryptophan catabolic process	1	0.07%
0008089	anterograde axon cargo transport	1	0.07%
0016236	macroautophagy	1	0.07%
0000085	G2 phase of mitotic cell cycle	1	0.07%
0050862	positive regulation of T cell receptor signaling pathway	1	0.07%
0007004	telomere maintenance via telomerase	1	0.07%
0014031	mesenchymal cell development	1	0.07%
0043588	skin development	1	0.07%
0051279	regulation of release of sequestered calcium ion into cytoplasm	1	0.07%
0009123	nucleoside monophosphate metabolic process	1	0.07%
0007272	ensheathment of neurons	1	0.07%
0045628	regulation of T-helper 2 cell differentiation	1	0.07%
0007631	feeding behavior	1	0.07%
0055002	striated muscle cell development	1	0.07%
0032637	interleukin-8 production	1	0.07%
0030240	muscle thin filament assembly	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0015991	ATP hydrolysis coupled proton transport	1	0.07%
0043392	negative regulation of DNA binding	1	0.07%
0031058	positive regulation of histone modification	1	0.07%
0007608	sensory perception of smell	1	0.07%
0043126	regulation of 1-phosphatidylinositol 4-kinase activity	1	0.07%
0042436	indole derivative catabolic process	1	0.07%
0031056	regulation of histone modification	1	0.07%
0016140	O-glycoside metabolic process	1	0.07%
0030174	regulation of DNA replication initiation	1	0.07%
0046928	regulation of neurotransmitter secretion	1	0.07%
0042434	indole derivative metabolic process	1	0.07%
0048260	positive regulation of receptor mediated endocytosis	1	0.07%
0018987	osmoregulation	1	0.07%
0003002	regionalization	1	0.07%
0007100	mitotic centrosome separation	1	0.07%
0000084	S phase of mitotic cell cycle	1	0.07%
0043012	regulation of fusion of sperm to egg plasma membrane	1	0.07%
0006370	mRNA capping	1	0.07%
0007035	vacuolar acidification	1	0.07%
0042430	indole and derivative metabolic process	1	0.07%
0043487	regulation of RNA stability	1	0.07%
0008354	germ cell migration	1	0.07%
0055001	muscle cell development	1	0.07%
0006475	internal protein amino acid acetylation	1	0.07%
0042402	biogenic amine catabolic process	1	0.07%
0007006	mitochondrial membrane organization and biogenesis	1	0.07%
0043128	positive regulation of 1-phosphatidylinositol 4-kinase activity	1	0.07%
0006637	acyl-CoA metabolic process	1	0.07%
0030866	cortical actin cytoskeleton organization and biogenesis	1	0.07%
0030838	positive regulation of actin filament polymerization	1	0.07%
0045627	positive regulation of T-helper 1 cell differentiation	1	0.07%
0000209	protein polyubiquitination	1	0.07%
0050715	positive regulation of cytokine secretion	1	0.07%
0046856	phosphoinositide dephosphorylation	1	0.07%
0006999	nuclear pore organization and biogenesis	1	0.07%
0046855	inositol phosphate dephosphorylation	1	0.07%
0050714	positive regulation of protein secretion	1	0.07%
0045766	positive regulation of angiogenesis	1	0.07%
0046854	phosphoinositide phosphorylation	1	0.07%
0043488	regulation of mRNA stability	1	0.07%
0051205	protein insertion into membrane	1	0.07%
0051798	positive regulation of hair follicle development	1	0.07%
0019439	aromatic compound catabolic process	1	0.07%
0043152	induction of bacterial agglutination	1	0.07%
0051797	regulation of hair follicle development	1	0.07%
0042670	retinal cone cell differentiation	1	0.07%
0009952	anterior/posterior pattern formation	1	0.07%
0006726	eye pigment biosynthetic process	1	0.07%
0051795	positive regulation of catagen	1	0.07%
0043489	RNA stabilization	1	0.07%
0006278	RNA-dependent DNA replication	1	0.07%
0042026	protein refolding	1	0.07%
0032020	ISG15-protein conjugation	1	0.07%
0051794	regulation of catagen	1	0.07%
0002260	lymphocyte homeostasis	1	0.07%
0008156	negative regulation of DNA replication	1	0.07%
0045851	pH reduction	1	0.07%
0048298	positive regulation of isotype switching to IgA isotypes	1	0.07%
0044258	intestinal lipid catabolic process	1	0.07%
0048610	reproductive cellular process	1	0.07%
0043129	surfactant homeostasis	1	0.07%
0009304	tRNA transcription	1	0.07%
0046782	regulation of viral transcription	1	0.07%
0016127	sterol catabolic process	1	0.07%
0042311	vasodilation	1	0.07%
0045768	positive regulation of anti-apoptosis	1	0.07%
0009303	rRNA transcription	1	0.07%
0006342	chromatin silencing	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0046330	positive regulation of JNK cascade	1	0.07%
0042312	regulation of vasodilation	1	0.07%
0048168	regulation of neuronal synaptic plasticity	1	0.07%
0043154	negative regulation of caspase activity	1	0.07%
0045471	response to ethanol	1	0.07%
0000132	establishment of mitotic spindle orientation	1	0.07%
0050891	body fluid osmoregulation	1	0.07%
0002262	myeloid cell homeostasis	1	0.07%
0001780	neutrophil homeostasis	1	0.07%
0019216	regulation of lipid metabolic process	1	0.07%
0051146	striated muscle cell differentiation	1	0.07%
0007183	SMAD protein complex assembly	1	0.07%
0007585	respiratory gaseous exchange	1	0.07%
0051053	negative regulation of DNA metabolic process	1	0.07%
0051453	regulation of cellular pH	1	0.07%
0050892	intestinal absorption	1	0.07%
0001781	neutrophil apoptosis	1	0.07%
0016441	posttranscriptional gene silencing	1	0.07%
0006651	diacylglycerol biosynthetic process	1	0.07%
0051452	cellular pH reduction	1	0.07%
0018401	peptidyl-proline hydroxylation to 4-hydroxy-L-proline	1	0.07%
0031333	negative regulation of protein complex assembly	1	0.07%
0007638	mechanosensory behavior	1	0.07%
0006586	indolalkylamine metabolic process	1	0.07%
0007193	G-protein signaling, adenylate cyclase inhibiting pathway	1	0.07%
0031269	pseudopodium formation	1	0.07%
0051775	response to redox state	1	0.07%
0045446	endothelial cell differentiation	1	0.07%
0009168	purine ribonucleoside monophosphate biosynthetic process	1	0.07%
0031268	pseudopodium organization and biogenesis	1	0.07%
0016054	organic acid catabolic process	1	0.07%
0046831	regulation of RNA export from nucleus	1	0.07%
0001754	eye photoreceptor cell differentiation	1	0.07%
0048589	developmental growth	1	0.07%
0042675	cone cell differentiation	1	0.07%
0009167	purine ribonucleoside monophosphate metabolic process	1	0.07%
0006707	cholesterol catabolic process	1	0.07%
0045444	fat cell differentiation	1	0.07%
0048144	fibroblast proliferation	1	0.07%
0030148	sphingolipid biosynthetic process	1	0.07%
0007252	I-kappaB phosphorylation	1	0.07%
0009166	nucleotide catabolic process	1	0.07%
0044236	multicellular organismal metabolic process	1	0.07%
0048145	regulation of fibroblast proliferation	1	0.07%
0045075	regulation of interleukin-12 biosynthetic process	1	0.07%
0042535	positive regulation of tumor necrosis factor-alpha biosynthetic process	1	0.07%
0010224	response to UV-B	1	0.07%
0016050	vesicle organization and biogenesis	1	0.07%
0006312	mitotic recombination	1	0.07%
0048863	stem cell differentiation	1	0.07%
0009161	ribonucleoside monophosphate metabolic process	1	0.07%
0051124	synaptic growth at neuromuscular junction	1	0.07%
0006975	DNA damage induced protein phosphorylation	1	0.07%
0042534	regulation of tumor necrosis factor-alpha biosynthetic process	1	0.07%
0048147	negative regulation of fibroblast proliferation	1	0.07%
0031272	regulation of pseudopodium formation	1	0.07%
0031958	corticosteroid receptor signaling pathway	1	0.07%
0006010	glucose 6-phosphate utilization	1	0.07%
0045625	regulation of T-helper 1 cell differentiation	1	0.07%
0007320	insemination	1	0.07%
0048864	stem cell development	1	0.07%
0048227	plasma membrane to endosome transport	1	0.07%
0051047	positive regulation of secretion	1	0.07%
0010155	regulation of proton transport	1	0.07%
0050879	organismal movement	1	0.07%
0031274	positive regulation of pseudopodium formation	1	0.07%
0048296	regulation of isotype switching to IgA isotypes	1	0.07%
0045900	negative regulation of translational elongation	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0048069	eye pigmentation	1	0.07%
0051045	negative regulation of membrane protein ectodomain proteolysis	1	0.07%
0046834	lipid phosphorylation	1	0.07%
0007176	regulation of epidermal growth factor receptor activity	1	0.07%
0045077	negative regulation of interferon-gamma biosynthetic process	1	0.07%
0050922	negative regulation of chemotaxis	1	0.07%
0050858	negative regulation of antigen receptor-mediated signaling pathway	1	0.07%
0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	1	0.07%
0051043	regulation of membrane protein ectodomain proteolysis	1	0.07%
0048066	pigmentation during development	1	0.07%
0018409	peptide or protein amino-terminal blocking	1	0.07%
0006012	galactose metabolic process	1	0.07%
0020027	hemoglobin metabolic process	1	0.07%
0043388	positive regulation of DNA binding	1	0.07%
0032297	negative regulation of DNA replication initiation	1	0.07%
0045453	bone resorption	1	0.07%
0048302	regulation of isotype switching to IgG isotypes	1	0.07%
0045839	negative regulation of mitosis	1	0.07%
0031365	N-terminal protein amino acid modification	1	0.07%
0043450	alkene biosynthetic process	1	0.07%
0032616	interleukin-13 production	1	0.07%
0051041	positive regulation of calcium-independent cell-cell adhesion	1	0.07%
0043491	protein kinase B signaling cascade	1	0.07%
0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	1	0.07%
