Table 1. Oligonucleotides for site-directed mutagenesis

Primer name	Sequence (5′ to 3′)	Description
C298A-F	CAG CTA AAT GAA TCT GTA GTA ATT AAC GCT ACA AGA CCC AAC AAC AAT ACA AG	For mutating cysteine 298 to alanine; deletes 1 *VspI* site
C298A-R	CTT GTA TTG TTG TTG GGT CTT GTA GCG TTA ATT ACT ACA GAT TCA TTT AGC TG	
C332A-F	TAG GAG ATA TCA GAC AAG CAC ATG CTA ACA TTA GTA GAG CAA AAT GGA ATA AC	For mutating cysteine 331 to alanine; creates 1 new *EcoRV* site
C332A-R	GTT ATT CCA TTT TGC TCT ACT AAT GTT AGC ATG TGC TTG TCT GAT ATC TCC TA	
C378A-F	CCA GAA ATT GTA ATG CAC AGT TTT AAT GCT GGA GGG GAA TTC TTC TAC TGT A	For mutating cysteine 378 to alanine; creates 1 new *EcoRI* site
C378A-R	TAC AGT AGA AGA ATT CCC CTC CAG CAT TAA AAC TGT GCA TTA CAA TTT CTG G	
C441A-F	CCC ATC ACA GGA CAA ATT AGA GCT TCA TCA AAC ATT ACA GGG CTG	For mutating cysteine 441 to alanine; deletes 1 *SspI* site
C441A-R	CAG CCC TGT AAT GTT TGA TGA AGC TCT AAT TTG TCC TGT GAT GGG	
C385A-F	TGT GGA GGG GAA TTC TTC TAC GCT AAT ACA GCA CAA CTG TTT AAT AG	For mutating cysteine 385 to alanine; creates 1 new *EcoRI* site
C385A-R	CTA TTA AAC AGT TGT GCT GTA TTA GCG TAG AAG AAT TCC CCT CCA CA	
C414A-F	GGA AAT GAC ATA ATC ACA CTC CAA GCC AGA ATA AAA	For mutating cysteine 414 to alanine ; creates 1 new

Primer name	Sequence (5′ to 3′)	Description
	CAA ATT ATT ATT ATG TGG C	*VspI* site
C414A-R	GCC ACA TAT TAA TAA TTT GTT TTA TTC TGG CTT GGA GTG TGA TTA TGT CAT TTC C	

Table 2. Peptide sequences corresponding to gp120s from SHIV 89.6p and HIV 89.6

Peptide	89.6p	89.6
1	TEKLWVTVYYGVPVWREATT	KEKTWVTIYYGVPVWREATT
2	GVPVWREATTTLFCASDAKA	GVPVWREATTTLFCASDAKA
3	TLFCASDAKAYDTEVHNVWA	TLFCASDAKAYDTEVHNVWA
4	YDTEVHNVWATHACVPTDPN	YDTEVHNVWATHACVPTDPN
5	THACVPTDPNPQEVVLGNVT	THACVPTDPNPQEVVLGNVTE
6	PQEVVLGNVTENFNMWKNNM	PQEVVLGNVTENFNMWKNNM
7	ENFNMWKNNMVDQMHEDIIS	ENFNMWKNNMVDQMHEDIIS
8	VDQMHEDIISLWDESLKPCV	VDQMHEDIISLWDESLKPCV
9	LWDESLKPCVKLTPLCVTLN	LWDESLKPCVKLTPLCVTLN
10	KLTPLCVTLNCTNLNITKNT	KLTPLCVTLNCTNLNITKNT
11	CTNLNITKNTTNLTSSSWGM	CTNLNITKNTTNPTSSSWGM
12	TNLTSSSWGMMEEGEIKNCS	TNPTSSSWGMMEKGEIKNCS
13	MEEGEIKNCSFYITTSIRNK	MEKGEIKNCSFYITTSIRNK
14	FYITTSIRNKVKKEYALFNR	FYITTSIRNKVKKEYALFNR
15	VKKEYALFNRLDVVPVKNTS	VKKEYALFNRLDVVPIENTN
16	LDVVPVKNTSNTKYRLISCN	LDVVPIENTNNTKYRLISCN
17	NTKYRLISCNTSVITQACPK	NTKYRLISCNTSVITQACPK
18	TSVITQACPKVSFQPIPIHY	TSVITQACPKVSFQPIPIHY
19	VSFQPIPIHYCVPAGFAILK	VSFQPIPIHYCVPAGFAMLK
20	CVPAGFAILKCNNKTFNGSG	CVPAGFAMLKCNNKTFNGSG
21	CNNKTFNGSGPCTNVSTVQC	CNNKTFNGSGPCTNVSTVQ
22	PCTNVSTVQCTHGIRPVVST	PCTNVSTVQCTHGIRPVVST
23	THGIRPVVSTQLLLNGSLAE	THGIRPVVSTQLLLNGSLAE
24	QLLLNGSLAEEDIVIRSEDF	QLLLNGSLAEEDIVIRSENF
25	EDIVIRSEDFTDNVKTIIVQ	EDIVIRSENFTDNAKTIIVQ
26	TDNVKTIIVQLNESVVINCT	TDNAKTIIVQLNESVVINCT
27	LNESVVINCTRPNNNTRERL	LNESVVINCTRPNNNTRRRL
28	RPNNNTRERLSIGPGRAFYA	RPNNNTRRRLSIGPGRAFYA
29	SIGPGRAFYARRNIIGDIRQ	SIGPGRAFYARRNIIGDIRQ
30	RRNIIGDIRQAHCNISRAKW	RRNIIGDIRQAHCNISRAKW
31	AHCNISRAKWNNTLQQIVIK	AHCNISRAKWNNTLQQIVIK
32	NNTLQQIVIKLREKFRNKTI	NNTLQQIVIKLREKFRNKTI
33	LREKFRNKTIAFNQSSGGDP	LREKFRNKTIAFNQSSGGD
34	AFNQSSGGDPEIVMHSFNCG	AFNQSSGGDPEIVMHSFNCG
35	EIVMHSFNCGGEFFYCNTAQ	EIVMHSFNCGGEFFYCNTAQ
36	GEFFYCNTAQLFNSTWNVAG	GEFFYCNTAQLFNSTWNVTG
37	LFNSTWNVAGGTNGTEGNDI	LFNSTWNVTGGTNGTEGNDI
38	GTNGTEGNDIITLQCRIKQI	GTNGTEGNDIITLQCRIKQI
39	ITLQCRIKQIINMWQKVGKA	ITLQCRIKQIINMWQKVGKA
40	INMWQKVGKAMYAPPITGQI	INMWQKVGKAMYAPPITGQI
41	MYAPPITGQIRCSSNITGLL	MYAPPITGQIRCSSNITGLL
42	RCSSNITGLLLTRDGGNSTE	RCSSNITGLLLTRDGGNSTE
43	LTRDGGNSTETETEIFRPGG	LTRDGGNSTETETEIFRPGG
44	TETEIFRPGGGDMRDNWRSE	TETEIFRPGGGDMRDNWRSE
45	GDMRDNWRSELYKYKVVRIE	GDMRDNWRSELYKYKVVRIE
46	LYKYKVVRIEPIGVAPTRAK	
47	PIGVAPTRAKRRTVQREKRA	