

Virus	Tier	Clade	Plasma ID50 Titer in TZM.bl Cells (1/x)					gp120-FT	
			10/1/2008	10/12/2009	9/9/2010	1/10/2013	2/1/2013	2/1/2013	
6535.3	1B	B	3,514	2,028	2,178	1,713	NT	NT	
QH0692.42	2	B	530	422	545	335	549	<40	
SC422661.8	2	B	973	630	650	1,008	752	<40	
PVO.4	3	B	1,384	548	800	2,046	905	55	
TRO.11	2	B	1,820	1,074	820	1,174	794	52	
AC10.0.29	2	B	3,655	1,884	1,709	1,586	1,040	<40	
RHPA4259.7	2	B	1,988	1,543	3,259	2,089	1,863	<40	
THRO4156.18	2	B	1,149	721	438	506	361	51	
REJO4541.67	2	B	2,112	1,576	1,133	2,143	919	<40	
TRJO4551.58	3	B	269	479	395	728	293	66	
WITO4160.33	2	B	268	221	127	732	164	<40	
CAAN5342.A2	2	B	6,032	2,197	1,367	1,906	851	<40	
BaL.26	1B	B	NT	NT	NT	NT	1,968	<40	
Du156.12	2	C	NT	1,000	NT	1,343	NT	NT	
Du172.17	2	C	NT	97	NT	468	NT	NT	
Du422.1	2	C	NT	636	NT	581	NT	NT	
ZM53M.PB12	2	C	NT	3,183	NT	1,715	NT	NT	
ZM135M.PL10a	2	C	NT	221	NT	425	NT	NT	
ZM197M.PB7	1B	C	NT	455	NT	1,062	NT	NT	
ZM214M.PL15	2	C	NT	412	NT	338	NT	NT	
Q23.17	1B	A	NT	3,592	NT	2,895	NT	NT	
Q259.d2.17	2	A	NT	2,873	NT	1,528	NT	NT	
Q461.e2	2	A	NT	77	NT	184	NT	NT	
Q168.a2	2	A	NT	1,303	NT	942	NT	NT	
3415.v1.c1	2	A	NT	1,097	NT	1,318	NT	NT	
0439.v5.c1	2	A	NT	499	NT	588	NT	NT	
0260.v5.c1	2	A	NT	3,519	NT	1,957	NT	NT	
3365.v2.c20	2	A	NT	869	NT	1,425	NT	NT	
T257-31	3	CRF02_AG	NT	97	NT	316	NT	NT	
263-8	2	CRF02_AG	NT	493	NT	1,104	NT	NT	
211-9	2	CRF02_AG	NT	108	NT	780	NT	NT	
MuLV (Neg)	Neg control	Neg control	24	30	<20	186	80	<40	

Table S1. N60 plasma neutralization potency and breadth from 2008-2013, Related to Figure 1. Plasma from patient N60 was tested against a panel of multiclade HIV pseudoviruses, demonstrating potency and breadth for more than 4 years. In the last column gp120-FT (plasma that was passed over a BaL-gp120 column) was tested against a panel of HIV pseudoviruses for neutralization (in each case, the gp120-FT loses potency compared to the parent plasma, confirming that the fraction affinity purified against the gp120 monomer contains the bulk of neutralizing antibodies). Numerical values given as ID50, the Inhibitory Dose 50. NT= not tested. Green boxes represent neutralization twice over background (MuLV) value.

Monoclonal Antibody		GenBank number	Epitope	Heavy Chain	Light chain	CDRL3 length	SHM (Heavy/Light)	Frequency of CDR3 (per 1000)		
								Peripheral plasmablast	Bone marrow 138-	Bone marrow 138+
Lineage 1	N60P1.1	MG791872 MG819662	CD4bs	1-2	κ1-5	5	36%/26%	0	2.48	1.62
	N60P2.1	MG819649 MG819677	CD4bs	1-2	κ1-5	5	38%/29%	0	2.48	0
	N60P25.1	MG819648 MG819664	CD4bs	1-2	κ1-5	5	33%/26%	0	2.48	0
	N60P31.1	MG819647 MG819665	CD4bs	1-2	κ1-5	5	42%/35%	0	2.48	0
Lineage 2	N60P22	MG819659 MG819666	CD4bs	4-31	κ3-20	9	9%/11%	1.62	2.48	9.69
	N60P38	MG819653 MG819667	CD4bs	4-31	κ3-20	9	9%/11%	0	2.48	0
Lineage 3	N60P30	MG819660 MG819670	CD4i (Cluster A)	1-2	κ3-20	8	21%/12%	0	2.48	0
Lineage 4	N60P36	MG819651 MG819671	CoR-BS (Cluster C)	1-69	κ3-20	8	11%/9%	0	4.96	4.85
Lineage 5	N60P39	MG819654 MG819672	CoR-BS (Cluster C)	1-69	κ3-20	9	11%/9%	0	2.48	1.62
	N6039.1	MG819656 MG819673	CoR-BS (Cluster C)	1-69	κ3-20	9	11%/9%	0	2.48	1.62
	N60P47	MG819655 MG819674	CoR-BS (Cluster C)	1-69	κ3-20	9	16%/6%	0	2.48	0
	N60P48	MG819657 MG819675	CoR-BS (Cluster C)	1-69	κ3-20	9	15%/6%	0	4.96	6.46
Lineage 6	N60P51	MG819658 MG819676	CoR-BS (Cluster C)	1-69	κ3-20	10	20%/9%	0	12.4	3.38
Lineage 7	N60P35	MG819650 MG819668	V3	5-51	λ6-57	9	18%/14%	0	2.48	4.85
	N60P37	MG819652 MG819669	V3	5-51	λ6-57	9	17%/16%	0	2.48	6.46