0042533	tumor necrosis factor-alpha biosynthetic process	1	0.07%
0044240	organismal lipid catabolic process	1	0.07%
0043414	biopolymer methylation	1	0.07%
0022600	digestive process	1	0.07%
0032615	interleukin-12 production	1	0.07%
0051040	regulation of calcium-independent cell-cell adhesion	1	0.07%
0019471	4-hydroxyproline metabolic process	1	0.07%
0001764	neuron migration	1	0.07%
0042062	long-term strengthening of neuromuscular junction	1	0.07%
0046463	acylglycerol biosynthetic process	1	0.07%
0006402	mRNA catabolic process	1	0.07%
0032612	interleukin-1 production	1	0.07%
0001867	complement activation, lectin pathway	1	0.07%
0048820	hair follicle maturation	1	0.07%
0043681	protein import into mitochondrion	1	0.07%
0006595	polyamine metabolic process	1	0.07%
0008206	bile acid metabolic process	1	0.07%
0048304	positive regulation of isotype switching to IgG isotypes	1	0.07%
0022413	reproductive process in single-celled organism	1	0.07%
0031341	regulation of cell killing	1	0.07%
0042231	interleukin-13 biosynthetic process	1	0.07%
0006930	substrate-bound cell migration, cell extension	1	0.07%
0042168	heme metabolic process	1	0.07%
0009267	cellular response to starvation	1	0.07%
0006596	polyamine biosynthetic process	1	0.07%
0000160	two-component signal transduction system (phosphorelay)	1	0.07%
0007194	negative regulation of adenylate cyclase activity	1	0.07%
0001766	lipid raft polarization	1	0.07%
0007413	axonal fasciculation	1	0.07%
0051665	lipid raft localization	1	0.07%
0007528	neuromuscular junction development	1	0.07%
0048305	immunoglobulin secretion	1	0.07%
0018184	protein amino acid polyamination	1	0.07%
0019827	stem cell maintenance	1	0.07%
0045123	cellular extravasation	1	0.07%
0046479	glycosphingolipid catabolic process	1	0.07%
0000072	M phase specific microtubule process	1	0.07%
0042921	glucocorticoid receptor signaling pathway	1	0.07%
0009268	response to pH	1	0.07%
0006597	spermine biosynthetic process	1	0.07%
0042097	interleukin-4 biosynthetic process	1	0.07%
0008216	spermidine metabolic process	1	0.07%
0019063	virion penetration into host cell	1	0.07%
0009441	glycolate metabolic process	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0016925	protein sumoylation	1	0.07%
0006750	glutathione biosynthetic process	1	0.07%
0017145	stem cell division	1	0.07%
0007416	synaptogenesis	1	0.07%
0031344	regulation of cell projection organization and biogenesis	1	0.07%
0046838	phosphorylated carbohydrate dephosphorylation	1	0.07%
0006688	glycosphingolipid biosynthetic process	1	0.07%
0032430	positive regulation of phospholipase A2 activity	1	0.07%
0048295	positive regulation of isotype switching to IgE isotypes	1	0.07%
0030004	monovalent inorganic cation homeostasis	1	0.07%
0006689	ganglioside catabolic process	1	0.07%
0000002	mitochondrial genome maintenance	1	0.07%
0009109	coenzyme catabolic process	1	0.07%
0008652	amino acid biosynthetic process	1	0.07%
0009895	negative regulation of catabolic process	1	0.07%
0046902	regulation of mitochondrial membrane permeability	1	0.07%
0007595	lactation	1	0.07%
0046546	development of primary male sexual characteristics	1	0.07%
0019987	negative regulation of anti-apoptosis	1	0.07%
0046839	phospholipid dephosphorylation	1	0.07%
0046549	retinal cone cell development	1	0.07%
0009250	glucan biosynthetic process	1	0.07%
0045617	negative regulation of keratinocyte differentiation	1	0.07%
0008215	spermine metabolic process	1	0.07%
0006427	histidyl-tRNA aminoacylation	1	0.07%
0030324	lung development	1	0.07%
0031346	positive regulation of cell projection organization and biogenesis	1	0.07%
0001960	negative regulation of cytokine and chemokine mediated signaling pathway	1	0.07%
0042789	mRNA transcription from RNA polymerase II promoter	1	0.07%
0030323	respiratory tube development	1	0.07%
0042090	interleukin-12 biosynthetic process	1	0.07%
0030150	protein import into mitochondrial matrix	1	0.07%
0000076	DNA replication checkpoint	1	0.07%
0045618	positive regulation of keratinocyte differentiation	1	0.07%
0006663	platelet activating factor biosynthetic process	1	0.07%
0043473	pigmentation	1	0.07%
0042058	regulation of epidermal growth factor receptor signaling pathway	1	0.07%
0031032	actomyosin structure organization and biogenesis	1	0.07%
0001773	myeloid dendritic cell activation	1	0.07%
0035235	ionotropic glutamate receptor signaling pathway	1	0.07%
0031503	protein complex localization	1	0.07%
0009247	glycolipid biosynthetic process	1	0.07%
0045908	negative regulation of vasodilation	1	0.07%
0009310	amine catabolic process	1	0.07%
0015804	neutral amino acid transport	1	0.07%
0007389	pattern specification process	1	0.07%
0008334	histone mRNA metabolic process	1	0.07%
0051890	regulation of cardioblast differentiation	1	0.07%
0051320	S phase	1	0.07%
0051891	positive regulation of cardioblast differentiation	1	0.07%
0008333	endosome to lysosome transport	1	0.07%
0042517	positive regulation of tyrosine phosphorylation of Stat3 protein	1	0.07%
0048293	regulation of isotype switching to IgE isotypes	1	0.07%
0002456	T cell mediated immunity	1	0.07%
0043006	calcium-dependent phospholipase A2 activation	1	0.07%
0015801	aromatic amino acid transport	1	0.07%
0048340	paraxial mesoderm morphogenesis	1	0.07%
0018146	keratan sulfate biosynthetic process	1	0.07%
0043547	positive regulation of GTPase activity	1	0.07%
0015800	acidic amino acid transport	1	0.07%
0031348	negative regulation of defense response	1	0.07%
0001573	ganglioside metabolic process	1	0.07%
0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	1	0.07%
0051252	regulation of RNA metabolic process	1	0.07%
0048008	platelet-derived growth factor receptor signaling pathway	1	0.07%
0046460	neutral lipid biosynthetic process	1	0.07%
0019317	fucose catabolic process	1	0.07%
0051893	regulation of focal adhesion formation	1	0.07%

Supplementary Table 3B. HIV-1 Human Protein Interaction Database: Distribution of biological process Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0031507	heterochromatin formation	1	0.07%
0042447	hormone catabolic process	1	0.07%
0009408	response to heat	1	0.07%
0030913	paranodal junction assembly	1	0.07%
0048006	antigen processing and presentation, endogenous lipid antigen via MHC class Ib	1	0.07%
0030947	regulation of vascular endothelial growth factor receptor signaling pathway	1	0.07%
0045909	positive regulation of vasodilation	1	0.07%
0031109	microtubule polymerization or depolymerization	1	0.07%
0006384	transcription initiation from RNA polymerase III promoter	1	0.07%
0046395	carboxylic acid catabolic process	1	0.07%
0048291	isotype switching to IgG isotypes	1	0.07%
0044241	lipid digestion	1	0.07%
0008211	glucocorticoid metabolic process	1	0.07%
0031065	positive regulation of histone deacetylation	1	0.07%
0048003	antigen processing and presentation of lipid antigen via MHC class Ib	1	0.07%
0051895	negative regulation of focal adhesion formation	1	0.07%
0006381	mRNA editing	1	0.07%
0001502	cartilage condensation	1	0.07%
0006730	one-carbon compound metabolic process	1	0.07%
0007019	microtubule depolymerization	1	0.07%
0001837	epithelial to mesenchymal transition	1	0.07%
0031063	regulation of histone deacetylation	1	0.07%
0006691	leukotriene metabolic process	1	0.07%
0043009	embryonic development (sensu the Vertebrata research community)	1	0.07%
0042441	eye pigment metabolic process	1	0.07%
0046148	pigment biosynthetic process	1	0.07%
0042416	dopamine biosynthetic process	1	0.07%
0046218	indolalkylamine catabolic process	1	0.07%
0050728	negative regulation of inflammatory response	1	0.07%
0051156	glucose 6-phosphate metabolic process	1	0.07%
0009582	detection of abiotic stimulus	1	0.07%
0007044	cell-substrate junction assembly	1	0.07%
0042109	tumor necrosis factor-beta biosynthetic process	1	0.07%
0032505	reproduction of a single-celled organism	1	0.07%
0051000	positive regulation of nitric-oxide synthase activity	1	0.07%
0006047	UDP-N-acetylglucosamine metabolic process	1	0.07%
0048290	isotype switching to IgA isotypes	1	0.07%
0042417	dopamine metabolic process	1	0.07%
0007263	nitric oxide mediated signal transduction	1	0.07%
0016202	regulation of striated muscle development	1	0.07%
0031280	negative regulation of cyclase activity	1	0.07%
0045861	negative regulation of proteolysis	1	0.07%
0044243	organismal catabolic process	1	0.07%
0030157	pancreatic juice secretion	1	0.07%
0006356	regulation of transcription from RNA polymerase I promoter	1	0.07%
0051896	regulation of protein kinase B signaling cascade	1	0.07%
0042594	response to starvation	1	0.07%
0030224	monocyte differentiation	1	0.07%
0000303	response to superoxide	1	0.07%
0019430	removal of superoxide radicals	1	0.07%
0048246	macrophage chemotaxis	1	0.07%
0043254	regulation of protein complex assembly	1	0.07%
0045869	negative regulation of retroviral genome replication	1	0.07%
0042462	eye photoreceptor cell development	1	0.07%
0042104	positive regulation of activated T cell proliferation	1	0.07%
0051898	negative regulation of protein kinase B signaling cascade	1	0.07%
0048628	myoblast maturation	1	0.07%
0045930	negative regulation of progression through mitotic cell cycle	1	0.07%
0000305	response to oxygen radical	1	0.07%
