SUPPLEMENTARY MATERIAL

Structural Analysis of Glycosylated Intact HIV-1 gp120-b12 Antibody Complex using Hydroxyl Radical Protein Footprinting

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Table S1

Glycosylation Site Identified	% Occupancy
88	100 %
135	76%
138	36%
141	25%
156	38%
160	100%
187	100%
188	41%
234	42%
241	56%
262	56%
276	85%
295	70%
301	62%
332	74%
339	69%
356	100%
362	81%
386	79%
392	79%
397	79%
406	79%
448	78%
463	100%

Figure S1

Alignments of gp120 sequences with available crystal structures to JRFL used by Modeller to generate a homology model

```
>P1;9B4C
structureX:9B4C:84:G :127:G ::::
------------------------------------------VVLENVTEHFNMWKNDMVEQMQEDIISLWDQSLKPCVK
LTPLCV--------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
------------------------------------------------------*
>P1;2B4C
structureX:2B4C:195:G :492:G ::::
--------------------------------------------------------------------------------
-------------------------------------------------------------------------------S
CDTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKTFNGKGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSD
NFTNNAKTIIVQLKESVEINCTRPNQNTRKSIHIGPGRAFYTTGEIIGDIRQAHCNISRAKWNDTLKQIVIKLREQFENK
TIV-FNHSSGGDPEIVMHSFNCGGEFFYCNSAQLFNSTWNNNTEGSNNTEGNTITLPCRIKQIINMWQEVGKAMYAPPIR
GQIRCSSNITGLLLTRDGGINENGTEIFRPGGGDMRDNWRSELYKYKVVKIE--*
>P1;4NCO
structureX:4NCO:44:A :493:A ::::
--VWKDAETTLFCASDAKAYETEKHNVWATHACVPTDPNPQEIHLENVTEEFNMWKNNMVEQMHTDIISLWDQSLKPCVK
LTPLCVTLQC-----TNVTNNITDDM-RGELKNCSFNMTTELRDKKQKVYSLFYR--------------------YRLIN
CNTSAITQACPKVSFEPIPIHYCAPAGFAILKCKDKKFNGTGPCPSVSTVQCTHGIKPVVSTQLLLNGSLAEEEVMIRSE
NITNNAKNILVQFNTPVQINCTRPNNNTRKSIRIGPGQAFYATGDIIGDIRQAHCNVSKATWNETLGKVVKQLRKHFGNN
TIIRFANSSGGDLEVTTHSFNCGGEFFYCNTSGLFNSTWISNT-----SVNDSITLPCRIKQIINMWQRIGQAMYAPPIQ
GVIRCVSNITGLILTRDGGSTNSTTETFRPGGGDMRDNWRSELYKYKVVKIEP-*
>P1;4R4H
structureX:4R4H:47:A :83:A ::::
-----EATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQE--------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
------------------------------------------------------*
>P1;3JWD
structureX:3JWD:42:A :83:A ::::
VPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQE--------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
------------------------------------------------------*
>P1;4TVP
structureX:4TVP:126:G :132:G ::::
--------------------------------------------------------------------------------
----CVTLQCT---------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
------------------------------------------------------*
>P1;4TVP
structureX:4TVP:150:G :194:G ::::
--------------------------------------------------------------------------------
-------------------------M-RGELKNCSFNMTTELRDKKQKVYSLFYRLDVVQIN---------SNKEYRLI-
---------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
------------------------------------------------------*
>P1;4HPO
structureX:4HPO:167:P :181:P ::::
--------------------------------------------------------------------------------
-------------------------------------------DKKQKVHALFYKLDI----------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
--------------------------------------------------------------------------------
------------------------------------------------------*
```

```
>P1;JRFL
sequence:JRFL:::::::0.00:0.00
VPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEVVLENVTEHFNMWKNNMVEQMQEDIISLWDQSLKPCVK
LTPLCVTLNCKDVNATNTTNDSEGTMERGEIKNCSFNITTSIRDEVQKEYALFYKLDVVPI--------DNNNTSYRLIS
CDTSVITQACPKISFEPIPIHYCAPAGFAILKCNDKTFNGKGPCKNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSD
NFTNNAKTIIVQLKESVEINCTRPNNNTRKSIHIGPGRAFYTTGEIIGDIRQAHCNISRAKWNDTLKQIVIKLREQFENK
TIV-FNHSSGGDPEIVMHSFNCGGEFFYCNSTQLFNSTWNNNTEGSNNTEGNTITLPCRIKQIINMWQEVGKAMYAPPIR
GQIRCSSNITGLLLTRDGGINENGTEIFRPGGGDMRDNWRSELYKYKVVKIEPL*
```