Table S2. Characteristics of isolated N60 P series antibodies, Related to Figure 3. mAb = monoclonal antibody. SHM = somatic hypermutation given as a percent of germline V region for heavy chains, and VJ region for light chains. CD4bs = CD4-binding site antibody. CoR-BS= Co-Receptor binding site antibody. Cluster A= competes with A32. Cluster C= competes with 19e and/or

mAb		Epitope	SF162 LS	BaL .26	SS 1198.1	6535.3	QH0692 .42	SC4226 61.8	PVO.4	TRO .11	AC10 0.29	RHPA 4259.7	THRO 4156.18	REJO 4541.67	TRJO 4551.58	WITO 4160.33	CAAN 5342.A2
Lineage 1	N60P1.1	CD4bs	12.92	>50	0.61	3.84	15.48	0.75	0.46	6.32	>25	4.22	>25	1.58	7.195	>25	1.64
	N60P2.1	CD4bs	>50	>50	1.84	>25	3.00	12.69	1.68	19.60	>25	15.68	>25	>25	>25	>25	6.73
	N60P25.1	CD4bs	30.99	>50	0.25	15.73	32.94	2.06	6.45	23.53	>50	1.45	>50	2.45	>50	>50	2.50
	N60P31.1	CD4bs	>50	>50	>50	>50	>50	>50	>50	1.81	>50	>50	31.04	>50	>50	>50	>50
Lineage 2	N60P22	CD4bs	1.28	5.532	5.67	10.64	36.84	>50	>50	>50	>50	>50	36.50	>50	>50	>50	>50
	N60P38	CD4bs	5.77	>50	7.98	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
Lineage 3	N60P30	CD4i (Cluster A)	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
Lineage 4	N60P36	CoR-BS (Cluster C)	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
Lineage 5	N60P39	CoR-BS (Cluster C)	3.19	>50	4.61	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
	N6039.1	CoR-BS (Cluster C)	0.48	14.124	1.21	>50	45.23	>50	>50	>50	>50	>50	>50	>50	>50	>50	>50
	N60P47	CoR-BS (Cluster C)	0.68	20.084	1.91	>40	>40	>40	>40	>40	>40	>40	>40	>40	>40	>40	>40
	N60P48	CoR-BS (Cluster C)	0.40	12.729	0.91	>40	20.24	>40	>40	>40	>40	>40	>40	>40	>40	>40	>40
Lineage 6	N60P51	CoR-BS (Cluster C)	0.32	8.963	1.03	>25	>25	>25	>25	>25	>25	>25	>25	>25	>25	>25	>25
Lineage 7	N60P35	V3	0.02	4.68	1.11	>25	>25	>25	>25	>25	>25	3.733	>25	>25	>25	>25	>25
	N60P37	V3	0.03	4.076	.99	>25	>25	>25	>25	>25	>25	11.62	>25	>25	>25	>25	>25

Table S3. Neutralization screening of N60 P series antibodies, Related to Figure 3. HIV-1 neutralization was tested against a panel of Tier 1-3 pseudoviruses (see Methods). Results given as IC50 (inhibitory concentration 50) in ug/ml. Green boxes represents neutralization.

mAb	Genbank number	Epitope	pI	Heavy chain	Light chain	CDRL3 length	SHM (Heavy/Light)	Frequency of CDR3 (per 1000)		
								Peripheral plasmablast	Bone marrow 138-	Bone marrow 138+
N49P6	MG819637 MG819642	CD4bs	8.9	1-2	λ 2-11	5	42%/28%	0	0	0.49
N49P7	MG819638 MG819643	CD4bs	8.8	1-2	λ 2-11	5	38%/31%	0	0	0.49
N49P7.1	MG819639 MG819644	CD4bs	8.8	1-2	λ 2-11	5	38%/31%	0	0	0.49
N49P11	MG819640 MG819645	CD4bs	8.4	1-2	λ 2-11	5	35%/30%	3.18	0	0
N49P9	MG819641 MG819646	CD4bs	8.7	1-2	λ 2-23	5	38%/42%	3.18	0	0.49