0051130	positive regulation of cell organization and biogenesis	1	0.07%
0048627	myoblast development	1	0.07%
0045197	establishment and/or maintenance of epithelial cell polarity	1	0.07%
0042461	photoreceptor cell development	1	0.07%
0000212	meiotic spindle organization and biogenesis	1	0.07%
0009650	UV protection	1	0.07%
0001570	vasculogenesis	1	0.07%
	unknown	138	9.53%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0003674	molecular_function	1448	100.00%
0005488	binding	1164	80.39%
0005515	protein binding	773	53.38%
0003824	catalytic activity	573	39.57%
0043167	ion binding	350	24.17%
0046872	metal ion binding	345	23.83%
0043169	cation binding	321	22.17%
0003676	nucleic acid binding	302	20.86%
0016787	hydrolase activity	258	17.82%
0004871	signal transducer activity	252	17.40%
0000166	nucleotide binding	244	16.85%
0003677	DNA binding	235	16.23%
0016740	transferase activity	235	16.23%
0017076	purine nucleotide binding	223	15.40%
0046914	transition metal ion binding	201	13.88%
0030554	adenyl nucleotide binding	178	12.29%
0030528	transcription regulator activity	173	11.95%
0005524	ATP binding	166	11.46%
0008270	zinc ion binding	157	10.84%
0004872	receptor activity	155	10.70%
0016772	transferase activity, transferring phosphorus-containing groups	153	10.57%
0005102	receptor binding	135	9.32%
0005509	calcium ion binding	130	8.98%
0016301	kinase activity	116	8.01%
0016773	phosphotransferase activity, alcohol group as acceptor	108	7.46%
0004672	protein kinase activity	97	6.70%
0003700	transcription factor activity	94	6.49%
0030234	enzyme regulator activity	93	6.42%
0016788	hydrolase activity, acting on ester bonds	92	6.35%
0005198	structural molecule activity	87	6.01%
0005215	transporter activity	85	5.87%
0004888	transmembrane receptor activity	84	5.80%
0004674	protein serine/threonine kinase activity	76	5.25%
0008134	transcription factor binding	76	5.25%
0016817	hydrolase activity, acting on acid anhydrides	69	4.77%
0003723	RNA binding	69	4.77%
0016462	pyrophosphatase activity	69	4.77%
0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	69	4.77%
0017111	nucleoside-triphosphatase activity	68	4.70%
0005125	cytokine activity	65	4.49%
0042578	phosphoric ester hydrolase activity	62	4.28%
0008092	cytoskeletal protein binding	59	4.07%
0016563	transcriptional activator activity	58	4.01%
0003712	transcription cofactor activity	58	4.01%
0008233	peptidase activity	57	3.94%
0016491	oxidoreductase activity	55	3.80%
0005057	receptor signaling protein activity	53	3.66%
0004175	endopeptidase activity	53	3.66%
0008289	lipid binding	51	3.52%
0000287	magnesium ion binding	47	3.25%
0003713	transcription coactivator activity	46	3.18%
0019001	guanyl nucleotide binding	45	3.11%
0046983	protein dimerization activity	44	3.04%
0003702	RNA polymerase II transcription factor activity	44	3.04%
0005525	GTP binding	44	3.04%
0019899	enzyme binding	43	2.97%
0003779	actin binding	42	2.90%
0015075	ion transporter activity	40	2.76%
0042802	identical protein binding	40	2.76%
0043565	sequence-specific DNA binding	38	2.62%
0030246	carbohydrate binding	38	2.62%
0016779	nucleotidyltransferase activity	37	2.56%
0016789	carboxylic ester hydrolase activity	35	2.42%
0003924	GTPase activity	35	2.42%
0005506	iron ion binding	34	2.35%
0005516	calmodulin binding	34	2.35%
0008083	growth factor activity	33	2.28%
0015267	channel or pore class transporter activity	33	2.28%
0042277	peptide binding	33	2.28%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0004857	enzyme inhibitor activity	33	2.28%
0016298	lipase activity	33	2.28%
0008081	phosphoric diester hydrolase activity	33	2.28%
0004620	phospholipase activity	32	2.21%
0005216	ion channel activity	31	2.14%
0015268	alpha-type channel activity	31	2.14%
0008415	acyltransferase activity	29	2.00%
0016791	phosphoric monoester hydrolase activity	29	2.00%
0016747	transferase activity, transferring groups other than amino-acyl groups	29	2.00%
0016746	transferase activity, transferring acyl groups	29	2.00%
0016757	transferase activity, transferring glycosyl groups	28	1.93%
0019955	cytokine binding	28	1.93%
0016798	hydrolase activity, acting on glycosyl bonds	27	1.86%
0005543	phospholipid binding	26	1.80%
0008047	enzyme activator activity	26	1.80%
0004930	G-protein coupled receptor activity	26	1.80%
0004713	protein-tyrosine kinase activity	25	1.73%
0008324	cation transporter activity	25	1.73%
0005200	structural constituent of cytoskeleton	24	1.66%
0016564	transcriptional repressor activity	24	1.66%
0001584	rhodopsin-like receptor activity	24	1.66%
0001664	G-protein-coupled receptor binding	23	1.59%
0016887	ATPase activity	23	1.59%
0009055	electron carrier activity	23	1.59%
0003899	DNA-directed RNA polymerase activity	23	1.59%
0004721	phosphoprotein phosphatase activity	23	1.59%
0042379	chemokine receptor binding	22	1.52%
0005529	sugar binding	21	1.45%
0005126	hematopoietin/interferon-class (D200-domain) cytokine receptor binding	21	1.45%
0019207	kinase regulator activity	21	1.45%
0008009	chemokine activity	21	1.45%
0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	21	1.45%
0051082	unfolded protein binding	20	1.38%
0001653	peptide receptor activity	20	1.38%
0030145	manganese ion binding	20	1.38%
0004702	receptor signaling protein serine/threonine kinase activity	20	1.38%
0016758	transferase activity, transferring hexosyl groups	20	1.38%
0016874	ligase activity	20	1.38%
0046982	protein heterodimerization activity	20	1.38%
0008528	peptide receptor activity, G-protein coupled	20	1.38%
0032403	protein complex binding	19	1.31%
0001871	pattern binding	18	1.24%
0016410	N-acyltransferase activity	18	1.24%
0035091	phosphoinositide binding	18	1.24%
0019887	protein kinase regulator activity	18	1.24%
0030414	protease inhibitor activity	17	1.17%
0008236	serine-type peptidase activity	17	1.17%
0043566	structure-specific DNA binding	17	1.17%
0004866	endopeptidase inhibitor activity	17	1.17%
0008565	protein transporter activity	17	1.17%
0042623	ATPase activity, coupled	17	1.17%
0005507	copper ion binding	17	1.17%
0008135	translation factor activity, nucleic acid binding	17	1.17%
0004252	serine-type endopeptidase activity	17	1.17%
0045182	translation regulator activity	17	1.17%
0004623	phospholipase A2 activity	17	1.17%
0004298	threonine endopeptidase activity	17	1.17%
0005261	cation channel activity	17	1.17%
0019904	protein domain specific binding	16	1.10%
0008080	N-acetyltransferase activity	16	1.10%
0016407	acetyltransferase activity	16	1.10%
0019900	kinase binding	16	1.10%
0030695	GTPase regulator activity	16	1.10%
0019992	diacylglycerol binding	16	1.10%
0005539	glycosaminoglycan binding	16	1.10%
0030247	polysaccharide binding	16	1.10%
0004629	phospholipase C activity	15	1.04%
0004402	histone acetyltransferase activity	15	1.04%
0005201	extracellular matrix structural constituent	15	1.04%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0019956	chemokine binding	15	1.04%
0004468	lysine N-acetyltransferase activity	15	1.04%
0016209	antioxidant activity	15	1.04%
0008201	heparin binding	15	1.04%
0004112	cyclic-nucleotide phosphodiesterase activity	15	1.04%
0019888	protein phosphatase regulator activity	14	0.97%
0004435	phosphoinositide phospholipase C activity	14	0.97%
0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	14	0.97%
0004114	3',5'-cyclic-nucleotide phosphodiesterase activity	14	0.97%
0005386	carrier activity	14	0.97%
0001637	G-protein chemoattractant receptor activity	14	0.97%
0042803	protein homodimerization activity	14	0.97%
0019901	protein kinase binding	14	0.97%
0016829	lyase activity	14	0.97%
0004950	chemokine receptor activity	14	0.97%
0015276	ligand-gated ion channel activity	14	0.97%
0051427	hormone receptor binding	14	0.97%
0004707	MAP kinase activity	14	0.97%
0004434	inositol or phosphatidylinositol phosphodiesterase activity	14	0.97%
0019208	phosphatase regulator activity	14	0.97%
0008194	UDP-glycosyltransferase activity	14	0.97%
0048503	GPI anchor binding	13	0.90%
0005083	small GTPase regulator activity	13	0.90%
0035257	nuclear hormone receptor binding	13	0.90%
0016251	general RNA polymerase II transcription factor activity	13	0.90%
0008601	protein phosphatase type 2A regulator activity	13	0.90%
0016853	isomerase activity	13	0.90%
0008146	sulfotransferase activity	12	0.83%
0016782	transferase activity, transferring sulfur-containing groups	12	0.83%
0019957	C-C chemokine binding	12	0.83%
0004386	helicase activity	12	0.83%
0016493	C-C chemokine receptor activity	12	0.83%
0003774	motor activity	12	0.83%
0016881	acid-amino acid ligase activity	11	0.76%
0003714	transcription corepressor activity	11	0.76%
0008378	galactosyltransferase activity	11	0.76%
0005179	hormone activity	11	0.76%
0005230	extracellular ligand-gated ion channel activity	11	0.76%
0003697	single-stranded DNA binding	11	0.76%
0001565	phorbol ester receptor activity	11	0.76%
0016879	ligase activity, forming carbon-nitrogen bonds	11	0.76%
0019838	growth factor binding	11	0.76%
0016814	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	11	0.76%
0004697	protein kinase C activity	11	0.76%
0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	10	0.69%
0004896	hematopoietin/interferon-class (D200-domain) cytokine receptor activity	10	0.69%
