Supplementary Information

Does Antibody Stabilize the Ligand Binding in GP120 of HIV-1 Envelope Protein? Evidence from MD Simulation

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Figure S1. The root mean square deviations of protein backbone, in presence and absence of the inhibitor, NBD-557.

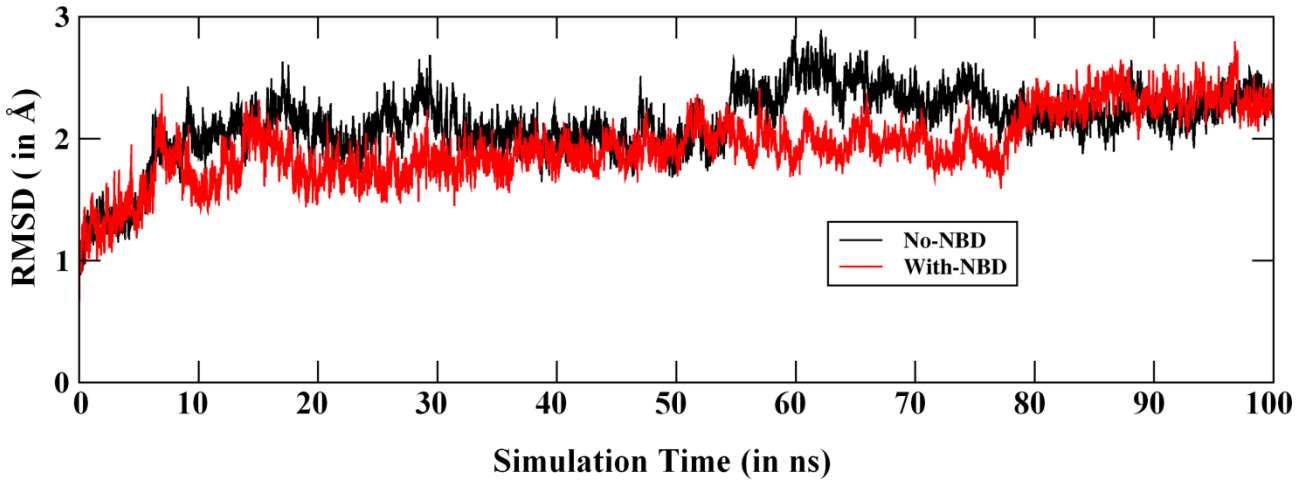

Figure S2. The distance between the Glu192 and Asn239 when there is no substrate. We note that H-bond interaction is very week when there is no substrate.