Table S4. Properties of N49 P series mAbs, Related to Figure 4. mAb = monoclonal antibody. SHM = somatic hypermutation (given as a percent of germline V region for heavy chains, and VJ region for light chains). CD4bs = CD4-binding site antibody. pI=isoelectric point

	N49-P7 Fab-gp120 _{93TH057} core _e	N60-P23 Fab-gp120 _{93TH057} core _e
Data collection		
Wavelength, Å	0.979	0.979
Space group	P2 ₁ 2 ₁ 2 ₁	C2
Cell parameters		
a, b, c, Å	61.4, 63.9, 255.3	127.6, 68.6, 119.4
α, β, γ, °	90, 90, 90	90, 111.4, 90
Complexes/a.u.	1	1
Resolution, (Å)	50-2.69 (2.74-2.69)	50-2.38 (2.43-2.38)
# of reflections		
Total	73,281	139,212
Unique	23,639	38,617
R _{merge} ^b , %	13.1 (74.9)	16.0 (90.8)
R _{pim} ^c , %	7.7 (42.9)	9.7 (62.5)
CC _{1/2} ^d	0.99 (0.67)	0.99 (0.47)
Wilson B _{factor} (1/Å ²) ^e	53	30
I/σ	9.3 (1.1)	9.7 (1.2)
Completeness, %	80.6 (72.2)	100 (99.0)
Redundancy	3.1 (3.2)	3.6 (2.9)
Refinement Statistics		
Resolution, Å	50.0 - 2.7	50.0 - 2.4
R ^f , %	22.5	21.4
R _{free} ^g , %	28.5	25.8
# of atoms		
Protein	5,822	5,905
Water	27	222
Ligand/Ion	170	133
Overall B value (Å) ²		
Protein	50	44
Water	33	36
Ligand/Ion	64	59
Root mean square deviation		
Bond lengths, Å	0.014	0.009
Bond angles, °	1.2	1.4
Ramachandran ^h		
favored, %	89.0	93.5
allowed, %	9.7	5.8
outliers, %	1.3	0.7
PDB ID	6BCK	5WB9

Table S5. Data collection and refinement statistics, Related to Figure 6.

Values in parentheses are for highest-resolution shell

^bR_{merge} = $\sum |I - \langle I \rangle| / \sum I$, where I is the observed intensity and $\langle I \rangle$ is the average intensity obtained from multiple observations of symmetry-related reflections after rejections

^cR_{pim} = as defined in (Weiss, 2001)

^dCC_{1/2} = as defined by Karplus and Diederichs (Karplus and Diederichs, 2012)

^eWilson B_{factor} as calculated in (Popov and Bourenkov, 2003)

^fR = $\sum \|F_o| - |F_c\| / \sum |F_o|$, where F_o and F_c are the observed and calculated structure factors, respectively

^gR_{free} = as defined by Brünger (Brünger, 1997)

^hCalculated with MolProbity

		N49_P7 Fab- gp120 _{93TH057} core _e	N60_P23 Fab- gp120 _{93TH057} core _e	N6 Fab- gp120 _{93TH057} core _e (5te6)	VRCO1- gp120 _{93TH057} core _e (3ngb)
Buried Surface Area, Å²	gp120 total	981	939	1132	1143
	Outer domain (OD)	774	872	1000	1036
	Inner domain (ID)	207	67	132	107
	Ratio of OD/ID	3.74	13.01	7.58	9.68
	Loop D of OD	339	346	332	322
	CD4 binding loop of OD	186	202	206	188
	Loop V5 of OD	164	209	339	301
	Heavy chain total	821	726	928	897
	FWR	54	158	146	136
	CDR H1	4	20	38	3
	CDR H2	489	435	621	598
	CDR H3	274	113	123	160
	Light chain total	138	243	251	306
	FWR	0	0	36	124
	CDR L1	9	67	43	50
	CDR L2	0	0	0	0
	CDR L3	129	176	172	132
	Heavy and light chain total	959	969	1179	1203

Table S6. Details of the N49_P7-gp120_{93TH057} core_e, N60_P23-gp120_{93TH057} core_e, N6-gp120_{93TH057} core_e, and VRCO1-gp120_{93TH057} core_e interfaces, Related to Figure 6. Results as calculated by the EBI PISA server (http://www.ebi.ac.uk/msd-srv/prot_int/cgi-bin/piserver)