0004518	nuclease activity	10	0.69%
0020037	heme binding	10	0.69%
0015026	coreceptor activity	10	0.69%
0035258	steroid hormone receptor binding	10	0.69%
0008234	cysteine-type peptidase activity	10	0.69%
0016303	phosphatidylinositol 3-kinase activity	10	0.69%
0003725	double-stranded RNA binding	10	0.69%
0048037	cofactor binding	10	0.69%
0004197	cysteine-type endopeptidase activity	10	0.69%
0046906	tetrapyrrole binding	10	0.69%
0015290	electrochemical potential-driven transporter activity	10	0.69%
0005085	guanyl-nucleotide exchange factor activity	10	0.69%
0004428	inositol or phosphatidylinositol kinase activity	10	0.69%
0004842	ubiquitin-protein ligase activity	10	0.69%
0019787	small conjugating protein ligase activity	10	0.69%
0005231	excitatory extracellular ligand-gated ion channel activity	10	0.69%
0016684	oxidoreductase activity, acting on peroxide as acceptor	10	0.69%
0035250	UDP-galactosyltransferase activity	10	0.69%
0035004	phosphoinositide 3-kinase activity	10	0.69%
0001727	lipid kinase activity	10	0.69%
0004601	peroxidase activity	10	0.69%
0015036	disulfide oxidoreductase activity	10	0.69%
0015923	mannosidase activity	10	0.69%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0015291	porter activity	10	0.69%
0005267	potassium channel activity	9	0.62%
0015035	protein disulfide oxidoreductase activity	9	0.62%
0016860	intramolecular oxidoreductase activity	9	0.62%
0019865	immunoglobulin binding	9	0.62%
0008237	metallopeptidase activity	9	0.62%
0043028	caspase regulator activity	9	0.62%
0004016	adenylate cyclase activity	9	0.62%
0009975	cyclase activity	9	0.62%
0004722	protein serine/threonine phosphatase activity	9	0.62%
0016849	phosphorus-oxygen lyase activity	9	0.62%
0003690	double-stranded DNA binding	9	0.62%
0050681	androgen receptor binding	9	0.62%
0050662	coenzyme binding	9	0.62%
0004725	protein tyrosine phosphatase activity	8	0.55%
0004867	serine-type endopeptidase inhibitor activity	8	0.55%
0005089	Rho guanyl-nucleotide exchange factor activity	8	0.55%
0004879	ligand-dependent nuclear receptor activity	8	0.55%
0015269	calcium-activated potassium channel activity	8	0.55%
0005164	tumor necrosis factor receptor binding	8	0.55%
0003682	chromatin binding	8	0.55%
0046870	cadmium ion binding	8	0.55%
0005088	Ras guanyl-nucleotide exchange factor activity	8	0.55%
0008026	ATP-dependent helicase activity	8	0.55%
0003823	antigen binding	8	0.55%
0019965	interleukin binding	8	0.55%
0019210	kinase inhibitor activity	8	0.55%
0050660	FAD binding	8	0.55%
0008066	glutamate receptor activity	8	0.55%
0003707	steroid hormone receptor activity	8	0.55%
0005244	voltage-gated ion channel activity	8	0.55%
0004860	protein kinase inhibitor activity	8	0.55%
0004497	monooxygenase activity	7	0.48%
0008022	protein C-terminus binding	7	0.48%
0005048	signal sequence binding	7	0.48%
0008509	anion transporter activity	7	0.48%
0008139	nuclear localization sequence binding	7	0.48%
0005537	mannose binding	7	0.48%
0005234	glutamate-gated ion channel activity	7	0.48%
0043492	ATPase activity, coupled to movement of substances	7	0.48%
0016909	SAP kinase activity	7	0.48%
0019199	transmembrane receptor protein kinase activity	7	0.48%
0004602	glutathione peroxidase activity	7	0.48%
0004222	metalloendopeptidase activity	7	0.48%
0003743	translation initiation factor activity	7	0.48%
0004907	interleukin receptor activity	7	0.48%
0003810	protein-glutamine gamma-glutamyltransferase activity	7	0.48%
0016820	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	7	0.48%
0003711	transcriptional elongation regulator activity	7	0.48%
0003746	translation elongation factor activity	7	0.48%
0048029	monosaccharide binding	7	0.48%
0004970	ionotropic glutamate receptor activity	7	0.48%
0016755	transferase activity, transferring amino-acyl groups	7	0.48%
0042626	ATPase activity, coupled to transmembrane movement of substances	7	0.48%
0051015	actin filament binding	7	0.48%
0016864	intramolecular oxidoreductase activity, transposing S-S bonds	6	0.41%
0005319	lipid transporter activity	6	0.41%
0003684	damaged DNA binding	6	0.41%
0008094	DNA-dependent ATPase activity	6	0.41%
0005496	steroid binding	6	0.41%
0015924	mannosyl-oligosaccharide mannosidase activity	6	0.41%
0030674	protein binding, bridging	6	0.41%
0003756	protein disulfide isomerase activity	6	0.41%
0042287	MHC protein binding	6	0.41%
0016862	intramolecular oxidoreductase activity, interconverting keto- and enol-groups	6	0.41%
0016505	apoptotic protease activator activity	6	0.41%
0005159	insulin-like growth factor receptor binding	6	0.41%
0005096	GTPase activator activity	6	0.41%
0016504	protease activator activity	6	0.41%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0004693	cyclin-dependent protein kinase activity	6	0.41%
0008656	caspase activator activity	6	0.41%
0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	6	0.41%
0016614	oxidoreductase activity, acting on CH-OH group of donors	6	0.41%
0019239	deaminase activity	6	0.41%
0031420	alkali metal ion binding	6	0.41%
0019958	C-X-C chemokine binding	6	0.41%
0019864	IgG binding	6	0.41%
0004714	transmembrane receptor protein tyrosine kinase activity	6	0.41%
0003704	specific RNA polymerase II transcription factor activity	5	0.35%
0004536	deoxyribonuclease activity	5	0.35%
0008499	UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity	5	0.35%
0004115	3',5'-cyclic-AMP phosphodiesterase activity	5	0.35%
0004289	subtilase activity	5	0.35%
0016494	C-X-C chemokine receptor activity	5	0.35%
0005253	anion channel activity	5	0.35%
0015926	glucosidase activity	5	0.35%
0004972	N-methyl-D-aspartate selective glutamate receptor activity	5	0.35%
0004691	cAMP-dependent protein kinase activity	5	0.35%
0048531	beta-1,3-galactosyltransferase activity	5	0.35%
0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NAD	5	0.35%
0008430	selenium binding	5	0.35%
0047498	calcium-dependent phospholipase A2 activity	5	0.35%
0004716	receptor signaling protein tyrosine kinase activity	5	0.35%
0030693	caspase activity	5	0.35%
0015293	symporter activity	5	0.35%
0003678	DNA helicase activity	5	0.35%
0003887	DNA-directed DNA polymerase activity	5	0.35%
0003709	RNA polymerase III transcription factor activity	5	0.35%
0004690	cyclic nucleotide-dependent protein kinase activity	5	0.35%
0004559	alpha-mannosidase activity	5	0.35%
0005178	integrin binding	5	0.35%
0004003	ATP-dependent DNA helicase activity	5	0.35%
0005132	interferon-alpha/beta receptor binding	5	0.35%
0001517	N-acetylglucosamine 6-O-sulfotransferase activity	5	0.35%
0030551	cyclic nucleotide binding	5	0.35%
0004519	endonuclease activity	5	0.35%
0008603	cAMP-dependent protein kinase regulator activity	5	0.35%
0004683	calmodulin regulated protein kinase activity	5	0.35%
0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	4	0.28%
0004095	carnitine O-palmitoyltransferase activity	4	0.28%
0005070	SH3/SH2 adaptor activity	4	0.28%
0050661	NADP binding	4	0.28%
0016741	transferase activity, transferring one-carbon groups	4	0.28%
0016208	AMP binding	4	0.28%
0047485	protein N-terminus binding	4	0.28%
0051020	GTPase binding	4	0.28%
0004000	adenosine deaminase activity	4	0.28%
0004705	JUN kinase activity	4	0.28%
0004708	MAP kinase kinase activity	4	0.28%
0005062	hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity	4	0.28%
0031402	sodium ion binding	4	0.28%
0004540	ribonuclease activity	4	0.28%
0051059	NF-kappaB binding	4	0.28%
0008307	structural constituent of muscle	4	0.28%
0008243	plasminogen activator activity	4	0.28%
0008375	acetylglucosaminyltransferase activity	4	0.28%
0008374	O-acyltransferase activity	4	0.28%
0003777	microtubule motor activity	4	0.28%
0017016	Ras GTPase binding	4	0.28%
0008373	sialyltransferase activity	4	0.28%
0004712	protein threonine/tyrosine kinase activity	4	0.28%
0003945	N-acetyllactosamine synthase activity	4	0.28%
0016416	O-palmitoyltransferase activity	4	0.28%
0004715	non-membrane spanning protein tyrosine kinase activity	4	0.28%
0031267	small GTPase binding	4	0.28%
0043176	amine binding	4	0.28%
0042288	MHC class I protein binding	4	0.28%
0004861	cyclin-dependent protein kinase inhibitor activity	4	0.28%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0017166	vinculin binding	4	0.28%
0046934	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	4	0.28%
0005254	chloride channel activity	4	0.28%
0015631	tubulin binding	4	0.28%
0019198	transmembrane receptor protein phosphatase activity	4	0.28%
0015144	carbohydrate transporter activity	4	0.28%
0008168	methyltransferase activity	4	0.28%
0016409	palmitoyltransferase activity	4	0.28%
0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms	4	0.28%
0005518	collagen binding	4	0.28%
0005262	calcium channel activity	4	0.28%
0016406	carnitine O-acyltransferase activity	4	0.28%
0051119	sugar transporter activity	4	0.28%
0005001	transmembrane receptor protein tyrosine phosphatase activity	4	0.28%
0030594	neurotransmitter receptor activity	4	0.28%
0030552	cAMP binding	4	0.28%
0004571	mannosyl-oligosaccharide 1,2-alpha-mannosidase activity	4	0.28%
0015457	auxiliary transport protein activity	4	0.28%
0051213	dioxygenase activity	4	0.28%
0042165	neurotransmitter binding	4	0.28%
0005275	amine transporter activity	4	0.28%