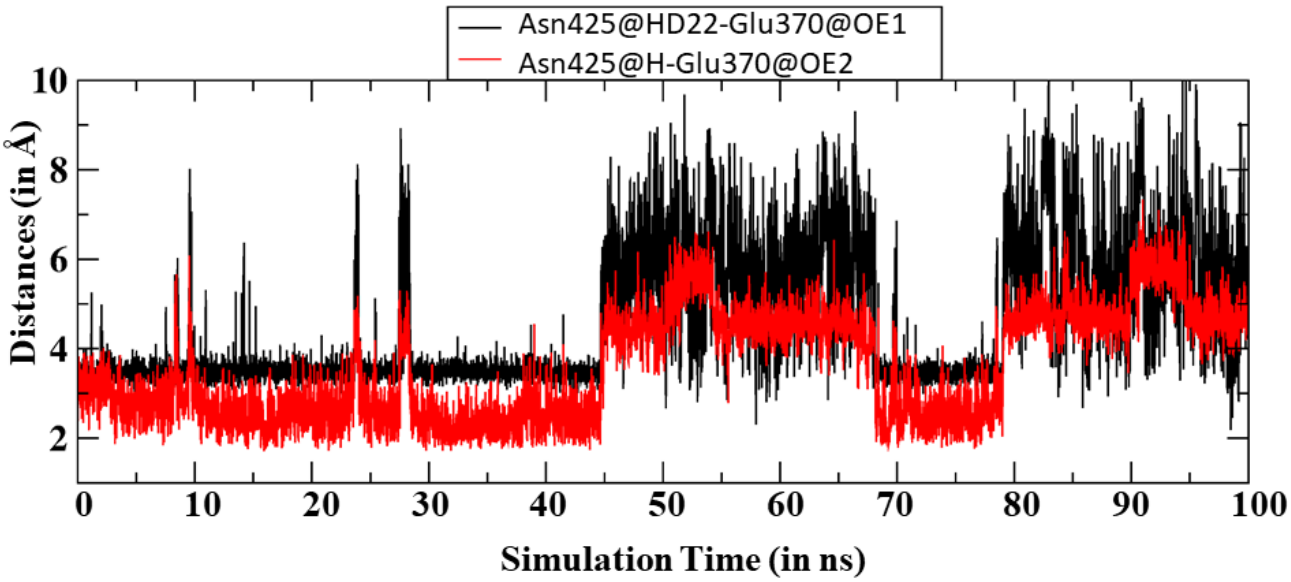

Table S1. The evolution of H-Bond for Glu370 and Asn425. H-bonds were calculated using VMD for most populated trajectory when NBD-557 binds gp120.

Found 2 hbonds.

donor	acceptor	occupancy
ASN425-Side	GLU370-Side	62.13%
ASN425-Main	GLU370-Side	3.56%

Figure S3. Hydrogen bond evolution with time for Glu370 and Asn425

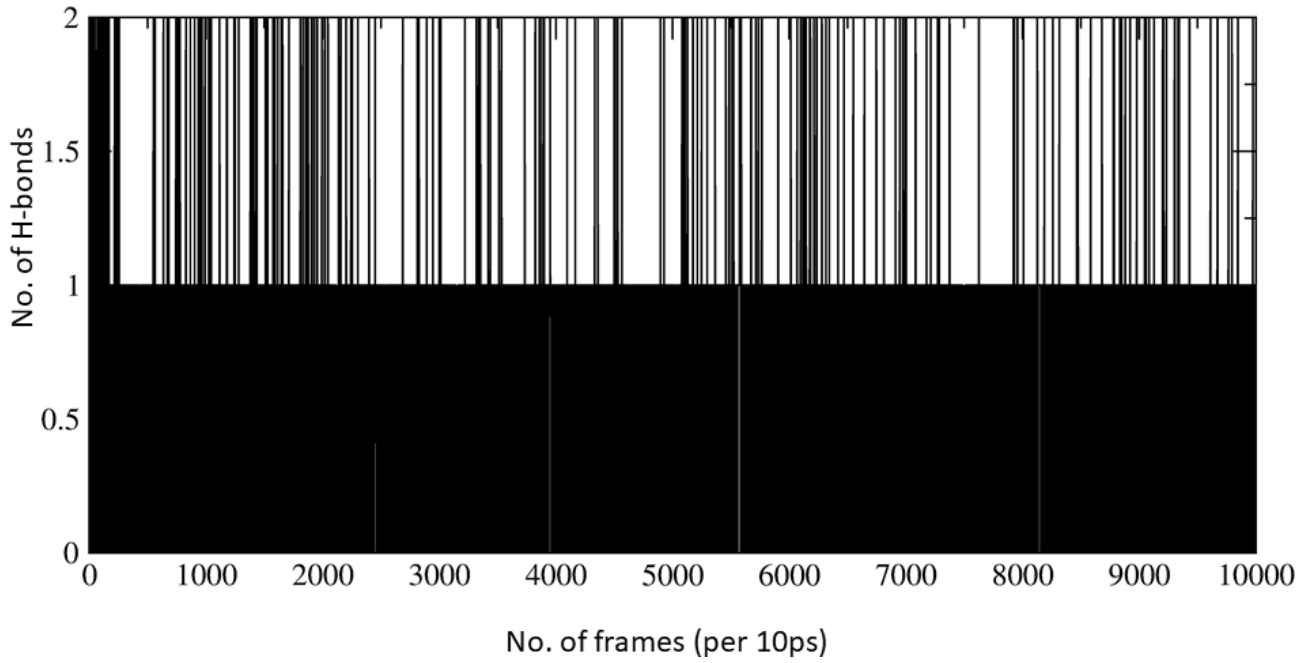

Table S2. The thermodynamic parameters for the N239G Mutant.