0042169	SH2 domain binding	4	0.28%
0035005	phosphatidylinositol-4-phosphate 3-kinase activity	3	0.21%
0003836	beta-galactoside alpha-2,3-sialyltransferase activity	3	0.21%
0016307	phosphatidylinositol phosphate kinase activity	3	0.21%
0016799	hydrolase activity, hydrolyzing N-glycosyl compounds	3	0.21%
0004198	calpain activity	3	0.21%
0003755	peptidyl-prolyl cis-trans isomerase activity	3	0.21%
0042166	acetylcholine binding	3	0.21%
0030159	receptor signaling complex scaffold activity	3	0.21%
0008339	MP kinase activity	3	0.21%
0003705	RNA polymerase II transcription factor activity, enhancer binding	3	0.21%
0000158	protein phosphatase type 2A activity	3	0.21%
0016811	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	3	0.21%
0005520	insulin-like growth factor binding	3	0.21%
0008329	pattern recognition receptor activity	3	0.21%
0004308	exo-alpha-sialidase activity	3	0.21%
0004911	interleukin-2 receptor activity	3	0.21%
0004889	nicotinic acetylcholine-activated cation-selective channel activity	3	0.21%
0043027	caspase inhibitor activity	3	0.21%
0005128	erythropoietin receptor binding	3	0.21%
0004527	exonuclease activity	3	0.21%
0015278	calcium-release channel activity	3	0.21%
0016651	oxidoreductase activity, acting on NADH or NADPH	3	0.21%
0030545	receptor regulator activity	3	0.21%
0004459	L-lactate dehydrogenase activity	3	0.21%
0001948	glycoprotein binding	3	0.21%
0008454	alpha-1,3-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity	3	0.21%
0046873	metal ion transporter activity	3	0.21%
0005184	neuropeptide hormone activity	3	0.21%
0046790	virion binding	3	0.21%
0008034	lipoprotein binding	3	0.21%
0015464	acetylcholine receptor activity	3	0.21%
0015238	drug transporter activity	3	0.21%
0005149	interleukin-1 receptor binding	3	0.21%
0005544	calcium-dependent phospholipid binding	3	0.21%
0016286	small conductance calcium-activated potassium channel activity	3	0.21%
0008095	inositol-1,4,5-triphosphate receptor activity	3	0.21%
0008191	metalloendopeptidase inhibitor activity	3	0.21%
0015370	solute:sodium symporter activity	3	0.21%
0043560	insulin receptor substrate binding	3	0.21%
0015082	di-, tri-valent inorganic cation transporter activity	3	0.21%
0008639	small protein conjugating enzyme activity	3	0.21%
0005021	vascular endothelial growth factor receptor activity	3	0.21%
0015288	porin activity	3	0.21%
0008159	positive transcription elongation factor activity	3	0.21%
0005154	epidermal growth factor receptor binding	3	0.21%
0015085	calcium ion transporter activity	3	0.21%
0004117	calmodulin-dependent cyclic-nucleotide phosphodiesterase activity	3	0.21%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0005247	voltage-gated chloride channel activity	3	0.21%
0008367	bacterial binding	3	0.21%
0004035	alkaline phosphatase activity	3	0.21%
0004784	superoxide dismutase activity	3	0.21%
0008017	microtubule binding	3	0.21%
0046943	carboxylic acid transporter activity	3	0.21%
0008238	exopeptidase activity	3	0.21%
0016763	transferase activity, transferring pentosyl groups	3	0.21%
0019825	oxygen binding	3	0.21%
0016721	oxidoreductase activity, acting on superoxide radicals as acceptor	3	0.21%
0016986	transcription initiation factor activity	3	0.21%
0004652	polynucleotide adenylyltransferase activity	3	0.21%
0003831	beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity	3	0.21%
0004767	sphingomyelin phosphodiesterase activity	3	0.21%
0005158	insulin receptor binding	3	0.21%
0015171	amino acid transporter activity	3	0.21%
0016247	channel regulator activity	3	0.21%
0016859	cis-trans isomerase activity	3	0.21%
0042608	T cell receptor binding	3	0.21%
0000146	microfilament motor activity	3	0.21%
0004812	aminoacyl-tRNA ligase activity	3	0.21%
0004840	ubiquitin conjugating enzyme activity	3	0.21%
0000049	tRNA binding	3	0.21%
0019209	kinase activator activity	3	0.21%
0042562	hormone binding	3	0.21%
0004709	MAP kinase kinase kinase activity	3	0.21%
0003950	NAD+ ADP-ribosyltransferase activity	3	0.21%
0043120	tumor necrosis factor binding	3	0.21%
0042605	peptide antigen binding	3	0.21%
0016997	alpha-sialidase activity	3	0.21%
0030235	nitric-oxide synthase regulator activity	3	0.21%
0005080	protein kinase C binding	3	0.21%
0017124	SH3 domain binding	3	0.21%
0005342	organic acid transporter activity	3	0.21%
0010181	FMN binding	3	0.21%
0050664	oxidoreductase activity, acting on NADH or NADPH, with oxygen as acceptor	3	0.21%
0003724	RNA helicase activity	3	0.21%
0004700	atypical protein kinase C activity	3	0.21%
0015294	solute:cation symporter activity	3	0.21%
0004689	phosphorylase kinase activity	3	0.21%
0005035	death receptor activity	3	0.21%
0019976	interleukin-2 binding	3	0.21%
0005217	intracellular ligand-gated ion channel activity	3	0.21%
0004457	lactate dehydrogenase activity	3	0.21%
0005220	inositol 1,4,5-triphosphate-sensitive calcium-release channel activity	3	0.21%
0003727	single-stranded RNA binding	3	0.21%
0016876	ligase activity, forming aminoacyl-tRNA and related compounds	3	0.21%
0004517	nitric-oxide synthase activity	3	0.21%
0042826	histone deacetylase binding	3	0.21%
0016875	ligase activity, forming carbon-oxygen bonds	3	0.21%
0005071	transmembrane receptor protein serine/threonine kinase signaling protein activity	3	0.21%
0008536	Ran GTPase binding	3	0.21%
0005072	transforming growth factor beta receptor, cytoplasmic mediator activity	3	0.21%
0008538	proteasome activator activity	3	0.21%
0005351	sugar porter activity	3	0.21%
0008426	protein kinase C inhibitor activity	3	0.21%
0046966	thyroid hormone receptor binding	2	0.14%
0019979	interleukin-4 binding	2	0.14%
0015405	P-P-bond-hydrolysis-driven transporter activity	2	0.14%
0046965	retinoid X receptor binding	2	0.14%
0046961	hydrogen-transporting ATPase activity, rotational mechanism	2	0.14%
0030508	thiol-disulfide exchange intermediate activity	2	0.14%
0005478	intracellular transporter activity	2	0.14%
0004685	calcium- and calmodulin-dependent protein kinase activity	2	0.14%
0019982	interleukin-7 binding	2	0.14%
0050220	prostaglandin-E synthase activity	2	0.14%
0005355	glucose transporter activity	2	0.14%
0008408	3'-5' exonuclease activity	2	0.14%
0004004	ATP-dependent RNA helicase activity	2	0.14%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0008133	collagenase activity	2	0.14%
0005076	receptor signaling protein serine/threonine kinase signaling protein activity	2	0.14%
0019966	interleukin-1 binding	2	0.14%
0003729	mRNA binding	2	0.14%
0048019	receptor antagonist activity	2	0.14%
0008138	protein tyrosine/serine/threonine phosphatase activity	2	0.14%
0016175	superoxide-generating NADPH oxidase activity	2	0.14%
0051540	metal cluster binding	2	0.14%
0004945	angiotensin type II receptor activity	2	0.14%
0004944	C5a anaphylatoxin receptor activity	2	0.14%
0019961	interferon binding	2	0.14%
0001608	nucleotide receptor activity, G-protein coupled	2	0.14%
0004126	cytidine deaminase activity	2	0.14%
0004942	anaphylatoxin receptor activity	2	0.14%
0003735	structural constituent of ribosome	2	0.14%
0019829	cation-transporting ATPase activity	2	0.14%
0051537	2 iron, 2 sulfur cluster binding	2	0.14%
0004558	alpha-glucosidase activity	2	0.14%
0008144	drug binding	2	0.14%
0051536	iron-sulfur cluster binding	2	0.14%
0019863	IgE binding	2	0.14%
0016891	endoribonuclease activity, producing 5'-phosphomonoesters	2	0.14%
0042132	fructose-bisphosphatase activity	2	0.14%
0032182	small conjugating protein binding	2	0.14%
0030617	transforming growth factor beta receptor, inhibitory cytoplasmic mediator activity	2	0.14%
0015399	primary active transporter activity	2	0.14%
0016893	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	2	0.14%
0008147	structural constituent of bone	2	0.14%
0003720	telomerase activity	2	0.14%
0008148	negative transcription elongation factor activity	2	0.14%
0016895	exodeoxyribonuclease activity, producing 5'-phosphomonoesters	2	0.14%
0001614	purinergic nucleotide receptor activity	2	0.14%
0004718	Janus kinase activity	2	0.14%
0004295	trypsin activity	2	0.14%
0004982	N-formyl peptide receptor activity	2	0.14%
0016502	nucleotide receptor activity	2	0.14%
0004406	H3/H4 histone acetyltransferase activity	2	0.14%
0004985	opioid receptor activity	2	0.14%
0004537	caspase-activated deoxyribonuclease activity	2	0.14%
0004119	cGMP-inhibited cyclic-nucleotide phosphodiesterase activity	2	0.14%
0042577	lipid phosphatase activity	2	0.14%
0005249	voltage-gated potassium channel activity	2	0.14%
0004859	phospholipase inhibitor activity	2	0.14%
0004379	glycylpeptide N-tetradecanoyltransferase activity	2	0.14%
0004666	prostaglandin-endoperoxide synthase activity	2	0.14%
0016776	phosphotransferase activity, phosphate group as acceptor	2	0.14%
0035014	phosphoinositide 3-kinase regulator activity	2	0.14%
0004177	aminopeptidase activity	2	0.14%
0008294	calcium- and calmodulin-responsive adenylate cyclase activity	2	0.14%
0001595	angiotensin receptor activity	2	0.14%
0042974	retinoic acid receptor binding	2	0.14%
0030374	ligand-dependent nuclear receptor transcription coactivator activity	2	0.14%
0046933	hydrogen-transporting ATP synthase activity, rotational mechanism	2	0.14%
0005123	death receptor binding	2	0.14%
0015239	multidrug transporter activity	2	0.14%
0042289	MHC class II protein binding	2	0.14%
0042975	peroxisome proliferator activated receptor binding	2	0.14%
0015078	hydrogen ion transporter activity	2	0.14%
0015077	monovalent inorganic cation transporter activity	2	0.14%
0004437	inositol or phosphatidylinositol phosphatase activity	2	0.14%
0043168	anion binding	2	0.14%
0003680	AT DNA binding	2	0.14%
0008422	beta-glucosidase activity	2	0.14%
0016835	carbon-oxygen lyase activity	2	0.14%
0001633	secretin-like receptor activity	2	0.14%
0004869	cysteine protease inhibitor activity	2	0.14%
0016831	carboxy-lyase activity	2	0.14%
0016830	carbon-carbon lyase activity	2	0.14%
0030547	receptor inhibitor activity	2	0.14%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0004917	interleukin-7 receptor activity	2	0.14%
0004529	exodeoxyribonuclease activity	2	0.14%
0015145	monosaccharide transporter activity	2	0.14%
0051087	chaperone binding	2	0.14%
0015101	organic cation transporter activity	2	0.14%
0004913	interleukin-4 receptor activity	2	0.14%
0008476	protein-tyrosine sulfotransferase activity	2	0.14%
0008173	RNA methyltransferase activity	2	0.14%
0003706	ligand-regulated transcription factor activity	2	0.14%
0005092	GDP-dissociation inhibitor activity	2	0.14%
0031072	heat shock protein binding	2	0.14%
0042162	telomeric DNA binding	2	0.14%
0045569	TRAIL binding	2	0.14%
0030295	protein kinase activator activity	2	0.14%
0004190	aspartic-type endopeptidase activity	2	0.14%
0019107	myristoyltransferase activity	2	0.14%
0005006	epidermal growth factor receptor activity	2	0.14%
0004572	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity	2	0.14%
0015149	hexose transporter activity	2	0.14%
0004194	pepsin A activity	2	0.14%
0008559	xenobiotic-transporting ATPase activity	2	0.14%
0016796	exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters	2	0.14%
0019104	DNA N-glycosylase activity	2	0.14%
0043548	phosphoinositide 3-kinase binding	2	0.14%
0004904	interferon receptor activity	2	0.14%
0042625	ATPase activity, coupled to transmembrane movement of ions	2	0.14%
0017056	structural constituent of nuclear pore	2	0.14%
0019201	nucleotide kinase activity	2	0.14%
0015459	potassium channel regulator activity	2	0.14%
0005044	scavenger receptor activity	2	0.14%
0030284	estrogen receptor activity	2	0.14%
0008607	phosphorylase kinase regulator activity	2	0.14%
0004785	copper, zinc superoxide dismutase activity	2	0.14%
0008459	chondroitin 6-sulfotransferase activity	2	0.14%
0004521	endoribonuclease activity	2	0.14%
0008186	RNA-dependent ATPase activity	2	0.14%
0045296	cadherin binding	2	0.14%
0005279	amino acid-polyamine transporter activity	2	0.14%
0019203	carbohydrate phosphatase activity	2	0.14%
0004759	serine esterase activity	2	0.14%
0015203	polyamine transporter activity	2	0.14%
0042056	chemoattractant activity	2	0.14%
0017069	snRNA binding	2	0.14%
0004520	endodeoxyribonuclease activity	2	0.14%
0031404	chloride ion binding	2	0.14%
0003964	RNA-directed DNA polymerase activity	2	0.14%
0019205	nucleobase, nucleoside, nucleotide kinase activity	2	0.14%
0045028	purinergic nucleotide receptor activity, G-protein coupled	2	0.14%
0005155	epidermal growth factor receptor activating ligand activity	2	0.14%
0050839	cell adhesion molecule binding	2	0.14%
0042910	xenobiotic transporter activity	2	0.14%
0031202	RNA splicing factor activity, transesterification mechanism	2	0.14%
0043130	ubiquitin binding	2	0.14%
0004331	fructose-2,6-bisphosphate 2-phosphatase activity	2	0.14%
0019903	protein phosphatase binding	2	0.14%
0042607	exogenous peptide antigen binding	2	0.14%
0019902	phosphatase binding	2	0.14%
0005160	transforming growth factor beta receptor binding	2	0.14%
0004461	lactose synthase activity	2	0.14%
0001537	N-acetylgalactosamine 4-O-sulfotransferase activity	2	0.14%
0005031	tumor necrosis factor receptor activity	2	0.14%
0045155	electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidas	2	0.14%
0030955	potassium ion binding	2	0.14%
0001540	beta-amyloid binding	2	0.14%
0019213	deacetylase activity	2	0.14%
0043125	ErbB-3 class receptor binding	2	0.14%
0004091	carboxylesterase activity	2	0.14%
0015925	galactosidase activity	1	0.07%
0015485	cholesterol binding	1	0.07%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0035259	glucocorticoid receptor binding	1	0.07%
0000175	3'-5'-exoribonuclease activity	1	0.07%
0019212	phosphatase inhibitor activity	1	0.07%
0031531	thyrotropin-releasing hormone receptor binding	1	0.07%
0015297	antiporter activity	1	0.07%
0015482	voltage-gated anion channel porin activity	1	0.07%
0015037	peptide disulfide oxidoreductase activity	1	0.07%
0015165	pyrimidine nucleotide sugar transporter activity	1	0.07%
0019211	phosphatase activator activity	1	0.07%
0001671	ATPase stimulator activity	1	0.07%
0004511	tyrosine 3-monooxygenase activity	1	0.07%
0008310	single-stranded DNA specific 3'-5' exodeoxyribonuclease activity	1	0.07%
0003953	NAD+ nucleosidase activity	1	0.07%
0004096	catalase activity	1	0.07%
0016423	tRNA (guanine) methyltransferase activity	1	0.07%
0015296	anion:cation symporter activity	1	0.07%
0008309	double-stranded DNA specific exodeoxyribonuclease activity	1	0.07%
0004771	sterol esterase activity	1	0.07%
0008757	S-adenosylmethionine-dependent methyltransferase activity	1	0.07%
0015038	glutathione disulfide oxidoreductase activity	1	0.07%
0008308	voltage-gated ion-selective channel activity	1	0.07%
0008504	monoamine transporter activity	1	0.07%
0042043	neurexin binding	1	0.07%
0005172	vascular endothelial growth factor receptor binding	1	0.07%
0030957	Tat protein binding	1	0.07%
0005528	FK506 binding	1	0.07%
0008199	ferric iron binding	1	0.07%
0008067	metabotropic glutamate, GABA-B-like receptor activity	1	0.07%
0051800	phosphatidylinositol-3,4-bisphosphate 3-phosphatase activity	1	0.07%
0005540	hyaluronic acid binding	1	0.07%
0050840	extracellular matrix binding	1	0.07%
0019905	syntaxin binding	1	0.07%
0015359	amino acid permease activity	1	0.07%
0018445	prothoracicotrophic hormone activity	1	0.07%
0016933	glycine-gated ion channel activity	1	0.07%
0042609	CD4 receptor binding	1	0.07%
0004634	phosphopyruvate hydratase activity	1	0.07%
0001530	lipopolysaccharide binding	1	0.07%
0005024	transforming growth factor beta receptor activity	1	0.07%
0005041	low-density lipoprotein receptor activity	1	0.07%
0016248	channel inhibitor activity	1	0.07%
0004765	shikimate kinase activity	1	0.07%
0015172	acidic amino acid transporter activity	1	0.07%
0004651	polynucleotide 5'-phosphatase activity	1	0.07%
0016566	specific transcriptional repressor activity	1	0.07%
0005527	macrolide binding	1	0.07%
0003893	epsilon DNA polymerase activity	1	0.07%
0042610	CD8 receptor binding	1	0.07%
0005153	interleukin-8 receptor binding	1	0.07%
0030274	LIM domain binding	1	0.07%
0015207	adenine transporter activity	1	0.07%
0015174	basic amino acid transporter activity	1	0.07%
0008320	protein carrier activity	1	0.07%
0005152	interleukin-1 receptor antagonist activity	1	0.07%
0008192	RNA guanylyltransferase activity	1	0.07%
0015205	nucleobase transporter activity	1	0.07%
0000739	DNA strand annealing activity	1	0.07%
0043559	insulin binding	1	0.07%
0015175	neutral amino acid transporter activity	1	0.07%
0005412	glucose:sodium symporter activity	1	0.07%
0043426	MRF binding	1	0.07%
0003809	thrombin activity	1	0.07%
0005174	CD40 receptor binding	1	0.07%
0004890	GABA-A receptor activity	1	0.07%
0043425	bHLH transcription factor binding	1	0.07%
0042903	tubulin deacetylase activity	1	0.07%
0005545	phosphatidylinositol binding	1	0.07%
0019204	nucleotide phosphatase activity	1	0.07%
0016806	dipeptidyl-peptidase and tripeptidyl-peptidase activity	1	0.07%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0045294	alpha-catenin binding	1	0.07%
0008455	alpha-1,6-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity	1	0.07%
0015491	cation:cation antiporter activity	1	0.07%
0016808	proprotein convertase activity	1	0.07%
0005147	oncostatin-M receptor binding	1	0.07%
0051117	ATPase binding	1	0.07%
0008187	poly-pyrimidine tract binding	1	0.07%
0015179	L-amino acid transporter activity	1	0.07%
0043138	3' to 5' DNA helicase activity	1	0.07%
0005146	leukemia inhibitory factor receptor binding	1	0.07%
0051219	phosphoprotein binding	1	0.07%
0008434	vitamin D3 receptor activity	1	0.07%
0004887	thyroid hormone receptor activity	1	0.07%
0043139	5' to 3' DNA helicase activity	1	0.07%
0048256	flap endonuclease activity	1	0.07%
0047555	3',5'-cyclic-GMP phosphodiesterase activity	1	0.07%
0004622	lysophospholipase activity	1	0.07%
0005144	interleukin-13 receptor binding	1	0.07%
0005011	macrophage colony stimulating factor receptor activity	1	0.07%
0016917	GABA receptor activity	1	0.07%
0000339	RNA cap binding	1	0.07%
0003890	beta DNA polymerase activity	1	0.07%
0005143	interleukin-12 receptor binding	1	0.07%
0005010	insulin-like growth factor receptor activity	1	0.07%
0004345	glucose-6-phosphate 1-dehydrogenase activity	1	0.07%
0043142	single-stranded DNA-dependent ATPase activity	1	0.07%
0008605	protein kinase CK2 regulator activity	1	0.07%
0005176	ErbB-2 class receptor binding	1	0.07%
0004347	glucose-6-phosphate isomerase activity	1	0.07%
0047429	nucleoside-triphosphate diphosphatase activity	1	0.07%