Energy Contribution	**Values (in kcal Mol)**	**Standard Error**
ΔE_{VDW}	-46.19	3.23
ΔE_{EEL}	-14.88	3.30
ΔE_{NPOLAR}	29.65	2.52
ΔE_{DISPER}	-5.28	0.32
ΔG_{gas}	-61.07	5.25
ΔG_{solv}	24.36	2.32
$\mathbf{\Delta H_{TOTAL}}$	**-36.71**	3.66

Figure S4. The residue mapping of simulated structures and crystal structure. The residues numbers in Table S3-S4 corresponds to simulated numbering.

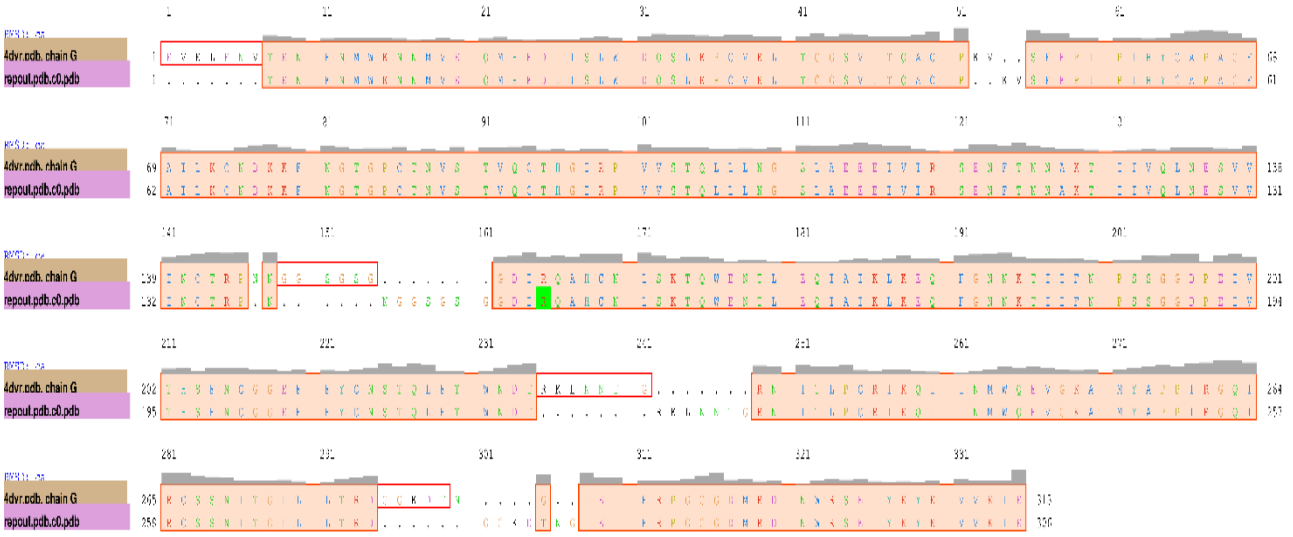

Figure S5. RMSD for entire 300 ns for gp120 with NBD-557 and with antibody.