0004348	glucosylceramidase activity	1	0.07%
0004883	glucocorticoid receptor activity	1	0.07%
0016534	cyclin-dependent protein kinase 5 activator activity	1	0.07%
0015283	apoptogenic cytochrome c release channel activity	1	0.07%
0005141	interleukin-10 receptor binding	1	0.07%
0050824	water binding	1	0.07%
0008200	ion channel inhibitor activity	1	0.07%
0005099	Ras GTPase activator activity	1	0.07%
0004445	inositol-polyphosphate 5-phosphatase activity	1	0.07%
0004523	ribonuclease H activity	1	0.07%
0004573	mannosyl-oligosaccharide glucosidase activity	1	0.07%
0005095	GTPase inhibitor activity	1	0.07%
0004618	phosphoglycerate kinase activity	1	0.07%
0004905	interferon-alpha/beta receptor activity	1	0.07%
0019237	centromeric DNA binding	1	0.07%
0004656	procollagen-proline 4-dioxygenase activity	1	0.07%
0005139	interleukin-7 receptor binding	1	0.07%
0004193	cathepsin E activity	1	0.07%
0004906	interferon-gamma receptor activity	1	0.07%
0005138	interleukin-6 receptor binding	1	0.07%
0003969	RNA editase activity	1	0.07%
0004192	cathepsin D activity	1	0.07%
0047273	galactosylgalactosylglucosylceramide beta-D-acetylgalactosaminyltransferase activity	1	0.07%
0004484	mRNA guanylyltransferase activity	1	0.07%
0005137	interleukin-5 receptor binding	1	0.07%
0008641	small protein activating enzyme activity	1	0.07%
0008995	ribonuclease E activity	1	0.07%
0008177	succinate dehydrogenase (ubiquinone) activity	1	0.07%
0005136	interleukin-4 receptor binding	1	0.07%
0004908	interleukin-1 receptor activity	1	0.07%
0030553	cGMP binding	1	0.07%
0005094	Rho GDP-dissociation inhibitor activity	1	0.07%
0008176	tRNA (guanine-N7-)-methyltransferase activity	1	0.07%
0004909	interleukin-1, Type I, activating receptor activity	1	0.07%
0004613	phosphoenolpyruvate carboxykinase (GTP) activity	1	0.07%
0005135	interleukin-3 receptor binding	1	0.07%
0016790	thiolester hydrolase activity	1	0.07%
0004525	ribonuclease III activity	1	0.07%
0043021	ribonucleoprotein binding	1	0.07%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0008175	tRNA methyltransferase activity	1	0.07%
0005134	interleukin-2 receptor binding	1	0.07%
0005432	calcium:sodium antiporter activity	1	0.07%
0004875	complement receptor activity	1	0.07%
0004611	phosphoenolpyruvate carboxykinase activity	1	0.07%
0005133	interferon-gamma receptor binding	1	0.07%
0005047	signal recognition particle binding	1	0.07%
0030165	PDZ domain binding	1	0.07%
0005517	calmodulin inhibitor activity	1	0.07%
0015197	peptide transporter activity	1	0.07%
0008424	glycoprotein 6-alpha-L-fucosyltransferase activity	1	0.07%
0004228	gelatinase A activity	1	0.07%
0000156	two-component response regulator activity	1	0.07%
0017046	peptide hormone binding	1	0.07%
0008859	exoribonuclease II activity	1	0.07%
0031625	ubiquitin protein ligase binding	1	0.07%
0005049	nuclear export signal receptor activity	1	0.07%
0030549	acetylcholine receptor activator activity	1	0.07%
0015198	oligopeptide transporter activity	1	0.07%
0004229	gelatinase B activity	1	0.07%
0043539	protein serine/threonine kinase activator activity	1	0.07%
0004439	phosphoinositide 5-phosphatase activity	1	0.07%
0030548	acetylcholine receptor regulator activity	1	0.07%
0004915	interleukin-6 receptor activity	1	0.07%
0030169	low-density lipoprotein binding	1	0.07%
0004438	phosphatidylinositol-3-phosphatase activity	1	0.07%
0001636	corticotrophin-releasing factor gastric inhibitory peptide-like receptor activity	1	0.07%
0031543	peptidyl-proline dioxygenase activity	1	0.07%
0005129	granulocyte macrophage colony-stimulating factor receptor binding	1	0.07%
0015368	calcium:cation antiporter activity	1	0.07%
0030546	receptor activator activity	1	0.07%
0046921	alpha(1,6)-fucosyltransferase activity	1	0.07%
0004363	glutathione synthase activity	1	0.07%
0030170	pyridoxal phosphate binding	1	0.07%
0008778	acyl-CoA thioesterase II activity	1	0.07%
0030171	voltage-gated proton channel activity	1	0.07%
0003918	DNA topoisomerase (ATP-hydrolyzing) activity	1	0.07%
0004051	arachidonate 5-lipoxygenase activity	1	0.07%
0030337	DNA polymerase processivity factor activity	1	0.07%
0030377	U-plasminogen activator receptor activity	1	0.07%
0004232	interstitial collagenase activity	1	0.07%
0030676	Rac guanyl-nucleotide exchange factor activity	1	0.07%
0017040	ceramidase activity	1	0.07%
0003917	DNA topoisomerase type I activity	1	0.07%
0004498	calcidiol 1-monooxygenase activity	1	0.07%
0005310	dicarboxylic acid transporter activity	1	0.07%
0008035	high-density lipoprotein binding	1	0.07%
0016519	gastric inhibitory peptide receptor activity	1	0.07%
0031545	peptidyl-proline 4-dioxygenase activity	1	0.07%
0008720	D-lactate dehydrogenase activity	1	0.07%
0003916	DNA topoisomerase activity	1	0.07%
0004235	matrilysin activity	1	0.07%
0016019	peptidoglycan receptor activity	1	0.07%
0016836	hydro-lyase activity	1	0.07%
0005313	L-glutamate transporter activity	1	0.07%
0045130	keratan sulfotransferase activity	1	0.07%
0016706	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutara	1	0.07%
0004180	carboxypeptidase activity	1	0.07%
0004999	vasoactive intestinal polypeptide receptor activity	1	0.07%
0008093	cytoskeletal adaptor activity	1	0.07%
0016314	phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase activity	1	0.07%
0002020	protease binding	1	0.07%
0016284	alanine aminopeptidase activity	1	0.07%
0043531	ADP binding	1	0.07%
0051717	inositol-1,3,4,5-tetrakisphosphate 3-phosphatase activity	1	0.07%
0008297	single-stranded DNA specific exodeoxyribonuclease activity	1	0.07%
0004998	transferrin receptor activity	1	0.07%
0004865	type 1 serine/threonine specific protein phosphatase inhibitor activity	1	0.07%
0008489	UDP-galactose:glucosylceramide beta-1,4-galactosyltransferase activity	1	0.07%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0004532	exoribonuclease activity	1	0.07%
0008296	3'-5'-exodeoxyribonuclease activity	1	0.07%
0004864	protein phosphatase inhibitor activity	1	0.07%
0016289	CoA hydrolase activity	1	0.07%
0019798	procollagen-proline dioxygenase activity	1	0.07%
0004179	membrane alanyl aminopeptidase activity	1	0.07%
0004113	2',3'-cyclic-nucleotide 3'-phosphodiesterase activity	1	0.07%
0016290	palmitoyl-CoA hydrolase activity	1	0.07%
0004567	beta-mannosidase activity	1	0.07%
0004566	beta-glucuronidase activity	1	0.07%
0004565	beta-galactosidase activity	1	0.07%
0008160	protein tyrosine phosphatase activator activity	1	0.07%
0004245	neprilysin activity	1	0.07%
0004246	peptidyl-dipeptidase A activity	1	0.07%
0016291	acyl-CoA thioesterase activity	1	0.07%
0016714	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pter	1	0.07%
0016774	phosphotransferase activity, carboxyl group as acceptor	1	0.07%
0008494	translation activator activity	1	0.07%
0008097	5S rRNA binding	1	0.07%
0017163	negative regulator of basal transcription activity	1	0.07%
0004248	stromelysin 1 activity	1	0.07%
0042708	elastase activity	1	0.07%
0004696	glycogen synthase kinase 3 activity	1	0.07%
0050321	tau-protein kinase activity	1	0.07%
0003906	DNA-(apurinic or apyrimidinic site) lyase activity	1	0.07%
0003691	double-stranded telomeric DNA binding	1	0.07%
0004726	non-membrane spanning protein tyrosine phosphatase activity	1	0.07%
0019002	GMP binding	1	0.07%
0009053	electron donor activity	1	0.07%
0004118	cGMP-stimulated cyclic-nucleotide phosphodiesterase activity	1	0.07%
0004988	mu-opioid receptor activity	1	0.07%
0005246	calcium channel regulator activity	1	0.07%
0019003	GDP binding	1	0.07%
0004987	kappa-opioid receptor activity	1	0.07%
0017108	5'-flap endonuclease activity	1	0.07%
0004723	calcium-dependent protein serine/threonine phosphatase activity	1	0.07%
0003847	1-alkyl-2-acetylglycerophosphocholine esterase activity	1	0.07%
0001882	nucleoside binding	1	0.07%
0008417	fucosyltransferase activity	1	0.07%
0008235	metalloexopeptidase activity	1	0.07%
0005326	neurotransmitter transporter activity	1	0.07%
0005112	Notch binding	1	0.07%
0000149	SNARE binding	1	0.07%
0030611	arsenate reductase activity	1	0.07%
0017026	procollagen C-endopeptidase activity	1	0.07%
0015643	toxin binding	1	0.07%
0016165	lipoxygenase activity	1	0.07%
0016635	oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor	1	0.07%
0004806	triacylglycerol lipase activity	1	0.07%
0005328	neurotransmitter:sodium symporter activity	1	0.07%
0000702	oxidized base lesion DNA N-glycosylase activity	1	0.07%
0045545	syndecan binding	1	0.07%
0004407	histone deacetylase activity	1	0.07%
0016896	exoribonuclease activity, producing 5'-phosphomonoesters	1	0.07%
0017022	myosin binding	1	0.07%
0051577	MyoD binding	1	0.07%
0031997	N-terminal myristoylation domain binding	1	0.07%
0047066	phospholipid-hydroperoxide glutathione peroxidase activity	1	0.07%
0030613	oxidoreductase activity, acting on phosphorus or arsenic in donors	1	0.07%
0004694	eukaryotic translation initiation factor 2alpha kinase activity	1	0.07%
0015932	nucleobase, nucleoside, nucleotide and nucleic acid transporter activity	1	0.07%
0003851	2-hydroxyacylsphingosine 1-beta-galactosyltransferase activity	1	0.07%
0005329	dopamine transporter activity	1	0.07%
0004980	melanocyte stimulating hormone receptor activity	1	0.07%
0017153	sodium:dicarboxylate symporter activity	1	0.07%
0030369	ICAM-3 receptor activity	1	0.07%
0015248	sterol transporter activity	1	0.07%
0030614	oxidoreductase activity, acting on phosphorus or arsenic in donors, with disulfide as acceptor	1	0.07%
0005504	fatty acid binding	1	0.07%

Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0008239	dipeptidyl-peptidase activity	1	0.07%
0004385	guanylate kinase activity	1	0.07%
0019826	oxygen sensor activity	1	0.07%
0001611	A2A adenosine receptor activity, G-protein coupled	1	0.07%
0019959	interleukin-8 binding	1	0.07%
0003721	telomeric template RNA reverse transcriptase activity	1	0.07%
0005330	dopamine:sodium symporter activity	1	0.07%
0051287	NAD binding	1	0.07%
0005104	fibroblast growth factor receptor binding	1	0.07%
0015266	protein channel activity	1	0.07%
0042834	peptidoglycan binding	1	0.07%
0004977	melanocortin receptor activity	1	0.07%
0004675	transmembrane receptor protein serine/threonine kinase activity	1	0.07%
0045502	dynein binding	1	0.07%
0019862	IgA binding	1	0.07%
0008143	poly(A) binding	1	0.07%
0016627	oxidoreductase activity, acting on the CH-CH group of donors	1	0.07%
0004844	uracil DNA N-glycosylase activity	1	0.07%
0005462	UDP-N-acetylglucosamine transporter activity	1	0.07%
0017114	wide-spectrum protease inhibitor activity	1	0.07%
0050749	apolipoprotein E receptor binding	1	0.07%
0008241	peptidyl-dipeptidase activity	1	0.07%
0005497	androgen binding	1	0.07%
0005066	transmembrane receptor protein tyrosine kinase signaling protein activity	1	0.07%
0008409	5'-3' exonuclease activity	1	0.07%
0051538	3 iron, 4 sulfur cluster binding	1	0.07%
0042301	phosphate binding	1	0.07%
0046030	inositol trisphosphate phosphatase activity	1	0.07%
0031727	CCR2 chemokine receptor binding	1	0.07%
0001609	adenosine receptor activity, G-protein coupled	1	0.07%
0030881	beta-2-microglobulin binding	1	0.07%
0032451	demethylase activity	1	0.07%
0004677	DNA-dependent protein kinase activity	1	0.07%
0004710	MAP/ERK kinase kinase activity	1	0.07%
0005100	Rho GTPase activator activity	1	0.07%
0051539	4 iron, 4 sulfur cluster binding	1	0.07%
0015252	hydrogen ion channel activity	1	0.07%
0008140	cAMP response element binding protein binding	1	0.07%
0030882	lipid antigen binding	1	0.07%
0016888	endodeoxyribonuclease activity, producing 5'-phosphomonoesters	1	0.07%
0003726	double-stranded RNA adenosine deaminase activity	1	0.07%
0050750	low-density lipoprotein receptor binding	1	0.07%
0008794	arsenate reductase (glutaredoxin) activity	1	0.07%
0019962	interferon-alpha/beta binding	1	0.07%
0008376	acetylgalactosaminyltransferase activity	1	0.07%
0004287	prolyl oligopeptidase activity	1	0.07%
0030884	exogenous lipid antigen binding	1	0.07%
0030353	fibroblast growth factor receptor antagonist activity	1	0.07%
0016174	NAD(P)H oxidase activity	1	0.07%
0047499	calcium-independent phospholipase A2 activity	1	0.07%
0005068	transmembrane receptor protein tyrosine kinase adaptor protein activity	1	0.07%
0019964	interferon-gamma binding	1	0.07%
0030515	snoRNA binding	1	0.07%
0004392	heme oxygenase (decyclizing) activity	1	0.07%
0004285	proprotein convertase 1 activity	1	0.07%
0016861	intramolecular oxidoreductase activity, interconverting aldoses and ketoses	1	0.07%
0005338	nucleotide-sugar transporter activity	1	0.07%
0035035	histone acetyltransferase binding	1	0.07%
0004839	ubiquitin activating enzyme activity	1	0.07%
0008533	astacin activity	1	0.07%
0004706	JUN kinase kinase kinase activity	1	0.07%
0019967	interleukin-1, Type I, activating binding	1	0.07%
0008118	N-acetyllactosaminide alpha-2,3-sialyltransferase activity	1	0.07%
0004704	NF-kappaB-inducing kinase activity	1	0.07%
0001848	complement binding	1	0.07%
0008398	sterol 14-demethylase activity	1	0.07%
0008383	manganese superoxide dismutase activity	1	0.07%
0048306	calcium-dependent protein binding	1	0.07%
0004017	adenylate kinase activity	1	0.07%

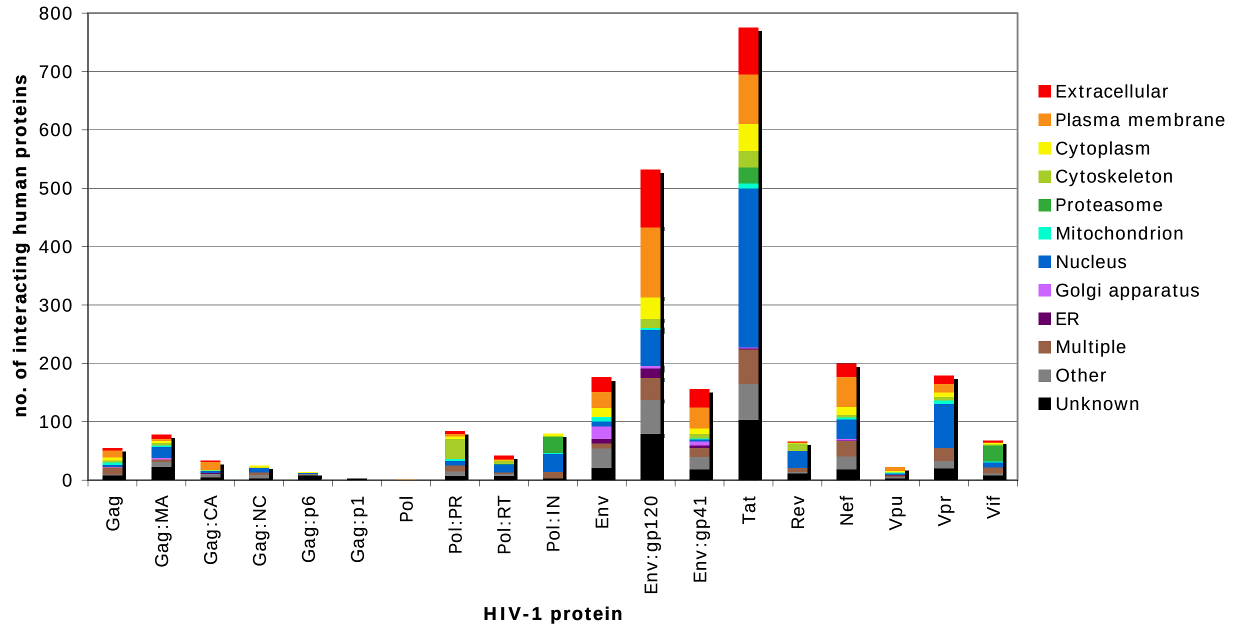
Supplementary Table 3C. HIV-1 Human Protein Interaction Database: Distribution of molecular function Gene Ontology terms associated with HIV-1 Human protein interactions

GO ID	GO name	# Proteins	Percent
0008384	IkappaB kinase activity	1	0.07%
0016594	glycine binding	1	0.07%
0004821	histidine-tRNA ligase activity	1	0.07%
0047915	ganglioside galactosyltransferase activity	1	0.07%
0005343	organic acid:sodium symporter activity	1	0.07%
0008534	oxidized purine base lesion DNA N-glycosylase activity	1	0.07%
0005487	nucleocytoplasmic transporter activity	1	0.07%
0005345	purine transporter activity	1	0.07%
0004680	casein kinase activity	1	0.07%
0016595	glutamate binding	1	0.07%
0004701	diacylglycerol-activated phospholipid-dependent protein kinase C activity	1	0.07%
0030911	TPR domain binding	1	0.07%
0045517	interleukin-20 receptor binding	1	0.07%
0048020	CCR chemokine receptor binding	1	0.07%
0048156	tau protein binding	1	0.07%
0004824	lysine-tRNA ligase activity	1	0.07%
0019981	interleukin-6 binding	1	0.07%
0051428	peptide hormone receptor binding	1	0.07%
0004014	adenosylmethionine decarboxylase activity	1	0.07%
0008539	proteasome inhibitor activity	1	0.07%
0019842	vitamin binding	1	0.07%
0019843	rRNA binding	1	0.07%
0004277	granzyme A activity	1	0.07%
0004145	diamine N-acetyltransferase activity	1	0.07%
0004830	tryptophan-tRNA ligase activity	1	0.07%
0004420	hydroxymethylglutaryl-CoA reductase (NADPH) activity	1	0.07%
0004276	furin activity	1	0.07%
0004682	protein kinase CK2 activity	1	0.07%
0004274	dipeptidyl-peptidase IV activity	1	0.07%
0016597	amino acid binding	1	0.07%
0030506	ankyrin binding	1	0.07%
0030228	lipoprotein receptor activity	1	0.07%
	unknown	112	7.73%

Supplementary Table 4A. HIV-1 Human Protein Interaction Database: Distribution of interactions based on cellular component Gene Ontology terms and individual HIV-1 proteins

HIV-1 Protein	Unknown	Other	Multiple	ER	Golgi apparatus	Nucleus	Mitochondrion	Proteasome	Cytoskeleton	Cytoplasm	Plasma membrane	Extracellular
Gag	8	2	12	0	1	3	4	0	4	5	12	4
Gag:MA	23	8	5	0	2	19	2	0	5	3	4	7
Gag:CA	5	6	0	1	0	4	1	0	0	1	13	2
Gag:NC	3	6	4	0	0	8	0	0	1	3	0	0
Gag:p6	8	3	0	0	0	2	0	0	0	1	0	0
Gag:p1	3	0	0	0	0	0	0	0	0	0	0	0
Pol	0	0	0	0	0	0	0	0	0	0	1	0
Pol:PR	7	8	10	0	0	8	3	0	35	4	4	5
Pol:RT	7	4	2	0	0	14	0	1	5	1	2	6
Pol:IN	3	0	11	0	0	31	2	28	0	5	0	0
Env	21	33	9	8	21	9	7	0	0	16	27	25
Env:gp120	79	59	37	16	5	61	4	0	15	37	120	99
Env:gp41	18	22	15	5	6	4	2	0	7	10	36	31
Tat	103	62	59	2	1	273	8	28	28	46	85	80
Rev	12	2	7	0	0	29	0	0	13	1	1	1
Nef	18	23	26	1	3	33	3	0	5	13	52	23
Vpu	3	3	2	1	0	3	1	0	0	3	6	0
Vpr	20	13	22	0	0	76	6	0	6	7	15	14
Vif	8	3	11	0	0	9	1	28	1	3	1	3

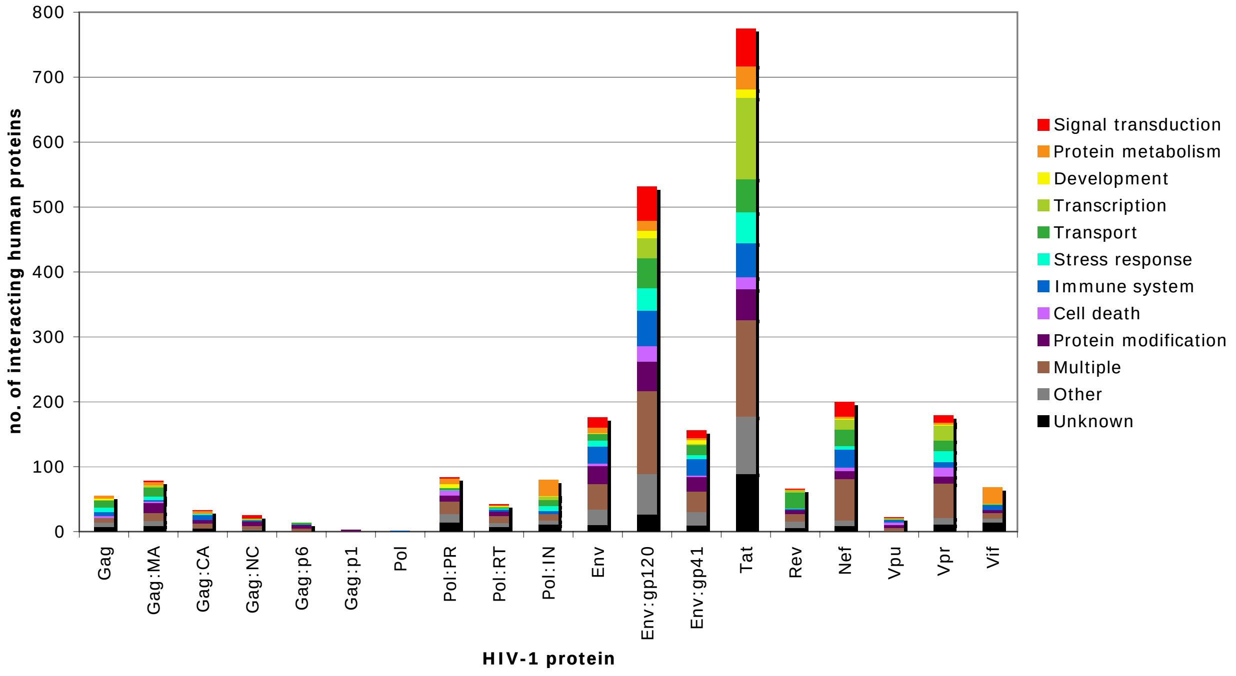
Supplementary Chart 1A. HIV-1 Human Protein Interaction Database: Distribution of interactions based on cellular component Gene Ontology terms and individual HIV-1 proteins



Supplementary Table 4B. HIV-1 Human Protein Interaction Database: Distribution of interactions based on biological process Gene Ontology terms and individual HIV-1 proteins

HIV-1 Protein	Unknown	Other	Multiple	Protein modification	Cell death	Immune system	Stress response	Transport	Transcription	Development	Protein metabolism	Signal transduction
Gag	7	7	7	0	3	6	7	11	1	2	4	0
Gag:MA	9	7	13	15	2	3	5	14	2	1	5	2
Gag:CA	5	0	7	6	0	8	1	0	1	0	4	1
Gag:NC	2	1	6	7	0	1	0	1	2	0	0	5
Gag:p6	0	0	5	5	0	1	0	3	0	0	0	0
Gag:p1	0	0	1	2	0	0	0	0	0	0	0	0
Pol	0	0	0	0	0	1	0	0	0	0	0	0
Pol:PR	14	13	19	10	7	0	1	3	0	6	9	2
Pol:RT	7	6	11	7	0	3	2	1	2	1	0	2
Pol:IN	11	6	10	0	0	5	7	10	5	1	25	0
Env	10	24	39	28	4	26	9	10	1	1	8	16
Env:gp120	26	63	127	46	24	54	35	46	31	11	16	53
Env:gp41	10	20	32	22	2	26	6	15	2	6	3	12
Tat	89	88	149	47	19	52	48	51	125	13	36	58
Rev	6	10	11	6	0	2	1	24	3	0	2	1
Nef	9	8	64	12	6	27	6	25	16	1	3	23
Vpu	0	1	5	4	4	4	0	1	1	0	1	1
Vpr	11	10	53	11	14	8	17	16	23	2	3	11
Vif	14	6	9	4	0	8	0	1	1	0	25	0

Supplementary Chart 1B. HIV-1 Human Protein Interaction Database: Distribution of interactions based on biological process Gene Ontology terms and individual HIV-1 proteins



Supplementary Table 4C. HIV-1 Human Protein Interaction Database: Distribution of interactions based on molecular function Gene Ontology terms and individual HIV-1 proteins

HIV-1 Protein	Unknown	Other	Multiple	Transporter	Structural molecule	Kinase	Receptor binding	Receptor	Transcription regulator	Transferase	Hydrolase	Nucleic acid binding	Metal ion binding
Gag	8	18	6	4	3	1	2	0	1	0	2	4	6
Gag:MA	7	14	6	12	6	11	9	1	1	2	2	3	4
Gag:CA	10	4	3	1	0	3	2	4	2	0	0	1	3
Gag:NC	3	8	3	1	2	0	0	0	3	0	3	1	1
Gag:p6	5	5	1	0	0	2	0	0	1	0	0	0	0
Gag:p1	3	0	0	0	0	0	0	0	0	0	0	0	0
Pol	0	1	0	0	0	0	0	0	0	0	0	0	0
Pol:PR	5	15	11	1	24	7	3	2	1	0	5	3	7
Pol:RT	1	0	11	1	6	8	7	0	3	0	1	4	0
Pol:IN	7	17	12	10	0	3	2	0	6	0	20	3	0
Env	22	13	34	4	5	18	14	6	3	27	16	0	14
Env:gp120	33	71	122	23	15	46	58	67	22	14	31	4	26
Env:gp41	27	16	31	7	11	3	16	8	3	5	14	0	15
Tat	74	104	148	14	38	44	48	37	111	7	52	56	42
Rev	4	6	11	6	14	8	0	1	4	1	1	9	1
Nef	11	30	27	12	7	19	24	21	21	1	13	1	13
Vpu	2	8	2	1	0	3	0	2	2	0	1	0	1
Vpr	10	32	30	9	8	16	13	10	20	2	12	7	10
Vif	7	14	12	1	2	3	4	0	3	1	19	1	1

Supplementary Chart 1C. HIV-1 Human Protein Interaction Database: Distribution of interactions based on molecular function Gene Ontology terms and individual HIV-1 proteins