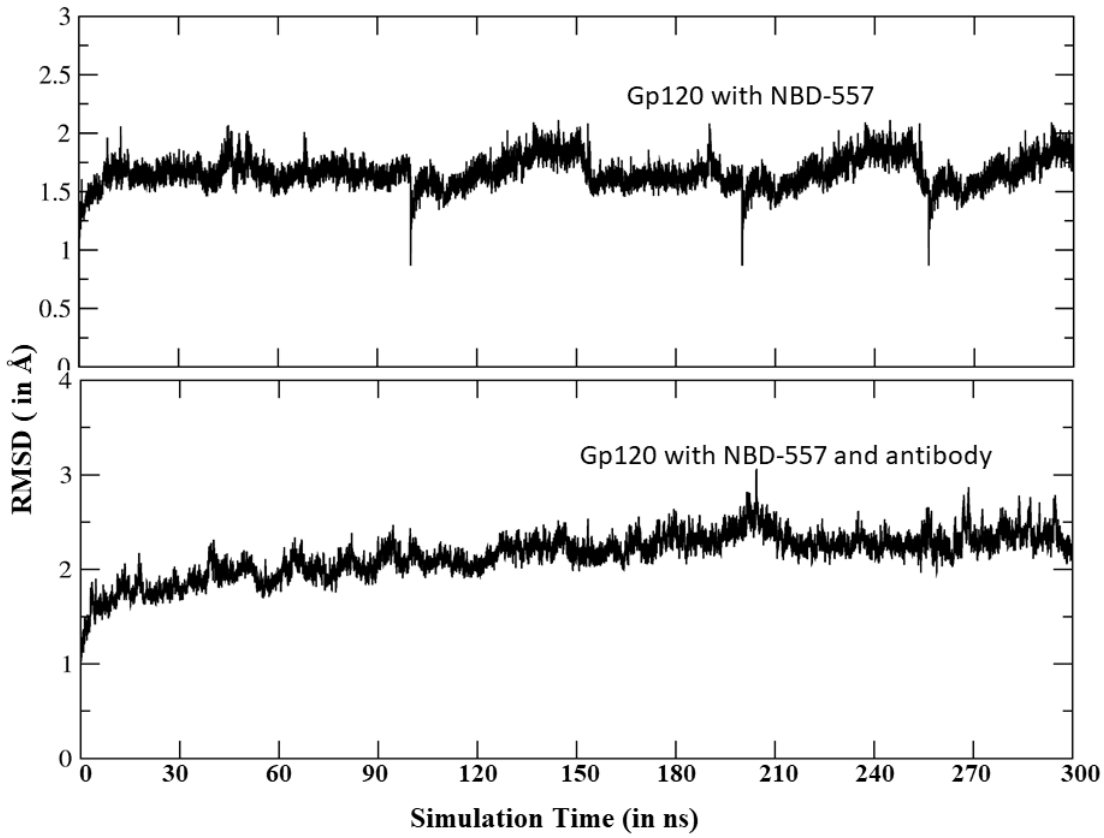

Table S3. Details of residuewise energy decompositions for interaction of NBD-557. All energy values are in kcal/mol. Data are shown as value ± standard error.

Total Energy Decomposition:

Resid 1	Resid 2	van der Waals	Electrostatic	Polar Solvation	Non-Polar Solv.	TOTAL
NBD 557	TRP 23	-0.800 ± 0.238	-0.130 ± 0.055	0.169 ± 0.054	-0.492 ± 0.140	-1.253 ± 0.382
NBD 557	VAL 93	-0.658 ± 0.199	0.198 ± 0.217	-0.318 ± 0.103	-0.291 ± 0.092	-1.069 ± 0.268
NBD 557	SER 94	-0.565 ± 0.136	-0.360 ± 0.100	0.134 ± 0.063	-0.207 ± 0.063	-0.998 ± 0.240
NBD 557	THR 95	-1.146 ± 0.240	-0.164 ± 0.188	0.249 ± 0.145	-0.817 ± 0.145	-1.879 ± 0.379
NBD 557	ASP 190	-0.636 ± 0.173	-0.501 ± 0.328	0.242 ± 0.292	-0.499 ± 0.152	-1.394 ± 0.357
NBD 557	PRO 191	-0.139 ± 0.021	0.150 ± 0.039	-0.115 ± 0.049	-0.000 ± 0.001	-0.105 ± 0.034
NBD 557	GLU 192	-2.357 ± 0.322	-1.218 ± 0.550	0.432 ± 0.484	-1.472 ± 0.160	-4.614 ± 0.610
NBD 557	ILE 193	-1.195 ± 0.254	0.073 ± 0.062	-0.054 ± 0.048	-1.127 ± 0.199	-2.303 ± 0.398
NBD 557	HID 196	-0.072 ± 0.013	-0.235 ± 0.055	0.138 ± 0.051	0.000 ± 0.000	-0.168 ± 0.034
NBD 557	SER 197	-0.937 ± 0.209	0.054 ± 0.216	-0.157 ± 0.145	-0.426 ± 0.087	-1.465 ± 0.338
NBD 557	PHE 198	-0.518 ± 0.131	-0.229 ± 0.102	0.099 ± 0.040	-0.123 ± 0.039	-0.771 ± 0.189
NBD 557	PHE 204	-0.752 ± 0.228	-0.283 ± 0.079	0.286 ± 0.043	-0.480 ± 0.076	-1.229 ± 0.257
NBD 557	TYR 206	-0.587 ± 0.142	-0.242 ± 0.200	0.036 ± 0.162	-0.335 ± 0.081	-1.128 ± 0.245
NBD 557	ILE 238	-0.781 ± 0.153	0.360 ± 0.103	-0.036 ± 0.049	-0.507 ± 0.108	-0.964 ± 0.202
NBD 557	ASN 239	-2.232 ± 0.399	-2.285 ± 0.723	0.397 ± 0.177	-1.568 ± 0.148	-5.688 ± 0.805
NBD 557	MET 240	-0.920 ± 0.197	0.711 ± 0.489	-0.476 ± 0.202	-0.416 ± 0.110	-1.102 ± 0.498
NBD 557	TRP 241	-2.046 ± 0.383	0.008 ± 0.218	0.117 ± 0.098	-1.259 ± 0.232	-3.181 ± 0.514
NBD 557	GLY 286	-0.416 ± 0.334	0.073 ± 0.298	0.022 ± 0.132	-0.274 ± 0.285	-0.596 ± 0.611
NBD 557	GLY 287	-0.941 ± 0.282	-0.235 ± 0.282	0.123 ± 0.175	-0.910 ± 0.241	-1.963 ± 0.515
NBD 557	MET 289	-0.779 ± 0.197	-0.012 ± 0.215	-0.060 ± 0.116	-0.584 ± 0.111	-1.434 ± 0.248

Table S4. Details of residuewise energy decompositions for interaction of antibody and gp120. All energy values are in kcal/mol. Data are shown as value ± standard error.

Total Energy Decomposition:

Resid 1	Resid 2	van der Waals	Electrostatic	Polar Solvation	Non-Polar Solv.	TOTAL
ASP 310	GLN 150	-0.208 ± 0.194	-2.305 ± 2.614	2.115 ± 2.231	-0.182 ± 0.227	-0.579 ± 0.919
TYR 312	ARG 149	-1.448 ± 0.332	-1.108 ± 0.808	-0.166 ± 0.578	-1.207 ± 0.254	-3.928 ± 0.832
TYR 312	LYS 235	-0.222 ± 0.068	1.205 ± 0.484	-1.765 ± 0.404	-0.127 ± 0.048	-0.909 ± 0.282
TYR 312	GLN 236	-1.012 ± 0.244	0.150 ± 0.485	-0.446 ± 0.316	-0.751 ± 0.144	-2.059 ± 0.450
LEU 329	ILE 237	-0.284 ± 0.104	-0.033 ± 0.013	0.066 ± 0.016	-0.352 ± 0.098	-0.604 ± 0.164
ASP 331	ARG 233	1.160 ± 0.969	-51.864 ± 2.007	32.894 ± 1.245	-0.536 ± 0.035	-18.346 ± 1.813
ASP 331	LYS 235	-0.204 ± 0.050	-29.633 ± 1.672	27.487 ± 1.239	-0.087 ± 0.033	-2.437 ± 0.651
GLU 333	ARG 233	-0.984 ± 0.314	-22.713 ± 2.701	23.804 ± 2.301	-1.013 ± 0.135	-0.905 ± 0.811
ASP 334	PRO 191	-0.731 ± 0.194	-2.548 ± 0.427	2.206 ± 0.355	-0.605 ± 0.134	-1.679 ± 0.374
ASP 334	ARG 233	-0.011 ± 0.621	-36.558 ± 2.139	29.505 ± 0.810	-0.553 ± 0.062	-7.616 ± 1.396
ASP 334	LYS 235	0.256 ± 0.708	-43.911 ± 2.874	34.074 ± 1.058	-0.571 ± 0.068	-10.152 ± 1.845
ASP 336	ARG 233	-0.087 ± 0.018	-22.654 ± 0.875	21.651 ± 0.640	-0.019 ± 0.011	-1.109 ± 0.337
ASP 336	LYS 235	0.507 ± 0.620	-47.018 ± 1.939	35.887 ± 0.752	-0.376 ± 0.037	-11.001 ± 1.200
ASP 336	ILE 237	-1.215 ± 0.244	2.300 ± 0.830	-2.176 ± 0.582	-0.937 ± 0.143	-2.028 ± 0.423
ASP 336	LYS 246	-0.050 ± 0.631	-42.962 ± 3.866	36.184 ± 1.825	-0.690 ± 0.136	-7.517 ± 2.089
MET 338	VAL 31	-0.531 ± 0.203	-0.033 ± 0.143	0.042 ± 0.110	-0.538 ± 0.175	-1.060 ± 0.359
MET 338	MET 248	-0.797 ± 0.256	-0.192 ± 0.220	0.065 ± 0.093	-0.732 ± 0.191	-1.656 ± 0.441

Table S5. Clustering of gp120 with NBD without antibody

#Cluster	Frames	Frac	AvgDist	Stdev	Centroid	AvgCDist
0	10565	0.218	1.636	0.208	3429	2.281
1	5912	0.127	1.591	0.202	6565	2.560
2	4520	0.121	1.688	0.237	1663	2.357
3	3824	0.115	1.591	0.215	6002	2.515
4	2729	0.102	1.599	0.198	2063	2.378
5	566	0.079	1.516	0.219	1146	2.349
6	532	0.074	1.559	0.199	261	2.618
7	502	0.070	1.572	0.215	5254	2.301
8	479	0.053	1.524	0.204	4824	2.257
9	295	0.041	1.520	0.246	684	2.419

Table S6. Clustering of gp120 with NBD in N239G mutant.

#Cluster	Frames	Frac	AvgDist	Stdev	Centroid	AvgCDist
0	10803	0.180	1.578	0.164	3230	2.037
1	5569	0.157	1.528	0.174	7695	2.173
2	4512	0.151	1.551	0.177	6321	2.142
3	3368	0.137	1.533	0.172	9362	2.120
4	3040	0.104	1.497	0.151	5347	2.089
5	2731	0.073	1.535	0.189	2134	2.050
6	1692	0.069	1.600	0.210	780	2.225
7	511	0.051	1.511	0.194	1689	2.107
8	454	0.045	1.531	0.199	328	2.429
9	120	0.032	1.519	0.195	1365	2.158

Table S7. Clustering of gp120 with NBD in presence of antibody.

#Cluster	Frames	Frac	AvgDist	Stdev	Centroid	AvgCDist
0	10934	0.493	2.508	0.523	4357	10.009
1	5370	0.137	2.621	0.632	7213	5.879
2	4963	0.096	2.731	0.843	5298	7.652
3	3900	0.090	2.597	0.689	9238	5.369
4	2473	0.047	2.130	0.518	8553	6.321
5	1367	0.037	2.230	0.642	9822	6.619
6	310	0.031	2.300	0.668	9471	6.176
7	306	0.031	1.918	0.408	6263	5.332
8	283	0.028	1.909	0.478	6013	5.813
9	94	0.009	1.677	0.416	6830	6.540